

Figure S4. Alignment of placental mammal AKB sequences. The alignment of the placental mammal AKB sequences used for the dN/dS analyses.

MATLAB multiple sequence alignment

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lcl|NM_004217.3 MAQKENSYPWPYGRQTAPSGSLTLPQVRLRKEPVTSPALVLMRSRNVQPTAAPGQKVM-E 59
lcl|XM_01511855 MAQKENAYPWPYGRQTAPSGSLTLPQVRLRKEPVTSPALVLMRSRNVQPTAAPGQKVV-E 59
lcl|NM_183084.2 MAQKENAYPWPYGRQTAQPGNLTLQVRLRKEPVTSPALVLMRSRNVQPTAAPGQKVV-E 59
lcl|XM_00401268 MAQKENAYPWPYGRQTAQPGNLTLQVRLRKEAVTPSALVLMRSRNVQPTAAPGQKVV-E 59
lcl|XM_844813.4 MTQKENAYPWPYGRQTTQPGNLTLQVRLRKEPATPSALVLMRSRNVQPTAAPGQKVV-E 59
lcl|XM_00399619 MAQKENAYPWPYGRQTTQPGNLTLQVRLRKEPATPSALVLMRSRNVQPTAAPGQKVV-E 59
lcl|NM_213919.2 MAQKENTYPWPYGRQTAQSGNLTLQVRLRKEAVTPSALVLMRSRNVQPTAAPGQKVV-E 59
lcl|XM_00150481 MTQKENAYPWPYGRQTAQSGNLTLQVRLRKEPATPSALVLMRSRNVQPTAAPGQKVV-E 59
lcl|XM_00443309 MAQKENAYPWPYGRQTAQSGNLTLQVRLRKEPVTSPALVLMRSRNVQPTAAPGQKVV-E 59
lcl|XM_00827074 MAQKENAYPWPYSRPTQSGNLTLQVRLRKEAATPSALVLMRSRNVQPTAAPGQKGM-E 59
lcl|XM_00587878 MTQKENAYPWPYGRQTAQCGNLTLQVRLRKEPATPSALVLMRSRNVQPTAAPGQKVV-E 55
lcl|XM_00468461 MAQKENAYPWPYGRQTAQSGNLTLQVRLRKEPATPSALVLMRSRNVQPTAAPGQKVV-E 59
lcl|XM_00341691 MAQKENAYPWPYGRQTAQSGNLTLQVRLRKEPATPSALVLMRSRNVQPTAAPGQKVV-E 60
lcl|XM_01994424 MAQKENAYPWPYGRQTAQSGNLTLQVRLRKEPVTSPALVLMRSRNVQPTAAPGQKVV-E 59
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lcl|NM_004217.3 NSSGTPDILTRHFTIDDFEIGRPLGKGKFGNVYLAREKKSCHFIVALKVLFKSQIEKEGVE 119
lcl|XM_01511855 NSSGTPNIMLRHFTIDDFEIGRPLGKGKFGNVYLAREKKSCHFIVALKVLFKSQIEKEGVE 119
lcl|NM_183084.2 NSSGTPNIPKRSFTIDDFEIGRPLGKGKFGNVYLAREKKSCHFIVALKVLFKSQIEKEGVE 119
lcl|XM_00401268 NSSGTLNIPKRSFTIDDFEIGRPLGKGKFGNVYLAREKKSCHFIVALKVLFKSQIEKEGVE 119
lcl|XM_844813.4 NSSGTPNFSMRSFTIDDFEIGRPLGKGKFGNVYLAREKKSCHFIVALKVLFKSQIEKEGVE 119
lcl|XM_00399619 NSSGTPNFSMRSFTIDDFEIGRPLGKGKFGNVYLAREKKSCHFIVALKVLFKSQIEKEGVE 119
lcl|NM_213919.2 NSSGTPNFSTRSFTIDDFEIGRPLGKGKFGNVYLAREKKSCHFIVALKVLFKSQIEKEGVE 119
lcl|XM_00150481 NSSGTPNLLMRSFTIDDFEIGRPLGKGKFGNVYLAREKKSCHFIVALKVLFKSQIEKEGVE 119
lcl|XM_00443309 NSSGTPNLLMRSFTIDDFEIGRPLGKGKFGNVYLAREKKSCHFIVALKVLFKSQIEKEGVE 119
lcl|XM_00827074 NSSGAPNF-TRPFTIDDFEIGRPLGKGKFGNVYLAREKKSCHFIVALKVLFKSQIEKEGVE 118
lcl|XM_00587878 NSMGTPN-LMRSFTIDDFEIGRPLGKGKFGNVYLAREKKSCHFIVALKVLFKSQIEKEGVE 114
lcl|XM_00468461 NSSGTPNLMRSFTIDDFEIGRPLGKGKFGNVYLAREKKSCHFIVALKVLFKSQIEKEGVE 119
lcl|XM_00341691 NSSGTPSLMRPFTIDDFEIGRPLGKGKFGNVYLAREKKSCHFIVALKVLFKSQIEKEGVE 120
lcl|XM_01994424 NNSRTPNFSMRSFTIDDFEIGRPLGKGKFGNVYLAREKKSCHFIVALKVLFKSQIEKEGVE 119
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lcl|NM_004217.3 HQLRREIEIQAHLLHPNILLRNYFYDRRRRIYILEYAPRGELYKELQKSCFTFDEQRTAT 179
lcl|XM_01511855 HQLRREIEIQAHLLHPNILLRNYFYDRRRRIYILEYAPRGELYKELQKSCFTFDEQRTAT 179
lcl|NM_183084.2 HQLRREIEIQAHLLHPNILLRNYFYDRRRRIYILEYAPRGELYKELQKSCFTFDEQRTAT 179
lcl|XM_00401268 HQLRREIEIQAHLLHPNILLRNYFYDRRRRIYILEYAPRGELYKELQKSCFTFDEQRTAT 179
lcl|XM_844813.4 HQLRREIEIQAHLLHPNILLRNYFYDRRRRIYILEYAPRGELYKELQKSCFTFDEQRTAT 179
lcl|XM_00399619 HQLRREIEIQAHLLHPNILLRNYFYDRRRRIYILEYAPRGELYKELQKSCFTFDEQRTAT 179
lcl|NM_213919.2 HQLRREIEIQAHLLHPNILLRNYFYDRRRRIYILEYAPRGELYKELQKSCFTFDEQRTAT 179
lcl|XM_00150481 HQLRREIEIQAHLLHPNILLRNYFYDRRRRIYILEYAPRGELYKELQKSCFTFDEQRTAT 179
lcl|XM_00443309 HQLRREIEIQAHLLHPNILLRNYFYDRRRRIYILEYAPRGELYKELQKSCFTFDEQRTAT 179
lcl|XM_00827074 HQLRREIEIQAHLLHPNILLRNYFYDRRRRIYILEYAPRGELYKELQKSCFTFDEQRTAT 178
lcl|XM_00587878 HQLRREIEIQAHLLHPNILLRNYFYDRRRRIYILEYAPRGELYKELQKSCFTFDEQRTAT 174
lcl|XM_00468461 HQLRREIEIQAHLLHPNILLRNYFYDRRRRIYILEYAPRGELYKELQKSCFTFDEQRTAT 179
lcl|XM_00341691 HQLRREIEIQAHLLHPNILLRNYFYDRRRRIYILEYAPRGELYKELQKSCFTFDEQRTAT 180
lcl|XM_01994424 HQLRREIEIQAHLLHPNILLRNYFYDRRRRIYILEYAPRGELYKELQKSCFTFDEQRTAT 179
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lcl|NM_004217.3 IMEELADALMYCHGKKVIHRDIKPENLLGLGKELIADFQWGSVHAPSLRRKTMCGTLDY 239
lcl|XM_01511855 IMEELADALMYCHGKKVIHRDIKPENLLGLGKELIADFQWGSVHAPSLRRKTMCGTLDY 239
lcl|NM_183084.2 IMEELADALTYCHAKKVIHRDIKPENLLGLRGELIADFQWGSVHAPSLRRKTMCGTLDY 239
lcl|XM_00401268 IMEELADALTYCHAKKVIHRDIKPENLLGLRGELIADFQWGSVHAPSLRRKTMCGTLDY 239
lcl|XM_844813.4 IMEELADALMYCHGKKVIHRDIKPENLLGLGKELIADFQWGSVHAPSLRRKTMCGTLDY 239
lcl|XM_00399619 IMEELADALTYCHGKKVIHRDIKPENLLGLGKELIADFQWGSVHAPSLRRKTMCGTLDY 239
lcl|NM_213919.2 IMEELADALTYCHGKKVIHRDIKPENLLGLGKELIADFQWGSVHAPSLRRKTMCGTLDY 239
lcl|XM_00150481 IMEELADALMYCHGKKVIHRDIKPENLLGLGKELIADFQWGSVHAPSLRRKTMCGTLDY 239
lcl|XM_00443309 IMEELADALTYCHGKKVIHRDIKPENLLGLGKELIADFQWGSVHAPSLRRKTMCGTLDY 239
lcl|XM_00827074 IMEELADALTYCHGKKVIHRDIKPENLLGLGKELIADFQWGSVHAPSLRRKTMCGTLDY 238
lcl|XM_00587878 IMEELADALMYCHGKKVIHRDIKPENLLGLGKELIADFQWGSVHAPSLRRKTMCGTLDY 234
lcl|XM_00468461 IMEELADALTYCHGKKVIHRDIKPENLLGLGKELIADFQWGSVHAPSLRRKTMCGTLDY 239
lcl|XM_00341691 IMEELADALMYCHGKKVIHRDIKPENLLGLRGELIADFQWGSVHAPSLRRKTMCGTLDY 240
lcl|XM_01994424 IMEELADALTYCHGKKVIHRDIKPENLLGLGKELIADFQWGSVHAPSLRRKTMCGTLDY 239
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lcl|NM_004217.3 LPPEMIEGRMHNEKVDLWICIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPPASVPMG 299
lcl|XM_01511855 LPPEMIEGRTHNEKVDLWICIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPPASVPTG 299
lcl|NM_183084.2 LPPEMIEGRTHNEKVDLWICIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPPASVPLG 299
lcl|XM_00401268 LPPEMIEGRTHNEKVDLWICIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPPASVPMG 299
lcl|XM_844813.4 LPPEMIEGRMHNEKVDLWICIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPPASVPTG 299
lcl|XM_00399619 LPPEMIEGRTHNEKVDLWICIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPPASVPTG 299
lcl|NM_213919.2 LPPEMIEGRTHNEKVDLWICIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPPASVPTG 299
lcl|XM_00150481 LPPEMIEGRTHNEKVDLWICIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPPASVPTG 299
lcl|XM_00443309 LPPEMIEGRTHNEKVDLWICIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPPASVPTG 299
lcl|XM_00827074 LPPEMIEGRTHNEKVDLWICIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPPASVPTG 298
lcl|XM_00587878 LPPEMIEGRTHNEKVDLWICIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPPASVPTG 294
lcl|XM_00468461 LPPEMIEGRTHNEKVDLWICIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPPASVPTG 299
lcl|XM_00341691 LPPEMIEGRMHNEKVDLWICIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPPASVPTG 300
lcl|XM_01994424 LPPEMIEGRTHNEKVDLWICIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPPASVPTG 299
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lcl|NM_004217.3 AQDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV* 345
lcl|XM_01511855 AQDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV* 345
lcl|NM_183084.2 AQDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV* 345
lcl|XM_00401268 AQDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV* 345
lcl|XM_844813.4 AQDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV* 345
lcl|XM_00399619 AQDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV* 345
lcl|NM_213919.2 AQDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV* 345
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tclIXM_00150481 AQDLISKLLRHNPSERLPLAQVSAHPWVAHSRRVLPPSALQSVP* 345
tclIXM_00443309 AQDLISKLLKHNPSERLPLAQVSAHPWVAHSRRVLPPAPQSVP* 345
tclIXM_00287074 AQDLISKLLRHNPSERLPLAQVSAHPWVAHSRRVLPPASAMQSA* 344
tclIXM_00587878 AQDLISKLLKHNPSERLPLAQVSAHPWVAHSRRVLPPSALQSVH* 340
tclIXM_00468461 AQDLITKLLKHNPSERLPLTQVSAHPWVAHSRRVLPPSALQSV* 345
tclIXM_00341691 AQDLISKLLKHNPSERLPLAQVSAHPWVAHSRRVLPPSALQSVP* 346
tclIXM_01994424 AQDLISKLLKHNPSERLPLAQVSAHPWVAHSRRVLPPSALQSV* 345
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