**Supplementary Information**

Evolutionary rates of body-size-related genes and ecological factors involved in driving body size evolution of squamates

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**Supplementary Information includes:**

**Supplementary TABLES S1-S16**

**TABLE | S1** GenBank accession numbers and sequence ID of body-size-related genes used in the study (##, unidentified; ‘predict’, predicted by GeMoMa).

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Genes/Species | *Anolis* *carolinensis* | *Crotalus* *tigris* | *Eublepharis* *macularius* | *Gekko* *japonicus* | *Hemiphyllodactylus* *yunnanensis* | *Hydrophis* *melanocephalus* | *Lacerta* *agilis* | *Laticauda* *laticaudata* | *Naja* *naja* |
| *ACAN* | XM\_003229774.3 | XM\_039359285.1 | predict | rna-Gja019622.1 | rna-Hyu09605.1 | predict | XM\_033167358.1 | predict | predict |
| *ADAMTS10* | XM\_003230509.3 | predict | predict | XM\_015414760.1 | predict | predict | predict | ## | predict |
| *ADIPOR1* | XM\_008123998.2 | predict | predict | rna-Gja011296.1 | rna-Hyu00369.1 | predict | XM\_033165603.1 | ENSLLTT00000025346 | ## |
| *ADIPOR2* | XM\_008110468.2 | XM\_039359206.1 | predict | rna-Gja020318.1 | rna-Hyu11242.1 | predict | XM\_033163210.1 | ENSLLTT00000023603 | predict |
| *AIP* | XM\_003214979.3 | predict | predict | rna-Gja014662.2 | predict | predict | XM\_033159732.1 | ENSLLTT00000019273 | predict |
| *AKT1* | XM\_008103699.1 | XM\_039352517.1 | predict | predict | predict | predict | XM\_033138566.1 | predict | ENSNNAT00000003825 |
| *AKT2* | XM\_003222834.3 | XM\_039361877.1 | predict | rna-Gja007404.1 | rna-Hyu10013.1 | predict | XM\_033158509.1 | predict | ENSNNAT00000030016 |
| *AKT3* | XM\_008117446.2 | XM\_039366468.1 | predict | rna-Gja001031.1 | rna-Hyu14552.1 | predict | XM\_033144373.1 | predict | ENSNNAT00000001521 |
| *BMP1* | XM\_016997197.1 | XM\_039354257.1 | predict | rna-Gja016336.2 | rna-Hyu04790.1 | predict | XM\_033171949.1 | predict | predict |
| *BMP10* | ## | XM\_039324271.1 | predict | rna-Gja016406.1 | rna-Hyu18986.1 | predict | XM\_033159165.1 | predict | predict |
| *BMP15* | XM\_008124584.2 | XM\_039354944.1 | predict | rna-Gja015638.1 | rna-Hyu03462.1 | predict | ## | predict | predict |
| *BMP2* | XM\_003215309.3 | XM\_039359446.1 | predict | rna-Gja000181.1 | rna-Hyu04000.1 | predict | XM\_033142840.1 | predict | predict |
| *BMP3* | XM\_008110983.2 | XM\_039350892.1 | predict | rna-Gja013614.1 | rna-Hyu12445.1 | predict | XM\_033160817.1 | predict | predict |
| *BMP4* | XM\_008123010.2 | XM\_039321018.1 | predict | rna-Gja011222.1 | rna-Hyu17817.1 | predict | XM\_033165194.1 | predict | predict |
| *BMP5* | XM\_003226063.3 | XM\_039320354.1 | predict | rna-Gja000399.1 | rna-Hyu04163.1 | predict | XM\_033143171.1 | predict | predict |
| *BMP6* | XM\_016995160.1 | XM\_039350278.1 | predict | rna-Gja012252.2 | rna-Hyu01828.1 | predict | ## | predict | predict |
| *BMP7* | XM\_008115241.2 | XM\_039343257.1 | predict | rna-Gja007138.1 | rna-Hyu00201.1 | predict | ## | predict | predict |
| *CCNB1* | XM\_003216345.3 | XM\_039333711.1 | predict | rna-Gja009277.1 | rna-Hyu16743.1 | predict | XM\_033164343.1 | ENSLLTT00000000294 | ENSNNAT00000008922 |
| *CCNB3* | XM\_003228113.2 | XM\_039354943.1 | predict | rna-Gja015641.1 | rna-Hyu03465.1 | predict | predict | ENSLLTT00000025587 | ENSNNAT00000019877 |
| *CDKN1A* | XM\_003220355.2 | XM\_039323211.1 | predict | rna-Gja006706.2 | rna-Hyu00560.1 | predict | XM\_033152568.1 | predict | predict |
| *CDKN1B* | XM\_008121663.2 | XM\_039354570.1 | predict | rna-Gja017258.2 | predict | predict | XM\_033148234.1 | ENSLLTT00000007524 | ENSNNAT00000023410 |
| *CDKN1C* | ## | XM\_039350751.1 | predict | rna-Gja011983.1 | rna-Hyu17150.1 | predict | XM\_033154351.1 | ENSLLTT00000004572 | predict |
| *CDKN2C* | XM\_003220281.3 | XM\_039319901.1 | predict | rna-Gja006531.2 | rna-Hyu00727.1 | predict | XM\_033152172.1 | ENSLLTT00000018904 | predict |
| *CDKN2D* | XM\_003216835.3 | XM\_039364315.1 | predict | rna-Gja001134.1 | rna-Hyu09478.1 | predict | XM\_033173581.1 | ENSLLTT00000016598 | ENSNNAT00000028103 |
| *CNP* | XM\_008113264.2 | XM\_039359113.1 | predict | rna-Gja017582.1 | rna-Hyu06931.1 | predict | XM\_033170337.1 | ENSLLTT00000003656 | predict |
| *COL10A1* | XM\_008120575.2 | XM\_039355513.1 | predict | rna-Gja000675.1 | predict | predict | XM\_033143639.1 | predict | predict |
| *EIF2AK3* | XM\_008113086.2 | XM\_039331642.1 | predict | rna-Gja013815.1 | rna-Hyu03043.1 | predict | XM\_033169071.1 | ENSLLTT00000025036 | predict |
| *EIF4EBP1* | XM\_008119665.1 | XM\_039332954.1 | predict | rna-Gja016282.1 | rna-Hyu04841.1 | predict | XM\_033172501.1 | ENSLLTT00000004264 | predict |
| *FBN1* | XM\_003229100.2 | XM\_039359016.1 | predict | XM\_015411782.1 | ## | predict | XM\_033167563.1 | ENSLLTT00000007681 | ENSNNAT00000031153 |
| *FGF4* | XM\_003214666.3 | XM\_039361461.1 | predict | rna-Gja011821.1 | rna-Hyu17295.1 | predict | XM\_033173233.1 | ENSLLTT00000016260 | predict |
| *FOXO1* | XM\_003215292.3 | XM\_039353304.1 | predict | rna-Gja000219.1 | rna-Hyu04034.1 | predict | XM\_033142770.1 | ENSLLTT00000000428 | ENSNNAT00000015897 |
| *FOXO3* | XM\_003215635.3 | XM\_039351147.1 | predict | rna-Gja000626.1 | rna-Hyu04309.1 | predict | XM\_033143556.1 | predict | ENSNNAT00000001477 |
| *FOXO4* | ## | XM\_039354825.1 | predict | rna-Gja015676.1 | rna-Hyu03496.1 | predict | XM\_033138142.1 | predict | predict |
| *FOXO6* | XM\_008121510.1 | XM\_039338253.1 | predict | rna-Gja007787.1 | rna-Hyu10349.1 | predict | XM\_033158019.1 | predict | predict |
| *GALNS* | XM\_008123578.2 | XM\_039330946.1 | predict | rna-Gja016889.2 | rna-Hyu05678.1 | predict | XM\_033156985.1 | ENSLLTT00000012946 | predict |
| *GDF1* | ## | XM\_039325015.1 | predict | rna-Gja005950.1 | rna-Hyu01319.1 | predict | XM\_033136830.1 | predict | predict |
| *GDF11* | XM\_008114414.2 | XM\_039338836.1 | predict | rna-Gja004103.1 | rna-Hyu15304.1 | predict | XM\_033138813.1 | predict | predict |
| *GDF2* | ## | XM\_039368595.1 | predict | rna-Gja011117.1 | rna-Hyu13444.1 | predict | XM\_033148437.1 | predict | predict |
| *GDF5* | XM\_003220471.3 | XM\_039319209.1 | predict | rna-Gja006957.1 | rna-Hyu00357.1 | predict | XM\_033153177.1 | predict | predict |
| *GDF6* | XM\_003219500.3 | XM\_039328916.1 | predict | rna-Gja012689.1 | rna-Hyu02071.1 | predict | XM\_033155614.1 | predict | predict |
| *GDF7* | XM\_003215463.3 | XM\_039364322.1 | predict | rna-Gja000252.1 | rna-Hyu04058.1 | predict | XM\_033145408.1 | predict | predict |
| *GDF9* | XM\_016991447.1 | XM\_039350836.1 | predict | rna-Gja003420.1 | rna-Hyu15890.1 | predict | XM\_033140042.1 | predict | predict |
| *GHR* | XM\_008102836.2 | XM\_039366353.1 | predict | XM\_015424478.1 | predict | predict | XM\_033163847.1 | ENSLLTT00000009946 | predict |
| *GPC1* | XM\_016992111.1 | XM\_039320553.1 | predict | rna-Gja010510.2 | rna-Hyu12951.1 | predict | XM\_033150210.1 | ## | predict |
| *GPC3* | predict | XM\_039354996.1 | predict | rna-Gja015698.1 | rna-Hyu03514.1 | predict | XM\_033137608.1 | predict | predict |
| *GPC4* | predict | XM\_039354780.1 | predict | rna-Gja015697.1 | rna-Hyu03513.1 | predict | XM\_033137336.1 | ENSLLTT00000000902 | predict |
| *GPC6* | XM\_008106861.2 | XM\_039337642.1 | predict | rna-Gja005660.1 | rna-Hyu09367.1 | predict | XM\_033147878.1 | ENSLLTT00000000618 | predict |
| *GRB10* | XM\_008112941.2 | XM\_039336396.1 | predict | XM\_015424873.1 | rna-Hyu02959.1 | predict | XM\_033171161.1 | predict | predict |
| *IGF1* | XM\_008110570.2 | XM\_039338185.1 | predict | rna-Gja008641.1 | predict | predict | XM\_033162260.1 | predict | predict |
| *IGF2* | XM\_008107927.2 | XM\_039350720.1 | predict | rna-Gja011994.1 | rna-Hyu17140.1 | predict | XM\_033154454.1 | predict | predict |
| *IGFBP1* | XM\_003222295.2 | XM\_039353938.1 | predict | rna-Gja013920.1 | rna-Hyu02940.1 | predict | XM\_033165782.1 | predict | ENSNNAT00000007217 |
| *IGFBP2* | XM\_016998075.1 | XM\_039321854.1 | ## | rna-Gja014741.2 | rna-Hyu05501.1 | predict | ## | predict | ENSNNAT00000023068 |
| *IGFBP3* | XM\_003222222.3 | predict | predict | rna-Gja013919.1 | rna-Hyu02939.1 | predict | XM\_033165557.1 | predict | ENSNNAT00000007252 |
| *IGFBP4* | XM\_008113472.1 | XM\_039353984.1 | predict | rna-Gja017605.1 | rna-Hyu07017.1 | predict | XM\_033168782.1 | predict | ENSNNAT00000024329 |
| *IGFBP5* | XM\_003214954.3 | XM\_039321781.1 | predict | rna-Gja014734.2 | rna-Hyu05502.1 | predict | XM\_033161450.1 | predict | ENSNNAT00000023126 |
| *IGFBP6* | XM\_008115096.2 | XM\_039344764.1 | ## | rna-Gja004254.2 | rna-Hyu15165.1 | predict | predict | predict | ENSNNAT00000026690 |
| *IGFBP7* | XM\_008116648.2 | XM\_039345235.1 | ## | rna-Gja009860.1 | rna-Hyu16187.1 | predict | XM\_033172696.1 | predict | ENSNNAT00000019174 |
| *INS* | XM\_003214757.3 | XM\_039350721.1 | predict | rna-Gja011993.1 | rna-Hyu17141.1 | predict | predict | predict | predict |
| *INSL5* | XM\_016997031.1 | predict | predict | rna-Gja020250.1 | rna-Hyu00839.1 | predict | XM\_033151860.1 | predict | predict |
| *IRS1* | XM\_003218293.2 | XM\_039350948.1 | predict | rna-Gja010451.1 | rna-Hyu12902.1 | predict | XM\_033150274.1 | predict | predict |
| *IRS2* | XM\_016996204.1 | XM\_039326285.1 | predict | rna-Gja000139.2 | rna-Hyu03962.1 | predict | XM\_033145331.1 | predict | predict |
| *IRS4* | predict | XM\_039348723.1 | predict | rna-Gja015925.2 | rna-Hyu03739.1 | predict | XM\_033137722.1 | predict | predict |
| *KCNJ2* | XM\_003224670.2 | XM\_039325463.1 | predict | XM\_015425799.1 | rna-Hyu15456.1 | predict | XM\_033138921.1 | ENSLLTT00000014164 | predict |
| *LCORL* | XM\_016993901.1 | XM\_039326495.1 | ## | rna-Gja013007.1 | rna-Hyu11905.1 | predict | XM\_033160887.1 | predict | predict |
| *LEPR* | XM\_008109307.2 | XM\_039347844.1 | predict | XM\_015425799.1 | predict | predict | XM\_033151876.1 | ENSLLTT00000016532 | predict |
| *MSTN* | XM\_003217420.3 | XM\_039322115.1 | predict | rna-Gja015171.1 | rna-Hyu05132.1 | predict | XM\_033168684.1 | predict | predict |
| *mTOR* | XM\_008121887.2 | XM\_039367368.1 | predict | XM\_015409471.1 | predict | predict | XM\_033159497.1 | ENSLLTT00000009968 | predict |
| *NOG* | predict | XM\_039343569.1 | predict | rna-Gja004054.1 | rna-Hyu15340.1 | predict | XM\_033138736.1 | ENSLLTT00000021598 | predict |
| *NPC1* | XM\_016992961.1 | XM\_039328557.1 | predict | rna-Gja012443.1 | rna-Hyu01662.1 | predict | XM\_033155039.1 | ENSLLTT00000006581 | predict |
| *NPC2* | XM\_003214383.3 | XM\_039351743.1 | predict | rna-Gja011494.1 | rna-Hyu17567.1 | predict | XM\_033142669.1 | ENSLLTT00000025867 | predict |
| *NPR2* | XM\_008124741.1 | XM\_039369033.1 | predict | rna-Gja009017.1 | rna-Hyu16996.1 | predict | XM\_033164105.1 | ENSLLTT00000009497 | predict |
| *NSD1* | XM\_008104944.2 | XM\_039356798.1 | predict | rna-Gja003226.1 | predict | predict | XM\_033140441.1 | ## | ENSNNAT00000026859 |
| *NSD2* | XM\_016996236.1 | XM\_039347629.1 | predict | rna-Gja010068.1 | rna-Hyu09492.1 | predict | XM\_033148417.1 | predict | predict |
| *NSD3* | XM\_008119823.2 | XR\_005557990.1 | predict | rna-Gja016337.2 | rna-Hyu04789.1 | predict | XM\_033172074.1 | predict | ENSNNAT00000013375 |
| *OBSL1* | XM\_008111858.2 | XM\_039354396.1 | predict | rna-Gja014669.1 | rna-Hyu05560.1 | predict | XM\_033159830.1 | predict | predict |
| *PLAG1* | XM\_008116164.1 | XM\_039351436.1 | predict | rna-Gja012523.1 | predict | predict | XM\_033155250.1 | predict | ENSNNAT00000028243 |
| *PLAGL2* | XM\_003227609.3 | XM\_039318882.1 | predict | rna-Gja007304.1 | predict | predict | XM\_033153868.1 | predict | ## |
| *PRKG2* | XM\_008110984.2 | XM\_039350891.1 | predict | rna-Gja013613.1 | rna-Hyu12444.1 | predict | XM\_033160928.1 | ## | predict |
| *RLN3* | XM\_003216768.3 | XM\_039329696.1 | predict | rna-Gja004573.1 | rna-Hyu14904.1 | predict | XM\_033173413.1 | predict | predict |
| *SH2B1* | XM\_008117506.2 | XM\_039335296.1 | predict | rna-Gja018094.1 | rna-Hyu07316.2 | predict | XM\_033169254.1 | predict | predict |
| *SH2B2* | ## | XM\_039333987.1 | predict | rna-Gja019017.1 | rna-Hyu08121.1 | predict | XR\_004427958.1 | predict | predict |
| *SH2B3* | XM\_008119880.2 | XM\_039362625.1 | predict | ## | rna-Hyu03119.1 | predict | XM\_033159257.1 | predict | predict |
| *SMO* | XM\_003228469.3 | XM\_039345718.1 | predict | rna-Gja008902.1 | rna-Hyu11383.1 | predict | XM\_033162534.1 | ENSLLTT00000006351 | predict |
| *SOX1* | XM\_008107076.2 | XM\_039359750.1 | predict | rna-Gja005588.1 | rna-Hyu09304.1 | predict | XM\_033147761.1 | predict | ENSNNAT00000010612 |
| *SOX10* | XM\_003227146.2 | XM\_039333526.1 | predict | rna-Gja008547.1 | rna-Hyu11077.1 | predict | XM\_033162295.1 | predict | ENSNNAT00000017261 |
| *SOX11* | XM\_008116083.2 | XM\_039331915.1 | predict | rna-Gja000322.1 | rna-Hyu04115.1 | predict | XM\_033143054.1 | predict | ENSNNAT00000002108 |
| *SOX12* | XM\_016996668.1 | XM\_039363850.1 | predict | rna-Gja007286.1 | rna-Hyu00081.1 | predict | XM\_033151051.1 | predict | ENSNNAT00000005227 |
| *SOX13* | XM\_003220368.3 | XM\_039340611.1 | predict | rna-Gja006780.1 | rna-Hyu00497.1 | predict | XM\_033152736.1 | predict | ENSNNAT00000015048 |
| *SOX14* | XM\_008106527.2 | XM\_039363714.1 | predict | rna-Gja010541.1 | rna-Hyu12991.1 | predict | XM\_033150115.1 | predict | ENSNNAT00000027856 |
| *SOX17* | XM\_003224318.3 | XM\_039351373.1 | predict | rna-Gja012507.1 | rna-Hyu01600.1 | predict | XM\_033155214.1 | predict | ENSNNAT00000003835 |
| *SOX18* | XM\_003220686.3 | XM\_039326957.1 | predict | rna-Gja007236.1 | rna-Hyu00126.1 | predict | XM\_033153753.1 | ## | ENSNNAT00000029216 |
| *SOX2* | ## | XM\_039321844.1 | predict | rna-Gja010261.1 | rna-Hyu12709.1 | predict | XM\_033148192.1 | predict | ENSNNAT00000006228 |
| *SOX21* | XM\_003218665.3 | predict | ## | rna-Gja005665.1 | rna-Hyu09371.1 | predict | XM\_033147885.1 | predict | ENSNNAT00000016400 |
| *SOX3* | XM\_008117936.2 | predict | predict | rna-Gja015729.1 | rna-Hyu03540.1 | predict | XM\_033137729.1 | predict | ENSNNAT00000012184 |
| *SOX30* | XM\_003223478.2 | XM\_039365481.1 | predict | rna-Gja003259.1 | rna-Hyu16023.1 | predict | XM\_033140371.1 | predict | predict |
| *SOX4* | XM\_008108797.1 | XM\_039322649.1 | predict | rna-Gja012294.1 | rna-Hyu01789.1 | predict | XM\_033154691.1 | predict | ENSNNAT00000021530 |
| *SOX5* | XM\_008110345.2 | XM\_039347420.1 | predict | rna-Gja008792.1 | rna-Hyu11287.1 | predict | XM\_033161785.1 | predict | ENSNNAT00000008490 |
| *SOX6* | XM\_008107338.2 | XM\_039344590.1 | ## | rna-Gja011947.1 | rna-Hyu17184.1 | predict | XM\_033153443.1 | predict | ENSNNAT00000026028 |
| *SOX7* | XM\_003230341.3 | XM\_039323544.1 | predict | rna-Gja001469.1 | rna-Hyu14170.1 | predict | XM\_033145158.1 | predict | ENSNNAT00000002436 |
| *SOX8* | XM\_003224758.3 | XM\_039349756.1 | predict | rna-Gja019927.1 | rna-Hyu11529.1 | predict | XM\_033167051.1 | predict | ENSNNAT00000026064 |
| *SOX9* | XM\_003224669.3 | XM\_039325522.1 | predict | rna-Gja003929.1 | rna-Hyu15458.1 | predict | XM\_033138926.1 | predict | ENSNNAT00000003366 |

**TABLE | S1 (continued)**

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Genes/Species | *Notechis* *scutatus* | *Pantherophis* *guttatus* | *Pantherophis* *obsoletus* | *Paroedura* *picta* | *Podarcis* *muralis* | *Pogona* *vitticeps* | *Protobothrops* *flavoviridis* | *Protobothrops* *mucrosquamatus* | *Ptyas* *mucosa* | *Python\_bivittatus* |
| *ACAN* | XM\_026681847.1 | XM\_034424626.1 | predict | gene-parPi\_0017450 | XM\_028705913.1 | XM\_020781675.1 | predict | predict | predict | XM\_007427154.1 |
| *ADAMTS10* | XM\_026681077.1 | XM\_034437757.1 | predict | gene-parPi\_0024564 | XM\_028713622.1 | XM\_020781187.1 | predict | XM\_015809941.1 | predict | XM\_015889014.2 |
| *ADIPOR1* | predict | XM\_034430517.1 | predict | gene-parPi\_0001232 | ## | XM\_020800150.1 | predict | ## | predict | XM\_025169305.1 |
| *ADIPOR2* | XM\_026663889.1 | XM\_034403448.1 | predict | gene-parPi\_0004626 | XM\_028745557.1 | XM\_020789048.1 | predict | XM\_015823740.1 | predict | XM\_007435023.2 |
| *AIP* | XM\_026665609.1 | XM\_034433816.1 | predict | gene-parPi\_0011916 | predict | XM\_020792092.1 | predict | XM\_015815188.1 | predict | XM\_007436956.3 |
| *AKT1* | XM\_026670115.1 | XM\_034418587.1 | predict | predict | XM\_028747722.1 | ## | predict | XM\_015831538.1 | predict | XM\_007420301.2 |
| *AKT2* | XM\_026687775.1 | XM\_034438311.1 | predict | gene-parPi\_0019415 | XM\_028741995.1 | XM\_020787178.1 | predict | XM\_015813903.1 | predict | XM\_007438600.3 |
| *AKT3* | XM\_026669404.1 | XM\_034428237.1 | predict | gene-parPi\_0015141 | XM\_028724127.1 | XM\_020787673.1 | predict | XM\_015822124.1 | predict | XM\_007422468.3 |
| *BMP1* | XM\_026681140.1 | XM\_034432941.1 | predict | gene-parPi\_0003627 | XM\_028708405.1 | XM\_020780295.1 | predict | XM\_015817975.1 | predict | XM\_007434809.3 |
| *BMP10* | XM\_026689396.1 | XM\_034430612.1 | predict | gene-parPi\_0003534 | XM\_028742159.1 | XM\_020780157.1 | predict | XM\_015811553.1 | predict | XM\_007442036.2 |
| *BMP15* | predict | XM\_034441777.1 | predict | predict | ## | XM\_020795807.1 | predict | XM\_029282935.1 | predict | XM\_025170082.1 |
| *BMP2* | XM\_026668524.1 | XM\_034432344.1 | predict | gene-parPi\_0013240 | XM\_028722205.1 | XM\_020793685.1 | predict | XM\_015813549.2 | predict | XM\_007427029.3 |
| *BMP3* | XM\_026676449.1 | XM\_034431199.1 | predict | predict | XM\_028744341.1 | XM\_020803172.1 | predict | XM\_015832355.1 | predict | XM\_007425362.2 |
| *BMP4* | XM\_026670247.1 | XM\_034433399.1 | predict | gene-parPi\_0025840 | XM\_028725147.1 | predict | predict | XM\_015822447.1 | predict | XM\_007436872.3 |
| *BMP5* | XM\_026665243.1 | XM\_034436697.1 | predict | gene-parPi\_0004221 | XM\_028722619.1 | XM\_020781800.1 | predict | XM\_015819889.1 | predict | XM\_007431739.2 |
| *BMP6* | XM\_026676670.1 | XM\_034429112.1 | predict | gene-parPi\_0009370 | predict | XM\_020797114.1 | predict | XM\_015810838.1 | predict | XM\_025176419.1 |
| *BMP7* | XM\_026664940.1 | XM\_034433071.1 | predict | gene-parPi\_0008867 | XM\_028735269.1 | XM\_020797472.1 | predict | XM\_015823851.1 | predict | XM\_007433611.2 |
| *CCNB1* | XM\_026670475.1 | XM\_034441042.1 | predict | gene-parPi\_0001814 | XM\_028748941.1 | XM\_020783740.1 | predict | XM\_015829950.1 | predict | XM\_007422277.3 |
| *CCNB3* | XM\_026684338.1 | XM\_034441766.1 | predict | predict | XM\_028715394.1 | XM\_020795849.1 | predict | XM\_015832487.1 | predict | XM\_025175696.1 |
| *CDKN1A* | predict | XM\_034414676.1 | predict | gene-parPi\_0003813 | XM\_028734001.1 | XM\_020795510.1 | predict | XM\_015815510.1 | predict | XM\_025163251.1 |
| *CDKN1B* | XM\_026679274.1 | XM\_034440384.1 | predict | gene-parPi\_0012286 | XM\_028728599.1 | XM\_020785790.1 | predict | XM\_029284044.1 | predict | ## |
| *CDKN1C* | XM\_026668288.1 | XM\_034416899.1 | predict | gene-parPi\_0013413 | XM\_028733541.1 | XM\_020788815.1 | predict | predict | predict | XM\_007433944.3 |
| *CDKN2C* | XM\_026665840.1 | XM\_034415062.1 | predict | gene-parPi\_0006275 | predict | predict | predict | XM\_015810922.1 | predict | XM\_007432276.3 |
| *CDKN2D* | XM\_026679665.1 | predict | predict | gene-parPi\_0023789 | XM\_028712777.1 | XM\_020791632.1 | predict | XM\_015820640.1 | predict | XM\_007430203.3 |
| *CNP* | XM\_026682772.1 | XM\_034415949.1 | predict | gene-parPi\_0017027 | XM\_028702746.1 | XM\_020811702.1 | predict | XM\_015832224.1 | predict | XM\_007428476.3 |
| *COL10A1* | XM\_026666702.1 | XM\_034409202.1 | predict | predict | XM\_028723223.1 | XM\_020810831.1 | predict | XM\_015821573.1 | predict | XM\_007429059.2 |
| *EIF2AK3* | XM\_026679877.1 | XM\_034416108.1 | predict | gene-parPi\_0022136 | XM\_028702243.1 | XM\_020807186.1 | predict | XM\_015831485.1 | predict | XM\_025166019.1 |
| *EIF4EBP1* | XM\_026671340.1 | XM\_034436873.1 | predict | gene-parPi\_0010907 | XM\_028708762.1 | XM\_020786156.1 | predict | ## | predict | XM\_025166228.1 |
| *FBN1* | XM\_026677102.1 | XM\_034434719.1 | predict | gene-parPi\_0020530 | XM\_028705573.1 | XM\_020790046.1 | predict | XM\_029284183.1 | predict | predict |
| *FGF4* | XM\_026664620.1 | XM\_034417295.1 | predict | gene-parPi\_0010257 | predict | ## | predict | XM\_015814077.1 | predict | XM\_007425531.1 |
| *FOXO1* | XM\_026668589.1 | XM\_034432245.1 | predict | gene-parPi\_0020291 | XM\_028722118.1 | XM\_020788033.1 | predict | XM\_015818674.1 | predict | XM\_025170230.1 |
| *FOXO3* | XM\_026666640.1 | XM\_034409122.1 | predict | gene-parPi\_0009318 | XR\_003705856.1 | XM\_020801330.1 | predict | predict | predict | predict |
| *FOXO4* | XM\_026684252.1 | XR\_004595420.1 | predict | gene-parPi\_0002044 | XM\_028714929.1 | XM\_020795884.1 | predict | XM\_029282942.1 | predict | XM\_025165310.1 |
| *FOXO6* | XM\_026679416.1 | XM\_034423581.1 | predict | gene-parPi\_0009764 | XM\_028742772.1 | XM\_020805980.1 | predict | predict | predict | predict |
| *GALNS* | XM\_026689757.1 | XM\_034426622.1 | predict | gene-parPi\_0006417 | XM\_028739979.1 | XM\_020788232.1 | predict | XM\_015811440.1 | predict | predict |
| *GDF1* | XM\_026687623.1 | XM\_034422580.1 | predict | predict | predict | XM\_020780965.1 | predict | XM\_015810689.1 | predict | XM\_007430334.3 |
| *GDF11* | XM\_026678705.1 | XM\_034412572.1 | predict | gene-parPi\_0012816 | XM\_028712311.1 | XM\_020782984.1 | predict | XM\_029283925.1 | predict | predict |
| *GDF2* | XM\_026688551.1 | XM\_034420080.1 | predict | predict | XM\_028728442.1 | XR\_002301987.1 | predict | XM\_015823137.1 | predict | XM\_025172421.1 |
| *GDF5* | XM\_026685207.1 | XM\_034414134.1 | predict | gene-parPi\_0001217 | XM\_028734745.1 | XM\_020782363.1 | predict | XM\_015815571.1 | predict | XM\_007429034.1 |
| *GDF6* | XM\_026690667.1 | XM\_034422321.1 | predict | predict | XM\_028736453.1 | XM\_020785266.1 | predict | XM\_015819636.1 | predict | XM\_007428883.2 |
| *GDF7* | XM\_026675589.1 | XM\_034431990.1 | predict | gene-parPi\_0013397 | XM\_028722337.1 | predict | predict | XM\_029285045.1 | predict | XM\_015889742.1 |
| *GDF9* | XM\_026685461.1 | XM\_034408740.1 | predict | predict | XM\_028717961.1 | predict | predict | XM\_015827112.2 | predict | XM\_007431889.2 |
| *GHR* | predict | XM\_034440812.1 | predict | gene-parPi\_0001683 | XM\_028747973.1 | XM\_020783630.1 | predict | XM\_015817122.2 | predict | XM\_007426732.3 |
| *GPC1* | XM\_026694963.1 | XM\_034439496.1 | predict | gene-parPi\_0000271 | XM\_028730983.1 | XM\_020786409.1 | predict | XM\_015816735.1 | predict | XM\_007438791.2 |
| *GPC3* | XM\_026687054.1 | XM\_034441587.1 | predict | predict | XM\_028714641.1 | XM\_020810324.1 | predict | XM\_015832425.1 | predict | XM\_007440630.2 |
| *GPC4* | XM\_026687060.1 | XM\_034441660.1 | predict | predict | XM\_028715943.1 | XM\_020795845.1 | predict | XM\_015832458.1 | predict | XM\_007442300.2 |
| *GPC6* | XM\_026668872.1 | XM\_034417392.1 | predict | predict | XM\_028728291.1 | XM\_020783492.1 | predict | XM\_015822600.1 | predict | XM\_007439892.2 |
| *GRB10* | XM\_026678346.1 | XM\_034416404.1 | predict | gene-parPi\_0024970 | XM\_028703027.1 | XM\_020806217.1 | ## | XM\_029284179.1 | predict | XM\_007425657.3 |
| *IGF1* | XM\_026695013.1 | XM\_034403031.1 | predict | predict | XM\_028747269.1 | XR\_002301546.1 | predict | XM\_015818227.2 | predict | XM\_007419939.2 |
| *IGF2* | XM\_026668274.1 | XM\_034416881.1 | predict | predict | XM\_028733745.1 | XM\_020788759.1 | predict | XM\_015828379.2 | predict | XM\_007424231.2 |
| *IGFBP1* | XM\_026681273.1 | XM\_034416450.1 | predict | predict | XM\_028750593.1 | XM\_020811237.1 | ## | XM\_015824572.1 | predict | XM\_007443407.2 |
| *IGFBP2* | XM\_026665506.1 | XM\_034421906.1 | predict | predict | XM\_028742484.1 | XM\_020805984.1 | predict | predict | predict | XM\_007420163.3 |
| *IGFBP3* | XM\_026681263.1 | XM\_034416443.1 | predict | ## | XM\_028749822.1 | XM\_020811238.1 | predict | XM\_015824594.1 | predict | predict |
| *IGFBP4* | XM\_026686038.1 | XM\_034415763.1 | predict | gene-parPi\_0018088 | XM\_028702464.1 | XM\_020805878.1 | predict | XM\_015832277.1 | predict | XM\_007437001.3 |
| *IGFBP5* | XM\_026665507.1 | XM\_034421893.1 | predict | gene-parPi\_0007922 | XM\_028742474.1 | XM\_020805180.1 | predict | XM\_015813070.1 | predict | XM\_007420164.2 |
| *IGFBP6* | XM\_026673894.1 | XM\_034419273.1 | predict | gene-parPi\_0016708 | XM\_028721259.1 | predict | predict | XM\_015819955.1 | predict | predict |
| *IGFBP7* | XM\_026688442.1 | XM\_034410887.1 | predict | gene-parPi\_0016079 | XM\_028712092.1 | XM\_020814928.1 | predict | XM\_015815357.1 | predict | XM\_007427011.3 |
| *INS* | XM\_026668141.1 | XM\_034418612.1 | predict | predict | predict | XM\_020788804.1 | predict | XM\_015823247.1 | predict | predict |
| *INSL5* | XM\_026665683.1 | XM\_034433266.1 | predict | predict | XM\_028733153.1 | XM\_020806096.1 | predict | predict | predict | predict |
| *IRS1* | XM\_026664269.1 | XM\_034439378.1 | predict | gene-parPi\_0000339 | XM\_028731109.1 | XM\_020792635.1 | predict | XM\_015815062.1 | predict | XM\_007420457.2 |
| *IRS2* | XM\_026679038.1 | XM\_034426894.1 | predict | predict | XM\_028721788.1 | XM\_020814835.1 | predict | XM\_029286039.1 | predict | XM\_025169158.1 |
| *IRS4* | XM\_026674628.1 | XM\_034435041.1 | predict | gene-parPi\_0018744 | XM\_028714350.1 | XM\_020784321.1 | predict | predict | predict | predict |
| *KCNJ2* | XM\_026675809.1 | XM\_034412714.1 | predict | gene-parPi\_0012170 | XM\_028713787.1 | XM\_020791307.1 | predict | predict | predict | XM\_007421675.2 |
| *LCORL* | XM\_026678839.1 | XM\_034442730.1 | predict | predict | XM\_028744220.1 | XM\_020812181.1 | predict | predict | predict | XM\_025165888.1 |
| *LEPR* | XM\_026665714.1 | XM\_034433267.1 | predict | predict | XM\_028733181.1 | XM\_020806097.1 | predict | predict | predict | XM\_007424892.1 |
| *MSTN* | XM\_026668007.1 | XM\_034429430.1 | predict | gene-parPi\_0018235 | XM\_028750472.1 | XM\_020802864.1 | predict | XM\_015817139.1 | predict | XM\_007425310.2 |
| *mTOR* | XM\_026684398.1 | XM\_034430195.1 | predict | gene-parPi\_0019663 | XM\_028740653.1 | XM\_020782169.1 | predict | XM\_029285652.1 | predict | XM\_025163051.1 |
| *NOG* | XM\_026680810.1 | XM\_034412491.1 | predict | gene-parPi\_0016911 | XM\_028711307.1 | ## | predict | XM\_015817225.1 | predict | XM\_007428647.2 |
| *NPC1* | XM\_026670329.1 | XM\_034429605.1 | predict | predict | XM\_028737172.1 | XM\_020785692.1 | predict | XM\_015821410.1 | predict | predict |
| *NPC2* | XM\_026664435.1 | XM\_034418105.1 | predict | gene-parPi\_0010413 | XM\_028719725.1 | XM\_020793876.1 | predict | XM\_015822209.1 | predict | XM\_007441386.2 |
| *NPR2* | XM\_026684950.1 | XM\_034441884.1 | predict | gene-parPi\_0016532 | XM\_028748189.1 | XM\_020800723.1 | predict | XM\_015828647.1 | predict | XM\_025175980.1 |
| *NSD1* | XM\_026673394.1 | XM\_034442278.1 | predict | gene-parPi\_0025495 | XM\_028718465.1 | XM\_020790667.1 | predict | XM\_029285900.1 | predict | XM\_025168133.1 |
| *NSD2* | XM\_026687223.1 | XM\_034415971.1 | predict | gene-parPi\_0017241 | XM\_028728860.1 | XM\_020805918.1 | predict | XM\_015820437.1 | predict | XM\_015889828.2 |
| *NSD3* | XM\_026681166.1 | XM\_034432942.1 | predict | gene-parPi\_0003626 | XM\_028708201.1 | XM\_020780291.1 | predict | XM\_015818822.1 | predict | XM\_007430417.3 |
| *OBSL1* | XM\_026665601.1 | XM\_034433802.1 | predict | gene-parPi\_0011923 | XM\_028740896.1 | XM\_020792117.1 | predict | XM\_029284004.1 | predict | XM\_007435699.2 |
| *PLAG1* | XM\_026692460.1 | XM\_034429805.1 | predict | gene-parPi\_0003013 | XM\_028736901.1 | XM\_020812962.1 | predict | XM\_015812378.1 | predict | XM\_025167923.1 |
| *PLAGL2* | ## | XM\_034405378.1 | predict | gene-parPi\_0024814 | XM\_028735599.1 | XM\_020807853.1 | predict | XM\_015823839.1 | predict | XM\_007439544.3 |
| *PRKG2* | XM\_026676513.1 | XM\_034431197.1 | predict | gene-parPi\_0007673 | XM\_028744438.1 | XM\_020803184.1 | predict | XM\_029287371.1 | predict | predict |
| *RLN3* | XM\_026681978.1 | XM\_034434410.1 | predict | predict | XM\_028712730.1 | XM\_020798753.1 | predict | XM\_015827367.1 | predict | XM\_025171372.1 |
| *SH2B1* | XM\_026677515.1 | XM\_034423351.1 | predict | gene-parPi\_0018915 | XM\_028702247.1 | XM\_020792776.1 | predict | XM\_015810291.1 | predict | XM\_007421440.2 |
| *SH2B2* | XM\_026672400.1 | XM\_034420870.1 | predict | predict | XM\_028707886.1 | XM\_020804996.1 | predict | XM\_029286571.1 | predict | XM\_025174142.1 |
| *SH2B3* | predict | XM\_034428628.1 | predict | gene-parPi\_0014241 | XM\_028741309.1 | XM\_020802705.1 | predict | XM\_029284045.1 | predict | predict |
| *SMO* | XM\_026691529.1 | XM\_034407099.1 | predict | ## | XM\_028746014.1 | XM\_020812446.1 | predict | XM\_015825840.1 | predict | XM\_007440857.2 |
| *SOX1* | XM\_026668852.1 | XM\_034418822.1 | predict | gene-parPi\_0000506 | XM\_028728115.1 | predict | predict | XM\_015821387.1 | predict | predict |
| *SOX10* | XM\_026694898.1 | XM\_034402787.1 | predict | gene-parPi\_0006744 | XM\_028746570.1 | XM\_020787743.1 | predict | XM\_015817261.1 | predict | XM\_007434407.3 |
| *SOX11* | XM\_026674288.1 | XM\_034432041.1 | predict | gene-parPi\_0004148 | XM\_028722480.1 | XM\_020782589.1 | predict | XM\_015827007.1 | predict | XM\_007428741.3 |
| *SOX12* | XM\_026694532.1 | XM\_034404871.1 | predict | gene-parPi\_0024683 | XM\_028735566.1 | XM\_020814668.1 | predict | XM\_015829281.1 | predict | XM\_025175052.1 |
| *SOX13* | XM\_026676852.1 | XM\_034414498.1 | predict | gene-parPi\_0003737 | XM\_028734211.1 | XM\_020797027.1 | predict | XM\_015832171.1 | predict | XM\_007425173.3 |
| *SOX14* | XM\_026667753.1 | XM\_034440321.1 | predict | gene-parPi\_0000224 | XM\_028730885.1 | XM\_020787458.1 | predict | XM\_015814165.1 | predict | XM\_007438980.1 |
| *SOX17* | XM\_026670437.1 | XM\_034429780.1 | predict | gene-parPi\_0002861 | XM\_028736953.1 | XM\_020795946.1 | predict | XM\_029285199.1 | predict | XM\_015888152.2 |
| *SOX18* | XM\_026692005.1 | ## | predict | predict | XM\_028735464.1 | XM\_020814395.1 | predict | XM\_015827360.1 | predict | XM\_025172960.1 |
| *SOX2* | predict | XM\_034438913.1 | predict | gene-parPi\_0018602 | XM\_028731643.1 | ## | predict | XM\_015828598.1 | predict | ## |
| *SOX21* | XM\_026668861.1 | XM\_034417516.1 | predict | gene-parPi\_0003184 | XM\_028728301.1 | predict | predict | XM\_015826608.1 | predict | ## |
| *SOX3* | XM\_026690830.1 | XM\_034441598.1 | predict | gene-parPi\_0001993 | XM\_028715451.1 | ## | predict | XM\_015832507.2 | predict | ## |
| *SOX30* | XM\_026682147.1 | XM\_034401529.1 | predict | predict | XM\_028718367.1 | XM\_020791364.1 | predict | XM\_015832120.1 | predict | XM\_007443891.3 |
| *SOX4* | predict | XM\_034429253.1 | predict | gene-parPi\_0007432 | XM\_028737589.1 | XM\_020781668.1 | predict | XM\_015831693.1 | predict | XM\_007432062.3 |
| *SOX5* | XM\_026678269.1 | XM\_034442598.1 | predict | predict | XM\_028746002.1 | XM\_020809978.1 | predict | XM\_015825047.1 | predict | XM\_007424150.2 |
| *SOX6* | XM\_026668336.1 | XM\_034416989.1 | predict | gene-parPi\_0007340 | XM\_028732368.1 | XM\_020802948.1 | predict | XM\_029283932.1 | predict | XM\_025162928.1 |
| *SOX7* | XM\_026671493.1 | XM\_034421309.1 | predict | gene-parPi\_0008523 | XM\_028725198.1 | XM\_020815847.1 | predict | XM\_015813769.1 | predict | XM\_007430523.3 |
| *SOX8* | XM\_026685814.1 | XM\_034420557.1 | predict | gene-parPi\_0022768 | XM\_028706020.1 | XM\_020805939.1 | predict | XM\_015824516.1 | predict | XM\_025175279.1 |
| *SOX9* | XM\_026675805.1 | XM\_034412719.1 | predict | predict | XM\_028713809.1 | XM\_020791275.1 | predict | XM\_015811091.1 | predict | XM\_007429906.3 |

**TABLE | S1 (continued)**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Genes/Species | *Ophiophagus* *hannah* | *Pseudonaja* *textilis* | *Salvator* *merianae* | *Shinisaurus* *crocodilurus* | *Thamnophis* *elegans* | *Thamnophis* *sirtalis* | *Thermophis* *baileyi* | *Varanus* *komodoensis* | *Zootoca* *vivipara* |
| *ACAN* | rna-L345\_04838.mrna | XM\_026709278.1 | ENSSMRT00000033805 | predict | XM\_032233151.1 | XM\_014055579.1 | predict | predict | XM\_035132014.1 |
| *ADAMTS10* | predict | XM\_026698997.1 | ENSSMRT00000003496 | predict | XM\_032212317.1 | predict | predict | predict | XM\_035120628.1 |
| *ADIPOR1* | rna-L345\_00125.mrna | predict | ENSSMRT00000025805 | predict | XM\_032237846.1 | XM\_014074644.1 | predict | predict | XM\_035128743.1 |
| *ADIPOR2* | predict | XM\_026718095.1 | ENSSMRT00000002538 | predict | XM\_032221384.1 | XM\_014068470.1 | predict | rna-EYD10\_16427 | XM\_035127345.1 |
| *AIP* | predict | XM\_026707861.1 | ENSSMRT00000015963 | predict | XM\_032218034.1 | XM\_014056809.1 | predict | predict | predict |
| *AKT1* | predict | XM\_026698587.1 | ENSSMRT00000002243 | predict | XM\_032235085.1 | XM\_014056354.1 | predict | predict | XM\_035104862.1 |
| *AKT2* | predict | XM\_026721508.1 | ENSSMRT00000003778 | predict | XM\_032228244.1 | XM\_014056399.1 | predict | rna-EYD10\_17828 | XM\_035119506.1 |
| *AKT3* | predict | XM\_026705238.1 | ENSSMRT00000015196 | predict | XM\_032215221.1 | XM\_014056810.1 | predict | predict | XM\_035108350.1 |
| *BMP1* | ## | predict | ENSSMRT00000028927 | predict | XM\_032229024.1 | predict | predict | predict | XM\_035138997.1 |
| *BMP10* | rna-L345\_15121.mrna | XM\_026715193.1 | ENSSMRT00000023322 | predict | XM\_032230062.1 | XM\_014058525.1 | predict | predict | XM\_035119718.1 |
| *BMP15* | predict | XM\_026716700.1 | ENSSMRT00000002949 | predict | ## | XM\_014069218.1 | predict | predict | ## |
| *BMP2* | predict | XM\_026710399.1 | ENSSMRT00000034452 | predict | XM\_032214290.1 | XM\_014068423.1 | predict | predict | XM\_035110119.1 |
| *BMP3* | predict | XM\_026718920.1 | ENSSMRT00000019351 | predict | XM\_032224540.1 | XM\_014067471.1 | predict | predict | XM\_035112545.1 |
| *BMP4* | rna-L345\_10492.mrna | XM\_026698724.1 | ENSSMRT00000014170 | predict | XM\_032236471.1 | XM\_014054780.1 | predict | ## | XM\_035100913.1 |
| *BMP5* | predict | XM\_026726551.1 | ENSSMRT00000017328 | predict | XM\_032217119.1 | predict | predict | rna-EYD10\_06908 | XM\_035109771.1 |
| *BMP6* | predict | XM\_026715078.1 | ENSSMRT00000009749 | predict | XM\_032222939.1 | ## | predict | predict | XM\_035124694.1 |
| *BMP7* | predict | XM\_026697457.1 | predict | predict | XM\_032217333.1 | ## | predict | predict | XM\_035122480.1 |
| *CCNB1* | predict | XM\_026714438.1 | ENSSMRT00000001450 | predict | XM\_032213746.1 | XM\_014069645.1 | predict | rna-EYD10\_03775 | XM\_035099888.1 |
| *CCNB3* | predict | XM\_026716620.1 | ENSSMRT00000003838 | predict | XM\_032228126.1 | ## | predict | rna-EYD10\_15844 | predict |
| *CDKN1A* | predict | XM\_026718195.1 | ENSSMRT00000031847 | predict | predict | XM\_014056585.1 | predict | rna-EYD10\_01494 | XM\_035122492.1 |
| *CDKN1B* | ## | XM\_026702158.1 | ENSSMRT00000011924 | ENSACAP00000004216 | XM\_032221499.1 | XM\_014064547.1 | predict | rna-EYD10\_05732 | XM\_035138382.1 |
| *CDKN1C* | predict | XM\_026706548.1 | ENSSMRT00000021320 | predict | XM\_032230322.1 | XM\_014058139.1 | predict | rna-EYD10\_08364 | XM\_035120955.1 |
| *CDKN2C* | predict | XM\_026707295.1 | ENSSMRT00000027618 | ENSGALP00000017133 | XM\_032218996.1 | XM\_014057359.1 | predict | rna-EYD10\_09260 | XM\_035124241.1 |
| *CDKN2D* | rna-L345\_11118.mrna | XM\_026716817.1 | ENSSMRT00000006853 | ## | predict | predict | predict | predict | XM\_035097494.1 |
| *CNP* | predict | XM\_026718289.1 | ENSSMRT00000010570 | predict | XM\_032235433.1 | XM\_014052701.1 | predict | rna-EYD10\_14164 | XM\_035134893.1 |
| *COL10A1* | predict | XM\_026726584.1 | ENSSMRT00000018912 | predict | XM\_032216598.1 | XM\_014053362.1 | predict | rna-EYD10\_00636 | XM\_035109119.1 |
| *EIF2AK3* | rna-L345\_02656.mrna | XM\_026717316.1 | ENSSMRT00000025474 | predict | XM\_032235316.1 | XM\_014068246.1 | predict | rna-EYD10\_14283 | XM\_035134679.1 |
| *EIF4EBP1* | rna-L345\_06274.mrna | XM\_026717229.1 | ENSSMRT00000033001 | predict | XM\_032228731.1 | XM\_014064710.1 | predict | rna-EYD10\_11459 | XM\_035140059.1 |
| *FBN1* | predict | XM\_026709584.1 | ENSSMRT00000033911 | ## | XM\_032232926.1 | ## | predict | predict | XM\_035132327.1 |
| *FGF4* | rna-L345\_04815.mrna | XM\_026704569.1 | ENSSMRT00000005831 | predict | XM\_032212980.1 | XM\_014066893.1 | predict | rna-EYD10\_02395 | XM\_035121451.1 |
| *FOXO1* | rna-L345\_03389.mrna | XM\_026710438.1 | ENSSMRT00000008497 | predict | XM\_032213476.1 | XM\_014061809.1 | predict | predict | XM\_035110210.1 |
| *FOXO3* | rna-L345\_01703.mrna | XM\_026726642.1 | ENSSMRT00000019967 | predict | XM\_032215089.1 | XM\_014075337.1 | predict | predict | XM\_035109282.1 |
| *FOXO4* | predict | XM\_026716645.1 | ENSSMRT00000005686 | predict | XM\_032227423.1 | predict | predict | predict | XM\_035112511.1 |
| *FOXO6* | rna-L345\_01312.mrna | predict | ENSSMRT00000004800 | predict | XM\_032228444.1 | XM\_014065696.1 | predict | predict | XM\_035117804.1 |
| *GALNS* | predict | XM\_026719758.1 | ENSSMRT00000010128 | predict | XM\_032230623.1 | XM\_014070409.1 | predict | predict | XM\_035117998.1 |
| *GDF1* | rna-L345\_00044.mrna | XM\_026698409.1 | ENSSMRT00000034866 | predict | XM\_032233810.1 | XM\_014059955.1 | predict | predict | XM\_035117887.1 |
| *GDF11* | predict | XM\_026711214.1 | ENSSMRT00000007307 | predict | XM\_032210714.1 | XM\_014068911.1 | predict | predict | XM\_035103919.1 |
| *GDF2* | predict | XM\_026720476.1 | ENSSMRT00000034560 | predict | XM\_032227040.1 | XM\_014053993.1 | predict | predict | XM\_035138168.1 |
| *GDF5* | rna-L345\_12290.mrna | XM\_026697325.1 | ENSSMRT00000004438 | predict | XM\_032218920.1 | XM\_014059299.1 | predict | predict | XM\_035122197.1 |
| *GDF6* | predict | XM\_026705937.1 | ENSSMRT00000010946 | predict | XM\_032222213.1 | XM\_014056065.1 | predict | predict | XM\_035126161.1 |
| *GDF7* | predict | XM\_026695354.1 | ENSSMRT00000006394 | predict | XM\_032214510.1 | predict | predict | predict | XM\_035110705.1 |
| *GDF9* | predict | XM\_026696116.1 | ENSSMRT00000027082 | predict | XM\_032212139.1 | XM\_014059657.1 | predict | predict | XM\_035105389.1 |
| *GHR* | predict | XM\_026716140.1 | ENSSMRT00000028543 | predict | XM\_032214232.1 | predict | predict | predict | XM\_035100739.1 |
| *GPC1* | predict | XM\_026701471.1 | ENSSMRT00000001920 | predict | XM\_032225564.1 | XM\_014065958.1 | predict | predict | XM\_035132470.1 |
| *GPC3* | predict | XM\_026716561.1 | ENSSMRT00000013187 | predict | XM\_032228556.1 | XM\_014069898.1 | predict | predict | predict |
| *GPC4* | predict | XM\_026716600.1 | ENSSMRT00000013182 | predict | predict | predict | predict | predict | XM\_035113664.1 |
| *GPC6* | predict | XM\_026708353.1 | ENSSMRT00000024494 | ## | XM\_032226094.1 | XM\_014058381.1 | predict | predict | XM\_035116476.1 |
| *GRB10* | rna-L345\_04201.mrna | XM\_026702339.1 | ENSSMRT00000014811 | predict | XM\_032237916.1 | XM\_014053612.1 | predict | predict | XM\_035137093.1 |
| *IGF1* | predict | XM\_026726539.1 | ENSSMRT00000024055 | predict | XM\_032221675.1 | predict | predict | predict | XM\_035128373.1 |
| *IGF2* | predict | XM\_026706561.1 | ENSSMRT00000021309 | predict | XM\_032221919.1 | XM\_014060943.1 | predict | predict | XM\_035121058.1 |
| *IGFBP1* | rna-L345\_14886.mrna | XM\_026702319.1 | ENSSMRT00000014515 | predict | XM\_032235413.1 | XM\_014069821.1 | predict | predict | XM\_035101383.1 |
| *IGFBP2* | predict | XM\_026707876.1 | ENSSMRT00000017396 | predict | XM\_032217081.1 | XM\_014074053.1 | predict | predict | XM\_035128175.1 |
| *IGFBP3* | rna-L345\_10695.mrna | XM\_026702321.1 | ENSSMRT00000014516 | predict | XM\_032237792.1 | XM\_014069824.1 | predict | rna-EYD10\_06181 | XM\_035101349.1 |
| *IGFBP4* | rna-L345\_05530.mrna | XM\_026722027.1 | ENSSMRT00000007850 | predict | XM\_032237890.1 | XM\_014073928.1 | predict | predict | XM\_035135458.1 |
| *IGFBP5* | predict | XM\_026708119.1 | ENSSMRT00000017394 | predict | XM\_032217093.1 | XM\_014076606.1 | predict | rna-EYD10\_11694 | XM\_035128162.1 |
| *IGFBP6* | predict | XM\_026713753.1 | ENSSMRT00000001846 | predict | XM\_032208882.1 | predict | predict | rna-EYD10\_13135 | predict |
| *IGFBP7* | predict | XM\_026723986.1 | ENSSMRT00000008739 | ## | XM\_032213057.1 | XM\_014062443.1 | predict | predict | XM\_035097398.1 |
| *INS* | predict | XM\_026706463.1 | ENSSMRT00000021310 | predict | XM\_032231439.1 | XM\_014064016.1 | predict | predict | XM\_035123834.1 |
| *INSL5* | predict | XM\_026700106.1 | ENSSMRT00000030239 | predict | XM\_032217265.1 | predict | predict | predict | XM\_035124201.1 |
| *IRS1* | predict | XM\_026701523.1 | ENSSMRT00000013277 | predict | XM\_032226024.1 | XM\_014057705.1 | predict | rna-EYD10\_10430 | XM\_035132694.1 |
| *IRS2* | predict | XM\_026707602.1 | ENSSMRT00000031945 | predict | XM\_032212708.1 | XM\_014070428.1 | predict | ## | XM\_035110389.1 |
| *IRS4* | ## | XM\_026703079.1 | ENSSMRT00000018321 | predict | XM\_032228395.1 | XM\_014065894.1 | predict | rna-EYD10\_08989 | predict |
| *KCNJ2* | predict | XM\_026701714.1 | ENSSMRT00000007385 | predict | XM\_032208525.1 | XM\_014065586.1 | predict | rna-EYD10\_16853 | XM\_035104075.1 |
| *LCORL* | ## | XM\_026699727.1 | ENSSMRT00000001350 | predict | XM\_032223898.1 | XM\_014069348.1 | predict | rna-EYD10\_05837 | XM\_035111647.1 |
| *LEPR* | rna-L345\_03808.mrna | predict | ENSSMRT00000030231 | predict | XM\_032217812.1 | XM\_014069825.1 | predict | predict | XM\_035122208.1 |
| *MSTN* | predict | XM\_026696903.1 | ENSSMRT00000030059 | predict | XM\_032223334.1 | XM\_014059699.1 | predict | predict | XM\_035136086.1 |
| *mTOR* | predict | XM\_026715849.1 | ENSSMRT00000023583 | ## | XM\_032231592.1 | XM\_014065414.1 | predict | rna-EYD10\_14004 | XM\_035117075.1 |
| *NOG* | rna-L345\_03161.mrna | XM\_026711222.1 | ENSSMRT00000032834 | predict | XM\_032210790.1 | XM\_014054379.1 | predict | predict | XM\_035107943.1 |
| *NPC1* | predict | XM\_026699294.1 | ENSSMRT00000018393 | predict | XM\_032223324.1 | XM\_014065522.1 | predict | predict | XM\_035125433.1 |
| *NPC2* | rna-L345\_04407.mrna | XM\_026711704.1 | ENSSMRT00000018954 | predict | XM\_032231461.1 | XM\_014057149.1 | predict | rna-EYD10\_02742 | XM\_035108573.1 |
| *NPR2* | rna-L345\_15815.mrna | XM\_026720789.1 | ENSSMRT00000030478 | predict | XM\_032212969.1 | predict | predict | rna-EYD10\_13433 | XM\_035100577.1 |
| *NSD1* | predict | XM\_026726392.1 | ENSSMRT00000010328 | predict | XM\_032211073.1 | XM\_014056171.1 | predict | rna-EYD10\_04240 | XM\_035105840.1 |
| *NSD2* | predict | XM\_026720448.1 | ENSSMRT00000034572 | predict | XM\_032226986.1 | predict | predict | predict | XM\_035137433.1 |
| *NSD3* | predict | XM\_026714982.1 | ENSSMRT00000028930 | predict | XM\_032228808.1 | XM\_014068293.1 | predict | predict | predict |
| *OBSL1* | predict | XM\_026708086.1 | predict | predict | XM\_032211909.1 | predict | predict | predict | XR\_004693285.1 |
| *PLAG1* | predict | XM\_026706187.1 | ENSSMRT00000015428 | predict | XM\_032222814.1 | XM\_014055649.1 | predict | rna-EYD10\_07703 | XM\_035125311.1 |
| *PLAGL2* | rna-L345\_16386.mrna | XM\_026722770.1 | ENSSMRT00000029571 | predict | XM\_032217401.1 | XM\_014074591.1 | predict | rna-EYD10\_05264 | XM\_035122822.1 |
| *PRKG2* | predict | XM\_026718908.1 | ENSSMRT00000019352 | predict | XM\_032224665.1 | XM\_014064915.1 | predict | predict | XM\_035112345.1 |
| *RLN3* | predict | XM\_026711562.1 | ENSSMRT00000025698 | predict | XM\_032208501.1 | predict | predict | predict | XM\_035141119.1 |
| *SH2B1* | rna-L345\_05653.mrna | XM\_026711837.1 | ENSSMRT00000006129 | predict | XM\_032235795.1 | predict | predict | rna-EYD10\_14592 | XM\_035136148.1 |
| *SH2B2* | predict | XM\_026708714.1 | ENSSMRT00000026991 | predict | XM\_032216392.1 | XM\_014075246.1 | predict | predict | XM\_035139936.1 |
| *SH2B3* | predict | XM\_026719359.1 | ENSSMRT00000013574 | predict | predict | predict | predict | predict | XM\_035120442.1 |
| *SMO* | predict | XM\_026722695.1 | predict | predict | XM\_032238800.1 | predict | predict | rna-EYD10\_00804 | XM\_035128625.1 |
| *SOX1* | ## | XM\_026708346.1 | ENSSMRT00000000855 | predict | XM\_032226656.1 | XM\_014066071.1 | predict | predict | XM\_035115911.1 |
| *SOX10* | rna-L345\_03015.mrna | XM\_026696098.1 | ENSSMRT00000023614 | predict | XM\_032221374.1 | XM\_014054960.1 | predict | predict | XM\_035128227.1 |
| *SOX11* | predict | XM\_026726518.1 | ENSSMRT00000009475 | predict | XM\_032214443.1 | XM\_014054087.1 | predict | predict | XM\_035109893.1 |
| *SOX12* | rna-L345\_14270.mrna | XM\_026725993.1 | ## | predict | XM\_032218981.1 | XM\_014070260.1 | predict | predict | XM\_035123490.1 |
| *SOX13* | predict | XM\_026715572.1 | ENSSMRT00000004343 | predict | XM\_032217658.1 | XM\_014076248.1 | predict | rna-EYD10\_01560 | XM\_035122774.1 |
| *SOX14* | predict | XM\_026701110.1 | ENSSMRT00000033564 | predict | XM\_032225565.1 | XM\_014071056.1 | predict | predict | XM\_035133606.1 |
| *SOX17* | rna-L345\_00910.mrna | XM\_026699190.1 | ENSSMRT00000015766 | predict | XM\_032222368.1 | XM\_014052941.1 | predict | predict | XM\_035125661.1 |
| *SOX18* | predict | XM\_026697763.1 | ENSSMRT00000028923 | predict | XM\_032218519.1 | predict | predict | rna-EYD10\_05307 | XM\_035122067.1 |
| *SOX2* | ## | XM\_026705716.1 | predict | predict | XM\_032225520.1 | XM\_014074915.1 | predict | predict | XM\_035132629.1 |
| *SOX21* | ## | XM\_026708391.1 | ENSSMRT00000024500 | ## | XM\_032226136.1 | predict | predict | predict | XM\_035116213.1 |
| *SOX3* | ## | XM\_026716606.1 | predict | predict | XM\_032238808.1 | XM\_014074551.1 | predict | rna-EYD10\_08828 | XM\_035125760.1 |
| *SOX30* | rna-L345\_09468.mrna | XM\_026696675.1 | ENSSMRT00000026655 | predict | XM\_032209232.1 | XM\_014070368.1 | predict | rna-EYD10\_04209 | XM\_035105758.1 |
| *SOX4* | predict | XM\_026699521.1 | ENSSMRT00000007416 | predict | XM\_032223212.1 | XM\_014057900.1 | predict | predict | XM\_035125354.1 |
| *SOX5* | predict | XM\_026710562.1 | ENSSMRT00000009838 | predict | XM\_032221305.1 | predict | predict | predict | XM\_035127879.1 |
| *SOX6* | predict | XM\_026706494.1 | ENSSMRT00000022512 | ## | XM\_032222712.1 | XM\_014058034.1 | predict | ## | XM\_035120083.1 |
| *SOX7* | predict | XM\_026715914.1 | ENSSMRT00000018410 | predict | XM\_032215987.1 | XM\_014054833.1 | predict | predict | XM\_035110869.1 |
| *SOX8* | predict | predict | ENSSMRT00000025559 | predict | XM\_032230930.1 | XM\_014074088.1 | predict | rna-EYD10\_15819 | XM\_035131990.1 |
| *SOX9* | rna-L345\_08850.mrna | XM\_026701718.1 | ENSSMRT00000007373 | predict | XM\_032209950.1 | XM\_014075535.1 | predict | rna-EYD10\_16856 | XM\_035104079.1 |

**TABLE | S2** Body size and genome assembly number of 28 species in squamates.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Species | Sub-order | Family | Max length (mm) | Length measure | Max mass (g) | Genome assembly number |
| *Pogona vitticeps* | Sauria | Agamidae | 250 | SVL | 574.92 | GCF\_900067755.1 |
| *Anolis carolinensis* | Sauria | Dactyloidae | 75 | SVL | 8.76 | GCF\_000090745.1 |
| *Eublepharis macularius* | Sauria | Eublepharidae | 170 | SVL | 114.58 | SRA45106 |
| *Hemiphyllodactylus yunnanensis* | Sauria | Gekkonidae | 54 | SVL | 3.48 | This study |
| *Gekko japonicus* | Sauria | Gekkonidae | 84.8 | SVL | 12.09 | This study |
| *Paroedura picta* | Sauria | Gekkonidae | 92.4 | SVL | 15.32 | GCA\_003118565.1 |
| *Zootoca vivipara* | Sauria | Lacertidae | 77 | SVL | 10.57 | GCF\_011800845.1 |
| *Podarcis muralis* | Sauria | Lacertidae | 78 | SVL | 10.98 | GCF\_004329235.1 |
| *Lacerta agilis* | Sauria | Lacertidae | 114 | SVL | 33.65 | GCF\_009819535.1 |
| *Shinisaurus crocodilurus* | Sauria | Shinisauridae | 197 | SVL | 143.91 | SRP093345 |
| *Salvator merianae* | Sauria | Teiidae | 501 | SVL | 4461.65 | GCA\_003586115.2 |
| *Varanus komodoensis* | Sauria | Varanidae | 1570 | SVL | 102477.74 | GCA\_004798865.1 |
| *Pantherophis guttatus* | Serpentes | Colubridae | 1830 | TL | 543.70 | GCF\_001185365.1 |
| *Pantherophis obsoletus* | Serpentes | Colubridae | 2565 | TL | 1281.36 | GCA\_012654085.1 |
| *Ptyas mucosa* | Serpentes | Colubridae | 3700 | TL | 3248.36 | GCA\_012654045.1 |
| *Thamnophis elegans* | Serpentes | Colubridae | 1090 | TL | 377.24 | GCF\_009769535.1 |
| *Thamnophis sirtalis* | Serpentes | Colubridae | 1400 | TL | 862.30 | GCF\_001077635.1 |
| *Thermophis baileyi* | Serpentes | Colubridae | 749 | TL | 138.85 | GCA\_003457575.1 |
| *Hydrophis melanocephalus* | Serpentes | Elapidae | 1230 | TL | 415.34 | GCA\_004320005.1 |
| *Laticauda laticaudata* | Serpentes | Elapidae | 1100 | TL | 317.42 | GCA\_004320025.1 |
| *Naja naja* | Serpentes | Elapidae | 2200 | TL | 1683.49 | GCA\_009733165.1 |
| *Notechis scutatus* | Serpentes | Elapidae | 2000 | TL | 1338.38 | GCF\_900518725.1 |
| *Ophiophagus hannah* | Serpentes | Elapidae | 5850 | TL | 17723.28 | GCA\_000516915.1 |
| *Pseudonaja textilis* | Serpentes | Elapidae | 2200 | TL | 1683.49 | GCF\_900518735.1 |
| *Python bivittatus* | Serpentes | Pythonidae | 9200 | TL | 197681.18 | GCF\_000186305.1 |
| *Crotalus tigris* | Serpentes | Viperidae | 910 | TL | 396.11 | GCF\_016545835.1 |
| *Protobothrops flavoviridis* | Serpentes | Viperidae | 2400 | TL | 6659.09 | GCA\_003402635.1 |
| *Protobothrops mucrosquamatus* | Serpentes | Viperidae | 1280 | TL | 1069.01 | GCF\_001527695.2 |

**TABLE | S3** Foreground branches of 28 squamate species used by branch-site model in the study.

|  |  |
| --- | --- |
| Dataset | Foreground branches |
| Sauria | The unified terminal branch of *S. merianae* and *V. komodoensis* |
| The terminal branch of *H. yunnanensis* |
| The terminal branch of *S. merianae* |
| The terminal branch of *V. komodoensis* |
| The ancestral branch of *P. muralis* and *L. agilis* (Lacertidae) |
| The ancestral branch of *P. picta* and *H. yunnanensis* (Gekkonidae) |
| Serpentes | The unified terminal branch of *N. naja* and *O. hannah* |
| The terminal branch of *N. naja* |
| The terminal branch of *O. hannah* |
| The terminal branch of *T. baileyi* |
| The ancestral branch of *P. obsoletus* and *P. guttatus* |
| The ancestral branch of *P. flavoviridis* and *P. mucrosquamatus* |
| The ancestral branch *T. elegans* and *T. sirtalis* |

**TABLE | S4** The microhabitat data of 28 squamate species in the study.

|  |  |  |  |
| --- | --- | --- | --- |
| Sauria | Microhabitat（logit transformation） | Serpentes | Microhabitat（logit transformation） |
| *Anolis carolinensis* | arboreal (2) | *Crotalus tigris* | terrestrial (1) |
| *Eublepharis macularius* | terrestrial (1) | *Hydrophis melanocephalus* | aquatic (3) |
| *Gekko japonicus* | terrestrial (1) | *Laticauda laticaudata* | aquatic (3) |
| *Lacerta agilis* | terrestrial (1) | *Notechis scutatus* | semi-arboreal (2) |
| *Paroedura picta* | terrestrial (1) | *Ophiophagus hannah* | terrestrial (1) |
| *Podarcis muralis* | semi-arboreal (3) | *Pantherophis guttatus* | semi-fossorial (5) |
| *Pogona vitticeps* | semi-arboreal (3) | *Pantherophis obsoletus* | semi-arboreal (2) |
| *Shinisaurus crocodilurus* | semi-aquatic (4) | *Naja naja* | semi-arboreal (2) |
| *Varanus komodoensis* | terrestrial (1) | *Pseudonaja textilis* | terrestrial (1) |
| *Zootoca vivipara* | terrestrial (1) | *Ptyas mucosa* | semi-arboreal (2) |
| *Salvator merianae* | terrestrial (1) | *Protobothrops mucrosquamatus* | terrestrial (1) |
| *Hemiphyllodactylus yunnanensis* | arboreal (2) | *Protobothrops flavoviridis* | terrestrial (1) |
|  |  | *Python bivittatus* | semi-fossorial (5) |
|  |  | *Thamnophis elegans* | terrestrial (1) |
|  |  | *Thamnophis sirtalis* | terrestrial (1) |
|  |  | *Thermophis baileyi* | semi-aquatic (4) |

**TABLE | S5** The climatic niche of 28 squamate species in the study.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Dataset | Species | Climatic-niche PC1 | Climatic-niche PC2 | Climatic-niche PC3 | Bio12 |
| Sauria | *Anolis carolinensis* | -0.2754 | -2.6360 | -0.4592 | 1278.00 |
| *Lacerta agilis* | 3.1150 | -7.0800 | 3.3042 | 508.12 |
| *Paroedura picta* | 1.6049 | 1.3969 | -0.4684 | 766.72 |
| *Podarcis muralis* | 0.7596 | -4.8873 | 1.9312 | 814.72 |
| *Salvator merianae* | -1.2379 | 0.5561 | -0.1846 | 1725.23 |
| *Zootoca vivipara* | 3.3863 | -7.9118 | 4.5940 | 578.95 |
| Serpentes | *Crotalus tigris* | 2.9310 | -0.5814 | -1.7904 | 361.65 |
| *Hydrophis melanocephalus* | -0.4445 | 1.1109 | 0.2799 | 1751.27 |
| *Laticauda laticaudata* | -3.8624 | 1.9024 | -0.0710 | 2445.59 |
| *Notechis scutatus* | -0.0183 | -3.2883 | 1.6963 | 915.85 |
| *Ophiophagus hannah* | -1.7197 | 1.6168 | 0.5990 | 2105.79 |
| *Pantherophis guttatus* | -0.4555 | -2.9104 | -0.0569 | 1335.52 |
| *Pantherophis obsoletus* | 0.6624 | -3.9619 | 0.5161 | 1118.33 |
| *Protobothrops mucrosquamatus* | 1.5896 | -1.1867 | 1.5764 | 1305.39 |
| *Thamnophis elegans* | 2.6660 | -5.8431 | 2.5364 | 503.87 |
| *Thamnophis sirtalis* | 2.1879 | -6.0852 | 2.7780 | 814.35 |
| *Thermophis baileyi* | 4.0501 | -6.3941 | 6.3743 | 291.67 |

**TABLE | S6** The ecoregion distribution of 28 squamate species in the study.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Species | Ecoregions | | | | | | | | | | | | |
| tropical South America | temperate South America | tropical middle America | the West Indies | Nearctic | Afro-tropical | Madagascar | western Palaearctic | eastern Palaearctic | south Asia | southeast Asia | Oceania | Total number |
| *Anolis\_carolinensis* |  |  |  |  | 1 |  |  |  |  |  |  |  | 1 |
| *Eublepharis\_macularius* |  |  |  |  |  |  |  |  | 1 | 1 |  |  | 2 |
| *Gekko\_japonicus* |  |  |  |  |  |  |  |  | 1 |  | 1 |  | 2 |
| *Hemiphyllodactylus\_yunnanensis* |  |  |  |  |  |  |  |  |  |  | 1 |  | 1 |
| *Lacerta\_agilis* |  |  |  |  |  |  |  | 1 | 1 |  |  |  | 2 |
| *Paroedura\_picta* |  |  |  |  |  |  | 1 |  | 1 |  | 1 |  | 3 |
| *Podarcis\_muralis* |  |  |  |  |  |  |  | 1 |  |  |  |  | 1 |
| *Pogona\_vitticeps* |  |  |  |  |  |  |  |  |  |  |  | 1 | 1 |
| *Salvator\_merianae* | 1 | 1 |  |  |  |  |  |  |  |  |  |  | 2 |
| *Shinisaurus\_crocodilurus* |  |  |  |  |  |  |  |  |  |  | 1 |  | 1 |
| *Varanus\_komodoensis* |  |  |  |  |  |  |  |  |  |  | 1 |  | 1 |
| *Zootoca\_vivipara* |  |  |  |  |  |  |  | 1 | 1 |  |  |  | 2 |
| *Crotalus\_tigris* |  |  |  |  | 1 |  |  |  |  |  |  |  | 1 |
| *Hydrophis\_melanocephalus* |  |  |  |  |  |  |  |  | 1 |  | 1 |  | 2 |
| *Laticauda\_laticaudata* |  |  |  |  |  |  |  |  | 1 | 1 | 1 | 1 | 4 |
| *Naja\_naja* |  |  |  |  |  |  |  |  |  | 1 | 1 |  | 2 |
| *Notechis\_scutatus* |  |  |  |  |  |  |  |  |  |  | 1 |  | 1 |
| *Ophiophagus\_hannah* |  |  |  |  |  |  |  |  | 1 | 1 | 1 |  | 3 |
| *Pantherophis\_guttatus* |  |  |  |  | 1 |  |  |  |  |  |  |  | 1 |
| *Pantherophis\_obsoletus* |  |  |  |  | 1 |  |  |  |  |  |  |  | 1 |
| *Protobothrops\_flavoviridis* |  |  |  |  |  |  |  |  | 1 |  |  |  | 1 |
| *Protobothrops\_mucrosquamatus* |  |  |  |  |  |  |  |  | 1 | 1 | 1 |  | 3 |
| *Pseudonaja\_textilis* |  |  |  |  |  |  |  |  |  |  | 1 |  | 1 |
| *Ptyas\_mucosa* |  |  |  |  |  |  |  |  | 1 | 1 | 1 |  | 3 |
| *Python\_bivittatus* |  |  |  |  |  |  |  |  |  | 1 | 1 |  | 2 |
| *Thamnophis\_elegans* |  |  |  |  | 1 |  |  |  |  |  |  |  | 1 |
| *Thamnophis\_sirtalis* |  |  |  |  | 1 |  |  |  |  |  |  |  | 1 |
| *Thermophis\_baileyi* |  |  |  |  |  |  |  |  | 1 |  |  |  | 1 |

**TABLE | S7** M0 models analyses in lizards and snakes.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genes | Sauria | | Serpentes | |
| lnL | ω value | lnL | ω value |
| *ACAN* | -16038.60 | 0.1945 | -10699.01 | 0.4107 |
| *ADAMTS10* | -8375.37 | 0.0503 | -6395.23 | 0.1899 |
| *ADIPOR1* | -3422.26 | 0.0091 | -3227.87 | 0.0062 |
| *ADIPOR2* | -4152.91 | 0.1311 | -2930.82 | 0.2134 |
| *AIP* | -3621.46 | 0.0614 | -2219.94 | 0.1112 |
| *AKT1* | -4132.10 | 0.0133 | -1879.22 | 0.0148 |
| *AKT2* | -5166.75 | 0.0118 | -2530.24 | 0.0369 |
| *AKT3* | -1607.84 | 0.0928 | -1495.98 | 0.0049 |
| *BMP1* | -8333.86 | 0.0477 | -949.97 | 0.1428 |
| *BMP10* | -5021.98 | 0.1587 | -4374.99 | 0.1404 |
| *BMP15* | -5010.28 | 0.1831 | -3298.27 | 0.1776 |
| *BMP2* | -5397.85 | 0.1102 | -2716.68 | 0.2038 |
| *BMP3* | -3789.44 | 0.1128 | -3363.95 | 0.1692 |
| *BMP4* | -2372.66 | 0.0395 | -2558.09 | 0.1600 |
| *BMP5* | -2450.20 | 0.0338 | -794.34 | 0.1853 |
| *BMP6* | -2263.88 | 0.0935 | -2020.67 | 0.1620 |
| *BMP7* | -2581.31 | 0.0391 | -2051.57 | 0.0595 |
| *CCNB1* | -5125.38 | 0.2089 | -2874.95 | 0.1783 |
| *CCNB3* | -5160.17 | 0.1694 | -3072.10 | 0.1131 |
| *CDKN1A* | -2402.07 | 0.2481 | -1305.04 | 0.2798 |
| *CDKN1B* | -2450.81 | 0.1700 | -628.08 | 0.4742 |
| *CDKN1C* | -1644.94 | 0.1007 | -863.00 | 0.1402 |
| *CDKN2C* | -2208.49 | 0.1382 | -1145.59 | 0.0626 |
| *CDKN2D* | -2371.19 | 0.1075 | -969.25 | 0.1340 |
| *CNP* | -5726.73 | 0.0896 | -3032.99 | 0.1739 |
| *COL10A1* | -7558.01 | 0.2021 | -5973.96 | 0.3379 |
| *EIF2AK3* | -7605.08 | 0.1120 | -6218.48 | 0.1961 |
| *EIF4EBP1* | -776.02 | 0.0893 | -705.40 | 0.3070 |
| *FBN1* | -27265.68 | 0.0617 | -16264.21 | 0.1233 |
| *FGF4* | -1415.08 | 0.0821 | -1077.40 | 0.0998 |
| *FOXO1* | -5784.79 | 0.1369 | -3345.65 | 0.1281 |
| *FOXO3* | -4567.88 | 0.0583 | -2860.23 | 0.0605 |
| *FOXO4* | -5308.21 | 0.1760 | -3841.07 | 0.0871 |
| *FOXO6* | -5293.20 | 0.0464 | -3509.27 | 0.0676 |
| *GALNS* | -6406.63 | 0.1051 | -2908.53 | 0.2207 |
| *GDF1* | -3708.78 | 0.0822 | -2538.02 | 0.1913 |
| *GDF11* | -1740.96 | 0.0023 | -1348.05 | 0.0121 |
| *GDF2* | -5484.30 | 0.2640 | -3726.64 | 0.3002 |
| *GDF5* | -2619.88 | 0.0374 | -609.53 | 0.3464 |
| *GDF6* | -2947.08 | 0.2025 | -1672.04 | 0.0610 |
| *GDF7* | -1085.21 | 0.0853 | -2224.35 | 0.1692 |
| *GDF9* | -6298.64 | 0.3201 | -3609.53 | 0.4389 |
| *GHR* | -9479.77 | 0.2826 | -5062.76 | 0.4490 |
| *GPC1* | -3762.13 | 0.1062 | -2828.16 | 0.1610 |
| *GPC3* | -2197.61 | 0.1976 | -2306.58 | 0.0977 |
| *GPC4* | -5302.31 | 0.0928 | -3095.81 | 0.0859 |
| *GPC6* | -3551.87 | 0.1393 | -563.16 | 0.4932 |
| *GRB10* | -4739.50 | 0.0825 | -2727.17 | 0.2121 |
| *IGF1* | -990.08 | 0.2544 | -558.23 | 0.4183 |
| *IGF2* | -2901.95 | 0.1687 | -1732.02 | 0.1205 |
| *IGFBP1* | -1463.92 | 0.3395 | -1783.14 | 0.4287 |
| *IGFBP2* | -2016.31 | 0.1546 | -710.44 | 0.1244 |
| *IGFBP3* | -1052.89 | 0.1214 | -889.52 | 0.2273 |
| *IGFBP4* | -596.76 | 0.2542 | -302.87 | 0.1380 |
| *IGFBP5* | -1301.73 | 0.0354 | -659.74 | 0.0710 |
| *IGFBP6* | -1862.96 | 0.1614 | -553.36 | 0.2972 |
| *IGFBP7* | -792.74 | 0.1344 | -653.07 | 0.3110 |
| *INS* | -1537.03 | 0.4255 | -814.49 | 0.3210 |
| *INSL5* | -2186.35 | 0.4089 | -1074.83 | 0.4910 |
| *IRS1* | -14068.88 | 0.1053 | -8306.61 | 0.1391 |
| *IRS2* | -10310.99 | 0.2288 | -7345.59 | 0.3389 |
| *IRS4* | -6293.53 | 0.0671 | -7577.01 | 0.0998 |
| *KCNJ2* | -4076.89 | 0.0356 | -2880.26 | 0.0479 |
| *LCORL* | -21645.07 | 0.3482 | -13199.10 | 0.4820 |
| *LEPR* | -9676.03 | 0.3445 | -1575.17 | 0.2751 |
| *MSTN* | -3686.32 | 0.0331 | -2327.11 | 0.1007 |
| *mTOR* | -24144.08 | 0.0120 | -8197.26 | 0.0136 |
| *NOG* | -1412.11 | 0.0327 | -1654.33 | 0.0637 |
| *NPC1* | -14993.56 | 0.1560 | -10791.36 | 0.3729 |
| *NPC2* | -2497.47 | 0.2393 | -1568.32 | 0.7590 |
| *NPR2* | -5192.56 | 0.0419 | -5133.28 | 0.0471 |
| *NSD1* | -8253.15 | 0.4263 | -6972.54 | 0.2618 |
| *NSD2* | -12181.26 | 0.1112 | -8325.89 | 0.0854 |
| *NSD3* | -14253.00 | 0.0674 | -2375.68 | 0.0772 |
| *OBSL1* | -12901.91 | 0.2025 | -1167.34 | 0.3010 |
| *PLAG1* | -3599.71 | 0.0652 | -2713.43 | 0.0958 |
| *PLAGL2* | -5857.16 | 0.0522 | -3213.06 | 0.0373 |
| *PRKG2* | -8378.40 | 0.0617 | -1344.55 | 0.1134 |
| *RLN3* | -2292.70 | 0.1663 | -1221.28 | 0.5123 |
| *SH2B1* | -6117.89 | 0.0434 | -3550.15 | 0.1490 |
| *SH2B2* | -4539.03 | 0.0510 | -2372.83 | 0.1060 |
| *SH2B3* | -6688.80 | 0.1865 | -2367.63 | 0.2376 |
| *SMO* | -6507.27 | 0.0633 | -822.80 | 0.1912 |
| *SOX1* | -312.50 | 0.0087 | -985.65 | 0.0523 |
| *SOX10* | -3389.96 | 0.0463 | -2226.13 | 0.0490 |
| *SOX11* | -4268.79 | 0.0586 | -1033.32 | 0.0500 |
| *SOX12* | -4098.75 | 0.0764 | -2400.75 | 0.0734 |
| *SOX13* | -5504.55 | 0.1327 | -2871.07 | 0.1141 |
| *SOX14* | -1365.11 | 0.0215 | -1208.05 | 0.0819 |
| *SOX17* | -2601.46 | 0.0568 | -884.87 | 0.1209 |
| *SOX18* | -3972.69 | 0.0591 | -1580.06 | 0.0646 |
| *SOX2* | -1815.14 | 0.0523 | -695.57 | 0.0170 |
| *SOX21* | -1524.05 | 0.0402 | -801.40 | 0.0089 |
| *SOX3* | -2618.44 | 0.0301 | -2531.73 | 0.0300 |
| *SOX30* | -3924.55 | 0.1412 | -3826.61 | 0.1670 |
| *SOX4* | -3298.52 | 0.0384 | -894.10 | 0.0049 |
| *SOX5* | -2582.24 | 0.0627 | -793.45 | 0.0706 |
| *SOX6* | -4998.76 | 0.0503 | -975.20 | 0.0613 |
| *SOX7* | -4631.98 | 0.1227 | -2105.89 | 0.1869 |
| *SOX8* | -5268.62 | 0.0459 | -2175.90 | 0.0618 |
| *SOX9* | -4571.05 | 0.0255 | -2325.43 | 0.0550 |

**TABLE | S8** Genes and sites detected to be under positive selection by site model in lizards.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Genes | Models | lnL | 2ΔlnL | df | *p* value | Positively selected sites (PP > 0.8) |
| *CDKN1B* | M8 | -2485.62 | 7.21 | 1 | 0.007 | 96R0.939, 102K0.982 |
| M8a | -2489.22 |
| *CDKN2C* | M8 | -2138.27 | 4.33 | 1 | 0.038 | Not allowed |
| M8a | -2140.43 |
| *COL10A1* | M8 | -7389.52 | 5.08 | 1 | 0.024 | 75L0.812, 84F0.904, 109A0.978, 137A0.973, 236H0.943, 274L0.831, 352F0.836, 368S0.990 |
| M8a | -7392.06 |
| *GHR* | M8 | -9310.40 | 6.70 | 1 | 0.010 | 163D0.932 |
| M8a | -9313.75 |
| *GRB10* | M8 | -4690.25 | 6.49 | 1 | 0.010 | 1H0.946, 2S0.877, 7S0.907, 9L0.855, 11A0.846, 13S0.932, 14S0.860, 15L0.914, 19S0.879, 21Q0.802, 22Q0.830, 31H0.959, 33L0.898, 34A0.898, 35V0.852, 36N0.963, 38T0.835, 41P0.823, 42V0.897, 47V0.856, 53T0.856, 55V0.853, 59C0.924, 73S0.916, 78L0.947, 80T0.923 |
| M8a | -4693.50 |
| *NPC1* | M8 | -14675.79 | 12.75 | 1 | 0.000 | 56H0.880, 105E0.962, 108I0.931, 431D0.926, 515V0.831, 908G0.937 |
| M8a | -14682.17 |
| *NSD1* | M8 | -8168.20 | 5.14 | 1 | 0.023 | 6G0.818, 13Y0.909, 97T0.807 |
| M8a | -8170.77 |
| *OBSL1* | M8 | -12636.89 | 22.05 | 1 | 0.000 | 299C0.904, 311Q0.969, 320A0.931, 340L0.967, 390R0.948, 428K0.833, 443S0.895, 520T0.904, 602V0.807, 779H0.825, 784H0.995 |
| M8a | -12647.92 |
| *SOX14* | M8 | -1336.04 | 3.99 | 1 | 0.046 | 113G0.980 |
| M8a | -1338.03 |

**TABLE | S9** Genes and sites detected to be under positive selection by site model in snakes.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Genes | M8\_lnL | M8a\_lnL | 2ΔlnL | df | *p* value | Positively selected sites (PP > 0.8) |
| *AKT1* | -1861.58 | -1865.12 | 7.09 | 1 | 0.008 | 55N0.975 |
| *BMP2* | -2692.67 | -2696.76 | 8.2 | 1 | 0.004 | 149Q0.980, 207V0.867 |
| *BMP4* | -2517.68 | -2521.51 | 7.67 | 1 | 0.006 | 103N0.991, 108V0.991, 109A0.867, 110T0.911, 112M0.964, 184T0.971 |
| *BMP6* | -1995.54 | -1998.38 | 5.68 | 1 | 0.017 | 7L0.975, 271C0.959 |
| *CNP* | -3004.05 | -3012.71 | 17.32 | 1 | 0.000 | 27R0.972, 180N0.997, 210P0.884, 354L0.973 |
| *COL10A1* | -5907.87 | -5915.6 | 15.46 | 1 | 0.000 | 75L0.813, 84F0.906, 109A0.979, 137A0.974, 236H0.944, 274L0.833, 352F0.838, 368S0.991 |
| *GDF9* | -3568.27 | -3571.21 | 5.88 | 1 | 0.015 | 3N0.919, 85I0.959, 308R0.932 |
| *GHR* | -5021.69 | -5027.27 | 11.15 | 1 | 0.001 | 3E0.914, 24I0.939, 48H0.915, 82T0.947, 92D0.988, 143I0.805 |
| *GPC3* | -2292.44 | -2294.48 | 4.07 | 1 | 0.044 | 216I0.843 |
| *GPC6* | -345.06 | -351.01 | 5.95 | 1 | 0.000 | 10S0.973, 21M1.000 |
| *IGF1* | -549.53 | -551.78 | 4.5 | 1 | 0.034 | Not allowed |
| *IGFBP4* | -294.33 | -296.57 | 4.47 | 1 | 0.035 | 28Q0.990 |
| *IRS2* | -7312.3 | -7316.28 | 7.97 | 1 | 0.005 | 835E0.932 |
| *IRS4* | -7537.29 | -7545.5 | 16.43 | 1 | 0.000 | 6V0.886, 466P0.826, 982D0.996 |
| *LCORL* | -13155.1 | -13158.3 | 6.44 | 1 | 0.011 | 262P0.836, 279Q0.908, 299G0.868, 330N0.817, 1169T0.808, 1497A0.886 |
| *NPC1* | -10618.6 | -10644.3 | 51.34 | 1 | 0.000 | 13E0.990, 67N0.846, 111Q0.999, 162V0.868, 182A0.957, 186M0.874, 212V0.905, 403S0.948, 406L0.992, 476V0.971, 479H0.985, 480H0.970, 482G0.803, 488Y0.809, 513D0.990, 604H0.995, 786R0.956, 906D0.967 |
| *NPC2* | -1533.06 | -1541.32 | 16.52 | 1 | 0.000 | 24F0.973, 38I0.937, 43G0.994, 44L0.985, 52V0.990, 74Y0.801, 77I0.931, 79H0.993, 82I0.906, 101H0.996, 102N0.890, 130S0.844, 134Q0.849, 136L0.930, 148S0.975 |
| *RLN3* | -1196.58 | -1207.75 | 22.34 | 1 | 0.000 | 55N1.000, 56L1.000 |
| *SH2B3* | -2329.91 | -2333.49 | 7.16 | 1 | 0.007 | 5A0.940, 116K0.927, 119T0.825, 120R0.879, 122C0.933, 123T0.910, 127M0.830, 132Q0.933, 134A0.801, 138H0.910 |
| *SOX13* | -2852.22 | -2854.55 | 4.66 | 1 | 0.031 | 157S0.982, 167S0.898, 373G0.905 |
| *SOX17* | -875.49 | -877.41 | 3.86 | 1 | 0.050 | 98W0.974 |

**TABLE | S10** Genes detected to be under disruptive selection by clade model (the terminal branches of large-bodied species as unified foreground branch).

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Dataset | Genes | Cmc\_lnL | M2a\_lnL | Background ω | Foreground ω | *p*-value | q-value |
| Sauria | *CCNB3* | -5098.24 | -5073.61 | 1.9084 | 17.2231 | 0.0000 | 0.0000 |
| *CDKN2C* | -2146.95 | -2139.45 | 2.9476 | 14.8311 | 0.0001 | 0.0002 |
| *COL10A1* | -7399.61 | -7391.29 | 2.6853 | 3.7175 | 4.52E-05 | 9.31E-05 |
| *FOXO1* | -5753.77 | -5726.95 | 0.0000 | 1.1060 | 0.0000 | 0.0000 |
| *GPC3* | -2135.61 | -2121.62 | 0.9703 | 3.6622 | 1.22E-07 | 3.16E-07 |
| *GPC4* | -5190.49 | -5168.04 | 0.0000 | 1.7686 | 0.0000 | 0.0000 |
| *GRB10* | -4704.49 | -4693.18 | 4.1646 | 11.9844 | 1.99E-06 | 4.77E-06 |
| *IGF1* | -964.91 | -979.11 | 0.0070 | 1.2753 | 9.90E-08 | 2.70E-07 |
| *INSL5* | -2156.04 | -2158.86 | 0.3829 | 1.0273 | 0.0174 | 0.0289 |
| *LEPR* | -9576.71 | -9615.74 | 0.1204 | 1.5212 | 0.0000 | 0.0000 |
| *mTOR* | -24072.60 | -24021.00 | 41.7790 | 52.4429 | 0.0000 | 0.0000 |
| *NSD3* | -14080.60 | -14075.90 | 4.4750 | 43.2900 | 0.0022 | 0.0040 |
| *OBSL1* | -12669.00 | -12644.70 | 3.1211 | 32.6249 | 0.0000 | 0.0000 |
| *SOX21* | -1501.91 | -1487.86 | 0.3450 | 2.4427 | 1.15E-07 | 3.06E-07 |
| Serpentes | *AKT1* | -1860.48 | -1865.12 | 4.5833 | 38.5891 | 0.0023 | 0.0092 |
| *BMP15* | -3249.03 | -3254.14 | 0.1169 | 998.9596 | 0.0014 | 0.0057 |
| *CDKN2C* | -1073.58 | -1080.98 | 0.0008 | 0.2543 | 0.0001 | 0.0007 |
| *IGFBP6* | -539.33 | -546.88 | 0.0000 | 3.3577 | 0.0001 | 0.0007 |
| *IRS4* | -7537.96 | -7545.46 | 12.4639 | 498.7288 | 0.0002 | 0.0007 |
| *NSD1* | -6813.90 | -6849.58 | 0.3495 | 3.6643 | 0.0000 | 0.0000 |
| *SOX11* | -1021.78 | -1029.53 | 0.0000 | 1.5254 | 8.31E-05 | 0.0007 |
| *SOX5* | -791.46 | -787.90 | 0.0232 | 4.1346 | 0.0077 | 0.0234 |

**TABLE | S11** Genes and sites detected to be under positive selection at the terminal branches of interest in lizards and snakes using branch-site model.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Dataset | Foreground | Genes | Ma\_lnL | Ma0\_lnL | Background(a/b)  Foreground(a/b) | *p*-value | Positively selected sites (PP > 0.8) |
| Sauria | *H. yunnanensis* (small) | *ACAN* | -15805.27 | -15825.28 | 0.087/1.000  999.000/999.000 | 0.0000 | 1S0.994, 11S0.992, 12P0.978, 15P0.855, 21A0.998, 23D0.986, 30L0.997, 32S0.995, 33N0.976, 40C0.994, 204I0.826, 894T0.988, 936S0.991, 994E0.984, |
| *FOXO6* | -5245.50 | -5256.17 | 0.031/1.000  20.668/20.668 | 0.0000 | 199A0.996, 202Q0.905, 206S1.000, 208M0.996, 210R0.901, 212P0.979, 213M0.912 |
| *GDF6* | -2900.27 | -2913.00 | 0.125/1.000  999.000/999.000 | 0.0000 | 88W0.843, 93Q0.817, 164C0.909, 166V0.999, 172P0.927, 175I0.891 |
| *GDF7* | -1070.98 | -1077.68 | 0.082/1.000  161.718/161.718 | 0.0003 | 2D0.845, 6G0.923, 31T0.999, 38A0.994, 39A0.922, 40P0.912, 41P0.943, 42S0.906, 43C0.999, 44C0.999, 46P0.999, 49R1.000 |
| *GHR* | -9314.55 | -9329.72 | 0.010/1.000  998.999/998.999 | 0.0000 | 3F0.886, 555L0.991, 556N0.957, 557K0.993, 560P0.980 |
| *IGFBP2* | -1967.07 | -1973.33 | 0.052/1.000  998.991/998.991 | 0.0004 | 138H0.982, 139E0.999, 140Q0.993 |
| *IRS2* | -10194.95 | -10203.59 | 0.132/1.000  999.000/999.000 | 0.0000 | 6R0.973, 7K0.918 |
| *S. merianae* (large) | *BMP15* | -4908.07 | -4913.21 | 0.077/1.000  21.257/21.257 | 0.0013 | 4P0.995, 8R0.974, 46T0.887, 205Q0.956 |
| *CDKN2C* | -2103.31 | -2132.07 | 0.048/1.000  451.764/451.764 | 0.0000 | 2A0.833, 3E0.952, 4P0.847, 5L0.975, 8E1.000, 10S0.857, 11T0.941, 13A0.858, 15R0.999, 16G0.999, 18L0.922, 21D0.995, 22V1.000, 23N0.999, 24A0.931, 25R0.870, 27G0.995, 28F0.999, 29G0.859, 30R0.998, 31T0.997, 33L0.997, 34Q0.914, 111A0.910 |
| *IRS2* | -10196.54 | -10202.41 | 0.132/1.000  18.835/18.835 | 0.0006 | 561T0.935, 571N0.823, 577K0.906 |
| *LEPR* | -9614.45 | -9622.04 | 0.238/1.000  30.801/30.801 | 0.0001 | 86N0.805, 91T0.807, 93E0.977, 95T0.970 |
| *V. komodoensis* (large) | *BMP10* | -4979.75 | -4987.66 | 0.118/1.000  998.918/998.918 | 0.0001 | 11V0.990, 12D0.935, 18S0.805, 22A0.947, 144E0.905 |
| *FOXO4* | -5258.20 | -5265.66 | 0.093/1.000  424.604/424.604 | 0.0001 | 5Q0.986, 11C0.919, 390T0.981, 391W0.902 |
| *IGF1* | -965.61 | -976.66 | 0.171/1.000  433.114/433.114 | 0.0000 | 19R0.992, 21E1.000, 23Y0.923, 25A0.997, 27V0.989, 28K0.885, 29K0.998, 30S0.998, 31A1.000, 32R0.940, 33K0.940, 33K0.949, 34E0.854, 36H0.906, 39N0.970 |
| *INS* | -1509.81 | -1522.15 | 0.181/1.000  72.254/72.254 | 0.0000 | 25L0.918, 26P0.947, 34H0.867, 41L0.982, 50R0.882, 62E0.979, 71N0.983, 76Y0.989 |
| *LEPR* | -10100.46 | -10110.50 | 0.234/1.000  234.929/234.929 | 0.0000 | 91Q0.869, 92E0.986, 98E0.966, 102K0.870, 104P0.882, 109D0.986 |
| *NSD1* | -8167.56 | -8174.34 | 0.173/1.000  998.998/998.998 | 0.0002 | 2D0.910, 13Y0.822, 427D0.879 |
| Serpentes | *T. baileyi* (small) | *FBN1* | -15919.07 | -15937.32 | 0.022/1.000  814.240/814.240 | 0.0000 | 854G0.923 |
| *IGF1* | -551.57 | -560.44 | 0.090/1.000  1.000/1.000 | 0.0000 | Not allowed |
| *PRKG2* | -1330.37 | -1336.17 | 0.059/1.000  999.000/999.000 | 0.0007 | 106Q0.831 |
| *SOX21* | -788.90 | -794.96 | 0.002/1.000  999.000/999.000 | 0.0005 | 89S0.988 |
| *O. Hannah* (large) | *BMP15* | -3236.18 | -3256.18 | 0.084/1.000  999.000/999.000 | 0.0000 | 3S0.997, 4A0.970, 6Q0.997 |
| *IGFBP6* | -537.29 | -542.78 | 0.000/1.000  23.719/23.719 | 0.0009 | 4R0.985, 5E0.801, 8A0.998, 12K0.998, 17K0.984, 18R0.945, 19G0.925, 24Q0.876, 25T0.989, 26E1.000, 28E1.000, 29P0.890, 30V0.983, 31A0.978 |
| *IGFBP7* | -638.37 | -648.07 | 0.160/1.000  188.493/188.493 | 0.0000 | 7C0.994, 9P0.998, 10K0.960, 14A0.989, 15T0.989, 19V0.942, 21K0.987, 22S0.991, 23R0.880, 24Y0.985, 26V0.856, 27C0.997, 29S0.997, 30T0.998, 34R0.876, 35A0.869, 37S0.969, 38L0.881 |
| *NSD1* | -6704.46 | -6820.29 | 0.050/1.000  504.197/504.197 | 0.0000 | 4Q0.830, 5S0.971, 8L0.957, 9N0.884, 12K0.995, 17C0.842, 22S0.997, 25D0.867, 26Q0.975, 30A0.987, 33V0.873, 34D0.953, 36H0.992, 38T0.905, 39L0.830, 40Q0.996, 41S0.992, 42K0.932, 44F0.867, 52Q0.985, 54Q0.998, 56A0.929, 59S0.987, 60S0.963, 61L0.922, 67S0.912, 69L0.983, 70P0.991, 72S0.993, 73T0.908, 74R0.998, 77S0.998, 78S0.890, 80S0.985, 84A0.993, 89L0.802, 90E0.998, 92V0.938, 93S0.947, 95A0.994, 96A0.983, 100S0.984, 101M0.898, 103P0.937, 106S0.964, 108R0.823, 112P0.997, 114K0.982, 117V0.904, 118P0.993, 121P0.896, 127Q0.973, 128R0.975, 129R0.806, 131L0.968, 133A0.809, 140S0.946, 141T0.949, 142Q0.980, 145T0.966, 146P0.978, 150G0.939, 153S0.998, 154H0.997, 156N0.971, 158Q0.980, 164P0.984, 167L0.995, 168L0.993, 171F0.978, 173L0.993, 175C0.993, 177G0.805, 180E0.876, 181M0.984, 184V0.812, 187N0.971, 190R0.996, 193C0.962, 199P0.991, 200T0.992, 203Q0.997, 205K0.998, 208R0.823, 210H0.990, 212T0.838, 214R0.975, 216G0.992, 217S0.994, 220C0.991, 221L0.851, 224Y0.833, 225C0.984, 226N0.999, 233G0.996, 234R0.996, 237W0.979, 238W0.997, 239P0.883, 240A0.855, 241E0.978, 244H0.834, 247V0.938, 250M0.968, 251E0.995, 253D0.997, 254V0.974, 255S0.971, 256S0.994, 257K0.999, 261A0.969, 268P0.813, 270P0.995, 272K0.969, 276E0.866, 278P0.997, 280C0.985, 284N0.962, 287L0.960, 290E0.998, 291C0.994, 293P0.991, 295A0.997, 297G0.993, 299G0.930 |
| *SOX11* | -994.96 | -1015.86 | 0.008/1.000  999.000/999.000 | 0.0000 | 131S0.878, 132S0.878, 133S0.894, 134S0.917, 135S0.901, 136S0.891, 137S0.858, 138S0.890, 139S0.998, 140P0.885, 144G0.998, 145T0.998, 146K0.878 |
| *P. bivittatus* (large) | *CDKN2C* | -1079.75 | -1086.75 | 0.006/1.000  602.658/602.658 | 0.0002 | 2V0.921, 4A0.982, 5E0.953, 6G0.954, 14L0.949, 16Q0.971 |
| *FBN1* | -15910.07 | -15929.04 | 0.021/1.000  451.033/451.033 | 0.0000 | 587P0.906, 674I0.927, 1166Q0.859, 1507Q0.930, 1607N0.996, 1612N0.989, 1615D0.895, 1618L0.982, 1626E0.948, 1627G0.949, 1629S0.976, 1631L0.953 |

**TABLE | S12** Genes and sites detected to be under positive selection at the ancestral branches of interest in lizards and snakes using branch-site model.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Foreground | Genes | Ma\_lnL | Ma0\_lnL | Background(a/b)  Foreground(a/b) | *p*-value | Positively selected sites (PP > 0.8) |
| The ancestral branch of *P. muralis and L. agilis* | *CCNB3* | -5091.53 | -5094.22 | 0.111/1.000  6.792/6.792 | 0.021 | 8V0.917, 25E0.802,  38P0.863, 158Q0.895 |
| *CNP* | -5669.70 | -5672.24 | 0.050/1.000  271.184/271.184 | 0.024 | 372A0.975 |
| *IGFBP3* | -1041.03 | -1043.00 | 0.065/1.000  999.000/999.000 | 0.047 | 7L0.804, 17D0.937 |
| *SOX9* | -4544.01 | -4545.94 | 0.015/1.000  534.599/534.599 | 0.049 | 261Q0.989 |
| *IRS2* | -10201.35 | -10203.71 | 0.134/1.000  66.941/66.941 | 0.030 | Not allowed |
| *SMO* | -6403.19 | -6405.79 | 0.041/1.000  19.304/19.304 | 0.023 | 301G0.801, 350N0.966 |
| The ancestral branch of *P. picta and H. yunnanensis* | *GDF6* | -2913.73 | -2916.77 | 0.138/1.000  365.046/365.046 | 0.014 | Not allowed |
| *GPC4* | -5187.22 | -5190.12 | 0.0440/1.000  50.201/50.201 | 0.016 | 300M0.994 |
| *IGFBP2* | -1973.11 | -1979.26 | 0.067/1.000  34.940/34.940 | 0.000 | 20S0.947, 25P0.970, 38K0.921 |
| *SH2B3* | -6600.76 | -6603.63 | 0.124/1.000  61.127/61.127 | 0.017 | 225S0.868 |
| *SOX11* | -4177.25 | -4181.24 | 0.030/1.000  998.999/998.999 | 0.005 | 221H0.993 |
| The ancestral branch of *P. obsoletus* and *P. guttatus* | *FBN1* | -15934.89 | -15937.46 | 0.022/1.000  81.934/ 81.934 | 0.024 | Not allowed |
| The ancestral branch of *P. flavoviridis* and *P. mucrosquamatus* | *LCORL* | -13154.27 | -13158.32 | 0.128/1.000  999.000/999.000 | 0.004 | Not allowed |
| The ancestral branch *T. elegans* and *T. sirtalis* | *ACAN* | -10630.68 | -10634.66 | 0.117/1.000  34.497/34.497 | 0.005 | 965D0.808 |
| *LCORL* | -13153.33 | -13157.80 | 0.130/1.000  151.258/151.258 | 0.003 | Not allowed |
| *NPC1* | -10641.08 | -10644.09 | 0.033/1.000  999.000/999.000 | 0.014 | Not allowed |

**TABLE | S13** Association analyses between gene evolution and microhabitat.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Dataset | Genes | Slope | R2 | *p*-value | F-statistic | AIC |
| Sauria | *BMP4* | − | 0.348 | 0.033 | 6.348 | -16.597 |
| *BMP6* | + | 0.388 | 0.018 | 7.983 | 5.214 |
| *CDKN1A* | + | 0.276 | 0.046 | 5.194 | -13.249 |
| *GALNS* | + | 0.501 | 0.006 | 12.031 | -5.949 |
| *IGFBP3* | + | 0.467 | 0.018 | 8.877 | 18.237 |
| *IGFBP6* | + | 0.364 | 0.029 | 6.724 | -11.706 |
| *SOX8* | − | 0.351 | 0.025 | 6.949 | -8.310 |
| Serpentes | *AKT1* | − | 0.909 | 0.008 | 41.099 | -8.475 |
| *CCNB3* | − | 0.335 | 0.018 | 7.536 | -16.780 |
| *FGF4* | − | 0.411 | 0.037 | 6.592 | -5.642 |
| *SH2B1* | − | 0.599- | 0.002 | 17.407 | -4.052 |
| *SOX6* | − | 0.432 | 0.032 | 7.073 | -11.453 |
| *SOX7* | − | 0.204 | 0.045 | 4.852 | -6.588 |

**TABLE | S14** Association analyses between gene evolution and number of ecoregions/rate of range expansion in species.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Ecological factors | Dataset | Genes | Slope | R2 | *p*-value | F-statistic | AIC |
| Number of ecoregions | Sauria | *AKT1* | − | 0.536 | 0.010 | 11.410 | -1.030 |
| *BMP1* | − | 0.448 | 0.010 | 9.929 | -13.775 |
| *IGF2* | − | 0.327 | 0.031 | 6.333 | -18.794 |
| *SOX5* | + | 0.302 | 0.037 | 5.752 | 4.720 |
| Serpentes | *ADIPOR2* | − | 0.374 | 0.007 | 9.962 | 0.108 |
| *FOXO1* | − | 0.201 | 0.047 | 4.767 | -11.882 |
| *GPC6* | + | 0.257 | 0.044 | 5.146 | -0.219 |
| *KCNJ2* | − | 0.334 | 0.011 | 8.525 | -1.618 |
| *SOX30* | − | 0.350 | 0.009 | 9.091 | -11.689 |
| Ecoregions/age | Sauria | *AKT1* | − | 0.365 | 0.038 | 6.180 | 2.110 |
| *BMP6* | − | 0.303 | 0.037 | 5.779 | 5.438 |
| *BMP7* | − | 0.302 | 0.037 | 5.757 | 6.109 |
| *FOXO1* | − | 0.293 | 0.040 | 5.548 | -11.935 |
| *GALNS* | − | 0.265 | 0.050 | 4.968 | -5.741 |
| *GDF9* | − | 0.304 | 0.037 | 5.804 | -12.112 |
| *IGFBP2* | − | 0.373 | 0.027 | 6.953 | -11.464 |
| *IGFBP6* | − | 0.383 | 0.025 | 7.201 | -12.236 |
| *IRS1* | + | 0.348 | 0.033 | 6.331 | -19.798 |
| *NSD2* | + | 0.443 | 0.011 | 9.742 | -27.980 |
| *PLAGL2* | − | 0.322 | 0.032 | 6.221 | -14.718 |
| Serpentes | *ADIPOR2* | − | 0.259 | 0.026 | 6.244 | 1.148 |
| *KCNJ2* | − | 0.236 | 0.033 | 5.626 | 0.587 |
| *SOX30* | − | 0.348 | 0.009 | 9.019 | -12.703 |

**TABLE | S15** Association analyses between gene evolution and climate.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Ecological factors | Dataset | Genes | Slope | R2 | *p*-value | F-statistic | AIC |
| PC1 | Sauria | *CDKN1B* | + | 0.585 | 0.047 | 8.048 | -2.595 |
| *NPC1* | + | 0.905 | 0.002 | 48.386 | -21.646 |
| *SOX11* | + | 0.901 | 0.002 | 46.574 | -7.561 |
| Serpentes | *CCNB1* | − | 0.480 | 0.011 | 10.237 | -2.484 |
| *CDKN1A* | − | 0.478 | 0.011 | 10.153 | -17.637 |
| *FBN1* | + | 0.506 | 0.013 | 10.209 | -14.003 |
| *SOX30* | + | 0.551 | 0.005 | 13.251 | -25.945 |
| PC2 | Sauria | *AKT1* | − | 0.656 | 0.032 | 10.524 | 1.451 |
| *BMP15* | + | 0.997 | 0.025 | 654.112 | -10.952 |
| *EIF4EBP1* | − | 0.819 | 0.008 | 23.685 | -2.333 |
| *GDF9* | − | 0.837 | 0.005 | 26.621 | -9.722 |
| *KCNJ2* | − | 0.644 | 0.034 | 10.056 | -6.947 |
| *SOX18* | + | 0.689 | 0.026 | 12.053 | -16.110 |
| *SOX5* | + | 0.710 | 0.022 | 13.215 | -8.527 |
| *SOX6* | − | 0.719 | 0.021 | 13.785 | -11.360 |
| Serpentes | *ADAMTS10* | − | 0.459 | 0.019 | 8.649 | -16.515 |
| *AKT1* | + | 0.998 | 0.018 | 1308.126 | -24.368 |
| *FBN1* | − | 0.494 | 0.014 | 9.793 | -13.419 |
| *FOXO6* | + | 0.380 | 0.026 | 7.136 | -14.307 |
| *GPC6* | + | 0.431 | 0.033 | 7.053 | -0.252 |
| *IGF1* | + | 1.000 | 0.003 | 49786.443 | -17.324 |
| *IGFBP6* | − | 0.326 | 0.049 | 5.360 | 14.533 |
| *KCNJ2* | − | 0.603 | 0.003 | 16.203 | -3.864 |
| *SOX30* | − | 0.488 | 0.010 | 10.535 | -25.007 |
| PC3 | Sauria | *CCNB1* | + | 0.599 | 0.044 | 8.468 | 3.371 |
| *FOXO6* | − | 0.636 | 0.036 | 9.737 | -2.127 |
| *GDF7* | − | 0.804 | 0.010 | 21.451 | -0.060 |
| *LEPR* | − | 0.609 | 0.041 | 8.788 | -7.712 |
| *SOX11* | + | 0.573 | 0.050 | 7.710 | 1.217 |
| *SOX6* | + | 0.787 | 0.012 | 19.514 | -13.036 |
| *SOX8* | + | 0.707 | 0.022 | 13.068 | -16.240 |
| Serpentes | *ADAMTS10* | + | 0.367 | 0.037 | 6.228 | -15.960 |
| *AIP* | + | 0.516 | 0.012 | 10.602 | -20.835 |
| *BMP2* | − | 0.325 | 0.039 | 5.815 | -11.847 |
| *CDKN1A* | − | 0.417 | 0.019 | 8.159 | -20.604 |
| *GPC1* | + | 0.391 | 0.031 | 6.774 | -17.750 |
| *LEPR* | − | 0.430 | 0.017 | 8.556 | -7.467 |
| *OBSL1* | − | 0.544 | 0.014 | 10.533 | -9.814 |
| *SOX7* | − | 0.305 | 0.045 | 5.383 | -3.660 |
| Bio1 | Sauria | *AIP* | − | 0.864 | 0.004 | 32.683 | -1.567 |
| *BMP15* | + | 0.998 | 0.018 | 1205.997 | -12.785 |
| *CCNB1* | − | 0.575 | 0.049 | 7.772 | 3.716 |
| *FOXO1* | − | 0.753 | 0.017 | 16.225 | -7.570 |
| *NOG* | − | 0.844 | 0.006 | 27.958 | -0.722 |
| *SOX14* | − | 0.881 | 0.041 | 23.144 | -0.031 |
| Serpentes | *AKT1* | + | 0.999 | 0.014 | 1973.355 | -25.601 |
| *FBN1* | − | 0.371 | 0.036 | 6.309 | -11.239 |
| *FOXO1* | − | 0.492 | 0.010 | 10.681 | -15.026 |
| *GPC1* | − | 0.330 | 0.048 | 5.427 | -16.795 |
| *IGFBP4* | − | 0.999 | 0.014 | 2194.580 | -13.064 |
| *LEPR* | + | 0.462 | 0.013 | 9.573 | -9.361 |
| *SH2B1* | − | 0.426 | 0.047 | 6.185 | -7.549 |
| *SOX30* | − | 0.309 | 0.044 | 5.465 | -21.208 |
| *SOX7* | + | 0.504 | 0.009 | 11.145 | -7.366 |
| Bio12 | Sauria | *CDKN1B* | − | 0.636 | 0.036 | 9.738 | -3.383 |
| *NPC1* | − | 0.802 | 0.010 | 21.198 | -17.254 |
| *PLAGL2* | − | 0.645 | 0.034 | 10.102 | -6.971 |
| *SOX11* | − | 0.750 | 0.016 | 16.004 | -1.996 |
| Serpentes | *ADIPOR2* | − | 0.388 | 0.024 | 7.345 | -1.080 |
| *BMP6* | + | 0.913 | 0.002 | 53.226 | -18.606 |
| *CCNB1* | + | 0.434 | 0.016 | 8.655 | -3.381 |
| *FBN1* | − | 0.654 | 0.003 | 17.988 | -17.750 |
| *LCORL* | + | 0.408 | 0.038 | 6.513 | -12.658 |
| *SOX30* | − | 0.646 | 0.002 | 19.216 | -28.558 |

**TABLE | S16** Association analyses between phenotypes and ecological factors (Significant *p*-value < 0.05 are boldfaced).

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Dataset | Factors | | Slope | R2 | *p*-value | F-statistic | AIC |
| Sauria | Microhabitat | Body length | − | -0.086 | 0.730 | 0.126 | 38.152 |
| PC1 | − | 0.138 | 0.251 | 1.797 | 25.022 |
| PC2 | + | 0.088 | 0.359 | 1.481 | 31.753 |
| PC3 | − | -0.063 | 0.466 | 0.703 | 26.542 |
| Bio1 | + | -0.109 | 0.516 | 0.507 | 29.255 |
| Bio12 | + | 0.230 | 0.190 | 2.489 | 7.897 |
| **Ecoregions** | **+** | **0.935** | **0.000** | **160.008** | **-34.143** |
| Ecoregions/age | + | 0.032 | 0.271 | 1.359 | -57.777 |
| Microhabitat | Body mass | − | -0.087 | 0.735 | 0.121 | 38.157 |
| PC1 | − | 0.137 | 0.252 | 1.793 | 25.026 |
| PC2 | + | 0.082 | 0.366 | 1.446 | 31.792 |
| PC3 | − | -0.071 | 0.474 | 0.670 | 26.585 |
| Bio1 | + | -0.125 | 0.541 | 0.445 | 29.338 |
| Bio12 | + | 0.230 | 0.189 | 2.494 | 7.893 |
| **Ecoregions** | **+** | **0.943** | **0.000** | **181.988** | **-35.602** |
| Ecoregions/age | + | 0.050 | 0.237 | 1.580 | -58.008 |
| Serpentes | Microhabitat | Body length | − | -0.040 | 0.527 | 0.421 | 58.764 |
| PC1 | − | -0.034 | 0.432 | 0.676 | 47.778 |
| PC2 | + | -0.095 | 0.726 | 0.131 | 54.642 |
| PC3 | − | -0.099 | 0.762 | 0.097 | 48.833 |
| Bio1 | + | 0.025 | 0.290 | 1.261 | 35.351 |
| Bio12 | + | 0.250 | 0.067 | 4.326 | 21.995 |
| Ecoregions | + | 0.011 | 0.297 | 1.172 | -8.457 |
| Ecoregions/age | + | 0.077 | 0.156 | 2.248 | -116.939 |
| Microhabitat | Body mass | − | -0.036 | 0.503 | 0.474 | 58.690 |
| PC1 | − | -0.065 | 0.549 | 0.387 | 48.111 |
| PC2 | + | -0.097 | 0.738 | 0.119 | 54.656 |
| PC3 | − | -0.108 | 0.876 | 0.026 | 48.920 |
| Bio1 | + | 0.011 | 0.320 | 1.106 | 35.518 |
| Bio12 | + | 0.173 | 0.112 | 3.098 | 23.058 |
| Ecoregions | + | -0.003 | 0.346 | 0.950 | -8.221 |
| Ecoregions/age | + | 0.068 | 0.170 | 2.092 | -116.785 |
| Squamates | Microhabitat | Body mass | − | 0.104 | 0.056 | 4.033 | 107.030 |
| PC1 | − | 0.098 | 0.119 | 2.738 | 73.679 |
| PC2 | + | -0.040 | 0.543 | 0.387 | 87.577 |
| PC3 | − | -0.010 | 0.375 | 0.838 | 75.071 |
| Bio1 | + | 0.108 | 0.107 | 2.936 | 66.061 |
| Bio12 | + | 0.124 | 0.091 | 3.263 | 31.309 |
| Ecoregions | + | -0.040 | 0.914 | 0.012 | -19.614 |
| Ecoregions/age | + | -0.030 | 0.626 | 0.243 | -159.970 |