1 >PRDM9_homSap. 13 prim gene CDH12 Homo..... sapiens..... (human)..... NM_020227 chr5 10 exon size 18,301 bp KRAB SSXRD SET C2H2 0 MSPEKSQEESPEEDTERTERKFM 0 0
VKDAFKDISIYFTKEEWAEMGDWEKTRYRNVRKNYNALITI 1 2 GLRATRPAFMCHRRQAIKLQVDDTEDSDEEWTPRQQ 1 2 VKPPWMALRVEQRKHQK 0 0 GMPKASFSNESSLKELSRTANLLNASGSEQAQKFVSPSGEASTSGQHSRLKL 1 2 ELRKKETEKMYSLRERKGHAYKEVSEPQDDDDYL 1 2
YCEMCQNFFIDSCAAHGPFTFVKDSAVDKGHPNRSALSLPPGLRIPSGIPQAGLGVWNEASDPLGLHFGPYEGRITDEEAANNGYSWL 0 0 ITKGRNCYEYVDGKDKSWANWMR 2 1 YVNCARDDEEQNLVAFQYHRQIFYRTCRVIRPGCELLVWYGDEYQGELGIKWGSKWKKELMAGR 1 2
EPKPEIHPCPSCCLAFSSQKFLSQHVERNHSSQNFPGPSARKLLQPENPCPGDQNQEQQYPDPRSRNDKTKQGEIEKERSKLLNKRTWQREISRAFSSPFKQGMGSCRVGKRIMEEESRTQGKVNPGNTGKLFVGVGISRIAK VKYGECGQGFSDKSDVITHQRTHTGEKP YVCRECGRFSWKSHLLSHQRTHTGEKP
YVCRECGRGFSWQSVLLTHQRTHTGEKP YVCRECGRGFSRQSVLLTHQRRHTGEKP YVCRECGRGFSRQSVLLTHQRHTGEKP YVCRECGRGFSWQSVLLTHQRTHTGEKP YVCRECGRGFSNKSHLLRHQRTHTGEKP YVCRECGRGFRDKSHLLSHQRTHTGEKP
YVCRECGRGFRDKSNLLSHQRTHTGEKP YVCRECGRGFSNKSHLLRHQRTHTGEKP YVCRECGRGFSDRSSLCTHQRTHTGEKP YVCRECGRGFSDKSLCTHQRTHTGEKP YVCREDE.....
2 >PRDM9_panTro. 19 prim gene CDH12 Pan..... troglodytes. (chimp)..... GU166820 chr5 frag assembly glitch in mid CD2H 0 MSPERSQEESPEGDTERTERKFM 0 0
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yCEMCQNFFIDSCAAHGPFTFVKDSAVDKGHPNRSALSLPPGLRIPSGIPQAGLRVWNEASDPPLGLHFGPYEGRITDEEAANSGYSWL 0 0 ITKGRNCYEYVDGKDKSWANWMR 2 1 YENCARDDEEQNLVSFQYHRQSFYRTCRVIRPGCELLVWYGDE GQELGIKWGSKWKKELMAGR 1 2
EPKPEIHPCPSCCLAFSSQKFLSQHVERNHSSQNFPGPSARKLLQPENPCPGDQNQEQQYPDPRSRNDKTKQGEIEKERSKLLNKRTWQREISRAFSSPFKQGMGSCRVGKRIMEEESRTQGKVNPGNTGKLFVGVGISRIAK VKYGECGQGFSDKSDVITHQRTHTGEKP YVCRECGRFSWKSHLLSHQRTHTGEKP
YVCRECGRFSVKSSLLSHRTHTGEKP YVCRECGRFSQGSHLLRHQRTHTGEKP YVCRECGRFSQGSHLLRHQRTHTGEKP YVCRECGRFSQGSALLIHQRTHTGEKP YVCREDE.....
3 >PRDM9_gorGor. -- prim gene cdh12 Gorilla..... gorilla..... (gorilla)..... CABD02290264 chr5 several contigs needed, most of ZNF domain missing 0 MSPERSQEESPEEDTERTERKFM 0 0
VKDAFKDISIYFTKEEWAEMGDWEKTRYRNVRKNYNALITI 1 2 GLRATRPAFMCHRRQAIKLQVDDTEDSDEEWTPRQQ 1 2 VKPPCMALRVEQRKHQK 0 0 GMPKASFSNESSLKELSRTANLLNASGSEQAQKFVSPPGEASTSGQHSRLKL 1 2 ELRKKETEGKMYSLRERKGHAYKEVSEPQDDDDYL 1 2
yCEMCQNFFIDSCAAHGPFTFVKDSAVDKGHPNRSALSLPPGLRIPSGIPQAGLGVWNEASDPLGLHFGPYEGRITDEEAANNGYSWL 0 0 ITKGRNCYEYVDGKDKSWANWMR 2 1 VVNCARDDEEQNLVAFQYHRQIFYRTCRVIRPGCELLVWYGDEYQGELGIKWGSKWKKELMAGR 1 2
EPKPEIHPCPSCCLAFSSQKFLSQHVERNHSSQNFPGPSARTLLQPENPCPGDQNQEQQYPDPRSRNDKTKQGEIEKERSKLLNKRTWQREISRAFSSPFKQGMGSCRVGKRIMEEESR TGQKVNPGNTGKLFVGVGISRIAK VKYGECGQGFSDKSDVITHQRTHTGEKP YVC.....
4 >PRDM9_ponAbe. 10 prim gene CDH12 Pongo..... abelii..... (orangutan)... XR_093432 chr5 frameshift extra a penultimate ZNF 0 MSPERSQEESPKGDTERTERKFM 0 0
VKDAFKDISIYFTKEEWTEMGDWEKTRYRNVRKNYKTLITI 1 2 GLRATRPAFMCHRRQAIKLQVDDTEDSDEEWTPRQQ 1 2 VKPPWMAFRGEQSKHQK 0 0 GMPKASFNNESSLKELSGTQNLLNTSGSEQAQKFVSPPGEASTSGQHSRLKL 1 2 ELRKKETEGTYSLRERKGHAYKEVSEPQDDDDYL 1 2
YCEMCQNFFIDSCAAHGPFTFVKDSAVDKGHPNRSALSLPPGLRIPSGIPQAGLGVWNEASDPLGLHFGPYEGRITDEEAANNGYSWL 0 0 ITKGRNCYEYVDGKDKSWANWMR 2 1 VVNCARDDEEQNLVAFQYHRQIFYRTCRVIRPGCELLVWYGDEYQGELGIKWGSKWKKELMPGR 1 2
EPKPEIHPCPSCCLAFSSQKFLSQHVERNHSSQNFPGPSARTLLQPENPCPGDQNQEQQYPDPRSRNDKTKQGEIEKERSKLLNKRTWQREISRAFSSPFKQGMGSCRVGKRIMEEESR TGQKVNPGNTGKLFVGVGISRIAK VKYGECGQGFSDKSDVITHQRTHTGEKP YVCRECGRFSWKSVLLSHQRTHTGEKP
YVCRECGRFSRRSVLLIHQRTHTGEKP YVCRECGRFSQGSVLLIHQRTHTGEKP YVCRECGRFSWKSVLLSHQRTHTGEKP YVCRECGRFSQGSVVFIHQRTHTGEKP YVCRECGRFSGKSVLFRHQRTHTGEKP YVCRECGRFSDKSGVCYHQRTHTRGEA
YVCRECGRGFSVKSNLLSHQRTHTEEKL YVCREDE.....
5 >PRDM9_nomLeu. 10 prim gene cdh12 Nomascus... leucogenys.. (gibbon)..... ADFV01015315 ADFV01015317 ADFV01015319 no CDH but best blastn favors PRDM9 0 MSPERSQEESPEEDTERTEQKPT 0 0
VKDAFKDISIYFTKEEWAEMGDWEKTRYRNVRKNYNALITI 1 2 GLRATRPAFMCHRRQAIKLQVDDTEDSDEEWTPRQQ 1 2 --- 0 0 --- 1 2 --- 1 2 AAHGPTFIKDSTVGKGHPNRSALSLPPGLRIGPSGIPQAGLGVWNEASDLPLGLHFGPYEGRITDEEAANNGYSWL 0 0
ITKGRNCYEYVDGKDKSWANWMR 2 1 --- 1 2 EPKAEIHPCPSCCLAFSSQKFLSQHVERNHSTQNFPGPSARKFLQPENPCPGDQNQEQQYSDPRSCNDKTKQGEIEKERSKLLNKRTWQREISRAFSSPKKQMGSCRVGKRIMEEESRTQGQKVNPGNTGKLFVGVGISRIAK VKYGECGQGFSDKSDVITHQRTHTGEKP
YVCRECGRGFSQKSSLLSHQRTHTGEKP YVCRECGRGFSDKSNLLSHQRTHTGEKP YVCRECGRGFSQKSSLLSHQRTHTGEKP YVCRECGRGFSDKSSLLRHQRTHTGEKP YVCRECGRGFSDKSDKSGVCYHQRTHTGEA
YVCRECGRGFSVKSNLLSHQRTHTGEKP YVCRECGRGFSDKSSLLRHQRTHTGEKP
6 >PRDM9_macNul. _9 prim gene CDH12 Macaca..... mulatta..... (rhesus)..... XM_001083675 chr6 exon 4 lost to Ns 0 MSPERSQEESPEEDTERTERKPT 0 0 VKDAFKDISIYFTKEEWAEMGDWEKTRYRNVRKNYNALITI 1 2
GLRATRPAFMCHRRQAIKLQVDDTEDSDEEWTPRQQ 1 2 --- 0 0 GMPKASFNNESSLKELSGTQNLLNTSGSEQAQKFVSPPGEASTSGQHSRLKL 1 2 ELRKKETEGGKMYSLRERKGHAYKEVSEPQDDDDYL 1 2
YCEMCQNFFIDSCAAHGPFTFIKDSAVEKGHPNRSALSLPPGLRIPSGIPQAGLGVWNEASDLPLGLHFGPYEGRITQDEEAANNGYSWL 0 0 ITKGRNCYEYVDGKDKSWANWMR 2 1 YVNCARDDEEQNLVAFQYHRQIFYRTCRVIRPGCELLVWYGDEYQGELGIKWGSKWKKELMAGR 1 2
EPKPEIHPCPSCCLAFSSQKFLSQHVERNHSTQNFPGPSARKFLPENLCSGDQNQEQQYSDPRSCNDKTKQGEIEKERSKLLNKRTWPREISRAFSSPFKQGMGSSRVGERMMEESRTQGKVNPGNTGKLFVGVGISRIAK VKYGECGQGFSDKSDVITHQRTHTGEKP YVCRECGRGFRDNSSLRCHQRTHTGEKP YLCRECGRGFRDNSSLRCHQRTHTGEKP YLCRECGRGFSDNSSLRYHQRTHTGEKP YLCRECGRGFRDNSSLRYHQRTHTGEKP YLCRECGRGFSVKSNLLSHQRTHTGEKP
YLCRECGRGFSVKSNLLSHQRTHTGEKP YLCRECGRGFSRKANLLSHQRTHTGEKP
8 >PRDM9_homSap. _3 prim gene GAS8+ Homo..... sapiens..... (human)..... genome chr16 TUBB3+ DEFB+ AFG3L1+ DBNDD1- GAS8+ PRDM7- 92% id 0 MSPERSQEESPEGDTERTERKFM 0 0
VKDAFKDISIYFTKEEWAEMGDWEKTRYRNVRKNYNALITV 1 2 GLRATRPAFMCHRRQAIKLQVDDTEDSDEEWTPRQQ 1 2 VKPPWMAFRGEQSKHQK 0 0 GMPKASFNNESSLRELSGTPNLLNTSDSEQAQKFVSPPGEASTSGQHSRLKL 1 2 ELRRKETEGKMYSLRERKGHAYKEISEPQDDDDYL 1 2
YCEMCQNFFIDSCAAHGPFTFVKDSAVDKGHPNRSALSLPPGLRIPSGIPQAGLGVWNEASDLPLGLHFGPYEGRITDEEAANNGYSWL 0 0 ITKGRNCYEYVDGKDKSWANWMR 2 1 YVNCARDDEEQNLVAFQYHRQIFYRTCRVIRPGCELLVWYGDEYQGELGIKWGSKWKKELMAGR 1 2
EPKPEIHPCPSCCLAFSSQKFLSQHVERNHSTQNFPGPSARKLLQPENPCPGDQNQERQYSDPRSCCNDKTKQGEIEKERSKLLNKRTWQREISRAFSSPFKQGMGSSRVGERMMEESRTQGKVNPGNTGKLFVGVGISRIAK VKYGECGQGFSWKSNLLSRQRTHTGEKP VYCRECGRGFSWKSDLLSHQRTHTGEKP
VYCRECERGFSRKSVLLIHQRTHRGDAP VCKKNE.....
9 >PRDM7_panTro. _2 prim pseu GAS8+ Pan..... troglodytes. (chimp)..... genome chr16 0 MSPERSQEESPEEDTERTERKFM 0 0 VKDAFKDISIYFTKEEWAEMGDWEKTRYRNVRKNYNALITI 1 2
GLRATRPAFMCHRRQAIKLQVDDTEDSDEEWTPRQQ 1 2 VKPPLMALRVEQRKHQK 0 0 GMPKASFSNESSLKELSRTANLLNASGSEQAQKFVSPPGEASTSGQHSRLKL 1 2 ELKKKETEGKMYSLRERKGHAYKEVSEPQDDDYL 1 2
YCEMCQNFFIDSCAAHGPFTFVKDSAVDKGHPNRSALSLPPGLRIPSGIPQAGLGVWNEASDLPLGLHFGYKGRITDEEAANNGYSWL 0 0 ITKGRNCYEYVDGKDKSWANWMR 2 1 YVNCARDDEEQNLVAFQYHRQIFYRTCRVIRPGCELLVWYGDEYQGELGIKWGSKWKKELMAGR 1 2
EPPKEIHPCPSCCLAFSSQKFLSQHVERNHSSQNFPGPSARKLQPENP PGDQNQERQYSDPRCCNDKTKGQEVKERSKLLNKWTWQREISRAFSSLPKGQMGSSRVGERMMEESRTQGKVNPGNTGKLFVGVGISRIAK VKYGECGQGFSRKSVLLIHQRTHNGEKP
VCRKDE.....
10 >PRDM7_gorGor. _3 prim pseu GAS8+ Gorilla..... gorilla..... (gorilla)..... genome chr15730 numerous frameshifts in terminal ZNF domain 0 MSPERSQEESPEGDTERTERKFM 0 0
VKDAFKDISIYFTKEEWAEMGDWEKTRYRNVRKNYNALITI 1 2 GLRATQPVFMCHRRQAIKLQVDDTEDSDEEWTPRQQ 1 2 --- 0 0 GMPKASFNNESSLKELSGTPNLLNTSGSEQAQKFVSPPGEASTSGQHSRRKL 1 2 ELRRKETEGKMYSLRERKGHAYKEISKPQDDDDYL 1 2
yCEMCQNFFIDSCAAHGPFTFVKDSAVDKHHPNRSALSLPPGLRIPSGIPQAGLGVWNEASDLPLGLHFGPYEGRITDEEAANNGYSWL 0 0 ITKGRNCYEYVDGKDKSWANWMR 2 1 YVNCARDDEEQNLVALQYHRQIFYRTCRVIRPGCELLVWYGDEYQGELGIKWGSKWKKELTAGR 1 2
EPPKEIHPCPSCCLAFSSQKFLSQHVERNHSSQNFPGPSARKLLQPENPCPGDQNQERQYSDPRCCNDKTKQGEIEKERSKLLNKRTWQREISRAFSSPFKQGMGSSRVGERMMEESRTQGKVNPGNTGKLFVGVGISRIAK VKYGECGQGFSWKSNLLSRQRTHTGEKP VYCRECGRGFSWKSDLLSHQRTHTGEKP
VYCRECGWGFSQKSNLLRHQRTHTGEKP YVCRECGRGFSRKSVLLIHQRTHTGEKP VCRKDE.....
11 >PRDM7_ponAbe. _4 prim pseu GAS8+ Pongo..... abelii..... (orangutan)... genome chr16 0 MSPERSQEESPEDDTERTERKPT 0 0 VKDAFKDISIYFTKEEWAEMGDWEKTRYRNVRKNYNALITI 1 2
GLRATRPAFMCHRRQAIKLQVDDTEDSDEEWTPRQQ 1 2 VKPPWMALRVEQRKHQK 0 0 GMPKASFNNESSLKELSRTANLLNASGSEQAQKFVSPPGEASTSGQHSRLKL 1 2 ELRSKETEGNTYSLRERKGHAYKEISEPQDDDDYL 1 2
YCEMCQNFFIDSCAAHGPFTFVKDSAVDKGHPNRSALSLPPGLRIPSGIPQAGLGVWNEASDLPLGLHFGPYEGRITKDEEAANNGYSWL 0 0 ITKGRNCYEYVDGKDKSWANWMR 2 1 YVNCARDDEEQNLVAFQYHRQIFYRTCRVIRPGCELLVWYGDEYQGELGIKWGSKWKKELMAGR 1 2
EPPKEIHPCPSCCLAFSSQKFLSQHVERNHSSQNFPGPSARKLLQANENCPGDQNQEQQYSDPRCCNDKTKQGEIEKERSKLLNKRTWQREISRAFSSAKQGMGSSRVGERMMEESGTQGKVNPGNTGKLFVGVGISRIAK VKYGECGQGFSVKSDVITHQRTHTGEKP YICRESGRGFTQKSGLLSHQRTHTGEKP
YVCRECGWGFSQKSNLLRHQRTHTGEKP YVCRECGRGFSRKSVLLIHQRTHTGEKP VCRKDE.....
12 >PRDM7_nomLeu. _5 prim pseu gas8+ Nomascus... leucogenys.. (gibbon)..... ADFV01125891 synteny implied by non-coding 0 --- 0 --- 1 2 --- 1 2 --- 1 2 IKSPWMAVRVEQSKHQK 0 0
GMPKASFNNESGLKELSGTQNLLNTSG EQARKFVSPPGEASTSGQHSRQKL 1 2 ELRRKETEGKMYSL ERKGHAYKEVSEPQDDDYL 1 2 yCEMCQNFFIDSCAAHGPFTFVKDSAVDKGHPNHSALSLPPGLRIPSGIPQAGLGVWNEASDLPLGLHFGYPEGRITDEEAANNGYSWL 0 0 ITKGRNCYEYVDGKDKS ANWMR 2 1
YVNCARDHEEQNLVAFQYHRQIFYRTCQVIKPGCELLVWYGDEYQGELGIKWGSKWKKELTAER 1 2 EPKPEIHPCPSCCLAFSSQKFLSQHVEQNHSSQNFPGPSARKLLQRENPCPGDQNQEQQYSDSRSCNDKTKQGEIEKERSKL NKRIWQREISRAFSSLPKGQMGSSRVGERMMEESRTGQKVNPGNTGKLFVGVGISRIAK
VKYGECGQGFSDKSDVIAHQHTHTGGKS .ICRECGWGFSQESHLLIHQRTHTGEKL YVCRECGQGFSQKSHLLSHQRTHTEEKP YVRRECGRGFSQKSNLLSHQRTHTEEKP YCRECGWGFSQKSHLLIHQRTHTGKKP VCRKDE.....
13 >PRDM7_macMul. _2 prim pseu GAS8+ Macaca..... mulatta..... (rhesus)..... genome chr20 frameshifts exon 5 and 10, exon 10 a to aa restores frame 0 --- 0 --- 1 2 --- 1 2
VKFPWMAFRVEQSKHQK 0 0 EMPKTSFNNESSLKELSGTSNLLSTSDSE AQKFASPPGEASTSGQHSRLKL 1 2 YCEMCQNFFIDSCAAHGPFTFVKDNAVNKGHPNRSALSLPPGLRIGPSGIPQAGLGVWNEASDLPLGLHFGPCEGRITDEEKAANSGYSWL 0 0
ITKGRNCYEYVDGKDKSWARKWMR 2 1 --- 1 2 EPKFEIYPCPSCCLAFSSQKFLSQHVERNHSSQNFPGPSARKLLQSENPCPGDQNQEQQYSDPRSCNDKTKQGEIEKERSKLLNKRTWQREILRAFTSPPKGQMGSSRVGERMMEEERTGQKANPGNTGKLFVGVEISRIAK VKYGECGQGFSGKSDVITHQRTHTEGKP
YVCRECGRFSQKSSLLSHQRTHTGEKP VCKKNE.....
14 >PRDM7_papHam. _2 prim pseu gas8+ Papio..... hamadryas... (baboon)..... genome contigs scattered 0 MSPERSQEESPEEDTERTEWKPM 0 0 VKDAFKDISIYFTKEEWAEMGDWEKTRYRNVRKNYNALITI 1 2
GLRATRPAFMCHRRQAIKLQVDDTEDSDEEWTPRQQ 1 2 VKPPWMAVRVEQSKHQK 0 0 GMPKASFNNESSLKEVSGMANLLNTSGSEQAQKFVSPPGEARTSGQHSRLKL 1 2 ELRKKETEGKMYSLRERKGHAYKEVSEPQDDDYL 1 2
YCEMCQNFFIDSCAAHGPFTFIKDSAVEKGHPNRSALSLPPGLRIPSGIPQAGLGVWNEASDLPLGLHFGYEGRITQDEEAANNGYSWL 0 0 ITKGRNCYEYVDGKDKSWANWMR 2 1 YVNCARDDEEQNLVAFQYHRQIFYRTCRVIRPGCELLVWYGDEYQGELGIKWGSKWKKELMAGR 1 2
EPPKEIYPCPSCCLAFSSQKFLSHHVERNHSSQNFPGTSTRKLLQPENPCPGKGKEEQQYPDPCNSNDKTKQGETEKERSKLLNIRTWQREMARAFSNPKKQMGSSRVEERMMEESRTQGKVNPGNTGKLFVGVGISRIAK AKYGECGQGFSGMSDVTGHQRTHTGEKP VYCRECGRGFSQKSHLLSHQRTHTGEKP
VYCRECGRGFSQKSSLLSHQRTHTGEKP VYCTECGRGFSRKSHLLSHQRTHTGEKP VYCRECGRGFSRKSHLLSHQGTHTGEKP VYCRECGRGFSRKSNLLSHQRHTGEKP VYCTECGRGFSQKSHLLSHQRTHTGEKP VYCRKCGRGFSQKSNLLSHQGTHTGEKP VYCRECGRGFSQKSHLLSHQRTHTGEKP
VYCRECGRGFSFKSALLRHQRTHTGEKP VYCRECGRGFSRKSHLLSHQGTHIGEKP VYCRECGRGFSRKSNLLSHQRHTGEKP YVRREDE.....
16 >PRDM7_tarSyr. -- prim pseu gas8+ Tarsius..... syrichta.... (tarsier)..... ABRT01100288 double frameshift in exon 5, ABRT01049286 0 --- 0 0 --- 1 2
GLRAPRPAFMCHRKRAIKPLVDDTEDSDEEWTPRQQ 1 2 --- 0 0 GMPRAPLSIVSSLKELSEMANLLNTSDSEQAWKFVSPSREASTSEQHSRKKL 1 2 EFRKKEIEVNMYSLRERKDCAYKEVNPEQDDDDYL 1 2
YCEQCQNFFIDSCATHGIPTFINDSAVDKGHPNRSALSLPPGLRIPSGIPQAGLGVWNEASDLPLGLHFGYPEGRITDEEAANNGYSWL 0 0 ITKGRNCYEYVDGKDKSWANWMR 2 1 YVNCARDDEEQNLVAFQYHRQIFYRTCRIIRPGCELLVWYGDEYQGELGIKWGSKWKKELMAGR 1 2 --- --- ---
17 >PRDM7_micNur. _8 prim gene gas8+ Mustela..... furonus..... (lemur) ABDC01433247 weak coverage (1 MSPEKSQEESPEEDTERTERKFM 0 0 vKDAFKDISIYFTKEEWAEMGDWEKTRYRNVRKNYNALITI 1 2
GLRATRPAFMCHRRQAIKLQVDDTEDSDEEWTPRQQ 1 2 VKPPWMARVEQRKHQK 0 0 GMPKASFNNESSLKELSRTANLLNASGSEQAQKFVSPSGEASTSGQHSRLKL 1 2 ELRKKETERKMYSLRERKGHAYKEVSEPQDDDYL 1 2
YCEKCQNFFIDSCAAHGPFTFVKDSAVDKGHPNRSALSLPPGLKIRPSGIPQAGLGVWNEASELPLGLHFGYEGQVTEDEEAANSGYSWL 0 0 ITKGRNCYEYVDGKDDSWANWMR 2 1 YVNCARDEEQNLVAFQYHRQIFYRTCRVIRPGCELLVWYGDEYQGELGIKWGSKWKKELTIRQ 1 2
EPPKEIHPCPSCSLAFSSQKFLSQHVKHTHSSQISPRTSGKKHLQPENPCPGDQNQEQQHSDPHSCNDKAKDQEVKERPKPFHKKTQQRGISRAFSSPPKGKMGSCREGKRINEEEPRTGQKVGPGDTGKLCAAGGISRISR VKYGDSQGSFSDKSNVIIHQRTHTGEKP YVCRECGRGFSQKSDLLKHQRTHTGEKP
YVCRECGRGSLLSHQRTHTGEKP YVGCRECGRGFSCKSSLLIHQRTHTGEKP YVCRECGRGFSCKSSLLIHQRTHTGEKP YVCRECGRGFSCKSSLLIHQRTHTGEKP YVCRECGRGFSCKSSLLIHQRTHTGEKP YVCRECGRGFSCKSSLLIHQRTHTGEKP YVCRECGRGLAALSTSTGHSQLLSH LPTPAKAGASKGSLLTLYISQCKETRN
18 >PRDM7_otoGar. _7 prim gene GAS8+ Otolemur... garnettii... (galago)..... genome good coverage 0 MSPEKSQEESPEEDTERTERKFM 0 0 VKDAFKDISIYFTKEEWAEMGDWEKTRYRNVRKNYNALITI 1 2
GLRATRPAFMCHRRQAIKLQVDDTEDSDEEWTPRQQ 1 2 VKHPWMAFRMEQSKRQK 0 0 ILKKCMLSFNMHLKELSGPASLPNISGSEQHQKHMSSPREASTSGQHSGRKS 1 2 DLRIKIEIEVRMYSLRERKGHAYKEVSEPQDDDYL 1 2
yCEKCQNFFIDNCAVHGPFTFVKDTAVEKGHPNRSVLSLPSGLGIRTSGIPQAGFGVWNEASDLPLGLHFGYEQVTEDEEAANSGYSWL 0 0 ITKGRNCYEYVDGKDESQGWNMR 2 1 YVNCARDEEEQNLVAFQYHRQIFYRTCVRIRPGCELLVWYGDEYQGELGIKWGSKWKKELTAGQ 1 2
EPKPEIHPCPSCSLAFSTQKFLSQHVERTHFSQISQGTSGKKNLRPQTPCPRDENQEQQHSDPHSRNDKTKQGEVKEMKSTSHKTQQSRISRIFSCPPKGQMGSSREGERMIEEEPRPDQKVGPGDTEKCVAIGISGIRK VKNRECVQSFSNKS NLRHQRTHTGEKP YMCRDCGRGFSHKSSLFRHQRTHTGEKP
VYCRDCGGFSQKANLLTHQRTHTGEKP VYCRDCQGGFSKAHLLRHQRTHTGEKP YVCRECCQGGFSQKAHLLRHQRTHTGEKP YVCRECCQGGFSQKSHLLRHQRTHTGEKP YVCRDCQGGFSQKSHLLRHQRTHTGEKP YVCRECGRGFSHSLFRHQRTHTGEKP YVCRDCGRGFSHQSHLLQHQRTHTGEKP
19 >PRDM7_tupBel. _9 prim gene noDet Tupaia..... belangeri... (tree_shrew).. AAPY01316756 most exons from traces 0 MRRYKSPEESPEGDAGRTEWKPT 0 0 VKDAFKDISYVFSKEEWAQMGEWEKIRYRNVRKNYTTLIAI 1 2
GLRAPRPAFMCHRKLAVKPHNDDAEDSDEEWTPRQQ 1 2 --- 0 0 --- 1 2 .....KMYSLRERKCGTYKEVHEPQDDDYL 1 2 yCEKCQNFFIDSCSAHGPFIFVKDSAVDKGSLNRSVLSLPPGLRIAPSGIPEAGLGVWNAATDLPLGLHFGYEGQITEDEEAANSGYSWL 0 0 ITKGRNCYEYVDGKDESCANWMR 2 1
YVNCARDDEEQNLVAFQYHRQIFYRTCRVIRPGCELLVWYGEEYQGELGIKWGSKWKSLWQGE 1 2 EPRPEIHPCLSCSLAFSSQKFLNQHVEHNHSSQRSLRTS .....QSSLIHRQRTHTGEKF YLCGECGRGFSRQSHLIHQRTHTGEKP YVCRECGRGFSQSHLIHQRTHTGEKP YCRKGE
VCGRECGRGFSQGSSLLHRQRTHTGEKP YVCRECGRGFSQGSSLLHRQRTHTGEKP YLCGECCGRGFSRQSHLIHQRTHTGEKP YSQPQLIHQRTHTGEKP YVCRECGRGFSQGSHLIHQRTHTGEKP YCRKGE
20 >PRDM9_oryCun. _8 glir gene other Oryctolagus cuniculus... (rabbit)..... genome Un0161 exon 2 ttt to tt restores frame; ZNF717+ DCAF4+ YAP1+ PRDM9- qTer 0 MSAAAPAEPSPGADAGQARGKPE 0 0
VQDAFRDISIYFSKEEWAEMGEWEKRYRNVRKNYCALVAI 1 2 GLRAPRPAFMCHRRLAVRARADDTEDSDEEWTPRQQ 1 2 VKPPWMAFRTEHSKHQK 0 0 GMPRLPVNNESSLKELSGTANLLKTTGSEEDQKFSPPKETRTSGQHSTRKL 1 2 GLRRKNIEVKMYSFRKRKSQAYKECSEPQDDDYL 1 2
YCEKCQNFFLDSCAVHGPIFVKDSAVDKGHPNRSVLSLPPGLRIPSGIPEAGLGVWNEASDLPLGLHFGYEGQVTEEEEAANSGYSWL 0 0 ITKGRNCYEYVDGKDRSWANWMR 2 1 YVNCARNDEEQNLVAFQYHKQIFYRTCQVIKPGCELLVWYGDEYQGELGIKWGSKWKELTAGR 1 2
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YACRECGRGFTVKSALITHQRTHTGEKP YACRECGRGFTVKSALISHQDTHTGEKP YACRECGRGFTVKSALISHQRTHTGEKP YACRECGRGFTQKSHLIHRLHARTGEKP YACRECGRGFTVKSDLISHQRTHTGEKP YACRECGRGFTVKSDSLISHQRTHTGEKP YACRVDE.....
21 >PRDM7_oryCun. _4 glir gene other Oryctolagus cuniculus... (rabbit)..... genome synteny novel 0 --- 0 0 --- 1 2 GLRAPRPAFMCHRRLAVRARADDTEDSDEEWTPRQQ 1 2 VKPPWMAFRTEHSKHQK 0 0
GMPRLPVNNESSLKELSGIANLLNTTGSEEQDKFSPPPKETRTSGQHSTRKL 1 2 GLRRKNIEVKMYSFRKRKSQAYKECSEPQDDDYL 1 2 YCEKCQNFFLDSCAVHGPIFVKDSAVDKGHPNRSVLSLPPGLRIPSGIPEAGLGVWNEASDLPLGLHFGYEGQVTEEEEAANSGYSWL 0 0 ITKGRNCYEYVDGKDRSWANWMR 2 1
YVNCARNDEEQNLVAFQYHKQIFYRTCQVIKPGCELLVWYGDEYQGELGIKWGSKWKELTAGR 1 2 EPKPEIHPCPSCSLAFSSHKFLSQHMECSHSSQIFPGAPARNHLQPANPCPGKEHQKLSDPQSWNDKNEQGDVKEKSRFSSKRTRQKAISRSFSSLPKGQVETSRSERMIEEEPRIGQELNPEDTGKSSVGAGLSRIAG
VKYRDCRQGLSDKSHLINGQRAHTGEKP YACRECGQSFTVKSNLISHQRTHTGEKP YACRECGRGFTQKSHLISHQRTHTGEKP YACRECGRGFTQKSNLISHQRTHTGEKP YACRVDE.....
22 >PRDM7_ochPri. -- prim gene noDet Ochotona... princeps.... (pika)..... AAYZ01312269 ubicus fragment, no orthologous terminal exon 0 --- 0 0 --- 1 2 --- 1 2 --- 0 0 --- 1 2 --- 1 2
yCEMCQNFFIESCAVHGSPTFVKD GHPHRSVLSLPSGLRIGPSGIPEAGLGVWNETTDLPLGLHFGPYEGQVTEEEEATNSGYSWL 0 0 ITKGRNRYEYVDGKDPSQANWMR 2 1 YVNCARNDEEQNLVAFQYHRQIFYRTCRAVRQGCELLVWYGDEYQGELGIKWGSKWKEELTAGR 1 2 --- --- ---
23 >PRDM7_ratNor. 10 glir gene PDCD2 Rattus..... norvegicus.. (rat)..... NM_001108903 chr1 FM103467 single transcript from body fat 0 MNTNKPEENSTEGDAGKLEWKPK 0 0
VKDEFKDISIYFSKEEWAEMGEWEKIRYRNVRKNYKNLISI 1 2 GLRAPRPAFMCYQRQAMKPQINDSEDSDEEWTPRQQ 1 2 VSPPWVPFRVKHSKQQK 0 0 ETPRMPLSDKSSVKEVFGIENLLNTSGSEHAQKPVCSPEEGNTSGQHSGKLI 1 2 ELRKRNVEVNYRLRERKGLAYEEVSEPQDDDYL 1 2
YCEKCQNFFIDSCPNHGPFLFVKDSMVDRGHPNHSVLSLPPGLRIPSGIPEAGLGVWNEASDLPVGLHFGPYEGQITEDEEAANSGYSWL 0 0 ITKGRNCYEYVDGQDESQANWMR 2 1 YVNCARDDEEQNLVAFQYHRQIFYRTCRVIRPGCELLVWYGDEYQGELGIKWGSKMKGFTAGR 1 2
ELRTEIHPCLLCSLAFSSQKFLTQHVEWNHRTEIFPGSARINPKFGDPCDSQLQEQHVDSQNKNDKASNEVKRKSKPRHWTRQRISTAFSSTLKEQMRSEESKRTVEELRTGQTTNTEDTVKSFIASEIS SIERQCGQYFSDKSNVNEHQKTHTGEKP YVCRECGRGFTQKSDLIKHQRTHTEEKP
YICRECGRGFTQKSDLIKHQRTHTGEKP YICRECGRGFTQKSDLIKHQRTHTEEKP YICRECGRGFTQKSSLIKHQRTHTGEKP YICRECGLGFTRKSNLIQHQRTHTGEKP YICRECGLGFTKSNLIRHLRTHTGEKP YICRECGLGFTRKSNLIQHQRTHTGEKP YICRECGRGFTWKSSLIQHQRTHTGEKP YICRECGRGFTWKSSLIQHQRTHTVEK.
24 >PRDM7_musMus. 12 glir gene PDCD2 Mus..... musculus.... (mouse)..... NM_144809 chr17 CN722438 eight transcripts, four from retina 0 MNTNKLEENSPEGDTGKFEWKPK 0 0
VKDEFKDISIYFSKEEWAEMGEWEKIRYRNVRKNYKMLISI 1 2 GLRAPRPAFMCYQRQAMKPQINDSEDSDEEWTPRQQ 1 2 VSPPWVPFRVKHSKQQK 0 0 ESSRMPSGESNVEKGSGIENLLNTSGSEHVQKPVSSLEEGNTSGQHSGKLI 1 2 ELRKKNVEVKMYRLRERKGLAYEEVSEPQDDDYL 1 2
YCEKCQNFFIDSCPNHGPFLFVKDSMVDRGHPNHSVLSLPPGLRIPSGIPEAGLGVWNEASDLPVGLHFGPYEGQITEDEEAANSGYSWL 0 0 ITKGRNCYEYVDGQDESQANWMR 2 1 YVNCARDDEEQNLVAFQYHRQIFYRTCRVIRPGCELLVWYGDEYQGELGIKWGSKMKGFTAGR 1 2
ELRTEIHPCLLCSLAFSSQKFLTQHMEWNHRTEIFPGTSARINPKFGDPCDSQLQEQHVDSQNKNDKASNEVKRKSKPRQRISTTFPSTLKEQMRSEESKRTVEELRTGQTTNTEDTVKSFIASEIS SIERQCGQYFSDKSNVNEHQKTHTGEKP YVCRECGRGFTQNSHLIQHQRTHTGEKP YVCRECGRGFTQKSDLIKHQRTHTGEKP
YVCRECGRGFTQKSDLIKHQRTHTGEKP YVCRECGRGFTQKSVLIKHQRTHTGEKP YVCRECGRGFTQKSVLIKHQRTHTGEKP YVCRECGRGFTAKSNLIQHQRTHTGEKP YVCRECGRGFTAKSNLIQHQRTHTGEKP YVCRECGRGFTAKSVLIQHQRTHTGEKP YVCRECGRGFTAKSVLIQHQRTHTGEKP
YVCRECGRGFTQKSDLIKHQRTHTGEKP YVCRECGWGFTQKSDLIQHQRTHTEK.
25 >PRDM7_musNol. 11 glir gene noDet Mus..... molossinus... (wild_mouse).. GU216230 full length deposit 0 MNTNKLEENSPEEDTGKFEWKPK 0 0 VKDEFKDISIYFSKEEWAEMGEWEKIRYRNVRKNYKMLISI 1 2
27

```
TCWVVRPGCELLVWYRDEYGQELSIK GSRHKSELTVRR 1      2 ---   ---    ---
34        >PRDM9d_oviAri  --      laur    gene    noDet   Ovis.......     aries.......    (sheep)......  genome  chr1 near end chr1      0 --- 0          0 --- 1 2 GLRATRLAFMHHCRQVIKPQVDDIEDSDEEWTPRQQ 1       2 --- 0 0 --- 1 2
--- 1   2 --- 0 0 ITKGRNCYEYVDGKDTSALANWMR 2      1 YVNCARDDEEQNLVAFQYDGQIFYRTCQVVRPGCELLVWYGDEYGQDLGIKRDSSGKSELAAGR 1   2 ---    ---    ---
35        >PRDM9c_oviAri  _4      laur    pseu    noDet   Ovis.......     aries.......    (sheep)......  genome  chr5 middle of 108,514,869 bp   0 --- 0          0 --- 1 2 GLRATRLAFMHHCRQVIKPQVDDIEDSDEEWTPRQQ 1       2 --- 0 0
GMSKALVSNKSSLKEMPGASKLLKTRGPKQAQIPVPAPREPSTSEQHPRQKV 1  2 --- 1 2                  HGLPTLVKDCAVEKGHANHSALSLSPGSSIRPSGIPEAGLGVWNKVSDLLLGLHFGSYVGQITDDEEAAKSGYSWL 0 0 --- 2 1 YVNGAQD KEQNLVAFLTHRQIFY
TCRVVRPGCELLVWYRDTYSQELSIKCGSRWKSELTASR 1      2 PMCSCSLAFSSQKFLSQHVKCNHPSQILLKTSARDRLQFEDPCFGNPNQQQQYSDLHSWSDKPEPSRESKEKPQPLLSKIRLRRISRASSYSSRGQMGGFRVHKRMREEPSTGKEVSPEDAGKLFMGEGVSRIMR        VKYGDCG GSKDRSSLMTHQRTHTGENF
YVCREYE.SFSEKSSLIKHQRTHTGEKP YVCRECWQSFGRKSTLTIHQRMHTHEKP CVCRECCGRSFSKKSTLITHQRTHTGQKP
36        >PRDM9b_oviAri  _2      laur    pseu    noDet   Ovis.......     aries.......    (sheep)......  genome  chrX not tandem: 62 mbp separation      0 MSPNRSPRENSTEGDAGRTEWKPM 0     0
AKDAFKDISIYFTKEEWAEMGEWEKIRYRNVKRNYEALIAI 1      2 GFRATQPAFMHHHRQVIKPQVDTEDSDEEEWTPRQQ 1       2 GKPSGMAFRGERSKHQK 0   0 RLSRGPLNVKSLSLKKLPGAAKLLKKTGSKAQGKPVPPPREARTPGQHPRHKV 1       2 ELRRKETEVKRYSLRERKGHVYQEVSELQDDDYL 1  2
yCEECQNFFIDSCAAHGPPTFVKDSAVEKGHANRSALTLPPGLSIRPSGIPEAGLGVWNEASDLPLGLHFGPYEGQVIYNEEASHSGYSWL 0   0 VTKGRNSYEYVDGKDTSLANWMR 2      1 YVNCARDDEEQNLVALQYHGQIFYRTCQVVRPGCELLVWYGDEYGEELGIKQDSRGKSKLSAQR 1    2
ELKPKIHPCASCSLFASSQKFLSQYVQPNHPSQILLRPSARDHLQFEDPCPGNQNEQQ YSDPHPSDKPEGCKAEKPFWLLKSMSVRISMASSYSPKGQMGSETHYRMTEEPSTSQKLNPEDIGKLFMGTGVSGIIK   IKYEECQVSKDRSSLITHEGTHTRSQS    YVCRECCGSFSVKSSLIRLQRTHTGEKP
Y.......................
37        >PRDM9a_oviAri  _9      laur    gene    noDet   Ovis.......     aries.......    (sheep)......  genome  chrX not tandem 0 MSPNRSPENSTEGDAGRTEWKPM 0     0 AKDAFKDISIYFTKEEWAEMGEWEKIRYRNVKRNYEALIAI 1    2
GFRATQPAFMHHHRQVIKPQVDTEDSDEEEWTPRQQ 1      2 GKPSGMAFRGERSKHQK 0   0 GMSRGPLSKVSSLKKLPGTTKLLKTSGSKQAQKPVPSSREARTSG HTRQKV 1       2 ELGRKETDMKRYSLRERKGHVYQEVSEPQDDDYL 1  2
yCQECQNFFINSCDAHGPPTFVKDSAVEKGHANRSALTLPPGLSIRLSGIPEAGLGVWNEASHLPLGLHFGPYEGQITDDEEAVNSGYSWL 0   0 --- 2 1 YVNCARHYEEQNLVAFQYHGQIFYRTCQVVRPGCELLVWYGDEYGEKLGIRCESRGKSMLAAGR 1    2
EPKPKIHPCASCSLFSSQKFLSQHVQRSHPSQILLRPSRPDHLQFEDPCPKGQNQQQRYSDPHSPSDKPEGQEPKERPHPLLKGPKLCIRLKRISTASSYTPKGQMGSSEVHEKNTEEPSTSQKLNPENTGKLFMEAGVSGIVR        VKYGEHEQGSKDKSSLITHERHTGEKEP    YVCKECGKSFNGRSNLTRHKRTHTGEKP
YVCRECGGSFSLKSILITHQRTHTGEKP YVCGECQGSFSEKSNLTRHKRTHTGEKP YVCRECGGSFSLKSILITHQRTHTGEKP YVCRECGRSFSVKSNLTRHKMTHTGEKP YVCGECQGSFSQKFHLIKHQRTHTGEKP YVCRECGRSFSAMSNLIRHQRTHTGEKP
YVCREC.....................
38        >PRDM9d_munMun  _4      laur    gene    noDet   Muntiacus...    muntjak.....   (muntjac)..... AC216498        frameshift exon 9 no syntenic loci; identities: 92kb 89ka 90kc  0 MRPNRSQEESTEGNAGRTERKPT 0     0
GKDAFKDISVYFSKEEWEEMGEWEKIRYRNMKRNYEALIAI 1      2 GFRATQPTFMHHRRQVIKSQVDDTEDSDEEWTPRQQ 1       2 GKPSSMAFRVEHSKHQK 0   0 RMSRAFLSNESGLKELPGAAKSLKTSDSKQANRVPHRHKARTPGQLPRQKV 1       2 ELRRKETGVKRYSLRERKGHVYQEVSEPQDDDYL 1  2
YCEECQNFFINSCAAHGPPTFVKDCAVEKGHADRSALTLPPGLSIRLSGIPDAGLGVWNEASDLPLGLHFGPYEGQITDDEEAANSGYAWL 0   0 ITKGRNCYQYVDGKDTSWANWMR 2      1 YVNCARDDEEQNLVAFQYHGQIFYRTCQVVRPGCELLVWCGDEYGQDLGIKRNSRGKSELVAGR 1    2
EPKPKIHPCASCSLFASSQKFLSQHIQRSHPSQTLLRPSERDLLQFEDPCPGNQNQRFSDPHSPSDKPEGQEHEAKDRPQPLLKSIRLKRISRASSCSPRGQMGGSGVHERMTEEPSTSQKLNPGDTGTLLTGAGVSGIMK    VKYGECQGGSKDRSSLSTHERTHTGEKP    YVCRECGQGFSGKPVLIRHQRTHTGEKP
YVCMECGRSFSAKSVLMTHHRTHTGEKP YICRECGQSFSQKIHLIRHQRIHTGE.P SVFRECE.......................
39        >PRDM9c_munMun  15      laur    gene    noDet   Muntiacus...    muntjak.....   (muntjac)..... AC154919        no syntenic loci AC204173 99% identical 0 MRPNRSPEESTEGDAGRTEQKPT 0     0
AKDAFKDISVYFSKEEWEEMGEWEKIRYRNMKRNYEVLIAI 1      2 GFRATRPDFMHHRRQVIKPQVDTEDSDEEWAPRQQ 1       2 GKPSSVAFRVEHSKHQK 0   0 RMSRAFLSNESGLKELPGAAKPLKTSGSKQANPVPHRHKARTPGQLPRQKV 1       2 ELRRKETGVKRYSLRERKGHVYQEVSKPQDDDYL 1  2
YCEECQNFFIDSCAAHGPPTFVKDCAVEKGHANRSALTLPPGLSIRLSGIPDAGLGVWNEASDLPLGLHFGPYEGQITDDEEAANSGYAWL 0   0 ITKGRDCYQYVDGKDTSWANWMR 2      1 YVNCARDDEEQNLVAFQYHGQIFYRTCQVIRPGCELLVWCGDEYGQDLGIKRNSRGKSELVAGR 1    2
EPKPKIHPCASCSLAFSSQKFLSQHIQRSHPSQTLLRPSERDLLQFEDPCPGNQNQRFSDPHSPSDKPEGQEAKDRPQPLLKSIRLKRISRASSYSPRGQMGSGVHELMTEEPSTSHKLNPEDTGTLLMGAGVSGIMT    VTYGECQGGSKDRSSLSTHERTTYTGEKF    YVCGECGRSFCQKAHLITHQRTHTGEKP YVCRECGQSFSRNSLLIRHQRIHTGEKP
YVCGECGRSFRDKSNLISHRRTHTGEKP YVCGECGQSFSDKSNLIRHQRTHAGEKP YVCGECGRSFNRKSHLITHQRTHTGEKP YACRECGQSFSQKSILITHQRTHTGEKP YVCRECGRSFSQKSSLLITHQRTHTGEKP YVCMECGRSFSQKTHLITHQRTHTGEKP
YVCGECGRSFSQKSLLITHQRTHTGEKP YVCGECGRSFSQKSLLITHQRTHTGEKP YICMECGRSFSQKTHLITHQRTHTGEKP YVCGECGRSFSDKSNLISHKRTHTGEKP YVCGKCGQSFSDKSNLISHKRTHTGEKP YVCRECGRSFNRKSLITHQRTHT.E.P YVCRECE.......................
40        >PRDM9b_munMun  13      laur    gene    noDet   Muntiacus...    muntjak.....   (muntjac)..... AC218859        no syntenic loci          0 MRPNTSPEESTEGDAGRTERKPT 0     0 AKDAFKDISVYFSKEEWEEMGDWEKSRYRNMKRNYEVLIAI 1    2
GFRATRPDFMHHRRQVIKPQVDDTEDSDEEWAPRQQ 1      2 GKPSSMAFRVEHSKHQK 0   0 RMSRAFLSNESGLKELPGAAKPLKTSGSKQANPVPHRHKARTPGQLPRQKV 1       2 ELRRKETGVKRYSLRERKGHVYQEVSKPQDDDYL 1  2
YCEECQNFFIDSCAAHGPPTFVKDCAVEKGHANRSALTLPPGLSIRLSGIPDAGLGVWNETSDLPLGLHFGPYEGQITDDEEAANSGYAWL 0   0 ITKGRNCYQYVDGKDTSWANWMR 2      1 YVNCARDDEEQNLVAFQYHGQIFYRTCQVIRPGCELLVWYGDEYGQDLGIKRNSRGKSELATGR 1    2
EPKPKIHPCASCSLAFSSQKFLSQHIQRSHPSQTLLRPSERDLLQFEDPCPGSQNQRYSDPHSPSDKPEGQEAKDRPQQLLKSIRLKRISRASYSPRGQMGSGVHERMTEEPSTSQKLNPEDTGTLLTGAGVSGIMR    VTYGCWKGSKDRSSLLTHERTHTGEKP    YVCGECGQSFHHGSVLIRHQRTHTGEKP
YVCGECGRSFSQKSVLIRHQRTHTGEKP YVCGECGRSFSQKSVLIRHQRTHTGEKP YVCGECGRSFSQKFHLIRHQRTHTGEKP YVCGECGRSFSQKSSLIRHQRTHTGEKP YVCGECGRSFSQKTHLIRHQRTHTGEKP YVCGECGRSFSQKSLLITHQRTHTGEKP YVCGECGRSFSQKSILITHQRTHTGEKP YVCMECGRSFSQKTHLITHQRTHTGEKP
YVCGECGRSFSQKSVLIRHQRTHTGEKP YVCGECGRSFSQKSLLITHQRTHTGEKP YVCGECGRSFSQKTHLSSHQRTHTGEKP YVCGECGRSFSQKSVLIRHQRTHTGEKP YVCQECGRSFSDKSNLISHKRTHMGEKP YVCRECGRSFIRKSVLIRHQRTHTGE.P YVCRECE.......................
42        >PRDM7_bosTau.  --      laur    pseu    GAS8+   Bos.........    taurus......   (cattle)......  genome  missing C2H2     0 MSPNRSPEESIEGDTGRTEWKPT 0     0 AKDAFKDISIYFCKEEWAQMG WEKIRYRNVKRNYEALITL 1   2 --- 1 2 --- 0 0
--- 1   2 --- 1 2 --- 0 0 --- 2 1 --- 1 2 ---   ---    ---
43        >PRDM7_turTru.  _9      laur    gene    gas8+   Tursiops....    truncatus...   (dolphin)..... ABRN01441536    no useful synteny       0 MSTDRWPEDSTEGDAGRTAWKPT 0     0 VKDAFKDISIYFSKEEWTEMGEWEKIRYRNVKKNYEALVTL 1    2
GLRAPRPAFMCHRRKAIKPQVDDTEDSDEEWTPRQQ 1      2 VKPSWNAFVEHSKHQK 0    0 AVPPVFLSNESSLKELPGAAQLGPKTSGSKQAQSPRPSPEAISAHHTRQKL 1       2 ERRAQGIVEVKMYSLRERKGHAYQEVSEPQDDDYL 1  2
yCEKCQNFFIDSCAAHGAPTFVKDCAVEKGHANRNSALTLPPGLSIRPSGIPEAGLGVWNEASDLPLGLSIRPSGIPEAGLGVWNEASDLPLGLHFGPYEGQITDDEEAANSGYSWL 0   0 ITKGRNCYEYVDGKDTSWANWMR 2      1 YVNCARDDEEQNLVAFQYHRQIFYRTCRVVRPGCELLVWYGDEYGQELGIKWGSGWKSQLVAGR 1    2
DPKPKIQPCGSCSLAFSSQKILSQHVECSHPSQVLPRTSARDRVQFEDPCPGYQNRQQQYSDPHSWSNKPECQEVKERSKPLLKKIRLGRISRAFSSSPKGQMGSSRAHERMMEAGPSTGQKVNPEATGKLLIGAGVSRVVK  VKYRSSGQGSKDRSSLTKHQRTHTGEKP    YVCGECGRDFSLKSDLIRHQRTHTGEKP
YVCGECGRDFSLKSGLISHQRTHTGEKP YVCGECGRDFSQKSGLIRHQRTHTGEKP YVCGECGRDFSLKSGLITHQRTHTGEKP YVCGECGRDFSQKSNLITHQRTHTGEKP YVCGECGRDFSQKSFLSKGLITHQRTHTGEKP YVCGECGRDFSRKSSYI...........
44        >PRDM7_lamPac.  _2      laur    gene    noDet   Lama........    paccos......   (llama)....... scaffolds      most exons from traces  0 --- 0          0 TFKDISIYFSKEEWTEMGEWEKIRYRNVERNYEALITI 1      2
GLRAPRPAFMCHRRKAIKPQVDDTEDSDEEWTPRQQ 1      2 --- 0 0 GMPRGPLSNQSSLKELSGTAKPLKTSGSGQAQKPFPPLGEASTSGRHSRQKL 1       2 ELRRKESQVKMYSLRERKGHAYQEVSEPQDDDYL 1  2 --- 0 0 ITKGRKCYEYVDGKDKYWANWMR 2      1
YVNCARDDEEQNLVAFQYHRQIFYRTCRVIRPGCELLVWYGEEYGQELGIKWGSKWKKSLWQGE 1      2 EPKYILCPSCSLAFSQKFLSQHVKHNHPSQILPRTAAGRHLEPEDPCPGNQNEQQQHSDHSWNDKPEGQEAEKERSKPFLKRILRLRRISARSAFSYSHKGQMGNSRVHDRMIEEEPSTGQKVNPKDTGKLFTWAGVSRTVE
VNYGEYGQGCKDTSHLTTHQRTHTGEKP    YVCRECGRGFTRKSNLTIHQRETHTGEK
YVCREC.....................
44        >PRDM7_susScr.  _9      laur    gene    GAS8+   Sus.........    scrofa......   (pig)......    FP476134        unordered HTGS not wgs mirassembly or inversion; not in genome browser  0 MRPDRRPREESPDPAAGSTERKAA 0     0
ATDAFKDISIYFSKEEWTEMGEWEKIRYRNVKRNYEALTTI 1      2 GLRAPRPAFMCHRRQAIKPQVDDTEDSDEEWTPRQQ 1       2 VKPCVAFAFVEHNHRQK 0   0 SDSRVPLSNESSLKELLTTAKVPTSSGSEQAQEPVSPPGEASTSRRSPGQEL 1       2 ARRKRCTEAKMYSLRERKGHAYQEVGEPQDDDYL 1  2
yCEKCQNFFIDSCAAHGPPTFVKDSAVDKGHPNRSALTLPPGLIRPSGIPEAGLGVWNEADLPLGLHFGPYEGQVTDDEEAANSGYSWL 0   0 ITKGRNCYEYVDGKDKSWANWMR 2      1 YVNCARDDEEQNLVAFQYHRQIFYRTCRVVRPGCELLVWYGDEYGQELGIKWGSKWKKELTAGI 1    2
EPKPKIHPCSCSLAFSSQRFLSQHVERSHPSQSLPRASARRGLQFEGPCPDNQNQQQQYPDPHSWDGTSESGDVKEGSKPFLERRRLRKTSRASSYAYPEGQMRSSRVRERMTEEEPSAGQKVNPEDTGRLTVFAGES    GILRVENGRYGPDSGLTRHPRTHTGEKP    HVCSECGRGFSVKSHLIRHQRTHTGEKP
YVCRECGRGFSVKSHLIRHQRTHTGEKP YVCRECGRGFSVKSSLITHQRTHTGEKP YVCRECGRGFSVKSHLIRHQRTHTGEKP YVCRECGRGFSKESSLVTHQRTHTGEKP YVCRECGRGFSVKSSLVTHQRTHTGEKP YVCRECGRGFSVKSNFITHQRTHTGEKP YVCRECGRGFSKESSLVTHQRTHTGEKP
YVCREGE.....................
46        >PRDM7_canFam.  _5      laur    pseu    GAS8+   Canis.......    familiaris..   (dog)......    genome  frameshift fixed to 6 ZNF; synteny MNS1 K1F1B intervening CDH3 oddity   0 --- 0          0 --- 1 2 --- 1 2
VKPSWVAFRMEQSKHQK 0     0 GIPRVPLSNKSSLKELSETAKLLNTSSPEQGGKSVSLPGKASTSGHHTRQKL 1       2 ELRRKDVEVKMYSLQERKGLAYQEVSEPQDDDYL 1  2 yCEK QTFFIDSCTVHGPPTFVKDSEVDKGQPNHSALTLPPGLRIRTSSIPQAGLGVWN ASDLPLGLHFGPYKGQITEDEEAANSGYSCL 0 0
ITKGRNCYEYVDGKDkSWANWMR 2      1 YMNCARDDEEQS LVAFQYHRQIFYRTFPGHQASCELLVWYGDEYSQELGIKWGSKWKSELTAGK 1    2 EPNPEIHPCFSCSL
AFSSQKFLSQHLEHNHPSQILPRISVREHFRPKDPCPGCQNQQQQQHSDPQRWNDRAKGQEGKERFKPLPKSIRQRRISRAFSTPCKGQTTCEGIVKEEPSAGSQKLNPEDTGKLIFKGVGMTRIIR  VKYRGCGRGFNDRSHLSRHQRTHTGENP    YVCRECGRGFIHRTNLIIHQRTHTGEKP YVCRECGTGFIQRSNLSIHQRTHTGEKP
YVCRECGRGFTQRSTLNEHQRTHTEEKP YVCRECGGSFTRRSTITHQRTHTGEKP YVCRECGSSFT.......................  KRSTWDPVVAQRFGACLMP.........  YVCRECGRGFSVKSHLIRHQRTHTGEKP
47        >PRDM7_felCat.  11      laur    gene    GAS8+   Felis.......    catus.......   (cat)......    genome  two contigs GAS8 implied by downstream CAD1    0 mSPLRFPEGSASRKARWKPT 0     0
AKDAFKDISIYFSKEEWTEMGDWEKIRYRNVKRNYEALMTI 1      2 GLRAPRPAFMCHRRQAIKPQVDVTEDSDEEWTPRQQ 1       2 VKPSWVASRVDQNKQHK 0   0 GTHRVPLSKESSLKDFSETAKLLNTSGSEQGQKPVSLPGEASTSGHHSRRKL 1       2 frRRKIGVKMYSLRERKGFAYQEVSEPQDDDYL 1  2
yCEKCQNFFIDSCAVHGPPTFVKDNAVGKGHPNRSALTLPPGLRIRPSSIPEAGLGVWNEASDLPLGTHFGPYEGQITDEEEAANSGYSWL 0   0 ITKGRNCYEYVDGKDNSWANWMR 2      1 YVNCARDDEEQNLVAFQYHRQIFYRTCRVIRPGCELLVWYGDEYGQELGIKWGSKWSKSELTAGK 1    2
EPGPDIHRCPSCSLAFSSQKFLSQHVECKHSSQSLPQISARKHFQPENPCPGDQNQQQQQHSDPHSWNDKAKCQEVKERSKPLLKSIKQRRISRAFSTPCKGQMGSSRVCEGMVEEGPSMGQMLNSEDTGKLFMGVGMSRIVR IKNRGCEGQFNDRSHFSRHQRTHKEEKP    SVCNEFRRDFSHKSALITHQRTHTGEKP
YVCRECGRGFTQRSNLFRHQRTHTGEKP YVCRECGRGFTWRSNLFTHQRTHTGEKP YVCRECGRGFTQRSNLFRHQRTHTGEKP YVCRECGRGFTQRSLFRHQRTHTGEKP YVCRECGRGFTQRSLLTHQRTHTGEKP YVCRECGRGFTQRSLTHQRTHTGEKP YVCRECGRGFTQRSLTHQRTHTGEKP YVCRECGRGFTQRSLTHQRTHTGEKP
YVCRECGRGFTQRSNLIRHQRTHTGEKP YVCRECGRGFTQRSNLIRHQRTHTGEKP YVCRECGRGFTQRSLIRHQRTHTGEKP YVCRECGRGFTQRSLTHQRTHTGEKP YVCRECGRGFTRPNLIGHQRTHTEALP INYISTTKEQM................
49        >PRDM9/pteVam.  15      laur    pseu    noDet   Pteropus....    vampyrus....   (bat)......    ABRP01232219    frameshift ttt to tttt fixed in last zinc finger; no blastx synteny     0 --- 0          0 --- 1 2 --- 1 2
vQPSWVAFVQEQSKHQK 0     0 AMPRVPLSNESSLKELSVIANPLKASGEEPGENQQPVYPPGKASASRPGHSRRKL 1       2 eLRRKGVEVKMDSLERERMGRVYQEVSEPQDDDYL 1  2 yCEKCQNFFIDSCAAHGSPIVFKDSEVDIGHPNHSALTLPLGLRIGPSIPEAGLGVWNEASDLPLGLLFGPYEGQVTDEDEEAANSKYSWM 0 0
mpKEGTAEKV DGKDESRAWNMR 2      1 YVNCARDDEEQNLVAFQYFRRQIFYRTCRVIMPGCELLVWYGDQGLIKWGSWKEKFAEK 1    2
EPKPEIHPCFSCSLAFSSRKFLSQHMKRSHPSQSLPGISARKHLQSKEPHPEDQSQQQQQQQHTDPCSWNDKAEGQEVKERSKPMLERNGQRKISRAFSKPPKGQMGSPRECERMMEAEPSTSQKVNPENTGKSSVGVGASRIVR     VKYGGCGHGFDDGSHFIRHQRTHSGEKP    FVCRECERGFNEKSSLTMHQRTHSGEKP
FVCREC.EGFSVKSSLIRHQRTYSGEKP FVCRECEQGFNEKSSLTMHQRTHSGEKP FFCRECEGFSVK.SSLIRHQRTHSGQKP FVCRECKRGFTQKSHLITHQRTHSGEKP FCRECER.GFTQKSHLIKHQRTHSGEKP FVCRECA.......................
50        >PRDM7_pteVam.  _7      laur    gene    GAS8+   Pteropus....    vampyrus....   (bat)......    ABRP01250178    4 distal exons of GAS8+-; unique F sweep in zinc finger; 15 ZNF dotplot no CAD1 0 MRPDRSPEEAPEGDTRRTGCKPK
0 0 AKDAFKDISIYFSKEEWTEMGDWEKIRYRNVERNYALQAI 1      2 GLRAPRPAFMCRRRQAIKPQVDDSEDSDEEWTPRQQ 1       2 --- 0 0 AMPRVPLSNESSLKELSVIANLLKASGSEQDQGKFVPPPGEASASRQHSRQKL 1    2 GLRRKGVEVKMYSLRERTGRVYQEVSEPQDDDYL 1  2
yCEKCQNFFIDSCAANGSPIFVKDSEVDIRHPNRSALTLPPGLRIGPSIPEAGLGVWNEASDLPLGLLFGPYEGQVTDEDEEAANSGYSWL 0   0 QGKGRNCYEYVDGKDESRAWNMR 2      1 YVNCARDDEEQNLVAFQYHRQIFYRTCRVVIRPGCELLVWYGDEYGQELGIKWGSKWKEELTAGR 1    2
EPKPAIHPCPSCSLAFSGQKFLSQHMKRSHPSQSLPGISARKHLQSKEPHPEDQSQQQNNDPRSWNDKAEGQEVKERSKPLLERNRQRKIFRAFSKPPKGQMGSPREYERMMEAEPSTSQKVNPENTGKSSVGVGASRIVI    VKYGGCHRGFDDGSHLIMHQRTHSGEKP    FVCRECERGFSKKSNLITHQRTHSGEKP
FVCRECERGFTRKSSLITHQRTHSGEKP FVCRECERGFTQKSHLITHQRTHSGEKP FVCRECERGFSEKSSLIKHQRTHSGEKP FVCRECERGFTQKSSLIKHQRTHSGEKP FVCRECERGFTQKSSLITHQRTHSGEKP FVRECERGFTQKSSLITHQRTHSGEKP FVCRECERGFTKESYLITHQRTHSGEKP FVCRECERGFTSKSSLIKHQRTHSGEKP
FVCRECERGFTQKSSLITHQRTHSGEKP FVCRECERGFTQKSHLITHQRTHSGEKP FVCRECERGFSKKSNLITHQRTHSGEKP FVCRECERGFTKESYLITHQRTHSGEKP FVGRECE.....................
51        >PRDM7_mycLuc.  _6      laur    gene    gas8+   Myotis......    lucifugus...   (bat)......    AAPR02062260    TGA stop codon; CpG hotspot for 8 CGA; SXXRD implies missing KRAB no CAD1  0 --- 0          0 --- 1 2
--- 1   2 --- 0 0 AKSRAPLSNESSLKELSGTANLLTTSGSEQTQKTVPPPGEASTSGQHRSKL 1      2 dLRRKEIEVKMYSLRERKCRVYQEISEPQDDDYL 1  2 YCEKCQNFFIDSCAVHGPPTFVKDSAVDKGHANRSALTLPPGLRIGPSGIPEAGLGVWNEEADLPLGLHFGPYEGQITDEDEAIANSGYSWL 0 0
ITKGRNCYEYVDGKDTSQANWMR 2      1 YVNCARDDEEQNLVAFQYHRQIFYRTCRVVRKGCELLVWYGEEYGQELGIKWGSKWKRELTAGR 1    2
EPKLEIHPCFSCSLAFSSQKFLSQHVERNHPSQILPGTSARNHLQFEDPSPGDQNQQQQHSDPHSWKDKAHSQEVKERSKPLLKKIRQRRIPRAFSYPPKGQMENFRMRERIMEEKPSIGRKVNPEDTGKLFMERNSRNVR  VQYGGCGRGFNDRASLIKHQRTHTGEKP    YVCRECEQGFTQKSSLIAHQRTHTGEKP
YVCRECEQGFSEKSRLIHHQRTHTGEKL YVCRECEQGFSVKSSLIRHQRTHTGEKL .FCRECEK.......................  ....................
53        >PRDM7_sorAra.  _8      laur    gene    noDet   Sorex.......    araneus.....   (shrew)....... AALT01000095    no useful synteny; upstream spectrin, IgG; GAS8 contig has no sign of pseudogene  0
MSLNRPAEMNTQGKARKLMLKPM 0      0 SKDAFKDISMYFSKEEWAEMGDWEKIRHRNVKRNYEELISI 1    2 GLRAAARPAFMSHRRQAIKTQLDDTEESDEEWTPNQQ 1       2 VKSLRVAFRAAEQSKHQK 0   0 GRSRTPISNESSSKELSGTRTLLNTKCTKQAQKFLPPGEASTSGHYSKPKL 1       2
ELRRKEPEVKMYSLRERKGRAYQEVSEPQDDDYL 1    2 YCENCQNFFINKCSAHGSPIFVKDNAVAKGHSNRSALTLPHGLRIGPSGIPEAGLGIWNEASDLPLGLHFGPYEGQITNDEEAANSGYSWL 0   0 ITKGRNCYEYVDGVDESLANWMR 2      1
YVNCARDYEEQNLVAFQYHRQIFYRTCRIIKPGCELLVWYGDEYGQELGIKWGSKWKSELTADR 1    2 EPKPEIYPCPCCSLAFSKNQKFLSRHVEHSHPSILLPGTSARTHPKSVNFCPGDQNQWQQHSDACNDKPDEPWNDKLEHHKSKGRSKPLKRKMGQKRISTAFPNLRSSKMGSSNKHETIMDKINTGQKENPKDTYRVFAGIGMPRIIR
DKHVTLRSRPTHRSKPTHRQRTHTGEKP    YVCRECGRGFSQKSHLITHQRTHTGEKP YVCRECCGRGFTDRSSLLTMQRTHTGEKP YVCRECGRGFSLKSSLLRHQRTHTGEKP YVCRECGRGFTDRSSLLTHQRTHTGEKP YVCRECGRGFSLKSSLLTHQRTHTGEKP YVCRECGRGFTDRSSLLTMQRTHTGEKP YVCRECGRGFSLKSSLLTHQRTHTGEKP
YVCRECCGRGFSRKSSLLRHQRTHTGEKP YVCES.......................
54        >PRDM9a_loxAfr  12      afro    gene    noDet   Loxodonta..     africana....   (elephant)..... genome  chr 153 novel synteny THEG+ MIER2+ PPAP2C PRDM9- ZNF699-     0 MSPARAAKKNPRGDVGSAGRTPT 0     0
aKDTFRDISIYFSKEEWAEMGEWEKFRYRNVKRNYEALVTI 1      2 GLRAPRPAFMCHRRQAIKAQVDNTEDSDEEWTPRQQ 1       2 VKPPSVASRAEQSRHQK 0   0 GTPKALLGNESSLKEVSGTAILLNTTGSEQAQKFVSSPGEASTSDQPSRWKL 1       2 ERRNNEVEVKMYNLRERKGLEYQEVSEPQDDDYL 1  2
yCEKCQNFFIDTCSVHGAPMFVKDSVVERGHPNRSALTVPPGLRIGPSSIPEAGLGVWNESALPLGLHFGPCEGQVTEDEEAANSGYSWL 0   0 ITKGRNCYEYVDGKNEAWANWMR 2      1 YVNRARDTEENKSAYQHRQIFYRTCRTCRVQPGCELLVWYGDEYGQELGIKWGSRWKKELTSGR 1    2
EPKPEIHPCPSCLAFSSQKFLSQYHVNHSHSSEPFPGTHARKHLPREDPRPGYERDSEQRHWNDSTGGPEDVSRP VIERTWEGEISACCSSLPRGHMGRSREGERMAETQSSPGLKVTLAK  VRWDEYGQGFGPKSHHITQQTKHSGKKP    CVCKECG GFRVKSLLKSHQMTHSGEKP YVCRECGRGFVKSLITHQRTHSGEKP
YVCRECGGFRWKSHLIRHQRTHSGEKP FVCSECGRGFSWKSGLITHQRTHTGEKP YVCRECGRGFSVKSYLITHQRTHTGEKP YVCRECGRGFSWKSHLITHQRTHSGEKP YVCRECGRGFSVQSHLITHQRTHSGEKP YVCRECGRGFSKSSLIRHRRTHSGEKP YVCRECDCG FSVKSLLITHQRTHSGEKP
YVCRECGRGFSKESYLISHQRTHSGEKP YVCSDCGRGFSVKSQLVSHKRTHSGEKP FVCREC RGFSVKSSLISHQRTHSGEKP YVCRECGRGFSVKSSLIKHQRTHSGEKP YVCRECGRGFGLKSYLITHQRTHTGEKP YICRECG GFSVKSSLITDQRTHTGEKP
YVCRECGRAFSKESSLISHHRTHPAEAV YVHRECG.......................  ....................
59        >PRDM7b_proCap  13      afro    pseu    noDet   Procavia...     capensis....   (hyrax)....... ABRQ01392668    CpG stop in ZNF1, 4aa insert exon 4, frameshift exon 5 c to cc, 4aa del exon 9 etc     0 --- 0          0
AKEYFRDISMFFS ERWVEMSESEKFCYRNMKRNCETTGAG 1      2 GIRVPHPAFMIHPRKTIKAQMDDSEDSDEDWTARQQ 1       2 AKPPSVASREELRKPQK 0   0 GPSRAPLRIKSSLKRVSEPAIVWSTADSEQAQERVQKPVLSRREASASDQPLRRKV 1    2 EPRRHEAEDKRYSLRGGTGPACQEVGEPQDDDYL 1  2
yCEECRNFFIDTCVAHGTPVFIKDISVERGHPNRLALTLPTGLRIGPSSIPDAGLGVWNEASELPPGLHFGPCEGQVTEDEEAANSGYSWL 0   0 VTKGRSCTEVYDGKNEALANWMR 2      1 YVRARDTEENKHLYRQIFYRTCRFQCELLVWGAEDSQALG    SRRTMELTSQK 1    2
EARPEIHPCPSCPLAFSTQKFLSYHVNHSHSSEPFPGTHARKHLPREDPRPGYERDSEQRHWNDSTGPGPEDVSRP VIERTWEGEISACCSSLPRGHMGRSREGERMAETQSSPGLKVTLAK  VRWDEYGQGFGPKSHHITQQTKHSGKKP    CVCKECG GFRVKSLLTHQRTHSGEKP
YVCRECGGFRWKSHLIRHQRTHSGEKP FVCSECGRGFSWKSGLITHQRTHTGEKP YVCRECGRGFSVKSYLITHQRTHTGEKP YVCRECGRGFSWKSHLIRHQRTHSGEKP YVCRQCGRGFSVQSHLIIHQRTHSLTHQRTHSGEKP YVCRECGGFSKESYLISHQRTHSGEKP YVCRDCG FSVKSLLTHQRTHSGEKP
YVCRECGRGFSKESYLISHQRTHSGEKP YVCSDCGRGFSVKSQLVSHKRTHSGEKP FVCREC RGFSVKSSLISHQRTHSGEKP YVCRECGRGFSVKSSLIKHQRTHSGEKP YVCRECGRGFGLKSYLITHQRTHTGEKP YICRECG GFSVKSSLITDQRTHTGEKP
YVCRECGRAFSKESSLISHHRTHPAEAV YVHRECG.......................  ....................
60        >PRDM7_dasNov.  _9      xena    pseu    TRAPP   Dasypus....     novemcinctus    (armadillo)... AAGV020462211    plus exon-by-exon traces, no GAS8 but facing TRAPPC3, frameshifts, tandem ZNF fragment  0 --- 0          0
AQDAFRDISIYFSREEWAEMGEWEKLAYRNVKRNYEALLAI 1      2 GLRAPRPAFMCHRKQSIKPQVDDAEDSDEEWTPRQQ 1       2 --- 0 0 --- 1 2 EPRRKGIDVKMYSLRERKGLAYEEVSEPQDDDYL 1  2
yCEKCQNFFIDSCTVHGPPIFVKDSAVDKGHPNRSALTLPSGLRIGPSGIPEAGLGIWNEASDLPLGLHFGPYEGQVTEDEEAANSGYSWL 0   0 ITKGRNYYEYVDGKDKSWANWMR 2      1 YVNCARNDDEEQNLVAFQYHRQIFYRTCRTIRPGCELLVWYGDEYGQELGIKWGSKWKKELTAEK 1    2
EPKPEIHPCPSCLAFSSEKFLSQVRRHHPSQSFPAACARHFQPGNPRPGEEPQQQHSDQCCWKDKAEGQTENRPKPLFERIKRMGSPRARYNPPRGQMGSRRGKRMMEIQPSGDQKANPEDTGKLFTWAGVSRRE RGQLFLGVGIFKTEV  IKPGENRGPFSDKSDHTSHQRTHTGEKP    YVCRECGRGFSNNSHLTRHQRTHTGVKP
YVCRECGGGFSVKSFLTHQRTHTVEKP yVCSECG GFSVKSTLITHQRTHTGEKP CVCRECGRGFNNKPDLTKHQRTHTGEKS YVCRECG GFSVKSTLIHQRTHTGEKP YVCRECGRGFSEKSNLTVHQRTHTGEKP YVCRECGRGFSVKSSLITHQRTHTGEKP
YVCMKSEVVVSNKSHLNSHRRMKCGHRT PPPPQL
61        >PRDM7_choHof   _2      xena    gene    noDet   Choloepus...    hoffmanni...   (sloth)....... ABVD01893961    fragmentary gene with indeterminate synteny     0 --- 0          0 --- 1 2 --- 1 2 --- 0 0 --- 1 2 --- 1 2
ycekcQNFFINCAAHGPPTLKDSAVGQPRHSALVIPPGLRIGPSIPEAGLGVWNEASDLPLGLHFGPYEGQVTEDEEAATSGYSWL 0   0 ITKGRNCYEYVDGKDKSCANWMR 2      1 YVNCARDDEEQNLVAFQYHRQIFYRTCRAIRPGCELLVWYGDEYGQELGIKWGSKWKKELTAEK 1    2
GLKPEIHPCPSCPLAFSTEKFLSQHVQRNHPSQIIPVVTYARKHLQPQDPRPGDQQQPQPHSDQCHCSDKAEDQETEKSKPLFESTKQ
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