

**Figure S5.** Alignment of placental mammal AKC sequences. The alignment of the placental mammal AKC sequences used for the dN/dS analyses.

MATLAB multiple sequence alignment

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lcl|NM_00101587  MSSPRAVVQLGKAQPAGE-----ELATANQTAQQPSSPAMRRLTVDDFEIGRPLGKGKF  54
lcl|XM_00109836  MSSPKAAVQLGRAQPAGE-----AVTAAANQTAQQPSSPAMRRLKIDDFEIGRPLGKGKF  54
lcl|XM_00521979  MSHRGRTARKAGGMQHAAA-----AGQTVPGAPTARRFTVDDFEIGRPLGKGKF  48
lcl|XM_00401544  MSHRGRTARKAGGMQPA---AGQSVPGAPAAARRFTIDDFEIGRPLGKGKF  48
lcl|XM_00561607  -----MLSGSAQPASE-GEKTQEQSKDAAGHVELSVPPGRRLTIDDFEIGRPLGKGKF  52
lcl|XM_00694080  -----MQSGSVQPAEEEEQTRDQGTAAAGLVELGMPVRRLTIEDFEIGRPLGKGKF  53
lcl|XM_02109730  -----MKSGSVQPAVA-----AAGQTVSNIPTGRRLTIDDFEIGRPLGKGKF  42
lcl|XM_00150199  MSLPEAVMKSGSVRPAVP-----TAGQSQPGFPNVRHLTIDDFEIGRPLGKGKF  49
lcl|XM_00443911  MSLPRAVMKLGVDVQSAGE-----TAGQTQPSFPTVRHFTIDDFEIGRPLGKGKF  49
lcl|XM_00824896  MQS-----GSSQAAGPAQPSVPLRRLTIEDFEIGRPLGKGKF  37
lcl|XM_01453723  MNPGFLLSIIAEKKEPWP-----SSPSGSRSLTIDDFDIRCPLGKGKF  44
lcl|XM_01273470  -----MKSGDAQAAGA-----AGGPALPVATVRRLTIDDFEIGRPLGKGKF  41
lcl|XM_00340664  MFTNVALSFARREWKELA-----PTERALYGDVLLERMRLTIDDFEIGRPLGKGKF  51
lcl|XM_01992887  -----MKSGSAQPAA-----VAGQTMPSTIPTVRRLTIDDFEIGRPLGKGKF  41
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lcl|NM_00101587  GNVYLARLKESHFIVALKVLFKSQIEKEGLEHQLRREIEIQAHLQHPNILRLYNYFHDAR 114
lcl|XM_00109836  GNVYLARLKESHFIVALKVLFKSQIEKEGLEHQLRREIEIQAHLQHPNILRLYNYFHDAR 114
lcl|XM_00521979  GNVYLARLKKNHFIVALKVLFKSQIEKEGLEHQLRREVEIQAHLQHPNILRLYNYFHDAR 108
lcl|XM_00401544  GNVYLARLKKNHFIVALKVLFKSQIEKEGLEHQLRREVEIQAHLQHPNILRLYNYFHDAR 108
lcl|XM_00561607  GNVYLARLKESHFIVALKVLFKSQIEKEGLEHQLRREIEIQAHLQHPNILRLYNYFHDAR 112
lcl|XM_00694080  GNVYLARLKESHFIVALKVLFKSQIEKEGLEHQLRREIEIQAHLQHPNILRLYNYFHDAR 113
lcl|XM_02109730  GNVYLARLKESHFIVALKVLFKSQIEKEGLEHQLRREIEIQAHLQHPNILRLYNYFHDAR 102
lcl|XM_00150199  GNVYLARLKESHFIVALKVLFKSQIEKEGLEHQLRREIEIQAHLQHPNILRLYNYFHDAR 109
lcl|XM_00443911  GNVYLARLKESHFIVALKVLFKSQIEKEGLEHQLRREIEIQAHLQHPNILRLYNYFHDAR 109
lcl|XM_00824896  GNVYLARLKDSHFIVALKVLFKSQIEKEGMEHQLRREIEIQAHLQHPNILRLYNYFHDAR  97
lcl|XM_01453723  GNVYLARLRDSHFIVALKVLFKSQLKEGMEHQLRREIEIQSHLQHPNILRLHNYFHDER 104
lcl|XM_01273470  GNVYLARLRRESRFLVALKVLFKSQIEKEGLEHQLRREVEIQAHLRHPNILRLYNYFHDAR 101
lcl|XM_00340664  GNVYLARLQENHFLVALKVLFKSQIEKEGLEHQLRREIEIQAHLQHPNILRLYNYFHDSR 111
lcl|XM_01992887  GNVYLARLKESHFIVALKVLFKSQIEKEGLEHQLRREIEIQAHLQHPNILRLYNYFHDAR 101
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lcl|NM_00101587  RVYLILEYAPRGELYKELQKSEKLDQRTATIIIEELADALTYCHDKKVIHRDIKPENLLL 174
lcl|XM_00109836  RVYLILEFAPRGELYKELQKSEKLDQRAATIIIEELADALTYCHEKKVIHRDIKPENLLL 174
lcl|XM_00521979  RVYLILEYAPKGELYKALQRSHTFDEQRTATIIIEELADALIYCHERKVIHRDIKPENLLL 168
lcl|XM_00401544  RVYLILEYAPKGELYKALQRSHTFDEQRTATIIIEELADALIYCHEKKVIHRDIKPENLLL 168
lcl|XM_00561607  RVYLILEYAPRGELYKELQKSHTLDEQHTATIMEELADALTYCHEKKVIHRDIKPENLLL 172
lcl|XM_00694080  RVYLILEYAPRGELYKELQKSNTLDEQHTATIMEELADALTYCHEKKVIHRDIKPENLLL 173
lcl|XM_02109730  RVYLILEYAPRGELYKELQKSHTLDEQRTATIMEELADALTYCHEKKVIHRDIKPENLLL 162
lcl|XM_00150199  RVYLILEYAPRGELYKELQKSHTLDEQRTATIMEELADALTYCHEKKVIHRDIKPENLLL 169
lcl|XM_00443911  RVYLILEYAPRGELYKELQKSHTLDEQRTATIMEELADALTYCHEKKVIHRDIKPENLLL 169
lcl|XM_00824896  RIYLILEYAPRGELYKELQKCHTLDEQRTATIMEELADALTYCHGKKVIHRDIKPENLLL 157
lcl|XM_01453723  XYVLILEYAPRGELYKELQKSHTIDEQSTATIMEELAHALAYCHENKVIHRDIKPENLLL 164
lcl|XM_01273470  RVYLILEYAPRGELYKELQNCHTLDEQRTATIIIEELADALTYCHEKKVIHRDIKPENLLL 161
lcl|XM_00340664  RVYLILEYAPRGELYKELQKSHRLDEQRTATIMEELADALIYCHEKKVIHRDIKPENLLL 171
lcl|XM_01992887  RMYLILEYAPRGELYKELQKSHTLDEQRTATVMEELADALTYCHEKKVIHRDIKPENLLL 161
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lcl|NM_00101587  GFRGEVKIADFGWSVHTPSLRRTKTCGTLDYLPPEMIEGRTYDEKVDLWCIGVLCYELLV 234
lcl|XM_00109836  GFRGEVKIADFGWSVHTPSLRRTKTCGTLDYLPPEMIEGRTYDEKVDLWCIGVLCYELLV 234
lcl|XM_00521979  GLMGEVKIADFGWSVHTPSLRRTTCGTLDYLPPEMIEGRTYDEKVDLWCIGVLCYELLV 228
lcl|XM_00401544  GLMGEVKIADFGWSVHTPSLRRTTCGTLDYLPPEMIEGRTYDEKVDLWCIGVLCYELLV 228
lcl|XM_00561607  GFKGEVKIADFGWSVHTPSLRRTKTCGTLDYLPPEMIERRTYNEKVDLWCIGVLCYELLV 232
lcl|XM_00694080  GFRGEVKIADFGWSVHTPSLRRTKTCGTLDYLPPEMIERRTYNETVDLWCIGVLCYELLV 233
lcl|XM_02109730  GFRGEVKIADFGWSVHTPSLRRTKTCGTLDYLPPEMIEGRTYNEKVDLWCIGVLCYELLV 222
lcl|XM_00150199  GFRGEVKIADFGWSVHTPSLRRTKTCGTLDYLPPEMIEGRTYNEKVDLWCIGVLCYELLV 229
lcl|XM_00443911  GFRGEVKIADFGWSVHTPSLRRTKTCGTLDYLPPEMIEGRTYNEKVDLWCIGVLCYELLV 229
lcl|XM_00824896  GFRGEVKIADFGWSVHTLSLRRTKTCGTLDYLPPEMIEGRTYDEKVDLWCIGVLCYELLV 217
lcl|XM_01453723  GLRGEVKIADFGWSVHTPSLRRTKTCGTLDYLPPEMVEQRTYSEMVDLWCIGVLCYELLV 224
lcl|XM_01273470  GYRGEVKIADFGWSVHTPSLRRTKTCGTLDYLPPEMIEGRTYNEKVDLWCIGVLCYELLV 221
lcl|XM_00340664  GLRGEVKIADFGWSVHTLSLRRTKTCGTLDYLPPEMIEGRTYDERVDLWCIGVLCYELLV 231
lcl|XM_01992887  GFRGEVKIADFGWSVHTPSLRRTKTCGTLDYLPPEMIEGRTYNEKVDLWCIGVLCYELLV 221
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lcl|NM_00101587  GYPFFESASHSETYRRILKVDVRFPLSMPLGARDLISRLRLRYQPLERLPLAQILKHPWVQ 294

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lcl|XM\_00109836 GYPFESTSHSETYRRILKVDVRFPLSMPLGARDLISKLLRYQPLERLPLAQILKHPWVQ 294  
lcl|XM\_00521979 GNPPFESASTSETYRRILKVDLRFPPSMSSGARDLISKLLRFQPLERLPLVRVLEHPWIR 288  
lcl|XM\_00401544 GNPPFESASTSETYRRILKVDLRFPPSMSSGARDLISKLLRFQPLERLPLVRVLEHPWIR 288  
lcl|XM\_00561607 GYPFESP SHNETYRRILKVDLRFPPSLPLGAQDLVSKLLRYQPLERLPLAQIMEHPWVR 292  
lcl|XM\_00694080 GNPPFESHSHNETYRRILKVDIRFPPSIPLGARDLISKLLRYQPLERLPLSQILEHPWVR 293  
lcl|XM\_02109730 GNPPFESASHNETYRRILKVDVRFPPSLPLGAQDLISRLLRYQPSDRLPLDQILEHPWVR 282  
lcl|XM\_00150199 GNPPFESNSHNETYRRILKVDVRFPPSIPLGAKDLISKLLRYQPLERLPLDQILEHPWVR 289  
lcl|XM\_00443911 GNPPFESNSHNETYRRILKVDVRFPPSIPLGAKDLISKLLRYQPLERLPLDQIMEHPWVR 289  
lcl|XM\_00824896 GNPPFESVSHNETYRRILKVDVKFPVTMSLGARDLISRLLRYQPSERLPLAQILRHPWVQ 277  
lcl|XM\_01453723 GNPPFKSSSYSETYRRILKVDVKFPPIPLGAQDLISKLLRYQPSERLLLAQVLQHPWVQ 284  
lcl|XM\_01273470 GKPPFESSTHNETYRRILKVDVRFPPSVPLGAQDLISSLLRYQPSERLPLAQILQHPWVR 281  
lcl|XM\_00340664 GNPPFESP SHNETYRRILKVDVRFPPSSMPGAQDLISKLLRYQPFERLALAQVLEHPWVQ 291  
lcl|XM\_01992887 GNPPFESP SHNETYRRILQVDVRFPPSMPLGAQDLISKLLRYQPSERLPLVQILEHPWVR 281  
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lcl|NM\_00101587 AHSRRVLPPCAQMAS\* 310  
lcl|XM\_00109836 VHSRRVLPPCAQMAS\* 310  
lcl|XM\_00521979 AHSQRLVPPSVPMF\* 304  
lcl|XM\_00401544 AHSQRLVPPSVQRAF\* 304  
lcl|XM\_00561607 AHSRRVLPPSVQMAS\* 308  
lcl|XM\_00694080 AHSRRVPPSVQMDS\* 309  
lcl|XM\_02109730 AHSRRVLPPSTQMVS\* 298  
lcl|XM\_00150199 AHSRRVLPPSAQMAS\* 305  
lcl|XM\_00443911 AHSRRVLPPSAQMAS\* 305  
lcl|XM\_00824896 AHSRRVLPPCAHPAS\* 293  
lcl|XM\_01453723 AHSRRVGPPAPAS\* 300  
lcl|XM\_01273470 MHSRRVLPPSAQVAS\* 297  
lcl|XM\_00340664 AHSQRLVPPSAQMAS\* 307  
lcl|XM\_01992887 AHSRRVLPPSAQMVS\* 297  
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