

Supplementary Figure 1

Genes showing multiple signs of adaptation (MSA)

Locus Name: Folate receptor 1 alpha (FOLR1)

ENSBTAT00000027602 FOLR1-201 folate receptor embryogenesis, folate homeostasis
 mouse: growth retardation, neural and cranofacial defects die at E10

PSG: (Giraffe) G47S|GGC/AGC; P48S|CCA/TCT; K61E|AAG/GAG; E222K|GAG/AAG; G235Q|GGG/CAG

PP2: (Giraffe) P49S, E223K;(Giraffe/Okapi) D51S, A22Q

Giraffe: P48S UPS, E54G UPS, R122T UPS, E222K UIS, G235Q UPS

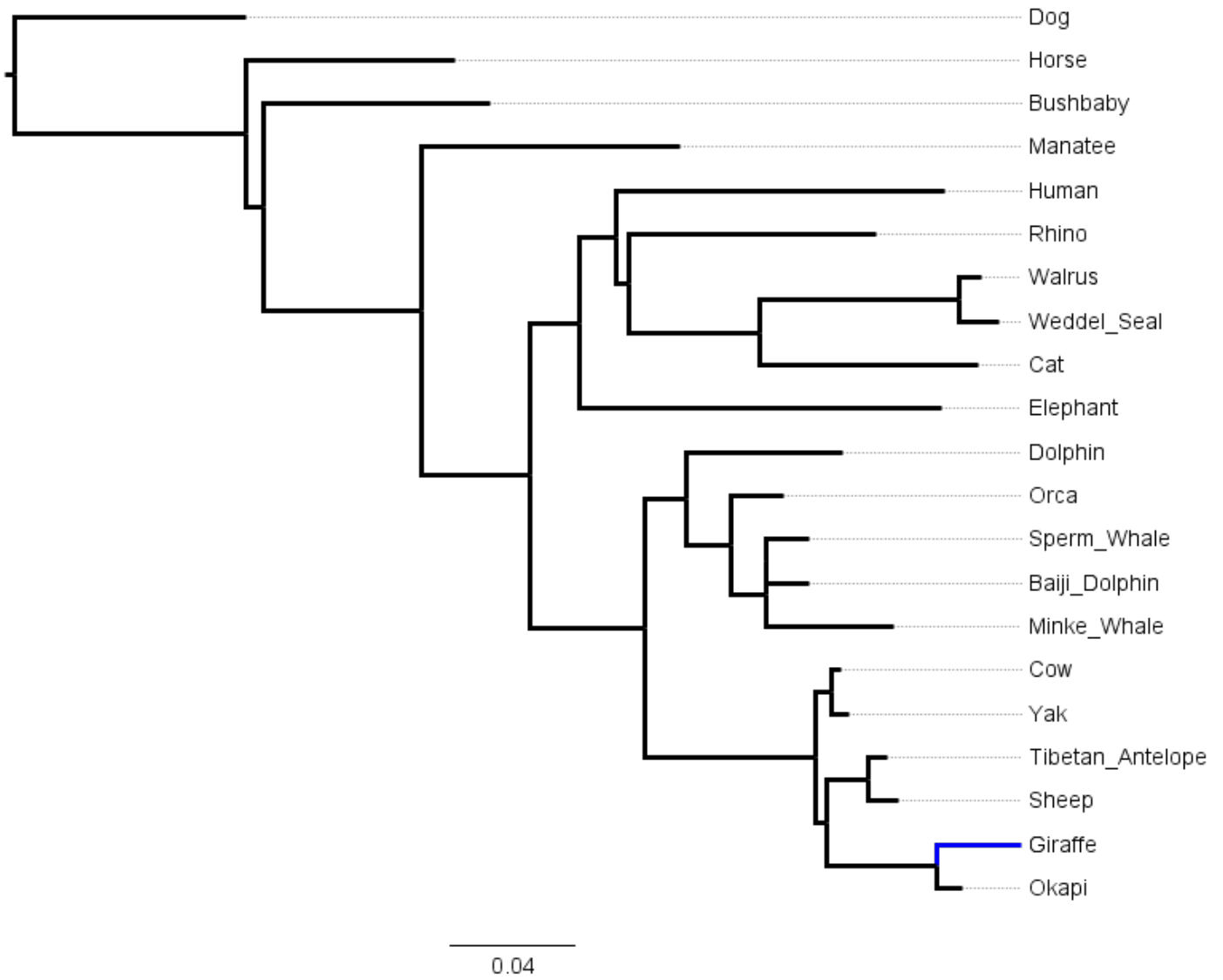
Okapi: A20S UPS

Protein sequence Alignment of Cow, Giraffe and Okapi FOLR1

Cow	1	MAWQMTQLLLLALVAAAWGAQAPRTPRARTDLLNVCM DAKHHKAE PGPEDSLHEQCSPWR	60
Giraffe	1	...K.....V.G.....N.....SS.S...G.....	60
Okapi	1	...K.....S.V.G.....N.....S.....	60
Cow	61	KNACCSVNTSIEAHKDISYLYRFNWDHCGKMEPACKRHF IQDTCLYECS PNLG P WIREVN	120
Giraffe	61	E.....	120
Okapi	61	120
Cow	121	QRWRKERV LGVPLCKEDCQSWWEDCRTSYTCKSNWHK GWNWTS GYNQCPVKAACHRFDFY	180
Giraffe	121	.T.....N.....I.....R..D.....	180
Okapi	121	.S.....N.....I.....R..D.....	180
Cow	181	FPTPAALCNEIWSHSYKVS NYSRGSGRCIQMWFDPFQGNPNEEVARFYAENPTSGSTPQG	240
Giraffe	181G.....K.....N.Q.....	240
Okapi	181G.....N.....	240
Cow	241	I	
Giraffe	241	.	
Okapi	241	.	

Newick Tree of Mammalian FOLR1

```
(dog:0.0755681, (horse:0.0677606, (bushbaby:0.073823, (manatee:0.0839709, ((human:0.10683,
(rhino:0.0803279, ((walrus:0.00727225, weddel_seal:0.0126104):0.065253,
cat:0.0713098):0.0423044):0.00400162):0.0122881, elephant:0.118106):0.0159987,
((dolphin:0.0509221, (orca:0.0171223, ((sperm_whale:0.0137419,
baiji_dolphin:0.0138767):0.000462631, minke_whale:0.041772):0.0109803):0.0150048):0.0134242,
((cow:0.00287772, yak:0.00545576):0.00515902, ((tibetan_antelope:0.00599731,
sheep:0.00962865):0.013353, (giraffe:0.0273562,
okapi:0.00815797):0.0355917):0.00359502):0.0559345):0.0372389):0.0352274):0.0517348):0.0053625):0.0755681);
```



Locus Name: Folate receptor 1 alpha (FOLR1)

Locus Name: Homeobox B3 (HoxB3)

ENSBTAT0000028563 HOXB3-201 homeobox transcription factor segmental identity, anterior axial skeleton, angiogenesis
mouse: defects in cervical vertebrae, atlas, formation of IXth cranial nerve

PP2: (Giraffe) S98I; (Giraffe/Okapi) M282I, P403A

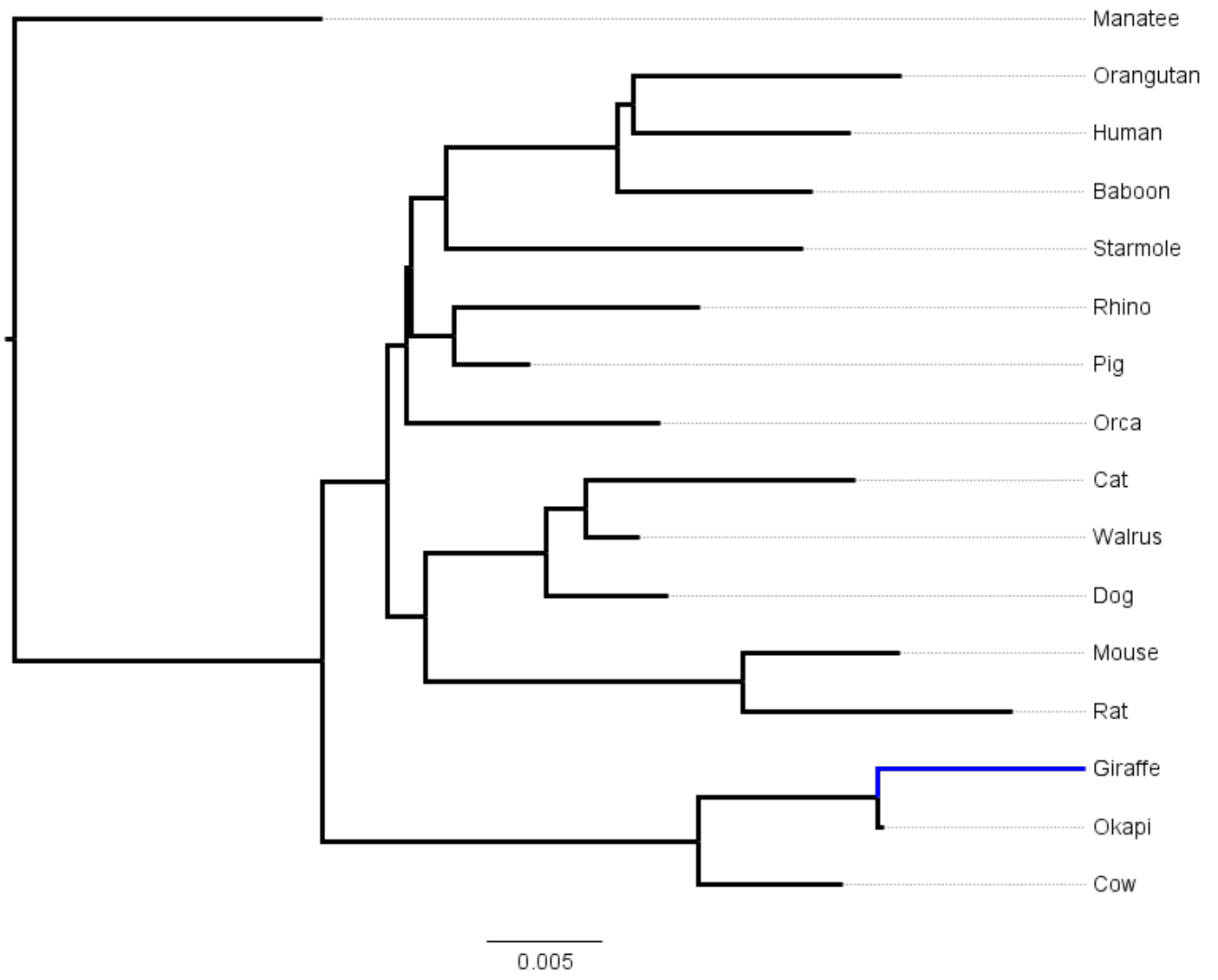
Giraffe: S98I UIS, G113S UPS,
Giraffe/Okapi: P115S UIS, M77I UIS, P398A UIS

Protein sequence Alignment of Cow, Giraffe and Okapi HoxB3

Cow	1	MQKATYYDNTAAALFGGYPSYPGSNGFGYDGGPPPPQAATHLESYQRSACSLQSLGNA	60
Giraffe	1E.....G	60
Okapi	1	60
Cow	61	APHAKGKELNGSCMRPGLASEPLPAPPSPPPSAAPTSTTSNSSNGGGPSKSGPPKCGAG	120
14540	61S.....I.....S.S.....	120
14541	61S.....S.....	120
Cow	121	SNSTLTKQIFPWMKESRQTSKLNSSPGTAEGCGSGGGGGGGSSGGGGGGGDKSPPGS	180
14540	121G.....G.....	183
14541	121G.....G.....	184
Cow	181	AASKRARTAYTSAQLVELEKEFHFNRYLCRPRRVEMANLLNLSEKIQIKIWFQNRMMKYKK	240
14540	184	243
14541	185	244
Cow	241	DQKAKGLASSSGGPPSPAGSPSQPMQSTAGFMNALHSMTPSYESPPPAFGKAHQNAYALP	300
14540	244I.....	303
14541	245I.....	304
Cow	301	SNYQPPLKGC GAPQKYPQTPAPDYEPHVLTNGGAYGTPMQGSPVYVGGGGYADPLPPP	360
14540	304	363
14541	305	364
Cow	361	AGPSLYGLNHLSSHPSGNLDYNGAPPMAFSQHGGPCDPHTYTDLSSHAPPQGRIQEA	420
14540	364A.....	423
14541	365A.....	424
Cow	421	PKLTHL	427
14540	424	430
14541	425	431

Newick Tree of Mammalian HoxB3

(manatee:0.0134567, ((cow:0.00638513, (giraffe:0.00908205, okapi:0.00026395):0.0078677):0.0164519, ((rat:0.011867, mouse:0.00691398):0.0138423, (dog:0.00532972, (walrus:0.00233832, cat:0.0118133):0.00175755):0.00524476):0.00171903, (orca:0.0111089, ((pig:0.00334083, rhino:0.0107775):0.00188319, (starmole:0.0156363, (baboon:0.0085923, (human:0.00948222, orangutan:0.0117216):0.000754308):0.00750944):0.00152221):0.000185431):0.000854271):0.00283764):0.0134567);



Locus Name: Homeobox B3 (HoxB3)

Locus name Homeobox B13 (HOXB13)

ENSBTAT00000019523 HOXB13-201 homeobox transcription factor segmental identity, posterior axial skeleton, angiogenesis
mouse: caudal vertebrae and angiogenesis impaired and overgrowth in all major structures derived from the tail bud

PP2 (Giraffe/Okapi): S122I, H160R, W195C

Giraffe: A108G UPS

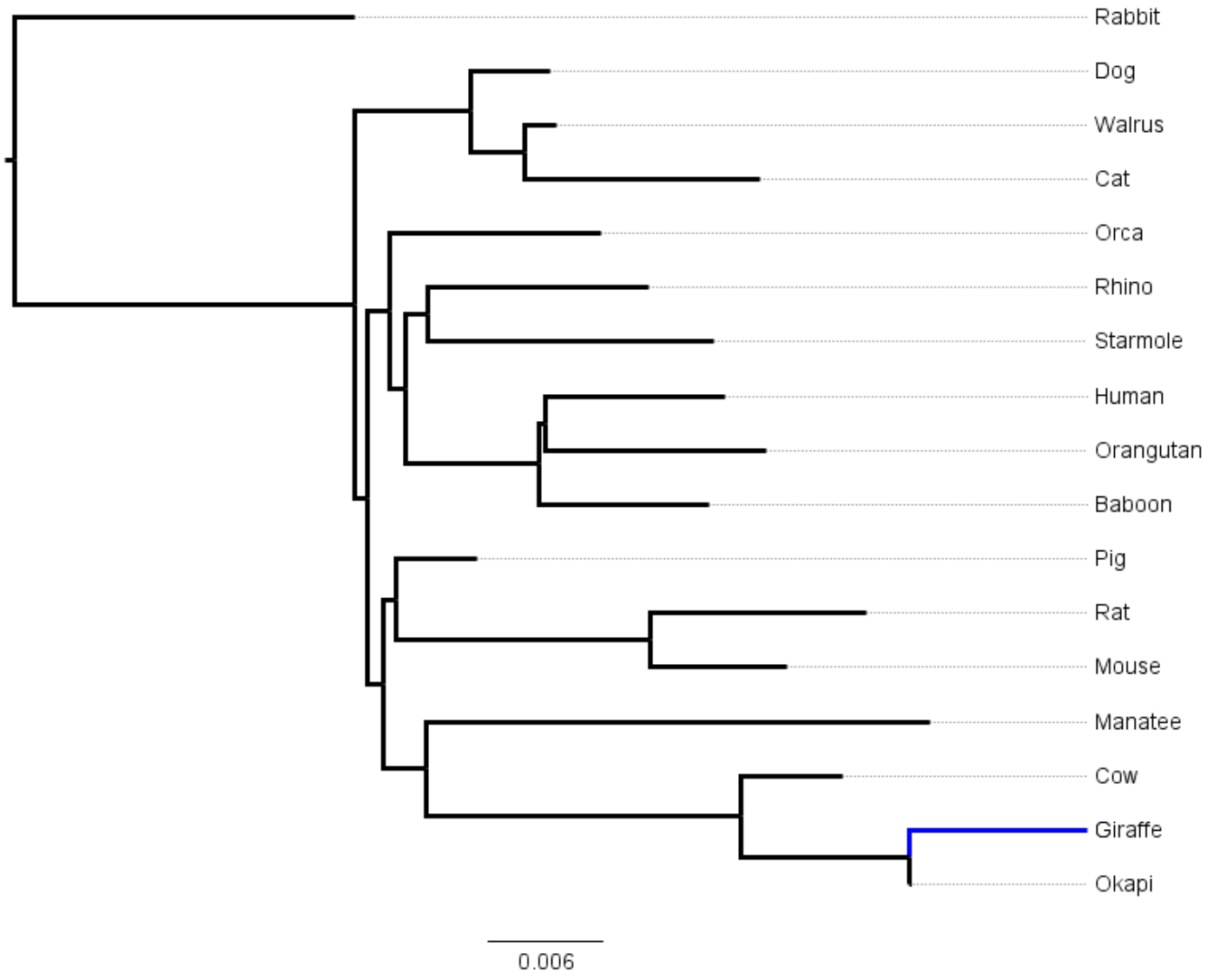
Giraffe/Okapi: S123I unique, APVP deletion unique, H160R UIS, W196C UIS,

Protein sequence Alignment of Cow, Giraffe and Okapi HOXB13

Cow	1	MEPSNYTTLDGAKEIEGLLGAGGSRNLVTHSPLTSHPTSAPTLM PAVNYAPLDLPGSAEP	60
Giraffe	1	...G.....T.....AA.....	60
Okapi	1	...G.....AA....L.....	60
Cow	61	PKQCHPCPGVPQGAS PAVPYGYFGGGYISCRVSRSSLKPCAQAATLAAYPAETPTS GEE	120
Giraffe	61G.....A....	116
Okapi	61T.....A....	116
Cow	121	YPSRPTTEFAFYPGYPGYPQMASYLDVSVVQTLGAPGEP RHDSL LPVDSYQPWALTGGWN	180
Giraffe	117	..I.....S.....V.....R.....S.....S...	176
Okapi	117	..I.....S.....V.....R.....S.....S...	176
Cow	181	SQMCCQGEQNPPGPFWKAAAFADSSSQHPPEGCTFR RGRKKRIPYSKGQLRELEREYSANK	240
Giraffe	177S.C.....V....D..A.....	236
Okapi	177S.C.....V....D..AL.....	236
Cow	241	FITKDKRRKISAATSLSERQITIW FQNRRVKEKKVLAKVKTS	282
Giraffe	237L...	278
Okapi	237L...	278

Newick Tree of Mammalian HOXB13

(rabbit:0.0180279, ((dog:0.00423827, (walrus:0.00170297, cat:0.0124487):0.002849):0.00610416, ((orca:0.0112771, ((rhino:0.0117203, starmole:0.0151466):0.00120006, (human:0.0095166, orangutan:0.0116872):0.000328021, baboon:0.00901859):0.00711139):0.000839773):0.00113203, ((pig:0.00433482, (rat:0.0115056, mouse:0.00727538):0.013488):0.000606871, (manatee:0.0266819, (cow:0.00537304, (giraffe:0.00941327, okapi:0):0.00887979):0.0166834):0.00225322):0.000864063):0.000653822):0.0180279);



Locus name Homeobox B13 (HOXB13)

Locus Name: Homeobox D9 (HOXD9)

ENSBTAT0000021336 HOXD9-201 HoxD9 homeobox transcription factor segmental identity, mid axial skeleton, forelimb development, angiogenesis
mouse: abnormalities in forelimb, lumbar, sacral, caudal vertebrae

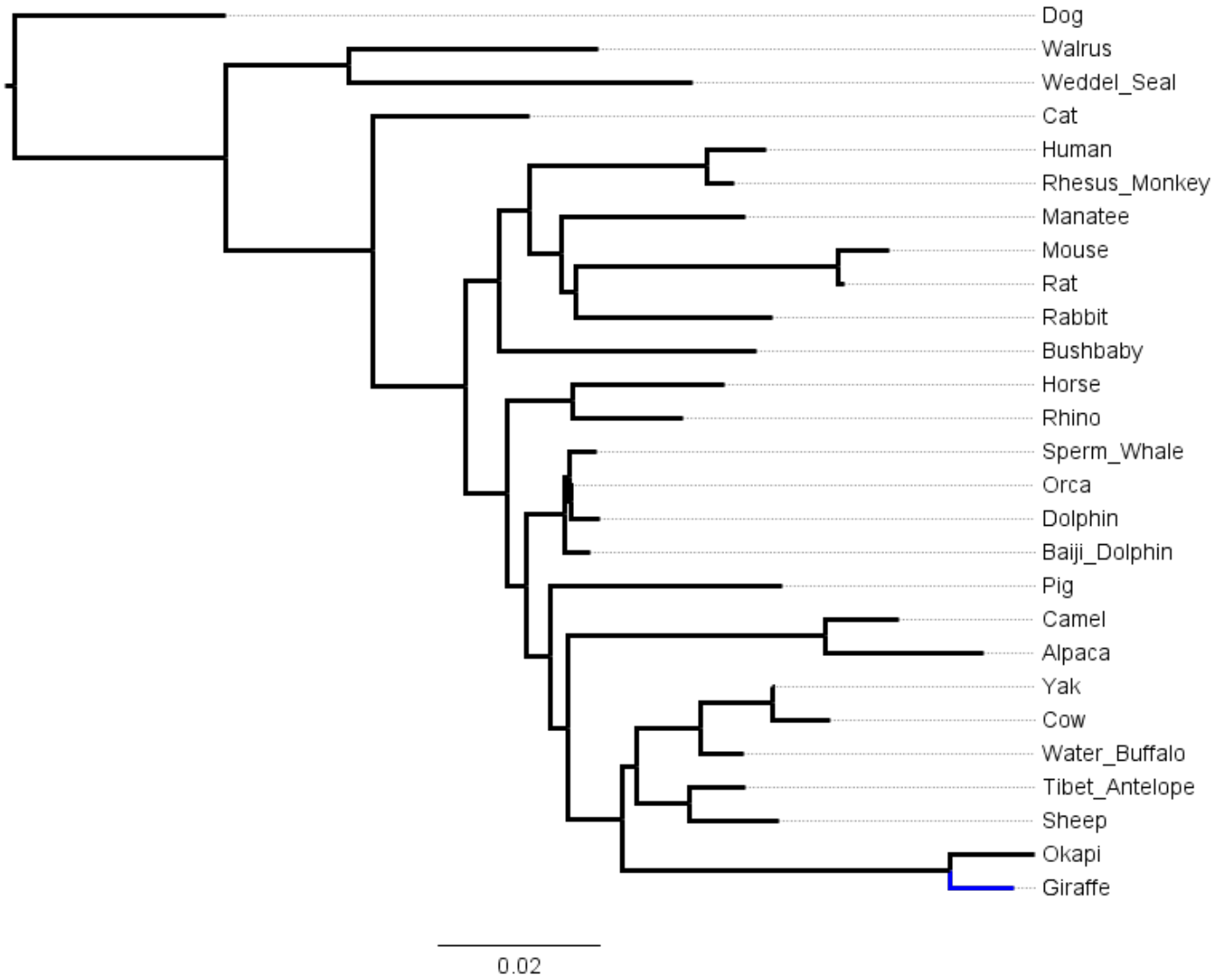
Giraffe: G124S UIS, GAGIGSGS deletion 219-226 UIS in cetartiodactyls
Okapi: S255L UPS

Protein sequence Alignment of Cow, Giraffe and Okapi HOXD9

Cow	1	MSSSGTLSNYYVDSLIGHEGDEVFAGRFGPPGPGAQGRPAGVADSPAAAAAEFASCSFAP	60
Giraffe	1	60
Okapi	1	60
Cow	61	KSAVFSASWSAVPAQPPAAAAAMSGLYHPYVPPPPLAASASEPGRYMRSWMEPLPGFPGGA	120
Giraffe	61	120
Okapi	61	120
Cow	121	GGGGGGGSGGGPGPGSPGSPGNRHYGIKPESGAAPTAAASTTSTSSSSSSSK	180
Giraffe	121	..SS..G.....-.....	179
Okapi	121	.S..S..G.....-.....	179
Cow	181	RTECSAARESQQSGGPEFSCNSFLRDKVAAAAAGGTGPGAGIGSGGAGGTSEPSACSDH	240
Giraffe	180-.....S.....	231
Okapi	180S.....	239
Cow	241	PSPGCPLKEEEKQHSQAPQQQLDPNNPAANWIHARSTRKKRCPYTKYQTTLELEKEFLFNM	300
Giraffe	232	291
Okapi	240L.....	299
Cow	301	YLTRDRRYEVARILNLTERQVKIWFQNRMRMKMKMSKEKCPKGD	345
Giraffe	292	336
Okapi	300	344

Newick Tree of Mammalian HOXD9

(dog:0.0260126, ((walrus:0.0305933, weddel_seal:0.0422303):0.0151606, (cat:0.0193117, (((human:0.00726759, rhesus_monkey:0.00335218):0.0218061, (manatee:0.0227011, (mouse:0.006319, rat:0.000698627):0.0322236, rabbit:0.0241599):0.00187279):0.00376309):0.00384313, bushbaby:0.0317558):0.00409975, (horse:0.0186464, rhino:0.0134474):0.00803063, ((sperm_whale:0.00335994, (orca:0, dolphin:0.00353369):0.000161231):0.000527845, baiji_dolphin:0.00299333):0.00476691, (pig:0.0284483, (camel:0.00906115, alpaca:0.0194144):0.0316376, (Giraffe:0.00771686, Okapi:0.0102379):0.0404145, ((sheep:0.0109289, tibet_antelope:0.00677159):0.00652728, (water_buffalo:0.00528391, (Cow:0.00713736, yak:0):0.00890192):0.00786959):0.00178088):0.00657298):0.00225435):0.00289114):0.0023088):0.0051923):0.0114512):0.0179872):0.0260126);



Locus Name: Homeobox D9 (HOXD9)

Locus Name: Caudal Type Homeobox 4 (CDX4)

ENSBTAT0000002260 CDX4-201 homeobox transcription factor segmental identity, posterior axial skeleton, heart development mouse: defects in axial skeleton development

PP2: (Giraffe) S250C; (Giraffe/Okapi) D140N; (Okapi) V246M

Giraffe: M93T UPS, S251C UIS

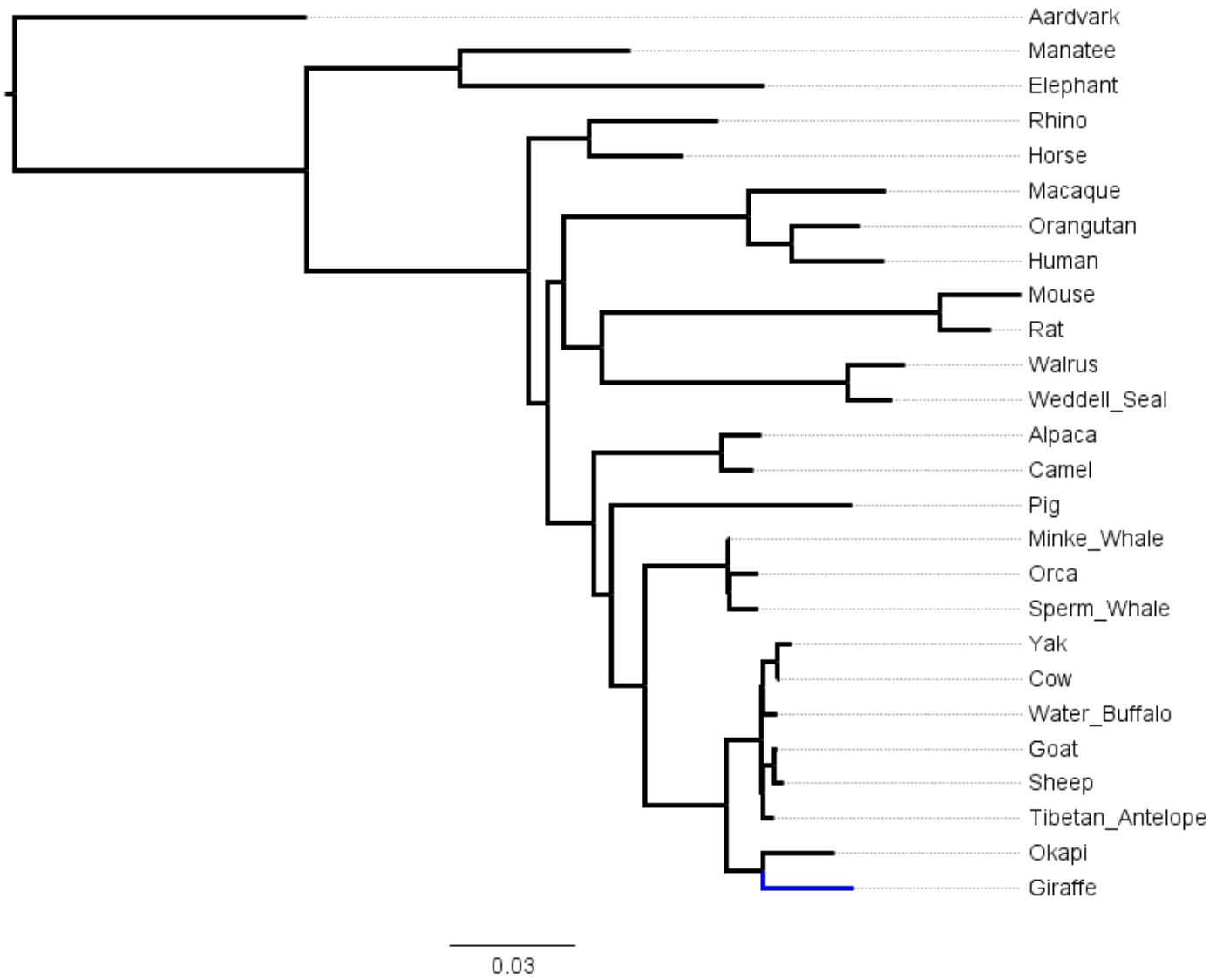
Giraffe/Okapi: T130P UPS, N140D UIS

Protein sequence Alignment of Cow, Giraffe and Okapi CDX4

Cow	1	MYRSCLEKEADMYSSTLRSPAGGGTAGAGATGDGGSPLPASNFAAAPSIAHYMGYPHMP	60
Giraffe	1S.....F..D.....	60
Okapi	1P.....D.....	60
Cow	61	GMDPHGPPPLGAWGSPYSPREDWSVYPGPSSTMGTVPMNDMSSSPAAFSSLEYSNLGPAG	120
Giraffe	61Q...T.....T.....P.....	120
Okapi	61V...T.....P.....	120
Cow	121	GGNSGSSLPTPAGGSLFPIDAGIADADESSRSRHSPIAWMRKTVQVTGKTRTKEKYRVV	180
Giraffe	121P.....N...--.....	178
Okapi	121P.....N...--..V.....	178
Cow	181	YTDHQRLLEKEFHCNRYITIRRKSELAVNLGLSERQVKIWFQNRRAKERKMIKKKISQF	240
Giraffe	179I.....	238
Okapi	181	238
Cow	241	ENSGGSVQSDSGSISPGELPNIFFTTPSAVRGFQPIEIQQVIVSE	285
Giraffe	239C.....T.....	283
Okapi	241M....D.....T.....	283

Newick Tree of Mammalian CDX4

(aardvark:0.0709835, (manatee:0.0414927, elephant:0.0743496):0.0375359, ((rhino:0.0313596, horse:0.0229299):0.0149351, ((Macaque:0.0334678, (orangutan:0.0167002, human:0.0228125):0.0104206):0.0451086, (mouse:0.0197583, rat:0.0126827):0.0823364, (walrus:0.0141256, weddell_seal:0.0108337):0.0598136):0.00930766):0.00360017, ((alpaca:0.00985501, Camel:0.00790838):0.0312197, (pig:0.0586732, (minke_whale:0, (orca:0.0070139, sperm_whale:0.0072217):0.000161725):0.0204831, (giraffe:0.022068, okapi:0.0175872):0.00900926, ((tibetan_antelope:0.00264641, (sheep:0.00257207, goat:0.00096776):0.00267596):0.000454067, (water_buffalo:0.00355976, (cow:0, yak:0.00357891):0.00354521):0.000438041):0.008455):0.0199578):0.00783972):0.00457048):0.010958):0.00487198):0.0541789):0.0709835);



Locus Name: Caudal Type Homeobox 4 (CDX4)

Locus Name: Homeobox protein notochord (NOTO)

ENSBTAT00000047327 NOTO-202 homeobox transcription factor embryonic somitogenesis,
mouse: notochord, axial skeleton, axial vs paraxial cell fate

PP2: (Giraffe) G98R, Y223H

Giraffe: Q115R UPS, D162G UIS, Y223H UIS, A257S UPS

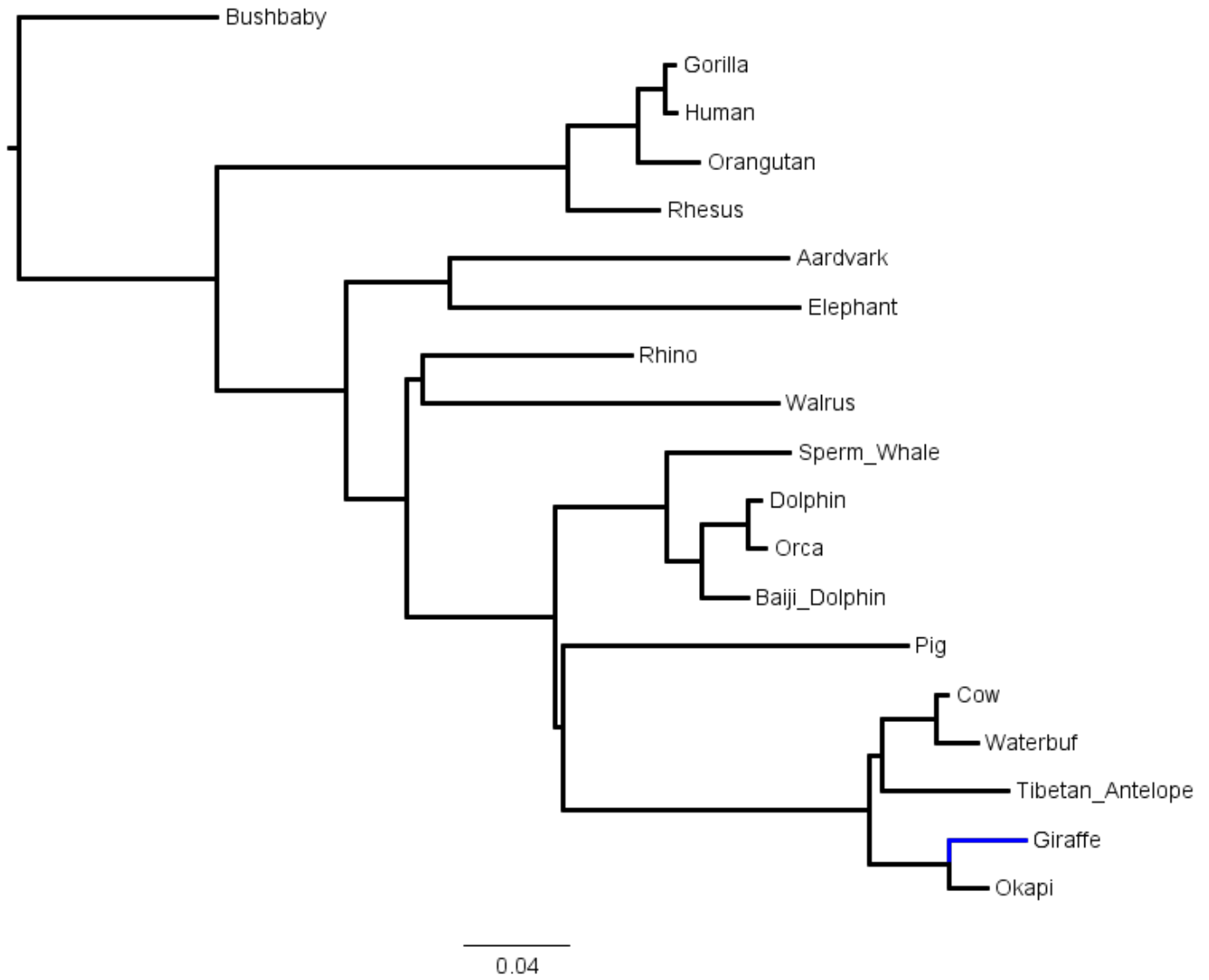
Giraffe/Okapi: R23H UPS, H81Y UPS, LP105-106PR UIS, H191Q UIS

Protein sequence Alignment of Cow, Giraffe and Okapi NOTO

Cow	1	MPSPGPRGCRPLPLSGAGVQQRSSRSRPPASPALPRGSANPGPARAPGRGLASSFSVEAI	60
Giraffe	1L....V...PH..G..G.....V....P.....V.....	60
Okapi	1L.....PH.....G.....S....PC.....	60
Cow	61	LARPDPRAPTTSPLSVSAGAHGDLWNVPSRPPAQALPGACPPTWLPCLSAGLHQPRPQP	120
Giraffe	61Y.....R.....PRA.....R.C...	120
Okapi	61Y.....W.....PRA....R....C...	120
Cow	121	PALRPLASHFCGLQGLSVTGLELVHCLGLWDPRDWAQAQDLQDTERSFKRIRTMFNLEQL	180
Giraffe	121Q.....G....Q.....	180
Okapi	121Q.....Q.....	180
Cow	181	EELKVFQKQHNIVGKKRAQLAAQLNLTENQVRVWFQNRVVKYQKQRLKLPASAMAAS	240
Giraffe	181Q.....H.....V...	240
Okapi	181Q.....V...	240
Cow	241	PDEPSSSDTSIQREDAESGMS	263
Giraffe	241S.....	263
Okapi	241	263

Newick Tree of Mammalian NOTO

(bushbaby:0.0742945, (((gorilla:0.00358939, human:0.00441074):0.00992558, orangutan:0.0225977):0.0265145, rhesus:0.034061):0.131246, ((aardvark:0.126819, elephant:0.130966):0.0388679, ((rhino:0.0780812, walrus:0.133037):0.00592613, ((sperm_whale:0.0459875, (dolphin:0.00480401, orca:0.00645338):0.017312, baiji_dolphin:0.0170391):0.0132068):0.0420243, (pig:0.128882, ((cow:0.0040265, waterbuf:0.0151691):0.0204709, tibetan_antelope:0.0470651):0.00501175, (giraffe:0.0284239, okapi:0.0143141):0.0299388):0.114692):0.0028508):0.0554365):0.0229346):0.04806):0.0742945);



Locus Name: Homeobox protein notochord (NOTO)

Locus Name: Jagged 1 homolog to Drosophila Serrate (JAG1)

ENSBTAT0000009631 JAG1-201 Notch ligand vertebrae development, cardiovascular, eye, kidney human: Alagille syndrome defects in heart and vertebrae abnormalities. mouse: right ventricular hypertrophy, overriding aorta, ventricular septal defects, coronary vessel abnormalities and valve defects

PP2: L134F

Giraffe: S916T UIS, S939P UIS

Giraffe/Okapi: V45P UPS, D72N UIS, L135F UIS, K854T UPS, SE909-910NQ UIS, K944R UIS, E995K UIS, A1015T UIS

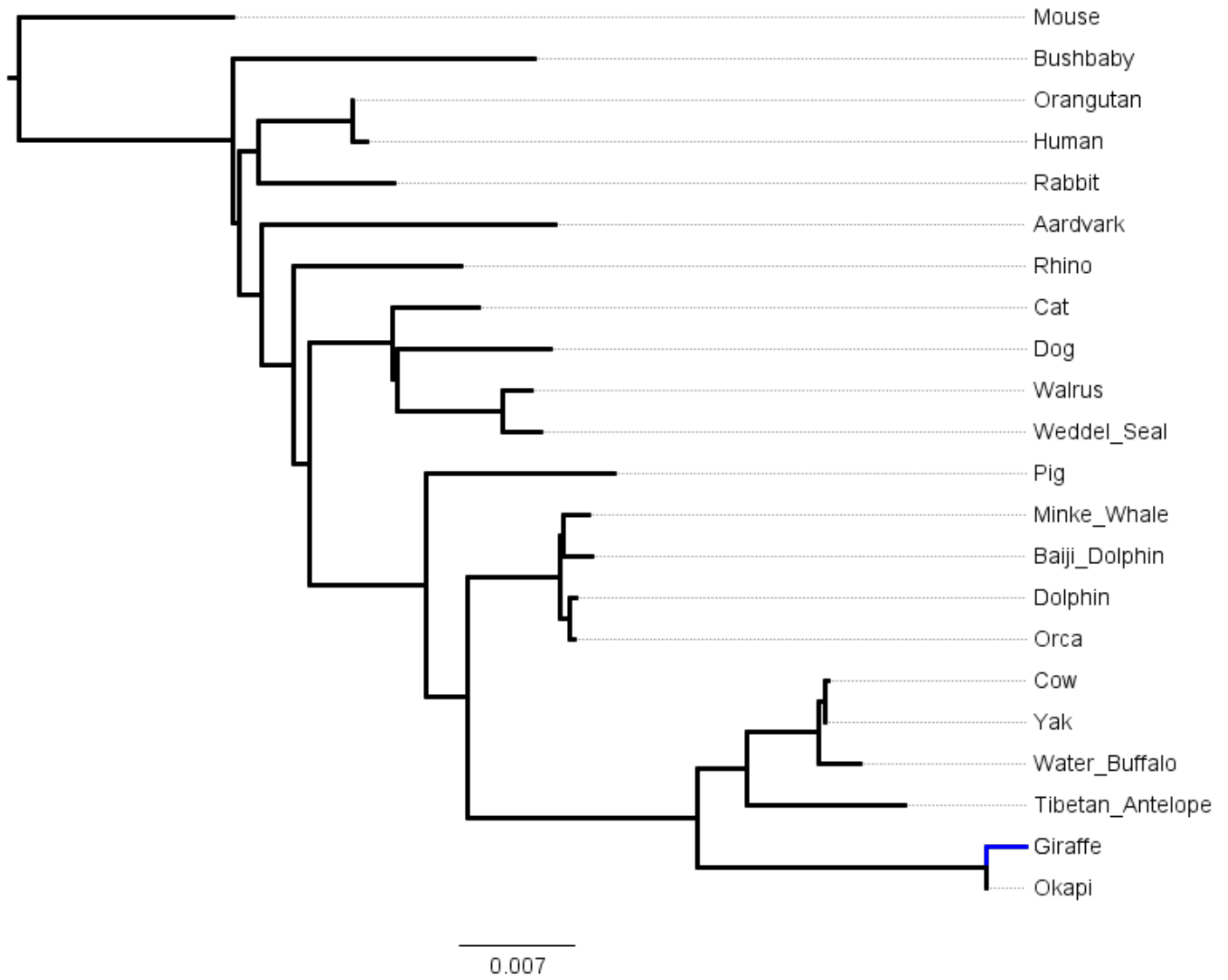
Protein sequence Alignment of Cow, Giraffe and Okapi JAG1

Cow	1	MRSRTRGRPGRPLSLLLALLCALRAKVCASGQFELEILSMENVNGELQNGNCCGGSRN	60
Giraffe	1P.....	60
Okapi	1P.....	60
Cow	61	PGDRKCSRDECDTYFKVCLKEYQSRVTAGGPCSFGSGSTPVIGNTFDLKASRGNERNRI	120
Giraffe	61N.....L.....DG....	120
Okapi	61N.....L.....DG....	120
Cow	121	VLPFSFAWPRSYYTLLEAWDSSNDTVQPDSIIIEKASYSGMINPGRQWQTLKQNTGVAHFE	180
Giraffe	121F.....L..R.....A.....	180
Okapi	121F.....L..R.....A.....	180
Cow	181	YQIRVTCDDYYYGFGCNKFCRPRDDFFGHYACDQNGNKTCMEGWMGPECNKAICRQGCSP	240
Giraffe	181	240
Okapi	181	240
Cow	241	KHGSKLPGDCRCQYGWQGLYCDKCIHPGCVHGTCEPWCCLCETNWWGGQLCDKDLNYC	300
Giraffe	241	300
Okapi	241	300
Cow	301	GTHQPCLNGGTCSENTGPKYQCSCPEGYSGPNCEIAEHACLSDPCHNRGCKETSLGFEC	360
Giraffe	301	360
Okapi	301	360
Cow	361	ECSPGWTGPTCSTNIDDCSPNNCAHGGTCQDLVNGFQCVCPPQWTGKTCQLDANECEAKP	420
Giraffe	361S.....K.....	420
Okapi	361S.....K.....	420
Cow	421	CVNARCKNLIASYYCNCLPGWMQNCNDININDCVGQCQNDASCRDLVNGYRCICPPGYA	480
Giraffe	421G...D.....Q.....	480
Okapi	421G...D.....Q.....	480
Cow	481	GDHCETDIDECASNPCLNGGHCQNEINRFQCLCPTGFSGNLCQLDIDYCEPNPCQNGAQC	540
Giraffe	481	540
Okapi	481	540
Cow	541	YNRASDYFCKCPEDYEGKNCSHLKDHCRTTPCEVIDSCTVAMASNDTPEGVRYISSNVCG	600
Giraffe	541	600
Okapi	541	600
Cow	601	PHGKCKSQSGGKFTCDCKNGFTGTYPHENINDCESNPCRNGGTCIDGVNSYACICSGGWE	660
Giraffe	601I.....	660
Okapi	601	660
Cow	661	GAHCETNINDCSQNPCHNGGSCRDLVNDFYCDCKNGWKGTCHSRDSQCDEATCNGGTC	720
Giraffe	661A.....	720
Okapi	661A.....	720
Cow	721	YDEGDAFKCMCPGGWEGTTCNIARNSSCLPSPCHNGGTCVVNGESFTCVCKEGWEGPICT	780
Giraffe	721	780
Okapi	721	780
Cow	781	QNTNDCSPHPCYNSGTCVDGENWYRCECAPGFAGPDCRININECQSSPCAFCATCVDEIN	840
Giraffe	781	840
Okapi	781	840

Cow	841	GYRCICPPGHSGAKCQEVSGRSCVTMGSVIPDGAKWDADCNACQCLDGRVACSKVWCGPR	900
Giraffe	841T.....I..M.....D.....	900
Okapi	841T.....I..M.....D.....	900
Cow	901	PCSLHRGHSECPGQSCVPILDTQCFVVRPCTGVGECRSSLQPVKTKCASDPYYQDNCAN	960
Giraffe	901K..NQ.....T.....P.....R...V.....	960
Okapi	901K..NQ.....R...V.....	960
Cow	961	ITFTFNKEMMSPGLTTEHICSELRLNLILKNVSAEYSIYIACEPSPSANNEIHVAISAED	1020
Giraffe	961K.....T.....	1020
Okapi	961K.....T.....	1020
Cow	1021	IRDDGNPIKEITDKIINLVSKRDGNSSLIAAAVAEVRVQRRLPKSRTDFLVPLLSSVLTVA	1080
Giraffe	1021R..D.....N.....	1080
Okapi	1021R..D.....N.....	1080
Cow	1081	WVCCLVTAFYWCVRKRRKPGSHARAASEDNTTNNVREQLNQIKNPIEKHGANTVPVKDYE	1140
Giraffe	1081I.....	1140
Okapi	1081I.....	1140
Cow	1141	SKNSKMSKIRTHNSEVEEDMDKHQQKARFAKQATYTLVDREEKPAHGTPAKHPNWTNKQ	1200
Giraffe	1141P.....	1200
Okapi	1141P.....	1200
Cow	1201	DNRDLESAQSLNRMEYIV	1219
Giraffe	1201	1219
Okapi	1201	1219

Newick Tree of Mammalian JAG1

```
(mouse:0.0130438, (bushbaby:0.0184162, ((orangutan:0, human:0.000829258):0.00576013,
rabbit:0.00830182):0.00113569, (aardvark:0.0179997, (rhino:0.0102121, ((cat:0.00525205,
(dog:0.00933142, (walrus:0.001755, weddel_seal:0.00235855):0.00642237):0.00031529):0.00507031,
(pig:0.0115497, ((minke_whale:0.00153792, baiji_dolphin:0.00175157):0.000250757,
(dolphin:0.000460762, orca:0.000360593):0.000571613):0.00560691, (((cow:0.000187183,
yak:0):0.000337076, water_buffalo:0.0025458):0.00437421, tibetan_antelope:0.00964462):0.00306327,
(giraffe:0.00240867, okapi:5.54004e-
05):0.0176221):0.0139723):0.00256881):0.00711842):0.000895776):0.00203781):0.00127203):0.00045141
4):0.0130438);
```



Locus Name: Jagged 1 homolog to Drosophila Serrate (JAG1)

Locus Name: delta-like three (DLL3)

ENSBTAT00000013852 DLL3-201 Notch ligand embryonic somitogenesis
mouse: disruption of somite boundaries, shortened trunk, vertebrae
malformed

PP2: (Giraffe/Okapi) L103M, R261G, P342L; (Okapi) G132D, G148C

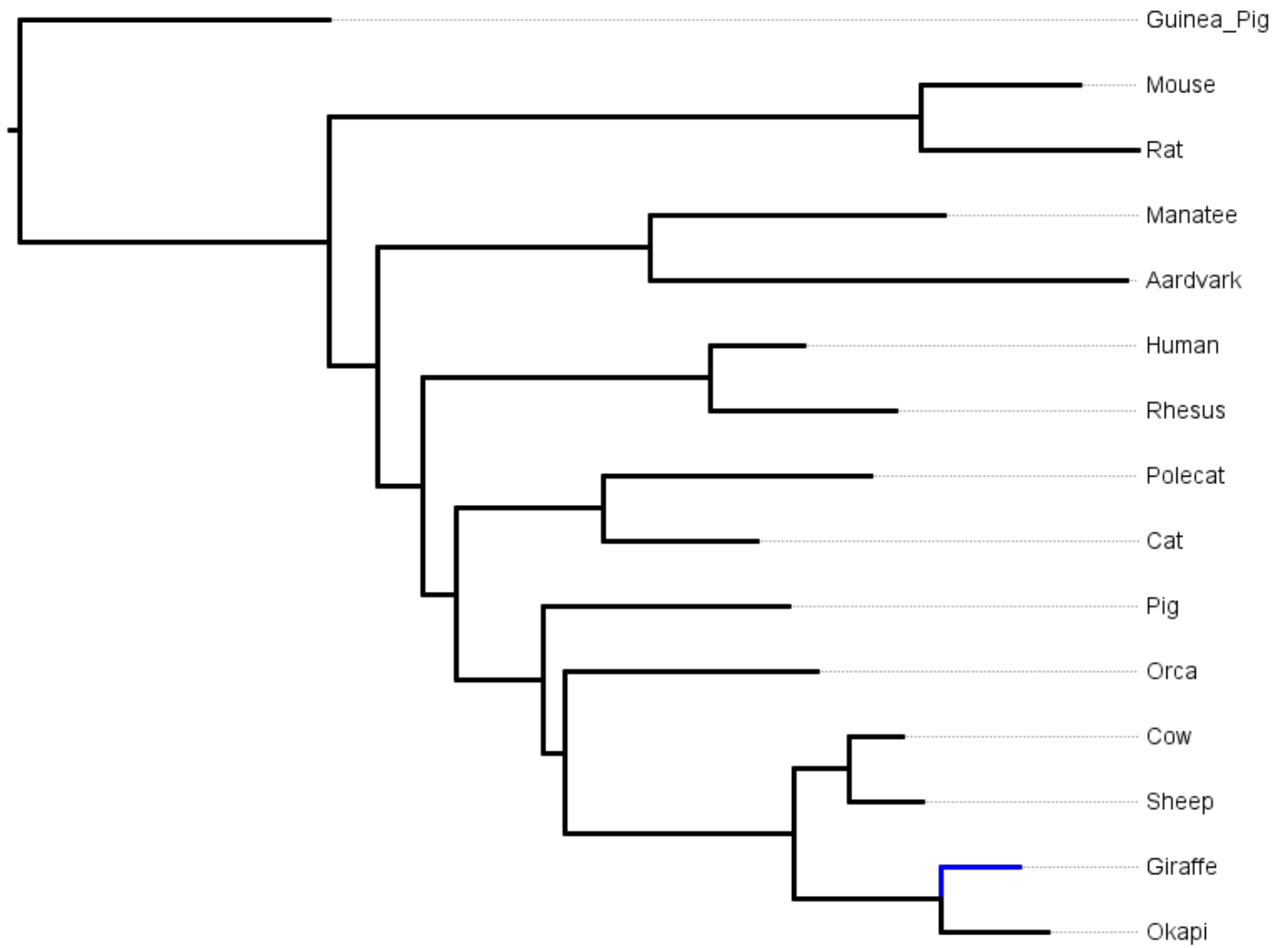
Giraffe: L10F UPS, G195A UPS, P197S UPS, L258F UIS, A475T UPS
Giraffe/Okapi: P7L UPS, E71D UIS, V89A UPS, L103M UIS, S254R UPS, R261G UIS, P526R UPS, R585P
Okapi: S69P UIS, G132D UPS, L143V UIS, G148C UIS

Protein sequence Alignment of Cow, Giraffe and Okapi DLL3

Cow	1	MVAPQMPQLLSSTVILALFFLPQAQFAGVFELQIHSFGPGPGTFRSPCKAGGSCRLFF	60	
Giraffe	1L..F.....A.....S.....	60	
Okapi	1L.....L.....A.....S.....	60	
Cow	61	RVCLKPGLSEETAETAEAPCTLGAALSARGPVYTAQPGALAPELRLPDGLLRVPFRDAWPGTF	120	
Giraffe	61D.....A.....P.....M.....T.....	120	
Okapi	61P.D.....A.....VP.....M.....	120	
Cow	121	SLIIETWREELGGQIGGAAWSLLARVAGRLLAAGGPWTRDVQRAGAWELRFSYRARCEP	180	DSL domain
Giraffe	121P.....R.....	180	
Okapi	121D.....P.....V..M.C..R.....T.....	180	
Cow	181	PAVGAACARLCRSRGAPLRCDPELRPCAPVEEECEAPPVCRAGCSPEHGFCEQPDECRL	240	
Giraffe	181A.S.....T..D...L.....	240	
Okapi	181T...D...L.....	240	
Cow	241	EGWTGPLCTIPVSSSSCLSSRGPSATTGCLVPGPGPCDGNPCANGGSCSETLGSFECTC	300	6 EGF repeats
Giraffe	241R..F..G.....	300	between DSL & TM
Okapi	241R.....G.....	300	
Cow	301	PRGFYGLRCEVSGVTCADGPCFNGGLCVGGADPDSAYICHCPPGFQGSNCEKRVDRCSLQ	360	
Giraffe	301T.....L.....	360	
Okapi	301T.....L.....K	360	
Cow	361	PCRNGGLCLDLGHALRCRCRAGFAGPRCEHDLEDCTGHTCANGGTCLEGGGARRCSCALG	420	
Giraffe	361	420	
Okapi	361	420	
Cow	421	FGGRDCRERADPCAARPCAAGGRCYAHFSGLVACAPGYMGARCEFPVHPDGAGALPAAQ	480	
Giraffe	421T.....	480	
Okapi	421	480	
Cow	481	PGLREGDPQRFLPPALGLLVAAGLAGAALLLVHVRRRGSPSRDTGPRLLAGTPEPSVHAL	540	TM domain
Giraffe	481	...Q.....S.R.....	540	
Okapi	481	...Q.....S.R.....	540	
Cow	541	PDALNNMRTQEGPGDGFSPSSDWNHPEDGDARSIIYVISAPSVYAREA	587	
Giraffe	541R.....L.....I..P..	587	
Okapi	541R.....I..P..	587	

Newick Tree of Mammalian DLL3

(guinea_pig:0.0460113, ((mouse:0.0238228, rat:0.0323618):0.0883706, ((manatee:0.0439186, aardvark:0.070948):0.0408664, ((human:0.0140158, rhesus:0.0278144):0.0428855, ((polecat:0.0399908, cat:0.0230087):0.0219097, (pig:0.0366227, (orca:0.0377216, ((cow:0.00797501, sheep:0.0109108):0.00810372, (giraffe:0.0116582, okapi:0.0159333):0.0219494):0.0343832):0.00320336):0.012967):0.00504953):0.0067664):0.00721435):0.0460113);



0.02

Locus Name: **delta-like three (DLL3)**

Locus Name: Neurogenic Locus Notch Homolog Protein 4 (Notch4)

ENSBTAT0000050083 NOTCH4-201 notch pathwaymesoderm development, angiogenesis, neurogenesis
 mouse: Homozygotes for null alleles exhibit no obvious phenotypic defects. However, in
 conjunction with Notch1 deficiency, embryonic, vascular, and nervous system defects are observed.

PP2 (Giraffe) D650N, Q750H, V1714I; (Giraffe/Okapi) G1893E; (Okapi) Q638M, A846T

Protein sequence Alignment of Cow, Giraffe and Okapi

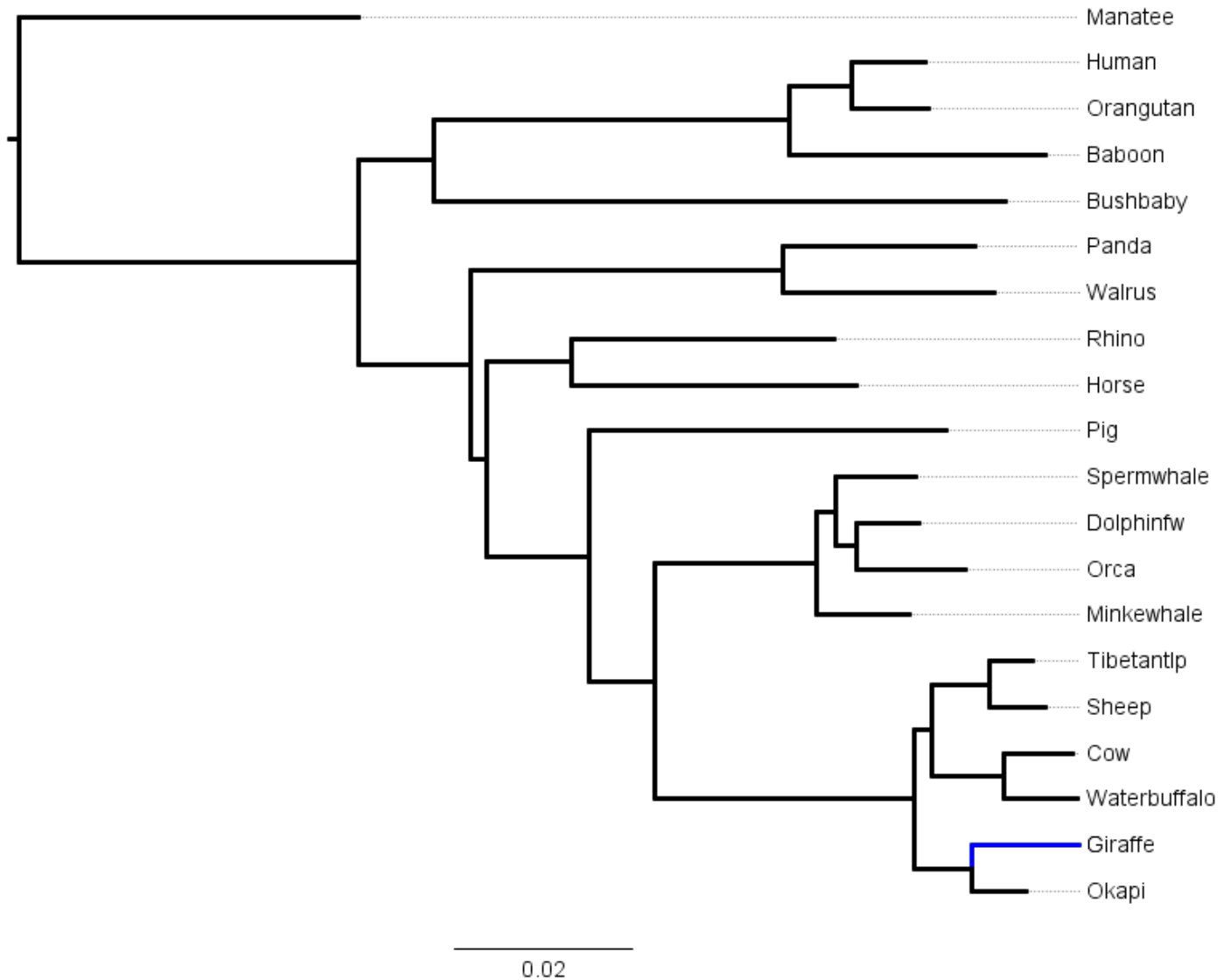
Cow	1	MQPPSLLLPLLLLLCQPVVTRTRGLQCGSFPEPCANGGTCLSLSQGQGTCCAPGFLGETC	60
Giraffe	1P.....R.....H.....	60
Okapi	1P.....R.....H.....	60
Cow	61	QFPDPCQDAQPCQNGGSCHTFLPTLPGSPGTPSPMAPSFFCTCPSGFTGDRCQAQIRDPC	120
Giraffe	61S..SA.....K...	120
Okapi	61S..S.....K...	120
Cow	121	SSFCSKMGRCHLQDSGRPRCSCMPGWTGEHCQLRDFCSANPCVNGGVCLATYPQIQCRCP	180
Giraffe	121A.....Q.....	180
Okapi	121A.....Q.....	180
Cow	181	PGFEGHACEHDVNECYLDPGPCPKGTTCHNTLGSCQCLCPAGREGPRCGLRPGPCTPRGC	240
Giraffe	181F.....S.....L.....M..	240
Okapi	181F.....D.....	240
Cow	241	LNGGTCQLVPGRDSTFHLCLCPPGFTGPSCEVNPDDCAGHCQNGGTCQDGLGTYTCLCP	300
Giraffe	241V.....	300
Okapi	241V.....	300
Cow	301	EAWTGWDCSEDVDECEVQGPPCRNGGTCQNSAGDFYCVCSVSGWGAGCEENLDDCVAAT	360
Giraffe	301H.....	360
Okapi	301H.....	360
Cow	361	CAPGSTCIDRVGSFSLCLPPGRTGLLCHMEDMCLSQPCHEEAQCSTNPLSGSTLCVCQPG	420
Giraffe	361	420
Okapi	361	420
Cow	421	YTGP TCHQDLDECQMAQQGPPSPCEHGGSCLNTPGSFECLCPPGYTGSRCEADHNECLSQP	480
Giraffe	421	480
Okapi	421	480
Cow	481	CHRG TCDLLLATFQCLCPPLEGQLCEVEIDE CASAPCLNQADCHDLLNGFQCICQPGF	540
Giraffe	481	.Q.....R.....N...S..R.V.R...	540
Okapi	481	.Q.....N.....R.V.R...	540
Cow	541	TGPRCEEDINECQSSPCANGGECQDQPGSFHCKCPPGFEGPRCQE EVDECLSGPCPTGAS	600
Giraffe	541Q.....	600
Okapi	541	..S..Q.....Q.....	600
Cow	601	CLDLPGAFLCVCPSGFTGHLCEIPLCAPNLCQPKQKQDQEDNAHCLCPDGNPGCVPTED	660
Giraffe	601Q.....P...R...SN.....	660
Okapi	601I...D...Q.....M...R.....	660
Cow	661	NCTCHHGHCQRSSCVCDGGWTGPECDDTLGGCVSTPCA HGGTCHPQPFYGNCTCPTGYTG	720
Giraffe	661E.....	720
Okapi	661	720
Cow	721	PTCSEEV TACHSGPCLNGGSCSPSPGGYTCTCPLSHTGLRCQTSIDHCASALCLNGGTCV	780
Giraffe	721S.A.....P.....	780
Okapi	721S.A.....P.....	780
Cow	781	NKPGTF SCLCTPGFQGP RCEGRTRPSCADSPCRNMATCQDSPQGP RCLCPPGYTG GSCQT	840
Giraffe	781	.R...S...A..H.....K.....	840
Okapi	781	.R...S...A.....K.....	840

Cow	841	LMDLCAQKPCPQNSHCLQTGPSFQCLCLQGWTFPLCNLPLSSCQKVALSQGTEVSSLCQN	900
Giraffe	841	900
Okapi	841	.V...T.....	900
Cow	901	GGVCIDSGPSHFCHCPPGFQGSICQDQVNPCESTRPCQHGATCVAQPNGYLCQCAPGYSGQ	960
Giraffe	901T.....	960
Okapi	901T.....R.....	960
Cow	961	NCSEEPDACQSQPCHNQGTICISKPGGFHCACPPGFVGLRCEGDVDECLDRPCHPTGTAAAC	1020
Giraffe	961L.....TP.....Y.....A.....	1020
Okapi	961L.....TP.....A.....	1020
Cow	1021	HSLANAFYCQCLPGHTGQWCEVELDPCQSQPCAHSQSCEATAGPPPGFTCHCPQGFEGPT	1080
Giraffe	1021G.....	1080
Okapi	1021G.....	1080
Cow	1081	CSHRAPSCGLHHCHHGGLCLPSPKPLPPRCACLNGYGGPDCLTPPAPSGCGPPSPCLHN	1140
Giraffe	1081P.....	1140
Okapi	1081	1140
Cow	1141	GSCSETPGLGGPGFRCSPPASSPGPRCQRPVKGCEGRSGDGACDAGCSGPGGNWDGGDC	1200
Giraffe	1141I.....D.....	1200
Okapi	1141	1200
Cow	1201	SLGVDPDPWKGCPSPHSRCWLLFRDQCHPQCDSEECFLFDGYDCETPPACIPAYDQYCRDHF	1260
Giraffe	1201Q.....T.....H...	1260
Okapi	1201T.....	1260
Cow	1261	HNGHCEKGCNTAECGWDDGDCRPELDGNSEWGPSLALLVVLSPSTLDQQLLALARVLSLTL	1320
Giraffe	1261I.....F.....A.....	1320
Okapi	1261	1320
Cow	1321	RVGLWVRKDSEKDMVYPYPGAQAEELGGTPDPSQQERAAQTEPTGKETDLSLSTGFVV	1380
Giraffe	1321R.....Q.....	1380
Okapi	1321R.....Q.....N.....	1380
Cow	1381	VMGVDSLHCGPERPASRCPWDPGLLLRFLAAMAAGALEPLLPGLLAAHPRAGTKPSAN	1440
Giraffe	1381R.....H.....E.....	1440
Okapi	1381R.....H.....E.....	1440
Cow	1441	QLPWPVLCSPVVGVLALLGALLVQLIRRRRREHGALWLPFGFTRRPRTQPVSRRRRPP	1500
Giraffe	1441	1500
Okapi	1441	1500
Cow	1501	LGEDSIGLKALKAEADMDEDGVVMCSVPKEGEEVQAEEMASPPKCQLWSLSSDCQELPQ	1560
Giraffe	1501E.....Q.....V.....	1560
Okapi	1501E.....H.....	1560
Cow	1561	AAMLTPPDSEMDVPDVTQGPDPVPLMSAVCCGGVESRTYQETWLGSPWPWEPLLEGG	1620
Giraffe	1561D..	1620
Okapi	1561D..	1620
Cow	1621	ACPQVHTVGTGETPLHLAARFSRPTAARRLLEAGANPNQPDRAGRTPHHTAADAAREVC	1680
Giraffe	1621	1680
Okapi	1621	1680
Cow	1681	QLLLRSRQTAVDARTEDGTTALMLAARLAVEDLVEELIAAQADVGARDKWGKTALHWAAA	1740
Giraffe	1681I.....	1740
Okapi	1681	1740
Cow	1741	VNNARAARSLAQAGADKDAQDGREQTPLFLAAREGAMEVAQLLLGLGAAQGLRDQAGLTP	1800
Giraffe	1741R.....	1800
Okapi	1741R.....	1800
Cow	1801	GDVARQRNHWDLLTLLEGAGPPEARHKPTPGRGAGTFQARARTASGSVPPRGGGAVPRCRT	1860
Giraffe	1801P.....	1860
Okapi	1801T.....A.....	1860

Cow	1861	LSAGARPQARTLSVDLAAHGGGAYSHCRSLSKGTGEGPPLRGRRFSAAGMRGPRPNPAMVR	1920
Giraffe	1861S.....E.....A.....	1920
Okapi	1861S.....E.....V..	1920
Cow	1921	GRPGVSAGSGGVAATVDWPCDWVPLGACGPASNTPIPPPCLTPSPERGSPQVAWGPPAHQ	1980
Giraffe	1921	..S..A.....A.....A.....	1980
Okapi	1921	..S..A.....A.....A.....	1980
Cow	1981	VIPLNAGGEGQK	1992
Giraffe	1981	1992
Okapi	1981	1992

Newick Tree of Mammalian NOTCH4

```
(manatee:0.0382014, (((human:0.00838792, orangutan:0.00875044):0.00688613,
baboon:0.0288976):0.040128, bushbaby:0.0643707):0.00864676, ((panda:0.0217116,
walrus:0.023918):0.0351746, ((rhino:0.0295228, horse:0.03205):0.00969203, (pig:0.0403091,
((spermwhale:0.00902558, (dolphinfw:0.00705352, orca:0.012218):0.00243441):0.00220093,
minkewhale:0.0105096):0.0180912, ((tibetantlp:0.00485875, sheep:0.00630344):0.0064468,
(cow:0.00781667, waterbuffalo:0.00837873):0.00808722):0.00212078, (giraffe:0.012021,
okapi:0.00621759):0.00658709):0.0291063):0.00746966):0.0116224):0.00173587):0.0127588):0.0382014;
```



Locus Name: Neurogenic Locus Notch Homolog Protein 4 (Notch4)

Locus Name: Fibroblast growth factor receptor-like 1 (FGFRL1)

ENSBTAT0000039444 FGFRL1-201 decoy FGF receptor cranofacial, axial & appendicular skeleton, heart, kidney mouse: multiple skeletal defects, delayed mineralization in cervical vertebrae, heart defects human: Wolf-Hirschhorn syndrome

PSG: T250A 0.908, D259G 0.905, F260S 0.910, F266L 0.909, K269R 0.918, K275R 0.908, E285D 0.906
PP2: (Giraffe) D259G, F260S, K269R, K275R, E285D

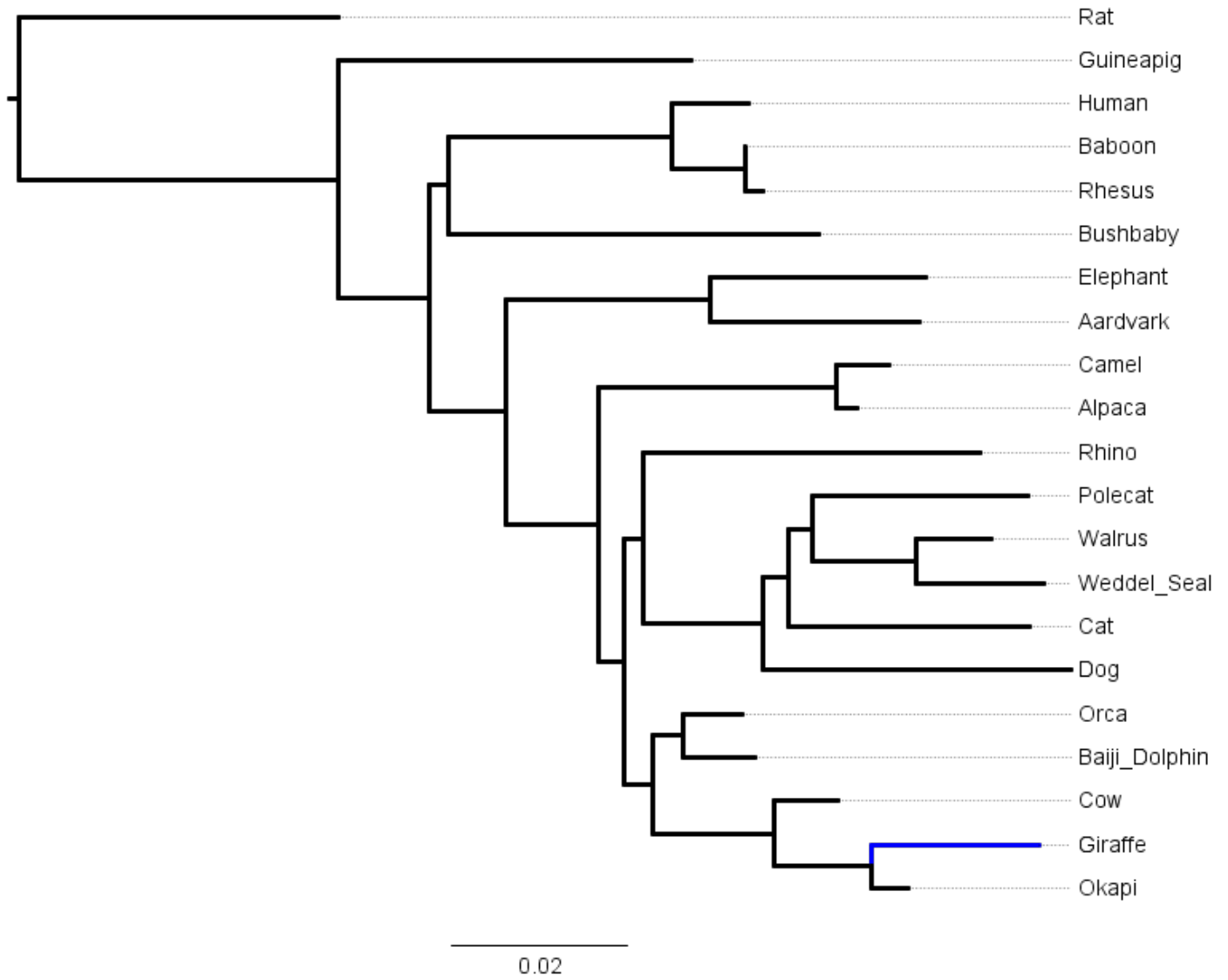
Giraffe: T250A UIS, D259G UIS, F260S UIS, F266L UIS, K269R UIS, K275R UIS, E285D UIS
Giraffe/Okapi: G254S UIS

Protein sequence Alignment of Cow, Giraffe and Okapi FGFRL1

Cow	1	MTPSPALVLP LLLLLL GALPPAAAARGP PRMADKV VPRQVARLGR TVRLQCPVEGDP PPLT	60
Giraffe	1	60
Okapi	1	60
Cow	61	MWTKDGR TIHGGWSRFRVLPQGLKVKEVEPEDAGAYVCKATNGFGSLSVNYTLIVMDDTS	120
Giraffe	61	120
Okapi	61	120
Cow	121	PGRESFGHDSSSGGQEDPASKQWARPRFTQPSKMRRRVIARPVGSSVRLKCVASGHPRPD	180
Giraffe	121G.....G.....	180
Okapi	121G.....	180
Cow	181	IMWMKDDQALTRPEAGEHRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQR	240
Giraffe	181	240
Okapi	181	240
Cow	241	TRSKPVL TGTHPVNTTVDFGGTTSFQCKVRSVDKPV IQWLKRVEYGAEGRYNSTIDVGGQ	300
Giraffe	241A.....GS.....L..R.....R.....D.....	300
Okapi	241	300
Cow	301	KFVVLPTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVLPDPKP	360
Giraffe	301	360
Okapi	301	360
Cow	361	PGPPVAPSSSTTSLPWPV VIGIPAGAVFIVGT VVLWLCQAKKKPCAPAPPAPHRPPATA	420
Giraffe	361	422
Okapi	361S.....	422
Cow	421	RDRGGDKDLPAPATVGS GPGVGLCEELGPPAAPQHLLGPGSATGPKLYPKLYTDTHTHH	480
Giraffe	423	.E.S.....T..PL.....A.....S.....	482
Okapi	423	.E.....T..PL.....T.....S.....	482
Cow	481	SHTHSHVEGKVHQHQH THYHC	501
Giraffe	483I..Q.	503
Okapi	483I..Q.	503

Newick Tree of Mammalian FGFRL1

(rat:0.0365636, (guineapig:0.0405323, ((human:0.00871237, (baboon:0, rhesus:0.00218068):0.00832846):0.025617, bushbaby:0.042395):0.00227335, ((elephant:0.024841, aardvark:0.0239686):0.0233709, ((camel:0.00607814, alpaca:0.00241458):0.0272582, ((rhino:0.0386203, ((polecat:0.0248259, (walrus:0.00855245, weddel_seal:0.0147311):0.0119796):0.00264384, cat:0.0275929):0.00302873, dog:0.035323):0.0135985):0.00230938, ((orca:0.00669743, baiji_dolphin:0.00821288):0.00352718, (cow:0.00721142, (giraffe:0.0192411, okapi:0.00419128):0.0111612):0.0139591):0.00336271):0.00286468):0.0106337):0.00882947):0.0104164):0.0365636);



Locus Name: Fibroblast growth factor receptor-like 1 (FGFRL1)

Locus Name: programmed cell death 2-like (PDCD2L)

ENSBTAT0000003327 PDC2L-201 transcriptional repressor programmed cell death
no mutants described for mouse or human

PP2: (Giraffe) D128G

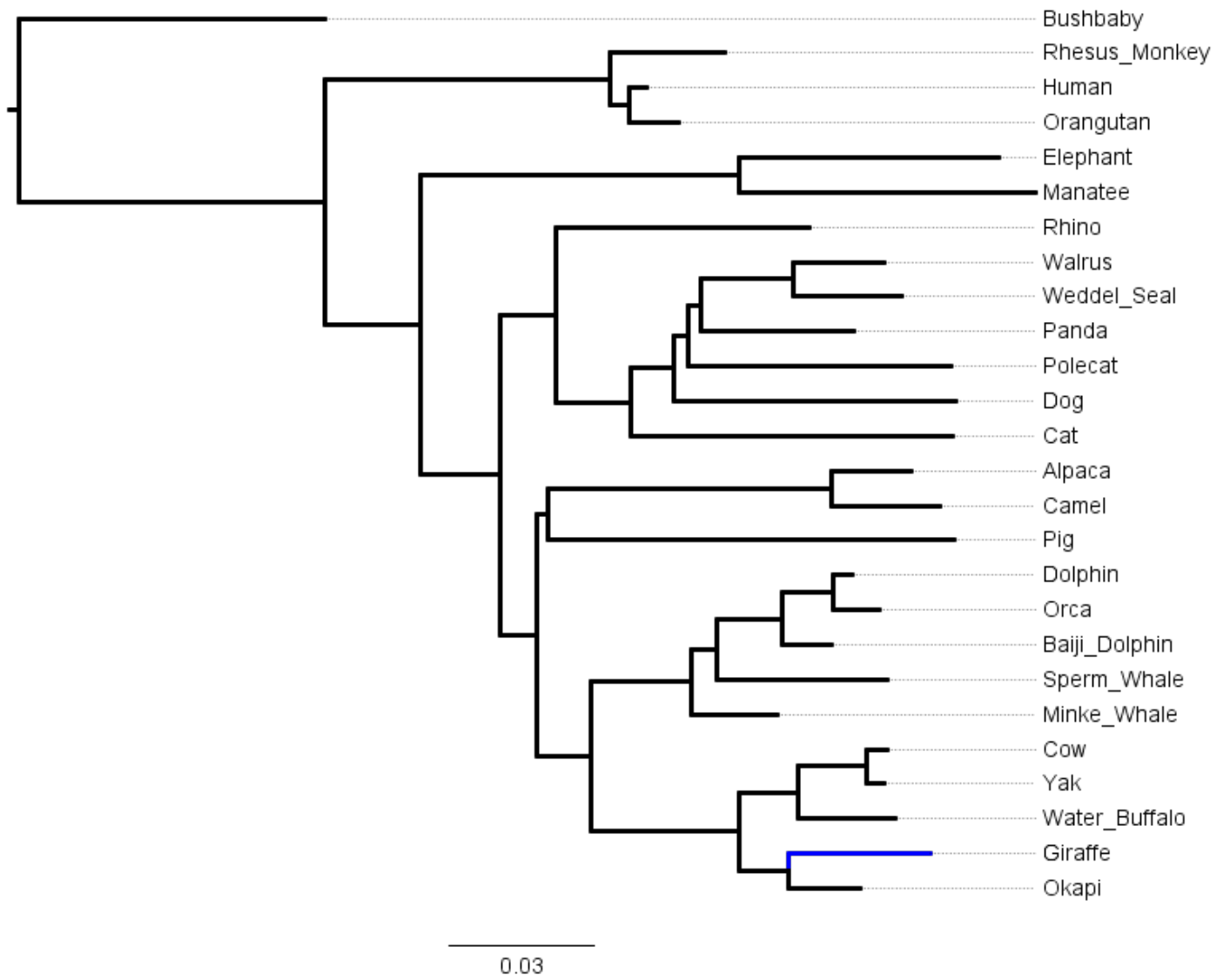
Giraffe: K6E UPS, V35D UPS, D128G UIS, A137S UPS, G181R UPS, K248R UIS
Okapi: T207M UPS, T285I UPS

Protein sequence Alignment of Cow, Giraffe and Okapi PDCD2L

Cow	1	MAAVRKPVLLGLRDAAVHGRPTGPSAWTASKLGGVDPDALPAVAAPRPVCELRCRQPLALVV	60
Giraffe	1	...A.E.....S.....D.....	60
Okapi	1	...A.....	60
Cow	61	QVYCPLEGS PFHRL LHVFACPRPECGSGGARSWKVFRSQCLQMREKETQDAQKQENGLTA	120
Giraffe	61	120
Okapi	61A.	120
Cow	121	EDWCEGADDWGS DSEEASPLQPVSEFGNDLSNAKDRDWTSQLQDLRLQDTPVPGVAPPAPP	180
Giraffe	121G.....S..P..I..D....S.....A.....	180
Okapi	121P..I..D....S.S.....H.....A.....	180
Cow	181	GGGPALPPSVPQFLPYIICVVD EDDYTD FDISLDHAQSLLREYQQREGVDMEQLLSQSLSS	240
Giraffe	181	RE.L...A.....S..N.....V.....K.....	240
Okapi	181	.E.L...V.....G.....M..V.....K.....	240
Cow	241	DGDEKYEKTVIKSGDKMFYKFMKRIAACQE QILRY SWSGEPLFLTCPTSEVTELPACSYC	300
Giraffe	241R.I.....H.	300
Okapi	241I.....I.....H.	300
Cow	301	GARRIFEFQLMPALVSM LRSANLDLSVEFGTIL IYTCEKSCWPQNDQAPMEEFCIIQEDP	360
Giraffe	301V.....V.....I.....	360
Okapi	301V.....I.....	360
Cow	361	DELLFK	366
Giraffe	361	366
Okapi	361	366

Newick Tree of Mammalian PDCD2L

(bushbaby:0.0637978, ((rhesus_monkey:0.0240491, (human:0.00359046, orangutan:0.0104749):0.0040552):0.0596258, ((elephant:0.0545039, manatee:0.0618291):0.0665387, ((rhino:0.0528277, (((walrus:0.0191956, weddel_seal:0.0226637):0.0193703, panda:0.0319915):0.0026076, polecat:0.0551402):0.00288622, dog:0.058893):0.00901244, cat:0.0672426):0.0157226):0.0117629, ((alpaca:0.0165552, camel:0.0225659):0.0593276, pig:0.08493):0.00229234, (((dolphins:0.00399435, orca:0.00976145):0.0106728, baiji_dolphin:0.0101595):0.0138221, sperm_whale:0.035824):0.00514097, minke_whale:0.0178994):0.0211134, ((cow:0.00437979, yak:0.0038508):0.0143783, water_buffalo:0.0205185):0.0122919, (giraffe:0.0295816, okapi:0.0150087):0.010454):0.0309843):0.0112464):0.00779422):0.0165112):0.0201117):0.0637978);



Locus Name: programmed cell death 2-like (PDCD2L)

Locus Name: cMyc

ENSBTAT0000011066 MYC-201 transcription factor cell proliferation, growth control, oncogene

mouse: Mutations affect growth and development of heart, pericardium, neural tube, vasculogenesis and erythropoiesis. Homozygous null mutants die by embryonic day 10.5. Heterozygotes have reduced body size and multiorgan hypoplasia;

PP2: (Giraffe) L3Y; (Giraffe/Okapi) G108S, P207S, A209D

Giraffe: L3Y UPS, V5A UPS, S79A UPS, A215S UPS

Giraffe/Okapi: R83K UPS, G108S UIS, A209D UPS, L224F UIS

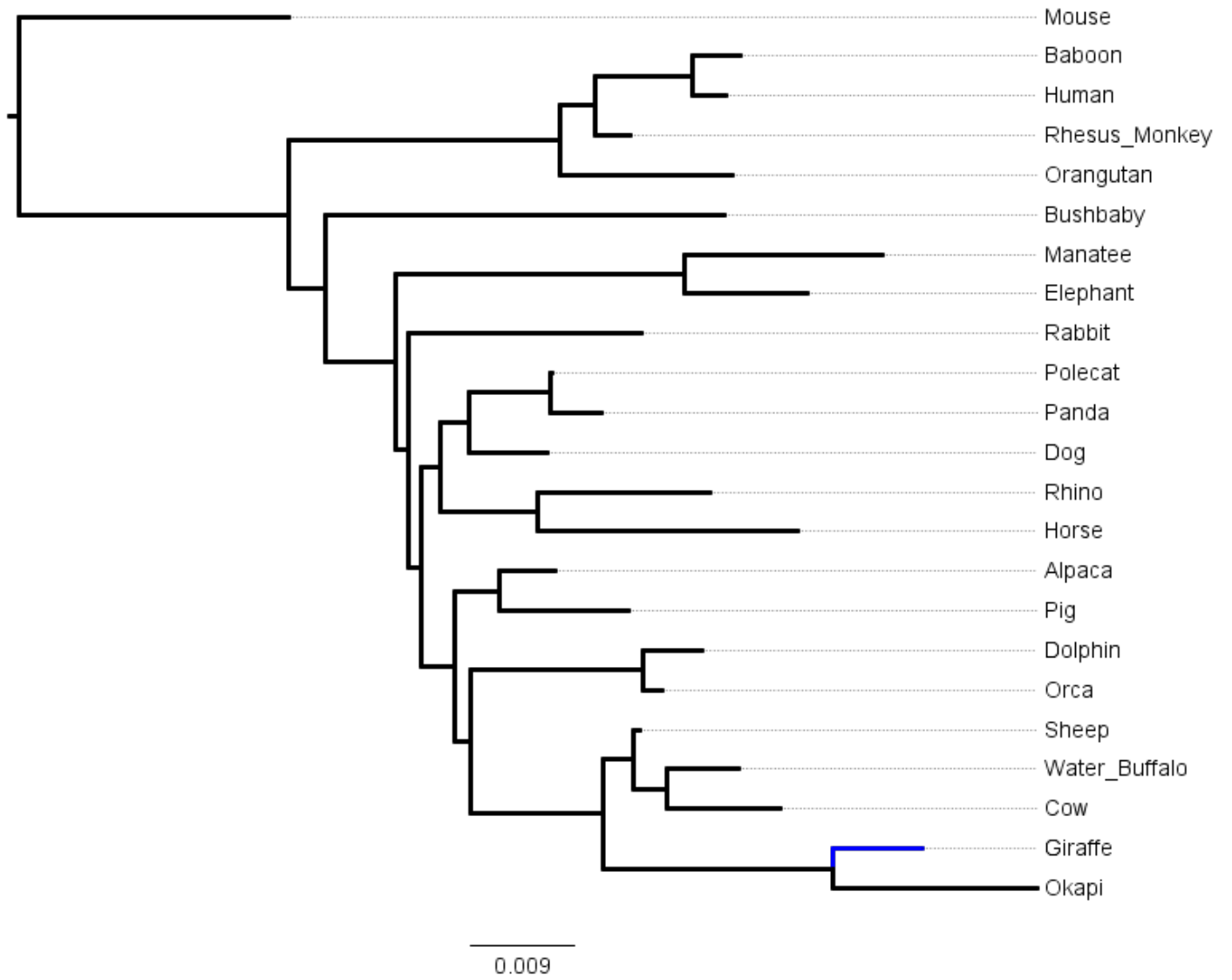
Okapi: L3H UPS, V5S UPS, N9H UPS, C25Y UIS, S347C UIS

Protein sequence Alignment of Cow, Giraffe and Okapi

Cow	1	MPLNVSFANKNYDLDDYDVQPYFYCDEEENFYHQQQQSELQPPAPSEDIWKKFELLPTPP	60
Giraffe	1	..Y.A...SR.....	60
Okapi	1	..H.S...HR.....H...Y.....	60
Cow	61	LSPSRRSGLCSPSYVAVASFSPRGDDDDGGGGSFSSADQLEMVTELLGGDMVNQSFICDPD	120
Giraffe	61F...A...K...G.....R.....S.....	120
Okapi	61F..T....K...G.....R.....S.....	120
Cow	121	DETLIKNIIIQDCMWSGFSAAAKLVSEKLASVQAARKDGGSPSPARGHGGCSTSSLYLQD	180
Giraffe	121	...F.....	180
Okapi	121	...F.....	180
Cow	181	LSAAASECIDPSVVFYPLNDSSSPKPCASPSTAFSPSSDLLSSAESSPRASPEPLAL	240
Giraffe	181S.D....S.....F.....	240
Okapi	181S.D....S.....F.....	240
Cow	241	HEETPPTTSSDSEEEQEDEEEDIVVSVEKRQPPAKRSESGSPSAGSHSKPPHSPLVLKRC	300
Giraffe	241	300
Okapi	241	300
Cow	301	HVSTHQHNYAAPSTRKDYPAAKRAKLDGRVVKQISNNRKCASPRSSDTEENDKRRTHN	360
Giraffe	301	360
Okapi	301T.....C.....	360
Cow	361	VLERQRRNELKRSFFALRDQIPELENNEKAPKVVILKKATAYILSVQAEQQKLKSEIDVL	420
Giraffe	361E...I..K...	420
Okapi	361T.E...I..K...	420
Cow	421	QKRREQLKLEQIRNSCA	439
Giraffe	421	R.....	439
Okapi	421	R.....	439

Newick Tree of Mammalian

(mouse:0.0233071, (((baboon:0.00407647, human:0.00278075):0.00844617, rhesus_monkey:0.00304353):0.00302863, orangutan:0.0149023):0.023451, (bushbaby:0.0344622, ((manatee:0.01719, elephant:0.0106576):0.0248904, (rabbit:0.020061, (((polecat:0.000163893, panda:0.00440234):0.00702407, dog:0.00677006):0.00247914, (rhino:0.0148197, horse:0.0224893):0.00844672):0.00170805, (alpaca:0.00484276, pig:0.0112688):0.00379907, ((dolphin:0.00517125, orca:0.00168597):0.0148027, ((sheep:0.000552616, (water_buffalo:0.00623665, cow:0.00983787):0.00286794):0.00254809, (giraffe:0.00773998, okapi:0.0175805):0.0197851):0.011432):0.00142065):0.00297063):0.00105204):0.00109731):0.00607101):0.00316987):0.0233071);



Locus Name: cMyc

Locus Name: E2F transcription factor 4 (E2F4)

ENSBTAT00000015999 E2F4-201 transcription factor cell proliferation, growth control, craniofacial, erythroid
mouse: mice die postnatally of an increased susceptibility to bacterial infection and exhibit craniofacial defects, erythroid abnormalities, and growth retardation.

PP2: P252H

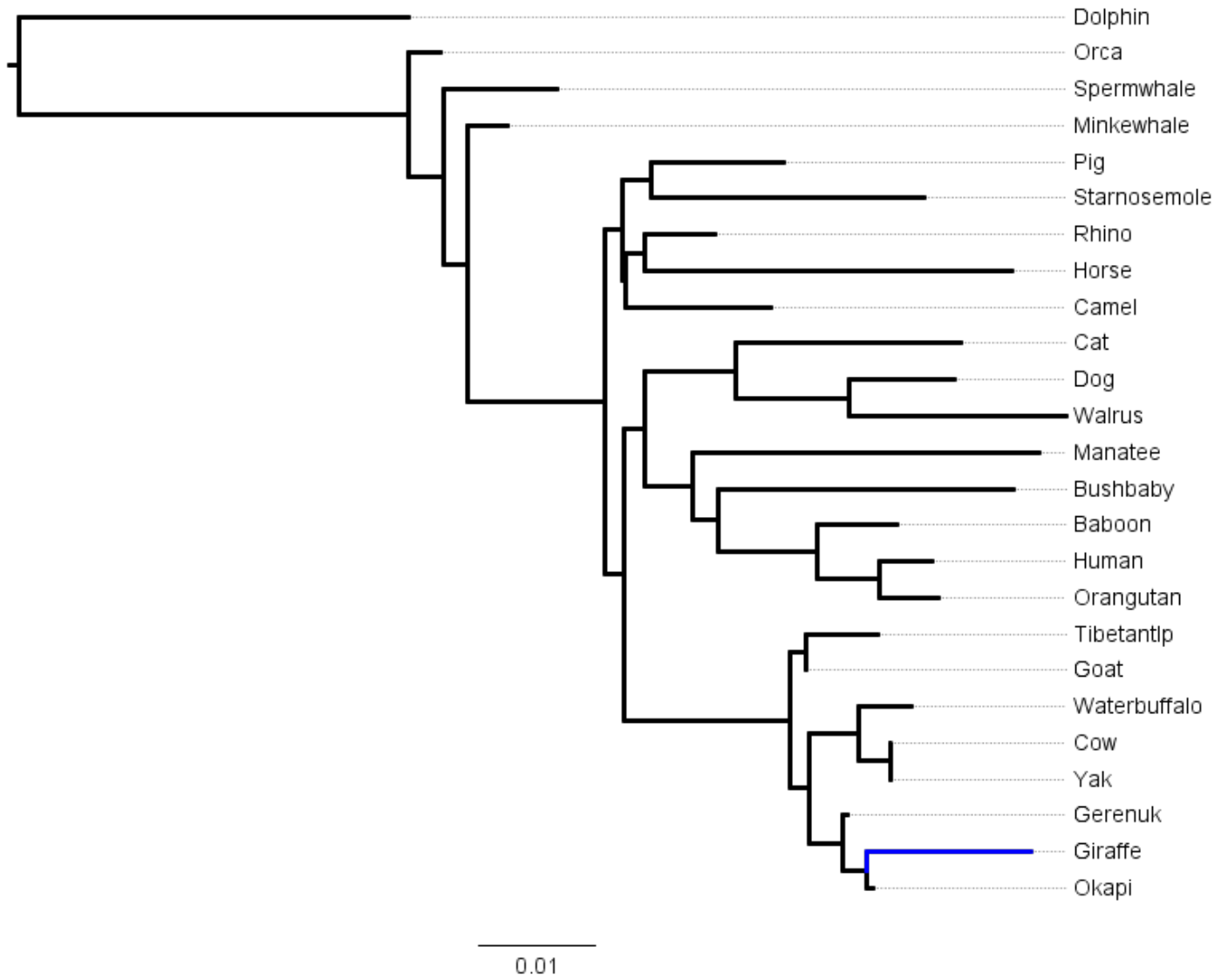
Giraffe: P252H UPS, P254L UPS, V255I UIS, S284N UPS, E286D UIS
Giraffe/Okapi/Gerenuk: V402A UIS

Protein sequence Alignment of Cow, Giraffe and Okapi E2F4

Cow	1	MAEAGPQAPPPPGTSPSRHEKSLGLLTTKFVSLIQEAKDGVLDLKLAAADTLAVRQKRRIYD	60
Giraffe	1	60
Okapi	1	60
Cow	61	ITNVLEGIGLIEKSKNSIQWKGVGPNCNTREIADKLIELKAEIEELQQREQLDQHKVW	120
Giraffe	61	120
Okapi	61	120
Cow	121	VQQSIRNVTEDEVHNSPHTLAYVTHEDICRCFAGDTLLAIRAPSGTSLEVPIPEGLNGQKK	180
Giraffe	121Q.....	180
Okapi	121Q.....	180
Cow	181	YQIHLKSVSGPIEVLLVNKEAWSSPPVAVVPPPEDLLQNPPAVSTPPLLKPSLAQPQD	240
Giraffe	181S.....A...S..	240
Okapi	181S.....A.....	240
Cow	241	ASRPSSPQATTPNPVPSSTEAQGVAGPAAEIPVSGGHGTESKDSGELSSSLPLGLAALDTR	300
Giraffe	241H.LI.....N..N.D.....	300
Okapi	241N.....	300
Cow	301	PLQSSALLDSSSSSSNSSSSGPNPSTSFPEPIKADPTGVLELPKELSEIFDPTRECMSEL	360
Giraffe	301	360
Okapi	301	360
Cow	361	LEELMSSEVFAPLLRLSPPPGDHDYIYNLDESEGVCDLFDVPVLNL	406
Giraffe	361A.....	406
Okapi	361A.....	406

Newick Tree of Mammalian E2F4

(dolphin:0.0338304, (orca:0.0028308, (spermwhale:0.0098671, (minke whale:0.0033991, (((waterbuffalo:0.00462629, (cow:0, yak:3.66971e-06):0.00282723):0.00429898, (gerenuk:0.000435762, (giraffe:0.0143575, okapi:0.000568709):0.0020552):0.0029183):0.00160793, (tibetantlp:0.00622668, goat:0):0.0013208):0.0144871, ((cat:0.0195981, (dog:0.00918394, walrus:0.0187758):0.00984373):0.00798754, (manatee:0.0301534, (bushbaby:0.0256082, (baboon:0.00694266, (human:0.00464845, orangutan:0.00513173):0.00531368):0.00860929):0.00230165):0.00415335):0.00175748):0.00161818, ((pig:0.0114845, starnosemole:0.0237023):0.00255027, ((rhino:0.00607722, horse:0.0319593):0.00163675, camel:0.0126628):0.0003507):0.00142501):0.011978):0.00212959):0.00304652):0.0338304);



Locus Name: E2F transcription factor 4 (E2F4)

Locus Name: E2F transcription factor 5 (E2F5)

ENSBTAT00000012342 E2F5-201 transcription factor cell proliferation, growth control, brain

mouse: Homozygous null mice develop non-obstructive hydrocephalus, ruffled coats, ataxic gait, and dehydration after weaning and die prematurely at an average age of 6 weeks. They exhibit dilated ventricles and cerebral cortex atrophy.

PP2: (Giraffe) S8C, T59A, V240M, P262T

Giraffe: H150R UIS, K162E UIS, T183V UPS, E199Q UIS, V202G UPS, I223V UIS

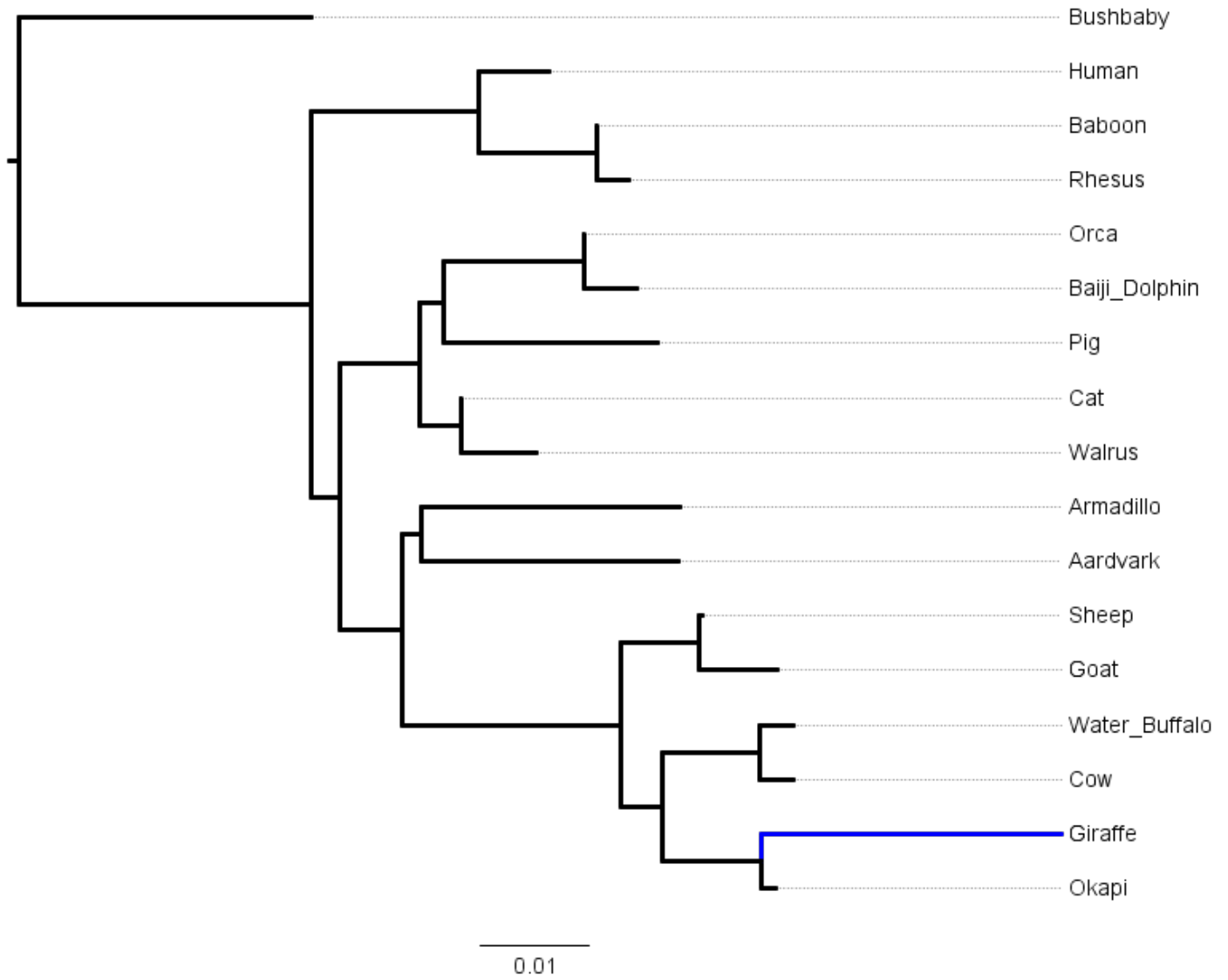
Giraffe/Okapi: V196M UIS

Protein sequence Alignment of Cow, Giraffe and Okapi E2F5

Cow	1	KQAADTLAVRQKRRIYDITNVLEGIDLIEKKSNSIQWKGVGAGCNTKEVIDRLKYLKAE	60
Giraffe	45	.A.....R.....	104
Okapi	1R.....	60
Cow	61	IEDLELKERELDQQKLWLQOSIKNVMDDSINNSTFSYVTHE DICNCFNGDTLLAIQAPSG	120
Giraffe	105	164
Okapi	61	120
Cow	121	TQLEVPIPEMGQNGQKKYQINLKSHSGPIHVLLINKESSSSKPVVFPVPPDDLAQPPSQ	180
Giraffe	165R.....E.M.....T.....	224
Okapi	121M.....T.....	180
Cow	181	PPTVPPHPKSSAVQSLPEPPVRSERSQPLQHTPATDLSSAGSISGDIIDELMSSDVFPLL	240
Giraffe	225	.SV.....T.A....Q..G....D.....V..V.....	284
Okapi	181	.S.....T.....S.....	240
Cow	241	RLSPTPADDYNFNLDDEGVCDFDVQILNY	272
Giraffe	285	316
Okapi	241	272

Newick Tree of Mammalian E2F5

(bushbaby:0.0270778, ((human:0.00661856, (baboon:0, rhesus:0.00298982):0.0109568):0.0154364, (((orca:0, baiji_dolphin:0.00488271):0.012942, pig:0.0197488):0.00219206, (cat:0, walrus:0.00690869):0.0037662):0.0074477, (armadillo:0.0238996, aardvark:0.0237464):0.00184229, ((sheep:0.000250682, goat:0.00726822):0.00727791, (water_buffalo:0.00319492, cow:0.00319492):0.00892585, (giraffe:0.0276732, okapi:0.00122529):0.00918804):0.0038863):0.0202626):0.00576561):0.00263753):0.0270778);



Locus Name: E2F transcription factor 5 (E2F5)

Locus Name: E26 avian leukemia oncogene homolog (**ETS2**)

ENSBTAT0000012144 ETS2-201 ETS transcription factor somitogenesis, heart development
mouse: expressed in posterior compartment of somites, short neck phenotype when overexpressed in mice

PP2: NO DAMAGING HITS

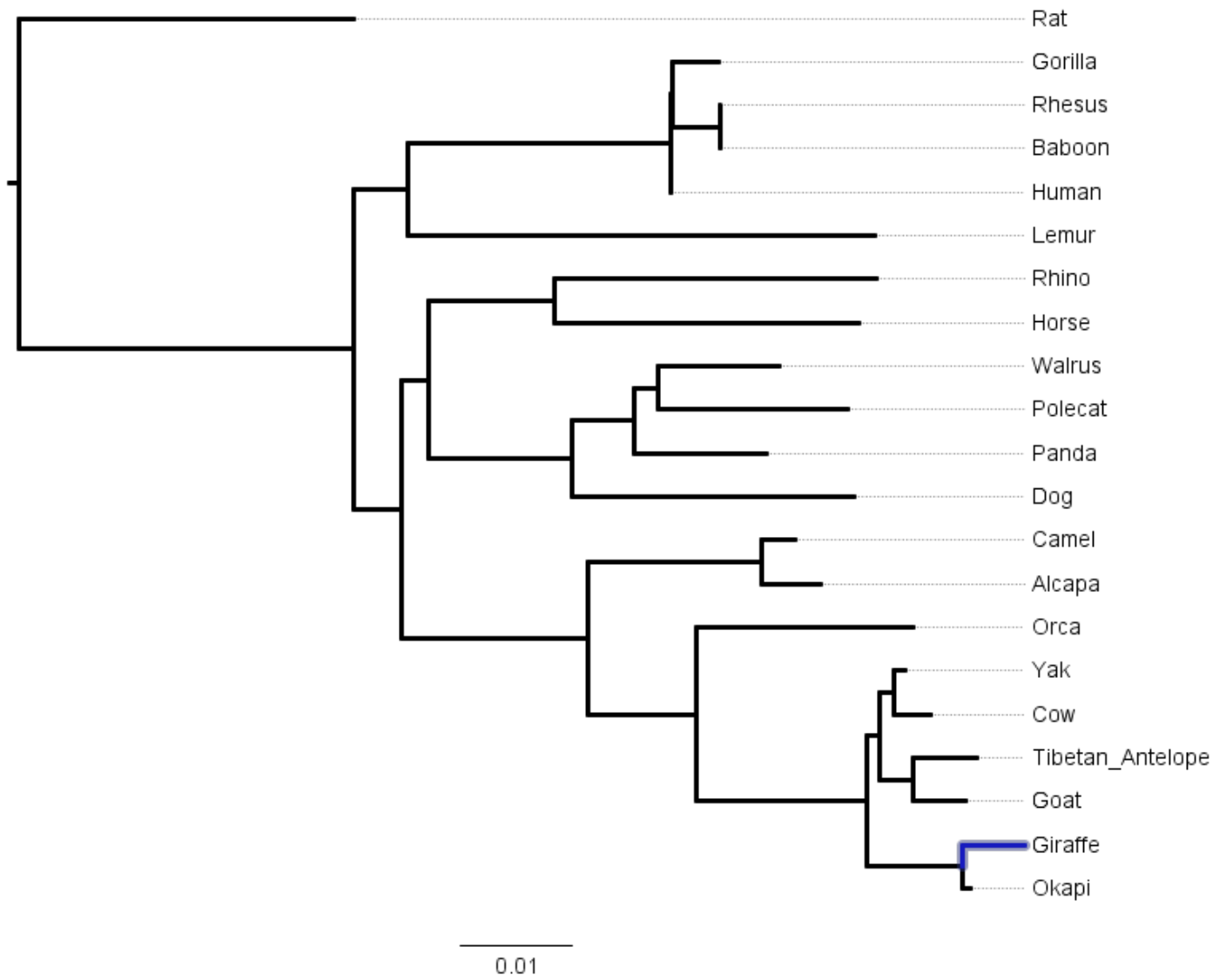
Giraffe/Okapi: S42A UIS

Protein sequence Alignment of Cow, Giraffe and Okapi ETS2

Cow	1	MNDFGIKNDQVAPVASSYRGTLKRQAAFDTFDGSL LAVFPSLNEEQTLQEVPTGLDSIS	60
Giraffe	1I..A.S.....	60
Okapi	1A.....	60
Cow	61	HDSANCELPLLTPCSKAVMSQALKATFSGFKKEQRRIGIPKNPWLWTEQQVCQWLLWATN	120
Giraffe	61	120
Okapi	61	120
Cow	121	EFSLVDVNLQRFGMTGQVLCNLGKERFLELAPDFVGDILWEHLEQMIKENQEKNEQYEE	180
Giraffe	121D.....T.....	180
Okapi	121D.....T.....	180
Cow	181	NSHLNSVPHWINSNSLGFGEQAPYGMQTQSYPKGGLLDGLCPASSAPSTLGPEQDFQMF	240
Giraffe	181I.....G.....	240
Okapi	181I.....G.....	240
Cow	241	PKARLNTVSVNYCSVGQDFPAGSLNLLSSASGKPRDHDSAETGGDSFESSESLQSWNSQ	300
Giraffe	241S.....S.....	300
Okapi	241S.....	300
Cow	301	SLLLDVQRVPSFESFEDDCSQSLGLSKPTMSFKDYIQDRSDPVEQKPVIPAAVLGFTG	360
Giraffe	301	360
Okapi	301	360
Cow	361	SGPIQLWQFLELLSDKSCQSFISWTGDGWEFKLADPDEVARRWGKRKNPKMNYEKLSR	420
Giraffe	361	420
Okapi	361	420
Cow	421	GLRYYYDKNIIHKTSKGKRYVYRFVCDLQNLGFTPEELHAILGVQPDTE	470
Giraffe	421	470
Okapi	421	470

Newick Tree of Mammalian ETS2

(rat:0.0303961, (((gorilla:0.00422325, (rhesus:0, baboon:0):0.00434222):0.000103139, human:0):0.0238534, lemur:0.0424498):0.0049381, (((rhino:0.0292759, horse:0.0276629):0.0114245, ((walrus:0.0109447, polecat:0.017169):0.00216096, panda:0.0119058):0.00563472, dog:0.0255789):0.0130936):0.00238709, (camel:0.00313301, alcapa:0.00537778):0.0157604, (orca:0.0196581, ((yak:0.000992099, cow:0.00327231):0.00131552, (tibetan_antelope:0.00585099, goat:0.0048445):0.00297886):0.00113061, (giraffe:0.00560933, okapi:0.000780512):0.00859034):0.0155565):0.00986514):0.0168361):0.00439006):0.0303961);



Locus Name: E2F transcription factor 5 (E2F5)

Locus Name: Transforming Growth Factor, Beta 1 (TGFB1)

ENSBTAT00000027261 TGFB1-201 secreted growth factor growth control, bone growth, heart mouse: wasting syndrome accompanied by a multifocal, mixed inflammatory cell response and tissue necrosis, leading to organ failure and death; Camurati-Engelmann disease (CE) [MIMOUSE:131300]: Autosomal dominant disorder characterized by hyperostosis and sclerosis of the diaphyses of long bones.

PSG (Giraffe) N230D 0.965*, G242T 0.977*, H276N 0.972*, N283D 0.966*, A360V 0.963*
PP2: None

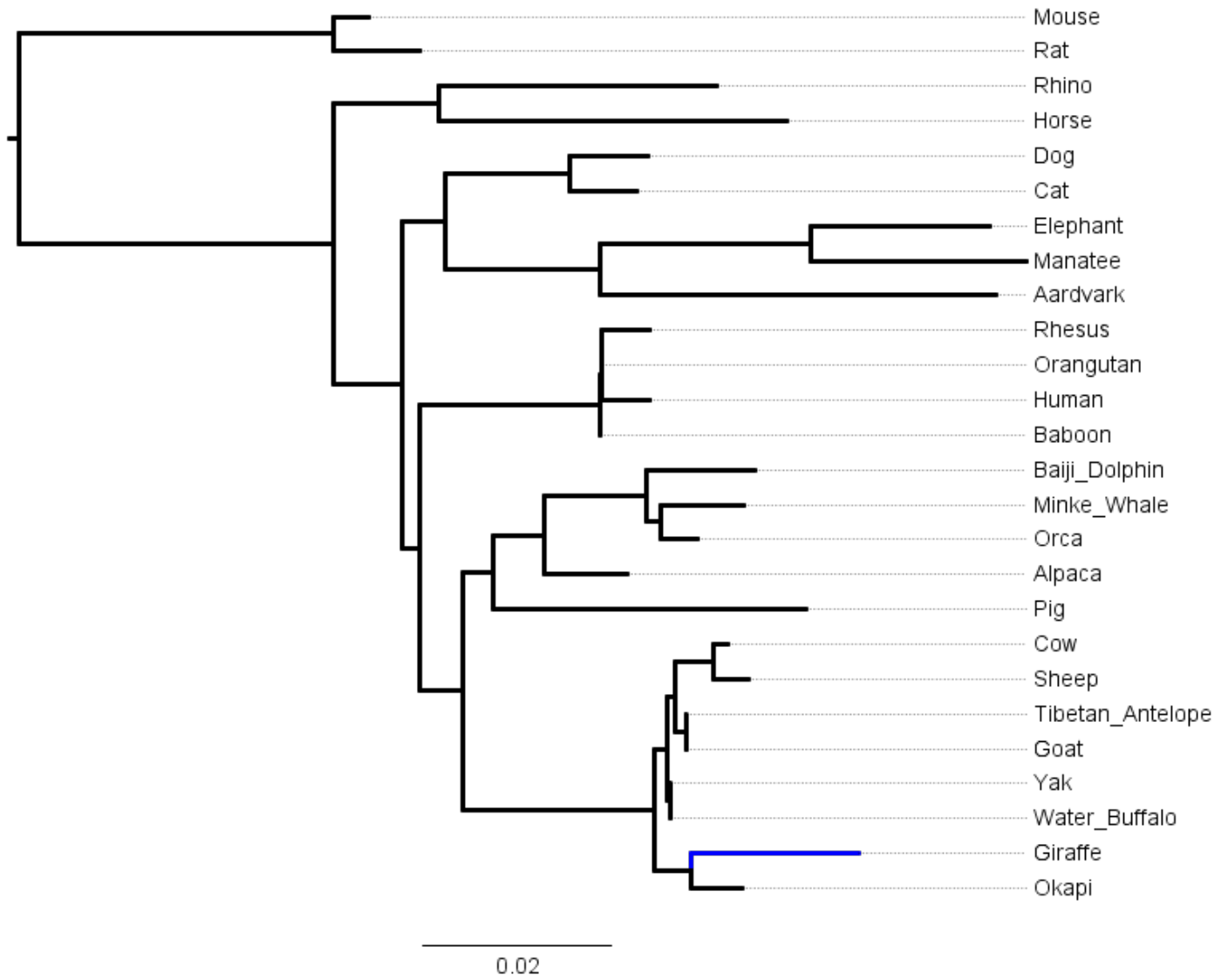
Giraffe: E215G UPS, N230D UIS, S241F UPS, G242T UPS, H275D UPS

Protein sequence Alignment of Cow, Giraffe and Okapi TGFB1

Cow	1	MPPSGLRLLPLLLLPLLWLLMLTPGRPVAGLSTCKTIDMELVKRKRIEAIKQILSKLRLA	60
Giraffe	1	60
Okapi	1L..L.....	60
Cow	61	SPPSQGDVPPGPLPEAILALYNSTRDRVAGESAETEPEPEADYYAKEVTRVLMVEYGNKI	120
Giraffe	61	120
Okapi	61	120
Cow	121	YDKMKSSSHSIYMFFNTSELREAVPEPVLLSRADVRLRLKLVKVEQHVELYQKYSNNSWR	180
Giraffe	121	.E.....EL.....	180
Okapi	121	.E.....EL.....	180
Cow	181	YLSNRL LAPSDSPEWLSFDVTVGVVRQWLTRREEIEGFRLSAHCSCDSKNTLQVDINGFS	240
Giraffe	181T...G.....D.....	240
Okapi	181T.....	240
Cow	241	SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNYCFSSTEKNCCVRQLYI	300
Giraffe	241	FT.....N.....D.....	300
Okapi	241	300
Cow	301	DFRKDLGWKWIHEPKGYHANFCLGPCYIWSLDTQYSKVLALYNQHNPASAAAPCCVPQA	360
Giraffe	301V	360
Okapi	301	360
Cow	361	LEPLPIVYVGRKPKVEQLSNMIVRSCKCS	390
Giraffe	361	390
Okapi	361	390

Newick Tree of Mammalian TGFB1

((mouse:0.00378357, rat:0.00912019):0.0334887, ((rhino:0.0293755, horse:0.0369224):0.0112504, ((dog:0.00837452, cat:0.00713029):0.0131879, (elephant:0.0190146, manatee:0.0227791):0.022475, aardvark:0.0421213):0.0164466):0.00456622, (((rhesus:0.00513782, orangutan:4.3558e-05):1.69522e-05, human:0.00513782):0.000183285, baboon:0):0.0190894, (((baiji_dolphin:0.0115145, minke_whale:0.00893155, orca:0.00397221):0.00145376):0.01084, alpaca:0.00873049):0.00543237, pig:0.0332531):0.00319142, (((cow:0.00139774, sheep:0.00374368):0.00406499, (tibetan_antelope:0, goat:0):0.00108642):0.000951564, (yak:0, water_buffalo:4.28948e-06):0.000333817):0.00134935, (giraffe:0.0178524, okapi:0.00549713):0.0038499):0.0202923):0.00459478):0.00189038):0.00728277):0.0334887);



Locus Name: Transforming Growth Factor, Beta 1 (TGFB1)

Locus Name: Aldehyde dehydrogenase family 16 member A1 (**ALDH16A1**)

ENSBTAT0000043139 ALDH16A1-201 aldehyde dehydrogenase eye development
mouse: abnormal retinal development in mouse

PP2: (Giraffe) W120R, E600H, H728Y; (Giraffe/Okapi) L262M; (Okapi) R129Q, R132Q, L704M

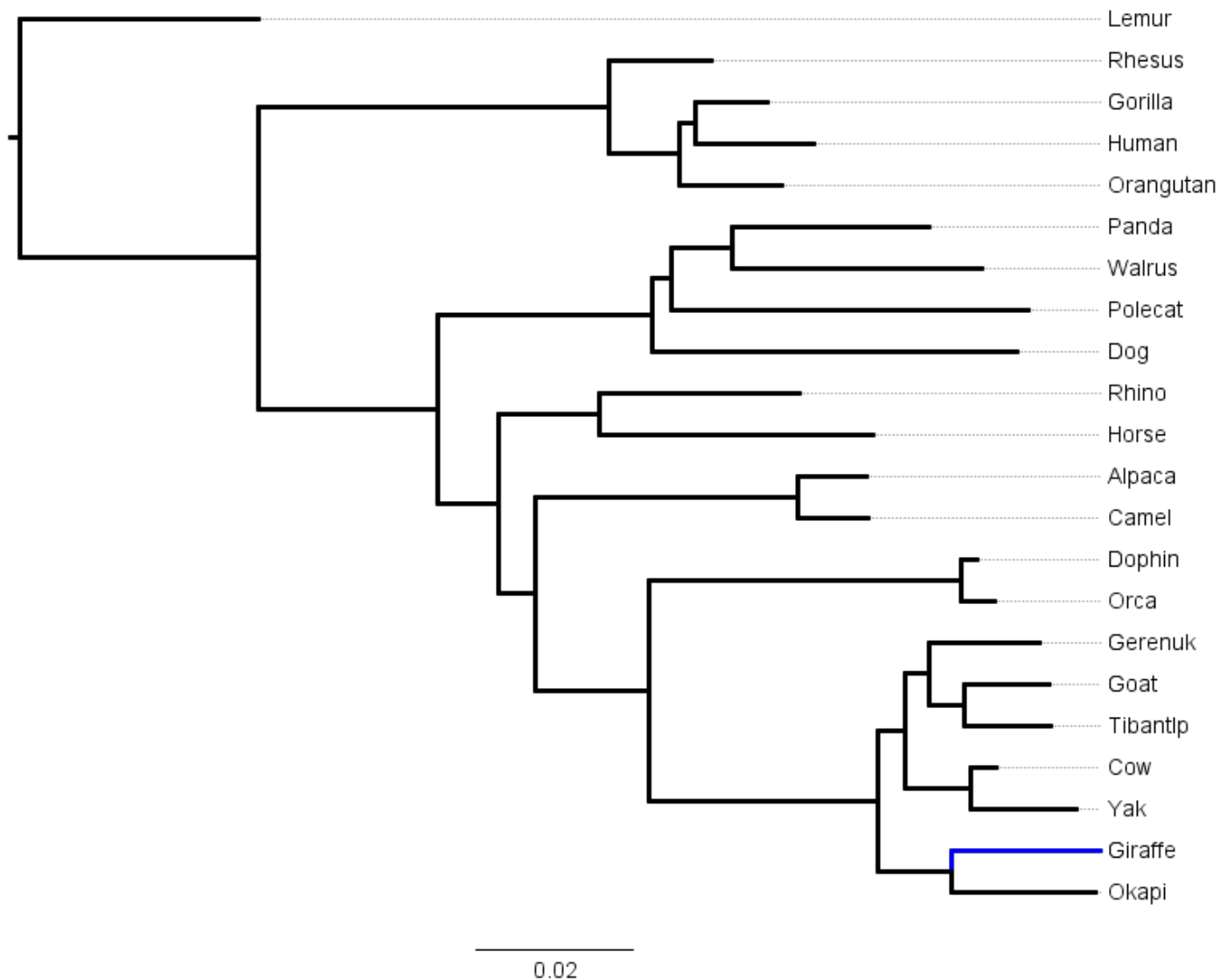
Giraffe: A7P UPS, A505T UPS, A561P UIS, Q598H UPS, N603S UPS, E669Q UPS, H726Y UIS, L740V UPS
Giraffe/Okapi: S174P UPS, L497V UPS

Protein sequence Alignment of Cow, Giraffe and Okapi ALDH16A1

Cow	1	MAARTASRACEIFTTLEYGPAPESHACALAWLDTQDRHLGHYVNGQWLKPEHRSSVPCQ	60
Giraffe	1P.....	60
Okapi	1N.....	60
Cow	61	DPITGENLASCLQAQSEDVAAAVEAARASLENWSTQPGAIRAQHLTRLAKVIQKHQRLW	120
Giraffe	61F.....R	120
Okapi	61F.....A...Q...	119
Cow	121	TLESVLTGRAVREVRDRDVPLAQQLLYHAVQAHTQEEALAGWEPMGVIGLILSPTFPFL	180
Giraffe	121P.....	180
Okapi	120Q..Q...--S.....N.....T.....M.P.....	177
Cow	181	DMMWRICPALAVGCTVVVLVPPASPTPLLLAQLAGELGPFPGILNVISGPASLGPVLAAQ	240
Giraffe	181	N.....S.....	240
Okapi	178	N.....Q.....S.....	237
Cow	241	PGVQKVAFCGAIEEGRALRRTLAWVPELGLALGAESLLLLTEVADVDSAVEGIVDAAWS	300
Giraffe	241M...G...S.....	300
Okapi	238M...G...S.S.....	297
Cow	301	DRSPGGLRLLIQEAVWDETMRRQLQERMGRRCGHGLDGAVDMGARGAAARDLAQRYVSEA	360
Giraffe	301	..G.....R.....T.....R..	360
Okapi	298	..G.....R.....T.....R..	357
Cow	361	QSQGAQVFQAGSEPSDSPFFPPTLVSDLPPASPTQAEVWPPLVVASPFRTAKEALAVAN	420
Giraffe	361V.....	420
Okapi	358V.....	417
Cow	421	GTPRGGASVWSERLGQALELAYGLVQGTVWINAHGLRDPVPTGGCKESGSSWHGGQDG	480
Giraffe	421M.....	480
Okapi	418H.....	477
Cow	481	LYEYLRPSGTPAWIPYLSKTLNYDAFGLALPSTL--PAGPET--GPAP--PYGLFVGGRF	534
Giraffe	481V..S...T.....-ILP.....GE..ET.....	537
Okapi	478V..S.....LL-.....GE..V.--.....	534
Cow	535	QAPGARSSRPIQDSQGSQGYVAEGGAKDIRGAVEAAHQAAPGWMSQSPAARAALLWALA	594
Giraffe	538N.H.....P.....G.....	597
Okapi	535H.....G.....	594
Cow	595	AALQRREPNLVSRLERHGVELKVAKAEVELSVKRLRAWGARVQAQGCALQVAELRGPVLR	654
Giraffe	598	..H...S.....	657
Okapi	595	654
Cow	655	LREPLGVLAIVCPDEWPLLAFLVSLAPALAHGNTVVLVPSGACPIPALEVCQEMATLLPA	714
Giraffe	658Q.....R.....	717
Okapi	655M.....	714
Cow	715	GLVNVVTGDRDHLTRCLALHQDIQALWYFGSAQGSQFVEWASAGNLKPVVVNRGCPRAWD	774
Giraffe	718Y.....V.....	777
Okapi	715	774
Cow	775	QEAEGAGPELGRRAARTKALWLPMD	800
Giraffe	778L.....	803
Okapi	775L.....	800

Newick Tree of Mammalian ALDH16A1

(lemur:0.030324, ((rhesus:0.0130267, ((gorilla:0.00903136, human:0.0149468):0.00214943, orangutan:0.013049):0.00892505):0.044449, (((panda:0.024959, walrus:0.0317876):0.00772496, polecat:0.0453532):0.00243257, dog:0.0463734):0.0271743, ((rhino:0.025468, horse:0.0349596):0.012711, ((alpaca:0.00868336, camel:0.00892807):0.033421, ((dolphin:0.00199813, orca:0.00425584):0.0396676, ((gerenuk:0.013941, goat:0.0107265, tibantlp:0.0109459):0.00452875):0.0031143, (cow:0.00310885, yak:0.0132754):0.00846929):0.00344326, (giraffe:0.0187481, okapi:0.0181837):0.00944829):0.0291017):0.0143796):0.00466941):0.007665):0.0227489):0.030324);



Locus Name: Aldehyde dehydrogenase family 16 member A1
(ALDH16A1)

Locus Name: Four And A Half LIM Domains 5 (FHL5)

ENSBTAT0000002359 FHL5-201 Four-half lim domains testis, heart, brain human:
GWAS for migraine headache, mouse: Male mice homozygous for disruptions of this gene have reduced
sperm counts and abnormal sperm

PSG: (Giraffe) D242G, N251T

PP2: (Giraffe): R35C

Giraffe: R35C UPS, E49A UPS, D242G UIS, N251T UIS, I284S UPS

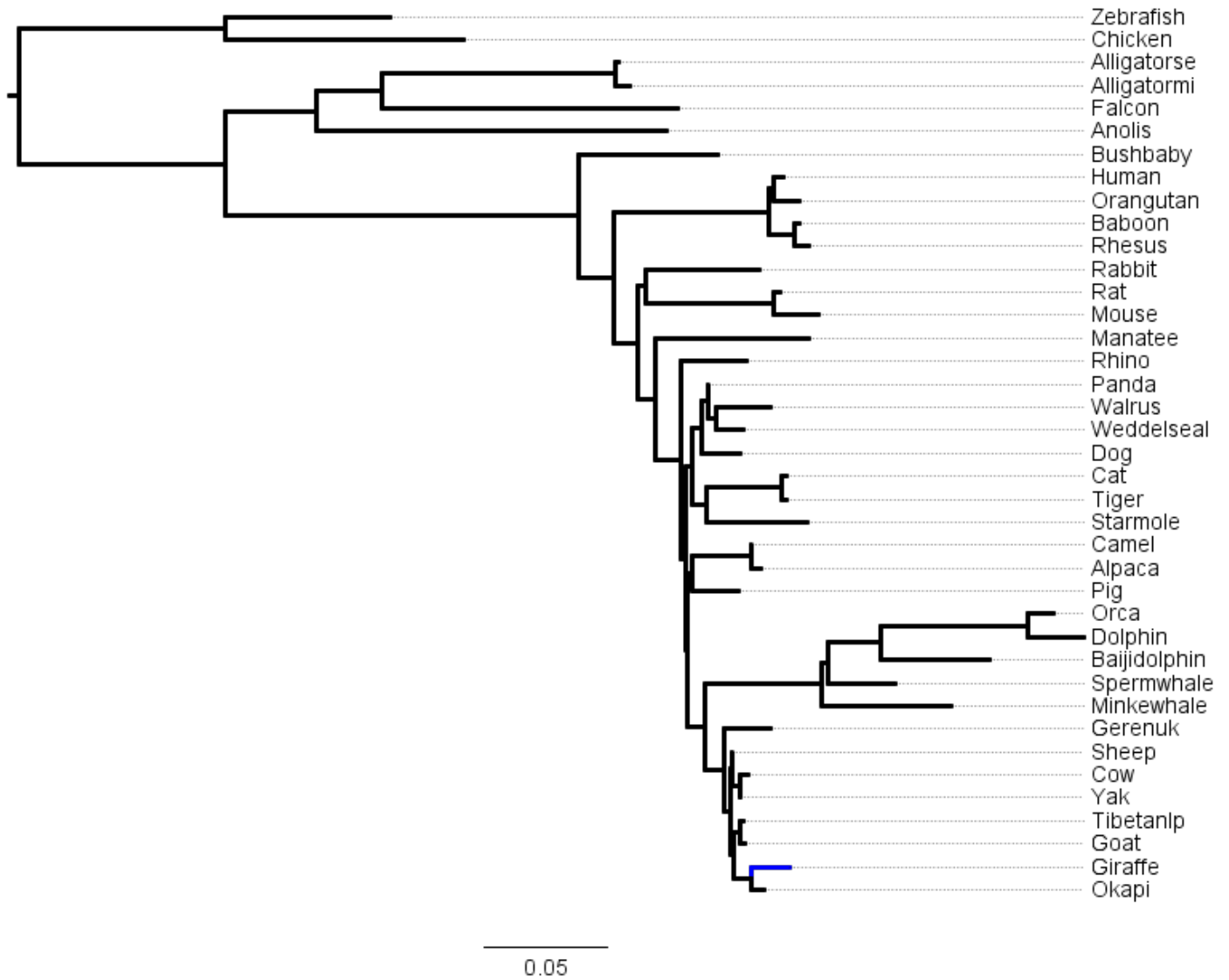
Giraffe/Okapi: D25N UIS

Protein sequence Alignment of Cow, Giraffe and Okapi FHL5

Cow	1	MTTPQFYCYCMASLLGKKYVLKDDNPYCVSCYDRIFSNYCEECKEPIESGSKDLCYKGH	60
Giraffe	1	...A.....N.....C.....A.....R	60
okapi	1	...A.....N.....V.....R	60
Cow	61	HWHEGCFNCTKCNHSLVEKPFPAKDERLLCSECYSNECSSKCFHCKKTIMPGSRKMEFKG	120
Giraffe	61	120
Okapi	61	120
Cow	121	NYWHETCFVCEHCRQPIGTKPLISKESGNYCVPCFEKEFAHYCSFCKKVITSGGITFRDQ	180
Giraffe	121H..	180
Okapi	121H..	180
Cow	181	PWHKECFLCSGCRKELCEEFFMSRDDYPFCLDCYNHLYAKKCAACTKPITGLRGAKFICF	240
Giraffe	181	240
Okapi	181	240
Cow	241	QDRQWHSECFNCGKCSVSLVGEGLTHNKEIFCRKCGSGVDTDI	284
Giraffe	241	.G.....T.....S	284
Okapi	241N.	284

Newick Tree of Mammalian FHL5

((zebrafishhuman:0.0668376, chicken:0.0970388):0.0833155, (((alligatorse:0.00130397, alligatormi:0.00586458):0.0948263, falcon:0.119757):0.0262781, anolis:0.14137):0.0374446, (bushbaby:0.0559843, ((human:0.00409343, orangutan:0.0100917):0.00187668, (baboon:0.00174038, rhesus:0.00532684):0.0106608):0.0630953, ((rabbit:0.0456561, (rat:0.00305221, mouse:0.0183025):0.0516199):0.00325014, (manatee:0.0622959, (rhino:0.026086, (((panda:0, (walrus:0.0215425, weddelseal:0.0106662):0.00351075):0.00246469, dog:0.0154795):0.00385592, ((cat:0.00176367, tiger:0.00176367):0.030445, starmole:0.0408813):0.00568553):0.00277947, ((camel:0, alpaca:0.00361645):0.0241293, pig:0.0191361):0.00176541, (((orca:0.0102221, dolphin:0.0221023):0.0599355, baijidolphin:0.0442202):0.0211295, spermwhale:0.0271777):0.00250532, minkewhale:0.052086):0.0474888, (gerenuk:0.0186301, (sheep:0.000223805, (cow:0.00328827, yak:0.000239075):0.00330981):0.000484349, ((tibetanlp:0.00154523, goat:0.00198212):0.0021112, (giraffe:0.0159476, okapi:0.00533138):0.0068569):0.00128658):0.00283108):0.00758024):0.00718322):0.000834176):0.00163687):0.0104579):0.00716852):0.00999347):0.01381):0.143717):0.0833155);



Locus Name: Four And A Half LIM Domains 5 (FHL5)

Locus Name: Integrin alpha 10 (ITGA10)

ENSBTAT00000011023 ITGA10-201 integrin alpha 10 heart, muscle articular cartilage
 mouse: Homozygous null mice display slightly shortened long bones and mild abnormalities in
 ephysiseal plate morphology.

PP2: Giraffe, N839D; Okapi, R821Q

Giraffe: A679T UIS, L755V UPS, N839D UIS, L942I UPS

Giraffe/Okapi: D116G UPS, G1053R UIS, K1078R UIS

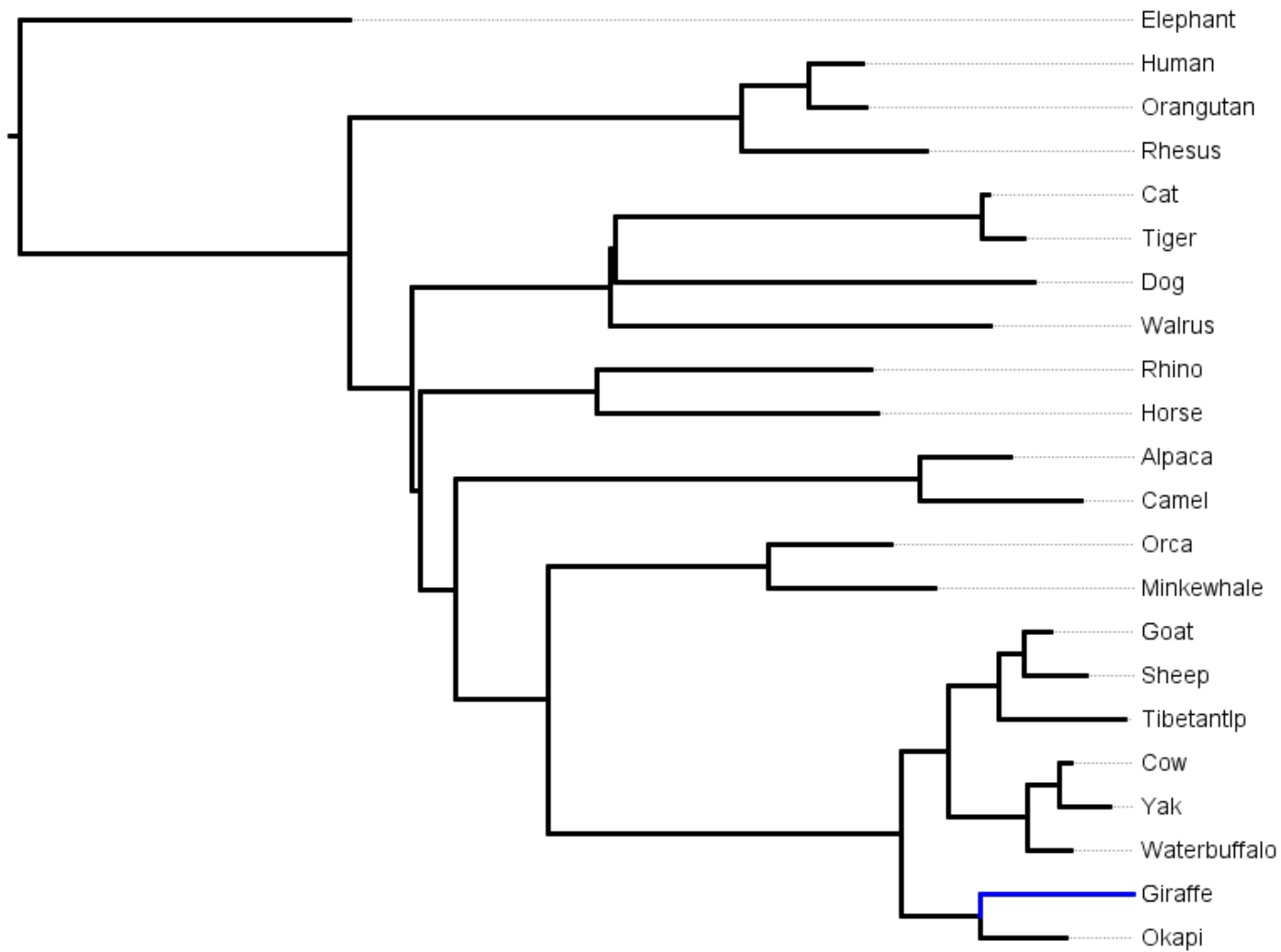
Protein sequence Alignment of Cow, Giraffe and Okapi ITGA10

Cow	1	MEFPLIPHLFLPLMFLTLGLCSSFNLDVHRPRLFLGPPAEAFGYSVLQHVGGGRQWMLVGA	60
Giraffe	1P.....R.....	60
Okapi	1P.....R.....	60
Cow	61	PWDGPGSDRRGDVYRCLVGGSSHSAPCAKGHLDHPLGNSSRPVAVNMHLGMSLLETGNGG	120
Giraffe	61G....	120
Okapi	61Y.....G....	120
Cow	121	FMACAPLWSRACGSSVFSSGICARVDASFRPQGLAPTAQRCPTYMDVVIVLDGSNSIYP	180
Giraffe	121	180
Okapi	121H.....	180
Cow	181	WSEVQTFLRRLVGRFLFIDPEQIQVGLVQYGESSVHEWSLGDFTKEEVVRAARNLSRREG	240
Giraffe	181	240
Okapi	181	240
Cow	241	RETKTAQAIMMACTEGFSQSRGGRPEAARLLVVVTDGESHDGEELPTALQACEAGRVTRY	300
Giraffe	241	300
Okapi	241R.....	300
Cow	301	GIAVLGHYLRQRDPSSFLREIRAIASDPDEKFFFNVTDEAALTDIVDALGDRIFGLEGS	360
Giraffe	301	360
Okapi	301T.....	360
Cow	361	HGENESSFGLEMSQIGFSTHQLKDGILFGMVGAYDWGGSVLWLEEGRRLFPRTALEDEF	420
Giraffe	361	420
Okapi	361	420
Cow	421	PPALQNHAAYLGYSVSSMFLRGRRFLSGAPRFSHRGKVIQFQKKGAVRVAQSLQGE	480
Giraffe	421R.....	480
Okapi	421R.....	480
Cow	481	QIGSYFGSELCPDIDGDTTDVLLVAAPMFLGPQNKETGRVYVYLVGQPSLLTLQRTLQ	540
Giraffe	481	540
Okapi	481	540
Cow	541	PESPQDARFGFAMGALPDLNQDGFADVAVGAPLEDGHRGALYLYHGAQRGVRPRPAQRIA	600
Giraffe	541H.....	600
Okapi	541H.....	600
Cow	601	AVAMPQALSIFYGRSVDGRLDLDGDDLVDVAVGAQGAAILLSSRPVRLAPSLDVTTPPAIS	660
Giraffe	601	..S.....V.....H.....	660
Okapi	601	..S.....	660
Cow	661	VVQRDCKRRGQEATCLSAALCFQVTSRTPGHWDRRFHVRFRTASLDEWTTAARAADFSGSQ	720
Giraffe	661T.....R..H...LQ.....T..V.....	720
Okapi	661R.....Q.....	720
Cow	721	RLSPRRLRLSVGNITCEQLHFHVLDTSYLRPVSLSVTFALDNTTKPGPVLDEGSPTSIR	780
Giraffe	721N...V.....VT.....	780
Okapi	721V.....T.....	780
Cow	781	KLVPFSKDCGPDNECVTDLVLQANMDIRGSRKDPFVVRGRRKVLVSATLENKKENAYNT	840
Giraffe	781D.....	840
Okapi	781Q.....	840

Cow	841	SLSLNFSRNLHLSSFTPQSNSPVKVECAAPTPHTRLCSVGHVPVFTGAKVTFLLLEFEFSC	900
Giraffe	841S.....S..A.....M.....	900
Okapi	841S.....S..A.....M.....	900
Cow	901	SFLLSQVLVRLTATSSSLERNGLRDNATAQTSAYIQYEPHLLFSSESTLHRYEVHPYGT	960
Giraffe	901I.....	960
Okapi	901I.....	960
Cow	961	PVGPPEFKTTLRVQNLGCYVVSGLIVSALLPAVAYGGNYFLSLSQVITNNASCTVQNLT	1020
Giraffe	961I.....	1020
Okapi	961I.....	1020
Cow	1021	EPPGPPVHPEELQHTSRLNESNTRCQVVRCHLGRRLAKGTEISVGLLRVLVHNEFFRRAKFK	1080
Giraffe	1021H.....R.....R..	1080
Okapi	1021H.....R.....R..	1080
Cow	1081	SLTVVSTFELSTEEGSVLLLTEASRWSESLLEVIQSRPVLISLWILIGSVLGLLLLLALL	1140
Giraffe	1081G.....H.....	1140
Okapi	1081G.....	1140
Cow	1141	VFCLWKLGF FARKKIPEEEKREDKLEQ	1167
Giraffe	1141E..E....	1167
Okapi	1141S...M....E..E....	1167

Newick Tree of Mammalian ITGA10

```
(Elephant:0.022716, (((Human:0.00371817, Orangutan:0.00402388):0.00461126,
Rhesus:0.0127369):0.0271021, (((Cat:0.000463002, Tiger:0.00297639):0.0253433,
Dog:0.0290155):0.000248483, Walrus:0.0262011):0.0137373, ((Rhino:0.0189875,
Horse:0.0194546):0.0122169, (Alpaca:0.00621601, Camel:0.0110714):0.0320862, ((Orca:0.00845164,
Minkewhale:0.0114551):0.0151917, (((Goat:0.00177715, Sheep:0.00423924):0.00173142,
Tibetantlp:0.00863256):0.00356924, (Cow:0.000848975, Yak:0.00344473):0.00214421,
Waterbuffalo:0.00302013):0.00556089):0.00324758, (Giraffe:0.0104911,
Okapi:0.00591051):0.00552424):0.0243155):0.00642702):0.00245339):0.00053918):0.00435728):0.022716
);
```

Locus Name: Integrin alpha 10 (ITGA10)

Locus name: Extracellular matrix protein 1 (**ECM1**)

ENSBTAT0000004959 ECM1-201 extracellular matrix protein endochondral bone formation and angiogenesis human: Lipoid proteinosis (LiP) [MIMOUSE:247100]: Rare autosomal recessive disorder characterized by generalized thickening of skin, mucosae and certain viscera. human height SNP

PP2: (Giraffe) V41M, S63F, T227M; (Giraffe/Okapitty) A15I, G161V

Giraffe: A7V UIS, V45M UPS, S67F UPS, S141N UPS, A230M UPS, T417A UPS

Giraffe/Okapi: T15I UPS, E78K UIS, I88V UPS, K104N UPS, G164V UIS, T245A UPS, Q339K UPS

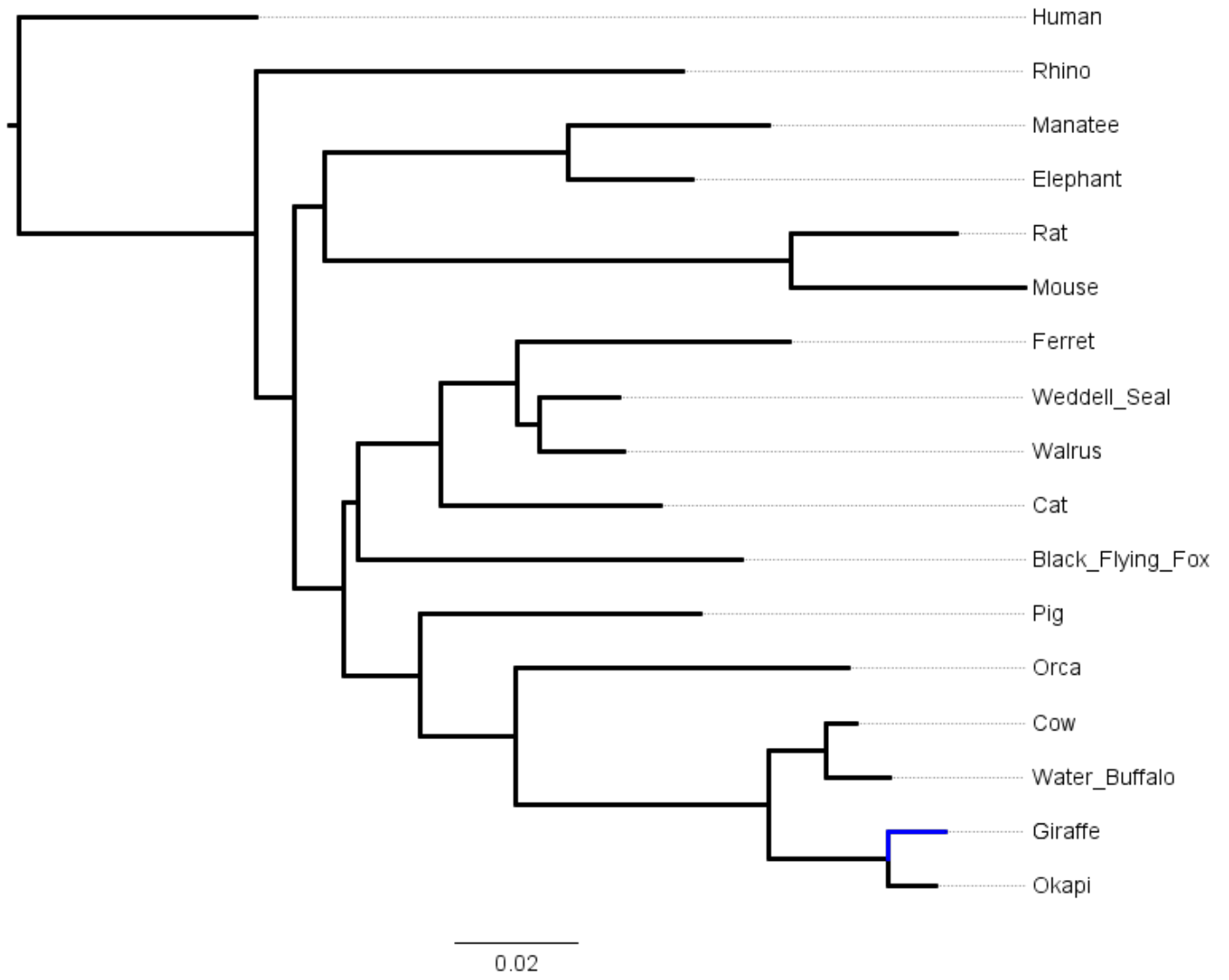
**Water buffalo used instead of Cow because cow sequence incomplete.

Protein sequence Alignment of Water Buffalo, Giraffe and Okapi ECM1

Water Buffalo	1	MGTMSGAAVLVLA	CLTVASV	ASDRGFK	APGQREL	GQPPLTH	PLQEVGY	AAPPSP	PLSRALP	60						
Giraffe	1V.....	I.....G...	S.....E...	Y....M.....	A....				60						
Okapi	1I.....	G.....S.....	E...Y.....	A....					60						
Water Buffalo	61	QGHPRTSQHSL	HFEQG	SEVQAS	PSQDAI	PLQEEL	PAPQL	PVEKKG	GPPLQ	EAIPLQEEL	120					
Giraffe	61D.F.....	..RK.....	E.V.....	LP.....	N.....				120						
Okapi	61D.....	..RK.....	E.V.....	LP.....	N.....				120						
Water Buffalo	121	PPPQVPIEQ	KEEKP	PAPSM	DHSPPE	PEPE	SWNPA	QHCQQ	GRPRR	GWGHR	LDGFP	GRPS	LDNL	180		
Giraffe	121N.N.....						GS.V.....						180		
Okapi	121N.....						GS.V.....						180		
Water Buffalo	181	DQICLPSRQ	HVVY	GPWN	LFPQT	GFSH	LSRQ	GETL	NLLET	GYRCC	RCRNR	ANRL	DCAE	LWV	240	
Giraffe	181H.PM.....												240		
Okapi	181H.PT.....												240		
Water Buffalo	241	EDAVTRFCE	AEFV	KTQ	PHGCC	KKQ	GEAR	LSCF	QEEA	PRPHY	QLRAC	PSHQ	PGIS	LGPEL	300	
Giraffe	241A.....												300		
Okapi	241A.....												300		
Water Buffalo	301	PFPPGLPT	VDNIK	NICH	LKRFR	SVPR	NLPAT	DSIQ	RQLQ	ALTR	LEAE	FQRCC	RQGN	NHTC	360	
Giraffe	301K.....												360		
Okapi	301K.....												360		
Water Buffalo	361	TWKAWED	TLDG	YCD	WEQAI	KTHH	HSCCN	YPPS	PLR	DECF	ARRA	PYPN	YDRD	ILTL	DLRSI	420
Giraffe	361R.....														420
Okapi	361R.....														420
Water Buffalo	421	TPNLMN	HLCG	NRRV	LSKHK	QIPG	LIQK	VTAR	CCDL	PFPE	QACCA	EEKSA	FIDEL	CGSRR	480	
Giraffe	421S.....												D.....	480	
Okapi	421Q.....												D.....	480	
Water Buffalo	481	NFWRDS	ALCCK	LSPG	DEQIN	CFNT	KYLR	NVAL	VTGD	TRDA	KGPRE	QGP	TQGT	NSSPT	SEP	540
Giraffe	481N.....												A.....	G.....	540
Okapi	481N.....												G.....		540
Water Buffalo	541	KEE	543													
Giraffe	541	...	543													
Okapi	541	...	543													

Newick Tree of Mammalian ECM1

(elephant:0.0750334, (((((human:0.0167993, orangutan:0.0113753):0.00957764, (macaque:0.0096667, baboon:0.0092029):0.027333):0.091352, lemur:0.107534):0.0199236, (((((Ailuropoda melanoleuca:0.00571839, polar_bear:0.0148253):0.0290693, (walrus:0.0392861, Weddell_seal:0.0414904):0.0078879):0.00731417, dog:0.0831403):0.0098806, (cat:0.00947357, tiger:0.00486409):0.0835722):0.0220459, ((camel:0.00519368, alpaca:0.00591778):0.0387242, ((sperm_whale:0.0414087, (minke_whale:0.0337845, (Chinese_dolphin:0.0201641, (orca:0.00563662, bottle_nose_dolphin:0.0092065):0.00995856):0.0111664):0.00183346):0.0469186, ((tibetan_antelope:0.00979868, goat:0.0111361):0.0101703, (yak:0.0136206, water_buffalo:0.0125033):0.00962957):0.00562099, (giraffe:0.0135262, okapi:0.0013169):0.0247143):0.066024):0.00660271):0.0157028):0.0183566):0.0750334);



Locus name: Extracellular matrix protein 1 (**ECM1**)

Locus Name: Tweety family member 2 (**TTYH2**)

ENSBTAT0000014618 TTYH2-201 chloride channel growth control, development
no mutants described for mouse or human; Drosophila mutants are flightless

PP2: (Giraffe) D38N; (Giraffe/Okapi) G384S
PSG: (Giraffe) K414R
Giraffe: D38N UIS, K414R UIS
Giraffe/Okapi: V105A UPS, G384S UIS, H521R UPS

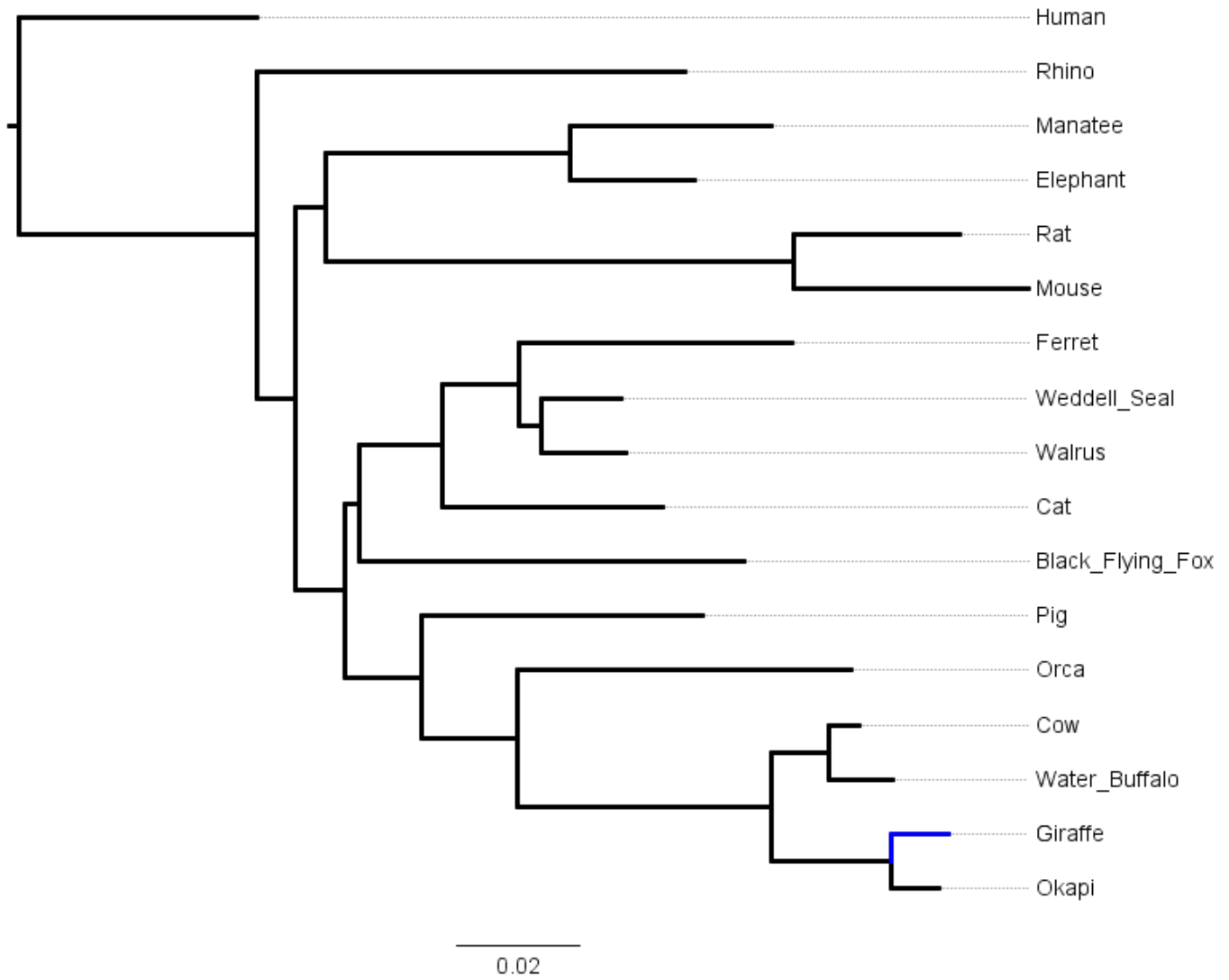
Protein sequence Alignment of Cow, Giraffe and Okapi TTYH2

Cow	1	MPAARVEYIAPWVWVWLHSVPHLGLRLQFVDSTFRPRDESYQESLLFLGLVAAVGLGLLV	60
Giraffe	1N.....	60
Okapi	1	60
Cow	61	LLAAYLVCVCCCRQDDAVQTKRPRSCCVTWTAVVAALICCAAVGVGFYGNSEANDGVYQL	120
Giraffe	61	..V.....G.....A.....	120
Okapi	61	..T.....G.....A.....	120
Cow	121	LYALDNNANHTFSGIDVLVSGTTQKMKVDLEQHLARLGEIFATRGDYLTQTLKFLQQTAGSI	180
Giraffe	121E.....A.....	180
Okapi	121R..E.....A.....M.....	180
Cow	181	IAQIAGVPVWTEVTEELTELANQTSSVEYYRWLSYLLLFVLDLVLCLLACLGLAKRSRCL	240
Giraffe	181	.V.M...T.....F.....	240
Okapi	181	.V.M...T.....Y...F.....	240
Cow	241	LASMLCCGVLALLFSWTSLAADAAAAGVTSDFCAAPDTFILNITEGQVRPEVTQYYLYCS	300
Giraffe	241A....L.....R.....	300
Okapi	241A....L.....R.....	300
Cow	301	QSASSPFQQALTVFQSRSLTAMQIQVAGLQFAVPRFPTAEKDLLGIQLLLNSSESGLHQL	360
Giraffe	301T.....	360
Okapi	301I.....T.....	360
Cow	361	TALLDCRGLHKDYLDALAGICYDGLEGLLYLGLFSLLAALAFSIMICLGPAAWKHCATRD	420
Giraffe	361S.....S.....R...S..	420
Okapi	361S.....	420
Cow	421	RDYDDIDDDDPFNPQARRIATHNPPRGQLRSFCSYSSGLGSQGLHPAQTISNAPVSEYM	480
Giraffe	421A.....T.....	480
Okapi	421A.....T.....	480
Cow	481	NQAALFGGNPRYENVPLIGRGSPPPTYSPSMRATYLSVADEHLRHYGNEFPG	533
Giraffe	481R.....	533
Okapi	481R.....	533

Newick Tree of Mammalian TTYH2

(Human:0.0382285, (Rhino:0.0688808, ((Manatee:0.0323078, Elephant:0.0200028):0.0393509, (Rat:0.026561, Mouse:0.0375202):0.075332):0.00474799, (((Ferret:0.043937, (Weddell_Seal:0.0128347, Walrus:0.0137355):0.00361613):0.0122243, Cat:0.0354042):0.0132597, Black_Flying_Fox:0.0616557):0.00252206, (Pig:0.0451661, (Orca:0.0538598, (Giraffe:0.00924067, Okapi:0.00778989):0.0190247, (Cow:0.00494582, Water_Buffalo:0.0102066):0.0090632):0.0410263):0.0153503):0.0123817):0.00775085):0.0063642):0.0382285);

Locus Name: Tweety family member 2 (**TTYH2**)



Locus Name: Tweety family member 2 (**TTYH2**)

Locus Name: CREB Binding Protein (CREBBP)

ENSBTAT00000005092 CREBBP-201 CBP histone acetylase angiogenesis, skeletal growth, regulates Hox protein activity human: Rubinstein-Taybi syndrome 1 (RSTS1) [MIMOUSE:180849]: A disorder characterized by craniofacial abnormalities, postnatal growth deficiency, broad thumbs, broad big toes, mental retardation and a propensity for development of malignancies.

PP2: Giraffe, A130T, G2171S; Giraffe/Okapi, A2268G

Giraffe: A259T UIS, T859P UIS, A1022V UPS, G2165S UIS

Giraffe/Okapi: PG2073-2074AS UISS, A2258G UIS

Protein sequence Alignment of Cow, Giraffe and Okapi CREBBP

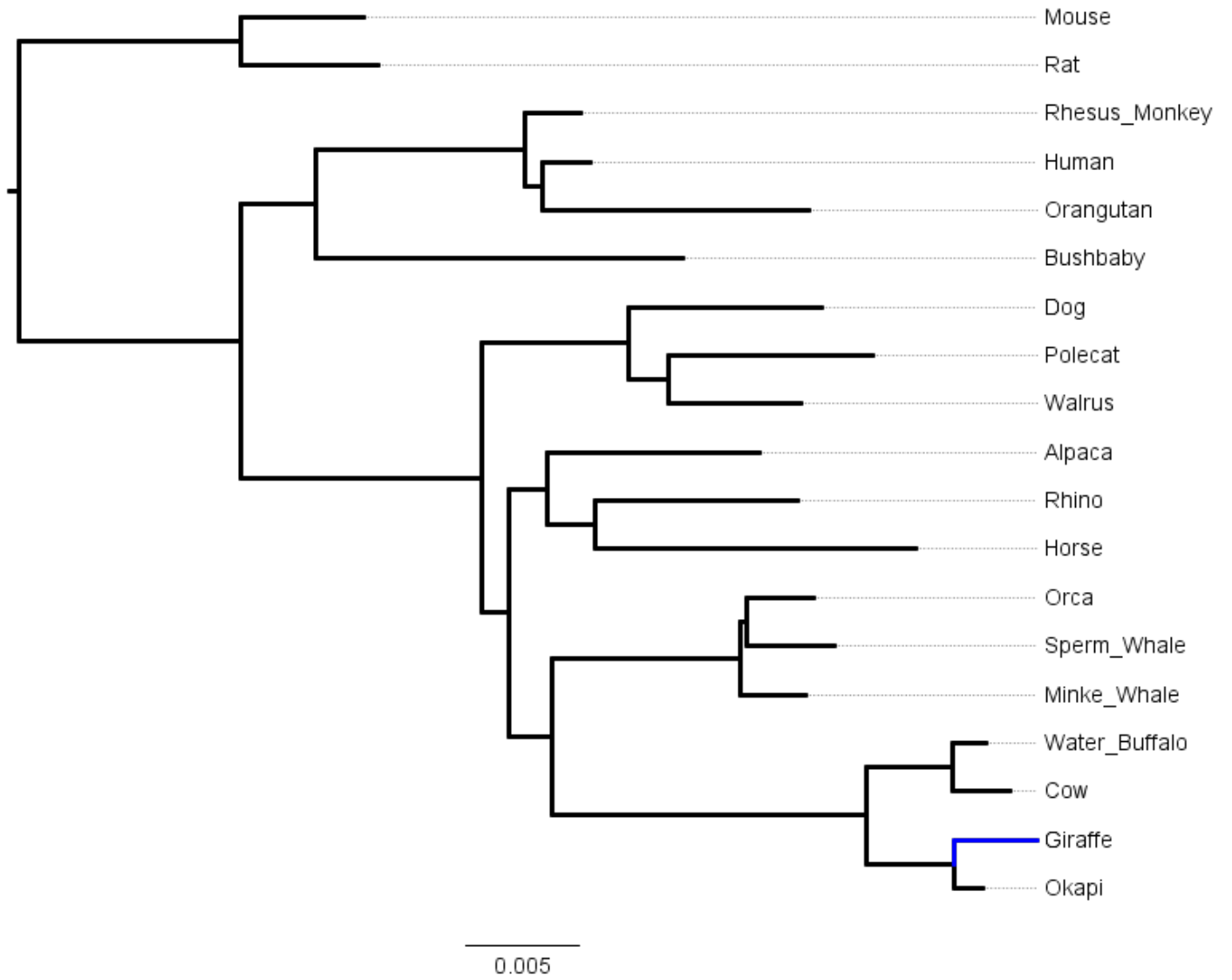
Cow	1	MAENLLDGPPNPKRAKLSSPGFSANDSTDFGSLFDLENDLPDELIPNGGELSLLNSGNLV	60
Giraffe	1	60
Okapi	1	60
Cow	61	PDAASKHKQLSELLRGGSSSSINPGIGNVSASSPAQQGLGSQAQQQPSSANMASLGAMGK	120
Giraffe	61G.....	120
Okapi	61G.....	120
Cow	121	SPLNQGDSSAPSLPKQAASTSGPTPPASQALNPQAQKQVGLVTSSPATSQTGPGICMNAN	180
Giraffe	121T.....	180
Okapi	121	180
Cow	181	FNQTHPGLLNSNSGHGLMNQAQQGQAQVMNGSLGAAGRGRGAGMPYPTPAMQGATSSVLA	240
Giraffe	181	..A.....S.....A.....	240
Okapi	181S.....T.....	240
Cow	241	ETLTQVSPQMASHAGLNTAQAGGMSKMGMTGNTSPFGQPFSSQTGGQQMGAPGVNPQLPSK	300
Giraffe	241S.....	300
Okapi	241	300
Cow	301	QSMVNSLPPFAADIKNASVTNVPNMPQMOTSVGIVPTQAIATGPTADPEKRKLIQQQLVL	360
Giraffe	301A..T.....S.....	360
Okapi	301A..T.....S.....	360
Cow	361	LLHAHKCQRREQANGEVRACALPHCRTMKNVNLNMTHTCQAGKACQVAHCASSRQIIISHWK	420
Giraffe	361S.....	420
Okapi	361S.....	420
Cow	421	NCTRHDCPVCLPLKNASDKRNQQTILGSPAGGIQNTIGSVGTGQQNATSLSNPNPIDPSS	480
Giraffe	421S.....	480
Okapi	421S.....	480
Cow	481	MQRAYAALGLPYLNQPQTQLQPQVPGQQAQPQTHQQMRSNLNPLGNPNMNI PAGGITTDQ	540
Giraffe	481	540
Okapi	481	540
Cow	541	QPSNLISESALPTSLGATNPLMNDGNSNGNIGTLSTIPAAAPPSSTGVRKSWHEHVTQDL	600
Giraffe	541	..P.....	600
Okapi	541	..P.....	600
Cow	601	RSHLVHKLQVAIFPTPDPAALKDRR MENLVAYAKKVEGDMYESANSRDEYYHLLAEKIYK	660
Giraffe	601	660
Okapi	601	660
Cow	661	IQKELEEKRRSRLHKQGILGNQPALSAPGTQPPGIPQAQFVRPPNGPMLPTVNRMQVSQG	720
Giraffe	661P.....S.....P.....	720
Okapi	661P.....S.....P.....	720
Cow	721	MNSFNPISLGNVQLPQAPMG PRAASPMNHSVPMNSMGVPGMAISPSRMPQPPNMMGAHA	780
Giraffe	721L...T	780
Okapi	721L.....	780
Cow	781	NSMMAQAPASQFLPQSQFPSSSGALS VSSVGMGQPAAQAGVPQGQVPGAALPNPLNMLG	840
Giraffe	781	840

Okapi	781T.....	840
Cow	841	PQASQLPCPFVTQPPLHQTPPPASTAAGMPSLQHHPAAGVTPPQPAAPTQPSTPASSSSGQ	900
Giraffe	841P.....	900
Okapi	841	900
Cow	901	TPTPTPGSVPSASQTQSTPTVQAAAQAQVTPQPQTPVQPPSVATPQSSQQQPTPVHTQPP	960
Giraffe	901	960
Okapi	901	960
Cow	961	GTPLSQTAASIDNRVPTPSSVASAETNSQQPGPEVPLEMKAEIKTEDTEPDAGEPKGEP	1020
Giraffe	961T.....	1020
Okapi	961	1020
Cow	1021	GATMMEEDLQGSSQVKEETDPTEQKSEPMEVDEKKTEVKVEAKEEEEEGSTNGTASQSTSP	1080
Giraffe	1021	.VA.....	1080
Okapi	1021	.VA.....	1080
Cow	1081	SQPRKKIFKPEELRQALMSTLEALYRQDPESLPPFRQVDPQLLGIPTYFDIVKNPMDLST	1140
Giraffe	1081P.....	1140
Okapi	1081P.....	1140
Cow	1141	IKRKLDTGQYQEPWQYVDDVWLMFNNAWLYNRKTSRVYKFCSKLAEVFEQEIDPVMQSLG	1200
Giraffe	1141	1200
Okapi	1141	1200
Cow	1201	YCCGRKYEFSPQTLCCYKQLCTIPRDAAYYSYQNRVYHFCEKCFTEIQGENVTLGDDPSQ	1260
Giraffe	1201	1260
Okapi	1201	1260
Cow	1261	PQTTISKDQFEKKNNDTLDPEPFVDCKECGRKMHQICVLHYDIIWPSGFVCDNCLKKTGR	1320
Giraffe	1261	1320
Okapi	1261	1320
Cow	1321	TRKENKFSAKRLQTTRLGNHLEDRVNKFLLRRQNHPEAGEVFVRRVASSDKTVEVKPGMKS	1380
Giraffe	1321	1380
Okapi	1321	1380
Cow	1381	RFVDSGEMSESFYRKTALFAFEEIDGVDVCFGMHVQEYGSDCPPNTRRVYISYLDSE	1440
Giraffe	1381	1440
Okapi	1381	1440
Cow	1441	HFFRPRCLRTAVYHEILIGYLEYVKLGYVTGHIWACPPSEGDDYIFHCHPPDQKIPKPK	1500
Giraffe	1441	1500
Okapi	1441	1500
Cow	1501	RLQEWYKMLDKAFAERI IHDYKDILKQANEDRLTSAKELPYFEGDFWPNVLEESIKELE	1560
Giraffe	1501T.....	1560
Okapi	1501T.....	1560
Cow	1561	QEEEEKKEESTAASETTEGSQGDSKNAKKNNKKTNKNKSSISRTNKKKPSMPNVSNDL	1620
Giraffe	1561A.....	1620
Okapi	1561A.....	1620
Cow	1621	SQKLYATMEKHKEVFFVIHLHAGPVIHTLPPIVDPDPLLSCDLMDGRDAFLT LARDKHWE	1680
Giraffe	1621N.....	1680
Okapi	1621N.....	1680
Cow	1681	FSSLRRSKWSTLCLMVELHTQGQDRFVYTCNECKHHVETRWHCTVCEDYDLCINCYNTKS	1740
Giraffe	1681	1740
Okapi	1681	1740
Cow	1741	HTHKMVKWGLGLDDEGGSQGEPPQSKSPQESRRLSIQRCIQSLVHACQCRNANCSLPSCQK	1800
Giraffe	1741	1800
Okapi	1741	1800
Cow	1801	MKRVVQHTKGCKRKTNGGCPVCKQLIALCCYHAKHCQENKCPVPFCLNIKHKLRQQQIQH	1860
Giraffe	1801	1860
Okapi	1801	1860

Cow	1861	RLQQAQLMRRRMATMNRNVPQQSLPSPTSAPPGTPTQQPSTPQTPQPPAQPPSPVMS	1920
Giraffe	1861	1920
Okapi	1861	1920
Cow	1921	PAGFPSVARTQPPTTVSTGKPTNQVPAPPPPAQPPAAVEAARQIEREAQQQQLYRVNI	1980
Giraffe	1921	1980
Okapi	1921	1980
Cow	1981	NNGMPPGRTGMVTPVVSQMAPVGLNVP RPQVSGPVVPTLPAGQWQAPIPQQQPMPGMFR	2040
Giraffe	1981	2040
Okapi	1981	2040
Cow	2041	PVMSMQAQPAVAGPRMSGVQPPRSISPGALQDLLRTLKSPSSPQQQQVLNILKSNPQLM	2100
Giraffe	2041	2100
Okapi	2041	2100
Cow	2101	AAFIKQRTAKYVASQPLQPPGLQAQPLHQPLQNLNAMQASGPRPGVPPQQQAMGG	2160
Giraffe	2101S.....G.....S	2160
Okapi	2101S.....G.....	2160
Cow	2161	LNPQGGALNIMNPGHNPSMASMNPQYREMLRRQLLQQQQQQQQQQQQGSGMAGGMA	2220
Giraffe	2161	...S.....AS.....-.....G.....	2219
Okapi	2161AS.....-.....G.....	2216
Cow	2221	GHSQFQQPPGAGYPPAMPQQRMQQHLPMQGSAMGPMMAQMGQLGQMGQPGLGADSTPNI	2280
Giraffe	2220	..G.....G.....	2279
Okapi	2217	..G.....T.....G.....	2276
Cow	2281	QQALQQRILQQQQMKQQMGSPGQPNPMSPPQHMLSGQPQASHLPGQQMATSLSSQVRSFA	2340
Giraffe	2280	2339
Okapi	2277	2336
Cow	2341	PVQSPRPQSQPPHSSPSPRIQPQPSPHHVSPQTGSPHPGLAVTMASSIDQGHLGNPEQSA	2400
Giraffe	2340	2399
Okapi	2337	2396
Cow	2401	MLPQLNTPNRSALSSELSLVGDTTGTLEKFEVGL	2435
Giraffe	2400	2434
Okapi	2397	2431

Newick Tree of Mammalian CREBBP

```
((mouse:0.0054413, rat:0.00609596):0.00984197, (((rhesus_monkey:0.00251445, (human:0.00218422,
orangutan:0.0118545):0.000778584):0.00922866, bushbaby:0.0162716):0.00335433, ((dog:0.00854825,
polecat:0.00905969, walrus:0.00584797):0.0017997):0.00653838, ((alpaca:0.0094531,
rhino:0.00897713, horse:0.0142625):0.00214399):0.00166158, (((orca:0.0029489,
sperm_whale:0.0039329):0.000244742, minke_whale:0.00283622):0.00837558,
((water_buffalo:0.00153525, cow:0.00257999):0.00379528, (giraffe:0.00365283,
okapi:0.00129566):0.00387512):0.0139488):0.00191949):0.00123868):0.0106762):0.00984197);
```

Locus Name: CREB Binding Protein (CREBBP)

Locus Name: Intraflagellar Transport 74 (IFT74)

ENSBTAT00000026073 IFT74-201 intraflagellar transport protein ciliogenesis kidney, heart, lung
mouse: heterotaxy syndrome (ambiguous lung lobation) with congenital heart disease, including a common atrium, double outlet right ventricle with atrioventricular septal defect, and dual inferior vena cavae.

PP2: (Giraffe/Okapi) Q7P, E386Q

Giraffe: I121M UIS, S469T UIS
Giraffe/Okapi: P7Q UPS, Q388E UIS

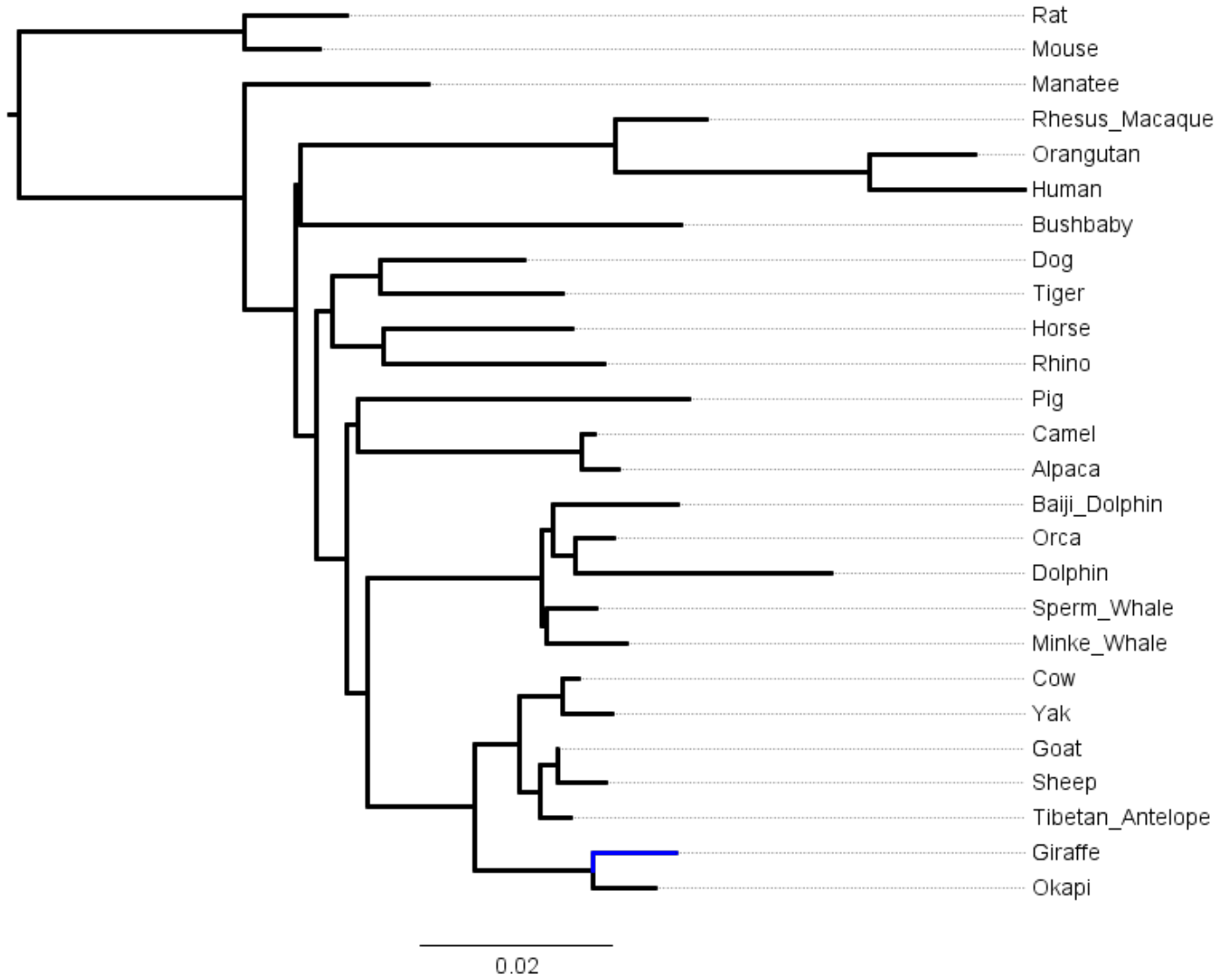
Protein sequence Alignment of Cow, Giraffe and Okapi IFT74

Cow	1	MASNHKPSAVRPVSRGGIGLTGRPPSGIRPPSGNIRVATGMPPGTARPGSRGGPIGTGGV	60
Giraffe	1Q.....I.....	60
okapi	1Q..L.....	60
Cow	61	LSSQIKVADRPVTQQGLSGMKTGMKGPQRQILDKSYLGLLRSKISELTTEINKLQKEIE	120
Giraffe	61V.....	120
Okapi	61V.....	120
Cow	121	MYNQENSVYLSYEKRAETLAVEIKEFQQLADYNMLADKLNTNTEMEEVMDYNMLKAQN	180
Giraffe	121	I.....	180
Okapi	121	180
Cow	181	DRETQSMDIIFTERQAKEKQIRSVEEEIEQEKQAAEGIIKNMSPEKQVKYIEMKTTNEKL	240
Giraffe	181D.....	240
Okapi	181	240
Cow	241	LQELDTLQQQLDSLNMKKESELESEIAHSQVKQEAVLLHEKLYELESHRDQMI AEDKNMGS	300
Giraffe	241K.....	300
Okapi	241K.....M.....	300
Cow	301	PMEERERLLKQVKEDNQEIASMERQLTDIKEKINQFNEEIRQLDMDLEEHQGE MNQKYKE	360
Giraffe	301S.....	360
Okapi	301	.T.....M...S.....	360
Cow	361	LKKREENMDTFIETFEDTKNQELERKAQIEASIVSLEHSSRNINRMKQISSITNQELKM	420
Giraffe	361E.....E...N.....	420
Okapi	361E.....E...N.....	420
Cow	421	MQDDLNFKSTEMQKSQSTARNLTSQSRLQLDLQKMDLLESKMTEEQQSLKNKIKQMITD	480
Giraffe	421E.....T.....	480
Okapi	421E.....	480
Cow	481	LETYNDLAALKSSGEEKKKLHQEKTVLSTRNFAFKKIMEKLNTEWETLKTQLQENETHS	540
Giraffe	481R.....C.....	540
Okapi	481R.....C.....	540
Cow	541	QLTNLERKQWHEQNNFVMKEFIATKSQESDYRPIMKNVSKQIAEYNKNIVDALHSMSRN	600
Giraffe	541QQ.....S....S.M.....	600
Okapi	541QQ.....S.M.....	600

Newick Tree of Mammalian IFT74

((rat:0.010688, mouse:0.00781656):0.0235145, (manatee:0.0190562, ((rhesus_macaque:0.0095176, (orangutan:0.0109874, human:0.0160446):0.0265336):0.0326271, bushbaby:0.0395034):0.000633869, ((dog:0.0149467, tiger:0.0189613):0.00506636, (horse:0.0195728, rhino:0.0229996):0.00537898):0.00157705, (pig:0.034436, (camel:0.00120612, alpaca:0.00381483):0.0232989):0.00112892, ((baiji_dolphin:0.0129324, (orca:0.00392894, dolphin:0.026535):0.00235439):0.00115393, (sperm_whale:0.00512886, minke_whale:0.00829456):0.000526762):0.0181528, (((cow:0.00166106, yak:0.00502798):0.0045889, ((goat:0, sheep:0.00503199):0.00186817, tibetan_antelope:0.00315708):0.00214983):0.00469667, (giraffe:0.00869598,

okapi:0.00641823):0.0123638):0.0110942):0.00206966):0.00321477):0.00225747):0.00522931):0.0235145);



Locus Name: Intraflagellar Transport 74 (**IFT74**)

Locus name: Abhydrolase domain-containing protein 2 (ABHD2)

ENSBTAT00000026579 ABHD2-201 abhydroloase smooth muscle cell migration
mouse: Increase of smooth muscle cell migration and of intimal and femoral artery hyperplasia

PP2: (Giraffe) F14S, V25A

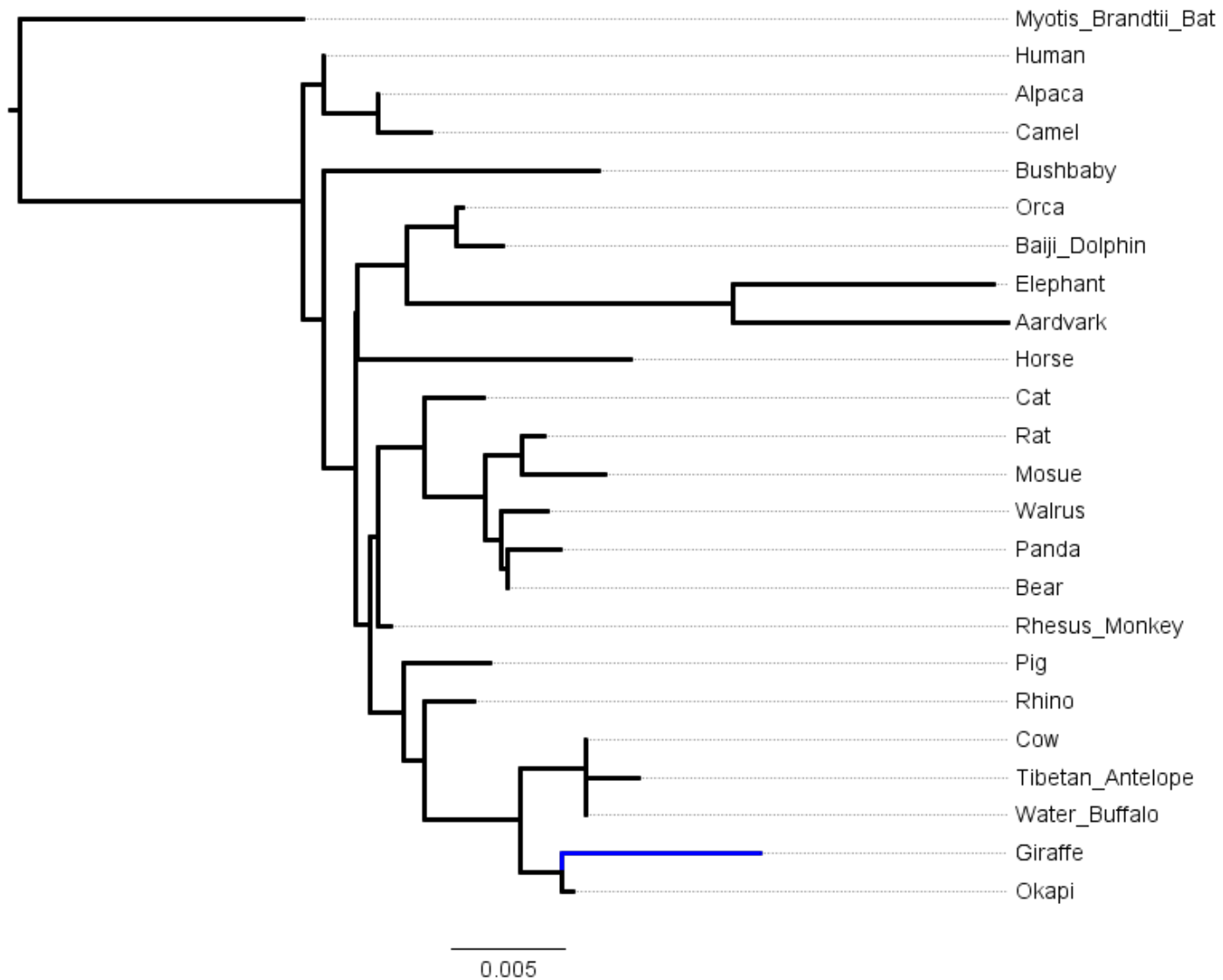
Giraffe: M5T UPS, T7A UIS

Protein sequence Alignment of Cow, Giraffe and Okapi ABHD2

Cow	1	MNAMMTESELPAVFDGVLAAVAALVYVIVRCLNLKSPPTAPPDLYFQDSGLSRFLKSCP	60
Giraffe	1T.A.....S.....A.....	60
Okapi	1	60
Cow	61	LLTKEYIIPPLIWGKSGHIQTALYGKMGRVRSHPYGHRKFITMSDGATSTFDLFEPLAEH	120
Giraffe	61	120
Okapi	61	120
Cow	121	CVGDDITMVICPGIANHSEKQYIRTFVDYAQKNGYRCAVLNHLGALPNIELTSPRMFTYG	180
Giraffe	121	...G.....	180
Okapi	121	...G.....	180
Cow	181	CTWEFGAMVNYIKKTYPLTQLVVVGFSLGGNIVCKYLGETQANQEKVLCVSVCCQGYALS	240
Giraffe	181	240
Okapi	181	240
Cow	241	RAQETFMQWDQCRRFYNFLMADNMKKIILSHRQALFGDHVKKPQSLEDTDLRSLYTATSL	300
Giraffe	241	300
Okapi	241	300
Cow	301	MQIDDNVMRKFFHGYNSLKEYEESCMRYLHRIYVPLMLVNAADDPLVHESLLAIPKSL	360
Giraffe	301T.....	360
Okapi	301T.....	360
Cow	361	EKRENVFVPLPHGGHLGFFEGSVLFPPEPLTWMDKLVVEYANAICQWERNKSQCSDEL	420
Giraffe	361	420
Okapi	361	420
Cow	421	EADLE	425
Giraffe	421	425
Okapi	421	425

Newick Tree of Mammalian ABHD2

(Myotis_Brandtii_Bat:0.0126674, ((Human:0, (Alpaca:0, Camel:0.00237069):0.0023949):0.000939286, (Bushbaby:0.0122577, (((Orca:0.000272192, Baiji_Dolphin:0.00208352):0.00220453, (Elephant:0.0115901, Aardvark:0.0122228):0.0145693):0.00222634, Horse:0.0121795):8.83777e-05, (((Cat:0.00264401, (Rat:0.000996293, Mosue:0.00372071):0.00164659, (Walrus:0.00206951, (Panda:0.00235655, Bear:0):0.000288992):0.000721738):0.00267525):0.00210213, Rhesus_Monkey:0.000552941):0.000377952, (Pig:0.00384487, (Rhino:0.0022047, ((Giraffe:0.0088849, Okapi:0.000549268):0.00182319, (Cow:0, (Tibetan_Antelope:0.0023623, Water_Buffalo:0):1.21775e-05):0.00292207):0.00431142):0.000888741):0.00155592):0.00062221):0.00141323):0.000919206):0.0126674);



Locus name: Abhydrolase domain-containing protein 2 (ABHD2)

Locus Name: Endoglin (ENG)

ENSBTAT0000054745 ENG-201 endoglin regulation of angiogenesis
mouse: defective vascular development, extra-arterial hematopoiesis, cardiac defects and die by embryonic day 11.0. Heterozygotes develop hemorrhagic telangiectasia causing strokes, fatal hemorrhage and heart failure

PP2: (Giraffe) S434, Q436S, R437Q; (Giraffe/Okapi) V426R, V427P, N428G, L430H, S431Q; (Okapi) T193M

Giraffe: C17F UIS

Giraffe/Okapi: D128H UPS, multi-UPS 419-427

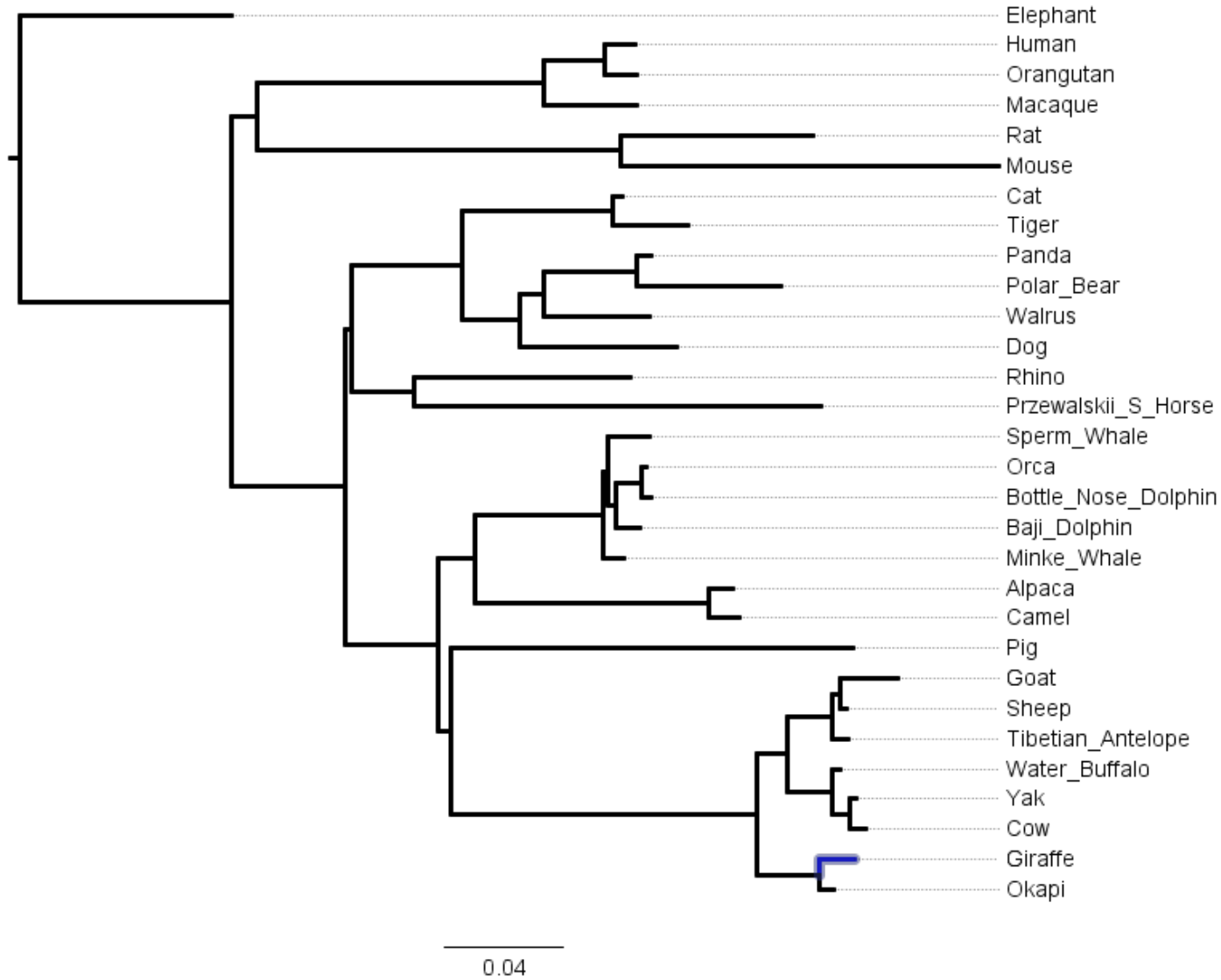
Protein sequence Alignment of Cow, Giraffe and Okapi ENG

Cow	1	MDRGVLCQAMALLLVVCSLGPTSLAETVYCDLQPVDSEVTVTSQVSEGCVAQIPDATLE	60
Giraffe	1A....I.....F..S.....K.....	60
Okapi	1A....V.....S.....K.....	60
Cow	61	VHVLFLTFLGDVSRLELTQTSKQGGIRPREVLLILSVNKSIFLKLQAPGIPLQLAYDSK	120
Giraffe	61E.Q.....A.....W.....P.	120
Okapi	61E.....P.	120
Cow	121	LVFHEALDANITQLPSFTTKDQLLNWANTQGSIASVAELSNPQSIFLRLDQASSPFCSCN	180
Giraffe	121H..T.....K.P.T.A...N..K..L.....A....S	180
Okapi	121H..T.....K.P...A...N..K..L.H.....A....S	180
Cow	181	LEPQKDMGHTLGWTPKAWGCRLEGVAGHKEAHILRILPGPEASPRTVTVKLELSCAWRDT	240
Giraffe	181E.S...Y.....W.....	244
Okapi	181M.E.S...Y.....W.....	244
Cow	241	DAAVLILQGPPYVSWLIEANHNMQIWTGTGEYSLKIFPDRINPGFQLPNTTQGLLGEARRL	300
Giraffe	245	E.....D.....	304
Okapi	245	E.....D.....	304
Cow	301	NASVVASFVELPVDVSLRTHSCGSLQPSPTPVEITTPNKGCNQELLLTLIQPKCSSD	360
Giraffe	305L.S....K.....	364
Okapi	305L.S....K.....	364
Cow	361	GMTLVLKKDLISTLLCTIKSLTFGDSSCQAKETEDEFVLSSGYSSCGMEVMENVVSNEVV	420
Giraffe	365T...W.....E.....G	426
Okapi	365T...W.....E.....G	426
Cow	421	IRLLSSSSPQRKKVQCINTDLSLQLGLYLSPHFLQASDTIELGQQGFVQVSVSPSIPEL	480
Giraffe	427	THQA.LP....-.....M.....N.....	485
Okapi	427	THQA.LL....-.....M.....N.....	485
Cow	481	MIQLESCQLNLGPDMEIVELIQGQEAKSSCVSLLSPSPSGDIRFSFLLRGMVPMPTTGI	540
Giraffe	486N.....L.....	545
Okapi	486L.....	545
Cow	541	LSCSVTMHPRIRSLEVHKTVSTRNLNIISTSLHDKGLVLPVAVLGITFGAFLIGALLTAALW	600
Giraffe	546V.A.....	605
Okapi	546V.A.....	605
Cow	601	YIYSHTRHPGKREPVVAVAAPASSESSSTNHSIGSTQSTPCSTSSMA	647
Giraffe	606	652
Okapi	606	652

Newick Tree of Mammalian ENG

((elephant:0.072431, (((human:0.010522, orangutan:0.0109859):0.0208525, macaque:0.0319625):0.0977316, (rat:0.0657712, mouse:0.128808):0.124244):0.00872041, (((cat:0.00336395, tiger:0.0261992):0.0512544, ((panda:0.0049737, polar_bear:0.0490313):0.0321168, walrus:0.036087):0.00816102, dog:0.0540564):0.01956):0.0375917, (rhino:0.073731, Przewalskii_s_horse:0.138861):0.0213191):0.00223153, (((sperm_whale:0.0141981, (orca:0.00166369, bottle_nose_dolphin:0.00288523):0.00870219, baiji_dolphin:0.00811665):0.00307396):0.00154817, minke_whale:0.00733948):0.0437027, (alpaca:0.00787746, camel:0.0104727):0.0799427):0.012384, (pig:0.136796, ((goat:0.0194578, sheep:0.0019086):0.00324475, tibetian_antelope:0.00545567):0.0151977, (water_buffalo:0.00266271,

(yak:0.00215987, cow:0.0055982):0.00590166):0.01563):0.0103541, (giraffe:0.0119799, okapi:0.00503603):0.0213213):0.104162):0.00441165):0.0318778):0.0389065):0.072431);



Locus Name: Endoglin (ENG)

Locus Name: Semaphorin 3E (SEMA3E)

ENSBTAT00000019866 SEMA3E-201 semaphorin 3E regulates angiogenesis and neuronal synaptogenesis in eye
 mouse: abnormal intersomitic vascular development and loss of the normal segmented somite pattern

PP2: (Giraffe) F227L

Giraffe: A39E UIS, F227L UIS, P694Q UIS
 Giraffe/Okapi: Y30S UIS, K313R UIS, V503I UIS
 Okapi: I393L UIS, D570E

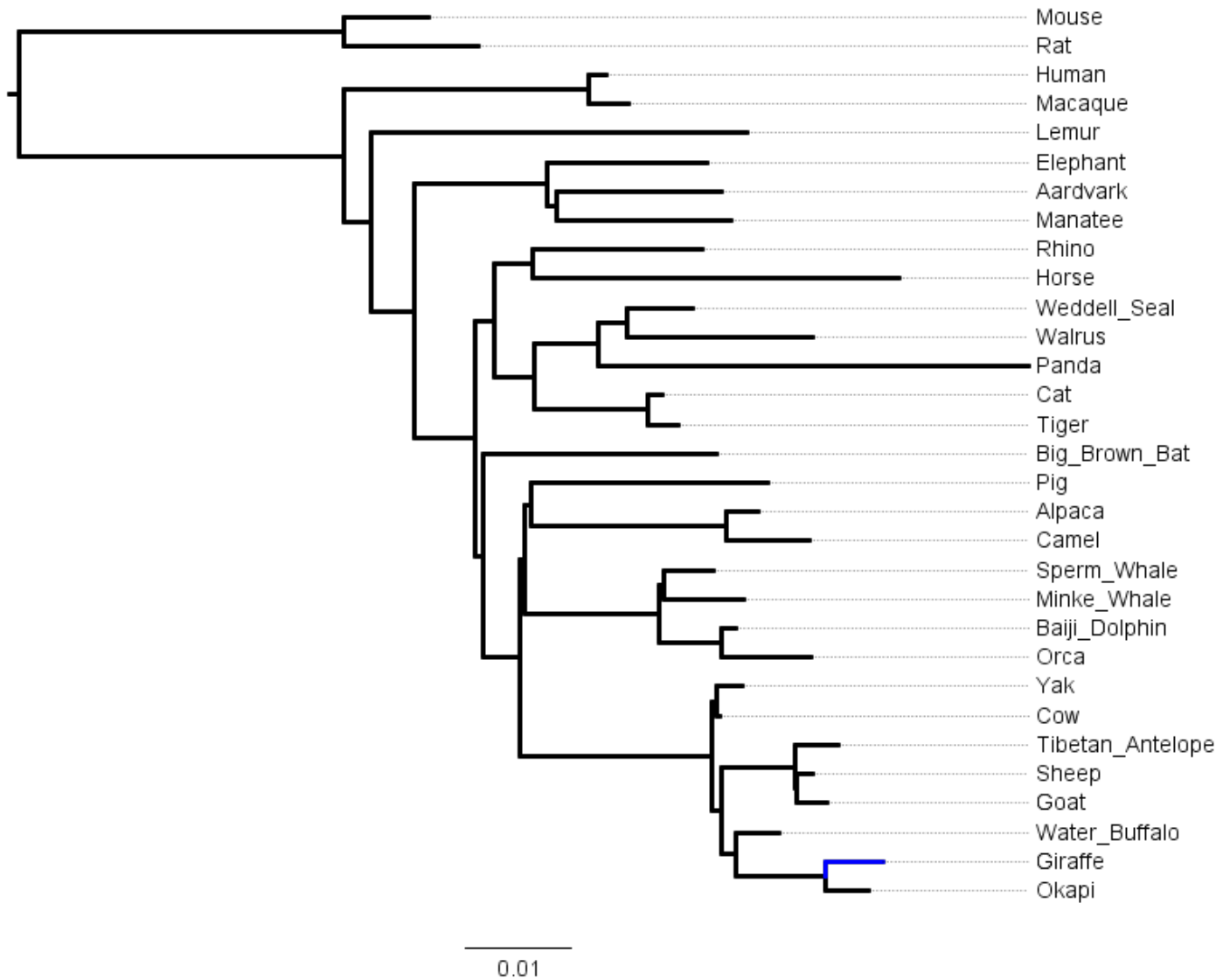
Protein sequence Alignment of Cow, Giraffe and Okapi SEMA3E

Cow	1	MLLDEYQERLQVGGKDLVYSLSLEHISGSYREIHWSTALKTEECIMKGNDASECANYVR	60
Giraffe	1I.....S.....E.....N.....	60
Okapi	1S.....N.....	60
Cow	61	VLHHYNRTHLLTCGTGAFDPLCAFIRVGYHLEAPLFHLESHRSERGRGRCPDFPSSSFIS	120
Giraffe	61	120
Okapi	61	120
Cow	121	TLIGSELFAGLYSDYWGRDAAIFRSLGRLAQIRTEHDDERLLKEPKFVGSYMIPDNEDRD	180
Giraffe	121	180
Okapi	121	180
Cow	181	DNKVYFFFTEKALEAENSAHAIYTRVGRLCVNDMGGQRILVKNKWFLLKARLVCSVPGMN	240
Giraffe	181L.....	240
Okapi	181	240
Cow	241	GIDTYFDELEDVFLHTRDHKNPVIIFGLFNTTSNIFRGHAICVYHMSSIRAAFNGPYAHK	300
Giraffe	241	300
Okapi	241	300
Cow	301	EGPEYHWSLYEGKVPYPRPGSCASKVNGGRYETTKDYRDDAIRFARSHPLMYQPIKPAHK	360
Giraffe	301R.....R	360
Okapi	301R.....R	360
Cow	361	KPILVKTGKYNLQKQIAVDRVEAEDGQYDVLFIGTDNGIVLKVITIIYNQETESMEEVILE	420
Giraffe	361	420
Okapi	361L.....	420
Cow	421	ELQIFKDPVPIISMEISSKRQQLYIGSASAVAQVRFHQCDMYGSACADCCCLARDPYCAWD	480
Giraffe	421	480
Okapi	421	480
Cow	481	GISCSRYPTGTHAKRRFRQRDVRHGNAAQQCFGQQFVGDALDKTEERLAYGIENNSTLL	540
Giraffe	481S.....I.....	540
Okapi	481S.....I.....	540
Cow	541	ECTPRSLQAKVIWFVQKGRDARKEEVKTDTRVVKMDLGLLFLRVRMDAGTYFCQTVSHS	600
Giraffe	541L.....	600
Okapi	541E.....E.....L.....	600
Cow	601	FVHTIRKITLEVVEEERVEEMFNKDFEEDRLHKMPCPAQSIIIPRGTKPWYKEFLQLIGYS	660
Giraffe	601V.....	660
Okapi	601V.....	660
Cow	661	NFQRVEEYCEKVVWCTDKKRKLLKMSPSKWYANPQEKLRPKTEHYRLPRHALDS	716
Giraffe	661Q.....	716
Okapi	661	716

Newick Tree of Mammalian SEMA3E

((mouse:0.00819491, rat:0.0130089):0.0312075, ((human:0.0017264, macaque:0.00388374):0.0235086, (lemur:0.0361279, ((elephant:0.0154507, (aardvark:0.0158782, manatee:0.0168242):0.000900524):0.0127502, ((rhino:0.0163994, horse:0.035285):0.00371721, ((Weddell_seal:0.00624211, walrus:0.0178236):0.00280579, panda:0.0413091):0.00617642, (cat:0.00132043, tiger:0.00288422):0.0110247):0.00386472):0.00176243, (big_brown_bat:0.0225403,

((pig:0.0228876, (alpaca:0.00319824, camel:0.00805387):0.0187613):0.000572052, ((sperm_whale:0.00483996, minke_whale:0.00782768):0.000373036, (baiji_dolphin:0.00130628, orca:0.00853232):0.00601937):0.012962):0.000514436, ((yak:0.00253409, cow:0.000267038):0.000442011, ((tibetan_antelope:0.0040512, (sheep:0.00140707, goat:0.00279758):0.000160362):0.0071345, (water_buffalo:0.00416397, (giraffe:0.00565158, okapi:0.00418703):0.00855504):0.00139084):0.000935351):0.0185334):0.00349495):0.000702794):0.00589418):0.00413213):0.00266778):0.0312075);



Locus Name: Semaphorin 3E (SEMA3E)

Locus Name: Jumonji, AT Rich Interactive Domain 2 (JARID2)

ENSBTAT0000017189 JARID2-201 modulates histone methyltransferase heart and nervous system development
 mouse: defective neural tube closure, impaired hematopoiesis and hypoplasia of liver, thymus and spleen. Homozygotes for another mutation die at birth with cardiac defects. In cardiac cells, it is required to repress expression of cyclin-D1 (CCND1) by activating methylation of 'Lys-9' of histone H3

PP2: (Giraffe/Okapi) S313P, E802D, K1124R

Giraffe: A256L UPS, A272G UPS

Giraffe/Okapi: N200T UIS, A291T UPS, N307S UPS, T310A UIS, S314P UIS, M325L UPS, P442S UPS, K1125R UIS

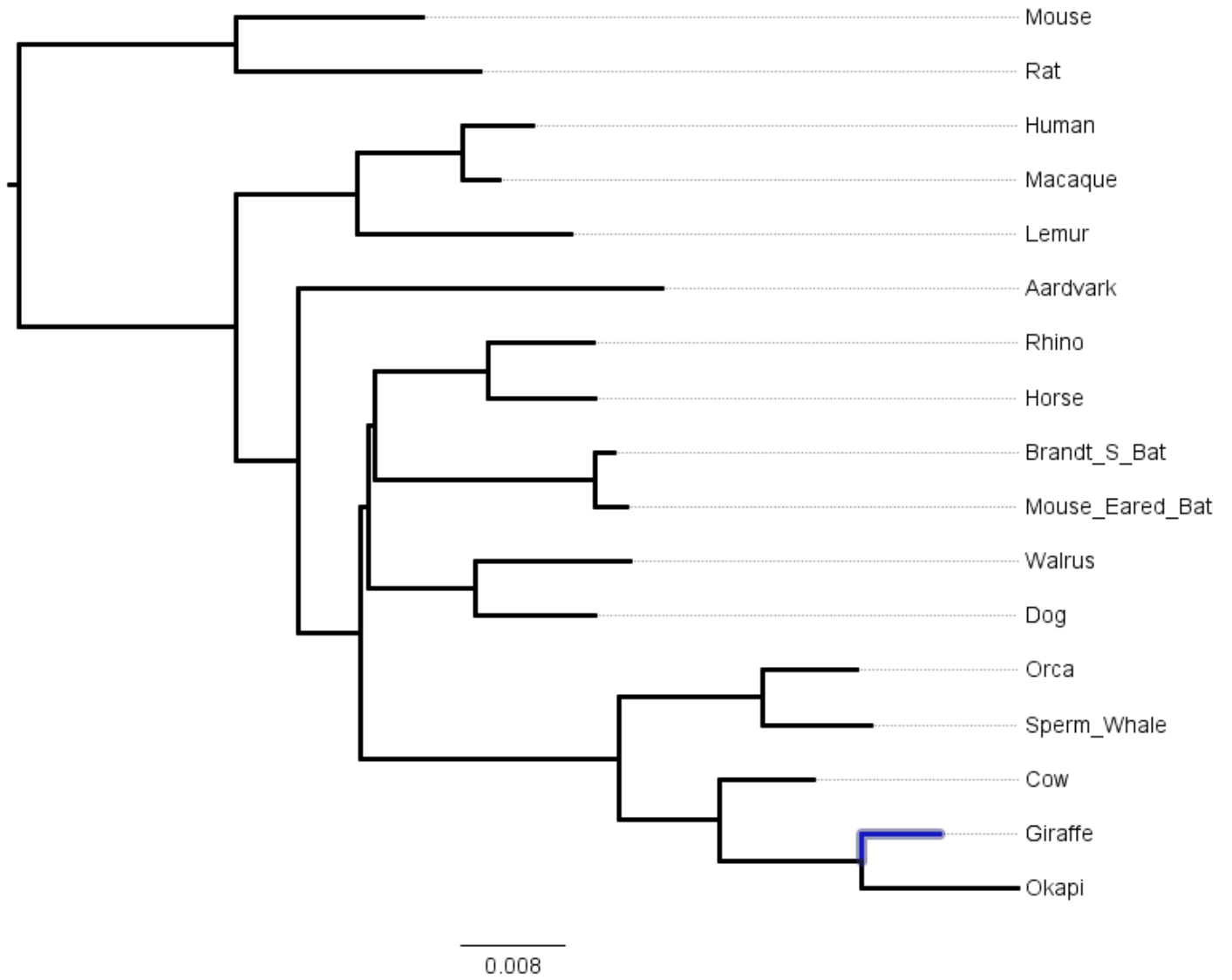
Protein sequence Alignment of Cow, Giraffe and Okapi JARID2

Cow	1	MSKERPKRNIIQKKYDDSDGIPWSEERVVRKVLVLSLKEFKNAQKRQHGEIGIPGSLKAVN	60
Giraffe	1	60
Okapi	1	60
Cow	61	GLLNGQSKGLGPASEQSENEKDDASQVSSTSNDVSSSDFEEGPSRKRPRLQAQRKFAQS	120
Giraffe	61	120
Okapi	61	120
Cow	121	QPNSPSTTPVKIVEPLPPATQISDLKRKPKTEDFLTFCLRGSPALPNSMVYFGSSQ	180
Giraffe	121	180
Okapi	121	180
Cow	181	DEEDVEEEDDETEDVKAATNNASSCQSTPRKKGKAHKHVHNGHVFNSSRSREKDPVQK	240
Giraffe	181T.....T.....	240
Okapi	181T.....T.....	240
Cow	241	HKSKEATPAKEKHS DARADARREQVSASHPPAAPAGSSAKGLAAHHHPALHRSAQDLR	300
Giraffe	241	.R.....EL.....A..Q..G.....R.....L.T.....	300
Okapi	241E.....A.V...V...V.....L.T.....	300
Cow	301	KQVSKVNGVTRMSSLGTSATSAKKMREVRPSPKTVKYTATVTKGTVTYTKAKRELVKET	360
Giraffe	301S..A...P...G.....L.....A	360
Okapi	301S.AA...P...G.....L.....R.A	360
Cow	361	KPHHHKPSAVNHTISGKTESSNAKTRKQVLSLGGASKSTGPAVNGLVKVSGRNLNPKSCTK	420
Giraffe	361R.....	420
Okapi	361A.....R.....H.....P.....	420
Cow	421	EVGGRQLREGLRNSKRRL EEVPPADKQPSPPKMKGAAGSAAEGPGRKAAPGPAEKAPLG	480
Giraffe	421AS.....M.....	480
Okapi	421	.G.....AS...Q.....V.....R..L.....P.	480
Cow	481	APGKKEAPERSLERNRPKRAAAGKGPGRQAHGKPDGGAPCENRSTSQSEPLPRPHEGAA	540
Giraffe	481	G....V.....S.....	540
Okapi	481	G....V.....S.....H.....	540
Cow	541	KAKEGAGRAGWAAMDEIPVLRPSAKEFHDPLVYIESVRPQVEKYGMCRVIPPPDWRPECK	600
Giraffe	541	600
Okapi	541	600
Cow	601	LNDEMRFVTQIQHIHKLGRRWGPNVQRLACIKKHLRSQGITMDELPLIGGCELDLCFFR	660
Giraffe	601	660
Okapi	601	660
Cow	661	LINEMGGMQQVTDLKKWNKLADMLRIPRTAQDRLAKIQEAYCQYLLSYDLSLSPEEHRRL	720
Giraffe	661	720
Okapi	661	720
Cow	721	KEVLMEKESLERRKGPLEGHTEQDYHRFHPLPRFEPKNGLINGVAHRNGFRSKLKEVGPA	780
Giraffe	721	780
Okapi	721T	780

Cow	781	QLKTGRRRLFAQEKEVVKEEEEEDKGILSDFHKCIYKGRSVSLTTFYRTARNIMMCFKSKE	840
Giraffe	781E.....	840
Okapi	781E.....	840
Cow	841	PAPAEIEQEYWRLVEEKDCHVAVHCGKVDNTNTHGSGFPVKGSEPFSSRHGWNLTVLPNNTG	900
Giraffe	841	900
Okapi	841	900
Cow	901	SILRHLGAVPGVTIPWLNIGMVFSTSCWSRDQNHLPYIDYLHTGADCIWYCIPAEEEHKL	960
Giraffe	901N..	960
Okapi	901N..	960
Cow	961	EDVVHTLLQANGTPGLQMLESNVMISPEVLCREGIKVHRTVQQSGQFVVCPPGSFVSKVC	1020
Giraffe	961V.....	1020
Okapi	961	1020
Cow	1021	CGYSVSETVHFATTQWTSMGFETAKEMKRRHIAPKPFMEKLLYQIAQAEAKKENGPTLST	1080
Giraffe	1021	1080
Okapi	1021	1080
Cow	1081	ISALLDELDRDTELRRQQLFEAGLHSSARYGSHDGSSAAPDGKKKPRKWLQLETSSERRCQ	1140
Giraffe	1081R.....	1140
Okapi	1081R.....	1140
Cow	1141	VCQHLCYLSMVVQENENVVFCLECALRHVEKQKSCRGLKLMYRYDEEQIISLVNQICGKV	1200
Giraffe	1141	1200
Okapi	1141	1200
Cow	1201	SGKNGSIENCLSKPTPKRGPRKRATVDVPPSRLASS	1236
Giraffe	1201	1236
Okapi	1201	1236

Newick Tree of Mammalian JARID2

((mouse:0.0143285, rat:0.0186293):0.0166807, (((human:0.00534, macaque:0.00271815):0.00815442, lemur:0.0164536):0.00922036, (aardvark:0.027892, (((rhino:0.00804583, horse:0.00816269):0.00868825, (Brandt_s_bat:0.00152453, mouse_eared_bat:0.00251263):0.0168041):0.000590236, (walrus:0.0118426, dog:0.00919531):0.00819426):0.000571848, ((orca:0.00718431, sperm_whale:0.0083205):0.0110135, (cow:0.00720798, (giraffe:0.00599024, okapi:0.0119704):0.0108826):0.00763952):0.0198209):0.00477126):0.00472721):0.0166807);



Locus Name: Jumonji, AT Rich Interactive Domain 2 (JARID2)

Locus Name: 25-hydroxyvitamin D-1 alpha hydroxylase (CYP27B1)

ENSBTAT00000022485 CYP27B1-201 25-hydroxyvitamin D-1 alpha hydroxylase bone development and calicium metabolism

mouse: hypocalcemia, hyperparathyroidism, growth retardation, rickets; human: ricketts

PSG (Giraffe) N353G

PP2: (Giraffe) G354N; (Giraffe/Okapi) S280F, P423L

Giraffe: R10K UIS, P33S UPS, R103C UPS, G354N UPS, V456I UPS

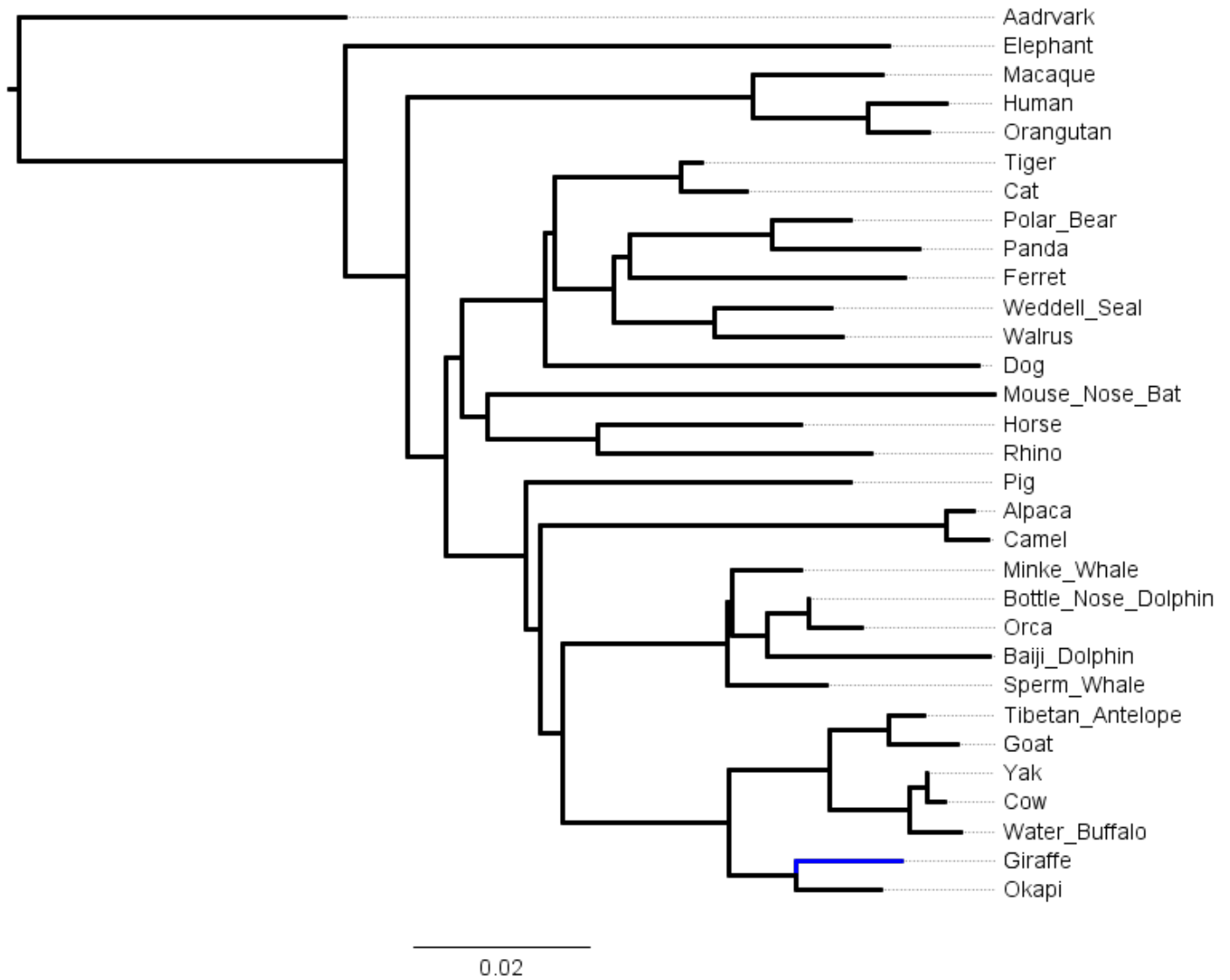
Giraffe/Okapi: V244I UPS, P423L UIS

Protein sequence Alignment of Cow, Giraffe and Okapi CYP27B1

Cow	1	MTQTLKFASRVFHRVRCPELGASLGRGSEAPRVLADIPGPSTPGFLAELFCKGGLSRL	60
Giraffe	1L..K.....D..S.....	60
Okapi	1L.....T.....D.....	60
Cow	61	HELQVQGAARFGPVWLASFQTVRTVYLAAPTLVEQLLRQEGPRPERCSFSPWTEHRRRRQ	120
Giraffe	61C.....A.....	120
Okapi	61V.....	120
Cow	121	RACGLLTAEGEEWQRLRSLLAPLRLRPQAAARYAGTLHGVRDLVRRRLRRQRGLGAGPPS	180
Giraffe	121H.....A	180
Okapi	121A	180
Cow	181	LVRDVAGEFYKFGLEGIAAVLLGSRGCLAEVPPDTETTFIRAVGSVVFVSTLLTMAMPSW	240
Giraffe	181N.....N	240
Okapi	181N.....N	240
Cow	241	LHRVVPGPWDRLCRDWDQMFQFAFAQQHVEQREAEVAMRNQSEKSEEDMGPGAHLTYFLLQK	300
Giraffe	241	...I.....S.FG.....RE	300
Okapi	241	...IL.....I.....S.FG.....RE	300
Cow	301	ELPAASILGNVTELLLAGVDTVSNTLSWALYELSRHPEIQTALHAEITAALGPGSSTQPS	360
Giraffe	301S.....N.....	360
Okapi	301S.....	360
Cow	361	ATALSQPLLLKAVVKEVLRRLYPVVPNGNSRVPDRDICVGEYIIPKNTLVTLCHYATSRDEA	420
Giraffe	361K.....D.....	420
Okapi	361K.....D.....	420
Cow	421	QFPEPNSFRPARWLGEQGPAPHPFASLPFGFGKRSCVGRRLAELELQMALAQILIHFEVQP	480
Giraffe	421	..L.....I.....N.....	480
Okapi	421	..L.....M.....N.....	480
Cow	481	EPGSAPVRPMTRTVLVPERSINLQFVDR	509
Giraffe	481	509
Okapi	481	509

Newick Tree of Mammalian CYP27B1

(aadrvark:0.0375242, (elephant:0.0622914, ((macaque:0.0148826, (human:0.00896279, orangutan:0.00691122):0.0132665):0.0395558, (((((tiger:0.00238673, cat:0.00750471):0.0145471, ((polar_bear:0.00899558, panda:0.016931):0.0163114, ferret:0.0316429):0.00178405, (Weddell_seal:0.013333, walrus:0.0146166):0.0115555):0.00679621):0.00106311, dog:0.0497564):0.00952142, (mouse_nose_bat:0.0582708, (horse:0.0232685, rhino:0.0313728):0.0127407):0.0028444):0.00178531, (pig:0.0372145, ((alpaca:0.00313167, camel:0.00477359):0.0464589, ((minke_whale:0.00783549, (bottle_nose_dolphin:0, orca:0.00599386):0.00475496, baiji_dolphin:0.0253801):0.00416045):0.000529713, sperm_whale:0.0114343):0.0188347, ((tibetan_antelope:0.00404073, goat:0.00784087):0.00682575, ((yak:1.66149e-05, cow:0.00195383):0.0019791, water_buffalo:0.00593403):0.00921975):0.0114662, (giraffe:0.0120963, okapi:0.00975338):0.0076539):0.0190941):0.00254586):0.00162077):0.00916863):0.00447796):0.00710974):0.0375242);



Locus Name: 25-hydroxyvitamin D-1 alpha hydroxylase (CYP27B1)

Locus name: Calcipressin-3 (RCAN3)

ENSBTAT0000023194 RCAN3-201 inhibits calcineurin A, binds troponin heart, brain, skeletal muscle, kidney, language SNP humans
no mutations in m/h; highest expression in heart, skeletal muscle kidney, liver and peripheral blood leukocytes. GWAS human linked to reading ability.

PP2: (Giraffe) S177R, S203G, E204G, T205A

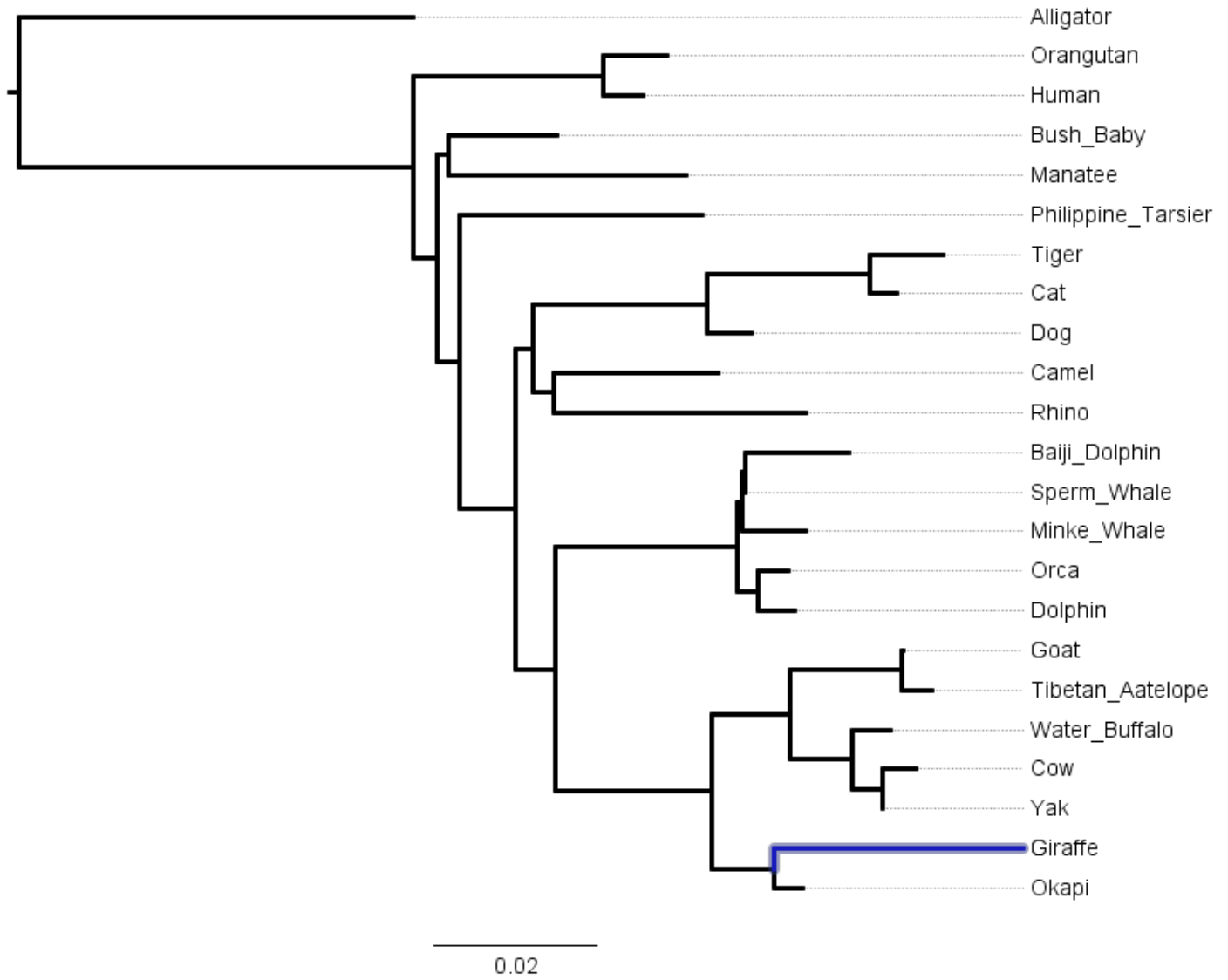
Giraffe: K177R UIS, S203G UIS, E204G UIS, T205A UIS, E206D UIS, E209A UIS, I218V UIS

Protein sequence Alignment of Cow, Giraffe and Okapi RCAN3

Cow	1	MLRDTMNSWNDSQSDLCSTDHEEEEEEMVFGENEDDLEEMMDLSDLPTSLFACRVHEAVFE	60
Giraffe	1A.K.....I.....S.....	60
Okapi	1A.K.....I.....S.....	60
Cow	61	VPEQKERFEALFTIYDDQVTFQLFKSFRRVRINFSKPEAAARARIELHETDFNGRKLKLY	120
Giraffe	61	120
Okapi	61	120
Cow	121	FAQVQMSGETRDKSYLQPPQPAKQFLISPPASPPVGWKQGGDATPVINYDLLCAVSKLGP	180
Giraffe	121S.....E..M.....R...	180
Okapi	121I.S.....E..M.....	180
Cow	181	GEKYELHAGTESTPSVVVHVCESETEEEEEETKNPKQKITQTRRPEPPTAALSEPRAFDCA	240
Giraffe	181GGAD..A.....V.....A.....	240
Okapi	181A.....	240
Cow	241	L	
Giraffe	241	.	
Okapi	241	.	

Newick Tree of Mammalian RCAN3

(alligator:0.0483704, ((orangutan:0.00770631, human:0.00482028):0.0231866, ((bush_baby:0.0132982, manatee:0.0290937):0.00139181, (Philippine_Tarsier:0.0295425, (((tiger:0.00911675, cat:0.00346237):0.019884, dog:0.00552053):0.0212035, (camel:0.0201789, rhino:0.0309182):0.00245174):0.00214144, (((baiji_dolphin:0.0126797, sperm_whale:0):0.000511953, minke_whale:0.00787482):0.000597203, (orca:0.00375068, dolphin:0.0045828):0.0025521):0.0222505, ((giraffe:0.030299, okapi:0.0034659):0.00771831, (goat:0.000308341, tibetan_Aatelope:0.00384968):0.0135723, (water_buffalo:0.00470648, (cow:0.00421536, yak:0):0.00364454):0.00754964):0.00965143):0.0191975):0.00471539):0.00686056):0.00281634):0.00283215):0.0483704);



Locus name: Calcipressin-3 (RCAN3)

Locus Name: CDC42 Effector Protein (Rho GTPase Binding) 2 (CDC42EP2; BORG1)

ENSBTAT00000045518 CDC42EP2-201 rho GTPase inhibit CDC42 heart
no mutations in m/h; highly expressed in heart

PSG: (Giraffe) F62L 0.932, Q74R 0.935, E80Q 0.937, P142L 0.933, T163P 0.931, A169T 0.933
PP2: Giraffe, P142L

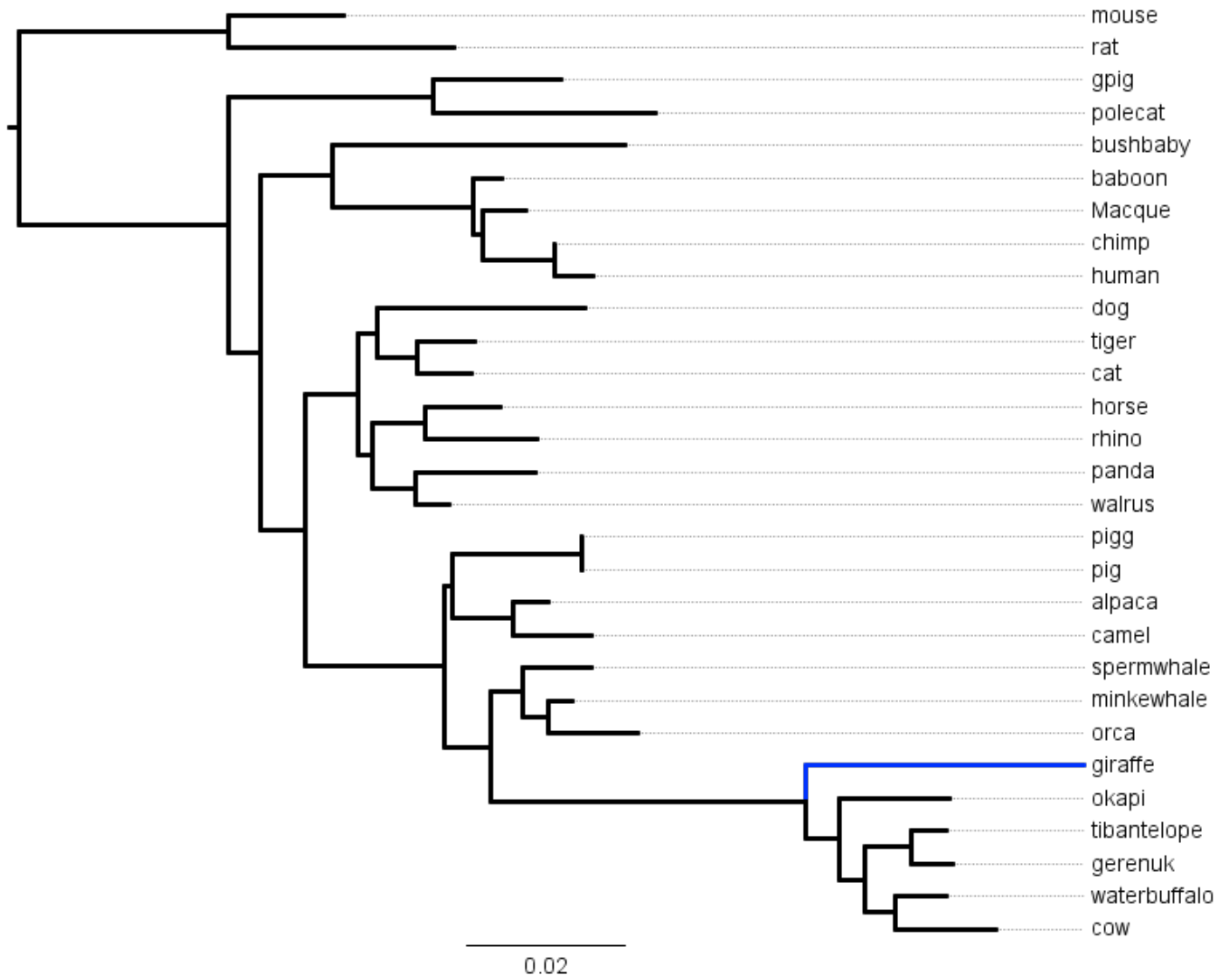
Giraffe: N49K UPS, F62L UIS, Q74E UPS, E80Q UPS, L163P UPS, A169T UPS
Okapi: G78V UPS, T137A UPS

Protein sequence Alignment of Cow, Giraffe and Okapi CDC42EP2

Cow	1	MSTKVPIYLKRGSRKGGKKEKLRDLLSSDMISPLGDFRHTIHIGSGGGNDTFGDISFLQG	60
Giraffe	1K.....	60
Okapi	1	60
Cow	61	KFHLLPGTAVDETQEDSGFEMPFQFTRTATLCGRELPDGPSPLLKNAISLPVIGGPQALT	120
Giraffe	61	.L.....AR.....Q.....	120
Okapi	61A...V.....	120
Cow	121	LPAAQAPPKPPRLHLETPQASPQEAGTVDVWRIPEAGAAHSELTTESGAEPPFLSHASSL	180
Giraffe	121P.L.....V.....GP.P...T.....	180
Okapi	121A..S.....G..P.....	180
Cow	181	LSLHVDLGPSILDDVLQIMDQDLGHLQIPT	210
Giraffe	181	210
Okapi	181	210

Newick Tree of Mammalian CDC42EP2

((mouse:0.0145936, rat:0.0283856):0.0262331, ((gpig:0.0159839, polecat:0.0278327):0.0258356, ((bushbaby:0.0366101, (baboon:0.00356704, (Macque:0.00548113, (chimp:0, human:0.00496303):0.00894311):0.00121776):0.0175749):0.00913156, (((giraffe:0.0348769, (okapi:0.0137486, ((tibantelope:0.00435601, gerenuk:0.00521358):0.00589585, (waterbuffalo:0.00656166, cow:0.0126709):0.00377406):0.00313783):0.00430068):0.03948, (spermwhale:0.00857386, (minke whale:0.00288067, orca:0.0112377):0.00324813):0.00395618):0.00592918, ((pigg:0, pig:0):0.0162874, (alpaca:0.00438069, camel:0.00980442):0.00761974):0.000994792):0.0175427, ((dog:0.026105, (tiger:0.0072252, cat:0.00689315):0.00494486):0.00250318, ((horse:0.00953455, rhino:0.0141094):0.00664547, (panda:0.0150295, walrus:0.00420301):0.00556832):0.00179352):0.00665173):0.00552213):0.00407209):0.0262331);



**Locus Name: CDC42 Effector Protein (Rho GTPase Binding) 2
(CDC42EP2; BORG1)**

Locus Name: Urotensin-2 (UTS2B)

ENSBTAT00000061012 UTS2B-201 urotensin 2, vasoconstrictor regulates blood pressure in the brain
no mutations in m/h described

PP2: (Giraffe) L81Q, L103V; (Okapi) L75V

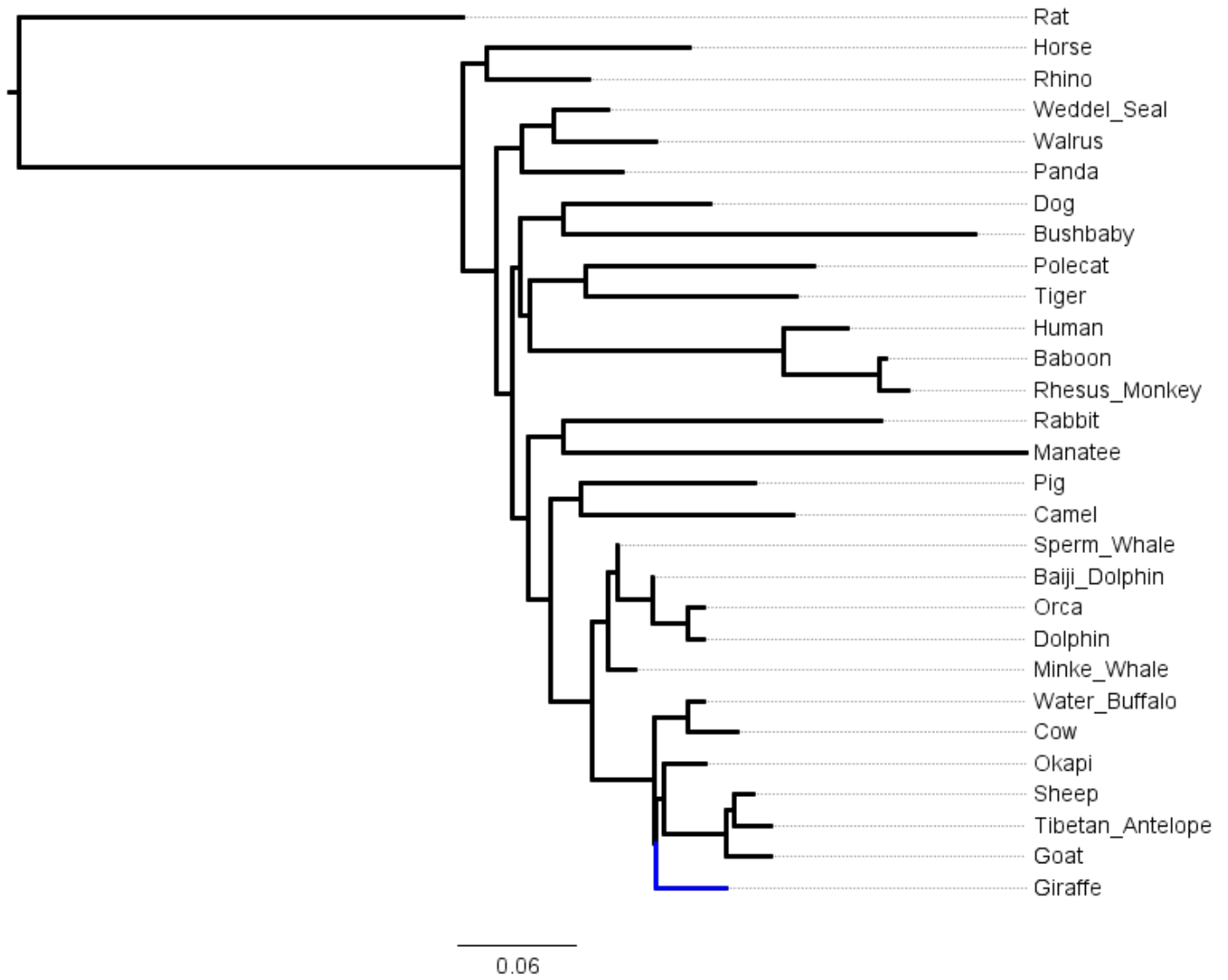
Giraffe: L81Q UPS, S97F UIS, G102S UPS, L103V UPS
Okapi: L75V UIS

Protein sequence Alignment of Cow, Giraffe and Okapi UTS2B

Cow	1	MNVILSTTLSFGLLTLLSVMIFLESVHGVYPYFVQGNELLPDKEDADGEELLLALLNKNFG	60
Giraffe	1C.....L...I.....T.....	60
Okapi	1C.....F.....L...I.....T.....	60
Cow	61	FQRPSNIDIELADKLEELNQLEKLKEQLMEAKDAEMSYAIDGLSSSHPNKRACFWKYCV	119
Giraffe	61N.....Q.....F....SV.....	119
Okapi	61N.V.....I.....	119

Newick Tree of Mammalian UTS2B

(rat:0.224501, ((horse:0.102568, rhino:0.0521938):0.0121468, (((weddel_seal:0.0276724, walrus:0.0517476):0.0163016, panda:0.0510553):0.0126691, (((dog:0.0744576, bushbaby:0.208502):0.0216221, (polecat:0.115453, tiger:0.107241):0.0275348, (human:0.0317029, baboon:0.00266853, rhesus_monkey:0.0144267):0.0484187):0.128325):0.00521252):0.00442636, ((rabbit:0.16054, manatee:0.233692):0.0177839, (pig:0.0880933, camel:0.107285):0.0154182, ((sperm_whale:0, baiji_dolphin:0, (orca:0.00849078, dolphin:0.00860448):0.0177554):0.0176492):0.00426715, minke_whale:0.0131005):0.00867836, ((water_buffalo:0.00838915, cow:0.0258089):0.0163519, (giraffe:0.0358681, (okapi:0.0206776, (sheep:0.00905644, tibetan_antelope:0.018346):0.00470059, goat:0.0230067):0.0310677):0.00427655):0.000482062):0.0319728):0.0211113):0.0108759):0.00849987):0.00778032):0.0170439):0.224501);



Locus Name: Urotensin-2 (UTS2B)

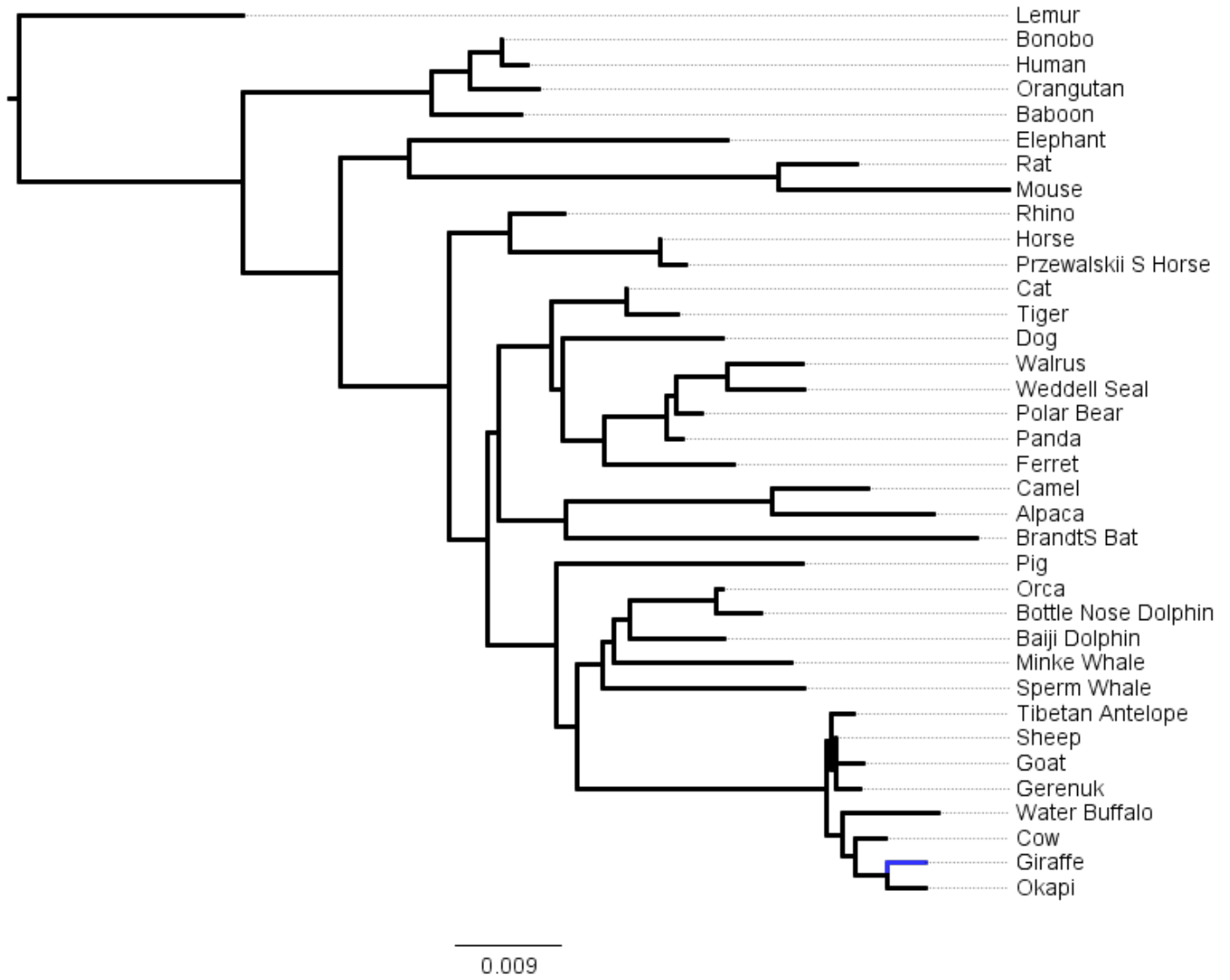
Locus Name: Alpha 1 Adrenergic Receptor **ADRA1A**

ENSBTAT0000044849 ADRA1A-201 adrenergic receptor regulation of blood pressure
 mouse: hypotension in mouse KO

PP2: (Giraffe) A422S
 PSG: (Giraffe) A422S
 Giraffe: A422S UIS

Protein sequence Alignment of Cow, Giraffe and Okapi ADRA1A

Cow	1	MVFLSGNASDSSNCTHPPPPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLSV	60
Giraffe	1	60
Okapi	1	60
Cow	61	THYYIVNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNVWAAVDVLCCTASIMGLCII	120
Giraffe	61	120
Okapi	61	120
Cow	121	SIDRYIGVSYPLRYPTIVTQKRLMALLCVWALSLSVISIGPLFGWRQPAPEDETICQINE	180
Giraffe	121	180
Okapi	121	180
Cow	181	EPGYVLFSAALGSFYVPLTIILVMYCRVYVVAKRERGLKSLKTDKSDSEQVTLRIHRKN	240
Giraffe	181	240
Okapi	181	240
Cow	241	AQVGGSGVTSANKKTHFSVRLKFSREKKAATLGIVVGCFLCWLPPFLVMPIGSFFPD	300
Giraffe	241	.P.....N.....	300
Okapi	241	.A.....N.....	300
Cow	301	FRPSETVFKIAFWLGYLNSCINPIIYPCSSQEFKAFQNVLRIQCLRRKQSSKHTLGYTL	360
Giraffe	301	360
Okapi	301	360
Cow	361	HAPSHVLEGQHKDLVRI PVGSAETFYKISKTDGVCEWKIFSSLPRGSARMAVARDPSACT	420
Giraffe	361A.....	420
Okapi	361A.....L.....	420
Cow	421	TARVRSKSFQVCCCLGPSTPSRGENHQIPTIKIHTISLSENGEEV	467
Giraffe	421	.S.....	467
Okapi	421	467



Locus Name: Alpha 1 Adrenergic Receptor **ADRA1A**

Locus Name: Alpha-2B adrenergic receptor (ADRA2B)

ENSBTAT00000012514 ADRA2B-201 adrenergic receptor regulation of vasoconstriction
 mouse: Homozygous null mice exhibit poor survival and breeding, lack the vasoconstrictor response
 to alpha2-adrenergic receptor agonists, and display background strain dependent postnatal
 respiratory failure. human: emotional stress response

PP2: S332G

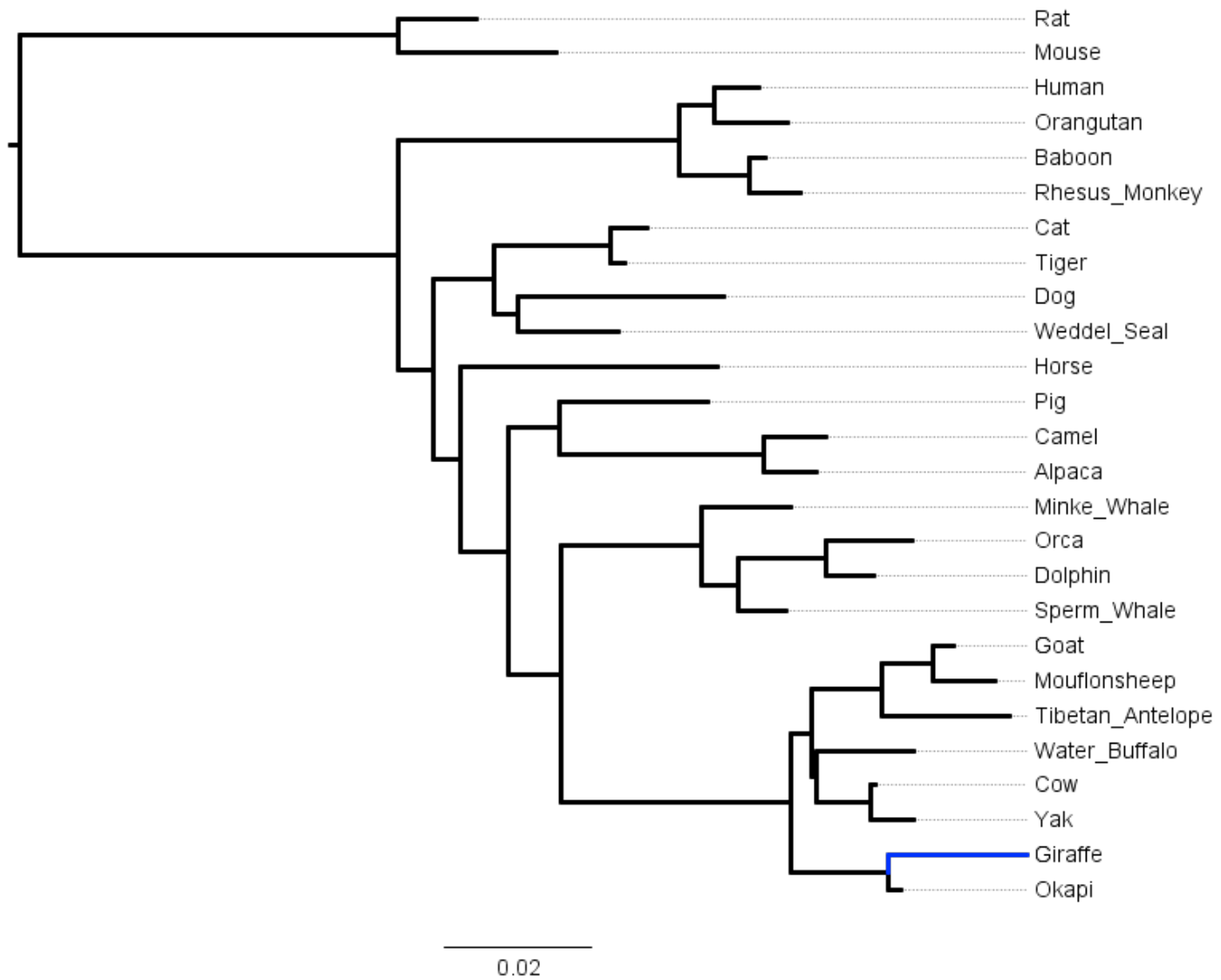
Giraffe: P267R UPS, A317V UIS, G329S UPS, R331Q UIS, G347A UIS, A349V UPS, H402Y UPS
 Giraffe/Okapi: A314S UPS, V400A UIS

Protein sequence Alignment of Cow, Giraffe and Okapi ADRA2B

Cow	1	MDHQEPYSVQATAAIAAVITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADIL	60
Giraffe	1	60
Okapi	1	60
Cow	61	VATLIIPFSLANELLGWYFWRTWCEVYLALDVLFTSSIVHLCAISLDRYWAVSRALEY	120
Giraffe	61A.....	120
Okapi	61A.....	120
Cow	121	NSKRTPRRIKFIILIVWLIAAVISLPLLIYKGDQGPPLARPQCKLNQEAWYILASSIGS	180
Giraffe	121	180
Okapi	121	180
Cow	181	FFAPCLIMILVYLRIYLIAKRSHCRGPRAKGGPGERESKQPHVPGEVSDSAKLPTLASQ	240
Giraffe	181AR.....	240
Okapi	181AR.....	240
Cow	241	LATPGEANGCSQPRPGEKGDGETPEAPGTFALPPSWPAIPKSGQGQKEGVCGSSPEEEAE	300
Giraffe	241H.....E.....DR.....N.....	300
Okapi	241E.....D.....N.....	300
Cow	301	EEEEEGCEPQALPASPASACSPPLQQPQGSRVLATLRGQVLLGRGTGTAGAQQWRRRTQL	360
Giraffe	301S.....S..V.....P...S.Q.....A.V.....	360
Okapi	301S.....P.....	360
Cow	361	SREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPQHCKVPHGLFQFFFWIGYCNSLNP	420
Giraffe	361A.Y.....	420
Okapi	361A.....	420
Cow	421	VIYTVFNQDFRRAFRRILCREWTQTAW	447
Giraffe	421I.....Q.....	447
Okapi	421I.....Q.....	447

Newick Tree of Mammalian ADRA2B

```
((Rat:0.0104148, Mouse:0.0213392):0.0511955, ((Human:0.00598824,
Orangutan:0.00979629):0.00481354, (Baboon:0.00215937,
Rhesus_Monkey:0.00687016):0.00947309):0.0377786, ((Cat:0.00489578, Tiger:0.00191474):0.0156221,
(Dog:0.0278336, Weddel_Seal:0.0136589):0.00306395):0.00838064, (Horse:0.0347292, (Pig:0.0199742,
(Camel:0.00859486, Alpaca:0.00715415):0.0274931):0.00686307, (Minke_Whale:0.0120515,
((Orca:0.0115844, Dolphin:0.00647579):0.0118757, Sperm_Whale:0.00637478):0.00508485):0.0189107,
(((Goat:0.00286248, Mouflonsheep:0.00838647):0.00671911, Tibetan_Antelope:0.0171775):0.00965908,
(Water_Buffalo:0.0131733, (Cow:0.00079359, Yak:0.00594049):0.00723812):0.00074093):0.0027817,
(Giraffe:0.0186536,
Okapi:0.00168747):0.0131997):0.0309802):0.00707524):0.00643335):0.00381393):0.00454996):0.0511955
);
```



Locus Name: Alpha-2B adrenergic receptor (ADRA2B)

Locus name: Angiotensin converting enzyme (**ACE**)

ENSBTAT00000061106 ACE-201 angiotensin I converting enzyme regulation of blood pressure
mouse: reduced systemic blood pressure, normocytic anemia, renal abnormalities, inability to
concentrate urine, and reduced male fertility

PP2: (Giraffe) W628G, R1242H; (Giraffe/Okapi) P405H; (Okapi) H861P

Giraffe: W628G UIS, A insertion 1045 UIS, R1242H UIS

Giraffe/Okapi: R242S UPS, T563P UPS, PDV866-888AEL UIS, P1151S UIS, (GP.V..GR)1235-1247(ST.Q..SH)
UIS, S1287G UPS

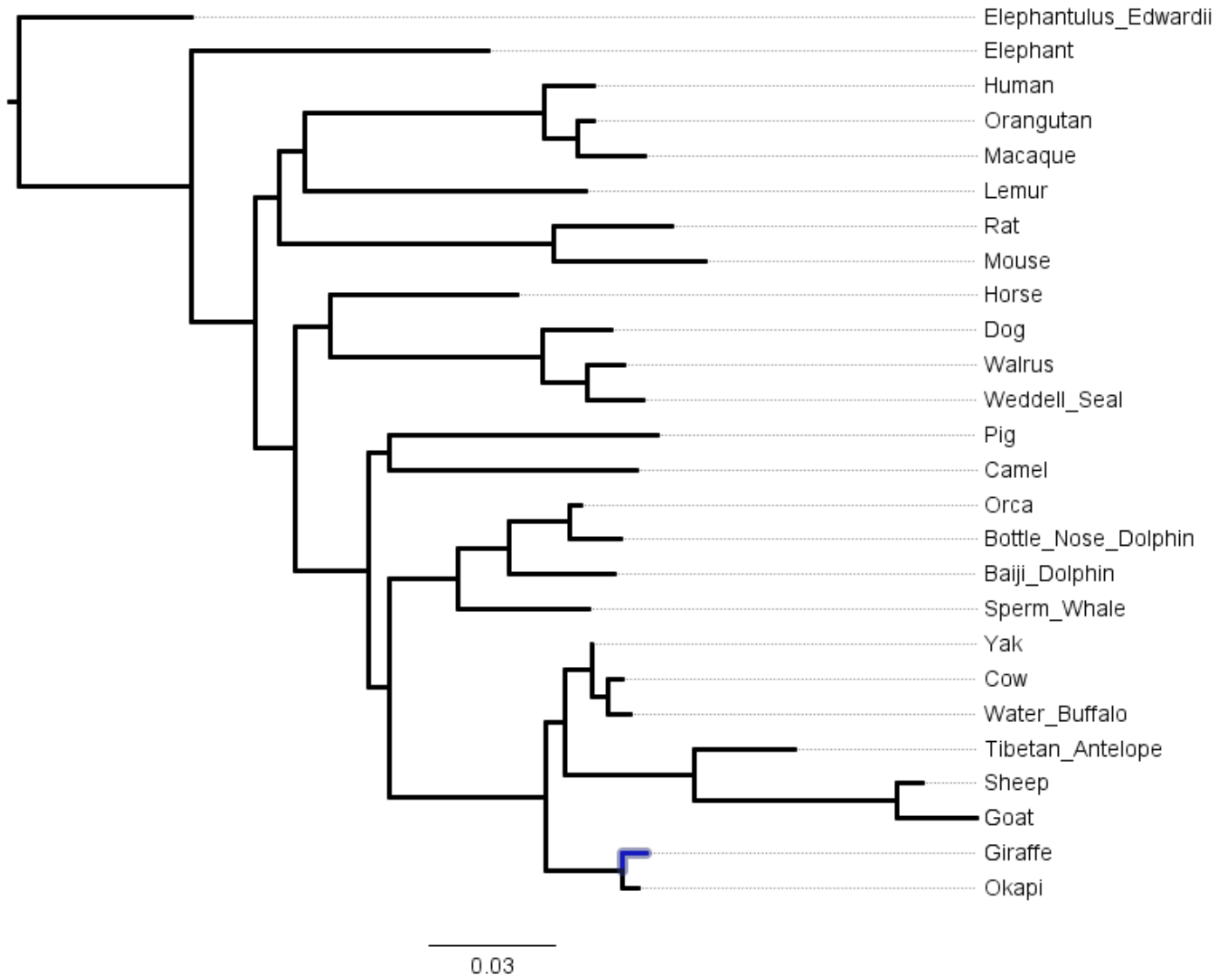
Protein sequence Alignment of Cow, Giraffe and Okapi ACE

Cow	1	MGAASGRRSPPLLLPLLLLLLPPPPVILELDPALQPGNFPADEAGAQIFAASFNSSAEQV	60
Giraffe	1W.....V.....D.....	60
Okapi	1W.....V.....D.....	60
Cow	61	LFQSTAASWAHDTNITEENARLQEEAALLSQEFSEAWGQKAKDLDFPVWQNFDTPTLLRI	120
Giraffe	61R.....I.....	120
Okapi	61R.....N...I.....	120
Cow	121	IGAVRTLGPANLDLEKRQKYNLLSNMSRIYSTAKVCFPNKTAPCWSLDPELTNILASSR	180
Giraffe	121V.....	180
Okapi	121V.....	180
Cow	181	SYTLLLYAWEGWHNAAGIPLKPLYQDFTALSNEAYKQDGFSDTGAYWRSWYDSPTFTEDL	240
Giraffe	181	..A.....R.....	240
Okapi	181	..A.....	240
Cow	241	ERLYQQLEPLYLNLHAYVRRALHRRYGDYINLRGPIPAHLLGNMWAQSWENIYDTVVVF	300
Giraffe	241	.S.....Y....K.....M....	300
Okapi	241	.S.....T.Y.....M....	300
Cow	301	PDKPNLDVTDVMVQKGNATHMFRVAEEFFTSLGLLPMPPEFWAESMLEKPSDGREVVCH	360
Giraffe	301ST.....	360
Okapi	301ST.....	360
Cow	361	ASAWDFYNRKDFRIKQCTRVMTDQLSTVHHEMGHVQYYLQYKGQHVSLRRGANPGFHEAI	420
Giraffe	361D.....	420
Okapi	361D.....	420
Cow	421	GDVLALSVESTPAHLHKIGLLDQVTNDTESDINYLKMALEKIAFLPFGYLVDQWRWGVFS	480
Giraffe	421	480
Okapi	421	480
Cow	481	GRTPPSRYNNDWYLRTRYQGICPPVVRNETHFDAGAKFHVPNVTPYIRYFVSVFLQFQF	540
Giraffe	481L.....	540
Okapi	481L.....	540
Cow	541	HEALCKEAGHQGPLHQCDIYQSTQAGAKLRALLQAGSSRPWQEVLDKDMVGSNDLDRPLL	600
Giraffe	541P.....	600
Okapi	541P.....	600
Cow	601	SYFQPVTQWLEEQNQNGEVLGWPEYQWRPMPDNYPEGIDLVSDEDEARKFVEEYDRRS	660
Giraffe	601G.....S.....	660
Okapi	601Q.....N.....	660
Cow	661	QVVWNEYAEANWNYSTDISTDNSKLLMEKNLQMANHTVKYGTWARKFDVTNFQATMKRM	720
Giraffe	661N.N.....K.....	720
Okapi	661N.N.....K.....	720
Cow	721	IKKIQDLERAALPTKELEEYNQILLDMETVYSVASVCHENGTCRLRLEPDLTNLMATSRNY	780
Giraffe	721V.....M....K....Q....K....S.	780
Okapi	721V.....K.....K.....S.	780
Cow	781	QDLAWAWKSWRDKVGRSILPYFPKYVELTNKAARLNGYQDGGDSWRSMYEMPFLLEELEQ	840
Giraffe	781V.....F.....T.....	840
Okapi	781V.....F.....T.....	840

Cow	841	LFQELQPLYLNLHAYVRRALHRHYGPDVINLEGPIPAHLLGNMWAQSWSNYDLVAPFPS	900
Giraffe	841AEL.....	900
Okapi	841P.....AEL.....	900
Cow	901	APKMDATEAMIKQGWTPLRMFKEADNFFTSLGLLPMPPEFWNKSMLEKPTDGREVVCHAS	960
Giraffe	901	960
Okapi	901	960
Cow	961	AWDFFNKGDFRIKQCTSVNMEDLVVAHHEMIGHIQYFMQYKDLPVTFREGANPGFHEAIGD	1020
Giraffe	961	1020
Okapi	961	1020
Cow	1021	VLALSVESTPHLHKINLLSSGDDGYEEDINFLMKMALEKIAFIPIFVDFLVDQWRWRVFDGS	1080
Giraffe	1021D.....	1081
Okapi	1021D.....	1080
Cow	1081	VTRENYNQEWWSLRLKYQGVCPPLARSQDDDFDPGAKFHIPASVPYVRYFVSFVIQFQFHQ	1140
Giraffe	1082V.....	1141
Okapi	1081V.....	1140
Cow	1141	ALCQAAGHQGPLHKCDIYQSKEAGKLLADAMKLGFSQPWPEAMRLITGQSNMSAAAMMTY	1200
Giraffe	1142S.....	1201
Okapi	1141S.....	1200
Cow	1201	FKPLLDWLVTENGRHEKLGWPQYNWTPNSARLEGPFVGSGRVNFGLNLEEQQARVGQW	1260
Giraffe	1202E.....ST.Q..SH.....	1261
Okapi	1201E.....ST.Q..S.....	1260
Cow	1261	VLLFLGVALLVATLGLTQRLFSIRHHSLRRPHRGPQFGSEVELRHS	1306
Giraffe	1262G.....H.....	1307
Okapi	1261G.....H.....	1306

Newick Tree of Mammalian ACE

```
(Elephantulus_edwardii:0.0411946, (elephant:0.0704335, (((human:0.0120756,
(orangutan:0.00370523, macaque:0.015684):0.00825184):0.0565632, lemur:0.06645):0.00623678,
(rat:0.0281724, mouse:0.0361543):0.0652831):0.00574888, ((horse:0.0444316, (dog:0.0164191,
(walrus:0.00850943, Weddell_seal:0.0130814):0.0109381):0.0501477):0.00829452, ((pig:0.0635755,
camel:0.058586):0.00494567, (((orca:0.00252518, bottle_nose_dolphin:0.0121079):0.0144663,
baiji_dolphin:0.0248234):0.0121141, sperm_whale:0.0311566):0.0161918, ((yak:0, (cow:0.00327061,
water_buffalo:0.00518782):0.00377227):0.00640482, (tibetan_antelope:0.023739, (sheep:0.0060831,
goat:0.0188735):0.0480138):0.0306322):0.00449784, (giraffe:0.00558065,
okapi:0.00365032):0.0180445):0.0371664):0.00510038):0.017292):0.00969575):0.0150436):0.0411946);
```



Locus name: Angiotensin converting enzyme (**ACE**)

Locus name: Somatostatin Receptor 2 (SSTR2)

ENSBTAT0000022785 SSTR2-201 somatostatin receptor behavior, eye, pancreas
mouse: Homozygotes for a null allele show elevated anxiety and locomotor and exploratory deficits

PP2: All benign

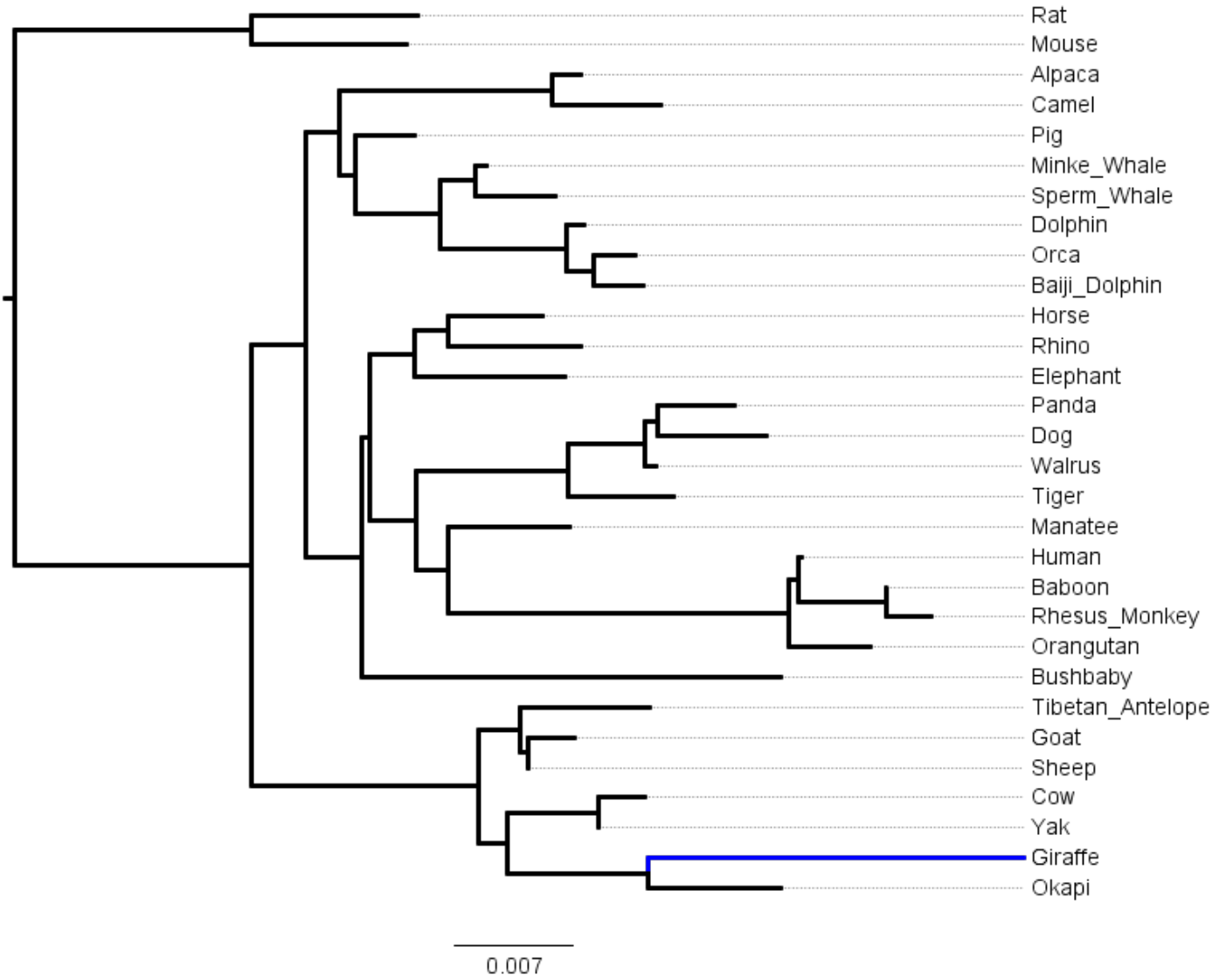
Giraffe: P12S UPS, V24M UPS, G25E UPS, I29V UPS, F229L UIS, D336E UIS

Protein sequence Alignment of Cow, Giraffe and Okapi SSTR2

Cow	1	MDLVSELNETQPWLTAPFDLNGSVGAANISNQTEPYDLASNVVLTFFIYFVVCIIIGLCGN	60
Giraffe	1	...A..F....S...S.....MET.DV.....A.....A.....	60
Okapi	1S.....D.....A..L..A.....	60
Cow	61	TLVIYVILRYAKMKTITNIYILNLAIADELFMLGLPFLAMQVALVHWPFGKAMCRVVMTV	120
Giraffe	61I.....	120
Okapi	61I.....	120
Cow	121	DGINQFTSIFCLTVMSIDRYLAVVHPIKSAKWRRPRTAKMINVAVWGVSLLVILPIMIYA	180
Giraffe	121	180
Okapi	121	180
Cow	181	GLRSNQWGRSSCTINWPGESGAWYTGFIYAFILGFLVPLTIICLCYLFIIIKVKSSGIR	240
Giraffe	181L.....	240
Okapi	181	240
Cow	241	VGSSKRKKSEKKVTRMVSIVVAVFIFCWLFPYIFNVSSVVAISPTPALKGMFDFVVVLT	300
Giraffe	241	300
Okapi	241	300
Cow	301	YANSCANPILYAFLSDNFKKSFQNVLCIVKVSCTDDGERSDSKQDKSRLNETTETQRTLL	360
Giraffe	301A.E.....	360
Okapi	301A.....T.....	360
Cow	361	NGDLQTSI	368
Giraffe	361	368
Okapi	361	368

Newick Tree of Mammalian SSTR2

((rat:0.00992787, mouse:0.00922574):0.0141798, (((alpaca:0.00168148, camel:0.00652659):0.0127307, (pig:0.00350426, (minke_whale:0.000650498, sperm_whale:0.00478433):0.00208782, (dolphin:0.00106841, (orca:0.00246721, baiji_dolphin:0.00296761):0.001649):0.00749814):0.00504175):0.00103442):0.00201469, (((horse:0.00567714, rhino:0.00796606):0.00198576, elephant:0.00896672):0.0026655, (((panda:0.00449213, dog:0.00640737):0.000763132, walrus:0.000586227):0.00464178, tiger:0.00629546):0.00905596, (manatee:0.00727576, (human:0.000189696, (baboon:4.28727e-05, rhesus_monkey:0.00267084):0.00525256):0.000559442, orangutan:0.00489409):0.0203181):0.001936):0.00276139):0.000444939, bushbaby:0.0249858):0.00341257):0.00315909, ((tibetan_antelope:0.00772093, (goat:0.00272831, sheep:0):0.000476007):0.00248115, (giraffe:0.0223613, okapi:0.00790698):0.00842764, (cow:0.00274314, yak:0):0.00543617):0.00169616):0.0135158):0.0141798);



Locus name: Somatostatin Receptor 2 (SSTR2)

Locus Name: fascin actin-bundling protein 1 (FSCN1)

ENSBTAT0000004145 FSCN1-201 fascin, organizes filamentous actin nervous system, eye
mouse: impaired migration of mature dendritic cells.

PP2: (Giraffe) A129T, S439W

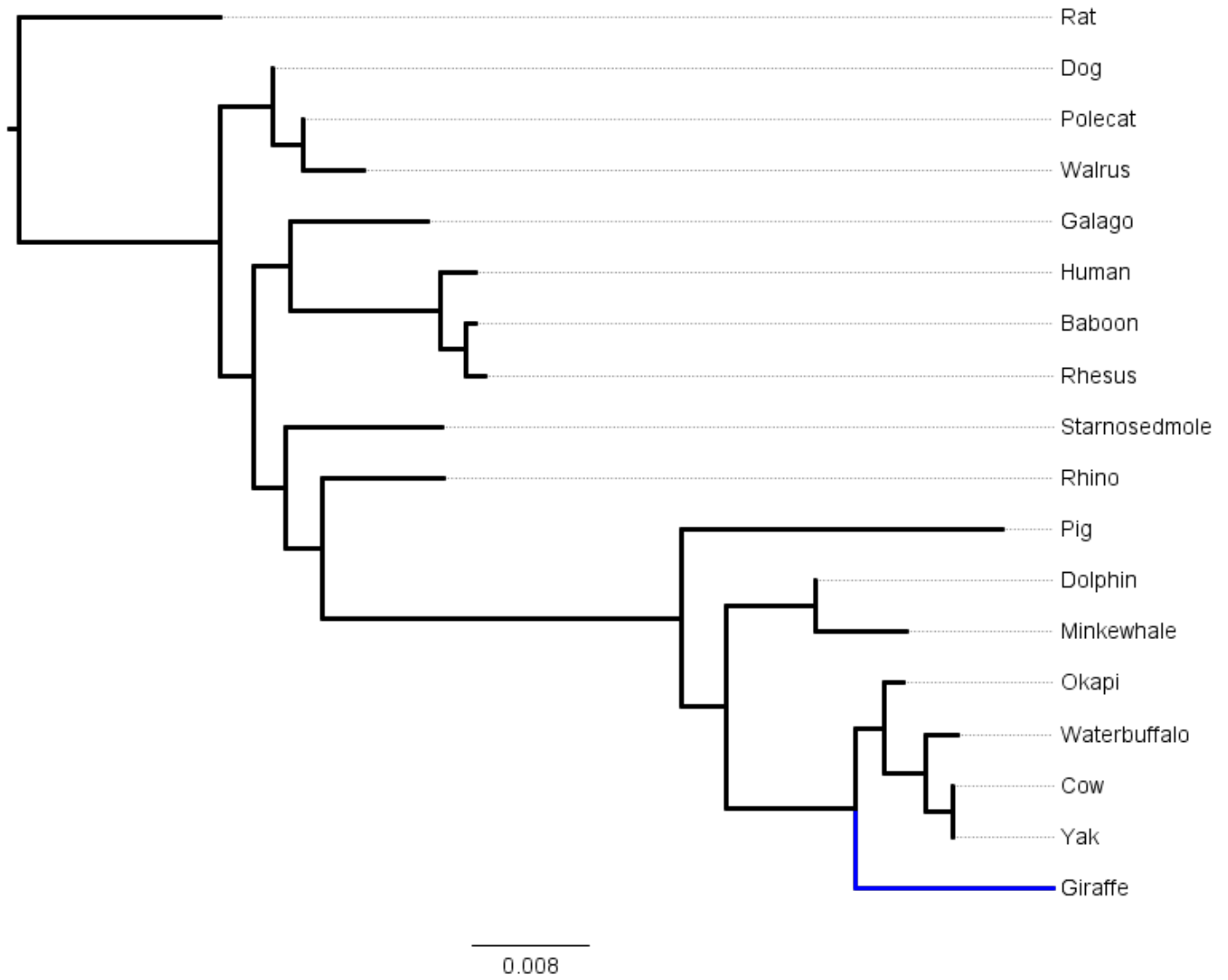
Giraffe: A129T UIS, I346V UPS, S350C UIS, S439W UIS, V465A UIS

Protein sequence Alignment of Cow, Giraffe and Okapi FSCN1

Cow	1	MTANGTAEALQIQFGLINCSNKYLTAETFGFKVNASASSLKKKQIWTLEQPPDEAGSAAV	60
Giraffe	1	60
Okapi	1G.....	60
Cow	61	CLRSHLGRYLAADKDGNTCEHEAPGADCRFLIVAHDDGRWSLQSEVHRRYFGGTEDRLS	120
Giraffe	61S.....A.....	120
Okapi	61A.....	120
Cow	121	CFAQTVSPAEEKSVHIAMHPQVNIYSLARKRYAHLGARPADDEISVDRDVPWGVDSLITLA	180
Giraffe	121T.....	180
Okapi	121	180
Cow	181	FQDQRYSLQTADHRFLRHDLVAHPEPATGYTLEFRSGKVAFRDCEGRYLAPSGPSGTL	240
Giraffe	181	240
Okapi	181	240
Cow	241	KAGKATKVGKDELFALEQSCAQVVLQAANERNVSTRQGMDSLANSQDEETDQETFQLEIDR	300
Giraffe	241	300
Okapi	241	300
Cow	301	DTKKCAFRTTHSGKYWTLTTGGVQSTASTKDARCYFDIEWRDRRIILRASNGKFVTAKN	360
Giraffe	301V...C.....	360
Okapi	301	360
Cow	361	GQLAASVETAGDSEFLMKLINRPIIVFRGEHGFICRKTGTLDANRSNYDVFQLEFRD	420
Giraffe	361	420
Okapi	361	420
Cow	421	GAYNIKDSTGKYWMVGNDSVTSSSDSPVDFFLFCFDYKVAIKVGGHYLKGDHAGVLKA	480
Giraffe	421S.W.....A.....A.....	480
Okapi	421T.....	480
Cow	481	CADTIDPTTLWEY	493
Giraffe	481	493
Okapi	481	493

Newick Tree of Mammalian FSCN1

(rat:0.0137084, ((dog:0, (polecat:0, walrus:0.00409865):0.00206885):0.00355177, ((galago:0.00929261, (human:0.0023545, (baboon:0.0006747, rhesus:0.00135576):0.00171471):0.0102139):0.00248441, (starnosedmole:0.0106757, (rhino:0.00825516, (pig:0.021789, ((giraffe:0.0133866, (okapi:0.00129707, (waterbuffalo:0.0022269, (cow:0, yak:4.95575e-05):0.00184229):0.00277217) :0.00196795):0.00884849, (dolphin:0, minke whale:0.00617017) :0.00616312):0.00298791):0.0244847):0.00245079):0.00217459):0.00226142):0.0137084);



Locus Name: fascin actin-bundling protein 1 (FSCN1)

Locus name: neurofibromin 2 (NF2)

ENSBTAT0000017489 NF2-201 merlin regulator of hippo pathway auditory functions
human: neurofibromatosis, deafness and balance disorder humans

PP2: All benign

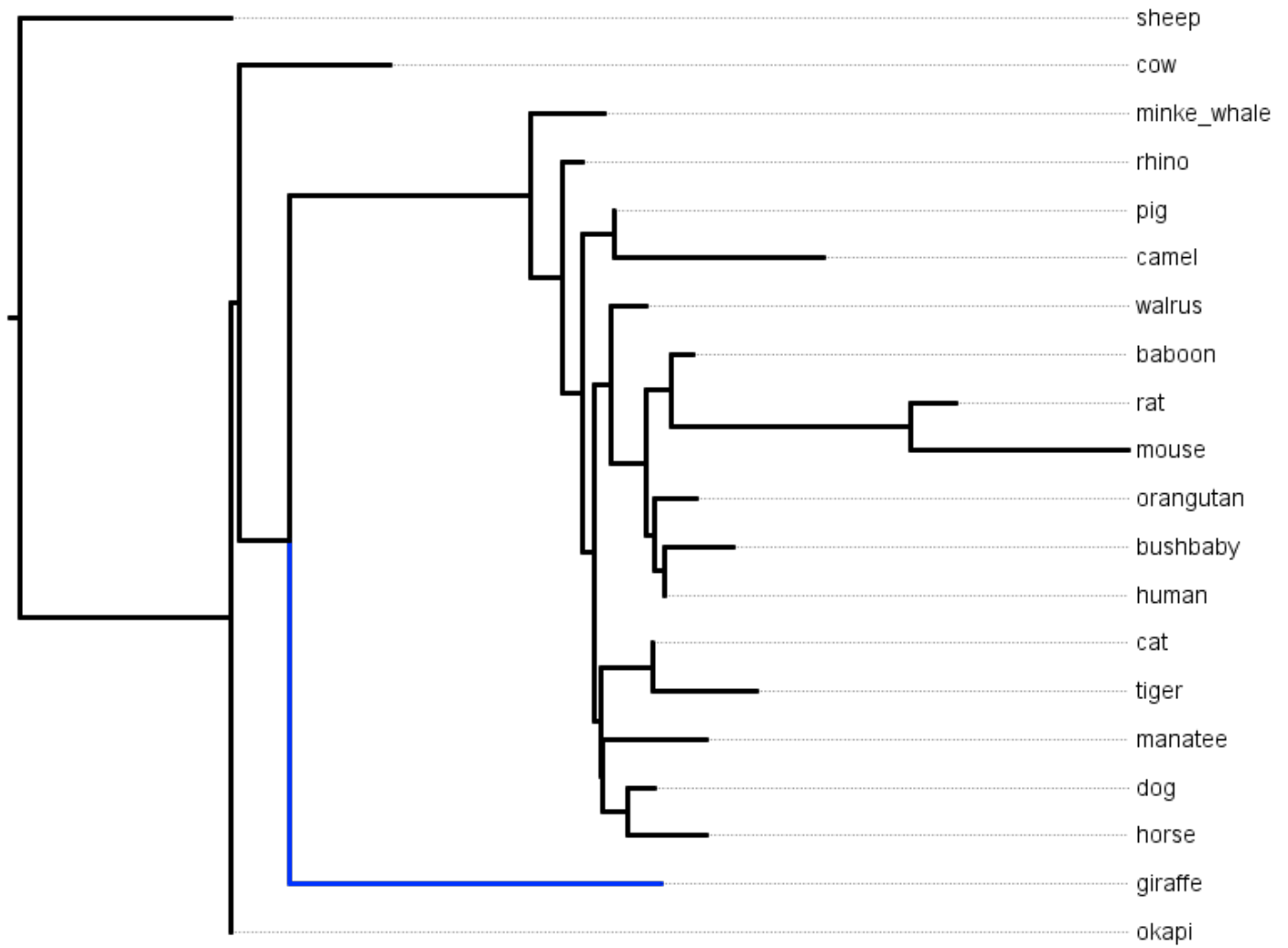
Giraffe: L453P UIS, M457T UPS, K514R UIS, M522A UPS, N527S UIS, D529E UIS

Protein sequence Alignment of Cow, Giraffe and Okapi NF2

Cow	1	MKWKGKDLFDLVCRTLGLRETWFFGLQYTIKDTVAWLKMDKKVLDHDSKEEPVTFHFLA	60
Giraffe	1	60
Okapi	1	60
Cow	61	KFYPENAEELVQEITQHLFFLQVKKQILDEKIYCPPEASVLLASYAVQAKYGDYDPSVH	120
Giraffe	61	120
Okapi	61	120
Cow	121	KRGFLAQEELLPKRVINLYQMTPEMWEERITAWYAEHRGRARDEAEMEYLKIAQDLEMYG	180
Giraffe	121	180
Okapi	121	180
Cow	181	VNYFTIRNKKGTELLLLGVDALGLHIYDPENKLTPKISFPWNEIRNISYSKDKEFTIKPLDK	240
Giraffe	181R.....	240
Okapi	181R.....	240
Cow	241	KIDVFKFNSSKLRVNKLILQLCIGNHDLFMRRRKADSLEVQOMKAQAREEKARKQMERQR	300
Giraffe	241	300
Okapi	241	300
Cow	301	LAREKQMREEAERTRDELERRLLQMKEEATMANEALMRSEETADLLAEKAQITEEEAKLL	360
Giraffe	301	360
Okapi	301	360
Cow	361	AQKAAEAEQEMQRIKATAIRTEEEKRLMEQKVLEAEVLALKMAEESERRAKEADQLKQDL	420
Giraffe	361	420
Okapi	361	420
Cow	421	QEAREAERRAKQKLEITTKPTYPPMNPLPAPLPPDMASFSLTGDSLFSDFKDTDMKRLS	480
Giraffe	421P...T...N.I.....	480
Okapi	421N.I.....	480
Cow	481	MEIEKEKVEYMEKSKHLQEQLNELKTEIEALRLKERETALDMLHNENS DRGGGSKHNTI	540
Giraffe	481R.....A...SAE.....S..	540
Okapi	481	540
Cow	541	KKLTLQSAKSRVAFFEEL	558
Giraffe	541	558
Okapi	541	558

Newick Tree of Mammalian NF2

```
(sheep:0.0072789, (okapi:0, (cow:0.00516242, (giraffe:0.012789, (minke_whale:0.00257861,
(rhino:0.000713123, ((pig:0, camel:0.00721896):0.00113334, (walrus:0.00117661,
((baboon:0.000782206, (rat:0.00155475, mouse:0.00744633):0.00827791):0.000850732,
(orangutan:0.00146506, (bushbaby:0.00238309,
human:0):0.000333503):0.000281676):0.00118389):0.000570996, ((cat:0,
tiger:0.00360505):0.00176099, (manatee:0.00361199, (dog:0.000892328,
horse:0.00269835):0.00088528):4.24795e-
05):0.000208882):0.000454465):0.000691512):0.00108222):0.00830701):0.00170362):0.00026333):0.0072
789);
```

Locus name: neurofibromin 2 (**NF2**)

Locus name: Cholinergic receptor nicotinic acid type 10 (CHRNA10)

ENSBTAT00000061577 CHRNA10-201 neuronal acetylcholine receptor auditory functions, pain reception
 mouse: impaired synaptic function and integrity of the olivocochlear system

PP2: (Giraffe) F412S

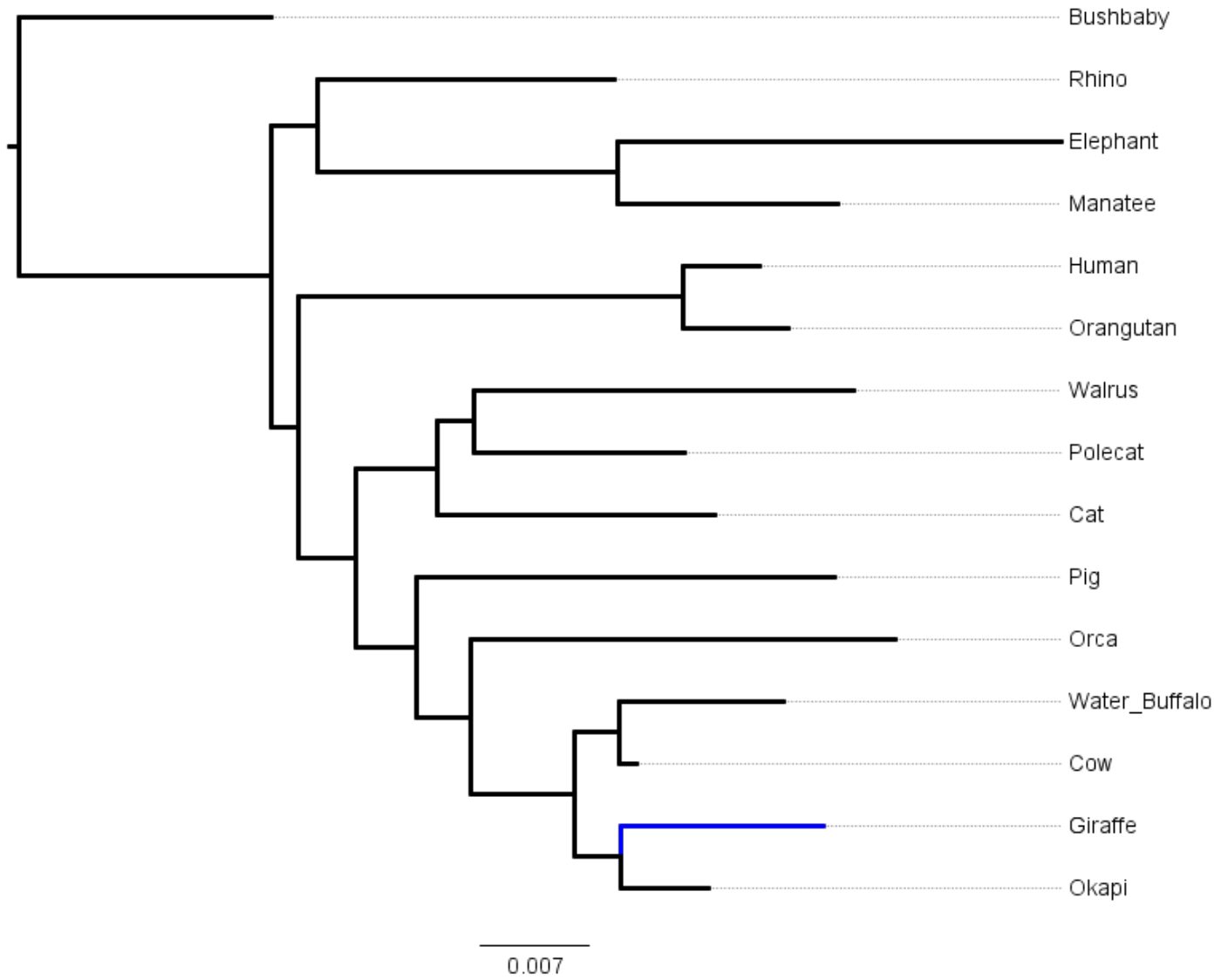
Giraffe: R369Q UPS, F412S UIS, M419V UIS

Protein sequence Alignment of Cow, Giraffe and Okapi CHRNA10

Cow	2	PECLGAEGRLAHKLFRLDFANYTSALRPVADTDQALNVTLEVTLSQIIDMDERNQVLTLY	61
Giraffe	2	61
Okapi	2	61
Cow	62	LWIRQEWTDAYLRWDPDPTYGGLDAIRIPSSLVWRPDIVLYNKADAQAPASASTNVVLRHD	121
Giraffe	62	121
Okapi	62	121
Cow	122	GAVRWDAPAITRSSCRVDVSAFPFDAQRCGLTFGSWTHGGHQLDVRPRGAAASLADFVEN	181
Giraffe	122	181
Okapi	122	181
Cow	182	VEWRVLGMPARRRVLTYGCCSEPYPDVFTLLLRRAAYVCNLLLPCVLISLLAPLAFH	241
Giraffe	182	241
Okapi	182H.....	241
Cow	242	LPADSGEKVS LGVTVLLALT V F Q L I L A E S M P P A E S V P L I G K Y Y M A T M T M V T F S T A L T I L I	301
Giraffe	242	301
Okapi	242	301
Cow	302	MNLHYCGPSARPVPAWARALLGRLARGLCVRRERGEPCGQSRPPESPSPQPPDRGTGPP	361
Giraffe	302Q.....Q.....	361
Okapi	302Q.....Q.....	361
Cow	362	AGPCHEPRCLCHQEALLRHVATIANAFHSHRAAQRREDWKRLARVMDRFFLGIFFSMAL	421
Giraffe	362Q...R.....Q.....S.....V..	421
Okapi	362	421
Cow	422	VMSLLVLRAL	432
Giraffe	422Q..	432
Okapi	422Q..	432

Newick Tree of Mammalian CHRNA10

(bushbaby:0.0161892, ((rhino:0.0191045, (elephant:0.0284532, manatee:0.0141192):0.0192858):0.00303032, ((human:0.00489306, orangutan:0.00674878):0.0247126, ((walrus:0.0244484, polecat:0.01357):0.00229231, cat:0.0178311):0.00522417, (pig:0.0268766, (orca:0.0272514, ((water_buffalo:0.0105222, cow:0.00111961):0.00290069, (giraffe:0.0130554, okapi:0.00563779):0.00300523):0.0066197):0.00354559):0.00383643):0.00371258):0.00178816):0.0161892);



Locus name: Cholinergic receptor nicotinic acid type 10
(**CHRNA10**)

Locus Name: PARK2 co-regulated-like (PACRGL)

ENSBTAT00000047431 PACRGL-201 E3 ubiquitin protein ligase parkin-like unknown substrate
expressed in brain
no mutations in m/h

PP2: (Giraffe) L156I

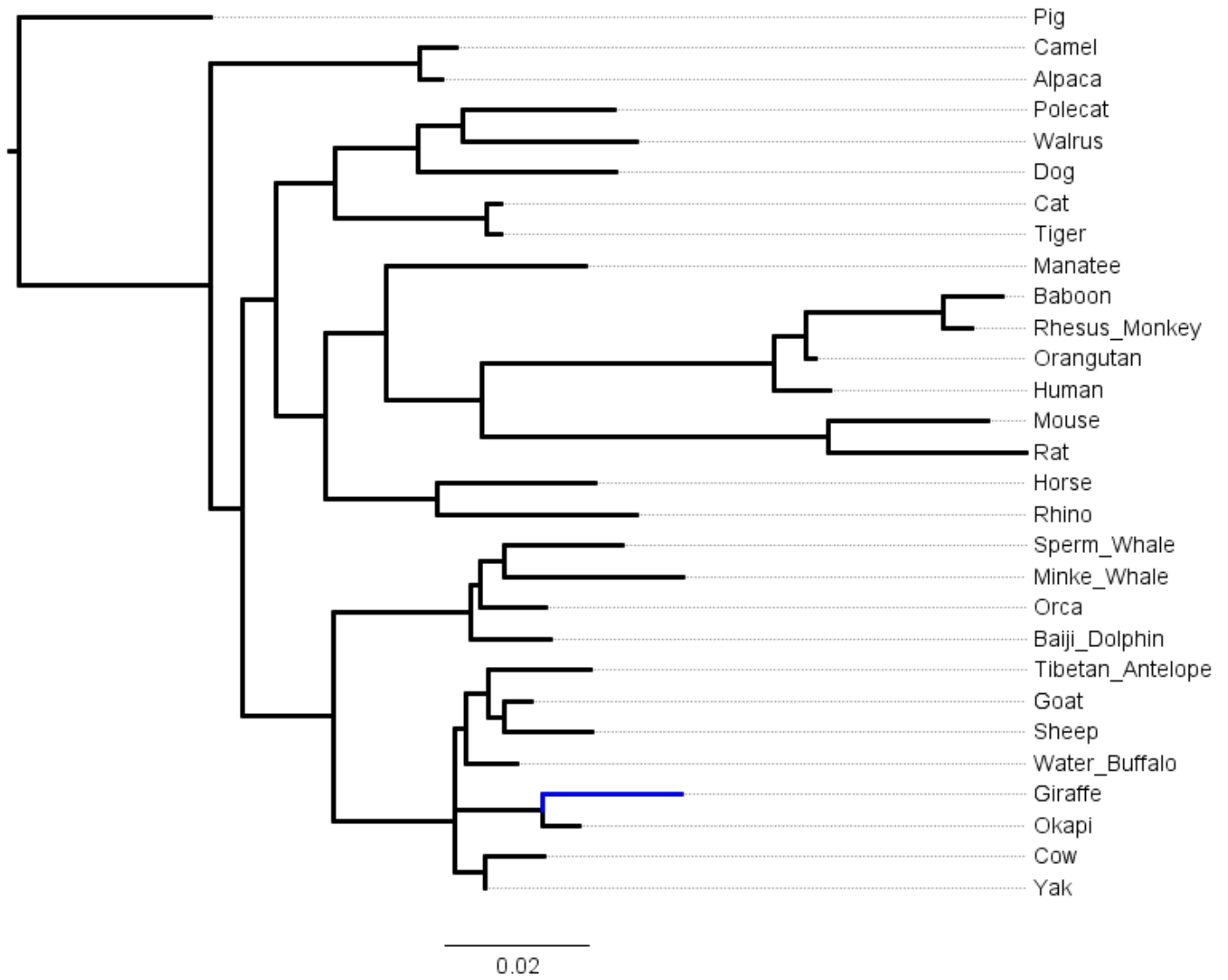
Giraffe: D21G UIS, L156I UIS, T219A UPS
Giraffe/Okapi: G9A UPS, D171N UIS

Protein sequence Alignment of Cow, Giraffe and Okapi PACRGL

Cow	1	MQKSEFHRGVQMRSLTDNCDQRTSSSAQVKHGTTVQQSKSSSSTSSPESARKLHPRPSD	60
Giraffe	1C..A....N.....G.....	60
Okapi	1C..A....N.....	60
Cow	61	KLNPKTINPFGEQSRAPSAFAAIYSKGGIPCRLVHGSVKHRLQWECPEKLPFDPLLITL	120
Giraffe	61	120
Okapi	61V..	120
Cow	121	AEGLRETKHPYTFVSKEGFRELLLVGTGAPEKAVPLLPRLLIPVLKAALVHVDDEVFERGLN	180
Giraffe	121H.....I.K.....N.....	180
Okapi	121K.....N.....	180
Cow	181	ALVQLSVVVGPAINDHLKHLTSLSKRLRDKKFKPEITTALQKLEQHGGSGSLIIIKSKI	240
Giraffe	181S.....A.....S.....	240
Okapi	181S.....	240
Cow	241	PTYCSICC	248
Giraffe	241	248
Okapi	241	248

Newick Tree of Mammalian PACRGL

(pig:0.0268583, ((camel:0.00508934, alpaca:0.00304088):0.0291624, (((((polecat:0.0210547, walrus:0.0243295):0.00631024, dog:0.0277088):0.0114588, (cat:0.00202021, tiger:0.00202021):0.0209913):0.00821082, ((manatee:0.0279144, (((baboon:0.00822717, rhesus_monkey:0.00394367):0.0191261, orangutan:0.00135305):0.00447901, human:0.00785994):0.0407379, (mouse:0.0223182, rat:0.0275053):0.0482884):0.0133719):0.00837059, (horse:0.0220272, rhino:0.0277962):0.0155863):0.00689242):0.00484492, (((sperm_whale:0.0163535, minke_whale:0.0248162):0.00342143, orca:0.00906974):0.00124775, baiji_dolphin:0.0109736):0.0192152, ((giraffe:0.0193302, okapi:0.00506371):0.012119, ((tibetan_antelope:0.0142917, (goat:0.0039665, sheep:0.0122947):0.00207989):0.00316881, water_buffalo:0.0070155):0.00148076):0.000167112, (cow:0.0081629, yak:0):0.00437129):0.0168449):0.0127507):0.00427376):0.0268583);



Locus Name: PARK2 co-regulated-like (PACRGL)

Locus Name: slit homolog 2 (SLIT2)

ENSBTAT00000061059 SLIT2-201 secreted axon guidance replusive protein axonal guidance
in the nervous system
mouse: perinatal lethality, abnormal ureteric bud development, multiple fused kidneys, multiple
ureters, and hydroureter; DKO with slit1 shows retinal axon guidance defects

PP2: (Giraffe) I488V, G1435E; (Giraffe/Okapi) V1405I

Giraffe: I486V UIS, G1433E UIS

Giraffe/Okapi: V1405I UIS

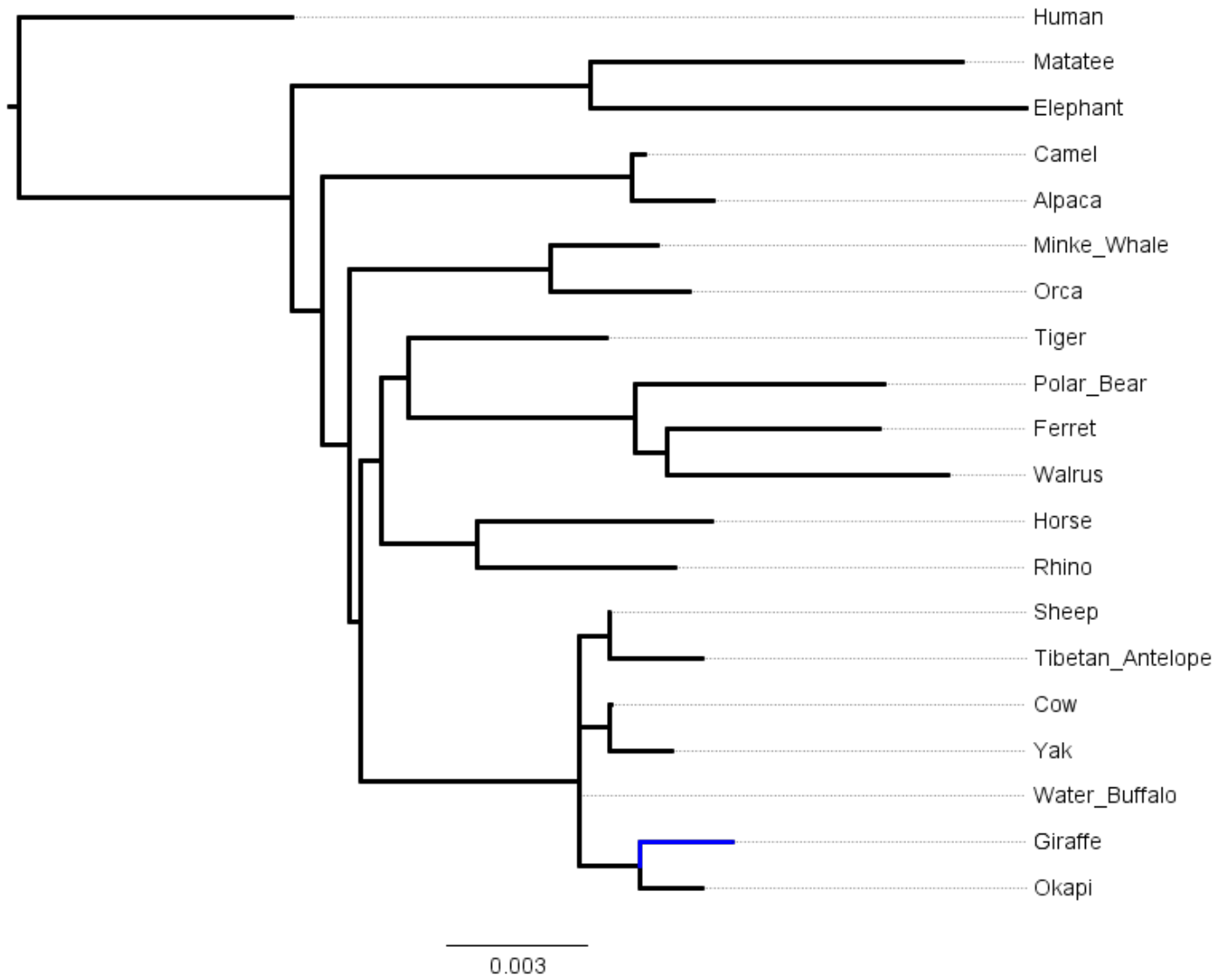
Protein sequence Alignment of Cow, Giraffe and Okapi SLIT2

Cow	1	MHGVGWTLSLSLGLVLAAILNEVAPQACPAQCSCSGSTVDCHGLALRSVPRNIPRNTERL	60
Giraffe	1	60
Okapi	1	60
Cow	61	DLNGNNITRITKTDFAGLRHLRVLQLMENKITTIERGAFQDLKELERLRLNRNHLQLFPE	120
Giraffe	61	120
Okapi	61	120
Cow	121	LLFLGTSKLYRLDLSENQIQAI PRKAFRGAVDIKKNLQLDYNHISCIEDGAFRALRDLEVL	180
Giraffe	121Q.....	180
Okapi	121Q.....	180
Cow	181	TLNNNNITRLSVASFNHMPKLRTRFLHSNNLYCDCHLAWLSDWLRQRPRVGLYTQCMGPS	240
Giraffe	181	240
Okapi	181	240
Cow	241	HLRGHNVAEVQKREFVCSGHQSFMAPSCSVLHCPAACTCSNNIVDCRGKGLTEIPTNLPE	300
Giraffe	241	300
Okapi	241	300
Cow	301	TITEIRLEQNSIKVIPPAGAFSPYKLRIDLSNNQISELAPDAFQGLRSLNSLVLYGNKI	360
Giraffe	301	360
Okapi	301	360
Cow	361	TELPKSLFEGFLFSLQLLLLNANKINCLRVDAFQDLHNLNLLSLYDNKLTIAKGTFSPLR	420
Giraffe	361	420
Okapi	361	420
Cow	421	AIQTMHLAQNPFFICDCHLKWLDYLHTNPIETSGARCTSPRRLANKRIGQIKSKKFRCSA	480
Giraffe	421	480
Okapi	421	480
Cow	481	KEQYFIPGTEDYRSKLSGDCFADLACPEKRCCEGTVDCSNQKLTIPDHIPOQYTAELRL	540
Giraffe	481V.....	540
Okapi	481	540
Cow	541	NNNEFTVLEATGIFKQLRKLINFSNNKITDIEEGAFEGASGVNEILLTSNRLENVQHK	600
Giraffe	541	600
Okapi	541	600
Cow	601	MFKGLESKLTMLRSNRISCVGNDSFIGLSSVRLLSLYDNQITTIAPGAFDTLHSLSTLN	660
Giraffe	601	660
Okapi	601	660
Cow	661	LLANPFNCNCYLAWLGEWLRKKRIVTGNPRCQKPYFLKEIPIQDVAIQDFTCDDGNDNS	720
Giraffe	661	720
Okapi	661	720
Cow	721	CSPLSRCPAECTCLDVTVVRCSNKALKVLPKGI PRDVTELYLDGNQFTLVPKELSNYKHLT	780
Giraffe	721R.....	780
Okapi	721	780

Cow	781	LIDLNNRISTLSNQSFNSMTQLLTLILSYNRLRCIPPRTFDGLKSLRLLSLHGNDISVV	840
Giraffe	781I.	840
Okapi	781I.	840
Cow	841	PEGAFNDLAALSHLAIGANPLYCDCNMQWLSDWVKSEYKEPGIARCAGPGEMADKLLLT	900
Giraffe	841	900
Okapi	841	...V.....	900
Cow	901	PSKKFTCQGPVDVNILAKCNPCLSNPCKNDGTCNNDPVDFYRCTCPYGFKGQDCDVPIHA	960
Giraffe	901	960
Okapi	901	960
Cow	961	CISNPCKHGGTCHLKEGEKDFWCICADGFEGENCEINVDDCEDNDCENNSTCVDGINNY	1020
Giraffe	961	1020
Okapi	961	1020
Cow	1021	TCLCPPEYTGELCEEKLDFAQDLNPCQHDSKILTPKGYKCDCTPGYIGEHCIDIDFDDC	1080
Giraffe	1021	1080
Okapi	1021	1080
Cow	1081	QDNCKNGAHCTDAVNGYTCTCEGYSGLFCEFSPPMVLPRTPPCDNFDCQNGAQCIIRI	1140
Giraffe	1081	1140
Okapi	1081	1140
Cow	1141	NEPICQCLPGYQGEKCEKLVSVNFVNKESYLQIPSAKVRPQTNITLQIATDEDSGILLYK	1200
Giraffe	1141	1200
Okapi	1141	1200
Cow	1201	GDKDHIAVELYRGRVRASYDTGSHPASAIYSVETINDGNFHVIVELLALDQSLSLSDVGGG	1260
Giraffe	1201	1260
Okapi	1201T.....	1260
Cow	1261	PKIITNLSKQSTLNFDSPLYVGGMPGKNNVAAALRQAPGQNGTSFHGCIRNLYINSELQD	1320
Giraffe	1261	1320
Okapi	1261	1320
Cow	1321	FRKVPMQTGILPGCEPCHKKVCAGHTCQPSSQAGFTCECEEGWTGPLCDQRTNDPCLGNK	1380
Giraffe	1321	1380
Okapi	1321	1380
Cow	1381	CVHGTCLPINAFAFSYSCKLEGHGGVLCDEEEDLFNPCQAIKCKHKGKRLSGLGQPYCECS	1440
Giraffe	1381I.....E.....	1440
Okapi	1381I.....	1440
Cow	1441	SGYTGDSCDREISCRGERIRDYYQKQGYAACQTTKKVSRLECRGGCAGGQCCGPLRSKR	1500
Giraffe	1441	1500
Okapi	1441	1500
Cow	1501	RKYSFECTDGSSFVDEVEKVVKCGCTRCAS	1530
Giraffe	1501	1530
Okapi	1501	1530

Newick Tree of Mammalian SLIT2

(human:0.00579445, ((matatee:0.00789571, elephant:0.00924464):0.00635343, ((camel:0.00025418, alpaca:0.00170853):0.00657847, ((minke_whale:0.0022852, orca:0.0029573):0.00426928, (((tiger:0.0042252, (polar_bear:0.00526635, (ferret:0.00454093, walrus:0.00597185):0.000651015):0.00483798):0.000552789, (horse:0.00498033, rhino:0.00421225):0.00201584):0.000443819, ((sheep:0, tibetan_antelope:0.00196769):0.000648594, ((cow:3.18391e-06, yak:0.00130486):0.000652231, water_buffalo:2.00589e-06):6.93232e-06):9.87529e-06, (giraffe:0.00194604, okapi:0.00132729):0.00130188):0.0046268):0.000258086):0.000559053):0.000665248):0.00579445);



Locus Name: slit homolog 2 (SLIT2)

Locus Name: Semaphorin 3A (**SEMA3A**)

ENSBTAT0000024139 SEMA3A-201 semaphorin 3A axonal guidance
mouse: patterning abnormalities of sensory and sympathetic neurons, abnormal embryonic bones and cartilaginous structures, cardiac defects, and high postnatal mortality

PP2: (Giraffe) L514F

Giraffe: I292V UIS, L514F UIS,
Giraffe/Okapi: H579Y UIS, I628V UIS, I629F UIS
Okapi: N43D UPS, A52D UPS

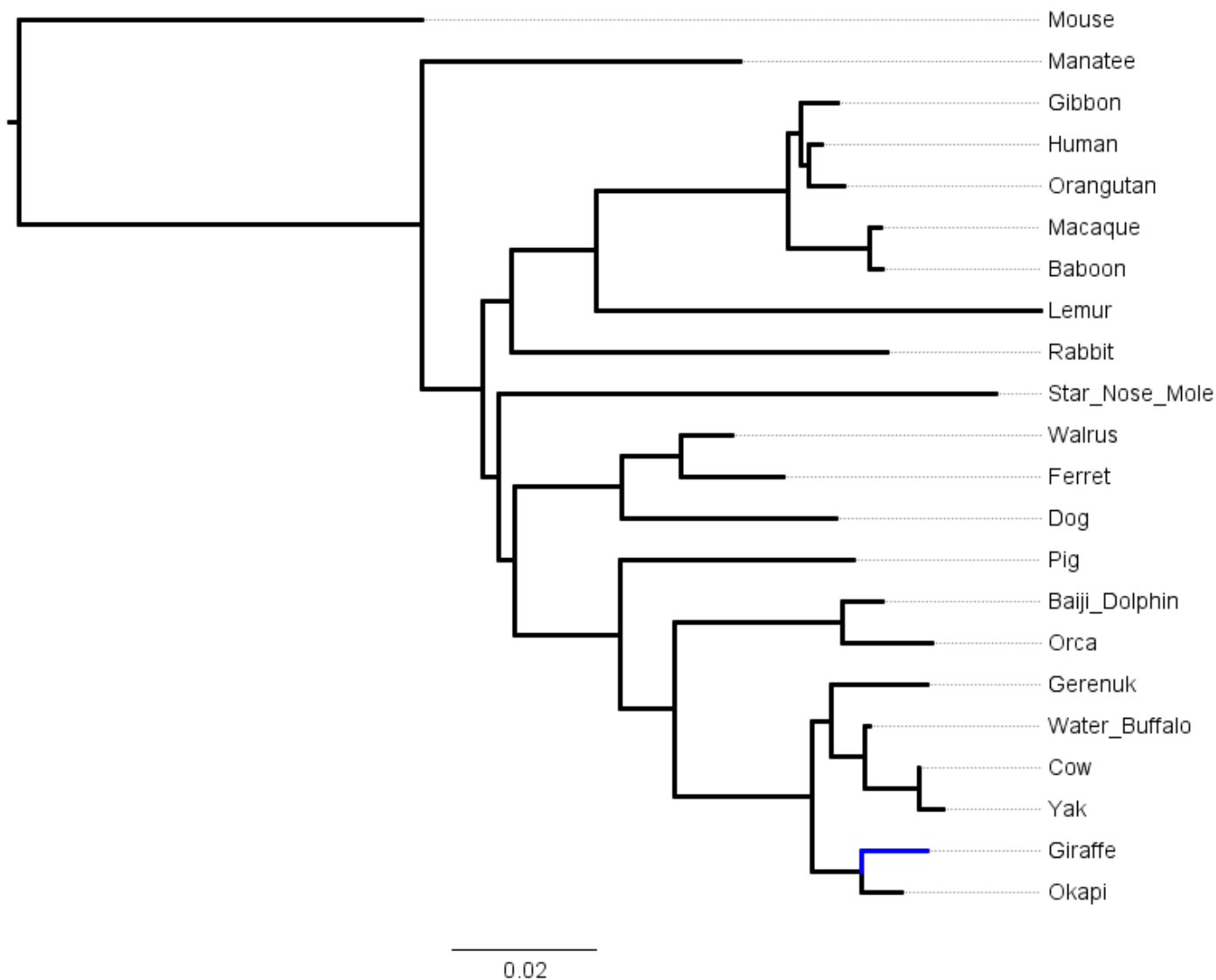
Protein sequence Alignment of Cow, Giraffe and Okapi SEMA3A

Cow	1	MGWFARIVCLFWGVLLTARANYQNGKNNVPRLLKLSYKEMLESNNVITFNGLANSSSYHTF	60
Giraffe	1T.....	60
Okapi	1T.....D.....D.....	60
Cow	61	LLDEERSRLYVVGAKDHIFSFNLVNIKDFQKIVWPVSYTRRDECKWAGKDILKECANFIKV	120
Giraffe	61	120
Okapi	61	120
Cow	121	LKAYNQTHLYACGTGAFHPVCTYIEIGHHPEDNIFKQLQDSHFENGRGKSPYDPKLLTASL	180
Giraffe	121	180
Okapi	121V.....	180
Cow	181	LIDGELYSGTAADFMGRDFAIFRTLGHHPHPIRTEQHDSRWLNDPRFISAHLIPESDNPED	240
Giraffe	181	240
Okapi	181	240
Cow	241	DKVYFFFRENAIDGEHTGKATHARIGQICKNDFGGHRSLVNKWTTFLKARLICSVPGPNG	300
Giraffe	241V.....	300
Okapi	241	300
Cow	301	IDTHFDELQDVFLMNSKDPKNPVVYGVFTTSSNIFKGSAVCMYSMSDVRVFLGPHYAHRD	360
Giraffe	301	360
Okapi	301	360
Cow	361	GPNYQWVPYQGRVPYPRPGTCCPSKTFGGFDSTKDLRDDVITFARSHPAMYNPVFPINNRP	420
Giraffe	361	420
Okapi	361	420
Cow	421	IMIKTDVNYQFTQIVVDRVDAEDGQYDVMFIGTDVGTVLKVVSI PKETWHDLEEVLL EEM	480
Giraffe	421	480
Okapi	421	480
Cow	481	TVFREPTTISAMELSTKQQQLYIGSTTGVTQLPLHRCDIYGKACAECCLARDPYCAWDGS	540
Giraffe	481F.....	540
Okapi	481	540
Cow	541	SCSRYFPTAKRRTRRQDIRNGDPLTHCSLDLQHHDNHHGHSFEERIIYGVENSTFLECSF	600
Giraffe	541Y.....	600
Okapi	541Y.....	600
Cow	601	KSQRALVYWQFQRRNEEPKEEIRVDDHIIRTEQGLLLRSLQRKDSGNYLCHAVEHGFMQT	660
Giraffe	601R.....VF.....	660
Okapi	601R.....A.....VF.....	660
Cow	661	LLKVTLEVIDTEHLEELLHKDDDDGSGSKTKETSNSMTPSQKVWYRDFMQLINHPNLNTMD	720
Giraffe	661	720
Okapi	661	720
Cow	721	EFCEQVWKRDRKQRRQRPGHQTQGSNSNKWHLQENKKGRRNRTHEFERAPRSV	772
Giraffe	721	772
Okapi	721	772

Newick Tree of Mammalian SEMA3A

((rat:0.00126554, mouse:0.00523226):0.00771245, (aardvark:0.0109108, (Brandt_s_bat:0.0132348, ((rhino:0.00888282, (macaque:0.00515895, (human:0.00259225,

orangutan:0.0013064):0.0118789):0.00557789):0.00109964, lemur:0.0130289):8.98605e-05,
 ((manatee:0.00491042, elephant:0.00944127):0.00344414, ((camel:0.00195809,
 alpaca:0.00323675):0.00514718, horse:0.00858057):0.00227274, (((tiger:7.82861e-05,
 cat:0.00121789):0.00508394, black_flying_fox:0.00796299):0.000553852, (Weddell_seal:0.00210906,
 walrus:0.00308578):0.000939603, ((panda:0.00325176, polar_bear:0.00194308):0.00328084,
 ((orca:0.000157567, baiji_dolphin:0.00243647):0.00266046, minke_whale:0.00384584):0.00319759,
 (water_buffalo:0.000820761, ((cow:0.00131248, (sheep:0.000379679, (tibetan_antelope:0.00227078,
 goat:0.00292406):0.000916491):0.000960902):3.31973e-05, (giraffe:0.00267287,
 okapi:0.00512959):0.00519282):0.000473033):0.00359753):0.00129819):0.000914216):0.000906283):0.00
 0465674):0.000806921):0.000777333):0.00136915):0.00256779):0.00771245);



Locus Name: Semaphorin 3A (**SEMA3A**)

Locus Name: Monooxygenase DBH-like 1 (MOXD1)

ENSBTAT00000025923 MOXD1-201 monooxygenase dopamine β-hydroxylase dopamine metabolism
human: episodic memory SNP

PSG: S20K|AGC/AAG

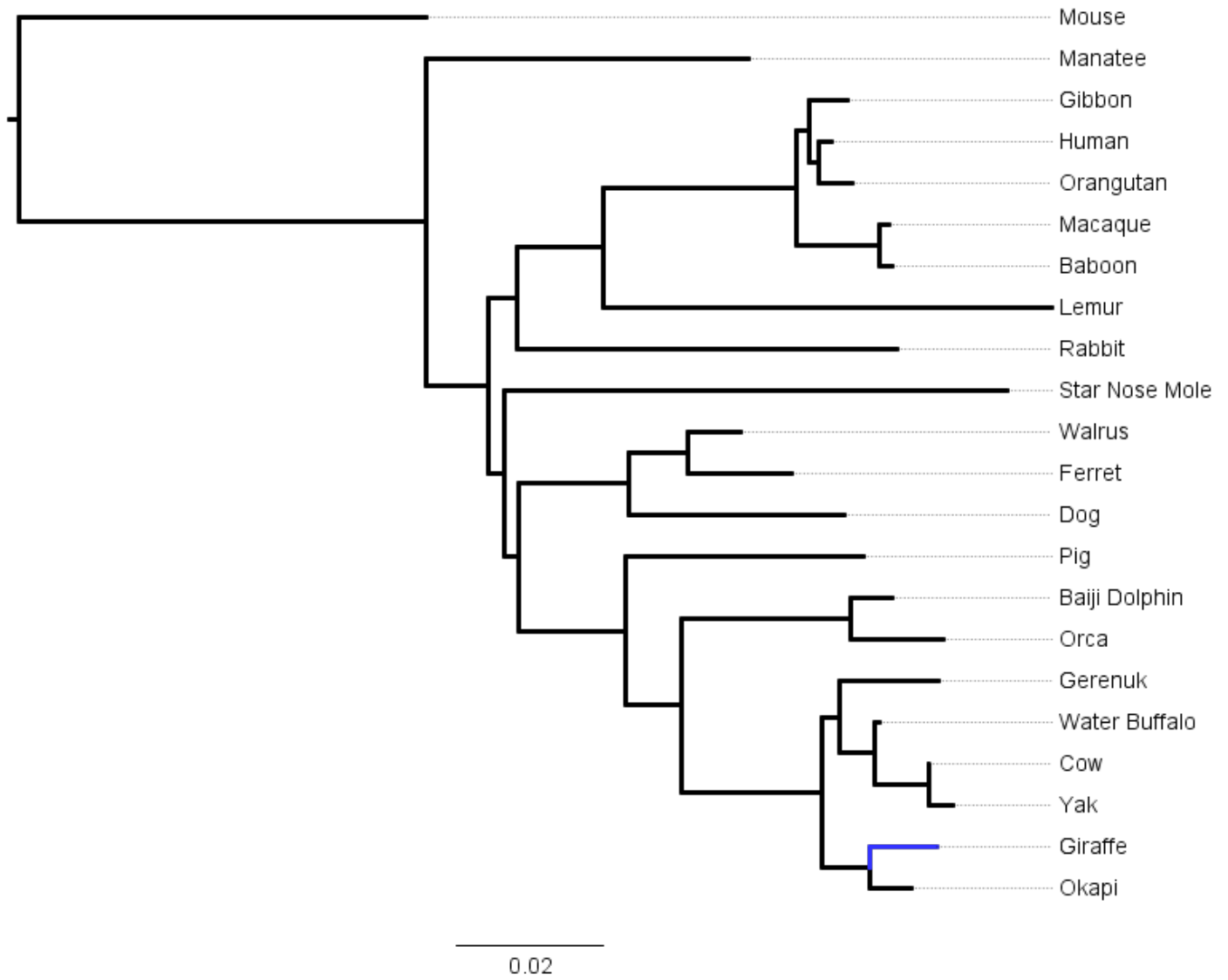
Giraffe: W23L UPS, S40K UPS, P43L UPS, A49V UIS
Giraffe/Okapi: S606A UPS, W613C UPS
Okapi: WP 23-24 deletion

Protein sequence Alignment of Cow, Giraffe and Okapi MOXD1

Cow	1	MCRWPLLLWGLLPRAAAGGSGWPFPHRTLLDSEGGKYWLSWGPRGGRLAFRLEVRTAGYV	60
Giraffe	1F.....L.L.....K..L...Q.V.....	60
Okapi	1-L.....	58
Cow	61	GFGFSSTGAMAAADIVGGVARGRPYLQDYFTNANRELKRKDAQQDYHLEYAMENSTHTVI	120
Giraffe	61P.....	120
Okapi	59P.....	118
Cow	121	EFTRELHTCDINDKSISESTVRVIWAYHHEDVGEAGPKYHESNRGTKSLRLLNPEKTSML	180
Giraffe	121	..A.....T.....N..	180
Okapi	119	..A.....M.....T.....NT.	178
Cow	181	STAIPYFDLVNQDVSIPNKGTTYWCQMFKIPMLQEKHHVIKVEPVIQKGHESLVHHILLY	240
Giraffe	181	..V.....P.....	240
Okapi	179	..V.....P.....	238
Cow	241	QCSSNFSDSVLDDGHECYHPNMPDAFLTCETVIFAWAIGGEGFSYPPHVGLSLGTPLDPH	300
Giraffe	241	300
Okapi	239	298
Cow	301	YVLLLEVHYDNPTYKEGLIDNSGLRFLFYTADIRKYDAGVIEAGLWVSLFHTIPPGLPDFRS	360
Giraffe	301	360
Okapi	299	358
Cow	361	EGHCTLECLEEAEAEKPSGIHVFAVLLHAHLAARGIRLRHFRKGEEMRLAYDDDFDFN	420
Giraffe	361	420
Okapi	359	418
Cow	421	FQEFQYLKKEEQTILPGDNLITECRYNTKDRARMTWGGLSTRNEMCLSYLLYPRINLTRC	480
Giraffe	421V.....	480
Okapi	419V.....	478
Cow	481	ASIPDIMEQLQFIGVKEIYRPVTTWPFIIKSPKQYRNLSFMDAMNFKWTKKEGLAFNKL	540
Giraffe	481K.....	540
Okapi	479K.....	538
Cow	541	VLSLPVMVRCSTKDNAEWSIQGMTALPPDIERPQAEPLVCGASSTSLRGNVCLELLLSF	600
Giraffe	541R.....	600
Okapi	539D.....R.....H.....	598
Cow	601	VVLGSSLSTRSLWP	615
Giraffe	601A..A...C.	615
Okapi	599A..A...C.	613

Newick Tree of Mammalian MOXD1

(Mouse:0.0557461, (Manatee:0.0440954, (((((Gibbon:0.00527691, (Human:0.00179691, Orangutan:0.00474981):0.0012874):0.0015707, (Macaque:0.00144472, Baboon:0.00182327):0.0112338):0.026656, Lemur:0.0614215):0.0117028, Rabbit:0.0519559):0.00396277, (Star Nose Mole:0.0688574, ((Walrus:0.00711941, Ferret:0.0143175):0.00813753, Dog:0.0296408):0.0149364, (Pig:0.0323803, ((Baiji Dolphin:0.00560225, Orca:0.0125361):0.023139, (Giraffe:0.00921503, Okapi:0.00557624):0.00667794, (Gerenuk:0.0134029, (Water Buffalo:0.00067413, (Cow:0, Yak:0.00327022):0.00751611):0.00475624):0.00254256):0.0190802):0.00763236):0.014648):0.00212052):0.00215234):0.00852775):0.0557461);



Locus Name: Monooxygenase DBH-like 1 (**MOXD1**)

Locus Name: Methylenetetrahydrofolate Dehydrogenase (NADP+ Dependent) 1 (MTHFD1)

ENSBTAT00000012704 MTHFD1-201 C-1-tetrahydrofolate synthase folate metabolism
 human: SNP association with neural tube defects and congenital heart defects, mouse: knockout is an embryonic lethal and heterozygotes exhibit ventricular septal defects

PP2: (Giraffe) A335V; (Okapi) V754I

Giraffe: A335V UIS, P367L UIS, Q548L UIS, D817N UIS, A893V UIS, A119T UPS, N248D UPS, S266R UPS

Giraffe/Okapi: L717I UIS

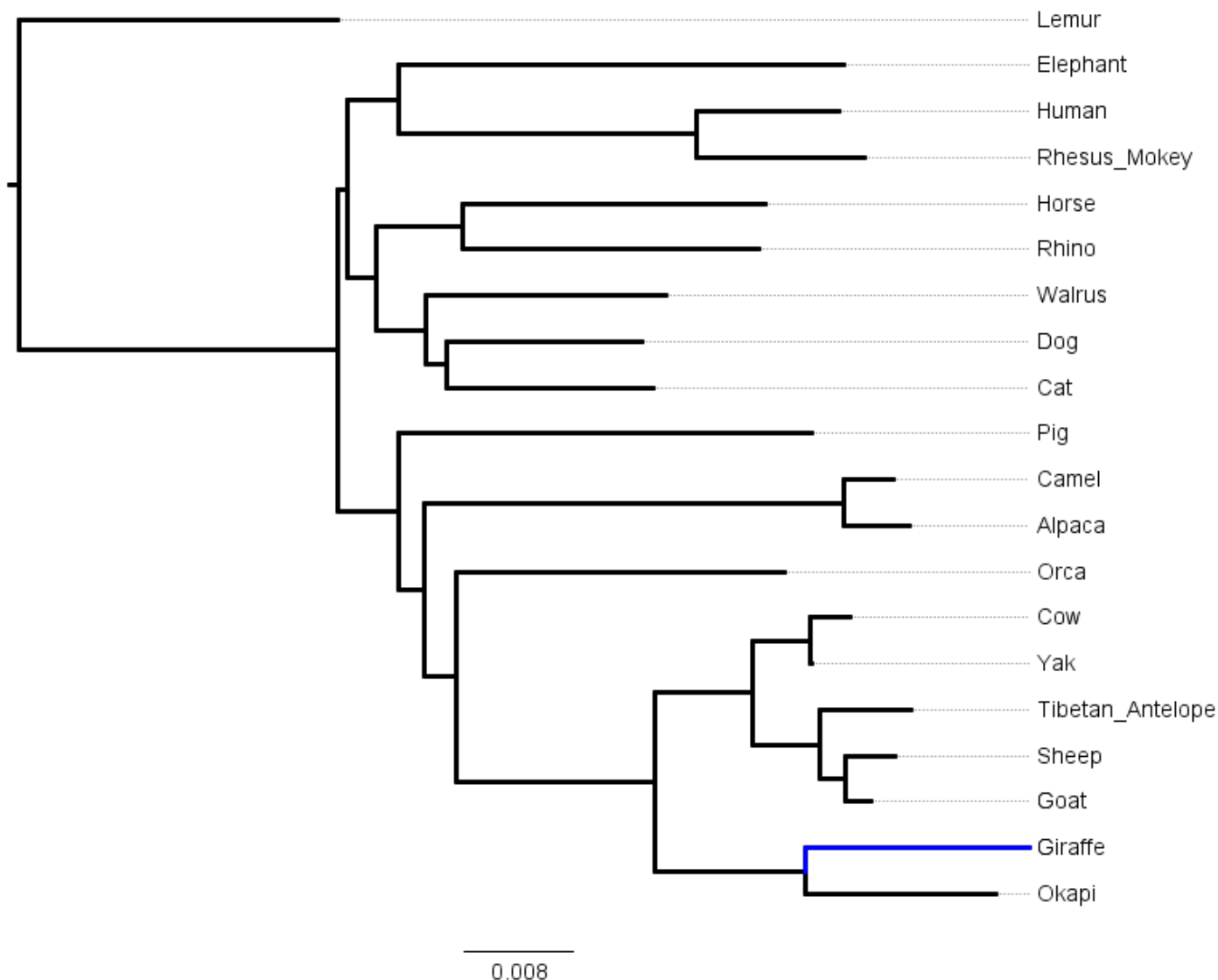
Protein sequence Alignment of Cow, Giraffe and Okapi MTHFD1

Cow	1	MAPAEILNGKVVSAQIKERLKNQVIQMKEEVPGFIPGLAILQVGNRDDSPLYINMKLKAA	60
Giraffe	1TR.R.....T.....	60
Okapi	1TR.R.....T.....	60
Cow	61	EEIGIKATHIKLPRATASEVLKICITSLNEDLTVHGFIVQLPLDSENPIETLVNAIAP	120
Giraffe	61	..V.....M.....T.....	120
Okapi	61	..V....K....S.R.....V..	120
Cow	121	EKDVDGLNSISAGKLARGDLSNCFIPCTPKGCLELIKETGVQIAGRHAVVVGRSKIVGAP	180
Giraffe	121	180
Okapi	121	180
Cow	181	MHDLNHNHATVTTCHSKTANLKEEISKDILVVAAGQPEMVKGWIKPGAIVIDCGINY	240
Giraffe	181N.....I.....	240
Okapi	181N..V.....V.....	240
Cow	241	VTDDTKPNGKKIVGDVAYTEAKERASFITVPPGGVGPMTVAMLMQSTVESAKRFLENFKP	300
Giraffe	241	.P....D...V.....L.....R.....K..T	300
Okapi	241	.P....G...V...V.L.....K...	300
Cow	301	GKWIIQYNKLNKTPVPSDIDISRSYKPKPIGNLAREVGLRTEEVELYGETKAKVLLSAL	360
Giraffe	301	.N.M....T.....S..V..I.....D.....V.	360
Okapi	301	.N.M....T.....S.....I.....D.....	360
Cow	361	ERLKHQPDGKYVVVTGITPTPLGEGKSTTTIGLVQALGTHLHQNVFACVRQPSQGPTFGI	420
Giraffe	361L.....A..L.....	420
Okapi	361	.W.....A.....	420
Cow	421	KGGAAGGGYSQVIPMEEFNHLTGDIAITAANNLVAAAIDARMFHEETQTDKALFNRLV	480
Giraffe	421	480
Okapi	421	480
Cow	481	PSVNGVRKFSDIQIRRLRRLGIEKTDPATLTDEEINRFARLDIDPETITWQRVLDTNDRF	540
Giraffe	481	540
Okapi	481	540
Cow	541	LRKITIGQAPTEKGHRSRTAQFDISVASEIMAVLALTSSLEDMRERLGKMOVASSKKGEPI	600
Giraffe	541L.....	600
Okapi	541N.....S.....	600
Cow	601	STEDLGVSGALTVLMKDAIKPNLMQTLGTPVVFVHAGPFANIAHGSSIIADRIALKLVG	660
Giraffe	601V.....	660
Okapi	601	660
Cow	661	PEGFVVTEAGFGADIGMEKFFNIKCRYSGLRPHVVVLVATVRALKMHGGGPTVTAGLPLP	720
Giraffe	661I...	720
Okapi	661I...	720
Cow	721	KAYIEEDLELVGKGFNSLKKQIENARMFVPPVVAVNAFKTDTEAELDLVSRLAKEHGAF	780
Giraffe	721E.....	780
Okapi	721	...V.....E.....I.....	780
Cow	781	DAVKCTHWAEGGKALALAEAVQRAAAPSSFQLLYDLKLPVEDKIRIIAQKIYGADNIE	840
Giraffe	781R.....N.....I.....D..	840
Okapi	781K.....D..	840

Cow	841	LLPEAQHKAEVYTKQGFGNLPICMAKTHLSLSHNPGLKGVPTGFVLPDIRASVGAGFL	900
Giraffe	841V.....	900
Okapi	841V.....V.....	900
Cow	901	YPLVGTMSTMPGLPTRPCFYDIDLDPETEQVNGLF	935
Giraffe	901	935
Okapi	901	935

Newick Tree of Mammalian MTHFD1

```
(lemur:0.0233642, ((elephant:0.0326464, (human:0.0104222,
rhesus_mokey:0.0123203):0.0218542):0.0037219, ((horse:0.0220978, rhino:0.021639):0.00637611,
(walrus:0.0175229, (dog:0.0142511,
cat:0.0150552):0.00154813):0.00367981):0.00207875):0.000659632, (pig:0.0301979,
(camel:0.00368962, alpaca:0.00490345):0.0306392, (orca:0.0240727, ((cow:0.003035,
yak:0.000178719):0.00422325, (tibetan_antelope:0.00668483, (sheep:0.00352919,
goat:0.00183277):0.00192923):0.00496905):0.00714463, (giraffe:0.0163896,
okapi:0.0139862):0.0110166):0.0144768):0.00232705):0.00182985):0.00446379):0.0233642);
```



Locus Name: Methylenetetrahydrofolate Dehydrogenase (NADP+ Dependent) 1 (MTHFD1)

Locus name: SLC17A1

ENSBTAT0000064064 SLC17A1-201 phosphate-sodium cotransporter kidney
no mutation in m/h described; human SNP for cholesterol homeostasis and hyperhomocysteinaemia

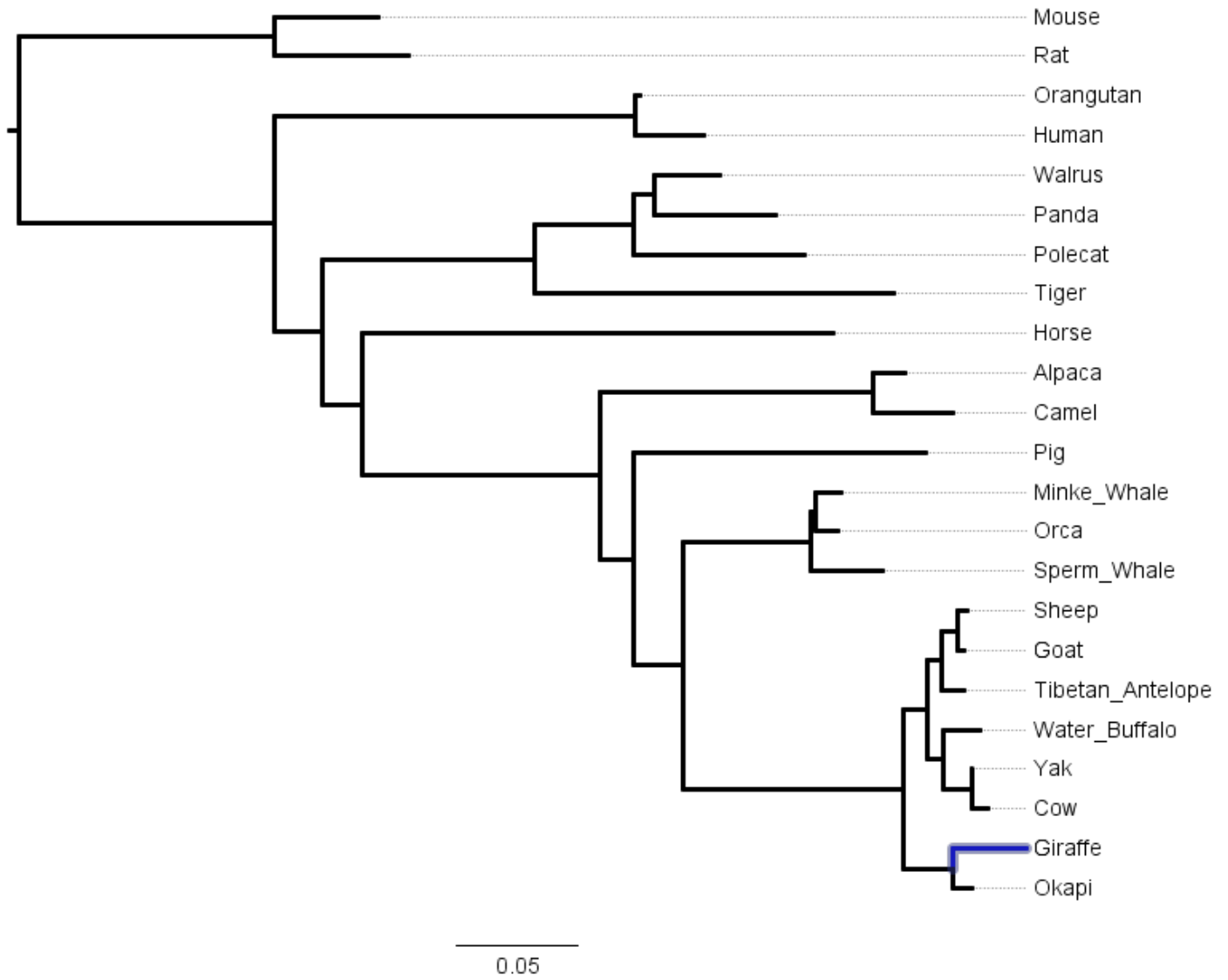
Giraffe: I142V UPS, G168A UPS, I204V UIS
Giraffe/Okapi: T263V UPS, S283G UPS, A365G, L389V UIS

Protein sequence Alignment of Water Buffalo, Giraffe and Okapi SLC17A1

Water Buffalo	1	MQVDNQVSPGKVPYFCSVRYGIAVFLLLCNVIIMSQRVCLSLTMIAMVNSTEPHGLSNTS	60
Giraffe	1R.....I.....V.....M.....	60
Okapi	1R.....I.....M.....	60
Cow	61	TKELQDNIKNPVYNWSTEIQGIMLSSIFYGVLISQIPAGYLSGIYSLKMKMIGFALLLSSL	120
Giraffe	61	120
Okapi	61	120
Cow	121	FTLLLPLAAEFGEILVVICRVIKGLFQGITLTTQQVWIKWAPPELGRLTALSLSGLLL	180
Giraffe	121TW.....V.....A.....IA...S.....	180
Okapi	121T.....V..V.....S.....	180
Cow	181	GPCIVLLITGFICDSLWPMVFIYFACGCALSVLWLFILFYEDPKDHPFISNREKEYITS	240
Giraffe	181V.....F.....Y..I.....	240
Okapi	181F.....Y..I.....	240
Cow	241	ALTQQVSSSTLIKVPKAMLKSTPLWVISLCNFAFFWSNTFLSIYIPIYIDYKLHVDVEE	300
Giraffe	241S...V.....S.....G..T.L.....N.K.	300
Okapi	241S...V.....G..T.....N.K.	300
Cow	301	NGLLSSPLHLFAWIFAVLAGYMADIFQTRNTFSLVTIRKLFSTLGLLLPSLFLSLCLLYLS	360
Giraffe	301G..IS.....I.....T.....	360
Okapi	301G.....I.....T.....	360
Cow	361	SSYYATIIFLILANSTGFSFAMGGIINVLVDIAPRYYGFLRGITNVIGLTGGLIASVTGI	420
Giraffe	361	.NF.G.....A.....LM...V.....V.....A.....	420
Okapi	361	.NF.G.....A.....LM...V.....	420
Cow	421	ILSEDAESPWLKIFLLMIANNMISLIFYLIFAKAEVQEWAKERQNTYL	468
Giraffe	421A.....F...G.....D.....	468
Okapi	421	...K.....F.....D.....	468

Newick Tree of Mammalian SLC17A1

((mouse:0.0421916, rat:0.0549928):0.103869, ((orangutan:0.00219056, human:0.0282513):0.14669, (((walrus:0.0263727, panda:0.0491226):0.00835653, polecat:0.0695857):0.0405544, tiger:0.146416):0.086042, (horse:0.191911, ((alpaca:0.0133032, camel:0.0329261):0.110951, (pig:0.118924, ((minke_whale:0.0101336, orca:0.00941223):0.00187525, sperm_whale:0.0289616):0.0522884, (((sheep:0.00399679, goat:0.00243415):0.00621533, tibetan_antelope:0.00890019):0.00599475, (water_buffalo:0.0147732, (yak:8.59446e-05, cow:0.00634499):0.0112915):0.0066585):0.00990888, (giraffe:0.0293547, okapi:0.0075743):0.0203731):0.0898591):0.0199903):0.0135566):0.0967838):0.0160838):0.019755):0.103869);



Locus name: SLC17A1

Locus name: Succinic semialdehyde dehydrogenase (**ALDH5A1**)

ENSBTAT0000029203 ALDH5A1-201 succinic semialdehyde dehydrogenase brain, clearance of GABA and hydroxybutyric acid
human: mental retardation, ataxia, seizures humans; mouse: reduced body weight, ataxia, seizures, gliosis of the hippocampus, and early death.

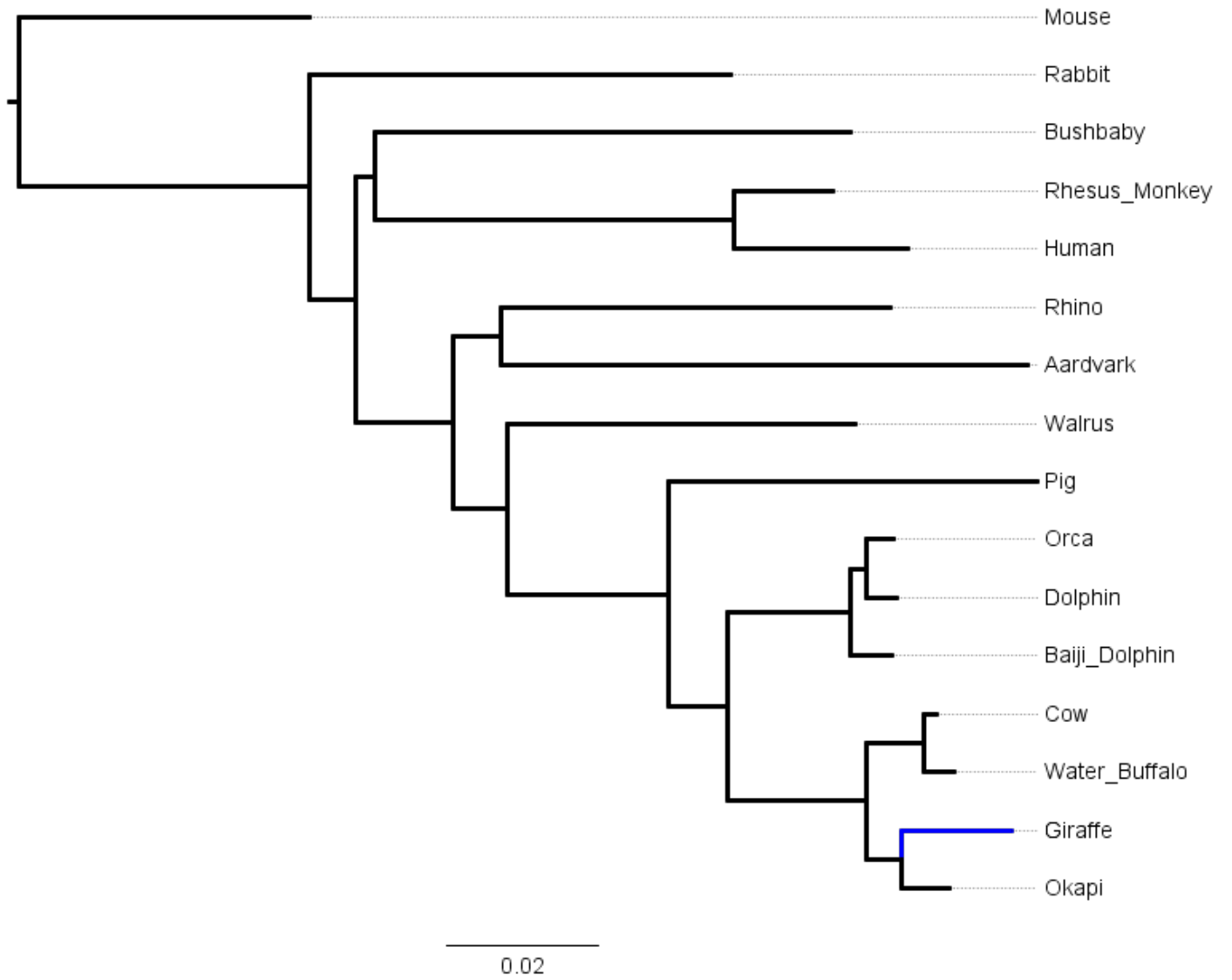
PP2: (Giraffe) A34I, V95M
Giraffe: R8L UPS, P31A UPS, V86M UPS, K402R UIS

Protein sequence Alignment of Cow, Giraffe and Okapi ALDH5A1

Cow	1	MATCLRLRSCAAPHLRRAPPSRICRPRADCPVAPIRGYARGPAGLSSALLRTDGFVGGGLW	60
Giraffe	1L.RP..C.....V.....A.....L.....	60
Okapi	1PS.Y.....QV...H.....	60
Cow	61	VSAATFPVHDPASGAELGLVADCGVPEARAAVRAAYEAFCSWRGVS AKERSLLRKWYD	120
Giraffe	61M.....	120
Okapi	61	120
Cow	121	LMIQNKDDLAKIITAESGKPLKEAQGEILYSANFLEWFSEEARRVYGDIIISTPAKERRAL	180
Giraffe	121	180
Okapi	121	180
Cow	181	VLKQPVGVAAVITPWNFP SAMITRKVGAALAAGCTVVVKPAEDTPFSALALAE LANQAGI	240
Giraffe	181L....I.....	240
Okapi	181L.....	240
Cow	241	PPGVYNVIPCSQKKAKEVGEALCTDPLVSKISFTGSTATGKVLLHHAANSVKRVS MELGG	300
Giraffe	241	300
Okapi	241	300
Cow	301	HAPFIVFDSANVDQAVAGAMASKFRNSGQTCVCSNRFLVQSGIHDSFVKKFAEAIKTNLH	360
Giraffe	301	360
Okapi	301	360
Cow	361	VGNGFDERTTQGPLINAKAVEKVEKHVSDAISKGATVVTGGKRHHVGKNFFEPTLLSNVT	420
Giraffe	361E.....A.....R..Q.....	420
Okapi	361E.....A.....Q.....	420
Cow	421	RDMLCSQEETFPGVPVPIKFNTEEEEAVAIANAANVGLAGYFYSQDPAQIWRVAERLEVGM	480
Giraffe	421D.....	480
Okapi	421D.....	480
Cow	481	VGVNEGLISSVECPFGGVKQSGLGREGSKYGIDEYLELKYVCFGGL	527
Giraffe	481	527
Okapi	481	527

Newick Tree of Mammalian ALDH5A1

(mouse:0.0385124, (rabbit:0.0560646, ((bushbaby:0.063082, (rhesus_monkey:0.0130375, human:0.0231304):0.04769):0.00264939, ((rhino:0.0515391, aardvark:0.0698163):0.00643962, (walrus:0.0459987, (pig:0.048716, ((orca:0.00366381, dolphin:0.00396989):0.00213718, baiji_dolphin:0.00551862):0.0163367, ((cow:0.00160601, water_buffalo:0.00411377):0.00756038, (giraffe:0.0146236, okapi:0.00647175):0.00455776):0.0185197):0.00768945):0.0213988):0.00733916):0.0129637):0.00610414):0.0385124);



Locus name: Succinic semialdehyde dehydrogenase (**ALDH5A1**)

Locus Name: 3-hydroxyisobutyrate dehydrogenase **HIBADH (3HIDH)**

ENSBTAT0000001374 HIBADH-201 3-hydroxyisobutyrate dehydrogenase mitochondrial, amino acid degradation
no mutation in m/h described

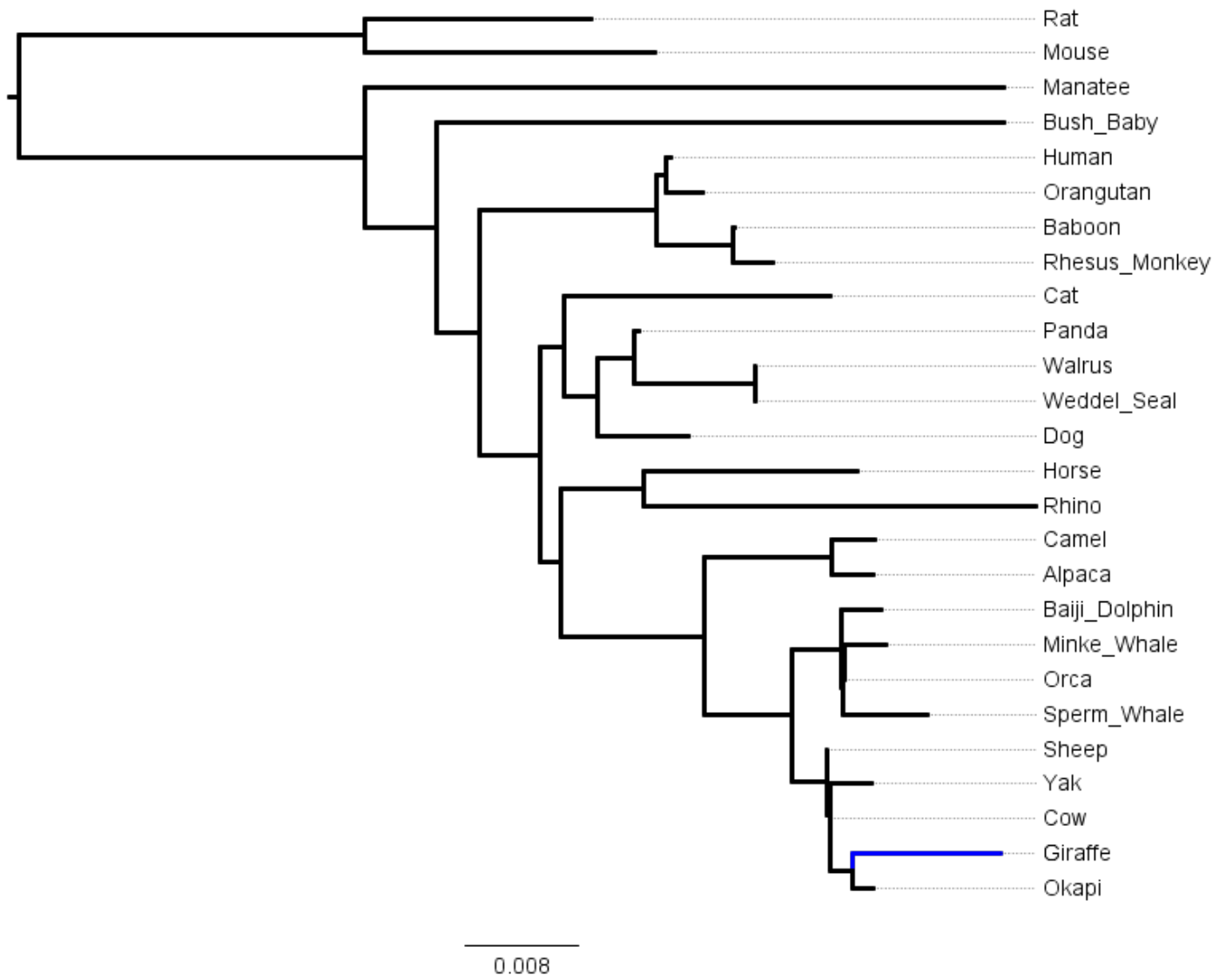
PP2: (Giraffe) A10V
Giraffe: A10V UPS, D265E UIS, D291E UPS

Protein sequence Alignment of Cow, Giraffe and Okapi HIBADH

Cow	1	MAASLRLRGAASGLRYWSRRQPPAVASLAAVCSRSMASKTPVGFIFVGNMGNPMAKNLMK	60
Giraffe	1V.....	60
Okapi	1	60
Cow	61	HGYPLIIYDVFPDACKEFLDAGEQVVSFPADVAEKADRIITMLPTSINAIEAYSGANGIL	120
Giraffe	61	120
Okapi	61	120
Cow	121	KKVKKGSLIDSSTIDPMVSKELAKEVEKMGAVFMDAPVSGGVAARSGNLTFMVGGVEE	180
Giraffe	121	180
Okapi	121	180
Cow	181	EFAAAQELLGCMGSNVVYCGAVGTGQAAKICNNLLLAISMIGTAEAMNLGIRLGLDPKLL	240
Giraffe	181	240
Okapi	181	240
Cow	241	AKILNMSSGRCWSSDTYNPVPVMDGVPSANNYQGGFGTTLMAKDLGLAQDSATSTKSPI	300
Giraffe	241TE.....E.....	300
Okapi	241I.....	300
Cow	301	LLGSQAHQIYRMMCAKGYSKKDFSSVFQFLREETF	336
Giraffe	301	336
Okapi	301	336

Newick Tree of Mammalian HIBADH

```
((rat:0.0159911, mouse:0.0204952):0.024398, (manatee:0.0452255, (bush_baby:0.0400822, ((human:0.000360217, orangutan:0.00262042):0.00063753, (baboon:0.000153016, rhesus_monkey:0.00282762):0.0053529):0.0125365, (cat:0.0188311, ((panda:0.000329437, (walrus:0, weddel_seal:0):0.00863935):0.00257591, dog:0.00643383):0.00234697):0.00171167, (horse:0.0149812, rhino:0.0275912):0.00590892, (camel:0.00306073, alpaca:0.00290947):0.00900709, (baiji_dolphin:0.00284379, (minke_whale:0.0029966, orca:0):5.56646e-05, sperm_whale:0.00592352):0.000143565):0.00351705, (sheep:0, (yak:0.00296328, (cow:0, (giraffe:0.0104891, okapi:0.00145161):0.00154322):3.97966e-05):0.000191481):0.0025478):0.00617726):0.0101173):0.00149611):0.00426352):0.00304448):0.00510457):0.024398);
```



Locus Name: 3-hydroxyisobutyrate dehydrogenase **HIBADH (3HIDH)**

Locus Name: Monocarboxylic acid transporter 1, (SLC16A1; MCT1)

ENSBTAT0000020102 SLC16A1-201 monocarboxylate transporter rumen epithelium, transport volatile fatty acids, butyrate
human: Symptomatic deficiency in lactate transport (SDLT) [MIMOUSE:245340]: Deficiency of lactate transporter may result in an acidic intracellular environment created by muscle activity with consequent degeneration of muscle and release of myoglobin and creatine kinase.

PP2: (Giraffe) G192E, A335P

Giraffe: G192E UIS, F246L UIS, W324R UPS, A335P UIS

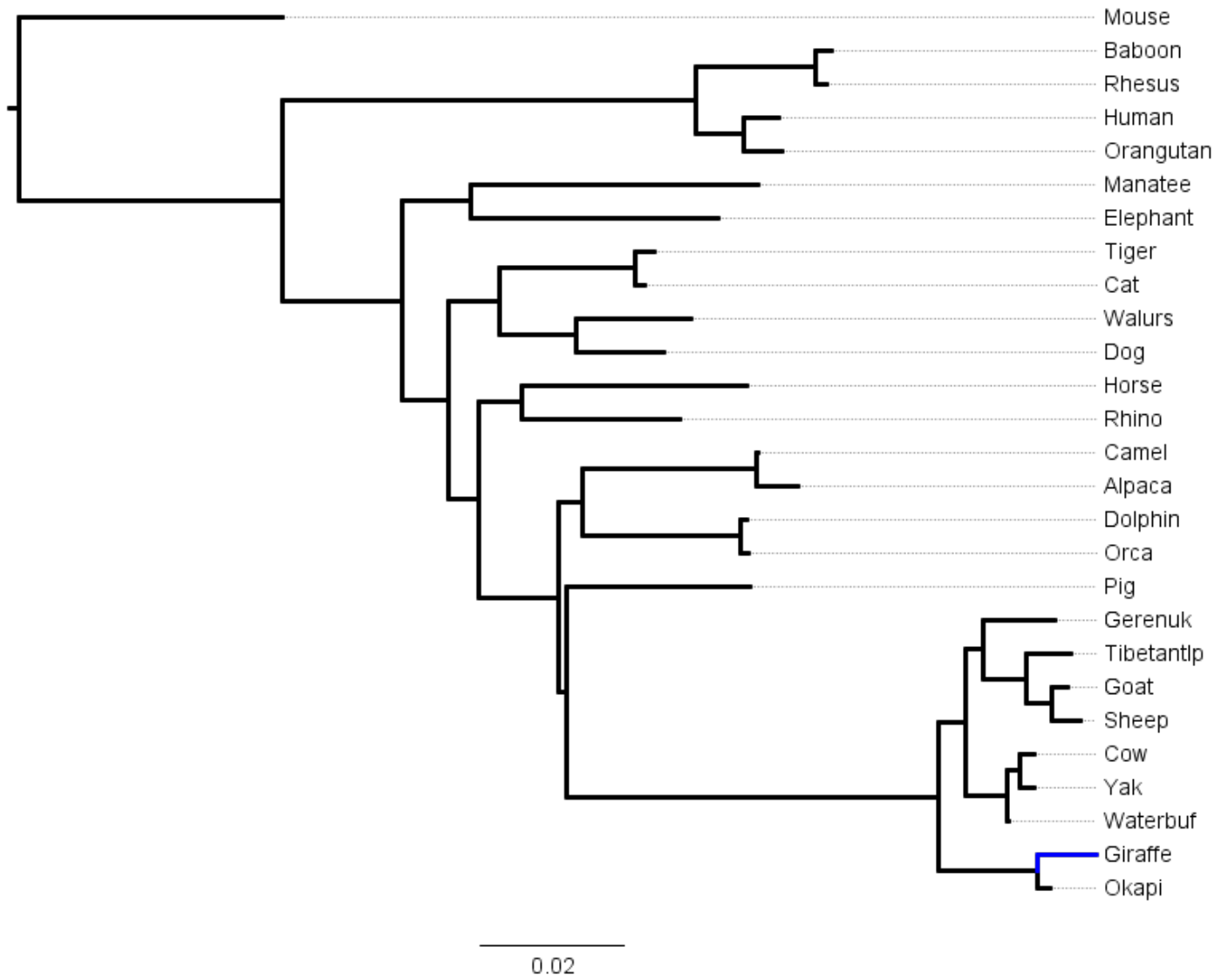
Giraffe/Okapi: I171T UIS

Protein sequence Alignment of Cow, Giraffe and Okapi MCT1

Cow	1	MPPAVGGPVGYPDPDGGWGWAVVIGAFISIGFSYAFPKSITVFFKEIEGIFNATTSEVSW	60
Giraffe	1V.....	60
Okapi	1V.....	60
Cow	61	ISSIMLAVMYGGPISSVLVKNKYSRPVMIVGGILSGSGLIAASFCNTVQELYFSVGVIG	120
Giraffe	61F..	120
Okapi	61F..	120
Cow	121	GLGLAFNLNPALTMIGKYFYKRRPLANGLAMAGSPVFLSTLAPLNQAFFMIYGWRGSFLI	180
Giraffe	121T.....	180
Okapi	121F.....T.....	180
Cow	181	LGLLLLNCCVAGALMRPIGPKPTTAEKEKSKGSLQEAGKYETKKGASDANTDLIGGNPKE	240
Giraffe	181E.....	240
Okapi	181	240
Cow	241	EKKSIFQTLNFTFLDLSLFKHRGFLLYLSGNVLMFFGLFTPLVFLSNYGKSKHYSSEKAAF	300
Giraffe	241L.....F.....	300
Okapi	241F.....	300
Cow	301	LLSILAFVDMVARPSMGLVANTKWVRPRVQYFFAASIIANGLCHLAAPLSSTYIELCIYA	360
Giraffe	301RI.....P..V.....	360
Okapi	301I.....V.....	360
Cow	361	GFFGFAGWLSSVLFETLMDLVGPQRFSSAVGLVTIVECCPVLLGPPVLGRLNDIYGDYK	420
Giraffe	361	420
Okapi	361	420
Cow	421	YTYWACGIILIVAGIYLFIMGINYRLLLEKEQKAQKQKESKDEETNVDVAEKPKPEVID	480
Giraffe	421A.....G.E.....T.	480
Okapi	421A.....G.E.....T.	480
Cow	481	AAESPEHKATEEDPKEAESPV	502
Giraffe	481I.V.....	502
Okapi	481I.V.....	502

Newick Tree of Mammalian MCT1

(mouse:0.0366203, ((baboon:0.00234744, rhesus:0.00166059):0.016673, (human:0.00488244, orangutan:0.00516807):0.00676165):0.0578562, (manatee:0.0401926, elephant:0.0346005):0.00957182, ((tiger:0.00272322, cat:0.00129286):0.0189166, (walurs:0.0162081, dog:0.012311):0.0105875):0.00718989, ((horse:0.0313634, rhino:0.0220628):0.00614059, ((camel:0.000177447, alpaca:0.00582861):0.0241509, (dolphin:0.000964546, orca:0.00103346):0.0220117):0.00336736, (pig:0.0255272, ((gerenuk:0.0101736, tibetantlp:0.00632708, (goat:0.00205463, sheep:0.00395143):0.00372973):0.00600986):0.00229364, ((cow:0.00200294, yak:0.00199708):0.0018109, waterbuf:0.000189113):0.00578455):0.00395114, (giraffe:0.00821691, okapi:0.00179335):0.0138139):0.05178):0.00113645):0.0113143):0.00418234):0.00638919):0.0168504):0.0366203);



Locus Name: Monocarboxylic acid transporter 1, (**SLC16A1**; **MCT1**)

Locus Name: Acyl-CoA Synthetase Medium-Chain Family Member 3 (ACSM3)

ENSBTAT0000008455 ACSM3-201 acyl-CoA synthetase medium-chain mitochondrial
mouse: deficiency is asymptomatic

PP2: All benign

Giraffe: K217T UIS, T433S UPS

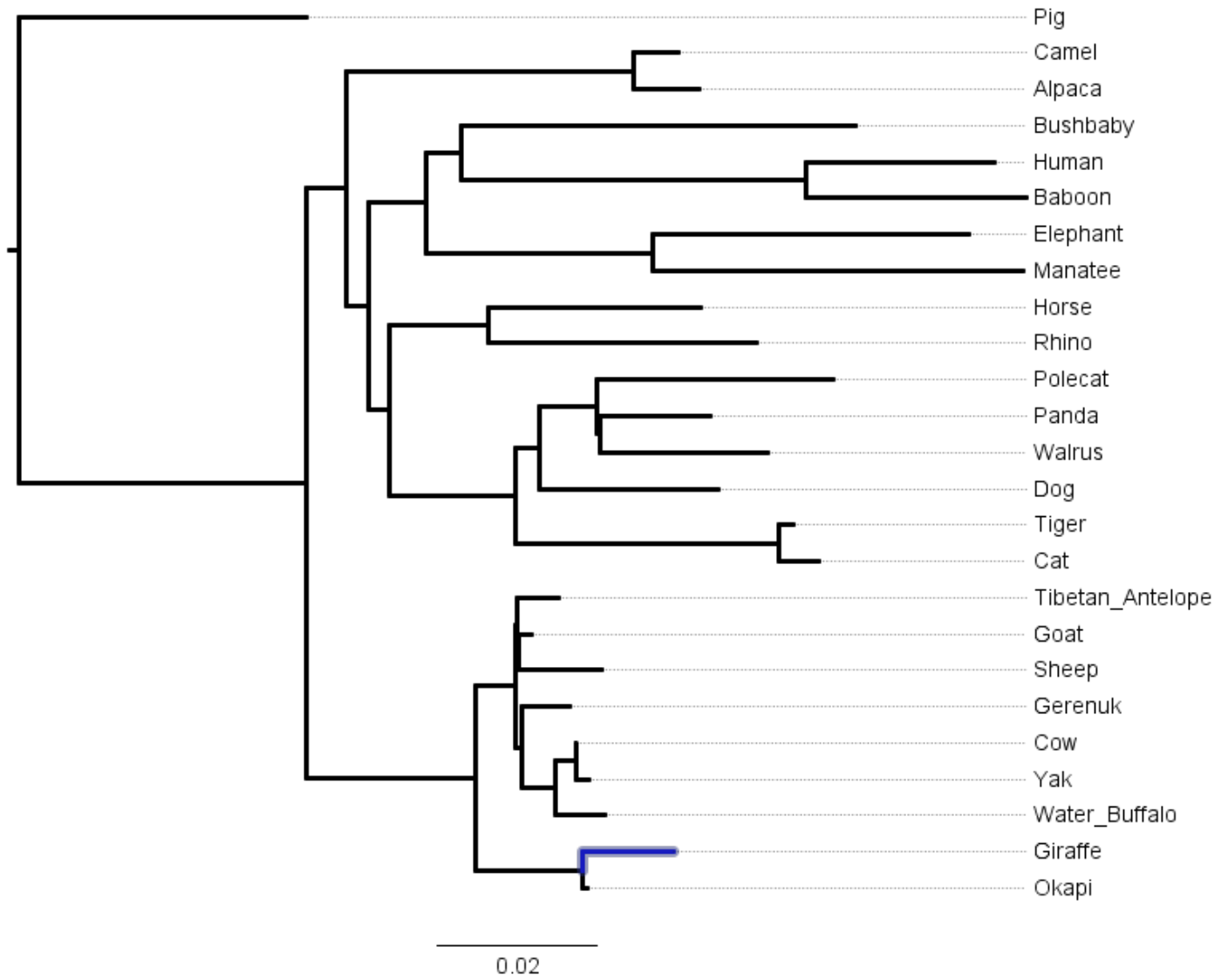
Giraffe/Okapi: F246Y UIS, V282L UPS, F283Y UIS, A320P UIS, S345T UIS, N543S UPS

Protein sequence Alignment of Cow, Giraffe and Okapi ACSM3

Cow	1	MKILLCAKYFQCPVIPGSMRALHKDYRTVTPQNFSNYESMKQDFKLEIPEYFNFAKDVL	60
Giraffe	1R.....LA.....D.....	60
Okapi	1R.....LA.....	60
Cow	61	QWTSMEKAGKKPSNPAFWWTNGNGEEVRSFEELGSLSRKFANILTEACGLQRGDRVILL	120
Giraffe	61	..N.....R.....I.....VI	120
Okapi	61	..N.....R.....I.....VI	120
Cow	121	LPRIPEWWLANIACLRTGTVLIPGTTQMTQKDILYRLQSSKAKCIITNEVLAPAVDAVAS	180
Giraffe	121	..K.....	180
Okapi	121	180
Cow	181	KCENLHSLKLVQSPPREGWENLKEMMKHASDNHTCVKTKHNEMMAIFFTSGTSGYPKMTG	240
Giraffe	181D..Q.....T.....S.....	240
Okapi	181S.....	240
Cow	241	HTHSSFGLGLSINGRFWLDLTPLDVMWNTSDTGWAKSAWSSVFPWIQACVFAHYLPRF	300
Giraffe	241Y.....LY.....	300
Okapi	241Y.....LY.....	300
Cow	301	EPTSILQTLKFPITVFCAPTAYRMLVQNDKASYKFKSLKHCVSAGEPINPEVTEQWRN	360
Giraffe	301P.....T.....	360
Okapi	301P.....T.....	360
Cow	361	RTGLDIYEGYQGTETVLIICGNFKGMKIKPGSMGKPSPAFDVKILDVNGNVLPKGEGDIG	420
Giraffe	361	420
Okapi	361	420
Cow	421	IRVRPNRPLGLFTHYIDNPTKTASTLRGNFYITGDRGYMDEDEGYFWFVSRADDIILSSGY	480
Giraffe	421S.....	480
Okapi	421	480
Cow	481	RIGPFVESALIEHPAVAESAUVSSPDPPIRGEVVKAFIVLNPDKSHDQEQLKKEIQEHV	540
Giraffe	481K.....	540
Okapi	481	540
Cow	541	KRNTAPYKYPRKVEFIQELPKTISGKIKRNELRKKEWETI	580
Giraffe	541	..S.....V.....	580
Okapi	541	..S.....V.....	580

Newick Tree of Mammalian ACSM3

(pig:0.036346, ((camel:0.00563085, alpaca:0.0082587):0.0362893, ((bushbaby:0.0498459, human:0.0236649, baboon:0.0276509):0.0436566):0.00444697, (elephant:0.0397854, manatee:0.0467067):0.0287065):0.00736451, (horse:0.0266564, rhino:0.0337895):0.0125289, ((polecat:0.0297458, (panda:0.0139341, walrus:0.0211644):0.000399972):0.00719307, dog:0.022576):0.00317441, (tiger:0.00182893, cat:0.00509157):0.0333636):0.0158113):0.00277917):0.00272705):0.00507594, (((tibetan_antelope:0.00509388, (goat:0.00164453, sheep:0.0104982):0.000114797):0.000176325, (gerenuk:0.00616657, (cow:0, yak:0.00174123):0.00252245, water_buffalo:0.00614327):0.00427353):0.0006959):0.00518214, (giraffe:0.0114731, okapi:0.000648542):0.0135766):0.02136):0.036346);



Locus Name: Acyl-CoA Synthetase Medium-Chain Family Member 3 (ACSM3)

Locus Name: Acyl-CoA Dehydrogenase (**ACADS**)

ENSBTAT0000009844 ACADS-201 acyl-CoA dehydrogenase short chain mitochondrial
mouse: viable but exhibit organic aciduria and develop hypoglycemia and fatty livers after
fasting

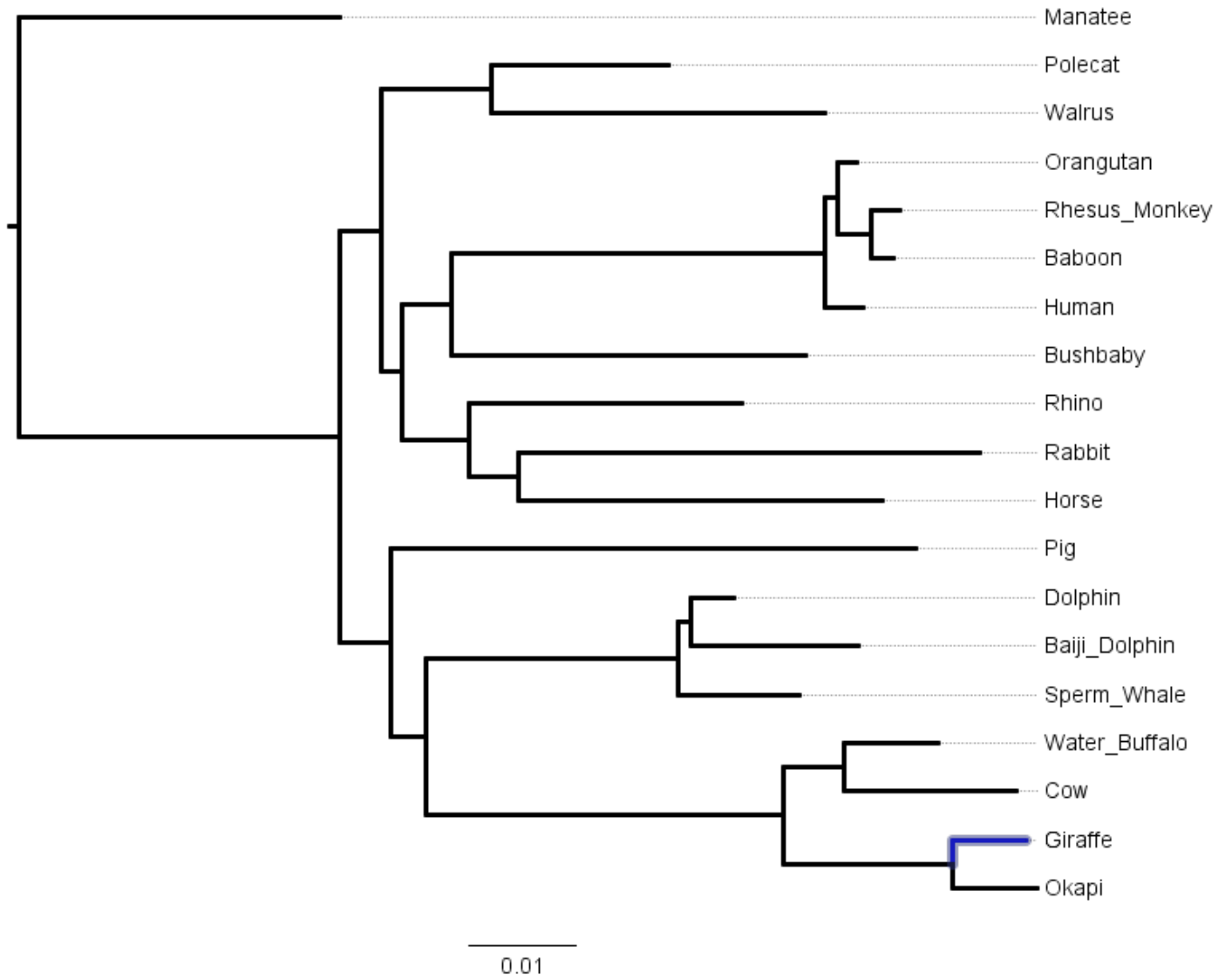
Giraffe: A9T UIS, H206R UPS
Giraffe/Okapi: E76K UPS, I186V UIS, S236T UIS, A318V UIS

Protein sequence Alignment of Cow, Giraffe and Okapi ACADS

Cow	1	MAATLLARACGLVRGAPCPWGWRRRLHTVYQSVELPETHQMLRQTCRDFAEKELFPPIAAQV	60
Giraffe	1T.....W.....	60
Okapi	1W.....L	60
Cow	61	DKEHRFPAAQVKMGELGLMAMNVPEELSGAGLDYLAISIAMEEISRGCASTGVIMSVNN	120
Giraffe	61K.....D.....	120
Okapi	61K.....D.....	120
Cow	121	SLYLGPIILKFGTKEQKQRWVAPFTSGDKIGCFALSEPGNGSDAGAAATTARADGDSWVLS	180
Giraffe	121T.....	180
Okapi	121T.....	180
Cow	181	GTKAWITNAWEASAVVFASTDRSLHNKGISAFVPMPTPGLTLGKKEDKLGIRASSTAN	240
Giraffe	181V..S.....A.....R.....T....	240
Okapi	181V.....A.....M.....T....	240
Cow	241	LIFEDCRIPKDSLLGEPGLGFKIAMQTLDTGRIGIASQALGIAQAALDCAVTYAENRSAF	300
Giraffe	241	...E.....S..M.....S.....	300
Okapi	241	...E.....S..M.....S.....N..	300
Cow	301	GAPLTKLQAIQFKLADMALALESARLLTWRAAMLKDNKKPFTKEAAMAKLAASEAATAIT	360
Giraffe	301G.....V.....	360
Okapi	301G.....V.....	360
Cow	361	HQAMQILGGMGYVKEMPAERHYRDARITEIYEGTSEIQRLVVAGHLLKSYRS	412
Giraffe	361T.....	412
Okapi	361T.....	412

Newick Tree of Mammalian ACADS

(manatee:0.0297308, ((polecat:0.0164476, walrus:0.0307837):0.010229, (((orangutan:0.0018263, rhesus_monkey:0.00275351, baboon:0.0021127):0.00304885):0.00122994, human:0.00364823):0.0344429, bushbaby:0.0327112):0.00463058, (rhino:0.0253092, (rabbit:0.0427137, horse:0.0337335):0.00463544):0.00614534):0.00193616):0.00378163, (pig:0.0484722, ((dolphin:0.00406857, baiji_dolphin:0.0155412):0.00110867, sperm_whale:0.0111876):0.0233502, ((water_buffalo:0.00862668, cow:0.0159471):0.00567232, (giraffe:0.00683494, okapi:0.00779998):0.0156148):0.0330674):0.00320999):0.00473364):0.0297308);



Locus Name: Acyl-CoA Dehydrogenase (**ACADS**)

Locus Name: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8 (**NDUFB8**)

ENSBTAT00000000100 NDUFB8-201 NADH dehydrogenase- ubiquinone subunit mitochondria electron transport
no mutation in m/h described; putative QTL for nutrient transformation in cattle

PP2: Giraffe, K34E; Giraffe/Okapi, L24M

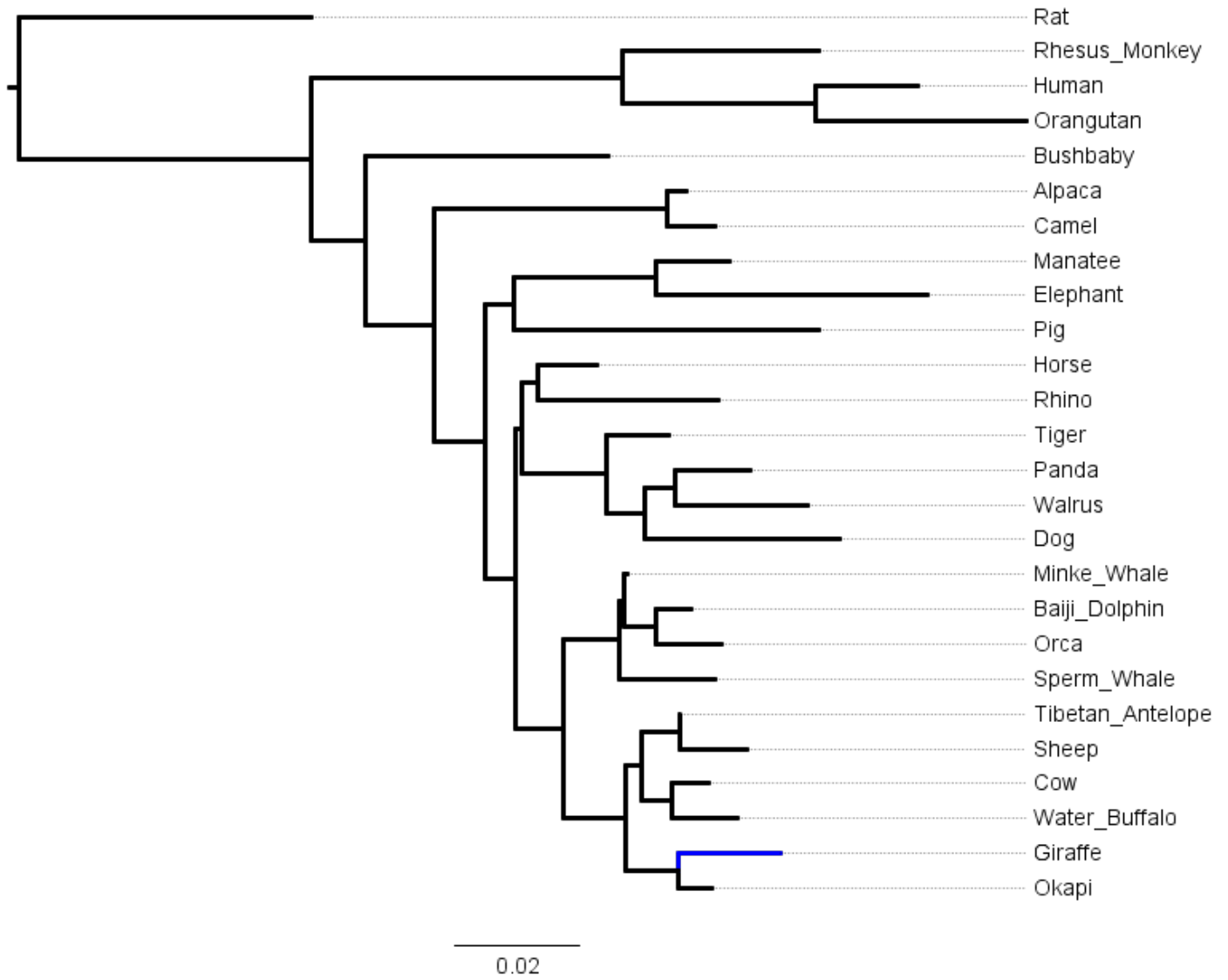
Giraffe: K34E UIS, Y72F UIS, L128F UPS

Protein sequence Alignment of Cow, Giraffe and Okapi NDUFB8

Cow	1	MAAARAGVLGVRWLQKAARNVVPLGARTASHITKDMLPGYPKTPPEERAAAANKYNMRVE	60
Giraffe	1M.....E.....	60
Okapi	1M.....F.....	60
Cow	61	DYEPYPDDGTGYGDYPKLPDRSQQERDPWYDWDHPDLRLNWGEPMHWDLDMYIRNRVDT	120
Giraffe	61M.F.....	120
Okapi	61M.....	120
Cow	121	PTPVNWNLMCKHLFGFVAFMLFMFWVGETYPAYQPVGPKQYPYNNLYLERGGDPNKEPEP	180
Giraffe	121F.....I.....T.....	180
Okapi	121I.....T.....	180
Cow	181	VVHYEI	186
Giraffe	181	186
Okapi	181	186

Newick Tree of Mammalian NDUFB8

(rat:0.0466707, ((rhesus_monkey:0.031416, (human:0.0161791, orangutan:0.0334381):0.0309388):0.0499067, (bushbaby:0.038833, ((alpaca:0.00311812, camel:0.00769301):0.0373299, ((manatee:0.0117701, elephant:0.0435207):0.0227242, pig:0.0488404):0.00452384, ((horse:0.0094675, rhino:0.0289028):0.0025596, (tiger:0.0101734, (panda:0.0118206, walrus:0.0209751):0.00499692, dog:0.0310593):0.00621582):0.013458):0.000986827, ((minke_whale:0.000394348, baiji_dolphin:0.00572374, orca:0.0105375):0.00501122):0.00093587, sperm_whale:0.0154388):0.00886842, ((tibetan_antelope:0, sheep:0.0109117):0.00602838, (cow:0.00580861, water_buffalo:0.0104526):0.00494835):0.00257955, (giraffe:0.0163783, okapi:0.00536341):0.00850647):0.00998073):0.007611):0.00488463):0.00821824):0.0108945):0.00873181):0.0466707);



Locus Name: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8 (**NDUFB8**)

Locus Name: Succinate dehydrogenase (SDHB)

ENSBTAT00000010949 SDHB-201 succinate dehydrogenase ubiquinone complex II mitochondria
electron transport and citric acid cycle
human: familial paraganglioma

Note MA1 and NZoo are identical except for C/R in lin1.

PP2: (Giraffe/Okapi) G20W

Giraffe: R12P UPS, P14S UPS, K55R UIS, A285S UIS, R11C UPS (MA1 only)

Giraffe/Okapi: G19S UPS, G20W UPS, G165R UPS

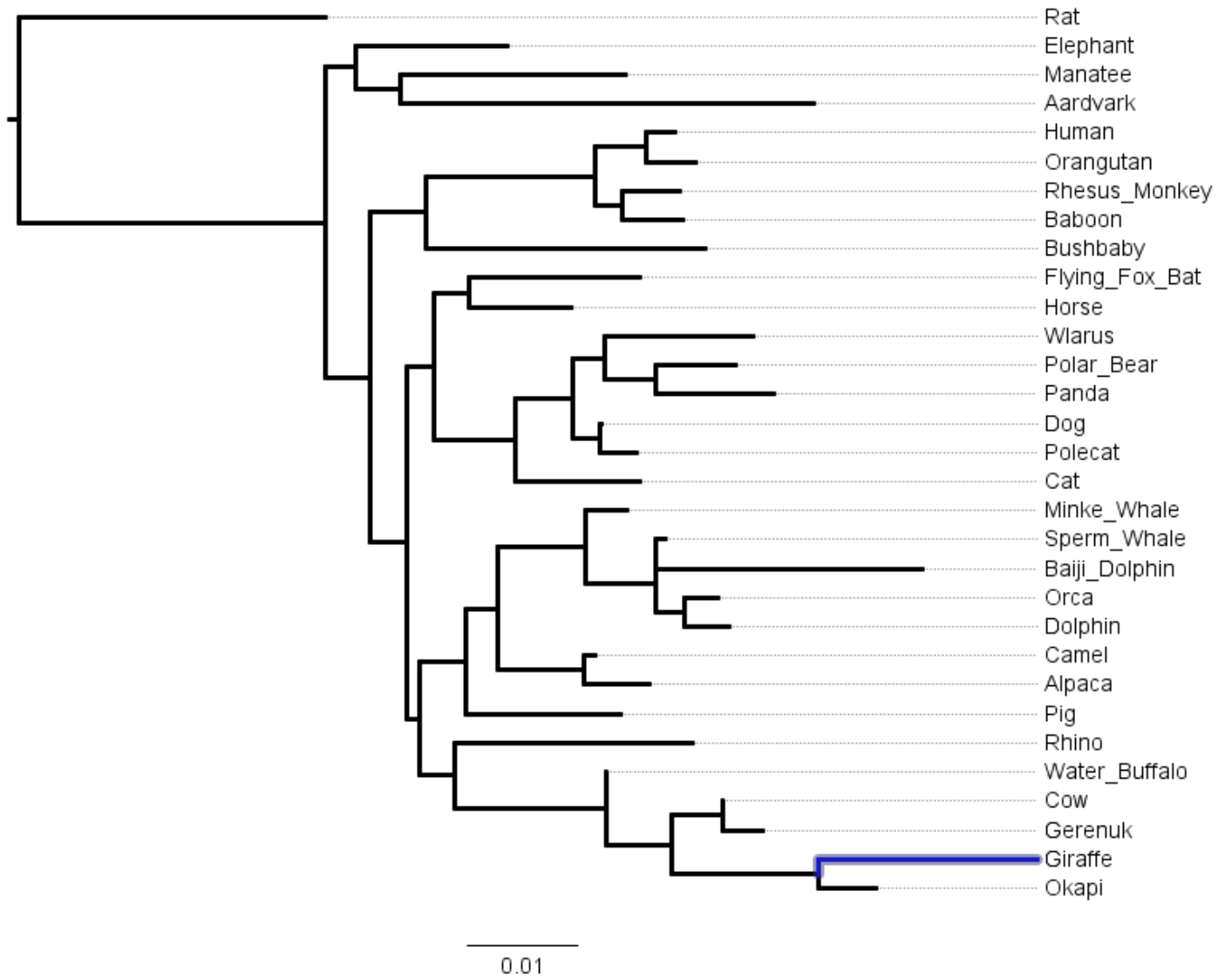
Okapi: A34V UPS

Protein sequence Alignment of Cow, Giraffe and Okapi SDHB

Cow	1	MAAVVALSLRRRFPAALGGARLQACRGAQTAAAAAPRIKKFAIYRWDPDKTGDKPHMQT	60
Giraffe	1P.S....SW.....V.....R.....	60
Okapi	1SW.....V.....	60
Cow	61	YEIDLNNCGPMVLDALIKIKNEIDSTLTFRRSCREGICGSCAMNINGGNTLACTRRIDTN	120
Giraffe	61	120
Okapi	61	120
Cow	121	LSKVSKIYPLPHMYVIKDLVPLSNFYAQYKSIIEPYLKKKDESQGGKEQYLQSIEDREKL	180
Giraffe	121	.N.....R.....	180
Okapi	121	.N.....R.....	180
Cow	181	DGLYECILCACSTSCPSYWWNGDKYLGPAVLMQAYRWMIDSRDDFTEERLAKLQDPFSL	240
Giraffe	181	240
Okapi	181	240
Cow	241	YRCHTIMNCTQTCPKGLNPGKAIKMMATYKEKQASA	280
Giraffe	241RRS..	280
Okapi	241R....	280

Newick Tree of Mammalian

```
(rat:0.0281864, ((elephant:0.0140475, (manatee:0.0207438,
aardvark:0.0381307):0.00414034):0.00275122, (((human:0.00262191,
orangutan:0.00454664):0.00469757, (rhesus_monkey:0.00524109,
baboon:0.00553121):0.00253636):0.0155736, bushbaby:0.0257615):0.00514465,
(((flying_fox_bat:0.0158236, horse:0.00949688):0.00310431, ((wlarus:0.0135686,
(polar_bear:0.00728323, panda:0.0109332):0.00461818):0.00298046, (dog:0.000146072,
polecat:0.00343176):0.00241848):0.00533172, cat:0.0114968):0.00740558):0.00249688,
(((minke_whale:0.00389848, ((sperm_whale:0.000771997, baiji_dolphin:0.0245485):6.3855e-05,
(orca:0.00312325, dolphin:0.0040453):0.00269294):0.00647283):0.00807418, (camel:0.00104348,
alpaca:0.00612507):0.00790473):0.00294939, pig:0.0143171):0.00421863, (rhino:0.0219161,
(water_buffalo:0, (giraffe:0.0199947, okapi:0.00523451):0.0135203, (cow:0,
gerenuk:0.00363408):0.00468624):0.00605696):0.0139869):0.00320491):0.00110757):0.00343791):0.0041
4917):0.0281864);
```



Locus Name: Succinate dehydrogenase (**SDHB**)

Locus Name: Proline Rich 19 (PRR19)

ENSBTAT00000017664 PRR19-201 proline rich protein 19 secreted tannin binding protein
no mutation in m/h described

PSG: (Giraffe) S335H
PP2: (Giraffe) P271T, L340R

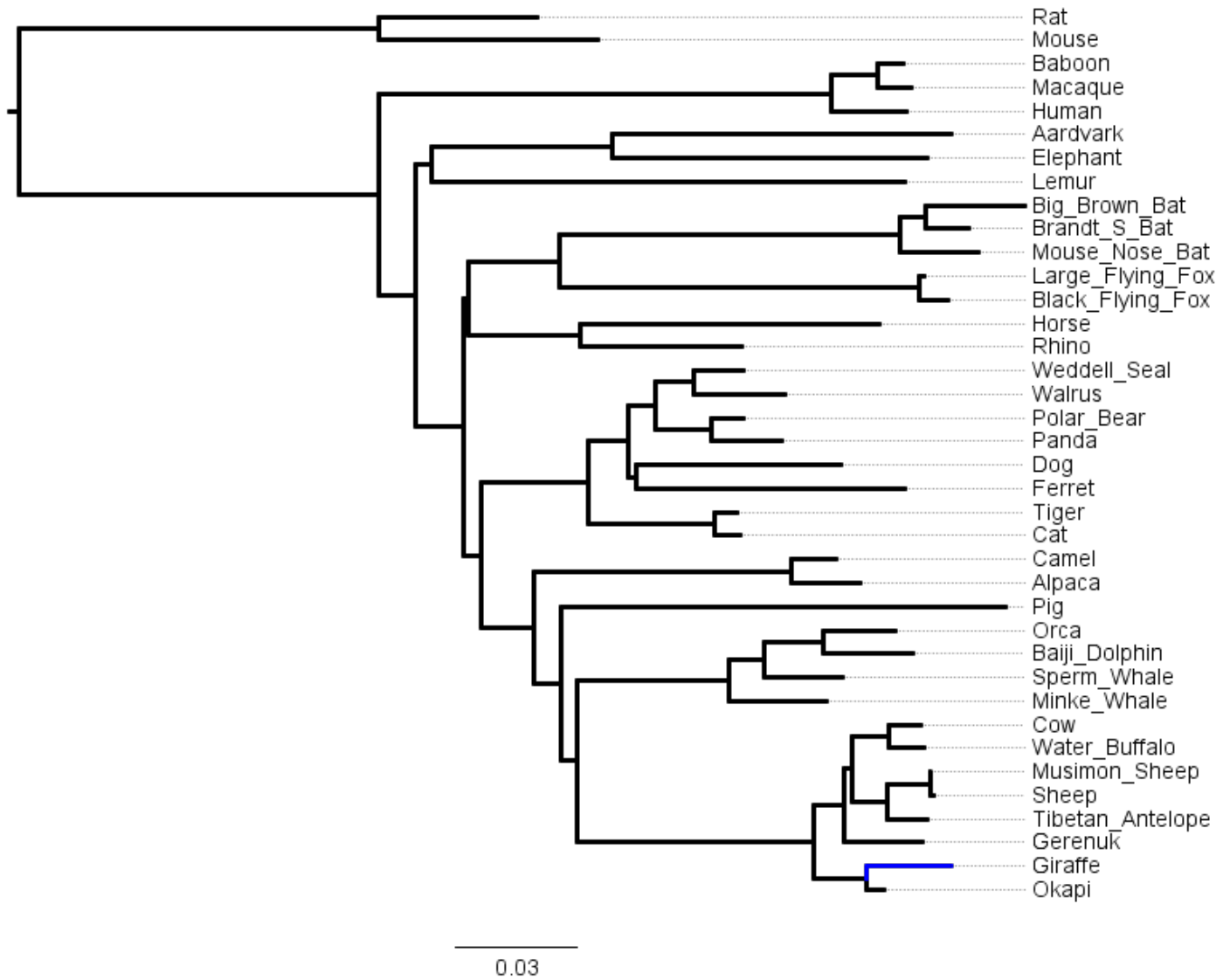
Giraffe: P270AV UPS, P271 UIS, G281R UPS, I310T UPS, S335H UPS, L340R UPS
Giraffe/Okapi: S49G UPS, P264S UPS

Protein sequence Alignment of Cow, Giraffe and Okapi PRR19

Cow	1	MDPGEPAKPFQOPEKPGRVRRRKRTRERNEALAGSRQPLTYQHPPVASRDPHMVLRNSV	60
Giraffe	1V...R..AC....M.G.....	60
Okapi	1V...RR.A....M.G.....	60
Cow	61	APTAAKLVVITQGRLSRDHRGLFNHEVKSLDVARLLSSESLELGTALTTKSSPSPGRGQ	120
Giraffe	61G...SA.....	120
Okapi	61G...S.....	120
Cow	121	QPSLQSRGKENQVPGGSGPGPPSPQLPDLEQLLQQLILPRAFPRRNLVQEARDAI	180
Giraffe	121Q.....	180
Okapi	121Q.....	180
Cow	181	VGTLQACHGCVPDLTLLVLRGCQPHLPGTDPGALKRQRMTFSPWINSPEQAPGEGRRRRQG	240
Giraffe	181E...P.....	240
Okapi	181E...P.....	240
Cow	241	TKELTFAVPTTSSTPTVHQVSLAPPKGPWPPPLSSLPSPSGAAWGPPTAFDLLKSIWLVA	300
Giraffe	241R...S....AT.....RV.....	300
Okapi	241R...S.....V.....	300
Cow	301	TPPPRPWGIGPPQLLPSPPLLRSSALDWSPSPAPLPSLSWMAQSSPEAWSFPPM	360
Giraffe	301T.....H....R....V.....	360
Okapi	301V.....	360
Cow	361	RLY	363
Giraffe	361	...	363
Okapi	361	...	363

Newick Tree of Mammalian PRR19

((rat:0.0386238, mouse:0.053525):0.0883841, ((baboon:0.00603163, macaque:0.00811335):0.0116231, human:0.0185133):0.110478, (((aardvark:0.0830881, elephant:0.0772208):0.0441121, lemur:0.115863):0.0041864, (((big_brown_bat:0.023928, Brandt_s_bat:0.01027):0.00653338, mouse_nose_bat:0.0193772):0.0832193, (large_flying_fox:0.00124157, black_flying_fox:0.00712677):0.0880732):0.0222939, (horse:0.0732935, rhino:0.0394889):0.0272606):0.00110741, (((Weddell_seal:0.0118746, walrus:0.0223234):0.00971802, (polar_bear:0.00807014, panda:0.0174659):0.0136758):0.00647727, (dog:0.0500977, ferret:0.0658449):0.00186069):0.010002, (tiger:0.00518627, cat:0.00608169):0.0313018):0.026254, ((camel:0.0110255, alpaca:0.0169129):0.0632447, (pig:0.10878, (((orca:0.0174325, baiji_dolphin:0.0219085):0.0147489, sperm_whale:0.0193722):0.00833998, minke_whale:0.0237239):0.037262, (((cow:0.00799261, water_buffalo:0.00867521):0.00915383, (musimon_sheep:0, sheep:0.000698761):0.0103752, tibetan_antelope:0.00989567):0.00886299):0.0016283, gerenuk:0.0191309):0.00752895, (giraffe:0.0207924, okapi:0.00431613):0.012737):0.0580005):0.00389828):0.00683237):0.0129994):0.00393652):0.012024):0.00872935):0.0883841);



Locus Name: Proline Rich 19 (PRR19)

Locus Name: RIBOSOMAL L10 PROTEIN MITOCHONDRIAL (MRP10)

ENSBTAT0000002395 MRPL10-201 ribosomal L10 protein mitochondrial protein synthesis
no mutation in m/h described; presumed essential gene

PSG: (Giraffe) V5T|GTG/ACG

Giraffe: V5T UPS, Q204L UIS

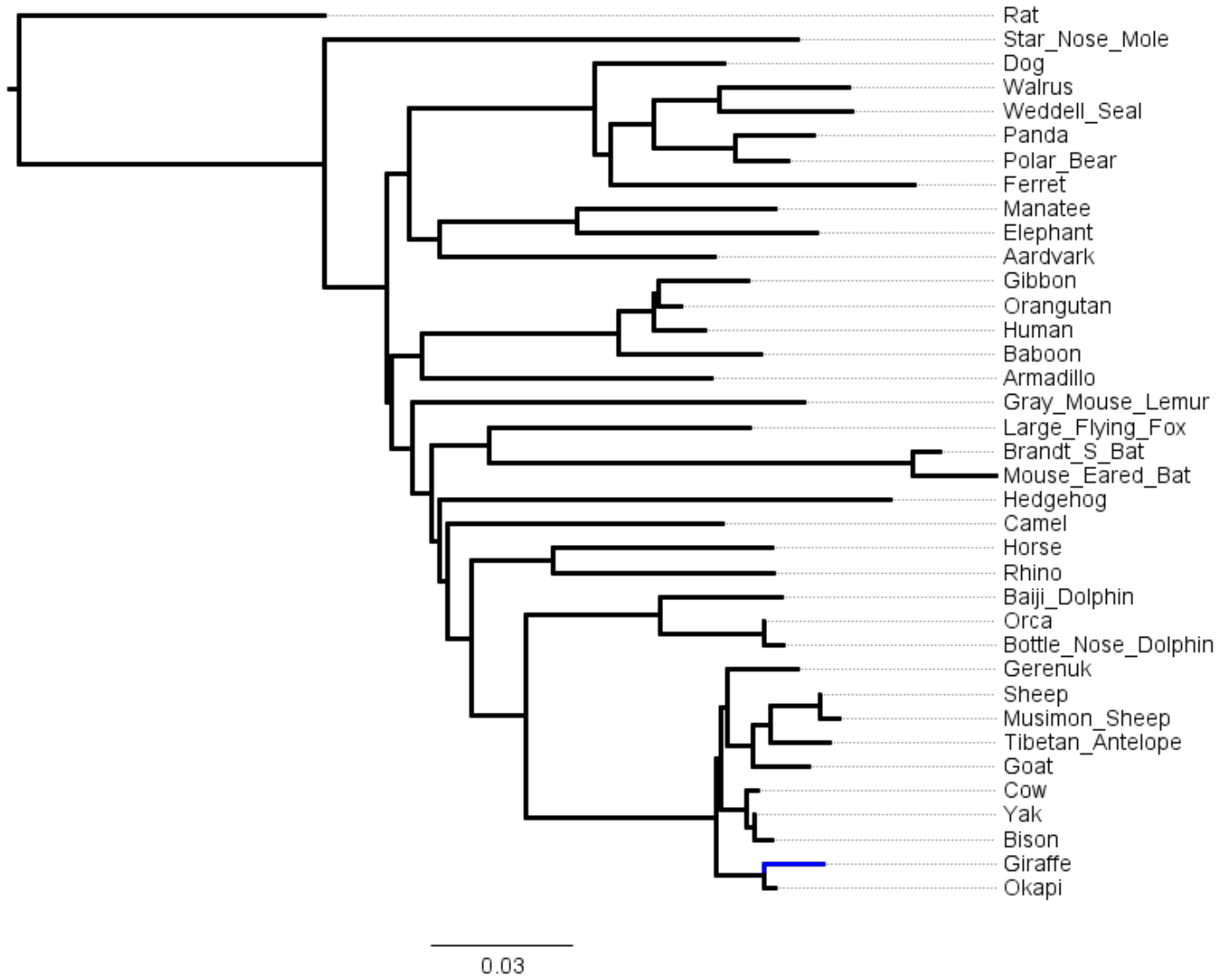
Giraffe/Okapi: V59L UPS

Protein sequence Alignment of Cow, Giraffe and Okapi MRP10

Cow	1	MAAAVAGMLRGGLLPQAGRLPTHQFIRYGSKAVTRHRRVMHFERQKLMVTEYIAPKPVV	60
Giraffe	1T.....I.....L.	60
Okapi	1I.....L.	60
Cow	61	NPRCLPPPPSPPQEETGLIRLLRREIAAVFRDNRMIAVCQNVAMSAEDKLLMRHQLRKHK	120
Giraffe	61R.....	120
Okapi	61	120
Cow	121	ILMKVFPNQILKPFLEDSKYQNLPLFVGHNLLVSEEPVKEMVRIKSVPFLLGGC	180
Giraffe	121M.....	180
Okapi	121M.....	180
Cow	181	IDDTILSRQGFINYSKLPALALAQGELVGGTLTLLTARTHSLQHHPLQLTALLDQYARQQ	240
Giraffe	181L.....A.....	240
Okapi	181A.....	240
Cow	241	HEGDPVVPASAQPDPPNPVQD	261
Giraffe	241V.....	261
Okapi	241	261

Newick Tree of Mammalian MRP10

(rat:0.0645262, (star_nose_mole:0.099884, ((dog:0.0272981, ((walrus:0.0275417, Weddell_seal:0.0280568):0.0135599, (panda:0.0165345, polar_bear:0.0109756):0.0171246):0.00912627, ferret:0.0641004):0.00334294):0.0391503, ((manatee:0.0418545, elephant:0.0505261):0.0290281, aardvark:0.0581608):0.00625984):0.00470102, (((((gibbon:0.0188812, orangutan:0.00446826):0.00117767, human:0.0109935):0.00751557, baboon:0.0303341):0.0412679, armadillo:0.0610013):0.00650589, (gray_mouse_lemur:0.0827197, ((large_flying_fox:0.0548505, (Brandt_s_bat:0.00579485, mouse_eared_bat:0.0174641):0.089278):0.0122031, (hedgehog:0.0953026, (camel:0.0578301, (horse:0.045932, rhino:0.0464486):0.0173674, ((baiji_dolphin:0.0253808, (orca:0, bottle_nose_dolphin:0.00399924):0.0217992):0.0284092, ((giraffe:0.0127051, okapi:0.00262143):0.00996322, ((gerenuk:0.0150397, ((sheep:0, musimon_sheep:0.00389757):0.0106477, tibetan_antelope:0.0126571):0.00366015, goat:0.0119038):0.00548156):0.00141166, (cow:0.00223277, (yak:0, bison:0.00385035):0.00161344):0.0055427):0.00084148):0.0401315):0.0115353):0.00501919):0.00175823):0.00166):0.00394547):0.00450686):0.000830059):0.0133847):0.0645262);



Locus Name: RIBOSOMAL L10 PROTEIN MITOCHONDRIAL (**MRP10**)

Locus Name: Mediator Of DNA-Damage Checkpoint 1 (MDC1)

ENSBTAT0000035900 MDC1-201 mediator DNA damage checkpoint dsDNA break repair, scaffold mouse: growth retardation and display increased susceptibility to ionizing radiation, male infertility, T and B cell abnormalities, and increased genomic instability

PP2: (Giraffe)L175F, S189L, G209R, S235G, V253M, E334K, L369Q, I400M, Q738P, A751S, E873Q, G960S, P969L, P1034S, S1057I, S1095F, R1114P, T1116S, P1136H, T1183R, T1269P, V1449M, T1474P, P1505L, A1785I, E1792D, P1827F, & A1911T. Giraffe and okapi share 15 PRD.

Protein sequence Alignment of Water Buffalo, Giraffe and Okapi MDC1

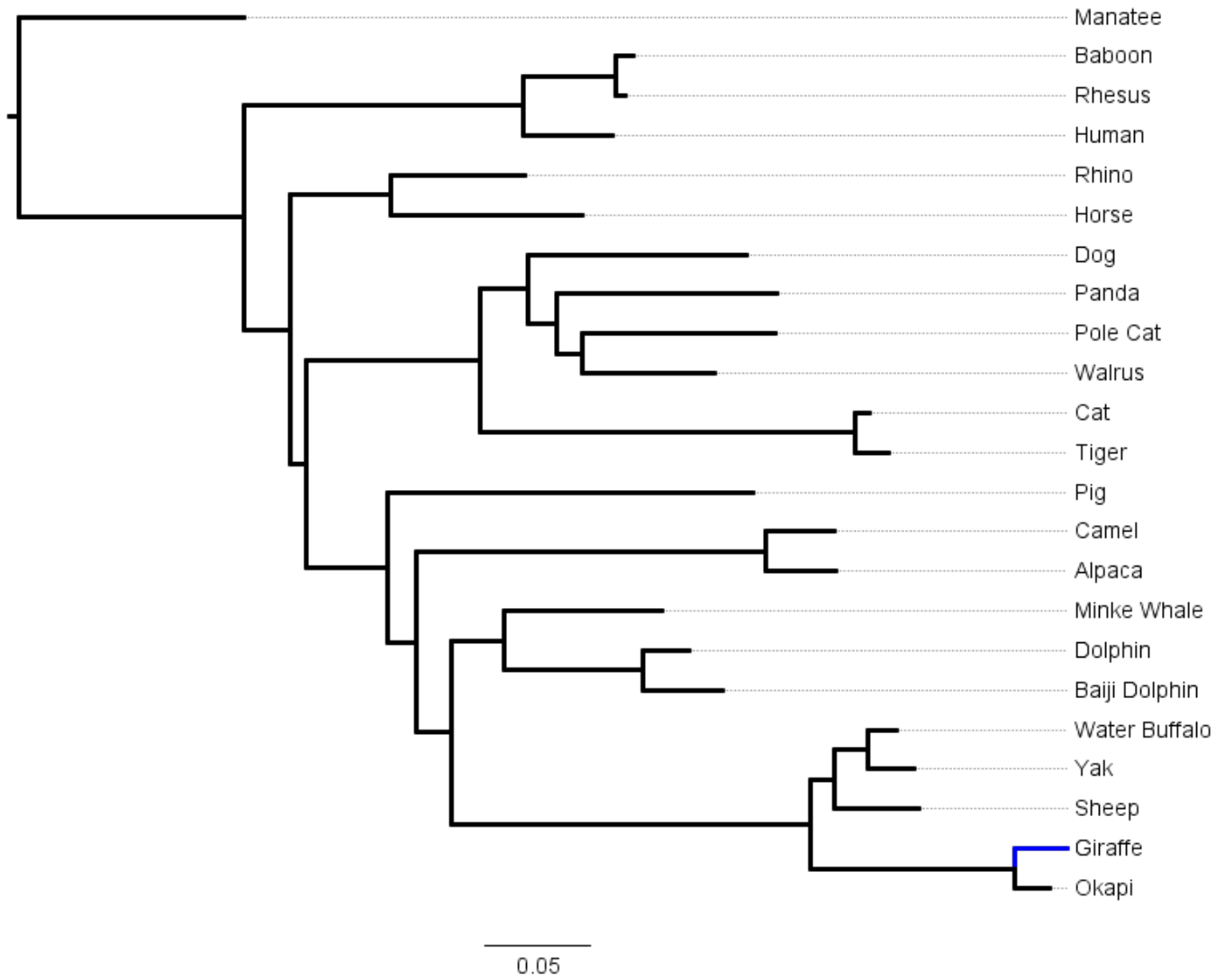
waterbuffalo	1	MEDTQILNWEVEEEEEVEERPSESLGYSLEPLGQLRIFSSSYGPEKDFPLYLGKMNIGRM	60
Giraffe	1V.....V...S.....HV.....	60
Okapi	1V.....V...S.....K.....H.....	60
Waterbuffalo	61	PDCSVALPFSSISKQHAVIEISAWDKAPVLRDCGSLNGTQILRPPKVLGPGVSHRLRDRE	120
Giraffe	61V.....Q.....Q.....	120
Okapi	61V.....Q.....Q.....	120
Waterbuffalo	121	LILFADLPCQYHRLDVPFVSRGPLTVEETPRVQGGTQPRLLLAEDSEEEVDSFLDKC	180
Giraffe	121	181
		\	
		R	
Okapi	121Q.....	180
Waterbuffalo	181	VVKGPRTSSLATVVPESDEEGPSPAPDGPSPAFNLSNTDDEESQESGAGEASSAPRR	240
Giraffe	182R.....A-----	235
Okapi	181	.A.....A-----	234
Waterbuffalo	241	GSAAEETEQPEPVTAIEIQIEKDQCSVKEKNRDEIERDVRNGVVPTGVILERSQPSGEDSD	300
Giraffe	236	.T.....K..M.....A.....K.....	295
Okapi	235	.TT.....R.....K.....I.....K...S.....	294
Waterbuffalo	301	TDVSDSESGPPRRLAGVVRPKRAWSCNFIDSNTDGEDEGIPATPAVVPKMERQIFHEAGTQS	360
Giraffe	296P.....G...N.K.....V.....	355
Okapi	295P.....G...N.K.....V.....	354
Waterbuffalo	361	PQAPGVARQQESPADGDTDIEEGEVPDRSQASMVIDSNTDDEEEVSAALTLARLRESQA	420
Giraffe	356A.....V.M.....A.....H...H.	412
Okapi	355R.....A.....V.....A.....H...H.	411
Waterbuffalo	421	GKWTRDPDAEEDRAQPVALLEQSASAGGSDTDVEEEGLPVERRGMVPGHMDREYSKK	480
Giraffe		-----	
Okapi		-----	
Waterbuffalo	481	SQHPPRSDTEGKEDKSSPGVHLERSQASAQVEDEVPLGPAVALPEKRQVQGIVWTHHTD	540
Giraffe		-----	
Okapi		-----	
Waterbuffalo	541	AEAEGGPAPLPLVLRLEEAWPPLAGDCKLDAENTSSAAAGVRKSQLPAEKDAGTTWDAAVP	600
Giraffe		-----	
Okapi		-----	
Waterbuffalo	601	EQDRALATGTQGGSSMAPGEQDLLPVSRENLADLVVDGTGTPGEPQPQREGAQTTRERE	660
Giraffe		-----	
Okapi		-----	
Waterbuffalo	661	PHGNRATDSGESLHDSLDLDPATQCFADRKNQSLEAAPSMEDEPTQAFLLPQEPGPS	720
Giraffe	410	-----F.....V..E.....V..V.....LP.....	458
Okapi	396	-----VA.E.....V.....LP.....	457
Waterbuffalo	721	CCSSQATGSLNEAWEVLATQPFPCPREYEASETQTAVTLLDTRASCPPPSRTAQEQHPES	780
Giraffe	459	...FP....D.....S.....S.....R...C.....	518
Okapi	458	...FP....D.....S.....C.....	517
Waterbuffalo	781	PVRAEALGMEGRGMQTVKDKGTQRETTERRVIPEGPPQNETKKLPSEGEREDVTGEEEL	840
Giraffe	519	..H..P.....M..P..A.....L.K.....	578
Okapi	518	..H..P.....M..P..A.....L.K.....	577

Waterbuffalo	841	IRGIQGREQNQVLARDTQSQESDKKVKASASTGRGMEIVKLETETPKETQEKEREKQTLAG	900
Giraffe	579D.....G.....Q.....M.....V.I.....	638
Okapi	578D.....V.....Q.....M.....I.....V.....	637
Waterbuffalo	901	EIFESEAGKLVVERESEVGGLEVKGPQELLDGRGPQMRTEAGGQDQKQASGPPSEPGAG	960
Giraffe	639A..N.A.....V.....L.X.....S.....P.L...	698
Okapi	638A..N.A.....I.....G.....P.....	697
Waterbuffalo	961	AGDLQGFSTDPVASGSQAGGGRGAPGSPRRQQRGDLNCEMPPAEKASRGDQESPDACLPP	1020
Giraffe	699LA.....R.....K.....G...S.....	758
Okapi	698LA.....R.....G...S.....	757
Waterbuffalo	1021	AAPEASAALPNLSIQIKHPAPQSLLFPSPAPLELPIPRTRENEQEAPETPFSSSELNS	1080
Giraffe	759T.....Q..S.....F.....	818
Okapi	758P.....T.....Q..S.....L.F.....	817
Waterbuffalo	1081	VHPEPKVVRPQGSPPVSSLPLEPHPTTPTGQPIALEPTSGVRSRSGTHSSFDVTASSVVPTA	1140
Giraffe	819	...K.....I.....H..P.....R.....FI....	878
Okapi	818	...N.....I.....Y.....P.....R.....	877
Waterbuffalo	1141	LALQPSTSTDQPVAPKPTLRAPRGRAQRSSVKTPEPNVRTDQPIAPELTAKATRGRAQRS	1200
Giraffe	879IT..R.....H.....S.S...V.....	938
Okapi	878II.....H.....S.P...V.....	937
Waterbuffalo	1201	SVKTPKPDNPTIPKQPSTSTDQPVTPKPTSRAPRGRTPKSSAKTPEPAVPTASELQPAA	1260
Giraffe	939TL.....L.....R..V.....V.....	998
Okapi	938T.....L.....R..V.....V.....	997
Waterbuffalo	1261	PKDQPVAPELTSRATRGRTRQRSSIKTSKPDSTAPEPQPSTSTDQPVTPKPTSRAPRGRTR	1320
Giraffe	999V.....M..T.....	1059
		\	
		P	
Okapi	998	LT.....V.....M..T....F.....	1058
		\	
		P	
Waterbuffalo	1321	PRSSSKTPEPVVSTASELQPSALTDQPVTPELTSRATRRAQRSSVKTDPDVTTPPELQ	1380
Giraffe	1060I.....L.....G.....S.....	1119
Okapi	1059T.....G.....	1118
Waterbuffalo	1381	PSTSTDQLVTPKRPSRAPRGRTRRSSAKTPEPVVPTASELQPSAPADQVGPWATQCRRH	1440
Giraffe	1120PT.....L.....S.....N.....R	1179
Okapi	1119PT.....L.....K.....R	1178
Waterbuffalo	1441	RSSVKTLEPVVPTVPEPQPSTSKDQSVAPEPTSQATQSQTHRSSVKTSPTEPTAPDLKP	1500
Giraffe	1180P....A.....G...K.....	1239
Okapi	1179P.....G.....	1238
Waterbuffalo	1501	SSPTDQPVTPKVIAQGGPSRTRASTASAVLVPTTPEFQCPVPSEQLSPDPIPEVNCSL	1560
Giraffe	1240S.....P.....L.....R	1299
Okapi	1239S.....S.....P.....R	1298
Waterbuffalo	1561	RPRATRKHGSPTAHVHEPCTAPPEPNSRSSRNQTHGAMKAAKLLSTIPEPAFAQLPEAPP	1620
Giraffe	1300YS.....RR..V..EP.....V..	1359
Okapi	1299S.....G..RR..V..EP.....V..	1358
Waterbuffalo	1621	HTPQMPKEEAADGSGFTPEPQPRASQNRKRPSATAHSPPLQKRLQGRVPOKAASLKEEE	1680
Giraffe	1360	.I..I..D.....K...H..A.IT.....F...K.....TI....	1420
		\	
		E	
Okapi	1359	.I..I.....K...C..A.IT.....K....V.V....	1419
		\	
		E	
Waterbuffalo	1681	NPAARPRKEEGVVIPGPGKRKREQTEESQGRPSRSLRRTKPVQESTAPKVLFTGVVDAR	1740
Giraffe	1421	...G.....LI.....	1480
Okapi	1420	...G.....I.....	1479

Waterbuffalo	1741	GERTVLALGGSLASSVAEASHLVTDRIIRRTVKFLCALGRGIPILSLAWLHESRKAGCFLP	1800
Giraffe	1481T.....	1540
Okapi	1480	1539
Waterbuffalo	1801	PDEYLVTDPEQEKNFGFSLREALSRARERRLLEGYEIHVTPGVQPPPPQMGEIINCCGGA	1860
Giraffe	1541Q.....Y.....	1600
Okapi	1540Q.....	1599
Waterbuffalo	1861	ILPSMPRSYKQORVVITCSQDFPRCAIPSRVGLPVLSPEFLLTGVLKQEVKPEAFSTV	1920
Giraffe	1601Y.....I.....	1660
Okapi	1600Y.....I.....	1659
Waterbuffalo	1921	EMSST	1925
Giraffe	1661	1665
Okapi	1660	.V...	1664

Newick Tree of Mammalian MDC1

(manatee:0.0873606, ((human:0.0506362, (baboon:0.0426609, rhesus:0.0216001):0.0201454):0.130203, ((rhino:0.0885826, horse:0.140875):0.0356451, ((cat:0.013552, tiger:0.0238696):0.10227, (dog:0.102894, (panda:0.0927121, (polecat:0.082205, walrus:0.069215):0.0078292):0.00246621):0.0230752):0.0619518, ((giraffe:0.0488042, (sheep:0.0362649, (waterbuffalo:0.0123944, yak:0.0225):0.019704):0.0140556):0.120944, (minke whale:0.032485, (dolphin:0.0209078, fwdolphin:0.0351586):0.0168106):0.0517353):0.0113368, (pig:0.162404, (camel:0.0307988, alpaca:0.0352585):0.0830175):0.0077372):0.0354452):0.00777303):0.019268):0.0873606);



Locus Name: Mediator Of DNA-Damage Checkpoint 1 (**MDC1**)

Locus Name: Exonuclease 1 (EX01)

ENSBTAT00000012365 EX01-201 exonuclease 1DNA mismatch repair, essential for meiosis
mouse: reduced life span, lymphoma development, and male/female sterility due to defective meiosis

PP2: (Giraffe) P587S

Giraffe: V142I UIS, G495D UIS, S579R UPS, P587S UIS, D639N UPS, S645R UIS, Q663E UPS, H714N UPS,
S733I UIS, R750K UIS, P796S UIS

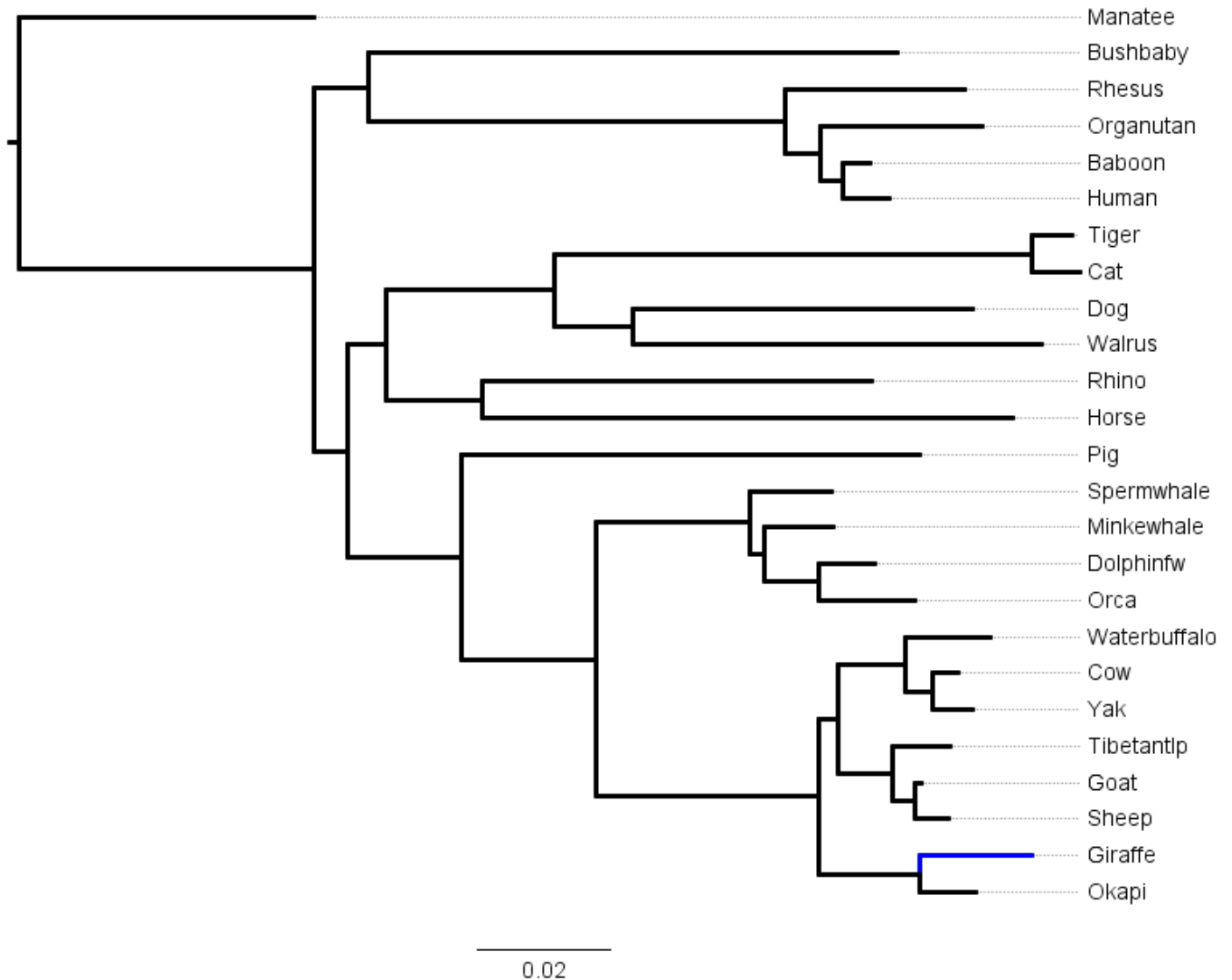
Giraffe/Okapi: E336K UIS, S492R UIS, S459G UPS, I606L UPS, T609A UIS

Protein sequence Alignment of Cow, Giraffe and Okapi Exo1

Cow	1	MGIHGLLQFIKEASEPIHIRKYKGQVVAVDTCWLHKGAVACA EK LAKGEPTEKYVGF	60
Giraffe	1V.....R....D.....	60
Okapi	1V.....R....D.....	60
Cow	61	KLVNMLLSHG I K P I L V F D G C T L P S K K E V E K S R R E R R Q A N L L K G K Q L L R E G K V S E A R E C F I	120
Giraffe	61	.F.....T	120
Okapi	61	.F.....T	120
Cow	121	RSINITH T M A H N V I K A A R S Q G V D C L V A P Y E A D A Q L A Y L N K A G I V Q A V I T E D S D L L A F G C K	180
Giraffe	121I.....	180
Okapi	121S.....	180
Cow	181	KVILKMDQFGNGLEVDQARLG MCKQLGDVFTEEKFRYMCILSGCDYLSSLRGIGLAKACK	240
Giraffe	181	240
Okapi	181	240
Cow	241	LLRLANNPDILKVV RK IGHY L K M N I T V P E D Y I K G F I R A N N T F L Y Q L V F D P I K R K L I P L N A	300
Giraffe	241I.....	300
Okapi	241I.....	300
Cow	301	YEDDVDPK T L S Y A G Q Y V D D S I A L Q I A L G N K D I N T L E Q I D H Y N P D T A M P A Q S R S H S W T D K A	360
Giraffe	301Q.....V.....K...D.....	360
Okapi	301V.....K...D.....	360
Cow	361	CQKSSNINSIWH R N Y C P R R E L D I V S D T K V K E N P S T V G I K Q V I S I K G L N L P R K S S I V K R P	420
Giraffe	361T.....	420
Okapi	361F.....T.....	420
Cow	421	RSEELSEDDMLDQYSTSFTKKIKKNSCEGNKSLNSSELF T P D L V D G T T V K K S L S T P P T T R	480
Giraffe	421M.....	480
Okapi	421M.....N.....	480
Cow	481	NKFAAFLQRKNEESGAVVPGTRIRFFSNLSADCIS K K A S S Q P L A E T A V T D K E T D A G E	540
Giraffe	481	...T...RD...I...T...N.....	540
Okapi	481	...T...R...T...N.....	540
Cow	541	PDCLEDK K L V D T S V S H N S S E Q I P D D V T V M A E E S Q S F K T S T F T R T I S P P T L G T L R S C F S W S	600
Giraffe	541G.....R.....S.....	600
Okapi	541T...L...G.....	600
Cow	601	GSLGDISRT P S P S T A L Q Q F R R K S D S S T S L P E N T E K S D I A P L K S D E S S D E S H P L H D V G C	660
Giraffe	601	...L..A.....I..L.NV...R.....W	660
Okapi	601	...L..A.....L..V.....W	660
Cow	661	SSQSQESMDLSPHN LNASKLSQPSSKSDSDSDCNFKSLDKQGNQKSKLHLHFHFSK K D T	720
Giraffe	661	..E.....E.....S.....N.....	720
Okapi	661I.....E.....S.....	720
Cow	721	PLRNKIPGLYKSSSVDSLSTTKIKPLV PARASGLSKKPPSVH K R N H H N A E N K P G L Q I K I N	780
Giraffe	721	L.....I...N.....K.....S.I.....Q.....	780
Okapi	721	L.....S.I.....Q.....	780
Cow	781	ELWKNFVFKK D S E K L P S C K K P D P L S P V K D N I Q L T P E E E D I F N N S E C M L V Q R A L F Q	835
Giraffe	781S.....H.....	835
Okapi	781H.....	835

Newick Tree of Mammalian EX01

```
(manatee:0.0445111, ((bushbaby:0.0799495, (rhesus:0.0269871, (organutan:0.0243306,
(baboon:0.00390335, human:0.00679214):0.00337844):0.0053381):0.0630245):0.0081005,
(((tiger:0.00598482, cat:0.00710319):0.0720242, (dog:0.0512731,
walrus:0.0616718):0.0117469):0.02554, (rhino:0.0587794, horse:0.0801692):0.0144952):0.00572285,
(pig:0.0691076, ((spermwhale:0.0124042, (minkewhale:0.0105979, (dolphinfw:0.00847203,
orca:0.0145474):0.00829768):0.0021954):0.0231251, ((giraffe:0.0170079,
okapi:0.00843537):0.0152493, ((waterbuffalo:0.012766, (cow:0.00382309,
yak:0.00582731):0.00425838):0.0101573, (tibetantlp:0.00874572, (goat:0.000995443,
sheep:0.00501062):0.00333675):0.00833323):0.00294327):0.0335305):0.0202126):0.017265):0.0050006) :
0.0445111);
```



Locus Name: Exonuclease 1 (EX01)

Locus Name: Nibrin (NBN)

ENSBTAT00000017598 NBN-201 component of MRN complex dsDNA break repair, chromosome integrity
mouse: impaired extraembryonic tissue growth and early embryonic death to growth retardation, lymphoid defects, lymphoma susceptibility, and failure of oogenesis. Null heterozygotes are cancer prone

PP2: (Giraffe) S278V, L490S

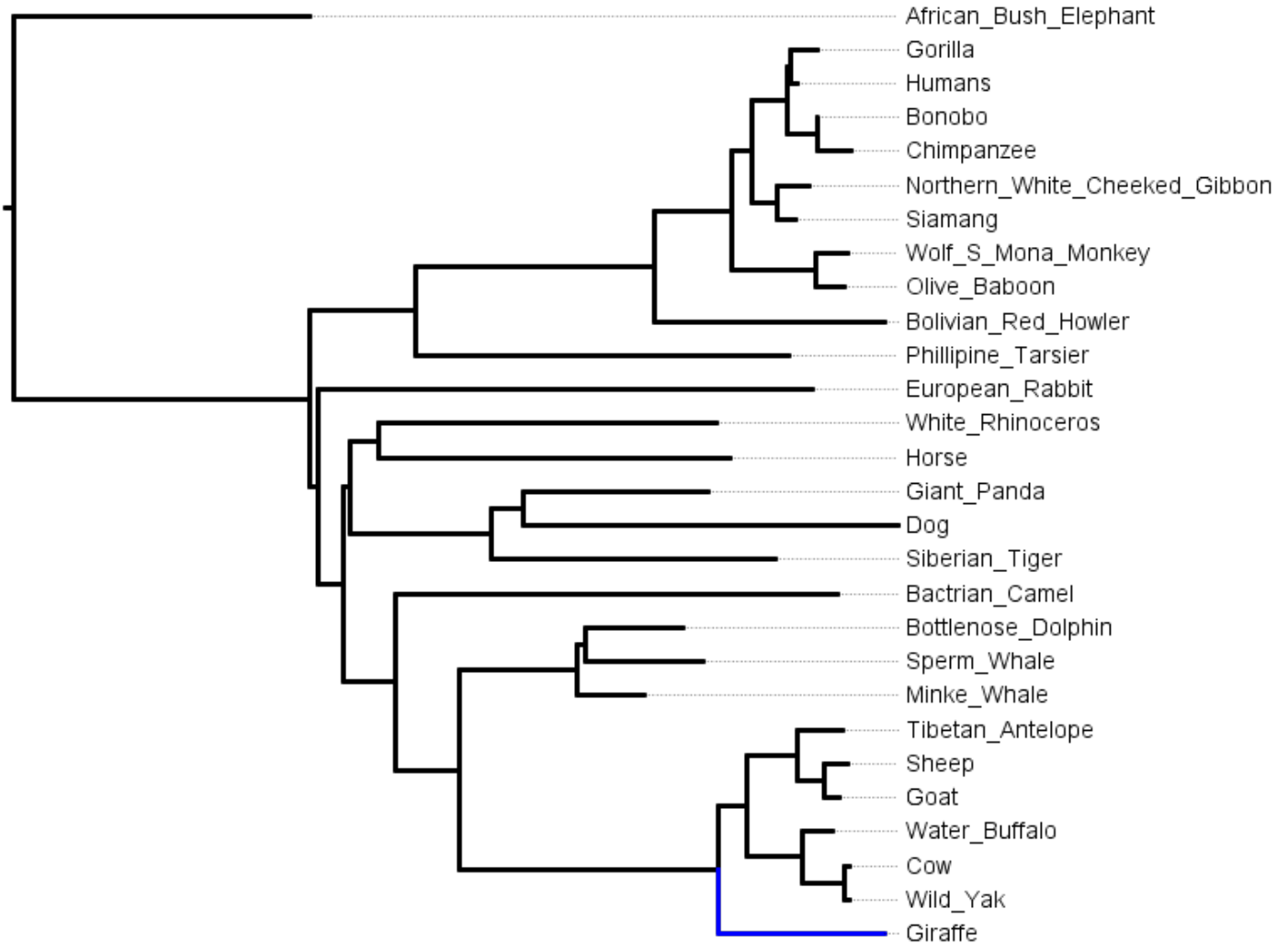
Giraffe: P6S UIS, P10L UPS, S277V UPS, H299R UPS, P339R UPS, L351V UIS, D372H UPS, H437P UPS, S463A UPS, Q474E UIS, T487V UPS, C489F UPS, N505T UPS, V516A UPS, N519K UPS, Y524H UPS, A525P UPS, P531A UPS, E572A UPS, I608T UPS, V735I UIS

Protein sequence Alignment of Cow, Giraffe and Okapi NBN

Cow	1	MWKLVPAAAGPAREPYRLLTGVEYIVGRKNCGILIEDDQSI SRNHATLTANFSVTNLSQTD	60
Giraffe	1S...L.....	60
Okapi	1Q.....	60
Cow	61	EIPVLTIKDNSKYGTFVNEEKMQNGLSQILKSGDRVTFGVFESKFRVEYEPLVACSSCLD	120
Giraffe	61	120
Okapi	61V.....	120
Cow	121	VSGKTALSHAILQLGGLTVNNWTEECTHLVMVSVKVTIKTICALICGRPIVKPEYFTEFL	180
Giraffe	121	180
Okapi	121R.....	180
Cow	181	KAVQSKKQLPEIESFYPPVDEPAIESKNIDL SGRQERKQIFKGKTFVFLNAKQHKKLSAA	240
Giraffe	181P.....GN.....	240
Okapi	181P.....	240
Cow	241	VIFGGGDARLITEENKEDDSFFSAPGTCVVDAGLTDSQTFIPDSQKKWIHSIMDILQRRG	300
Giraffe	241E.....V..L.....H.	300
Okapi	241T.....LV.....Q.	300
Cow	301	LRPIPEAEIGLAVLFVTTENYCDPQQQPSTGLKTTTPGPSLSQALPANENLMPNASVNTT	360
Giraffe	301I.....R.....V.....	360
Okapi	301I.....K...D...A.	360
Cow	361	TYVADTESEQADTCMDLSEPKKEIKIFGMEPKCRILSQETSTVKKPHKISSNNNIVSNTL	420
Giraffe	361	A.....H.....	420
Okapi	361	A.....V.....S.....	420
Cow	421	VRMKIPNYQLSPTKVPVHNKSRGWPSQHQQTNSIRDYFQPLTSPQKRERDEENQEMSLSK	480
Giraffe	421F.P.....K.....ATK.....E..S..	480
Okapi	421F.....K.....N..K.....	480
Cow	481	SARMETSCSLLLEQTQPTTSLIRKNKDEHLSQNVLVEENPDNSYADTNVKPTVKNYANKSL	540
Giraffe	481V.F..S.....A.S...T...P....A.KT...HP..DL.A.....	540
Okapi	481I.....S...I.....GK.....L.....	540
Cow	541	FTENLKSKKRKEIDDLAIEDEVLEQLFKDTELESEVVKVQKQEEDINVRKRLRLDKETN	600
Giraffe	541	...K...N.....A.....P...M...	600
Okapi	541	...K...E.....E.....T...P...I...	600
Cow	601	VTFNDETIPESNKISQENEIKKKCELKKESSLWSTKELSNCELQDGDEMPLPKKVLLTEFR	660
Giraffe	601	..C...T.....G.....G.....R.....	660
Okapi	601	A.....E.....G.P.....	660
Cow	661	SLVVCNSTSRNASNVNNDY GELKNFKKFKKVTFPGAGKLPHIIGGSDLIAHHARKNTELE	720
Giraffe	661	...R.....S.....	720
Okapi	661S.....	720
Cow	721	EWLRQEME VQNQHAKEDSLADDLFRYNPNVKRRR	754
Giraffe	721I.....	754
Okapi	721	754

Newick Tree of Mammalian NBN

```
(African_Bush_Elephant:0.0703092, (((((((Gorilla:0.00656225, Humans:0.00142722):0.000893651,
(Bonobo:4.3724e-05, Chimpanzee:0.00794575):0.00717268):0.00826899,
(Northern_White_cheeked_Gibbon:0.00747707, Siamang:0.00453136):0.00596178):0.00471753,
(Wolf_s_Mona_Monkey:0.00776341, Olive_Baboon:0.00693344):0.0197714):0.018193,
Bolivian_Red_Howler:0.0544405):0.0568263, Phillipine_tarsier:0.0885859):0.0246784,
(European_Rabbit:0.116838, ((White_Rhinoceros:0.0799503, Horse:0.0831269):0.00665034,
(Giant_Panda:0.0434426, Dog:0.088366):0.00765649,
Siberian_Tiger:0.0672528):0.0333086):0.00192851, (Bactrian_Camel:0.104846,
((Bottlenose_Dolphin:0.0231422, Sperm_Whale:0.0277381):0.00210022,
Minke_Whale:0.0160832):0.0276671, (giraffe:0.0393298, ((Tibetan_Antelope:0.0110148,
(Sheep:0.00560167, Goat:0.0037381):0.00645804):0.0117507, (Water_Buffalo:0.00736511,
(Cow:0.00137023,
Wild_Yak:0.00128582):0.0100501):0.0129403):0.00678369):0.0613014):0.015145):0.0124811):0.00567769
):0.0019239):0.0703092);
```



0.03

Locus Name: Nibrin (NBN)

Locus Name: Meiotic Recombination 11 Homolog A (MRE11A)

ENSBTAT0000011748 MRE11A-201 component of MRN complex dsDNA break repair, chromosome integrity
 mouse: chromosome instability human: Ataxia-telangiectasia-like disorder 1 (ATLD1)
 [MIMOUSE:604391]: A rare disorder characterized by progressive cerebellar ataxia, dysarthria, abnormal eye movements, and absence of telangiectasia. Hypersensitivity to ionizing radiation.

PP2: All benign
 PSG: D647S

Giraffe: N34H UIS, A539D UIS, A564T UPS, A566G UPS, S590L UPS, D647S UIS
 Giraffe/Okapi: F660L UPS, M699V UPS

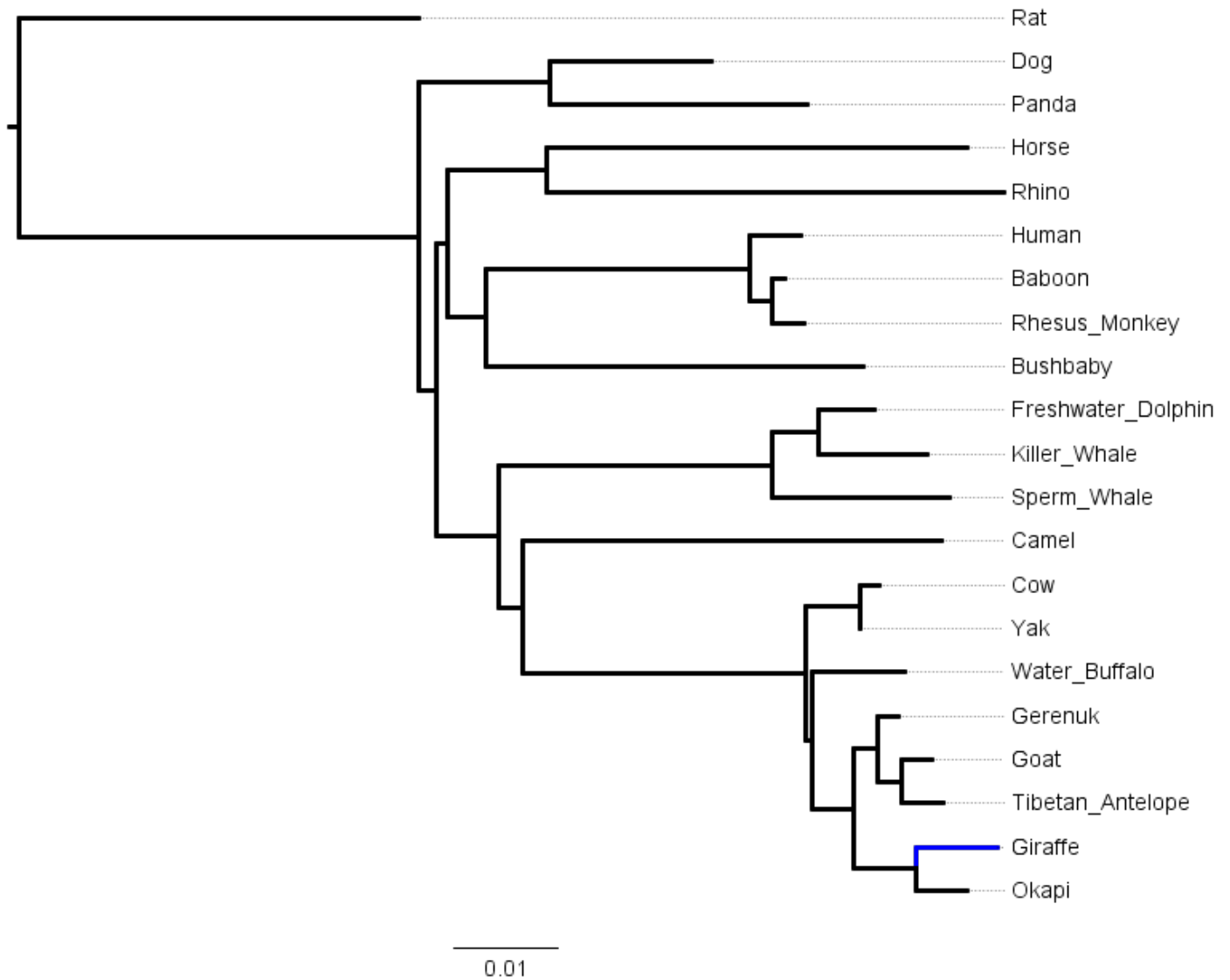
Protein sequence Alignment of Cow, Giraffe and Okapi MRE11A

Cow	1	MSPADALDDENTFKILVATDIHLGFMEKDAVRGNDTFVTLDEILRLAQENDVDFILLGGD	60
Giraffe	1H.....F.....	60
Okapi	1F.....	60
Cow	61	LFHENKPSRKTLLHTCLELLRKYCMGDRPVQFEILSDQSVNFGFSKFPWVNYQDGNLNISV	120
Giraffe	61I	120
Okapi	61I	120
Cow	121	PVFSIHGNHDDPTGADALCALDILSCAGFVNHFGRSMSVEKIDISPVLLQKGSTKIALYGL	180
Giraffe	121V.....	180
Okapi	121V.....	180
Cow	181	LGSIPDERLYRMFVNKKVTMLRPKEDENSWFNLFVIHQNRSKHGSTNFIPFQFLDDFIDL	240
giraffe	181	240
okapi	181	240
Cow	241	VIWGHEHECKIAPTQKNEQQLFYVSQPGSSVVTSLSPGEAVKKHIGLLRIKGRKMMQKIP	300
Giraffe	241	300
Okapi	241	300
Cow	301	LRTVRQFFMEDVVLADHPDIFNPDNPKVTQVIQNFCEKVEEMLENAERERLGNSSQPEK	360
Giraffe	301D.....R.....	360
Okapi	301D.....G.....R.....	360
Cow	361	PLIRLRVDYSGGFEPFVLRFSQKFVDRVANPKDVIHFFRHREQKENTGEEINFGKFISK	420
Giraffe	361	420
Okapi	361	420
Cow	421	PSEGTTLRVEDLVKQYFQTAEKNVQLSLLTERGMGEAVQEFVDKEEKDAIEELVKYQLEK	480
Giraffe	421	480
Okapi	421	480
Cow	481	TQRFLKERHIDALEDKIDEVRRFRFRESRQKNTNEEDDEVREAMSRARALRSQSEDAASAL	540
Giraffe	481D.....	540
Okapi	481	540
Cow	541	TAEDLMSIDLAEQMADSDSISIKAAANKGRGRGRGQRGGRGQNSMSRRGSQRGRAGTSLE	600
Giraffe	541IT.G.....V.....L.....	600
Okapi	541IM.....V.....	600
Cow	601	ISTQGRGSKATTSTSRNMSIIDAFKSTRQQPSRVATKNTYEVIEVDESDEEDVFLTTF	660
Giraffe	601S.....I.....L	660
Okapi	601I.....L	660
Cow	661	KTDQRGSSTSSSSKPMSSQSQITKGVDFESDEEDDDDDPFMNLSCLRNR	709
Giraffe	661AR.....V.....	709
Okapi	661AR.....E.....V.....V.....	709

Newick Tree of Mammalian MRE11A

(rat:0.038408, ((Dog:0.0155616, panda:0.024859):0.0125348, (((Horse:0.0403516, rhino:0.0438057):0.00950569, ((Human:0.00498374, (baboon:0.0011894, rhesus_monkey:0.00307501):0.00212889):0.0252834, bushbaby:0.0362617):0.00368096):0.001105, ((Freshwater_Dolphin:0.00537519, Killer_Whale:0.0103065):0.00456771,

Sperm_Whale:0.0170226):0.0262469, (camel:0.0401972, ((Cow:0.0017424, Yak:0):0.00531566,
 (Water_Buffalo:0.00877464, ((Gerenuk:0.00202422, (Goat:0.00302343,
 Tibetan_Antelope:0.00407389):0.00223722):0.00230315, (Giraffe:0.00787458,
 Okapi:0.00490096):0.00594156):0.00393068):0.000720289):0.0270679):0.00240898):0.00592855):0.00170
 572):0.038408);



Locus Name: Meiotic Recombination 11 Homolog A (MRE11A)

Locus Name: Nucleic Acid Binding Protein 1, SOSB2, (NABP1)

ENSBTAT00000024821 NABP1-201 component of SOSS complex dsDNA break repair, chromosome integrity
no mutation in m/h described

PP2: (Giraffe) G157C; (Okapi) G157V

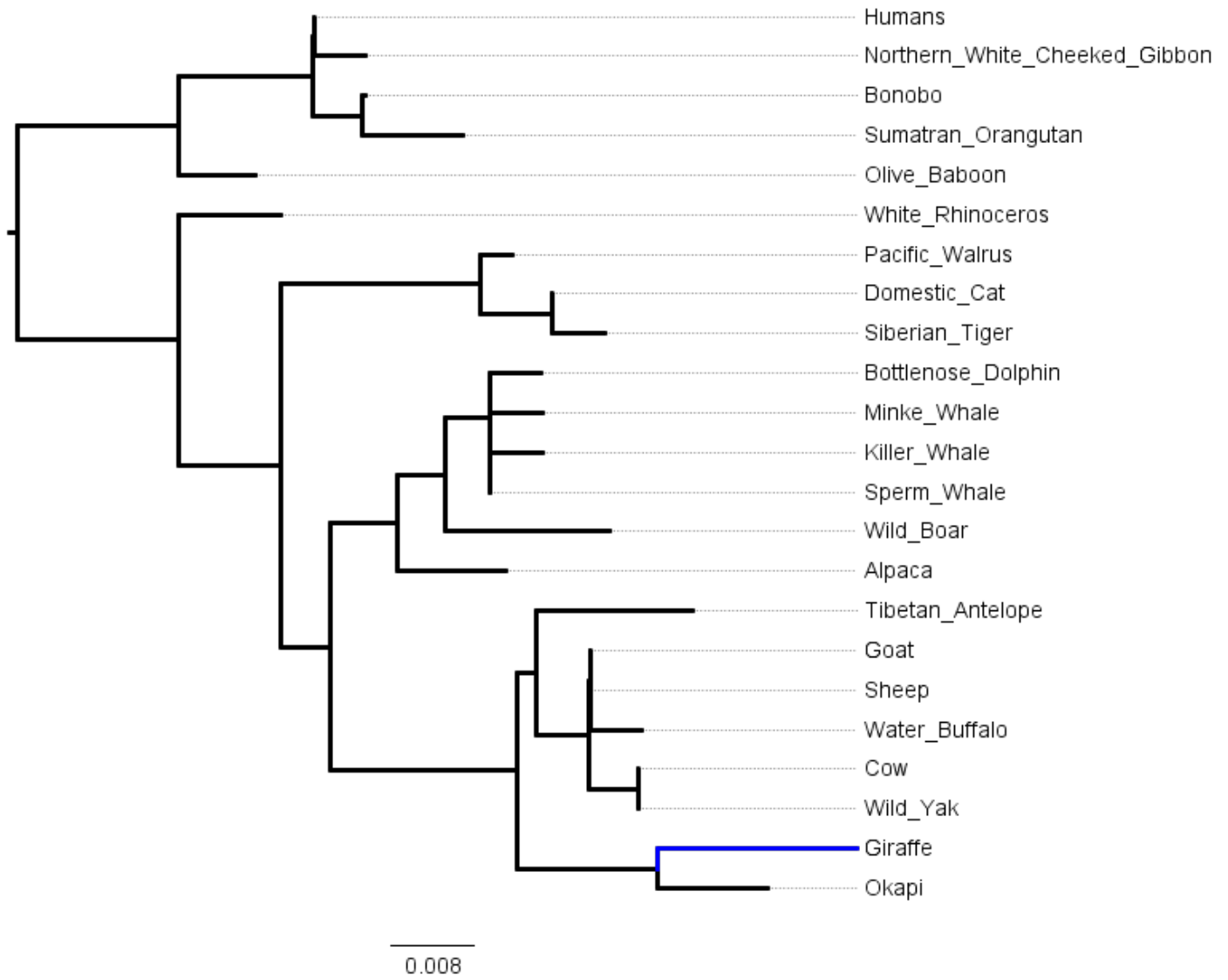
Giraffe: P8F UPS, K15R UIS, S139R UPS, G157C UPS, A185P UIS
Giraffe/Okapi: T192S UIS

Protein sequence Alignment of Cow, Giraffe and Okapi NABP1

Cow	1	MNGVRDPPLFIKDIKPLKLNLVVFFIVLEIGRVTKTKDGHEVRSCKVADKTGSITISVWD	60
Giraffe	1F.....R.....	60
Okapi	1N.L.....	60
Cow	61	EIGGLIQPGDIIRLTRGYASMWKGLTLYTGRGGELQKIGEFMVSSELPNFSEPNPDYR	120
Giraffe	61	120
Okapi	61	120
Cow	121	GQQNKGAHNEQKNNMNNNNVGTGTGTFGPMGNVQTGAEARGCQFSYAGRSNGRGPINPQ	180
Giraffe	121R.....V.....CP.....L....	180
Okapi	121V.....VP.....L....	180
Cow	181	LPGTANNQTVMTTISNGRDPRAFKR	206
Giraffe	181P.....S.....	206
Okapi	181S.....	206

Newick Tree of Mammalian NABP1

((((Humans:1.35158e-05, Northern_White_cheeked_Gibbon:0.00490052):0.000173763,
(Bonobo:0.000230472, Sumatran_Orangutan:0.00962198):0.0047895):0.0126725,
Olive_Baboon:0.00724493):0.0153951, (White_Rhinoceros:0.00969271, ((Pacific_Walrus:0.0029945,
(Domestic_Cat:0, Siberian_Tiger:0.00492291):0.00688252):0.0190245,
(((Bottlenose_Dolphin:0.00487486, (Minke_Whale:0.00492623, Killer_Whale:0.00492623):2.9495e-05,
Sperm_Whale:0):5.13674e-05):0.00420664, Wild_Boar:0.015666):0.0046031,
Alpaca:0.0103256):0.00635077, ((giraffe:0.018899, okapi:0.0105192):0.0133158,
(Tibetan_Antelope:0.0147935, ((Goat:0, (Sheep:4.49295e-05, Water_Buffalo:0.00486911):4.64641e-
05):0.000157009, (cow:0, Wild_Yak:1.22161e-
05):0.00472713):0.00489268):0.00182553):0.0178111):0.00476268):0.0096721):0.0153951);



Locus Name: Nucleic Acid Binding Protein 1, SOSB2, (NABP1)

Locus Name: Nudix (Nucleoside Diphosphate Linked Moiety X)-Type Motif 15 (NUDT15)

ENSBTAT00000025978 NUDT15-201 8-oxo-dGTP diphosphatase DNA repair
human: SNP associated with thiopurine-induced early leukopenia

PP2: (Giraffe) G41C,

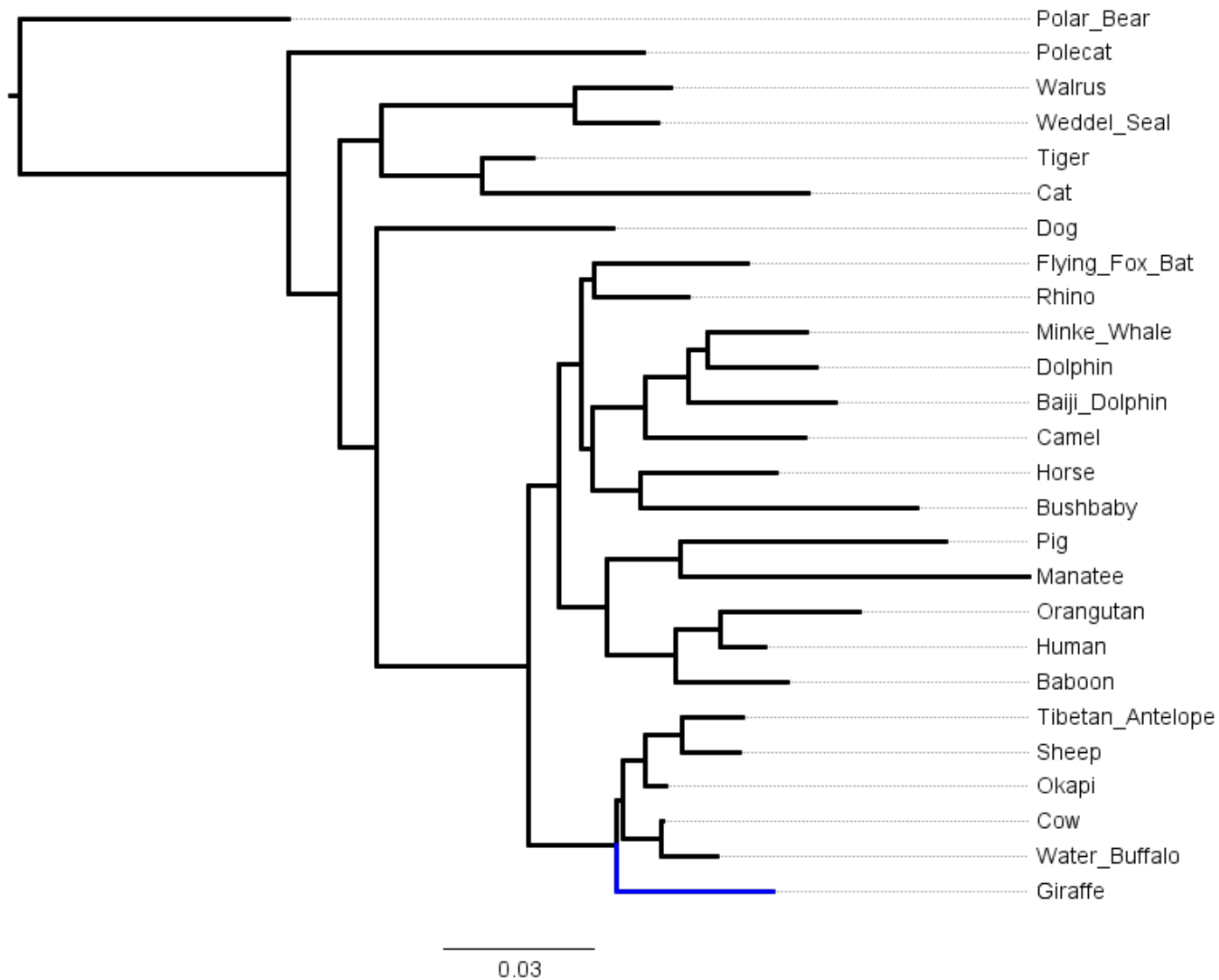
Giraffe: F38S UPS, G41C UIS, S42G UPS

Protein sequence Alignment of Cow, Giraffe and Okapi NUDT15

Cow	1	MTASVEPRGRRPGVGVVVVTSGRHPRCVLLGKRKGSFGAGSFQLPGGHLEFGETWEECA	60
giraffe	1S..CG...S.....	60
okapi	1R.....	60
Cow	61	QRETWEEAALHLKKNVRFASVVNSFIEKENYHYVTILMKGEVDLTHDSEPKNVEPEKNESW	120
Giraffe	61V.....	120
okapi	61V.....	120
Cow	121	EWVPWEEFPPLDQLFWGLRCLKEQGYDPFKEDLDHLVGKYGSHLEVNKEIH	171
Giraffe	121A.....T.	171
okapi	121A.....	171

Newick Tree of Mammalian NUDT15

(polar_bear:0.054059, (polecat:0.0716555, ((walrus:0.0192266, weddel_seal:0.0164991):0.0390647, (tiger:0.0104963, cat:0.0655627):0.020215):0.00836249, (dog:0.0476442, (((flying_fox_bat:0.0308995, rhino:0.0191318):0.00240289, (((minke_whale:0.0198181, dolphin:0.0219912):0.00377589, baiji_dolphin:0.029413):0.00875072, camel:0.0323124):0.0104892, (horse:0.0271261, bushbaby:0.0555545):0.0096214):0.00228131):0.00462611, ((pig:0.0534803, manatee:0.0699637):0.0149886, (orangutan:0.0281216, human:0.00915845):0.0089688, baboon:0.0225089):0.0140251):0.00950781):0.00607612, (giraffe:0.0315998, ((tibetan_antelope:0.0121413, sheep:0.0115307):0.00753406, okapi:0.00430192):0.00439255, (cow:0.000458753, water_buffalo:0.0113064):0.00758047):0.00142054):0.0176639):0.0304707):0.00753779):0.0103838):0.054059);



**Locus Name: Nudix (Nucleoside Diphosphate Linked Moiety X) -
Type Motif 15 (NUDT15)**

Locus Name: SAC3 domain containing 1 (SAC3D1)

ENSBTAT0000002904 SAC3D1-201 SAC3 domain containing protein centrosome duplication and mitotic progression

mouse: null allele had increased numbers of myeloid and erythroid progenitor cells. Mice homozygote for a null allele had these features plus mild spleen and thymus hyperplasia, an increased T cell proliferative response, and enhanced IgM secretion by B cells to IL-5.

PP2: (Giraffe) P36S, D46H

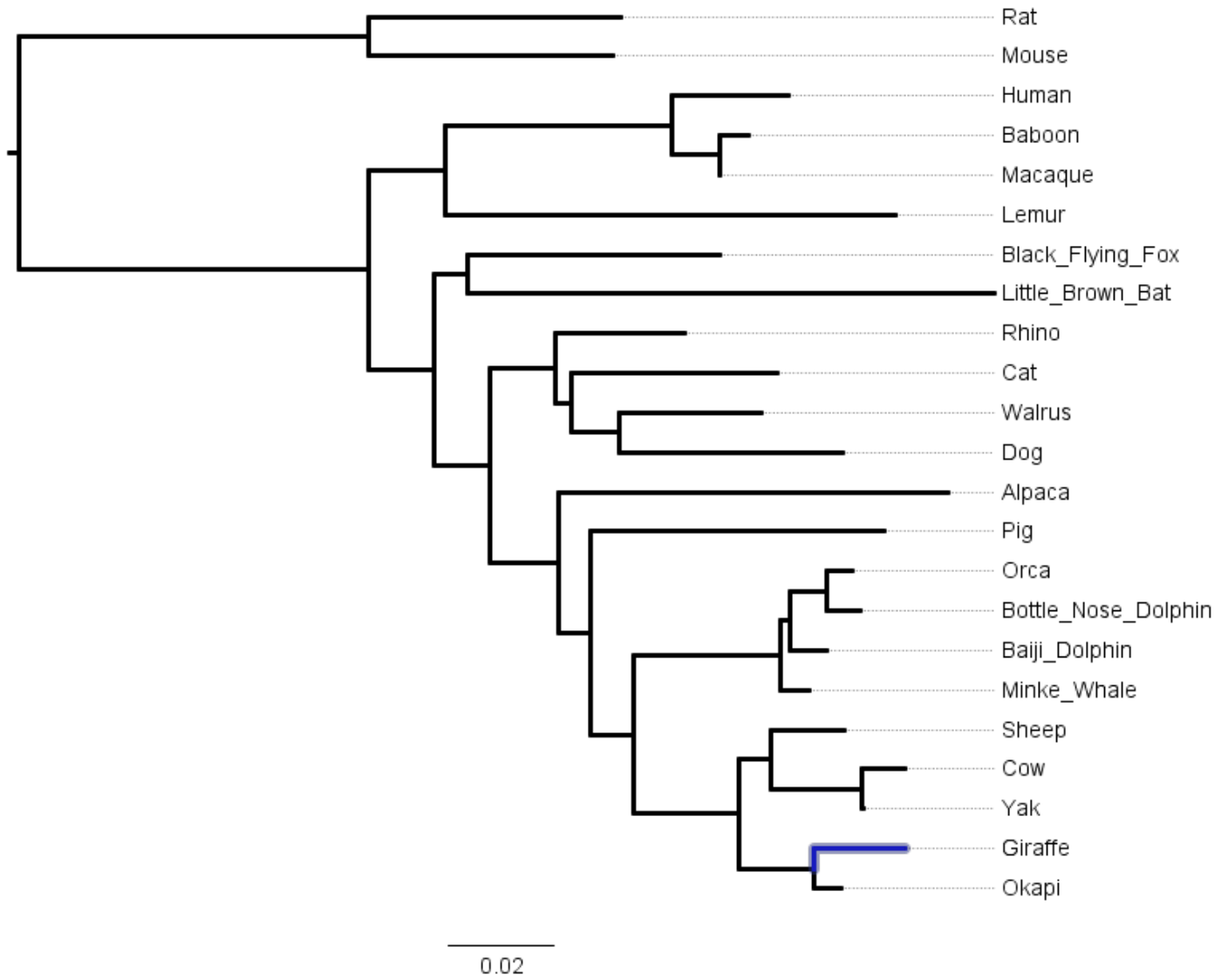
Giraffe: P36S UPS, D46H UIS, E85D UIS, GQ 269-270 deletion UIS
Giraffe/Okapi: T90N UPS, A228S UPS, G302E UIS

Protein sequence Alignment of Cow, Giraffe and Okapi SAC3D1

Cow	1	MPGYELPVGTCCLDMCPAAERAQREKERLHRFEVVPGCRRDRPRADPQRAVKEYSRPAAG	60
Giraffe	1AS..PG.....H.....	60
Okapi	1A....G.....	60
Cow	61	KNRPPPSQLRPPSVLLATVRYLASEVAERTDASCAEVASFVADRLRAVRLDLALQTASDV	120
Giraffe	61	.I.....D...N.....S....	120
Okapi	61	.I.....N.....S....	120
Cow	121	ETALVLESALAVLLAVVARLGNATHGVPDPLLQAQVQESFGSLRRCYALGAGPHPRQA	180
Giraffe	121A.....	180
Okapi	121	.A.....A.....	180
Cow	181	TFQGLFLLYNLGSVEALHEILRLPALRSCPALRTALAVDSAFREGNAARLFRLRLTPY	240
Giraffe	181V.Q.....A.....S.....M...	240
Okapi	181V.Q.....A.....F.....S.....	240
Cow	241	LQSCAVQCHVGRARRGALARLARLALSTPGQTLPLGFMVHLLALDGPNEARDLCQAHGLPL	300
Giraffe	241--.....K.....	298
Okapi	241K.....	300
Cow	301	DGQERVVFLRGRYTEEGLPPAGTCQIILVGNKLGRTLEDVAMAEEDAEVDRPTTEV	358
Giraffe	299	.E.....V.....V.....P.A	356
Okapi	301	.E.....C.....V.....V.....-.....P.A	355

Newick Tree of Mammalian SAC3D1

((rat:0.0481168, mouse:0.0464892):0.0668792, (((human:0.0222544, (baboon:0.00562448, macaque:0):0.00904964):0.0431507, lemur:0.0859029):0.0146379, ((black_flying_fox:0.0479258, little_brown_bat:0.100247):0.00646711, (rhino:0.0247291, (cat:0.039166, (walrus:0.0270068, dog:0.0424409):0.00919329):0.00319157):0.0123405, (alpaca:0.074389, (pig:0.0561884, (((orca:0.0048984, bottle_nose_dolphin:0.00633791):0.00712948, baiji_dolphin:0.00700041):0.00168236, minke_whale:0.00535034):0.0279719, ((giraffe:0.0173528, okapi:0.00531299):0.0142441, (sheep:0.0140873, (cow:0.00822133, yak:0.000217642):0.0173079):0.00614948):0.0199847):0.00830785):0.00618363):0.0129237):0.0107031):0.0124859):0.0668792);



Locus Name: SAC3 domain containing 1 (SAC3D1)

Locus Name: HAUS augmin-like complex, subunit 2 (HAUS2, CEP27)

ENSBTAT00000045340 CEP27-201 centrosomal protein 27 centrosome assembly, cytokinesis
no mutation in m/h described

PP2: (Giraffe) E59K; (Giraffe/Okapi) R110K, N186D

Giraffe: E59K UIS, S83T UPS, A234I UPS

Giraffe/Okapi: R110K UIS, N186D UIS, K213T UIS

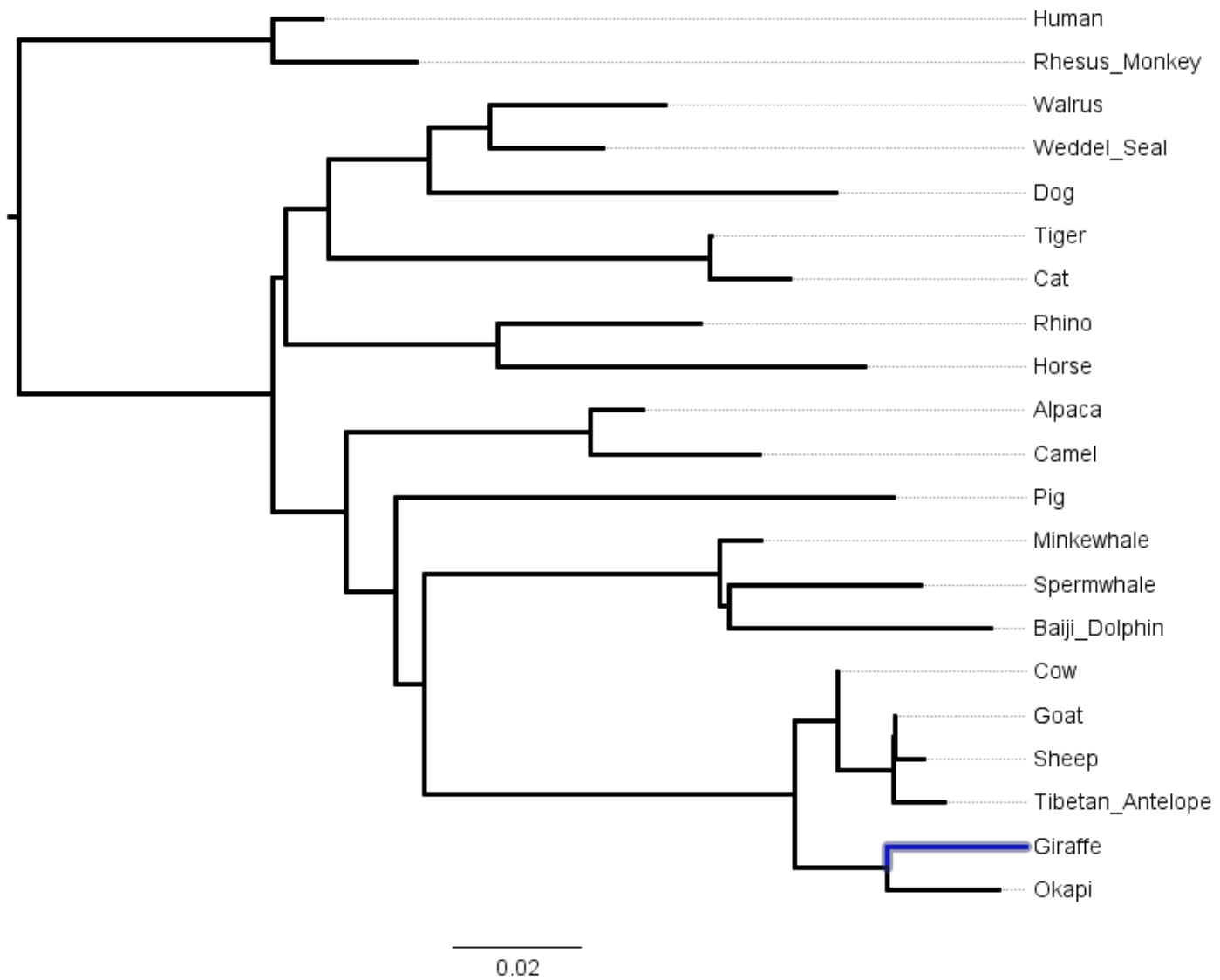
Okapi: V140I UIS, E182K UIS, L213V UPS

Protein sequence Alignment of Cow, Giraffe and Okapi HAUS2

Cow	1	MAAANPWPDPATAPNAAGLLGLGHFITSELVTEEMLNISKKSTSCFVNFSRLQQITDIQAEI	60
Giraffe	1	..T.S.....Q.....K.	60
Okapi	1Q.....	60
Cow	61	YQKNLEIELLSLEKDAADVHPSFLAQKCHSLQSMNNHLEAVLKEKRSLRQRLLKPMCQG	120
Giraffe	61T.....K.....	120
Okapi	61K.....	120
Cow	121	NLPIEAVYHRYMVHLLLELAVTFIERLEDHLETIRNIPHLDADLKKMSTALAKMDILVTET	180
Giraffe	121	180
Okapi	121I.....	180
Cow	181	EELAENILKWREQQKEVSSYIPKILAEKNSLHKHDVIVPPLPLTSKVNVTINAK	235
Giraffe	181D.....T..A.....I.	235
Okapi	181	.K...D.....F.....T..A.....V.....	235

Newick Tree of Mammalian HAUS2

((human:0.00781634, rhesus_monkey:0.0224282):0.0395964, (((walrus:0.0273919, weddel_seal:0.0177438):0.00942989, dog:0.0634805):0.0157581, (tiger:0.000307832, cat:0.0125407):0.059509):0.00673875, (rhino:0.0316379, horse:0.0574269):0.033083):0.00201224, ((alpaca:0.0081809, camel:0.0264615):0.0381112, (pig:0.077705, (minkewhale:0.00665894, (spermwhale:0.0297894, baiji_dolphin:0.0407829):0.00156408):0.0460076, (cow:0, (goat:0, sheep:0.00431966):0.000442935, tibetan_antelope:0.00812269):0.00862458):0.00663573, (giraffe:0.0215924, okapi:0.0174681):0.0142901):0.0578789):0.00438738):0.00787604):0.0114256):0.0395964);



Locus Name: HAUS augmin-like complex, subunit 2 (HAUS2, CEP27)

Locus Name: RCC1 Domain Containing 1 (RCCD1)

ENSBTAT00000024803 RCCD1-201 histone demethylase complex chromosome segregation
no mutation in m/h described

PP2: (Giraffe) P157R; (Giraffe/Okapi) R5C, A177T, A283S

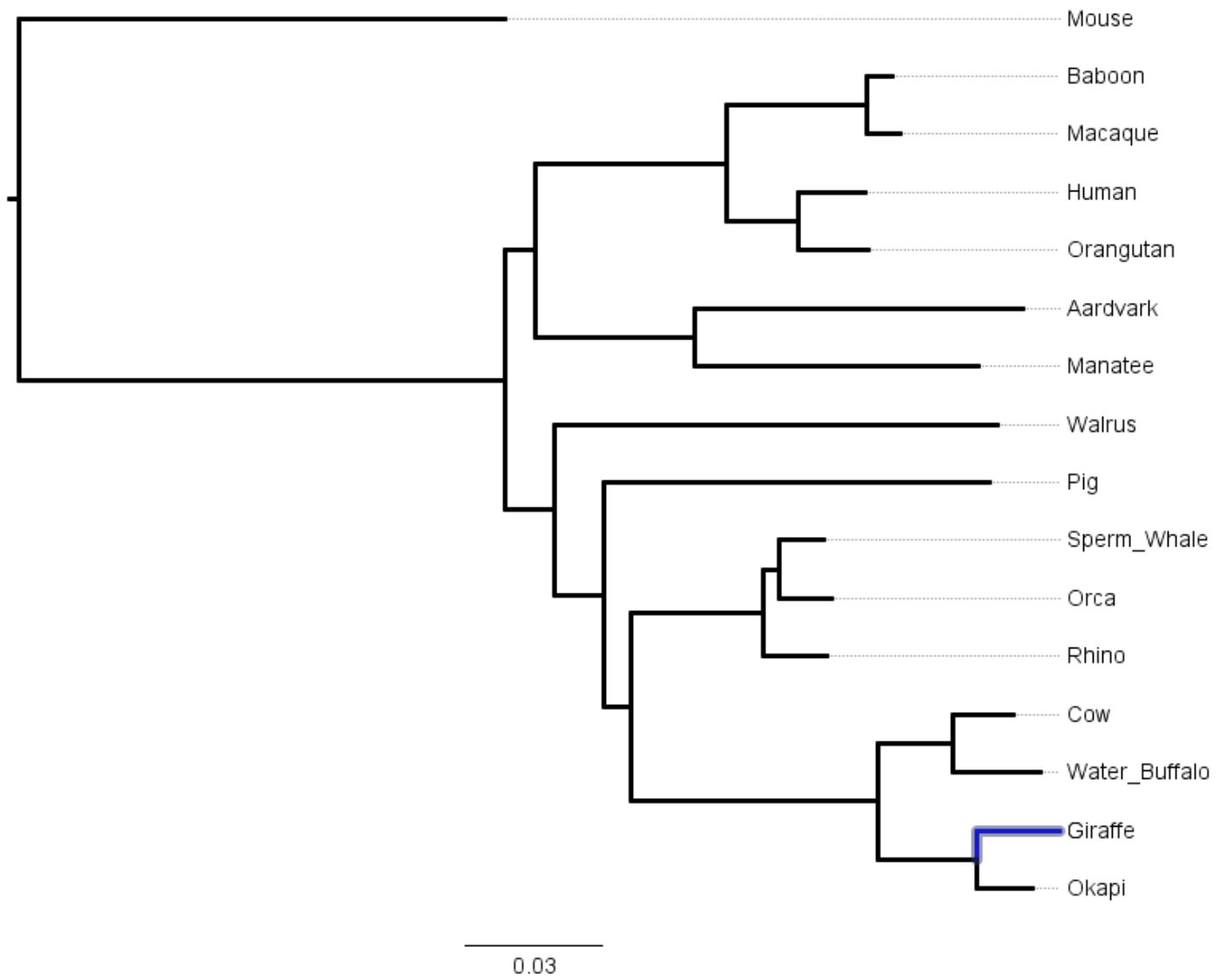
Giraffe: E3K UPS, E122Q UPS, H123S UPS, P157R UIS, P200S UPS, A214V UIS
Giraffe/Okapi: R5C UPS, G124V UPS, A177T UPS, T257S UPS, S275P UPS, S298T UPS

Protein sequence Alignment of Cow, Giraffe and Okapi RCCD1

Cow	1	MDEERRGTWFGFGFCGFGQALGSGGLGRQVHSPEPLRTPGGSLGVCRVASWSYTAFAVTRG	60
Giraffe	1	..K.C.....D.....	60
Okapi	1C.....D.....	60
Cow	61	GRVQLSGAAGGTADGCTDAWASEELLVLLRAGPGAGAEIQAWAPGSAMRGDPLWSQAVQE	120
Giraffe	61A.G.....L..E.....	120
Okapi	61A.G.....K.....L..E.....	120
Cow	121	AEHGPSRDETQAGLLPLLPCARAYVSPRPPFYRPLAPTLRARRLELGAEHALLLDAAGQV	180
Giraffe	121	.QSV.....V.P.....R.....T...	180
Okapi	121	..RV.....P.....V.....T...	180
Cow	181	FSWGAGRHRGQLGHGTLEAEPEPRLLLEALQGLRMAEVAAGGWHSVCLSETGDIYIWGNES	240
Giraffe	181S.....P.V.....	240
Okapi	181P.....	240
Cow	241	GQLALPTKSLAEDGKTTAGEASGLEEDGSEVKRGSAGEDGAPAPFIAVQFPALDLSPG	300
Giraffe	241S.....D...Q...VPG.....S.....T..	300
Okapi	241S.....D...Q...VPG.....S.....T..	300
Cow	301	SEAVKVSCGRSHTAVLTRTGELYTWGWGKYQLGHKDTTTLDRPCRVEYFVDKQLQVRTV	360
Giraffe	301	360
Okapi	301	..I.....	360
Cow	361	SCGPWNTYVYAVEKEKS	377
Giraffe	361	377
Okapi	361--	375

Newick Tree of Mammalian RCCD1

(mouse:0.105706, (((baboon:0.00581647, macaque:0.00757101):0.0303074, (human:0.0144056, orangutan:0.0152905):0.0155866):0.0415576, (aardvark:0.0712829, manatee:0.0615056):0.0347084):0.00671051, (walrus:0.0965316, (pig:0.0838172, ((sperm_whale:0.00979843, orca:0.0114241):0.0036096, rhino:0.0138793):0.0287441, ((giraffe:0.0176997, okapi:0.0119964):0.0215354, (cow:0.0132835, water_buffalo:0.01907):0.016207):0.0539794):0.0056637):0.0108573):0.0107874):0.105706);



Locus Name: RCC1 Domain Containing 1 (RCCD1)

Locus Name: HAUS Augmin-Like Complex, Subunit 6 (HAUS6)

ENSBTAT00000031479 HAUS6-201 mitotic spindle assembly centrosome integrity cytokinesis
 human: GWAS study mapped pulmonary tuberculosis susceptibility to 8 loci including HAUS6

PP2: (Giraffe) A53T, C699R, L882G; (Giraffe/Okapi) G26Y, L127T, A194T, K342G, S854H; (Okapi)
 L127T, P500Q, L840Q, S899Y

PSG: L882G

Giraffe: A52T UIS, N240S UPS, D686G UIS, C700R UIS, L882G UPS

Giraffe/Okapi: C26Y UPS, I127T UPS, A194T UIS, F799S UIS, S854H UPS, R297S UPS

Protein sequence Alignment of Cow, Giraffe and Okapi HAUS6

Cow	1	MSSAWVTSFEKARLWMYLQALGFEPCLATIACGNTVSHTQFGVNMFDKLNRFDAFHIVSYF	60
Giraffe	1Y.....H.....T.....	60
Okapi	1Y.....H.....	60
Cow	61	LFQTLDKSLTKEVFKHCWPPFDQKRDFEVRKLFCEWLKKISAECGSSFPQVVGSLFLFPV	120
Giraffe	61E.....C.....	120
Okapi	61C.....	120
Cow	121	GPKFIHIMYHFARFVAVKYIKTHSKNSSIRFTETFNVKPQDLHICLARCLVARNRFLQVL	180
Giraffe	121T.....	180
Okapi	121T.....	180
Cow	181	QREDCVTRKYQENAQLSVKQVRNLRSECMGLENQIKKMEPCDDQSNIQEKIQKVRSLWTN	240
Giraffe	181T.....Q..M.....S	240
Okapi	181T.....Q.....S	240
Cow	241	VNETLMFLEKEREVSSVLSLDNNYTLDGTDIAINIPSLLLDKIEKQMCQLHTGNIYEAG	300
Giraffe	241N.....I.....	300
Okapi	241N.....I.....	300
Cow	301	KLNILTVPFWLLNEVLKVMKCECCQTDQARLTIDLHFLEKETRFQKERLSDLKHMRYKITE	360
Giraffe	301Y.....R..G..R.....	360
Okapi	301Y.....R..G..R.....	360
Cow	361	ALKTIRHSIVEKQEEWHKKWKEFLGLSPFSIIKGSTPAVDLLPPMSPLSFDPAEEAYAR	420
Giraffe	361	D.....I.....S.....	420
Okapi	361	D.....I.....R.....	420
Cow	421	SILLQYPASLPVTPKQHIQENNCRRASDTLETKSDPPNSPASFPPLQVPVPLGGDIVTLE	480
Giraffe	421V.....A.....L.....S.....	480
Okapi	421V.....A.....L.....S.....	480
Cow	481	KDTKLVTLREKNETVPKKTPEFNVENSSSNIVKNTDSSACGGSLPAKKSNPQKEQDHL	540
Giraffe	481	.E..I.....K..D.....A.....A.....	540
Okapi	481	.N..I.....T..Q..K..D.....A.....S.....	540
Cow	541	VEEVARAVLSNSPQLSEEKVKLEELIDSLISNPFLTRSQIPRTPENLISEIRSSWRKAV	600
Giraffe	541G.....D.....	600
Okapi	541G.....D.....	600
Cow	601	DTEDNRSTEPIQVDTERREELPESLPVHNQEFMSASFLSAATVSNSSHSHLPEEKVVS	660
Giraffe	601	EI.....H.....D.....	660
Okapi	601	EI.....H.....D.....L..	660
Cow	661	DCLECVQKPVVTTTCIGEPPTQNPDDLKNDIICMQLDCTTLQNKLETSQIETFSPAV	720
Giraffe	661G.....R.....H.....	720
Okapi	661N.....	720
Cow	721	GNRRNVLSSEEDNIKISDQSKASYKDFSMYNSMLWNCFQVSSEISSFKDGFILHET	780
Giraffe	721E.....HK.....G.....	780
Okapi	721E.....HK.....G.....	780
Cow	781	LPEVGHISLISPSSTEATFNLEPNSPMHSGIFTEDVVGEKQTTPESDFNLQATCSGYEAL	840
Giraffe	781SK.....R.....	840
Okapi	781SK.....R.....R.....Q	840

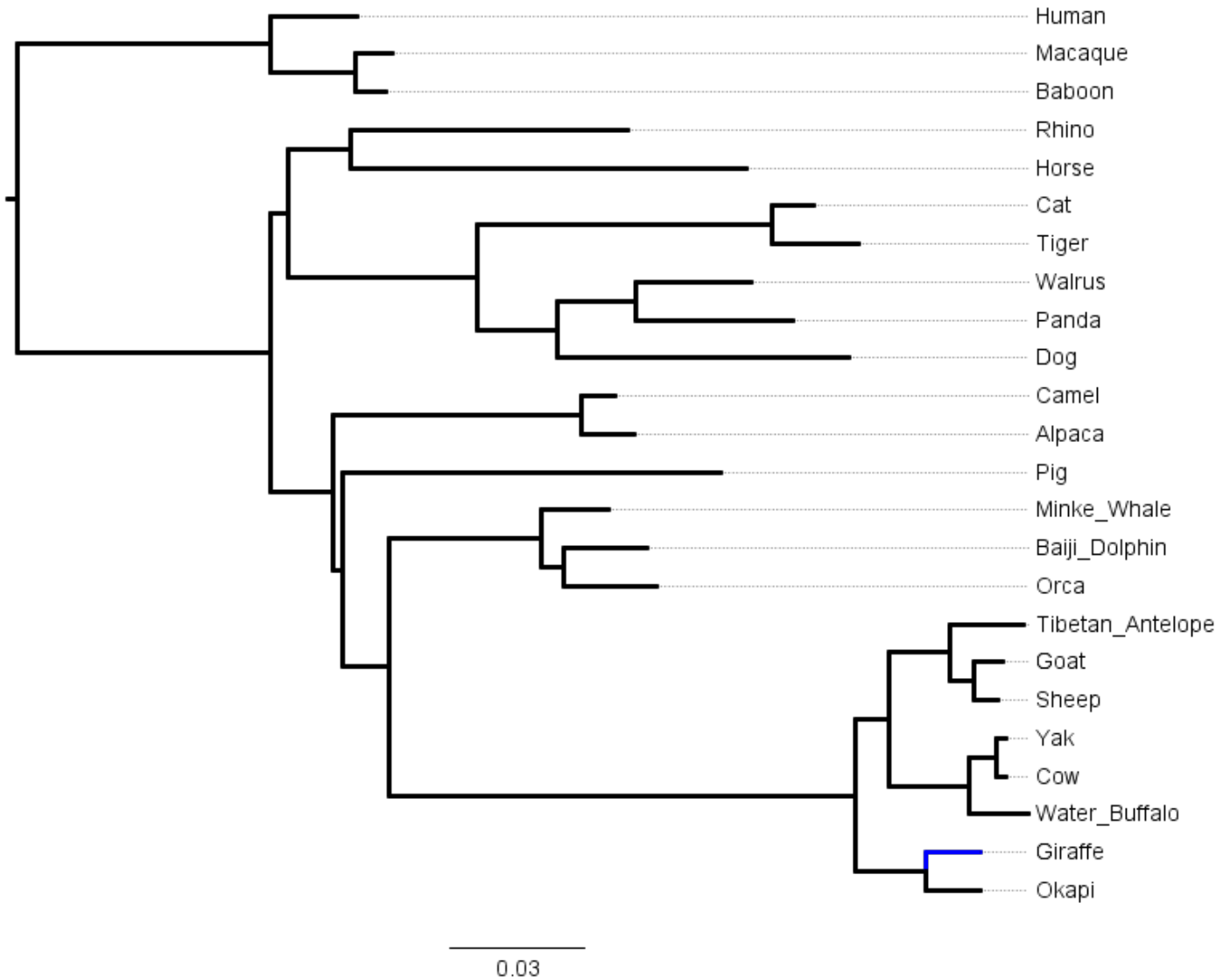
Cow	841	KKSPSKQREEIYLSNPEILERHKPELSLTPQKMQTDDMLNFLGIHDLHIDYTKPSSRMSL	900
Giraffe	841	...L.....H.....L.S.....N.....G.....S...	900
Okapi	841	...L.ER.....H.....L...F...N.....S.Y.	900
Cow	901	GERKRSLSPLIKFSPVEQLKTTIPCSLGELLSNLTEEEIILNKSLDAEVSPSDSTR	956
Giraffe	901N.....P.....L.S.....K.....L..	956
Okapi	901N.....P.....K.....L..	956

Newick Tree of Mammalian HAUS6

```

((human:0.0194397, (macaque:0.00812563, baboon:0.00662755):0.019272):0.0570848,
(((rhino:0.0623698, horse:0.0890501):0.0140823, ((cat:0.00924832, tiger:0.0194657):0.0663829,
((walrus:0.0260784, panda:0.0356352):0.017548, dog:0.0656536):0.0180032):0.0426137):0.00404989,
((camel:0.00742002, alpaca:0.0119366):0.0560334, (pig:0.0853386, ((minke_whale:0.0149833,
(baiji_dolphin:0.0186215, orca:0.0206927):0.00512539):0.034174, ((tibetan_antelope:0.0165858,
(goat:0.00656066, sheep:0.0054682):0.00551236):0.0137305, (yak:0.00210216,
cow:0.00209073):0.00634826, water_buffalo:0.0132339):0.0181573):0.00730959, (giraffe:0.0121769,
okapi:0.0121782):0.0157611):0.105023):0.0106529):0.00214122):0.0141138):0.0570848);

```



Locus Name: HAUS Augmin-Like Complex, Subunit 6 (HAUS6)

Locus Name: Rho GTPase Activating Protein 15 (**ARHGAP15A**)

ENSBTAT0000061453 ARHGAP15-201 Rho GTPase-activating protein trypanosome resistance
mouse: reduced leukocyte numbers and abnormally shaped macrophage. Chemotactic responses of
macrophage are normal while neutrophile chemoattraction and bacterial pagocytosis are increased.

PP2: (Giraffe) L14R, I177T

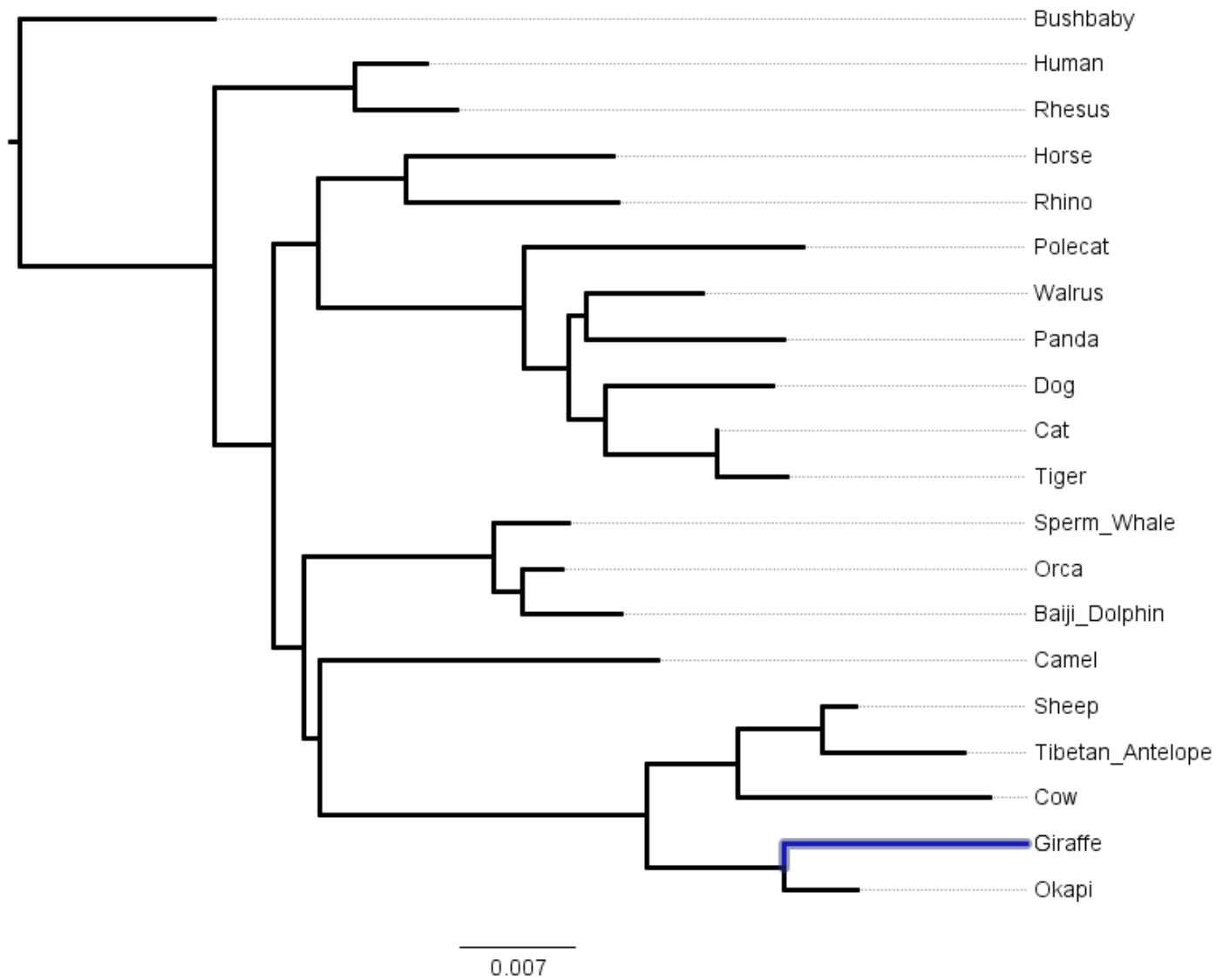
Giraffe: Q122P UIS, I177T UIS

Protein sequence Alignment of Cow, Giraffe and Okapi ARHGAP15A

Cow	1	MQKSTNSDIPVETLNPTRQGTGAVQMRIKNANSHHDRLSQSKSMILTEVGKVTEPISRHR	60
Giraffe	1T...R.....DA.....	60
Okapi	1T.....D.....V....	60
Cow	61	RNHSQHILKDVIPPLEQLMVEKEGYLQKAKIADGGKLRKNWTTSWIVLSSRKIEFYKES	120
Giraffe	61V.....S.....N.....	120
Okapi	61V.....S.....N.....	120
Cow	121	KQQALSNMKTGNKPESVDLCGAHIEWAKEKSSRKNVFQITTLSGNEFLLQSDIDFIILDW	180
Giraffe	121	.P.....A.....T.E.	180
Okapi	121A.....	180
Cow	181	FHAIKNAIDRLPKDPSSHRSRNLELFKIQRSSSTELLSHYDSDTKEQKPEHRKSLMFRLLH	240
Giraffe	181V.....	240
Okapi	181I.....	240
Cow	241	SASDTSKDNRVKSRLKKFITRRPSLKTLEKGLIKDQIFGSHLHTLCEREKSTVPRFVKQ	300
Giraffe	241N.....	300
Okapi	241N.....	300
Cow	301	CIEAVEKRGLDVDGIYRVSGNLATIQLRFIVNQEEKLNLDDSQWEDIHVVTGALKMFFR	360
Giraffe	301	360
Okapi	301	360
Cow	361	DLPEPLFPYSFFEQFVEAIAIKKQDNNTRIEAIAKSLVQKLPNPNRDTMKVLFGHLTKIVARA	420
Giraffe	361S.....	420
Okapi	361S.....K.	420
Cow	421	SKNLMSTHSLGIVFGPTLLRAEDESIGNMAVHMVYQNQIAELMLSAYDQIFS	471
Giraffe	421	.Q.....Q.....T.....E..K...	471
Okapi	421	.Q.....Q.....N.T.....E..K...	471

Newick Tree of Mammalian ARHGAP15A

(bushbaby:0.0118693, ((human:0.0043642, rhesus:0.0062181):0.00859842, (((((giraffe:0.0147509, okapi:0.00450219):0.00839461, ((sheep:0.00200696, tibetan_antelope:0.00868854):0.00515523, cow:0.0153501):0.00557623):0.0198966, camel:0.0205926):0.000958678, (sperm_whale:0.00458877, (orca:0.00240179, baiji_dolphin:0.00605502):0.00176742):0.0115323):0.00185767, ((horse:0.0126713, rhino:0.0129193):0.00529789, (polecat:0.0170393, ((walrus:0.00708325, panda:0.0120471):0.00103587, (dog:0.0102075, (cat:0, tiger:0.0042562):0.00681543):0.00219187):0.00279409):0.0124646):0.00276319):0.00361606):0.0118693);



Locus Name: Rho GTPase Activating Protein 15 (**ARHGAP15A**)

Locus Name: Lactoperoxidase (LPO)

ENSBTAT00000016986 LPO-201 lactoperoxidase antibacterial in milk
 GWAS study in cattle maps susceptibility to bronchial respiratory disease

PP2: (Giraffe) A155T, T179S, Y289C, A373V, G651W, H675Y; (Giraffe/Okapi) S302P, E355V

Giraffe: V14M UPS, S118F UIS, G651W UIS, H675Y UPS
 Giraffe/Okapi: S302P UIS, E355V UIS, L367V UPS

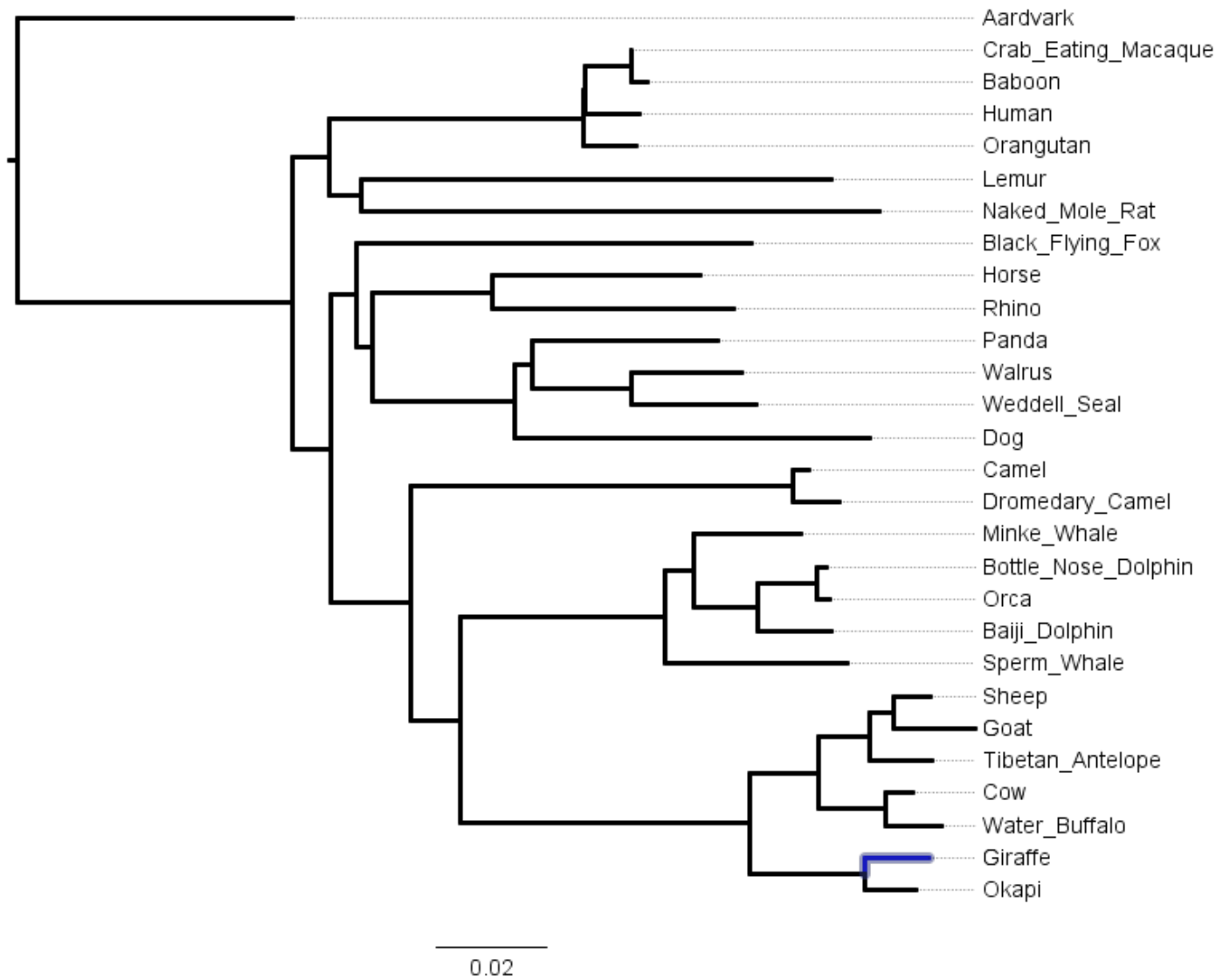
Protein sequence Alignment of Cow, Giraffe and Okapi LPO

Cow	1	MWVCLQLPVFLASVTLFEVAASDTIAQAASSTTTISDAVSKVKIQVNKAFLDSRTRLKTTL	60
Giraffe	1H.....M.....N...T.....	60
Okapi	1H.....N...T.....	60
Cow	61	SSEAPTQQLSEYFKHAKGRTRTAIRNGQVWEESLKRRLRRDRTLNTVTDPSLDLTALSWE	120
Giraffe	61R.....Q.....F..	120
Okapi	61R.....Q.....F...L.....	120
Cow	121	VGCGAPVPLVKCDENSPYRTITGDCNNRRSPALGAANRALARWLP AEYEDGLALPFGWTQ	180
Giraffe	121T.....S.....S.	180
Okapi	121S.....S.....	180
Cow	181	RKTRNGFRVPLAREVSNKIVGYLDEEGVLDQNRSLLFMQWQIVDHDLDFA PETELGSNE	240
Giraffe	181N.....V.....S.	240
Okapi	181N.....V.....S.	240
Cow	241	HSKTQCEEYCIQGDNCFPIMFPKNDPKLKTQKCMPPFRAGFVCPTPPYQSLAREQINAV	300
Giraffe	241	...A...H.....C.....	300
Okapi	241	...A...H.....T.....	300
Cow	301	TSFLDASLVYGSEPSLASRLRNLSSPLGLMAVNQEAWDHGLAYLPFNKKPSPCEFINTT	360
Giraffe	301	.P.....D.....V.....	360
Okapi	301	.P.....D.....V.....	360
Cow	361	ARVPCFLAGDFRASEQIILLATAHTLLLREHNRLARELKKLNPHWNGEKLYQEARKILGAF	420
Giraffe	361	.Q...V...S.V.....AS.....K.....D.....	420
Okapi	361	.Q...V...S.V.....S.....K.....D.....	420
Cow	421	IQIITFRDYLPVILGSEMOKWIPPYQGYNNSVDPRI SNVFTFAFRFGHMEVPSTVSRLDE	480
Giraffe	421L.....	480
Okapi	421L.....	480
Cow	481	NYQPWGPEAELPLHTLFFNTWRIKDGIDPLVRGLLAKKSKLMNQDKMVTSELRNKLFQ	540
Giraffe	481E.....LY.....	540
Okapi	481E.....LY.....	540
Cow	541	PTHKIHGFDLAAINLQRCRDHGMPPGYNSWRGFCGLSQPKTLKGLQTVLKNKILAKKLMDL	600
Giraffe	541A.....L..	600
Okapi	541A.....L..	600
Cow	601	YKTPDNIDIWIGGNAEPMVERGRVGPLLACL LGRQFQQIRDGDRFWWENPGVFTEKQRDS	660
Giraffe	601A.....I.....W.....	660
Okapi	601A.....S...I...L.R.....	660
Cow	661	LQKVSFSRLICDNTHITKVP LHAFAQANNYPHDFVDCSTVDKLDLSPWASREN	713
Giraffe	661V...Y.....G....AI.....	713
Okapi	661V.....V.....G....AI.....	713

Newick Tree of Mammalian LPO

(aardvark:0.0501076, (((((crab_eating_macaque:0, baboon:0.00289749):0.00857466, human:0.00988003):0.00028666, orangutan:0.0096434):0.0465617, (lemur:0.0860017, naked_mole_rat:0.0947617):0.00580509):0.00668931, (black_flying_fox:0.0723435, (horse:0.0378994, rhino:0.0442298):0.0218112, (panda:0.0339126, walrus:0.0203033, Weddell_seal:0.0227582):0.0181913):0.00301572, dog:0.0646278):0.0260308):0.00307433):0.00465552, (camel:0.00280621, dromedary_camel:0.00850957):0.0698379, (((minke_whale:0.0194947, (bottle_nose_dolphin:0.00185447, orca:0.00236792):0.0107734, baiji_dolphin:0.0134454):0.0115035):0.00532388, sperm_whale:0.0334334):0.0374344,

((giraffe:0.0118233, okapi:0.00944058):0.0211749, (((sheep:0.00660276, goat:0.0146914):0.00438947, tibetan_antelope:0.0112999):0.00949666, (cow:0.0051338, water_buffalo:0.0104369):0.0122571):0.0126386):0.05275):0.00898427):0.0147262):0.00703359):0.0501076);



Locus Name: Lactoperoxidase (LPO)

Locus Name: Semaphorin 7A (SEMA7A)

ENSBTAT0000015210 SEMA7A-201 semaphorin 7A cell migration, adhesion, immune response
mouse: impaired development of olfactory tract

PSG: (Giraffe) R107H|CGC/CAC
PP2: All benign

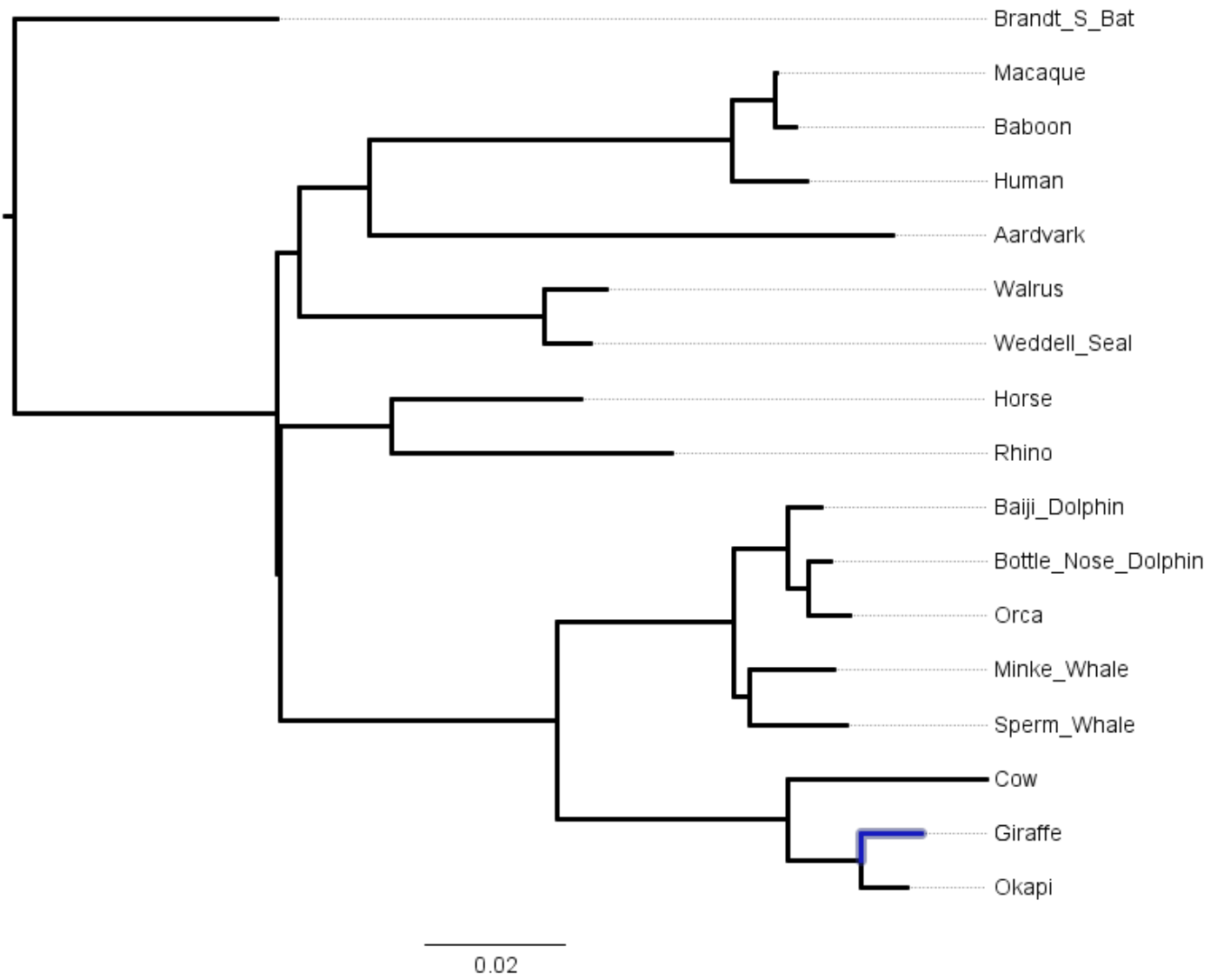
Giraffe: T428A UIS, TL656-657RV UISs
Giraffe/Okapi: R24W UPS, V95A UPS, W300R UIS, Q423H UIS

Protein sequence Alignment of Cow, Giraffe and Okapi SEMA7A

Cow	1	MTPPPSRCTALGAPRARVSSSLARSFPLWLLQLVWTAASQGHSKSGPRISAVWKGRA	60
Giraffe	1P..W.G...R.....P.....H.	60
Okapi	1P..W.G...R.....P.....T.H.	60
Cow	61	GQDHVDFGSTEPHTVLFHEPGSSSVWVGGRNRIYVFAFSKGRNASVRTVNI GSTKGS CRD	120
Giraffe	61S.V.A.D.....MH.....	120
Okapi	61S..Q.....S.V.A.D.....M.....	120
Cow	121	KQDCGNYITLLEKQNEGLLACGTNARRPSCWILVND SVEFLGERKGYAPFSPDENS L VLF	180
Giraffe	121	...E.....AV.....	180
Okapi	121	...E.....AV.....	180
Cow	181	DGDEVYSTIRKQEYNGKIPRFRIKGEIELYTS DTVMQNPQFIKATIVHQDQAYDDKIYY	240
Giraffe	181	240
Okapi	181	240
Cow	241	FFREDNPDKNPEAPLNVS RVAQLCRGDQGGESSLSVSKWNTFLKAMLVCS DATTNKNFNR	300
Giraffe	241A.....W	300
Okapi	241A.....W	300
Cow	301	LQDVFLLPDPNGQWKDTRVYGVFSNPWNYS AVCVYSLGDIDKVFCTSSLKGYHSSLPNPR	360
Giraffe	301	360
Okapi	301	360
Cow	361	PGKCLPDRQPIPTETFQVADSHPEVVQRVEPMGPLKAPLFH SKYHYQKVVVHRMHASNGE	420
Giraffe	361T.....	420
Okapi	361T.....	420
Cow	421	TFHVLYLTDTDKGTIHKVLEPGWEHGLVFNILEIQPFRRAAAIQAMSLDADRRKLYVNSQ	480
Giraffe	421A.....V...KR.....	480
Okapi	421V...R.....	480
Cow	481	WEVSQVPLDLCELYTGGCHGCLMARDPYCGWYQDR CVSIYSSQEPVLQSI SPVDPHKGCP	540
Giraffe	481V.....H.....N..E.....	540
Okapi	481V.....H.....N..E.....	540
Cow	541	NPKPEQAPLQKVS LAQNSRYLSCPME SRHATYSWRHENSVEQSCEPGHQSPNCILFIEN	600
Giraffe	541	600
Okapi	541	600
Cow	601	LTDLHYGHYYCEAQEDSYLREAQHWELLREDSAMTS QLLGHACTLATS L WLGVLPTLILG	660
Giraffe	601G.....R.....R.....RV...	660
Okapi	601G..F.....R.....	660
Cow	661	LLVH	664
Giraffe	661	664
Okapi	661	664

Newick Tree of Mammalian SEMA7A

(Brandt_s_bat:0.0374918, (((((macaque:0.000115098, baboon:0.0029015):0.00606498, human:0.0106665):0.051877, aardvark:0.0746724):0.00991221, (walrus:0.0086756, Weddell_seal:0.00652284):0.0350117):0.00327992, ((horse:0.0270289, rhino:0.0400769):0.0157669, ((baiji_dolphin:0.00469115, (bottle_nose_dolphin:0.00324284, orca:0.00584826):0.00290453):0.00779418, (minke_whale:0.0120336, sperm_whale:0.0139448):0.00222698):0.0252228, (cow:0.0282195, (giraffe:0.00857852, okapi:0.00659686):0.0104437):0.033028):0.0393207):0.000607242):0.0374918);



Locus Name: Semaphorin 7A (SEMA7A)

Locus Name: V-Rel Avian Reticuloendotheliosis Viral Oncogene Homolog (REL)

ENSBTAT00000020447 REL-201 v-rel oncogene lymphocyte and ketatinocytes growth and development
 mouse: defects in lymphocyte proliferation, humoral immunity, cytokine production

PSG: Q305E

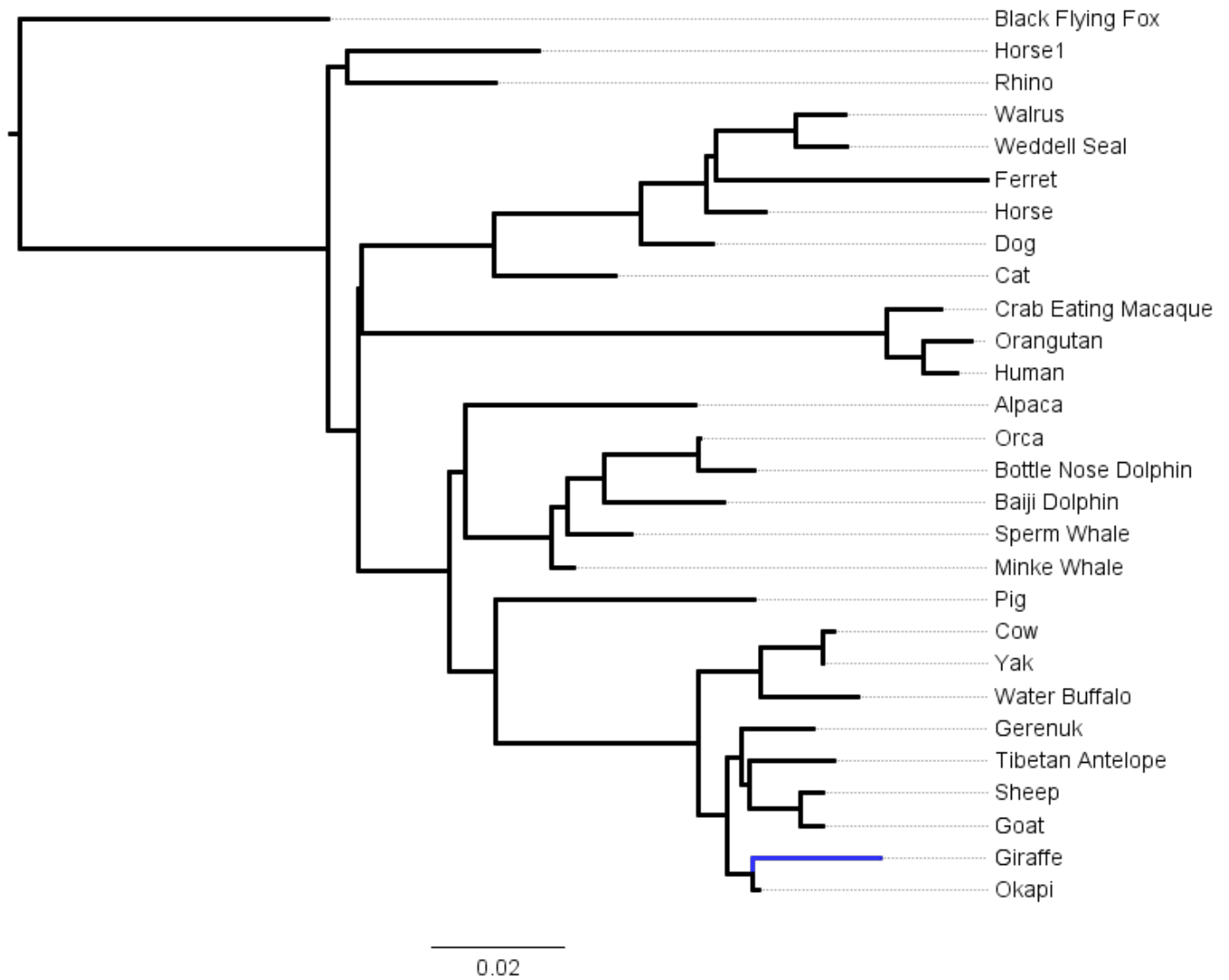
PP2: Q574P

Giraffe: L163F UIS, A291T UIS, Q301Y UPS, Q305E UIS, P319S UPS, H390P UPS, S472N UIS, Q574P UIS

Protein sequence Alignment of Cow, Giraffe and Okapi REL

Cow	1	MASGGFNPCIEIIEQPRQRGMRFYKCEGRSAGSIPGEHSTDNNRITYPSIQILNYYGK GK	60
Giraffe	1	60
Okapi	1	60
Cow	61	VRITLVTKNDPYKPHPHDLVKGKDCRDGYEAEFGQERRPLFFQNLGIRCVKKKEVKDAVI	120
Giraffe	61E.I.	120
Okapi	61E.I.	120
Cow	121	SRVRAGINPFNVPEQQLLDIEDCDLNVVRLCFQVFLPDEHGNTTALPPVVSNIYDNRA	180
Giraffe	121	..I.....F..T.....	180
Okapi	121	..I.....T.....	180
Cow	181	PNTAELRICRVNKNCGSVKGGDEIFLLCDKVQKDDIEVRFVLDWEAKGVFSQADVHRQV	240
Giraffe	181E.....	240
Okapi	181E.....	240
Cow	241	AIVFKTPPYCKAIIIEPVTVMQLRRPSDQEVSESMDFRYLPDEKDTYGNKAKKQKTLLF	300
Giraffe	241T.....T.....	300
Okapi	241T.....	300
Cow	301	HKLWQDCGVNFPERPRPSPLGPTGEGRFIKKEPNLFSHGAVLPETSRPVSSQAESYSSS	360
Giraffe	301	Y...E.....S.....	360
Okapi	301	Q.....	360
Cow	361	ASISSTLSHPASAMLPMTQSSSGWSSVAHPTSRVNTNSLSSFSTGTLSSNSQVIPPFL	420
Giraffe	361P...H.....G.....S..	420
Okapi	361I.....I.....G.....	420
Cow	421	EMSDLNVSNACIYNNNTNDIGRMEASSVSPADLYSISDASMLPNCVNMITPSNDSMRETD	480
Giraffe	421A.....G.....N.....	480
Okapi	421A.....G.....	480
Cow	481	NPRLVSMNLENPSCNSVLDPRDLRQLHQMSPPSMSTVTSSTTAYVAQSEAFEGSDFNCA	540
Giraffe	481S.....S.....F.....	540
Okapi	481S.....S.....F.....	540
Cow	541	DNSMINEAGPSNSTNANSHGFGPNSQYSGIGAMQNEQLSDSF AF E F F K V	589
Giraffe	541G.....S..Q.....P.....P....Q.	589
Okapi	541G.....S..Q.....P....Q.	589

Newick Tree of Mammalian REL



Locus Name: V-Rel Avian Reticuloendotheliosis Viral Oncogene Homolog (REL)

Axis inhibition protein 1 (AXIN2)

ENSBTAT0000042542 AXIN2-201 negative regulator of Wnt signaling embryonic somitogenesis and skeletal development

mouse: premature fusion of cranial sutures, enhanced expansion of osteoprogenitors, accelerated ossification, increased osteoblast proliferation and differentiation

Confirmed 5aa del in MA1, Reticulated and Rothschild

PP2: (Giraffe/Okapi) K486P, F679C

Giraffe: VPRLP 7-11 deletion UIS, Q165H UIS, S428C UIS, P489A UIS, A645P UPS

Giraffe/Okapi: I302M UIS, M312L UIS, M605V UPS

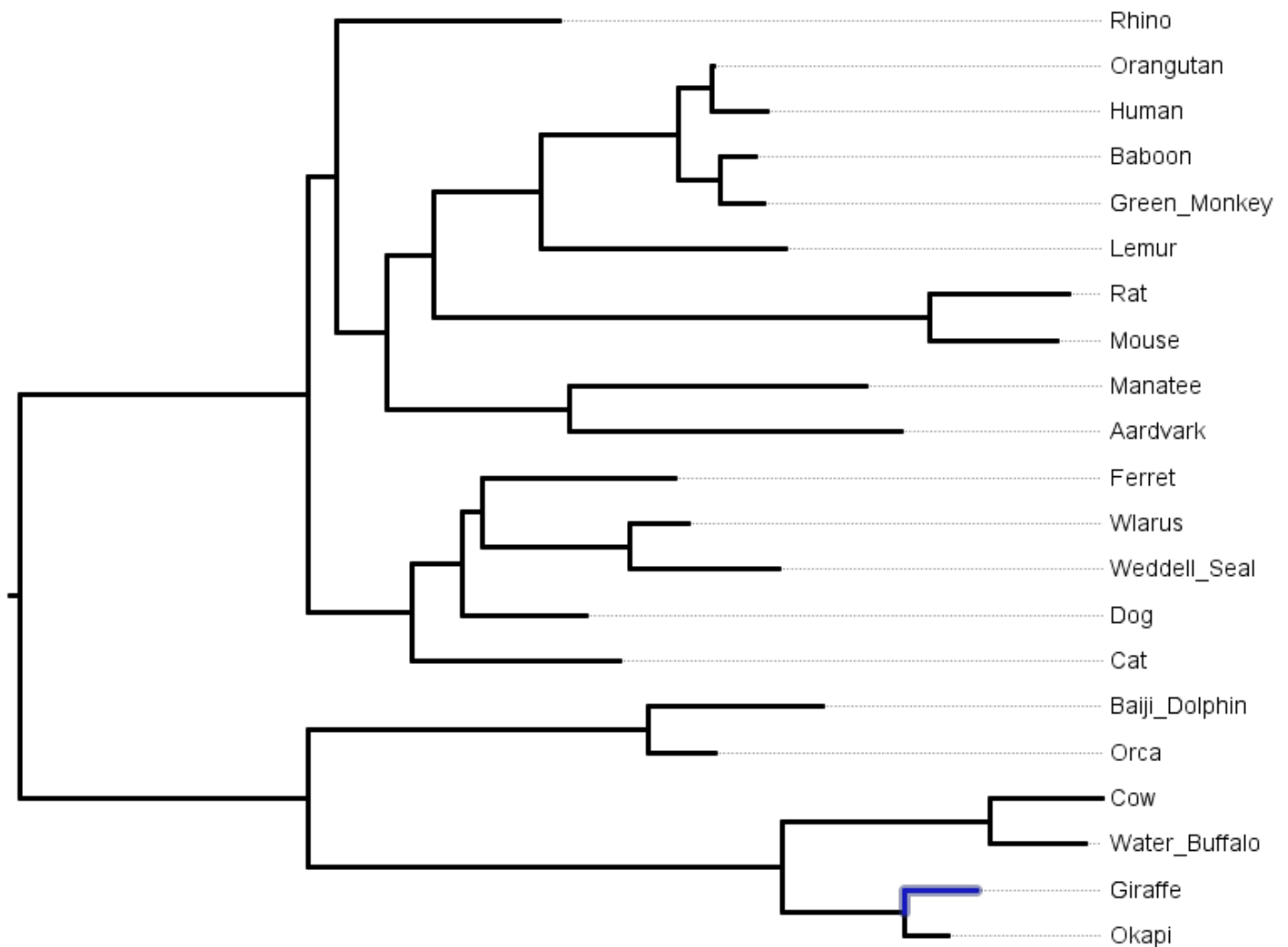
Protein sequence Alignment of Cow, Giraffe and Okapi AXIN2

Cow	1	MSSAVLVPRLPDPSSSFREDAPRPPVPGEEGETPPCQPGVVGKGPAAKASPVSPSARRNEG	60
Giraffe	1-----.....P.....P...S.....	55
Okapi	1L.....P...S.....	60
Cow	61	GLGEPEGRASPDSPLTRWTKSLHSLLDGDGAYLFRFTFLEREKCVDTLDFWFACNGFRQM	120
Giraffe	56	115
Okapi	61	120
Cow	121	NLKDAKTLRVAKAIYKRYIENNSIVSKQLKPKATKTYIRDSIKKQQIDSVMFDQAQTEVQA	180
Giraffe	116H.....	175
Okapi	121	180
Cow	181	VMEENAYQTFLTSDICLQYVGSNGENPAYLSQGGLGSLRLVCGYLPTLNEEEEWTCADEFK	240
Giraffe	176M.....Y.E..R.....V.H.....	235
Okapi	181M.....Y.E..R.....V.H.....	240
Cow	241	CKLPPTVVGSLSSKTLRATASARAMDTIESGYRSFRRSDPVNPHYVHVGSGYVFAPAASANDS	300
Giraffe	236T.....	295
Okapi	241T.....	300
Cow	301	EISSDALTDSSMSMTDSSVDGVPYRVSQKQLQREMHRSVKANGQVSLPHFPTRHRLPK	360
Giraffe	296	.M.....L.....	355
Okapi	301	.M.....L.....	360
Cow	361	EMTPVEPAAFAAELIARLEKLETRHSLEERLQQIQEEDKEGVELAPGSREAGPAP	420
Giraffe	356T.....R.....S.....	415
Okapi	361T.....R.....S.....V.....	420
Cow	421	HALCLLPSSSYEEDPQTILDDHLSRVLKTPGCQSPGVGRYSRARS PDHHRHHLQSHRA	480
Giraffe	416	.P.....C.....A...	475
Okapi	421	.P.....A...	480
Cow	481	LPPPGGPLEPAVAVPASCSSLGARGFVSRQATKHIHHHYIHHHAGPRTRDEAEAEAPRAR	540
Giraffe	476APA.I.....T...V.....E.....	535
Okapi	481SPA.L.....T...V.....E.....	540
Cow	541	CPCVPVGGADYSCCAKCKSHPGVPEPPGAAQLGWTRSSVPTSSRGGAPARRSTAPAREAG	600
Giraffe	536A.....LG.....T...A.....	604
Okapi	541A.....XG.....A.....	608
Cow	601	APGGMGSLQPPGEEGDRTPVWVQWVLESERPGKPKPHSAQSTKRAYPTESARTSPAERAG	660
Giraffe	605	...V.....A.....T.....P.....A.....	664
Okapi	609	P...V.....A.....T.....A.....	668
Cow	661	RHHLWGGSTGHPRAVPRAHPACTQDSSVPLTPPNTLAQLEEACRRLAEVSKPPKQRCCA	720
Giraffe	665T.....A...A.....	724
Okapi	669T.....A...A.....	728
Cow	721	AGQQRDRSHPGMPGTPFSSPSPASEDHKEPKKLAGMHALQASELVVTTYFFCGEEIPY	780
Giraffe	725AL.Q...A.....V.....	784
Okapi	729AL.Q...A.....V.....	788

Cow	781	RRMLKAQSLTLGHFKEQLSKKGNRYRYFKKASDEFACGAVFEEVWDDEVVLPMEYGRILG	840
Giraffe	785	844
Okapi	789	848
Cow	841	KVERID	846
Giraffe	845	850
Okapi	849	854

Newick Tree of Mammalian AXIN2

```
((rhino:0.0231316, (((((orangutan:0.000135022, human:0.00581387):0.00350805, (baboon:0.00373345, green_monkey:0.00460499):0.0042932):0.0142304, lemur:0.0253743):0.0111668, (rat:0.0145529, mouse:0.0132807):0.0515446):0.00502125, (manatee:0.0308067, aardvark:0.0344936):0.0191671):0.00514728):0.00296164, ((ferret:0.0200918, (wlarus:0.00611816, Weddell_seal:0.015519):0.0153809):0.00212345, dog:0.0129166):0.00523803, cat:0.0216697):0.0107635):0.03006, ((baiji_dolphin:0.0181628, orca:0.00697578):0.0354123, ((cow:0.0115613, water_buffalo:0.00994656):0.0216675, (giraffe:0.00736486, okapi:0.00449796):0.0127801):0.0493753):0.03006);
```



0.02

Axis inhibition protein 1 (AXIN2)

Locus Name: Peripherin PRPH2

ENSBTAT0000007836 PRPH2-201 perpherin-2 visual function
m common cause of retinitis pigmentosa, human: retinal degeneration

PSG: P10Q

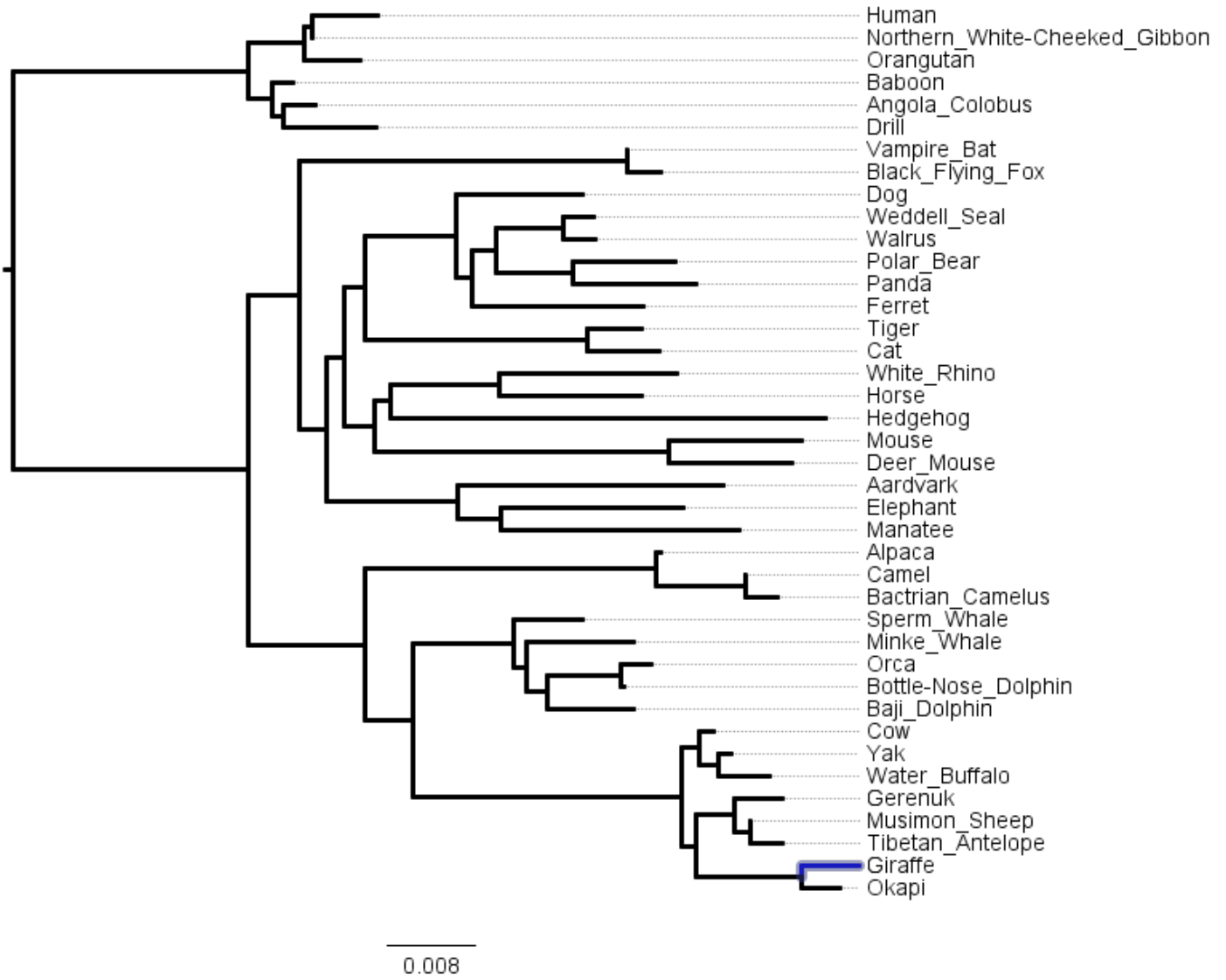
Giraffe: P10Q UIS

Protein sequence Alignment of Cow, Giraffe and Okapi PRPH2

Cow	1	MALLKVKFDQKKRVKLAQGLWLMNWFSVLAGIIIFGLGLFLKIELRKRSDVMNNSSESHFV	60
Giraffe	1P.....E.....	60
Okapi	1E.....	60
Cow	61	PNSLIGVGVLSVFNLSLAKGKICYDALDPAKYAKWKPWLKPYLAVCVLNFVFLVALCCF	120
Giraffe	61T.....	120
Okapi	61M.....T.....	120
Cow	121	LLRGSLESTLAHGLKNGMKFYRDTDTPGRCFMKKTIDMLQIEFKCCGNGFRDWFEIQWI	180
Giraffe	121	180
Okapi	121	180
Cow	181	SNRYLDFSSKEVKDRIKSNVDGRYLDGVVFPSCCNPSRPRCIQYQLTNNSAHYSYDHQT	240
Giraffe	181	240
Okapi	181	240
Cow	241	EELNLWLRGCRAALLSYYSNLMNTTGAVTLLVWLFVETITVGLRYLHTALEGMANPEDPE	300
Giraffe	241N.....I.....I.....	300
Okapi	241N.....I.....	300
Cow	301	CESEGWLLEKSVPETWKAFLESVKKLGKGNQVEAEGEDAGQAPAAG	347
Giraffe	301S.....	347
Okapi	301S.....	347

Newick Tree of Mammalian PRPH2

((((Human:0.00588561, Northern_White-Cheeked_Gibbon:0):0.000738324, Orangutan:0.00507583):0.00517584, (Baboon:0.0018958, (Angola_Colobus:0.0030238, Drill:0.0086045):0.00100277):0.00214564):0.0214713, ((Vampire_Bat:0, Black_Flying_Fox:0.00301012):0.0299616, (((Dog:0.0115878, ((Weddell_Seal:0.00282626, Walrus:0.00297089):0.00615544, (Polar_Bear:0.00927793, Panda:0.0111622):0.00708484):0.0021069, Ferret:0.015548):0.00158817):0.00829999, (Tiger:0.00497386, Cat:0.00665444):0.0202934):0.00184041, (((White_Rhino:0.0162639, Horse:0.013068):0.00991163, Hedgehog:0.039621):0.00142509, (Mouse:0.0121093, Deer_Mouse:0.0112857):0.0267635):0.00278664):0.00161864, (Aardvark:0.0242448, (Elephant:0.0166021, Manatee:0.0217036):0.00396617):0.0119554):0.00254992):0.00461297, ((Alpaca:0.000514034, (Camel:0, Bactrian_Camelus:0.00296152):0.00820715):0.0264655, ((Sperm_Whale:0.00617751, (Minke_Whale:0.00976298, (Orca:0.00273464, Bottle-nose_dolphin:0.000159718):0.00675668, Baji_Dolphin:0.00782157):0.00192789):0.0010987):0.00927823, ((Cow:0.00123748, (Yak:0.00116035, Water_Buffalo:0.0046368):0.00166535):0.00163245, ((Gerenuk:0.00436983, (Musimon_Sheep:0, Tibetan_Antelope:0.00291997):0.00143578):0.00357245, (Giraffe:0.00518775, Okapi:0.00352069):0.00962686):0.00127879):0.0245697):0.00432251):0.0106901):0.0214713);



Locus Name: Peripherin PRPH2

Locus Name: NF-X1-type zinc finger protein (NFXL1)

ENSBTAT0000061348 NFXL1-201 NF-X1-type skeletal growth
 mouse: reduced body length and short tibia

PP2: None
 PSG: T616M

Giraffe: P441A UIS, PT615-616LM UIS with M(TS)UPS

Protein sequence Alignment of Cow, Giraffe and Okapi NFXL1

Water Buffalo	1	MEASWRQVAGGRGRARGRTAAPSSGNVHLRGAGGGREKGSVGAAGPGLSPGGAATPAA	60
Giraffe	1A.....I...	60
Okapi	1A.G.....	60
Water Buffalo	61	AGSSARRCPAGSEAPQTSVAGELMSQKKFEEIKKANQAAAKKIVEEHFSSSEEGDED	120
Giraffe	61G..S..R.....I.....	120
Okapi	61G..S.....I.....	120
Water Buffalo	121	EGKRGKIVANTFITYTTQTGDGDVRELERTKQYVNEAFQAGAMTCLICIASVKRNQAVWSC	180
Giraffe	121T.....	180
Okapi	121T.....	180
Water Buffalo	181	SGFCFIFHMPCIQKWAKDSQFLVSSLTDDDFGKRDPWPCPKCRFEYKRSDTPSRYYCYC	240
Giraffe	181	240
Okapi	181	240
Water Buffalo	241	GKVEDPPLDPWLVPHSCGQVCERDFKPCSGHKCLLLCHPGPCPPCKMVTTCYCKKAKP	300
Giraffe	241P.....	300
Okapi	241P.....	300
Water Buffalo	301	IPRCSAKEWSCQLPCGRKLLCGQHKECNPCHAGSPPCPRVSRQKVCVCGKRVAERSCAS	360
Giraffe	301S.....A.....	360
Okapi	301A.....	360
Water Buffalo	361	PLWHCDQVCGKTLPCGNHTCEQVCHVGACGDCPRSGKRFCPCQKSKFSLPCTEDVPTCGD	420
Giraffe	361	420
Okapi	361	420
Water Buffalo	421	SCDKVLECGIHRCSQRCHRGPCETCRQEVEKHCRCGKHTKRMPCCHKPYLCETKCVKMRDC	480
Giraffe	421A.....	480
Okapi	421	480
Water Buffalo	481	QKHQCRKCCPGNCPDQNCGRITLGCNRHKCPSVCHRGSYPCPETVDVKCNCNGTKVT	540
Giraffe	481	540
Okapi	481S.....	540
Water Buffalo	541	VPCGRERTTRPPKCKEQCSRPTCHHTSQEKHRCHFGSCPPCHQPCQKVLKCGHLCPAP	600
Giraffe	541	600
Okapi	541	600
Water Buffalo	601	CHDQALIKQTGRHQPTGPWEQPSFAFIQTALPCPPCQVPIPMECLGKHEVSPLPCHAVG	660
Giraffe	601LM.....	660
Okapi	601L.....	660
Water Buffalo	661	PYSCKRACGRITLTCQNHTCMKECHKVTETDSDTKKAGPECLHCEECSKSRPSGCPHP	720
Giraffe	661V.....N.....	720
Okapi	661V.....N.....T..	720
Water Buffalo	721	CVLPCHPGECPPCVQMLRIKCHKITSLYVECRKITTADVNEKNLLSCCKNQCPKELPCG	780
Giraffe	721I.....	780
Okapi	721I.....	780
Water Buffalo	781	HRCCKEMCHPGECPFNCNQKVKLRCPCPKRIKKEVQC�KVNRENQISIECDTTCKEMKQKASE	840
Giraffe	781R.....	840
Okapi	781R.....	840

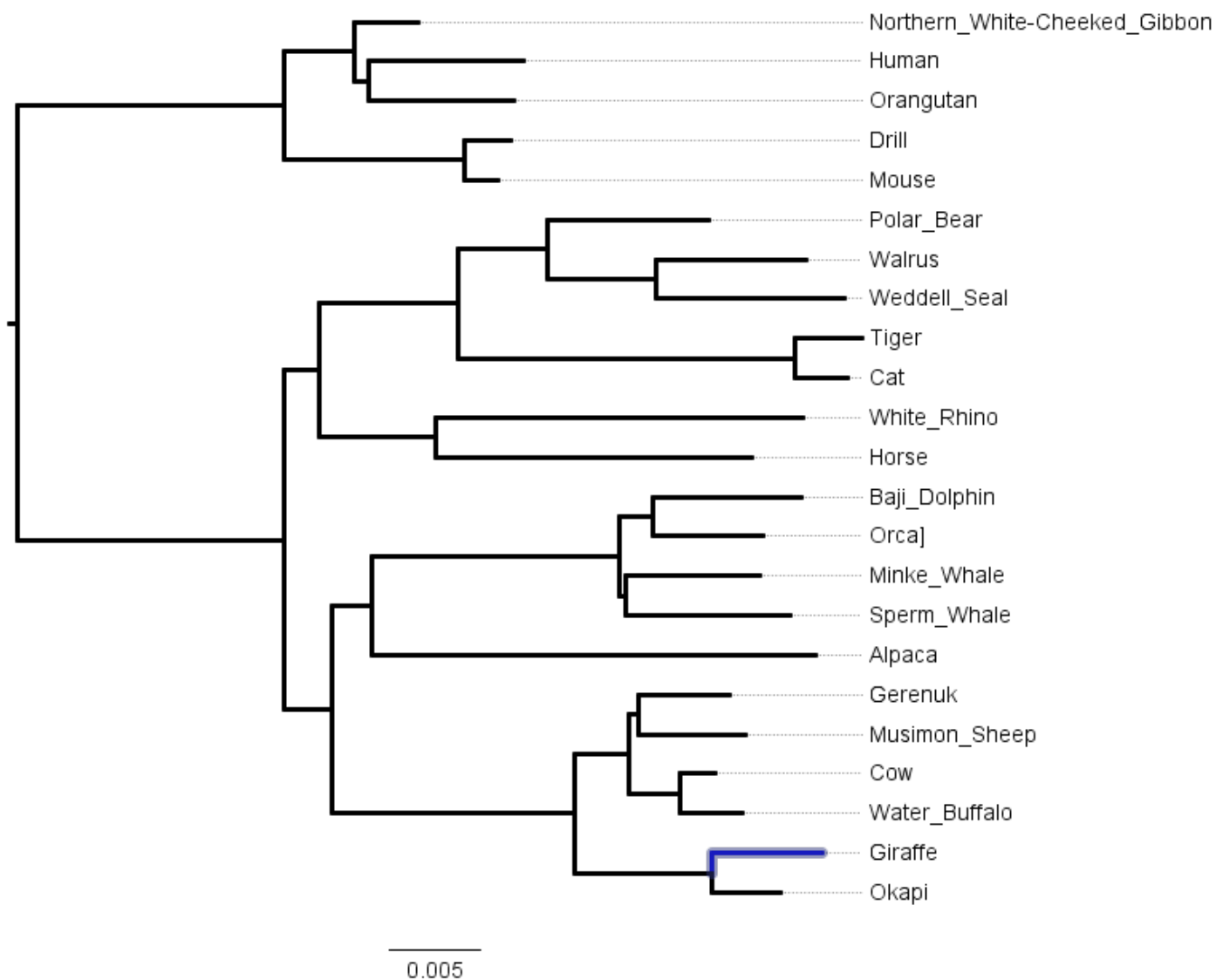
Water Buffalo	841	LKEAEAKAALEEEKRRQQAEELEAFENRLKGRRKKNRKRDEVAVELTLWQKYKYLLFPLCA	900
Giraffe	841	900
Okapi	841	900
Water Buffalo	901	IVVVVFAWYIANAVD	915
Giraffe	901	V.....L...	915
Okapi	901L...	915

Newick Tree of Mammalian NFXL1

```

(((Northern_White-Cheeked_Gibbon:0.00359942, (Human:0.00856959,
Orangutan:0.00803366):0.000796594):0.00387898, (Drill:0.00255115,
Mouse:0.00184931):0.0100495):0.0147522, (((Polar_Bear:0.00890291, (Walrus:0.00830195,
Weddell_Seal:0.0104325):0.0060435):0.00490846, (Tiger:0.0036526,
Cat:0.00291921):0.0186251):0.00768872, (White_Rhino:0.0203383,
Horse:0.017495):0.00639622):0.00200009, (((Baji_Dolphin:0.00819689,
'Orca]:0.00609741):0.00184553, (Minke_Whale:0.00741933,
Sperm_Whale:0.00909252):0.000375473):0.0136695, Alpaca:0.0245246):0.00224885,
((giraffe:0.0060733, okapi:0.00381162):0.00758221, ((gerenuk:0.00506027,
Musimon_Sheep:0.00592907):0.000498578, (cow:0.00199488,
Water_Buffalo:0.00348461):0.00280918):0.00297043):0.013462):0.00267698):0.0147522);

```



Locus Name: NF-X1-type zinc finger protein (NFXL1)

Supplementary Table 1 Gene Annotations of giraffe and okapi

We used gene annotations for assemblies of the cow and dog genomes to identify putative coding regions for giraffe and okapi, as follows. We downloaded gene models for the cow assembly called bosTau4 from Ensembl (www.ensembl.org). The union of all intervals annotated as coding, as well as 150 bp flanks, were used to extract sequence from the bosTau4 assembly, forming the mapping target. Giraffe reads were mapped to the target using lastz (www.bx.psu.edu/miller_lab/dist/README.lastz-1.02.00/README.lastz-1.02.00a.html) Mapping required an alignment with at least 60% of the read length as matched bases, and at least 3 matches better than the second best alignment. Lastz scoring was as follows.

Nucleotide substitutions:

	A	C	G	T
A	11	-33	-20	-39
C	-33	16	-30	-20
G	-20	-30	16	-33
T	-39	-20	-33	11

gap_open_penalty = 40, gap_extend_penalty = 4, hsp_threshold = 300, x_drop = 80 and y_drop = 80. The analogous process was used to align reads to the dog canFam3 assembly. To allow for the additional evolutionary distance between giraffe and the assembly, we used the following, less stringent lastz scores.

Nucleotide substitutions:

	A	C	G	T
A	11	-22	-10	-28
C	-22	15	-20	-10
G	-10	-20	15	-22
T	-28	-10	-22	11

gap_open_penalty = 30, gap_extend_penalty = 3, hsp_threshold = 300, x_drop = 60 and y_drop = 60. The okapi reads were processed just as for giraffe.

Supplementary Table 2 Genome Assemblies of giraffe and okapi

Summary of genome assemblies of giraffe and okapi

	<i>Giraffa camelopardalis tippelskirchi</i>		<i>Okapia johnstoni</i>	
Assembly size (Gb)	2,92		3,28	
GC-content %	41,5		42,3	
Number of scaffolds	2051673		3721563	
Total size of scaffolds (nt)	2923614156		3279649410	
Longest scaffold (nt)	5618088		2167669	
Number of scaffolds > 500 nt	121921	5,90%	191750	5,20%
Number of scaffolds > 1K nt	60763	3,00%	106272	2,90%
Number of scaffolds > 10K nt	13235	0,60%	27730	0,70%
Number of scaffolds > 100K nt	5782	0,30%	7270	0,20%
Number of scaffolds > 1M nt	342	0,00%	62	0,00%
N50 scaffold length (nt)	339613		104593	
L50 scaffold count	2088		6933	
scaffold %A	28,39		27,74	
scaffold %C	20,17		20,3	
scaffold %G	20,06		20,21	
scaffold %T	28,08		27,41	
scaffold %N	3,29		4,33	
Percentage of assembly in scaffolded contigs	82,80%		69,90%	
Ave. length of breaks (20 or more Ns) between contigs	1170		1620	
Number of contigs	2133680		3808993	
Number of contigs in scaffolds	101091		124674	
Number of contigs not in scaffolds	2032589		3684319	
Total size of contigs (nt)	2827601364		3137992281	
Longest contig (nt)	540046		592595	
Number of contigs > 500 nt	187457	8,80%	251065	6,60%
Number of contigs > 1K nt	121879	5,70%	159155	4,20%
Number of contigs > 10K nt	50330	2,40%	54534	1,40%
Number of contigs > 100K nt	4159	0,20%	3359	0,10%
Number of contigs > 1M nt	0	0,00%	0	0,00%
N50 contig length (Kb)	47286		33770	
L50 contig count	16327		22986	

Mapping reads to genome assemblies of giraffe and okapi

	<i>Giraffa camelopardalis tippelskirchi</i>			<i>Okapia johnstoni</i>		
	PE	MP	Adaptor-clipped MP	PE	MP	Adaptor-clipped MP
Number of reads	570222616	156989988	134919530	541205364	134600726	117136186
Coverage (resp. mapped coverage)	29.26x (28.44x)	8.05x (6.44x)	6.63x (5.67x)	24.75x (23.65x)	6.16x (4.98x)	5.08x (4.40x)
Number of mapped reads (out of total)	563495089 (98.82%)	155254040 (98.89%)	134692225 (99.83%)	537760172 (99.36%)	132951488 (98.77%)	116902286 (99.80%)
Percentage of PCR duplicate reads*	N/A	43,00%	N/A	N/A	64,00%	N/A
Insert size average (bp)	527.4	4610.1	4630,4	541.9	4271	4274,8
Insert size standard deviation (bp)	132.4	3623	3623,7	157.2	3584.4	3591,3
Number of reads in pairs that map to the same scaffold	518811698	110023320	107539588	447699474	81993204	80146978
Number of reads in pairs that map to the same scaffold in PE orientation**	518139122 (99.87%)	44469980 (40.42%)	43154754 (40.13%)	445077876 (99.41%)	34908928 (42.58%)	34157932 (42.62%)
Number of reads in pairs mapping to the same scaffold in MP orientation**	672576 (0.13%)	65553340 (59.58%)	64384834 (59.87%)	2621598 (0.59%)	47084276 (57.42%)	45989046 (57.38%)
Mismatch rate (over all mapped bases)	1.11%	0.26%	0.16%	0.63%	0.44%	0.30%

Prepared MP libraries are MP that have been processed by the NextClip software, then given to the assembler instead of the original MP contamination in MP libraries.

Coverage is the total number of bases in the reads, divided by the genome size. Mapped coverage is the number of mapped bases, divided

*as detected by NextClip software ** out of all reads mapping to the same scaffold

Supplementary Table 4 Genes exhibiting positive selection in giraffe and okapi**giraffe: over (+) under (-) representation**

Biological Process	P value
lysosomal transport	+ 0.023
natural killer cell activation	+ 0.023
immune response	+ 0.029
angiogenesis	+ 0.033
protein ADP-ribosylation	+ 0.035
blood circulation	+ 0.037
response to pheromone	+ 0.046
nervous system development	- 0.046
protein phosphorylation	- 0.052
cellular defense response	+ 0.055
neuronal action potential propagation	+ 0.057
sex determination	+ 0.057
protein metabolic process	- 0.075
mRNA transcription	+ 0.089
cell-matrix adhesion	+ 0.091
mRNA processing	- 0.101
response to stimulus	+ 0.108
mitochondrion organization	+ 0.111
mitochondrial transport	+ 0.111
macrophage activation	+ 0.12
cellular protein modification process	- 0.127
mRNA splicing via spliceosome	- 0.147
anion transport	+ 0.148
immune system process	+ 0.149
B cell mediated immunity	+ 0.164
ectoderm development	- 0.171
cell communication	- 0.171
antigen processing and presentation	+ 0.2
protein transport	- 0.209
lipid metabolic process	+ 0.212
RNA catabolic process	+ 0.218

okapi: over (+) under (-) representation

Biological Process	P value
nervous system development	- 0.03
protein methylation	+ 0.063
sensory perception of taste	+ 0.075
phosphate-containing compound metabolic process	+ 0.087
cellular amino acid metabolic process	- 0.095
sensory perception of pain	+ 0.098
sensory perception of chemical stimulus	+ 0.098
cell adhesion	+ 0.106
biological adhesion	+ 0.106
mitochondrion organization	+ 0.121
mitochondrial transport	+ 0.121
steroid metabolic process	+ 0.123
ectoderm development	- 0.124
muscle organ development	- 0.125
cholesterol metabolic process	+ 0.128
localization	- 0.129
glycolysis	+ 0.133
system development	- 0.135
transport	- 0.151
cell-cell signaling	- 0.156
protein metabolic process	+ 0.156
regulation of liquid surface tension	+ 0.166
transcription DNA-dependent	- 0.173
antigen processing and presentation	+ 0.176
Unclassified	+ 0.178
transcription from RNA polymerase II promoter	- 0.179
exocytosis	+ 0.18
proteolysis	+ 0.185
protein acetylation	+ 0.187
developmental process	- 0.189
blood circulation	+ 0.191

Supplementary Table 5 Genes exhibiting multiple signs of adaptation (MSA) in giraffe

Gene ¹	Protein Function	Stage Tissue/Organ/Function	Protein Divergence ² branch length	Substitutions at		PolyphenZ PRD ⁴ number	PSG ⁵
				Fixed Sites ³ number	p-value		
HOXB3	homeobox transcription factor	segmental identity, anterior axial skeleton, angiogenesis	G-mammals	G-2US; GO-3US	n.s.	GO-1PRD	n.s.
HOXB13	homeobox transcription factor	segmental identity, posterior axial skeleton, angiogenesis	GO-mammals	GO-5US, 4aadel	n.s.	GO-3PRD	n.s.
CDX4	homeobox transcription factor	segmental identity, posterior axial skeleton, heart develop.	GO-cetartiodactyls	G-2US, GO-1US	n.s.	G-1PRD, GO-1PRD	n.s.
NOTO	homeobox transcription factor	embryonic somitogenesis,	G-mammals	G-2US, GO-2US	n.s.	G-2PRD, GO-2PRD	n.s.
JAG1	Notch ligand	vertebrae development, cardiovascular, eye, kidney	G-mammals	G-2US, GO-6US	n.s.	GO-1PRD	n.s.
DLL3	Notch ligand	embryonic somitogenesis	GO-cetartiodactyls	G-1US, GO-4US	n.s.	GO-3PRD	n.s.
NOTCH4	notch pathway	mesoderm development, angiogenesis, neurogenesis	G-mammals	G-8US, O?	n.s.	G-3PRD, GO-1PRD	n.s.
FGFRL1	decoy FGF receptor	cranofacial, axial & appendic. skeleton, heart, kidney	G-cetartiodactyls	G-7US; GO-1US	4.00E-06	G-3PRD	7 P< 0.09
FOLR1	folate receptor	embryogenesis, folate homeostasis	G-cetartiodactyls	G-3US	n.s.	G-2PRD	5*
PDCD2L	transcriptional repressor	programmed cell death	G-pecorans	G-3US; GO-1US	n.s.	G-2PRD	n.s.
MYC	transcription factor	cell proliferation, growth control, oncogene	GO-mammals	G-3US, GO-2US	n.s.	G-1PRD, GO-3PRD	n.s.
E2F5	transcription factor	cell proliferation, growth control, brain	G-mammals	G-4US, GO-1US	0.00011	GO-2PRD	n.s.
E2F4	transcription factor	cell proliferation, growth control, cranofacial, erythroid	G-pecorans	G-2US, GO-1US	n.s.	G-1 PRD	n.s.
ETS2	ETS transcription factor	somitogenesis, heart development	G-mammals	GO-1US	n.s.	n.s.	n.s.
TGFB1	secreted growth factor	growth control, bone growth, heart	G-cetartiodactyls	G-1US	n.s.	n.s.	5*
ALDH16A1	aldehyde dehydrogenase	eye development	GO-mammals	G-3US	n.s.	G-3PRD, GO-1PRD	n.s.
FHL5	Four-half lim domains	testis, heart, brain	G-pecorans	G-2US, GO-1US	n.s.	G-1 PRD	2*
ITGA10	integrin alpha 10	heart, muscle articular cartilage	G-mammals	G-2US, GO-2US	n.s.	G-1 PRD	n.s.
ECM1	extracellular matrix protein	endochondral bone formation and angiogenesis	G-cetartiodactyls	G-1US, GO-2US	n.s.	G-3PRD, GO-2PRD	n.s.
TTYH2	chloride channel	growth control, development	G-cetartiodactyls	G-2US, GO-1US	n.s.	G-1PRD, GO-1PRD	1*
CREBBP	CBP histone acetylase	angiogenesis, skeletal growth, regulates Hox protein activity	G-mammals	G-3US, GO-US	n.s.	G-3PRD	n.s.
PTGES2	prostaglandin E synthase	heart, brain regulates smooth muscle contraction	G-pecorans	G-1US	n.s.	G-1 PRD	n.s.
IFT74	intraflagellar transport protein	ciliogenesis kidney, heart, lung	G-pecorans	G-2US, GO-2US	n.s.	G-1 PRD	n.s.
ABHD2	abhydroloase	smooth muscle cell migration	G-cetartiodactyls	G-1US	n.s.	G-1PRD	n.s.

ENG	endoglin	regulation of angiogenesis	unremarkable	G-1US	n.s.	G-1PRD, GO-5PRD	n.s.
SEMA3E	semaphorin 3E	regulates angiogenesis and neuronal synaptogenesis in eye	G-cetartiodactyls	G-1US, GO-3US	n.s.	G-1 PRD	n.s.
JARID2	modulates histone methyltransferase	heart and nervous system development	GO-mammals	GO-4US	n.s.	GO-3PRD	n.s.
CYP27B1	25-hydroxyvitamin D-1 alpha hydroxylase	bone development and calcium metabolism	unremarkable	G-1US, GO-1US	n.s.	n.s.	1*
NFXL1	NF-X1-type	skeletal growth	G-cetartiodactyls	G-2US	n.s.	n.s.	1*
AXIN2	negative regulator of Wnt signaling	embryonic somitogenesis and skeletal development	unremarkable	G-2US & 5aadel, GO-2US	n.s.	GO-2PRD	n.s.
RCAN3	inhibits calcineurin A, binds troponin	heart, brain, skeletal muscle, kidney, language SNP humans	G-mammals	G-7US	3.70E-06	G-3PRD	n.s.
BORG1	rho GTPase inhibit CDC42	heart	G-mammals	G-1US	0.00216	n.s.	6 P<0.09
UTS2B	urotensin 2, vasoconstrictor	regulates blood pressure in the brain	Giraffe>okapi	G-1US	n.s.	G-2PRD, GO-1PRD	n.s.
ADRA1A	adrenergic receptor	regulation of blood pressure	unremarkable	G-1US	n.s.	G-1PRD	1*
ADRA2B	adrenergic receptor	regulation of vasoconstriction	GS-mammals	G-3US, GO-1US	0.00203	n.s.	n.s.
ACE	angiotensin I converting enzyme	regulation of blood pressure	unremarkable	G-3US, GO-1US	n.s.	G-2PRD, GO-1PRD	n.s.
SSTR2	somatostatin receptor	behavior, eye, pancreas	G-mammals	G-2US, GO-1US	0.00836	n.s.	n.s.
FSCN1	fascin, organizes filamentous actin	nervous system, eye	G-mammals	G-4US	n.s.	G-2PRD	n.s.
NF2	merlin regulator of hippo pathway	auditory functions	G-mammals	G-4US	n.s.	n.s.	n.s.
CHRNA10	neuronal acetylcholine receptor	auditory functions, pain reception	G-pecorans	G-2US	n.s.	G-1PRD	n.s.
SLIT2	secreted axon guidance replusive protein	axonal guidance in the nervous system	G-cetartiodactyls	G-2US, GO-1US	n.s.	n.s.	n.s.
SEMA3A	semaphorin 3A	axonal guidance	GO-cetartiodactyls	G-2US, GO-3US	n.s.	G-1PRD	n.s.
MOXD1	monoxygenase dopamine β -hydroxylase	dopamine metabolism	unremarkable	G-1US, GO-1US	n.s.	n.s.	1*
PRPH2	perpherin-2	visual function	G-mammals	G-1US	n.s.	n.s.	1*
ALDH5A1	succinic semialdehyde dehydrogenase	brain, clearance of GABA and hydroxybutyric acid	G-cetartiodactyls	G-1US	n.s.	G-2PRD	n.s.
MTHFD1	C-1-tetrahydrofolate synthase	folate metabolism	G-mammals	G-5US, GO-1US	n.s.	G-1PRD	n.s.
SLC17A1	phosphate-sodium cotransporter	kidney	G-mammals	G-1US, GO-1US	n.s.	G-1PRD, GO-5PRD	n.s.
HIBADH	3-hydroxyisobutyrate dehydrogenase	mitochondrial, amino acid degradation	G-cetartiodactyls	G-1US	n.s.	G-1PRD	n.s.
MCT1	monocarboxylate transporter	rumen epithelium, transport volatile fatty acids, butyrate	G-mammals	G-3US, GO-1US	0.045	G-1PRD	n.s.

ACSM3	acyl-CoA synthetase medium-chain	mitochondrial	G-cetartiodactyls	G-1US, GO-4US	n.s.	n.s.	n.s.
ACADS	acyl-CoA dehydrogenase short chain	mitochondrial	GO-mammals	G-1US, GO-3US	n.s.	n.s.	n.s.
NDUFB8	NADH dehydrogenase-ubiquinone subunit	mitochondria electron transport	G-cetartiodactyls	G-2US	n.s.	G-1PRD, GO-1PRD	n.s.
SDHB	succinate dehydrogenase ubiquinone complex II	mitochondria electron transport and citric acid cycle	G-mammals	G-2US	n.s.	GO-1PRD	n.s.
PRR19	proline rich protein 19	secreted tannin binding protein	G-cetartiodactyls	G-1US	n.s.	G-2PRD	1*
MRP10	ribosomal L10 protein	mitochondrial protein synthesis	unremarkable	G-1US	n.s.	G-1PRD	1*
MDC1	mediator DNA damage checkpoint	dsDNA break repair, scaffold	G-mammals	G-6US, GO-3US 264aadel	n.s.	G-13PRD, GO-15PRD	n.s.
EXO1	exonuclease 1	DNA mismatch repair, essential for meiosis	G-cetartiodactyls	G-7US, GO-3US	n.s.	G-1PRD	n.s.
Nibrin	component of MRN complex	dsDNA break repair, chromosome integrity	G-cetartiodactyls	G-4US	n.s.	G-2PRD	n.s.
MRE11	component of MRN complex	dsDNA break repair, chromosome integrity	G-cetartiodactyls	G-3US	n.s.	n.s.	1*
SOSB2	component of SOSS complex	dsDNA break repair, chromosome integrity	G-mammals	G-2US, GO-1US	0.02544	G-1PRD, GO-1PRD	n.s.
NUDT15	8-oxo-dGTP diphosphatase	DNA repair	G-pecorans	G-2US	n.s.	G-2PRD	n.s.
SAC3D1	SAC3 domain containing protein	centrosome duplication and mitotic progression	unremarkable	G-3US, GO-1US	n.s.	G-2PRD	n.s.
HAUS2	centrosomal protein 27	centrosome assembly, cytokinesis	G-mammals	G-1US, GO-3US	n.s.	G-1PRD, GO-1PRD	n.s.
RCCD1	histone demethylase complex	chromosome segregation	G-mammals	G-2US	n.s.	G-1PRD, GO-3PRD	n.s.
HAUS6	mitotic spindle assembly	centrosome integrity cytokinesis	Pecorans>>mammals	G-5US, GO-6US	n.s.	G-3PRD, GO-5PRD	1*
ARHGAP15	Rho GTPase-activating protein	trypanosome resistance	G-mammals	G-2US	n.s.	n.s.	n.s.
LPO	lactoperoxidase	antibacterial in milk	unremarkable	G-2US, GO-2US	n.s.	G-6PRD, GO-2PRD	n.s.
SEMA7A	semaphorin 7A	cell migration, adhesion, immune response	unremarkable	G-3US, GO-2US	n.s.	n.s.	1*
REL	v-rel oncogene	lymphocyte and ketatinocytes growth and development	G-cetartiodactyls	G-6US	0.00127	G-1PRD, GO-1PRD	1*
PACRGL	E3 ubiquitin protein ligase parkin-like	unknown substrate expressed in brain	G-cetartiodactyls	G-2US, GO-1US	n.s.	G-1PRD	n.s.

Abbreviations: G=giraffe, O=okapi, GO= giraffe and okapi, m=mouse, h=human, US=unique substitution at a fixed site in other mammals, PRD=probably damaging polyphen 2 score, PSG=positively selected genes using branch-site test

SNP=single nucleotide polymorphism, GWAS=genome wide association study, n.s.=not statistically significant

¹ Homologous cattle transcript identification is listed in Supplementary Figure 1.

- ² Protein divergence is the relative branch length of giraffe (G) compared to other species on the phylogenetic protein tree. For example "G-mammals" means that giraffe has the longest branch length among all mammals compared. See Supplementary Figure 1 for gene trees. Phylogenetic tree analysis was by PhyML likelihood-based tree-searching algorithm and n=100 bootstrapping.
- ³ Unique substitutions at fixed sites refers to amino acid substitutions in giraffe and/or okapi that at sites that are otherwise fixed for another amino acid in all other mammals compared. number of US sites = the number of US positions in the specific protein. p-value for US = are proteins that display an a larger number of unique amino acid substitutions at fixed sites than expected as compared to other mammals.
- ⁴ Polyphen2 PRD = amino acid substitutions in giraffe and/or okapi that are predicted to be "probably damaging" or probably alter function-structure of the protein
- ⁵ PSG = positive selected sites as determined by branch-site test. PSG test was performed using the coding sequences giraffe and okapi and all mammalian species of high quality in the public databases of NCBI and Ensembl. The number of positively selected sites and overall statistical significance are given.

Supplementary Table 6 Survey of major developmental genes for evidence of significant changes in giraffe compared to other eutherians

Gene Cluster/Pathway	Gene	Survey results based on amino acid sequence divergence and attributes of amino acid substitutions
Homeobox Genes	HoxA1	Unremarkable
Homeobox Genes	HoxA2	Unremarkable
Homeobox Genes	HoxA3	Unremarkable
Homeobox Genes	HoxA4	Unremarkable
Homeobox Genes	HoxA5	Conserved (with okapi and cow)
Homeobox Genes	HoxA6	Conserved (with okapi and cow)
Homeobox Genes	HoxA7	Unremarkable
Homeobox Genes	HoxA9	Unremarkable
Homeobox Genes	HoxA10	Unremarkable
Homeobox Genes	HoxA11	Unremarkable
Homeobox Genes	HoxA13	Unremarkable
Homeobox Genes	Even-skipped	Unremarkable
Homeobox Genes	HoxB1	Unremarkable
Homeobox Genes	HoxB2	Unremarkable
Homeobox Genes	HoxB3	Remarkable
Homeobox Genes	HoxB4	Unremarkable
Homeobox Genes	HoxB5	Unremarkable
Homeobox Genes	HoxB6	Conserved (with okapi and cow)
Homeobox Genes	HoxB7	Unremarkable
Homeobox Genes	HoxB8	Conserved (with okapi and cow)
Homeobox Genes	HoxB9	Conserved (with okapi and cow)
Homeobox Genes	HoxB13	Remarkable
Homeobox Genes	HoxC4	Unremarkable
Homeobox Genes	HoxC5	Conserved (with okapi and cow)
Homeobox Genes	HoxC6	Conserved (with okapi and cow)
Homeobox Genes	HoxC8	Conserved (with okapi and cow)
Homeobox Genes	HoxC9	Conserved (with okapi and cow)
Homeobox Genes	HoxC10	Unremarkable
Homeobox Genes	HoxC11	Unremarkable
Homeobox Genes	HoxC12	Unremarkable
Homeobox Genes	HoxC13	Unremarkable
Homeobox Genes	HoxD1	Unremarkable
Homeobox Genes	HoxD3	Unremarkable
Homeobox Genes	HoxD4	Unremarkable
Homeobox Genes	HoxD8	Unremarkable
Homeobox Genes	HoxD9	Remarkable
Homeobox Genes	HoxD10	Unremarkable
Homeobox Genes	HoxD11	Unremarkable
Homeobox Genes	HoxD12	Unremarkable
Homeobox Genes	HoxD13	Unremarkable
Homeobox Genes	Even-skipped 2	Unremarkable

Homeobox Genes	CDX1	Unremarkable
Homeobox Genes	CDX2	Unremarkable
Homeobox Genes	CDX4	Remarkable
Homeobox Genes	Meox1	Unremarkable
Homeobox Genes	Meox2	Unremarkable
Homeobox Genes	TBX18	Unremarkable
Homeobox Genes	PBX1	Conserved (with okapi and cow)
Homeobox Genes	MEIS1	Conserved (with okapi and cow)
Homeobox Genes	NKX3-2	Unremarkable
Homeobox Genes	NKX3-1	Unremarkable
Homeobox Genes	LDB1	Conserved (with okapi and cow)
Homeobox Genes	SHOX2	Remarkable
Homeobox Genes	CREBBP	Remarkable
Homeobox Genes	IRX6	Unremarkable
Homeobox Genes	NOTO	Remarkable
Homeobox Genes	PRRX1	Unremarkable
TGF β Pathway		
TGF β Pathway	BMP4	Unremarkable
TGF β Pathway	BMP5	Unremarkable
TGF β Pathway	TGFB1	Remarkable
TGF β Pathway	TGFBR2	Unremarkable
TGF β Pathway	GDF8	Unremarkable
FGF Pathway		
FGF Pathway	FGF8	Conserved (with okapi and cow)
FGF Pathway	FGF19	Unremarkable
FGF Pathway	FGFR2	Unremarkable
FGF Pathway	FGFR3	Unremarkable
FGF Pathway	FGFR4	Unremarkable
FGF Pathway	FGF4	Unremarkable
FGF Pathway	FGF3	Unremarkable
FGF Pathway	FGFR1	Unremarkable
FGF Pathway	FGFRL1	Remarkable
FGF Pathway	TCF15	Unremarkable
FGF Pathway	FGF21	Unremarkable
FGF Pathway	FGF1	Unremarkable
FGF Pathway	DUSP6	Unremarkable
FGF Pathway	FRS2	Unremarkable
FGF Pathway	GRB2	Conserved (with okapi and cow)
FGF Pathway	SOS1	Conserved (with okapi and cow)
FGF Pathway	BCL2L11	Unremarkable
FGF Pathway	EFNA1	Unremarkable
FGF Pathway	EPHB3	Unremarkable
FGF Pathway	HSPG2	Unremarkable
FGF Pathway	SHH	Unremarkable
FGF Pathway	PTPN11	Unremarkable
FGF Pathway	GAB1	Unremarkable
FGF Pathway	RAS	Unremarkable
FGF Pathway	RAF1	Unremarkable

FGF Pathway	FGF2	Unremarkable
FGF Pathway	Sprouty2	Unremarkable
FGF Pathway	Perlecan	Unremarkable
WNT Signalling Pathway		
WNT Signalling Pathway	WNT3A	Unremarkable
WNT Signalling Pathway	MYC	Remarkable
WNT Signalling Pathway	Rock1	Unremarkable
WNT Signalling Pathway	ZIC1	Unremarkable
WNT Signalling Pathway	VDR	Unremarkable
WNT Signalling Pathway	AXIN2	Remarkable
WNT Signalling Pathway	FZD7	Unremarkable - missing sequence
WNT Signalling Pathway	FZD5	Unremarkable - missing sequence
WNT Signalling Pathway	CDC73	Conserved (with okapi and cow)
WNT Signalling Pathway	PHLDA1	Sequencing missing in giraffe and okapi
WNT Signalling Pathway	DVL2	Unremarkable
WNT Signalling Pathway	HDAC9	Unremarkable - missing sequence
WNT Signalling Pathway	DACT1	Unremarkable - missing sequence
WNT Signalling Pathway	TNFRSF19	Unremarkable - missing sequence
WNT Signalling Pathway	FZD3	Unremarkable
WNT Signalling Pathway	HAS2	Conserved (with okapi and cow)
WNT Signalling Pathway	PPP2R1A	Unremarkable
WNT Signalling Pathway	APC	Unremarkable
WNT Signalling Pathway	SMAD4	Unremarkable
WNT Signalling Pathway	LRP5	Unremarkable
WNT Signalling Pathway	DKK1	Unremarkable
WNT Signalling Pathway	FRZB	Unremarkable
WNT Signalling Pathway	TCF15	Unremarkable
WNT Signalling Pathway	FZD1	Unremarkable
WNT Signalling Pathway	CtBP1	Unremarkable
WNT Signalling Pathway	FZD9	Unremarkable
WNT Signalling Pathway	FZD4	Unremarkable
WNT Signalling Pathway	SMARCA5	Unremarkable
WNT Signalling Pathway	CER1	Unremarkable
WNT Signalling Pathway	DVL1	Unremarkable
WNT Signalling Pathway	GSK3A	Unremarkable
WNT Signalling Pathway	GSK3B	Unremarkable
WNT Signalling Pathway	SP5	Conserved (with okapi and cow)
Notch Pathway		
Notch Pathway	DTX3L	Unremarkable
Notch Pathway	MESP2	Unremarkable
Notch Pathway	LFNG	Unremarkable
Notch Pathway	MFNG	Unremarkable
Notch Pathway	DLL1	Unremarkable
Notch Pathway	DLL3	Remarkable
Notch Pathway	JAG1	Remarkable
Notch Pathway	DLL4	Unremarkable
Notch Pathway	APH1B	Unremarkable
Notch Pathway	HES7	Unremarkable

Notch Pathway	Ripply2	Unremarkable
Notch Pathway	PSN1	Unremarkable
Notch Pathway	PSN2	Unremarkable
Notch Pathway	Notch1	Unremarkable
Notch Pathway	Notch4	Remarkable
Notch Pathway	Notch2	Unremarkable
Notch Pathway	DLK1	Unremarkable
Notch Pathway	DLK2	Unremarkable
Notch Pathway	NUMBL1	Unremarkable
Notch Pathway	HES7	Unremarkable
Notch Pathway	HEY2	Unremarkable
Notch Pathway	PSEN1	Unremarkable
Notch Pathway	HES1	Unremarkable
Notch Pathway	MESP2	Unremarkable
Notch Pathway	NKD1	Unremarkable
Notch Pathway	RTF1	Unremarkable
Notch Pathway	NRARP	Conserved (with okapi and cow)
Hedgehog Pathway		
Hedgehog Pathway	CDX2	Unremarkable
Hedgehog Pathway	SHH	Unremarkable
Hedgehog Pathway	GLI3	Unremarkable
Hedgehog Pathway	SMO	Unremarkable
Hedgehog Pathway	TRPS1	Unremarkable
Hedgehog Pathway	IHH	Unremarkable
Hedgehog Pathway		
Others		
Others	Sox9	Unremarkable