```
1       >PRDM9_homSap.  13      prim    gene    CDH12   Homo.......     sapiens.....    (human).......  NM_020227       chr5 10 exon size
18,301 bp KRAB SSXRD SET C2H2   0 MSPEKSQEESPEEDTERTERKPM 0     0 VKDAFKDISIYFTKEEWAEMGDWEKTRYRNVKRNYNALITI 1   2
GLRATRPAFMCHRRQAIKLQVDDTEDSDEEWTPRQQ 1  2 VKPPWMALRVEQRKHQK 0   0 GMPKASFSNESSLKELSRTANLLNASGSEQAQKPVSPSGEASTSGQHSRLKL 1        2
ELRKKETERKMYSLRERKGHAYKEVSEPQDDDYL 1    2 YCEMCQNFFIDSCAAHGPPTFVKDSAVDKGHPNRSALSLPPGLRIGPSGIPQAGLGVWNEASDLPLGLHFGPYEGRITEDEEAANNGYSWL 0 0
ITKGRNCYEYVDGKDKSWANWMR 2       1 YVNCARDDEEQNLVAFQYHRQIFYRTCRVIRPGCELLVWYGDEYGQELGIKWGSKWKKELMAGR 1    2
EPKPEIHPCPSCCLAFSSQKFLSQHVERNHSSQNFPGPSARKLLQPENPCPGDQNQEQQYPDPHSRNDKTKGQEIKERSKLLNKRTWQREISRAFSSPPKGQMGSCRVGKRIMEEESRTGQKVNPGNTGKLFVGVGISRI
AK      VKYGECGQGFSVKSDVITHQRTHTGEKL    YVCRECGRGFSWKSHLLIHQRIHTGEKP YVCRECGRGFSWQSVLLTHQRTHTGEKP YVCRECGRGFSRQSVLLTHQRRHTGEKP
YVCRECGRGFSRQSVLLTHQRRHTGEKP YVCRECGRGFSWQSVLLTHQRTHTGEKP YVCRECGRGFSWQSVLLTHQRTHTGEKP YVCRECGRGFSNKSHLLRHQRTHTGEKP
YVCRECGRGFRDKSHLLRHQRTHTGEKP YVCRECGRGFRDKSNLLSHQRTHTGEKP YVCRECGRGFSNKSHLLRHQRTHTGEKP YVCRECGRGFRNKSHLLRHQRTHTGEKP
YVCRECGRGFSDRSSLCYHQRTHTGEKP YVCREDE....................
2       >PRDM9_panTro.  19      prim    gene    CDH12   Pan........     troglodytes.    (chimp).......  GU166820        chr5 frag assembly
glitch in mid C2H2      0 MSPERSQEESPEGDTERTERKPM 0     0 VKDAFKDISIYFTKEEWAEMGDWgKTRYRiVKMNYNALITi 1   2
GLRATRPAFMCHRRQAIKLQVDDTEDSDEEWTPRQQ 1  2 VKPPWMAFRGEQSKHQK 0   0 GMPKASFNNESSLkELSGmPNLLNTSgSEQAQKPVSPPGEASTSGQHSRLKL 1        2
ELRRKETvGKMYSLRERKGHAYKEISEPQDDDYL 1    2 yCEMCQNFFIDSCAAHGPPTFVKDSAVDKGHPNRSALSLPPGLRIGPSGIPQAGLRVWNEASDPPLGLHSGPYEGQITEDEEAANSGYSWL 0 0
ITKGRNCYEYVDGKDKSwANWMR 2       1 YENCARDDEEQNLVSFQYHRQSFYRTCRVIRPGCELLVWYGDE GQELGIKWGSKWKKELMAGR 1    2
EPKPEIHPCPSCCLAFSSQKFLSQHVERNHSSQNFPGPSARKLLQPENPCPGDQNQEQQYPDPRSRNDKTKGQEIKERSKLLNKRTWQREISRAFSSPPKGQMGSCRVGKRIMEEESRTGQKVNPGNTAKLFVGVGISRI
AK      VKYGECGQGFSDKSDVITHQRTHTGGKP    YVCRECGRGFSWKSHLLSHQRTHTGEKP YVCRECGRGFSVKSSLLSHQRTHTGEKP YVCRECGRGFSVKSSLLSHRTTHTGEKP YVCRECGRGFSVKSSLLSHQRTHTGEKP
YVCRECGRGFSQQSNLLSHQRTHTGEKP YVCRECGRGFSVKSSLLSHQRTHTGEKP YVCRECGRGFSVKSSLLSHQRTHTGEKP YVCRECGRGFSKQSHLLSHQRTHTGEKP
YVCRECGRGFSVQSNLLSHQRTHTGEKL YVCRECGRGFSQQSHLLRHQRTHTGEKP YVCRecgrgfsqqshLLSHQRTHTGEKP YVCRECGRGFSVKSSLLSHQRTHTGEKP
YVCRECGRGFSKQSHLLSHQRTHTGEKP YVCRECGRGFSQQSHLLSHQRTHTGEKP YVCRECGRGFSQQSHLLRHQRTHTGEKP YVCRECGRGFSVKSSLLSHQRTHTGEKP
YVCRECGRGFSVKSSLLSHQRTHTGEKP YVCRECERGFSQQSHLLRHQRTHTGEKP YVCRECGRGFSRQSALLIHQRTHTGEKP VCREDE....................
3       >PRDM9_gorGor.  --      prim    gene    cdh12   Gorilla....     gorilla.....    (gorilla).....  CABD02290264    chr5 several contigs
needed, most of ZNF domain missing      0 MSPERSQEESPEEDTERTERKPM 0     0 VKDAFKDISIYFTKEEWAEMGDWEKTRYRNVKRNYNALITI 1   2
GLRATRPAFMCHRRQAIKLQVDDTEDSDEEWTPRQQ 1  2 VKPPCMALRVEQRKHQK 0   0 GMPKASFSNESSLKELSRTANLLNASGSEQAQKPVSPPGEASTSGQHSRLKL 1        2
ELRKKETEGKMYSLRERKGHAYKEVSEPQDDDYL 1    2 yCEMCQNFFIDSCAAHGPPIFVKDSAVDKGHPNRSALSLPPGLRIGPSGIPQAGLGVWNEASDLPLGLHFGPYKGRITEDEEAANNGYSWL 0 0
ITKGRNCYEYVDGKDKSWANWMR 2       1 YVNCARDDEEQNLVAFQYHRQIFYRTCRVIRPGCELLVWYGDEYGQELGIKWGSKWKKELMAGR 1    2
TGQKVNPGNTGKLFVGVGISRIAK        VKYGECGQGFSVKSDVITHQRTHTGEKP    YVC.......................
4       >PRDM9_ponAbe.  10      prim    gene    CDH12   Pongo......     abelii......    (orangutan)...  XR_093432       chr5 frameshift
extra a penultimate ZNF 0 MSPERSQEESPkGDTERTERKPM 0     0 VKDAFKDISIYFTKEEWTEMGDWEKTRYRNVKRNYKTLITI 1   2
GLRATRPAFMCHRRQAIKLQVDDTEDSDEEWTPRQQ 1  2 VKPPWMAFRGEQSKHQK 0   0 GMPKASFNNESSLKELSGTQNLLNTSGSEQAQKPVSPPGEASTSGQHSTLKI 1        2
ELRRKETEGKTYSLRERKGHAYKEVSEPQDDDYL 1    2 YCEMCQNFFIDSCAAHGPPTFVKDSAVDKGHPNRSALSLPPGLRIGPSGIPQAGLGVWNEASDLPLGLHFGPYEGRITEDKEAANNGYSWL 0 0
ITKGRNCYEYVDGKDKSWANWMR 2       1 YVNCAWDDEEQNLVAFQYHRQIFYRTCRVIRPGCELLVWYGDEYGQELGIKWGSKWKKELMPGR 1    2
EPKPEIHPCPSCCLAFSSQKFLSQHVERNHSSQNFPGPSARKLLQPENPCPGDQNHEQQYSDPRSCNDKTKGQEIKERSKLLNKRTWQREISRAFSSPPKGQMGSCRVGKRIMEEESRTGQKVNPGNTGKLFVGVGISRI
AK      VKYGECGQGFSDKSDVITHQRTHTGGRS    YVCRECGRGFSRQSVLLIHQRTHTGEKP YVCRECGRGFSRRSVLLIHQRTHTGEKP YVCRECGRGFSQQSVLLIHQRTHTGEKP
YVCRECGRGFSRRSVLLIHQRTHTGEKP YVCRECGRGFSWKSVLLRHQRTHTGEKP YVCRECGRGFSWKSVLLRHQRTHTGEKP YVCRECGRGFSQQSVVFIHQRTHTGEKP YVCRECGRGFSGKSVLFRHQRTHTGEKP
YVCRECGRGFSDKSGVCYHQRTHTRGEA 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 VKDAFKDISIYFTKEEWAEMGDWEKTRYRNVKRNYNALITI 1   2
GLRATRPAFMCHRRQAIKLQVDDTEDSDEEWTPRQQ 1  2 --- 0 0 --- 1 2 --- 1 2
AAHGPPTFIKDSTVGKGHPNRSALSLPPGLRIGPSGIPQAGLGVWNEASDLPLGLHFGPYEGRITEDEEAANNGYSWL 0        0 ITKGRNCYEYVDGKDKSWANWMR 2     1 --- 1 2
EPKAEIHPCPSCCLAFSSQKFLSQHVARHHSSQNFPGPSARKFLQPENPCPGDQNQEQQYSDPRSCNDKTKGQEIKERSKLLNKRTWQREISRAFSSSPKVQMGSCRVGKRIIEESRTGQKVNPGNTGQLFVGVGISRIA
E       VKYGECGQGFSVKSDVITHQRTHTGEKL    YLCRECGRGFSVKSSLLSHQRTHTGEKP YVCRECGRGFSKKSNLLSHQRTHTGEKP YVCRECGRGFSDKSSLLRHQRTHTGEKP
YVCRECGRGFSQKSSLLSHQRTHTGEKP YVCRECGRGFSQKSSLLSHQRTHTGEKP YVCRECGRGFSDKSSLLRHQRTHTGEKP YVCRECGRGFSQKSSLLSHQRTHTGEKP
YVCRECGRGFSVKSNLLSHQRTHTGEKP YVCRECGRGFSDKSSLLRHQRTHTGEKP
6       >PRDM9_macMul.  _9      prim    gene    CDH12   Macaca.....     mulatta.....    (rhesus)......  XM_001083675    chr6 exon 4 lost to
Ns      0 MSPERSQEESPEEDTERTERKPT 0     0 VKDAFKDISIYFTKEEWAEMGDWEKTRYRNVKRNYNALITI 1   2 GLRATRPAFMCHRRQAIKLQVDDTEDSDEEWTPRQQ 1        2
--- 0   0 GMPKASFNNESSLKEVSGMANLLNTSGSEQAQKPVSPPGEARTSGQHSRLKL 1        2 ELRRKETEGKMYSLRERKGHAYKEVSEPQDDDYL 1  2
YCEMCQNFFIDSCAAHGPPTFIKDSAVEKGHPNRSALSLPPGLRIGPSGIPQAGLGVWNEASDLPLGLHFGPYEGRITQDEEAANNGYSWL 0   0 ITKGRNCYEYVDGKDKSWANWMR 2     1
YVNCARDDEEQNLVAFQYHRQIFYRTCRVIRPGCELLVWYGDEYGQELGIKWGSKWKKELMAGR 1      2
EPKPEIHPCPSCCLAFSSQKFLSQHVERNHSTQNFPGPSARRLFQPENLCSGDQNQEQQYSDPRSCNDKTKGQEIKERSKLLNKRTWPKEISRAFSSPPKGQMGSSRVGERMMEEEYRTGQKVNPENTGKLFVGVGISRI
AK      VKYGECGQGFSDKSDVIIHQRTHTGEKP    YLCRECGRGFSQKSSLRRHQRTHTGEKP YLCRECGRGFRDNSSLRYHQRTHTGEKP YLCRECGRGFSNNSGLCYHQRTHTGEKP
YLCRECGRGFSDNSSLHRHQRTHTGEKP YLCRECGRGFSNNSGLRYHQRTHTGEKP YLCRECGRGFSNNSGLRHHQRTHTGEKP YLCRECGRGFSQKANLLRHQRTHTGEKP
YLCRECGRGFSQKADLLSHQRTHTGEKP VCRKDE....................
7       >PRDM9_papHam.  11      prim    gene    cdh12   Papio......     hamadryas...    (baboon)......  genome  contigs scattered       0
--- 0   0 --- 1 2 --- 1 2 VKPPWMAFRVEQSKHQK 0   0 EMPKTSFSNESSLKELSGTPNLLSTSGSEQAQKPASPPGEASTSGQHSRLKL 1        2
ELRRKEAEGKMYSLRERKGHAYKEVSELQDDDYL 1    2 ycEMCQNFFIDSCAAHGPPTFVKDSAVNKGHPNRSALSLPPGLRIGPSGIPQAGLGVWNEASDLPLGLHFGPYEGRITEDKEAANNGYSWL 0 0
ITKGRNCYEYVDGKDKSWANWMR 2       1 --- 1 2
EPKPEIHPCPSCCLAFSSQKFLSQHVERNHSTQNFPGPSARRLLQPENLCSGDQNQEQQYSDPCSCNDKTKGQEIKERSKLLNKRTWQKEISRAFSSPPKGQMGSSRVGERMMEEESRTGQKVNPENIGKLFVEVGISRI
AK      VKYGECGQGFSGKSDVITHQRTHTEGKP    YLCRECGRGFSQKSNLLRHQRTHTGEKP YLCRECGRGFRDNSSLRCHQRTHTGEKP YLCRECGRGFRDNSSLRCHQRTHTGEKP
YLCRECGRGFSDNSSLRYHQRTHTGEKP YLCRECGRGFRDNSSLRYHQRTHTGEKP YLCRECGRGFSVKSNLLSHQRTHTGEKP YLCRECGRGFSDNSSLRCHQRTHTGEKP
YLCRECGRGFSQMSHLRCHQRTHTGEKP YLCRECGRGFSVKSNLLSHQRTHTGEKP YVCRECGRGFSRKANLLSHQRTHTGEKP
8       >PRDM7_homSap.  _3      prim    gene    GAS8+   Homo.......     sapiens.....    (human).......  genome  chr16 TUBB3+ DEFB+ AFG3L1+
DBNDD1- GAS8+ PRDM7- 92% id     0 MSPERSQEESPEGDTERTERKPM 0     0 VKDAFKDISIYFTKEEWAEMGDWEKTRYRNVKMNYNALITV 1   2
GLRATRPAFMCHRRQAIKLQVDDTEDSDEEWTPRQQ 1  2 VKPPWMAFRGEQSKHQK 0   0 GMPKASFNNESSLRELSGTPNLLNTSDSEQAQKPVSPPGEASTSGQHSRLKL 1        2
ELRRKETEGKMYSLRERKGHAYKEISEPQDDDYL 1    2 YCEMCQNFFIDSCAAHGPPTFVKDSAVDKGHPNRSALSLPPGLRIGPSGIPQAGLGVWNEASDLPLGLHFGPYEGRITEDEEAANSGYSWL 0 0
ITKGRNCYEYVDGKDKSSANWMR 2       1 YVNCARDDEEQNLVAFQYHRQIFYRTCRVIRPGCELLVWYGDEYGQELGIKWGSKWKKELMAGR 1    2
EPKPEIHPCPSCCLAFSSQKFLSQHVERNHSSQNFPGPSARKLLQPENPCPGDQNQERQYSDPRCCNDKTKGQEIKERSKLLNKRTWQREISRAFSSPPKGQMGSSRVGERMMEEESRTGQKVNPGNTGKLFVGVGISRI
AK      VKYGECGQGFSDKSDVITHQRTHTGGKP    YVCRECGRgFSRKSDLLSHQRTHTGEKP YVCRECERGFSRKSVLLIHQRTHRGDAP VCRKDE....................
9       >PRDM7_panTro.  _2      prim    pseu    GAS8+   Pan........     troglodytes.    (chimp).......  genome  chr16   0
MSPERSQEESPEEDTERTERKPM 0       0 VKDAFKDISIYFTKEEWAEMGDWEKTRYRNVKRNYNALITI 1   2 GLRATRPAFMCHRRQAIKLQVDDTEDSDEEWTPRQQ 1        2
VKPPLMALRVEQRKHQK 0     0 GMPKASFSNESSLKELSRTANLLNASGSEQAQKPVSPPGEASTSGQHSRLKL 1        2 ELKKKETEGKMYSLRERKGHAYKEVSEPQDDDYL 1  2
YCEMCQNFFIDSCAAHGPPTFVKDSAVDKGHPNRSALSLPPGLRIGPSGIPQAGLGVWNEASDLPLGLHFGPYKGRITEDEEAANNGYSWL 0   0 ITKGRNCYEYVDGKDKSWANWMR 2     1
YVNCARDDEEQNLVAFQYHRQIFYRTCRVIRPGCELGIKWGSKWKKELMAGR 1      2 EPKPEIHPCPSCCLAFSSQKFLSQHVERNHSSQNFPGPSARKLQPENP
PGDQNQERQYSDPRCCNDKTKGQEVKERSKLLNKWTWQREISRAFSSLPKGQMGSSRVGERMMEEESRTGQKVNPGNTGKLFVGVGISRIAK    VKYGECGQGFSVKSDVITHQRTHTGEKP
YVCRECGQGFSRKSVLLIHQRTHRGEKP VCRKDE....................
10      >PRDM7_gorGor.  _3      prim    pseu    GAS8+   Gorilla....     gorilla.....    (gorilla).....  genome  chr15730 numerous
frameshifts in terminal ZNF domain      0 MSPERSQEESPEGDTERTERKPM 0     0 VKDAFKDISIYFTKEEWAEMGDWEKTRYRNVKRNYNALITI 1   2
GLRATQPVFMCHRRQAIKLQVDDTEDSDEEWTPRQQ 1  2 --- 0 0 GMPKASFNNESSLKELSGTPNLLNTSGSEQAQKPVSPPGEASTSGQHSRRKL 1        2
ELRRKETEGKMYSLRERKGHAYKEISKPQDDDYL 1    2 yCEMCQNFFIDSCAAHGPPTFVKDSAVDKGHPNRSALSLPPGLRIGPSGIPQAGLGVWNEASDLPLGLHFGPYEGRITEDKEAANSGYSWL 0 0
ITKGRNCYEYVDGKDKSWANWMR 2       1 YVNCARDDEEQNLVALQYHRQIFYRTCRVIRPGCELLVWYGDEYGQELGIKWGSKWKKELTAGR 1    2
EPKPEIHPCPSCCLAFSSQKFLSQHVERNHSSQNFPGPSARKLLQPENPCPGDQNQERQYSDPRCCNDKTKGQEIKERSKLLNKRTWQREISRAFSSPPKGQMGSSRVGERMMEEESRTGQKVNPGNTGKLFVGVGISRI
AK      VKYGECGQGFSWKSNLLRHQRTHTGGKP    YVCRECGRGFSWKSDLLSHQRTHTGEKP YVCRECGRGFSWKSNLLSHQRTHTGEKP
11      >PRDM7_ponAbe.  _4      prim    gene    GAS8+   Pongo......     abelii......    (orangutan)...  genome  chr16   0
MSPERSQEESPEDDTERTERKPT 0       0 VKDAFKDISIYFTKEEWAEMGDWEKTRYRNVKRNYNALITI 1   2 GLRATRPAFMCHRRQAIKLQVDDTEDSDEEWTPRQQ 1        2
VKPPWMALRVEQRKHQK 0     0 GMPKASFNNESSLKELSETANLLNASGSEQAQKPVSPPGEASTSGQHSRLKL 1        2 ELRSKETEGNTYSLRERKGHAYKEISEPQDDDYL 1  2
yCEMCQNFFIDSCAAHGPPTFVKDSAVDKGHPNRSALTLPPGLRIGPSGIPQAGLGVWNEASDLPLGLHFGPYEGRITKDEEAANNGYSWL 0   0 ITKGRNCYEYVDGKDKSWANWMR 2     1
YVNCARDDEEQNLVAFQYHRQIFYRTCRVIRPGCELLVWYGDEYGQELGIKWGSKWKKELMAGR 1      2
EPKPEIHPCPSCCLAFSSQKFLSQHVERNHSSQNFPGPSARHLLQAENPCPGDQNQEQQYSDPDCCNDKTKGQEIKERSKLLNKRTWQREISRAFSSSAKGQMGSSRVGERMMEEESGTGQKVNPGNTGKLFVGVGISRI
AK      VKYGECGQGFSVKSDVITHQRTHTGEKP    YICRESGRGFTQKSGLLSHQRTHTGEKP YVCRECGWGFSQKSNLLRHQRTHTGEKP YVCRECGRGFSRKSVLLIHQRTHTGEKP
VCRKDE....................
12      >PRDM7_nomLeu.  _5      prim    pseu    gas8+   Nomascus...     leucogenys..    (gibbon)......  ADFV01125891    synteny implied by
non-coding      0 --- 0         0 --- 1 2 --- 1 2 IKSPWMAVRVEQSKHQK 0   0 GMPKASFNNESGLKELSGTQNLLNTSG EQARKPVSPPGEASTSGQHSRQKL 1        2
ELRRKETEGKMYSL ERKGHAYKEVSEPQDDDYL 1    2 yCEMCQNFFTDSCAAHGPPTFVKDSAVDKGHPNHSALSLPPGLRIGPSGIPQAGLGVWNEASDLPLGLHFGPYEGRITEDEEAANNGYSWL 0 0
ITKGRNCYEYVDGKDKS ANWMK 2       1 YVNCARDHEEQNLVAFQYHRQIFYRTCQVIRPGCEPLVWYGDEYGQELGIKWGSKWKKELTAER 1    2
EPKPEIHPCPSCCLVFTSQKFLSQHVECNHSSQNFPGPSARKLLQRENPCPGDQNQEQQYSDSRSCNDKTKGQEIKERSKL
NKRIWQRKISRAFSSLPKGQMGSSRVGERMMEEESRTGQKVNPGNTGKLFVGVGISRIAK    VKYGECGQGFSDKSDVIAHQGTHTGGKS    .ICRECGWGFSQESHLLIHQRTHTGEKL
```

YVCRECGQGFSQKSDLLSHQRTHTGEKP YVRRECGRGFSQKSNLLSHQRTHTEEKP YVCRECGWGFSQKSHLLIHQRTHTGKKP 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 0 --- 1 2 --- 1 2 VKPPWMAFRVEQSKHQK 0 0 EMPKTSFNNESSLKELSGTPNLLSTSDSE
AQKPASPPGEASTSGQHSRLKL 1 2 ELRRKETEGKMYSLRERKRHAYKEASELQHDDYL 1 2
YCEMCQNFFIDSCAAHGPPTFVKDNAVNKGHPNRSALSLPPGLRIGPSGIPQAGLGVWNEASDLPLGLHFGPCEGRITEDKEAANSGYSWL 0 0 ITKGRNCYEYVDGKDKSWAKWMR 2 1 --- 1 2
EPKPEIYPCPSCCLAFSSQKFLSQHVERNHSSQNFPGPSARKLLQSENPCPGDQNQEQQYSDPSSCNDKTKGQEIKERSKLLNKRTWQREILRAFTSPPKGQMGSSRVGERMMEEEFRTGQKANPGNTGKLFVGVEISRI
AK VKYGECGQGFSGKSDVITHQRTHTEGKP YVCRGCGRRFSQKSSLLRHQRTHTGEKP VCKKNE.....
14 >PRDM7_papHam. _2 prim pseu gas8+ Papio..... hamadryas... (baboon)..... genome contigs scattered 0
MSPERSQEESPEEDTERTEWKPM 0 0 VKDAFKDISIYFTKEEWAEMGDWEKTRYRNVKRNYNALITI 1 2 GLRATRPAFMCHRRQAIKLQVDDTEDSDEEWTPRQQ 1 2
VKPPWMAVRVEQSKHQK 0 0 GMPKASFNNESSLKEVSGMANLLNTSGSEQAQKPVSPPGEARTSGQHSRLKL 1 2 ELRRKETEGKMYSLRERKGHAYKEVSEPQDDDYL 1 2
YCEMCQNFFIDSCAAHGPPTFIKDSAVEKGHPNRSALSLPPGLRIGPSGIPQAGLGVWNEASDLPLGLHFGPYEGRITQDEEAANNGYSWL 0 0 ITKGRNCYEYVDGKDKSWANWMR 2 1
YVNCARDDEEQNLVAFQYHRQIFYRTCRVIRPGCELLVWYGDEYGQELGIKWGSKWKKELMAGR 1 2
EPKPEIYPCPSCCLAFSSQKFLSQHVERNHSSQNFPGPSARKLLQSENPCPGDQNQEQQYSDPSSCNDKTKGQEIKERSKLLNKRTRQRQILRAFTSPPKGQMGSSRVGERMMKEEFRTGQKANPGNTGKLFVGVEISRI
AK VKYGECGQGFSDKSDVVIHQRTHTREKP YVYRgCGQGFSIKSNLLRHQRIHTGEKP
15 >PRDM7_calJac. 12 prim gene GAS8+ Callithrix. jacchus..... (marmoset).... XR_090591 chr20 one frameshift
in repeat area chr20 terminus 0 MSPERSQEESPEGDTGRTEQKPM 0 0 VKDAFKDISMYFSKEEWAEMGDWEKTRYRNMKRNYNALITI 1 2
GLRATRPAFMCHRRQAIKLQVDDTEDSDEEWTPRQQ 1 2 VKPPGMAFRVGQSKHQK 0 0 GMPKASFGNESSLKKLSGTANVLNTSGPEQAQKPVSPPGEASTSGQHSRLKL 1 2
ELRRKDTEEKMYSLRERKGLAYKEVSEPQDDDYL 1 2 yCEICQNFFIDSCAAHGPPTFVKDSAVDKGHPNHAALSLPPGLRIGPSGIPQAGLGVWNEASDLPLGLHFGPYEGRVTEDEEAASSGYSWL 0 0
ITKGRNCYEYVDGKDKSWANWMR 2 1 YVNCARDDEEQNLVAFQYHRQIFYRTCRVIRPGCELLVWYGDEYGQELGIKWGSKWKKELMAGR 1 2
ESKPEIHPCPSCCLAFSSQKFLSHHVERNHSSQNFPGTSTRKLLQPENPCPGKQKEEQQYFDPCNSNDKTKGQETKERSKLLNIRTWQREMARAFSNPPKGQMGSSRVEERMMEEESRTGQKVNPVDTGKLFVGVGISRI
AK AKYGECGQGFSDMSDVTGHQRTHTGEKP YVCRECGRGFSQKSALLSHQRTHTGEKP YVCRECGRGFSQKSHLLSHQRTHTGEKP YVCTECGRGFSQKSVLLSHQRTHTGEKP
YVCTECGRGFSRKSNLLSHQRTHTGEKP YVCRECGRGFSRKSALLSHQRTHTGEKP YVCRKCGRGFSQKSNLLSHQGTHTGEKP YVCTECGRGFSQKSHLLSHQRTHTGEKP
YVCRKCGRGFSQKSNLLSHQRTHTGEKP YVCRECGRGFSFKSALLRHQRTHTGEKP YVCRECGRGFSRKSHLLSHQGTHIGEKP YVCRECGRGFSRKSNLLSHQRIHTGEKP
YVRREDE.....
16 >PRDM7_micMur. _8 prim gene gas8+ Microcebus. murinus..... (lemur)..... ABDC01433247 weak coverage 0
MSPEKSQEESPEEDTERTERKPM 0 0 vKDAFKDISIYFTKEEWAEMGDWEKTRYRNVKRNYNALITI 1 2 GLRATRPAFMCHRRQAIKLQVDDTEDSDEEWTPRQQ 1 2
VKPPWMALRVEQRKHQK 0 0 GMPKASFSNESSLKELSRTANLLNASGSEQAQKPVSPSGEASTSGQHSRLKL 1 2 ELRKKETERKMYSLRERKGHAYKEVSEPQDDDYL 1 2
YCEKCQNFFIDSCAAHGPPTFVKDSAVDKGHPNRSALSLPPGLKIRPSGIPQAGLGVWNEASELPLGLHFGPYEGQVTEDEEAANSGYSWL 0 0 ITKGRNCYEYVDGKDDSWANWMR 2 1
YVNCARDEEEQNLVAFQYHRQIFYRTCQVIRPGCELLVWYGDEYGQELGIKWGSKWKEELTIRQ 1 2
EPKPEIHPCPSCSLAFSSQKFLSQHVKHTHSSQISPRTSGRKHLQPENPCPGDQNQEQQHSDPHSCNDKAKDQEVKERPKPFHKKTQQRGISRAFSSPPKGKMGSCREGKRIMEEEPRTGQKVGPGDTDKLCAAGGISRI
SR VKYGDSGQSFSDKSNVIIHQRTHTGEKP YVCRECGRGFSQKSDLLKHQRTHTGEKP YVCRECGRGFSQKSHLLRHQRTHTGEKP YVCRECGRGFSQKSDLLIHQRTHTGEKP
YVCRECGRGFSCKSHLLIHQRTHTGEKP YVCRECGRGFSCKSSLLIHQRTHTGEKP YVCRGVWGEALAESQTSSYTRGHTQGRS PVFAGRVSKSLALNYISTATGGHLLTSH
LPTPALGGASKGSLLTLYISQECKETRN
17 >PRDM7_otoGar. _7 prim gene GAS8+ Otolemur... garnettii... (galago)..... genome good coverage 0
MSPEKSQEESPEEDTERTERKPM 0 0 VKDAFKDISIYFTKEEWAEMGDWEKTRYRNVKRNYNALITI 1 2 GLRATRPAFMCHRRQAIKLQVDDTEDSDEEWTPRQQ 1 2
VKHPWMAFRMEQSKRQK 0 0 ILKKCMLSFNMHLKELSGPASLPNISGSEQHQKHMSSPREASTSGQHSGRKS 1 2 DLRIKEIEVRMYSLRERKGHAYKEVSEPQDDDYL 1 2
yCEKCQNFFIDNCAVHGPPTFVKDTAVEKGHPNRSVLSLPSGLGIRTSGIPQAGFGVWNEASDLQLGLHFGPYEGQVTEDEEAANSGYSWL 0 0 ITKGRNCYEYVDGKDESQGNWMR 2 1
YVNCARDEEEQNLVAFQYHRQIFYRTCRVIRPGCELLVWYGDEYGQELGIKWGSKWKKELTAGQ 1 2
EPKPEIHPCPSCSLAFSTQKFLSQHVERTHPSQISQGTSGRKNLRPQTPCPRDENQEQQHSDPNSRNDKTKGQEVKEMSKTSHKKTQQSRISRIFSCPPKGQMGSSREGERMIEEEPRPDQKVGPGDTEKFCVAIGISGI
VK VKNRECVQSFSNKS NLRHQRTHTGEKP YMCRDCGRGFSHKSSLFRHQRTHTGEKP YVCRDCGRGFSLKANLLTHQRTHTGEKP YVCRDCGQGFSQKAHLLRHQRTHTGEKP
YMCRDCGQGFSRKAYLLTHQRTHTGEKP YVCRDCGQGFSQKAHLLTHQRTHTGEKP YVCRDCGRGFSHKSSLFRHQRTHTGEKP YICRDCG
18 >PRDM7_tarSyr. -- prim pseu gas8+ Tarsius.... syrichta.... (tarsier)..... ABRT011082008 double frameshift in
exon 5, ABRT010499286 0 --- 0 0 --- 1 2 GLRAPRPAFMCHRKRAIKPLVDDTEDSDEEWTPRQQ 1 2 --- 0 0
GMPRAPLSIVSSLKELSEMANLLNTSDSEQAWKPVSPSREASTSEQHSRKKL 1 2 EFRKKEIEVNMYSLRERKDCAYKEVNEPQDDDYL 1 2
YCEQCQNFFIDSCATHGIPTFINDSAVDKGHPNRSALSLPPGLRIGPSGIPQAGLGVWNEASELPLGLHFGPYEGQITDDEEAANSGYSWL 0 0 ITKGRNCYEYVDGKDKSWANWMR 2 1
YVNCARDDEEQNLVAFQYHRQIFYRTCRIIRPGCELLVWYGDEYGQELGIKWGSKWKKELMAGR 1 2 --- --- ---
19 >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 VQDAFRDISIYFSKEEWAEMGEWEKIRYRNVKRNYCALVAI 1 2
GLRAPRPAFMCHRRLAVRARADDTEDSDEEWTPRQQ 1 2 VKPPWMAFRTEHSKHQK 0 0 GMPRLPVNNESSLKELSGTANLLKTTGSEEDQKPSFPPKETRTSGQHSTRKL 1 2
GLRRKNIEVKMYSFRKRKSQAYKECSEPQDDDYL 1 2 YCEKCQNFFLDSCAVHGPPIFVKDSAVDKGHPNRSVLSLPPGLRIGPSGIPEAGLGVWNEASDLPLGLHFGPYEGQITEEEEAANSGYSWL 0 0
ITKGRNCYEYVDGKDRSWANWMR 2 1 YVNCARNDEEQNLVAFQYHKQIFYRTCQVIKPGCELLVWYGDEYGQELGIKWGSKWKEELTAGR 1 2
EPKPEIHPCPSCSLAFSSHKFLSQHMERSHSSQIFPGAPARNHLQPANPCPGKEHQKLSDPQSWNDKNEGQDVKEKSRFSSKRTRQKAISRSFSSLPKGQVETSREGERMIEEEPRIGQELNPEDTGKSSVGAGLSRIAG
VKYRDCRQGLSDKSHLINGQRAHTGEKP YACRECERGFTVKSNLISHQRTHTGEKP YACRECGRGFTVKSALTTHQRTHTGEKP YACRECGRGFTVKSHLISHQRTHTGEKP
YACRECGRGFTVKSALITHQRTHTGEKP YACRECGQGFTVKSNLISHQRTHTGEKP YACRECGRGFTQKSHLINHLRAHTGEKP YACRECGRGFTVKSDLISHQRTHTGEKP
YACRVDE.....
20 >PRDM7_oryCun. _4 glir gene other Oryctolagus cuniculus... (rabbit)..... genome synteny novel 0 --- 0
0 --- 1 2 GLRAPRPAFMCHRRLAVRARADDTEDSDEEWTPRQQ 1 2 VKPPWMAFRTEHSKHQK 0 0
GMPRLPVNNESSLKELSGIANLLNTTGSEEDQKPSFPPKETRTSGQHSTRKL 1 2 GLRRKNIEVKMYSFRKRKSQAYKECSEPQDDDYL 1 2
YCEKCQNFFLDSCAVHGPPIFVKDSAVDKGHPNRSVLSLPPGLRIGPSGIPEAGLGVWNEASDLPLGLHFGPYEGQITEEEEAANSGYSWL 0 0 ITKGRNCYEYVDGKDRSWANWMR 2 1
YVNCARNDEEQNLVAFQYHKQIFYRTCQVIKPGCELLVWYGDEYGQELGIKWGSKWKEELTAGR 1 2
EPKPEIHPCPSCSLAFSSHKFLSQHMECSHSSQIFPGAPARNHLQPANPCPGKEHQKLSDPQSWNDKNEGQDVKEKSRFSSKRTRQKAISRSFSSLPKGQVETSREGERMIEEEPRIGQELNPEDTGKSSVGAGLSRIAG
VKYRDCRQGLSDKSHLINGQRAHTGEKP YACRECGQSFTVKSNLISHQRTHTGEKP YACRECGRGFTQKSHLIRHQRTHTGEKP YACRECGQSFTWKSNLISHQRTHTGEKP
YACRVDE.....
21 >PRDM7_ochPri. -- glir gene noDet Ochotona... princeps.... (pika)..... AAYZ01312269 dubious 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
YVNCARNDEEQNLVAFQYHRQIFYRTCRAVRQGCELLVWYGDEYGQELGIKWGSKWKEELTAGR 1 2 --- --- ---
22 >PRDM7_ratNor. 10 glir gene PDCD2 Rattus..... norvegicus.. (rat)..... NM_001108903 chr1 FM103467 single
transcript from body fat 0 MNTNKPEENSTEGDAGKLEWKPK 0 0 VKDEFKDISIYFSKEEWAEMGEWEKIRYRNVKRNYKMLISI 1 2
GLRAPRPAFMCYQRQAIKPQINDNEDSDEEWTPKQQ 1 2 VSSPWVPFRVKHSKQQK 0 0 ETPRMPLSDKSSVKEVFGIENLLNTSGSEHAQKPVCSPEEGNTSGQHFGKKL 1 2
KLRRKNVEVNRYRLRERKDLAYEEVSEPQDDDYL 1 2 YCEKCQNFFIDSCVVDRGHPNHSVLSLPPGLRIGPSGIPEAGLGVWNEASDLPVGLHFGPYKGQITEDEEAANSGYSWL 0 0
ITKGRNCYEYVDGQDESQANWMR 2 1 YVNCARDDEEQNLVAFQYHRKIFYRTCRVIRPGRELLVWYGDEYGQELGIKWGSKMKKGFTAGR 1 2
ELRTEIHPCFLCSLAFSSQKFLTQHVEWNHRTEIFPGASARINPKPGDPCPDQLQEHFDSQNKNDKASNEVKRKSKPRHKWTRQRISTAFSSTLKEQMRSEESKRTVEEELRTGQTTNIEDTAKSFIASETS
RIERQCGQCFSDKSNVSEHQRTHTGEKP YICRECGRGFSQKSDLIKHQRTHTEEKP YICRECGRGFTQKSDLIKHQRTHTEEKP YICRECGRGFTQKSDLIKHQRTHTGEKP
YICRECGRGFTQKSDLIKHQRTHTEEKP YICRECGRGFTQKSSLIRHQRTHTGEKP YICRECGLGFTQKSNLIRHLRTHTGEKP YICRECGLGFTRKSNLIQHQRTHTGEKP
YICRECGQGLTWKSSLIQHQRTHTGEKP YICRECGRGFTWKSSLIQHQRTHTVEK.
23 >PRDM7_musMus. 12 glir gene PDCD2 Mus..... musculus.... (mouse)..... NM_144809 chr17 CN723438 eight
transcripts, four from retina 0 MNTNKLEENSPEEDTGKFEWKPK 0 0 VKDEFKDISIYFSKEEWAEMGEWEKIRYRNVKRNYKMLISI 1 2
GLRAPRPAFMCYQRQAMKPQINDSEDSDEEWTPKQQ 1 2 VSPPWVPFRVKHSKQQK 0 0 ESSRMPFSGESNVKEGSGIENLLNTSGSEHVQKPVSSLEEGNTSGQHSGKKL 1 2
KLRKKNVEVKMYRLRERKGLAYEEVSEPQDDDYL 1 2 YCEKCQNFFIDSCPNHGPPLFVKDSMVDRGHPNHSVLSLPPGLRISPSGIPEAGLGVWNEASDLPVGLHFGPYEGQITEDEEAANSGYSWL 0 0
ITKGRNCYEYVDGQDESQANWMR 2 1 YVNCARDDEEQNLVAFQYHRKIFYRTCRVIRPGCELLVWYGDEYGQELGIKWGSKMKKGFTAGR 1 2
ELRTEIHPCLLCSLAFSSQKFLTQHMEWNHRTEIFPGTSARINPKPGDPCSDQLQEQHVDSQNKNDKASNEVKRKSKPRQRISTTFPSTLKEQMRSEESKRTVEELRTGQTTNTEDTVKSFIASEIS
SIERQCGQYFSDKSNVNEHQKTHTGEKP YVCRECGRGFTQNSHLIQHQRTHTGEKP YVCRECGRGFTQKSDLIKHQRTHTGEKP YVCRECGRGFTQKSDLIKHQRTHTGEKP
YVCRECGRGFTQKSVLIKHQRTHTGEKP YVCRECGRGFTQKSVLIKHQRTHTGEKP YVCRECGRGFTAKSVLIQHQRTHTGEKP YVCRECGRGFTAKSNLIQHQRTHTGEKP
YVCRECGRGFTAKSVLIQHQRTHTGEKP YVCRECGRGFTAKSVLIQHQRTHTGEKP YVCRECGRGFTQKSNLIKHQRTHTGEKP YVCRECGWGFTQKSDLIQHQRTHTREK.
24 >PRDM7_musMol. 11 glir gene noDet Mus..... molossinus.. (wild_mouse).. GU216230 full length deposit
0 MNTNKLEENSPEEDTGKFEWKPK 0 0 VKDEFKDISIYFSKEEWAEMGEWEKIRYRNVKRNYKMLISI 1 2 GLRAPRPAFMCYQRQAMKPQINDSEDSDEEWTPKQQ 1 2
VSPPWVPFRVKHSKQQK 0 0 ESSRMPFSGESNVKEGSGIENLLNTSGSEHVQKPVSSLEEGNTSGQHSGKKL 1 2 KLRKKNVEVKMYRLRERKGLAYKEVSEPQDDDYL 1 2
YCEKCQNFFIDSCPNHGPPLFVKDSMVDRGHPNHSVLSLPPGLRISPSGIPEAGLGVWNEASDLPVGLHFGPYEGQITEDEEAANSGYSWL 0 0 ITKGRNCYEYVDGQDESQANWMR 2 1
YVNCARDDEEQNLVAFQYHRKIFYRTCRVIRPGCELLVWYGDEYGQELGIKWGSKMKKGFTAGR 1 2
ELRTEIHPCLLCSLAFSSQKFLTQHMEWNHRTEIFPGTSARINPKPGDPCSDQLQEQHVDSQNKNDKASNEVKRKSKPRQRISTTFPSTLKEQMRSEESKRTVEELRTGQTTNTEDTVKSFIASEIS
SIERQCGQYFSDKSNVNEHQKTHTGEKP YVCRECGRGFTAKSNLIQHQRTHTGEKP YVCRECGRGFTQKSVLIQHQRTHTGEKP YVCRECGRGFTQKSDLIKHQRTHTGEKP
YVCRECGRGFTAKSNLIQHQRTHTGEKP YVCRECGRGFTEKSSLIKHQRTHTGEKP YVCRECGWGFTAKSNLIQHQRTHTGEKP YVCRECGRGFTQKSSLIKHQRTHTGEKP
YVCRECGRGFTAKSNLIQHQRTHTGEKP YVCRECGWGFTQKSNLIKHQRTHTGEKP YVCRECGWGFTQKSDLIQHQRTHTR.EK
25 >PRDM7_dipOrd. -- glir gene noDet Dipodomys.. ordii..... (kangaroo_rat) genome dubious fragment, no
orthologous terminal exon 0 --- 0 0 --- 1 2 GLKAPRPVFMCHRRQAIKPQVDDTDDSDEEWTPGRQ 1 2 --- 0 0 --- 1 2
elRTKEVKMRMYSLRERKSYAYEEISEPQDDDYL 1 2 yCEQCQNFFINSCTVHGPPIFVRDNVVDKGHYDRSVLSLPPGLRIRQSSIPEAGLGVWNEESDLPLGLHFGPYEGQITEDEDAANSGYSWM 0 0

ITKGRNCYVYVDGKDKSQANWMR 2 1 YVNCARYDEEQNLVAFQYHRQIFYRTCRVIKAGCELLVWYGDEYGQELGIKWGSKWKRELTAgr 1 2 --- --- ---
26 >PRDM7_speTri. -- glir gene noDet Spermophilu tridecemline (squirrel).... AAQQ01308561 plus exon by exon
traces 0 --- 0 0 --- 1 2 GFRAPRPAFMCHQRQTIKLQMDDTEDSDEEWTPRQQ 1 2 --- 0 0
LKPEVLLSNESSLKELSGTANLLNTSGSEQVQKPVSPLREASASRQHSRRKL 1 2 ELRTKEVEVKMYSLRERKGHAYKEVSEPQDDDYL 1 2
yCDKCQNFFMDSCPVHGPPTFIKDSVVNKDHSNHSTLSLPLGLRIGPSSIPEAGLGVWNEATDLPLGLHFGPYRGQITEDEEAANSGYSWL 0 0 ITKGRNCYEYVDGKDESQANWMR 2 1
YVNCARDDEEQNLVAFQYHRQIFYRTCRVIRPGCELLVWYGDEYGQELGIKWGSKWKKELSAGR 1 2
EPKPEIHPCPSCSLAFSSQKFLSQHVDRSHPSQIFPGTSMRKKLIPGDSSPRDQLQEQQHPDPHGWNDKARGQEVQGSLKPTHKGTRQRGISSPPKGQMGRSEESERMMEDDLKADQEINPEDTDKILVGVEMSRI
--- ---
27 >PRDM9a_bosTau _7 laur gene noDet Bos..... taurus..... (cattle)..... NW_003053109 chr1 0
MSQNRSPEERTKGDAGRTEWKLT 0 0 AKDAFKDISIYFSKEEWAEMGEWEKTGYRNVKRNYEVLIAI 1 2 GLRATQPAFMHHRRQVIKPQGDDTEDSDEEWTPQHQ 1 2
GKPSRKAFRMEHRKHQK 0 0 GKSRGPLSKVSSLKKLQGAAKLLNTSGSKWAQKPANPPRETRTLEQHSRQKV 1 2 ELRRKETDMKRYSLRERKGHVYQEVSEPQDDDYL 1 2
YCQECQNFFIDSCDAHGPPTFVKDSAVEKGHANRSVLTLPPGLSIKLSGIPEAGLGVWNEASHLPLGLHFGPYEGQITDDKEAINSGYSWL 0 0 ITKGRNSYEYVDGKDTSLaNWMR 2 1
YVNCARHYEEQNLVAFQYHGQIFYRTCQVVRPGCELLVWYGDEYGEKLGIKCESRGKSMFAAGr 1 2
ESKPKIHPCASCSLAFSSQKFLSQHVQHNHPSQTLLRPSARDYLQPEDPCPGSQNQQQRYSDPHSPSDKPEGREVKDRPQPLLKSIRLKRISRASSYSPRGQMGASGVHERITEEPSTSQKPNPEDTGKLFMGAGVSGII
K VKYGECGQGSKDRSSLITNQRTHTGEKP YVCGECGQSFNQKSTLITHQRTHTGEKP YVCGECGRSFNQKSTLITHQRTHTGEKP YVCGECGRSFSQKSTLIKHQRTHTGEKP
YVCGECGQSFNQKSTLITHQRTHTGEKP YVCGECGQSFNQKSTLITHQRTHTGEKP YVCGECGRSFSRKSTLITHQRTHRGEKL CLQGV.....
28 >PRDM9b_bosTau _5 laur gene noDet Bos..... taurus..... (cattle)..... DAAA02065087 chrU aaaaa fixed to
aaaaaa in exon 2 KRAB SSXRD SET C2H2 0 MSPNRSPENSTEGDAGRTEWKPM 0 0 AKDAFKDISIYFTKEEWAEMGEWEKIQYRNVKRNYEALIAI 1 2
GFRATQPGFMHHGRQVLKSQVDDTEDSDEEWTPRQQ 1 2 GKPSGMAFRGEPSKHPK 0 0 RLSRGPLNKVSSLKKLPGAAKLLKKSGSKQAQKPVPPPREARTPGKHPRHKV 1 2
ELRRKETEVKRYSVRERKGHVYQEVSEPQDDDYL 1 2 YCEECQNFFIDSCAAHGPPTFVKDSAVEKGHANRSALTLPPGLSIRPSGIPEAGLGVWNEASDLPLGLHFGPYEGQIIYNEEDSNSGYCWL 0 0
VTKGRNSYEYVDGKDTSLANWMR 2 1 YVNCARDDEEQNLVALQYHGQIFYRTCRVVRPGCELLVWYGDEYGEELGIKQDKRGKSKLSAQR 1 2
AKMHPCASCSLAFSSQKFLSQHVQRNHPSQTLLRPSARDHLQPEDPCPGNQNQQQRYSDPHSPSDKPEGRKAKDRPQPLLKSIKLKRISRASSYSPRGQVGRSGVHERITEEPSTSQKLNPEDTGKLFMGAGVSGIIK
VKYRECGQGSKDRSSLITHERTHRAEAL CLRRVWAKLQSEVPLLVMHQRTHTGEKL YVCGECGKSFSQKSPLIRHQRTHTGEKP YVCGECGKSFSQKSPLIRHQRTHTGKKP
YVCRECGRSFSDKSH.HTPEYTHRGEAL HLRGVWA.....
29 >PRDM9c_bosTau -- laur gene noDet Bos..... taurus..... (cattle)..... XM_002699750 chrX GO353654 4-cell
embryo transcript no zinc downstream despite 43k bp 0 MSPNRSPENSTEGDAGRTEWKPM 0 0 AKDAFKDISIYFTKEEWAEMGEWEKIRYRNVKRNYEALIAI 1 2
GFRATQPGFMHHRRQVLKPQVDDTEDSDEEWTPRQQ 1 2 GKPSGMAFRGERSKHQK 0 0 RLSRGPLNKVSSLKKLPGAAKLLKKSGSKQAQKPVPPPREARTPGKHPRHKV 1 2
ELRRKETKVKRYSVRERKGHVYQEVSEPQDDDYL 1 2 YCEECQNFFIDSCAAHGPPTFVKDSAVEKGHANRSALTLPPGLSIRPSGIPEAGLGVWNEASDLPLGLHFGPYEGQIIYNEEDSHSGYCWL 0 0
VTKGRNSYEYVDGKDTSLANWMR 2 1 YVNCARDDEEQNLVALQYHGQIFYRTCRVVRPGCELLVWYGDEYGEELGIKQDKRGKSKLSAQR 1 2 --- --- ---
30 >PRDM9d_bosTau _9 laur gene noDet Bos..... taurus..... (cattle)..... genome chrX proximal tandem 0
MRPNTSPEESTERDAGRTEWKPT 0 0 AKDAFKDISVYFSKEEWEEMGEWEKIRYRNVKRNYEALIAI 1 2 GFRATRPAFMHHRRQVIKLQADDTEDSDEEWTPRQQ 1 2
GKLSSMAFRVEHNKHQN 0 0 TMSRAPLSKEFSLKELPGAAKLLKTSGSKQAQKLVPPPGKARTPGQHPRQKV 1 2 ELRRKETEVKRYSLRERKGHVYQEVSEPQDDDYL 1 2
YCEECQSFFIDSCAAHGPPIFVKDCAVEKGHANRSALTLPPGLSIRESSIPEAGLGVWNEVSDLPLGLHFGPYEGQITDDEEAANSGYSWL 0 0 ITKRRNCYEYVDGKDTSLANWMR 2 1
YVNCARDDEEQNLVALQYHGQIFYRTCQVVRPGCELLVWYGDEYGQDLGIKRESSRKSELAGPR 1 2
EPKPKIYPCASCCLSFSSQKFLSQHVQRNHPSQILLRPSIGDHLQPEDPCPGSQNQQQRYSDPHSLSDKPEGREPKERPHPLLKGPKLCIRPKRISTASSYPPKGQMGGSEVHERMTEEPSTSQKLNPEDTGKLFMEAGV
SGIVR VNYGDHEQGSKDRSSLITHEKIHTGEKP YVCKECGKSFNGRSDLTKHKRTHTGEKP YACGECGRSFSFKKNLITHKRTHTREKP YVCRECGRSFNEKSRLTIHKRTHTGEKP
YVCGDCGQSFSLKSVLITHQRTHTGEKP YVCGECGRSFNEKSRLTIHKRTHTGEKP YVCGDCGQSFSLKSVLITHQRTHTGEKP YVCGECGQSFNEKSRLTIHKRTHTGEKP
YACGDCGQSFSLKSVLITHQRTHTGEKP YVCMECE.....
31 >PRDM9e_bosTau _9 laur gene noDet Bos..... taurus..... (cattle)..... genome chrX distal tandem 0
MRPNRSPEESTEGDAGRTEWKPM 0 0 AKDAFKDISIYFSKEEWEEMGEWEKIRYRNVKRNYEVLITI 1 2 GFRAARPAFMHHRRQVIKPQVNDIKDSDEEWTPRQQ 1 2
GKPFSMAFRVEHSKHQK 0 0 GMSRAPLSKESSLKELPGAAKLLKTSGCKQAQKLVPPPRKARTPEQHPRQKV 1 2 ERRRKETGVKRYSLREREGLVYQEVSEPLDDDYL 1 2
YCEECQSFFIDICAAHRPPTFVKDCAVEKGHANCSALTLPPGLSIRLSGIPEAGLGVWNEASDLPLGLHFGPYEGQITDDKEAAHSRYSWL 0 0 ITKGRNCYEYVDGKDTSLANWMR 2 1
YVNCARDDEEQNLVALQYQGQIFYRTCQVVRPGCELLVWYGDEYGWDLSIKQDSRGKNKLAAGR 1 2
EPKPKIYPCASCCLSFSSQKFLSQHVQRNHPSQILLRPSIGDHLQPEDPCPGSQNEQQRYSDPHSLSDKPEGREPKERPHPLLKGPKLCIRLKRISTASSYPPKGQMGGSEVHERMTEEPSTSQKLNPEDTGKLFMEAGV
SGIVR VKYGEHEQDSKDKSSLITHEKIHTGEKP YVCTECGKSFNWKSDLTKHKRTHSEEKP YACGECGRSFSFKKNLIIHQRTHTGEKP YVCGECGRSFSEKSNLTKHKRTHTGEKP
YACGECGQSFSFKKNLITHQRTHTGEKP YVCGECGRSFSEKSRLTTHKRTHTGEKP YVCGDCGQSFSLKSVLITHQRTHTGEKP YVCRECGRSFSVISNLIRHQRTHTGEKP
YVCRECEQSFREKSNLVRHQRTHTGEKP YVCMECE.....
32 >PRDM9e_oviAri -- laur pseu noDet Ovis..... aries..... (sheep)..... genome chr 18 cow has PDRM7
pseudogene; sheep GAS8 is on sheep chr14 0 --- 0 0 --- 1 2 GLRAP PPFMYHRRQVIKPQVDDIEDSDEEWTPRQQ 1 2 --- 0 0 --- 1 2
ELRRKETEMKIYSLQKRKGHMYQEVSDPQDDNYL 1 2 ycEKCQNF INSCAAHGPPTFVKDCVVEKGHASCSALtLSPGLSIRPSGIPEAGLRVWNEASDLPLGLHFGPYKGQITDDEEVANSRYFWL 0 0
--- 2 1 YVNCAQDDEEQNLVAFQYHRQIFS TCWVVRPGCELLVWYRDEYGQELSIK GSRHKSELTVRR 1 2 --- --- ---
33 >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 ITKGRNCYEYVDGKDTSLANWMR 2 1
YVNCARDDEEQNLVALQYQGQIFYRTCQVVRPGCELLVWYGDEYGQDLGIKRDSSGKSELAAGR 1 2 --- --- ---
34 >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
PMCSCSLAFSSQKFLSQHVKCNHPSQILLKTSARDRLQPEDPCPGNPNQQQQYSDLHSWSDKPESRESKEKPQPLLKSIRLRRISRASSYSSRGQMGGFRVHKRMREEPSTGKEVSPEDAGKLFMGEGVSRIMR
VKYGDCG GSKDRSSLMTHQRTHTGENP YVCREYE.SFSEKSSLIKHQRTHTGEKP YVCRECWQSFGRKSTLITHQRMHTREKP CVCRECGRSFSKKSTLITHQRTHTGQKP
35 >PRDM9b_oviAri _2 laur pseu noDet Ovis..... aries..... (sheep)..... genome chrX not tandem: 62 mbp
separation 0 MSPNRSPENSTEGDAGRTEWKPM 0 0 AKDAFKDISIYFTKEEWAEMGEWEKIRYRNVKRNYEALIAI 1 2 GFRATQPAFMHHHRQVIKPQVDDTEDSEEEWTPRQQ 1
2 GKPSGMAFRGERSKHQK 0 0 RLSRGPLNKVSSLKKLPGAAKLLKKTGSKQAQKPVPPPREARTPGQHPRHKV 1 2 ELRRKETEVKRYSLRERKGHVYQEVSELQDDDYL 1 2
yCEECQNFFIDSCAAHGPPTFVKDSAVEKGHANRSALTLPPGLSIRPSGIPEAGLGVWNEASDLPLGLHFGPYEGQVIYNEEASHSGYSWL 0 0 VTKGRNSYEYVDGKDTSLANWMR 2 1
YVNCARDDEEQNLVALQYHGQIFYRTCQVVRPGCELLVWYGDEYGEELGIKQDSRGKSKLSAQR 1 2 ELKPKIHPCASCSPAFSSQKFLSQYVQPNHPSQILLRPSARDHLQPEDPCPGNQNEQQ
YSDPHSPSDKPEGCKAKERPPWLLKSMSVRISMASSYSPKGQMRGSETHYRMTEEPSTSQKLNPEDIGKLFMGTGVSGIIK IKYEECGQVSKDRSSLITHEGTHTREQS
YVCRECGQSFSVKSSLIRLQRTHTGEKP Y.....
36 >PRDM9a_oviAri _9 laur gene noDet Ovis..... aries..... (sheep)..... genome chrX not tandem 0
MSPNRSPENSTEGDAGRTEWKPM 0 0 AKDAFKDISIYFTKEEWAEMGEWEKIRYRNVKRNYEALIAI 1 2 GFRATQPAFMHHHRQVIKPQVDDTEDSEEEWTPRQQ 1 2
GKPSGMAFRGERSKHQK 0 0 GMSRGPLSKVSSLKKLPGTTKLLKTSGSKQAQKPVPSSREARTSG HTRQKV 1 2 ELGRKETDMKRYSLRERKGHVYQEVSEPQDDDYL 1 2
yCQECQNFFINSCDAHGPPTFVKDSAVEKGHANRSALTLPPGLSIRLSGIPEAGLGVWNEASHLPLGLHFGPYEGQITDDKEAVNSGYSWL 0 0 --- 2 1
YVNCARHYEEQNLVAFQYHGQIFYRTCQVVRPGCELLVWYGDEYGEKLGIRCESRGKSMLAAGR 1 2
EPKPKIHPCASCSLSFSSQKFLSQHVQRSHPSQILLRPSPRDHLQPEDPCPGKQNQQQRYSDPHSPSDKPEGQPEKERPHPLLKGPKLCIRLKRISTASSYTPKGQMGGSEVHEKMTEEPSTSQKLNPENTGKLFMEAGV
SGIVR VKYGEHEQGSKDKSSLITHERIHTGEKP YVCKECGKSFNGRSNLTRHKRTHTGEKP YVCRECGQSFSLKSILITHQRTHTGEKP YVCGECGQSFSEKSNLTRHKRTHTGEKP
YVCRECGQSFSLKSILITHQRTHTGEKP YVCRECGRSFSVKSNLTRHKMTHTGEKP YVCGECGQSFSQKPHLIKHQRTHTGEKP YVCRECGRSFSAMSNLIRHQRTHTGEKP
YVCRECGRSFSAMSNLIRHQRTHTGEKP YVCREC.....
37 >PRDM9d_munMun _4 laur gene noDet Muntiacus.. muntjak..... (muntjac)..... AC216498 frameshift exon 9 no
syntenic loci; identities: 92%b 89%a 90%c 0 MRPNRSQEESTEGNAGRTERKPT 0 0 GKDAFKDISVYFSKEEWEEMGEWEKIRYRNMKRNYEALIAI 1 2
GFRATQPTFMHHRRQVIKSQVDDTEDSDEEWTPRQQ 1 2 GKPSSMAFRVEHSKNQK 0 0 RMSRAPLSNESGLKELPGAAKSLKTSDSKQARNPVPHHRKARTPGQLPRQKV 1 2
ELRRKETGVKRYSLRERKGHVYQEVSEPQDDDYL 1 2 YCEECQNFFINSCAAHGPpTFVKDCAVEKGHANRSALTLPHGLSIRLSGIPDAGLGVWNKVSDLALGLHFGPYKGQITDNEEAANSGYAWL 0 0
ITKGRDCYQYVDGKDTSWANWMR 2 1 YVNCARDDEEQNLVAFQYHGQIFYRTCQVVRPGCELLVWGDEYGQDFGIKRNSRGKSELAAGR 1 2
EPKPKIHPCASCSLTFSSQKFLSQHIQCSHPPQTLLRPSERDLLQPEDPCPGNQNQQQRYSDPHSPSDKPEGHEAKDRPQPLLKSIRLKRISRASSCSPRGQMGGSGVHERMTEEPSTSQKLNPGDTGTLLTGAGVSGIM
K VKYGECGQGSKDRSSLSTHERTHTGEKP YVCRECGQSFSGKPVLIRHQRTHTGEKP YVCMECGRSFSAKSVLMTHHRTHTGEKP YICRECGQSFSQKIHLIRHQRIHTGE.P
SVFRECE.....
38 >PRDM9c_munMun 15 laur gene noDet Muntiacus.. muntjak..... (muntjac)..... AC154919 no syntenic loci
AC204173 99% identical 0 MRPNRSPEESTEGDAGRTEQKPT 0 0 AKDAFKDISVYFSKEEWEEMGDWEKIRYRNMKRNYEVLIAI 1 2
GFRATRPDFMHHRRQVIKPQVDDTEDSDEEWAPRQQ 1 2 GKPSSVAFRVEHSKHQK 0 0 RMSRAPLSNESGLKELPGAAKPLKTSGSKQAQNPVPHHRKARTPGQLPRQKV 1 2
ELRRKETGVKRYSLRERKGHVYQEVSKPQDDDYL 1 2 YCEKCQNFFIDSCAAHGPPTFVKDCAVEKGHANRSLLTLPPGLSIRLSGIPDAGLGVWNEASDLPLGLHFGPYEGQITDDEEAANSGYAWL 0 0
ITKGRDCYQYVDGKDTSWANWMR 2 1 YVNCARDDEEQNLVAFQYHGQIFYQTCQVVRPGCELLVWCGDEYGQDLGIKRNSRGKSELVAGR 1 2
EPKPKIHPCASCSLAFSSQKFLSQHIQRSHPSQTLLRPSERDLLQPEDPCPGNQNQRFSDPHRPSDRPQPLLKSIRLKRISRASSYSPRGQMGGSGVHELMTEEPSTSHKLNPEDTGTLLMGAGVSGIMR
VTYGECGQGSKDRSSLTTHERTYTGEKP YVCGECGRSFCQKAHLITHQRTHTGEKP YVCRECGQSFSRNSLLIRHQRIHTGEKP YVCGECGRSFRDKSNLISHRRTHTGEKP
YVCGECGQSFSDKSNLIRHQRTHAGEKP YVCGECGRSFNRKSHLITHQRTHTGEKP YACRECGQSFSQKSILITHQRTHTGEKP YACRECG.SFSQKSILITHQRTHTGEKP
YVCGECGRSFSQKSLLITHQRTHTGEKP YVCMECGRSFSQKTHLITHQRTHTGEKP YVCGECGRSFSQKSLLITHQRTHTGEKP YVCGECGRSFSQKSLLITHQRTHTGEKP
YICMECGRSFSQKTHLITHQRTHTGEKP YVCGKCGQSFSDKSNLISHKRTHTGEKP YVCRECGRSFNRKSLLITHQRTHT.E.P YVCRECE.....
39 >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 RMSRAPLSNESGLKELPGAAKPLKTSGSKQAQNPVPHHRKARTPGQLPRQKV 1        2 ELRRKETGVKRYSLRERKGHVYQEVSKPQDDDYL 1  2
YCEECQNFFIDSCAAHGPPTFVKDCAVEKGHANRSALTLPPGLSIRLSGIPDAGLGVWNETSDLPLGLHFGPYEGQITDDEEAANSGYAWL 0   0 ITKGRNCYQYVDGKDTSWANWMR 2     1
YVNCARDDEEQNLVAFQYHGQIFYRTCQVIRPGCELLVWYGDEYGQDLGIKRNSRGKSELATGR 1      2
EPKPKIHPCASCSLAFSSQKFLSQHIQRSHPSQTLLRPSERDLLQPEDPCPGSQNQRYSDPHSPSDKPEGQEAKDRPQQLLKSIRLKRISRASSYSPGGQMGGSGVHERMTEEPSTSQKLNPEDTGTLLTGAGVSGIMR
        VTYGECWKGSKDRSSLTTHERTHTGEKP    YVCGECGQSFHHGSVLIRHQRTHTGEKP YVCGECGRSFSQKSVLIRHQRTHTGEKP YVCGECGRSFSQKSVLIRHQRTHTGEKP
YVCGECGRSFSQKAHLITHQRTHTGEKP YVCGECGRSFSQKTHLISHKRTHTGEKP YVCGECGRSFCQKSALIRHQRAHTGEKP YVCGECGRSFIQKSDFIRHQRTHTGEKP
YVCRECGQSYSDKTVLITHERTHTGEKP YVCGECGRSYSDKTVLITHERTHTGEKP YVCGECGRSFLWKSALIRHQRTHTGEKP YACGDCGRSFNQKSNFIRHQRTHTGEKP
YVCGECWRSFSQKSSSSDTRGHTQGRRP VCRECG..SFSQKSHLISHQRTHTEEKP YVCRECE.....................
40      >PRDM9a_munMun  _7      laur    gene    noDet   Muntiacus..     muntjak.....    (muntjac).....  AC225653        unordered contigs
htgs; no synteny tag stop instead of aag K      0 MRPNRSPEESTEGDAGRTEQKPT 0     0 AKDAFKDISVYFSKEEWEEMGEWEKIRYRNVKRNYEALIAI 1   2
GFRATRPDFMHHCRQVIKPQVDDTEDSDEEWTPRQQ 1  2 GKPSSMAFRVKHSKHQK 0   0 GMSRAPLIKESSLKELLGAAKLMKTSGSKQAQNPVPHPRKARTPGQHPRQKV 1        2
ELTRKETGVKRYSLRERKGHVYQEVSEPQDDDYL 1    2 YCEECQNFFIDSCAAHGLPTFVKDCAVEKGHANRSALTLPPGLSIRLSGIPDAGLGVWNEESDLPLGLHFGPYEGQITDDEEAANSGYAWL 0 0
ITKGRNCYQYVDGKDTSWANWMR 2       1 YVNCARDDEEQNLVAFQYHGQIFYRTCQVIRPGCELLVWYGDEYGQDLGIKRNSRGKSELAAGR 1    2
EPKPKIHPCASCSLAFTSQKFLSQHIQRSHPAQTLLRPSERNLLQPEHPCPGSQNQRYSDPHSLSDKPEGQEAKDRPQPLLKSIRLKRISRASSYSPGGQMGGSGVHERMKDEPSTSQKLNPEDTGTLLTGAGVSGIMR
        VTYGECGKGSKDRSSLTTHERTHTGEKP    YACRECGRSFRQKSDFITHQRTHTGEKP YVCGQCGRSFGRKFALIRHQRIHTGEKP YVCRECGQSFSQKTHLSSHQRTHTGEKP
YVCGECGRSFSQKSVLIRHQRTHTGEKP YVCQECGRSFSDKSNLISHKRTHMGEKP YVCRECGRSFIRKSVLIRHQRTHTGE.P YVCRECE.....................
41      >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
---     ---     ---
42      >PRDM7_turTru.  _9      laur    gene    gas8+   Tursiops...     truncatus...    (dolphin).....  ABRN01441536    no useful synteny
        0 MSTDRWPEDSTEGDAGRTAWKPT 0     0 VKDAFKDISIYFSKEEWTEMGEWEKIRYRNVKKNYEALVTL 1   2 GLRAPRPAFMCHRRQAIKAQVGDPEDSDEEWTPRQQ 1        2
VKPSWVAFRVEHSKHQK 0     0 AVPPVPLSNESSLKKLPGAAQLQKASGPAQAQSPAPPPGAASTSAWHTRQKL 1        2 ERRAKQIEVKMYSLRERKGHVYQEVSEPQDDDYL 1  2
yCEKCQNFFIDSCAAHGAPTFVKDSAVEKGHPNRSALTLPPGLSIRPSGIPEAGLGVWNEASDLPLGLHFGPYEGQITEDEEAANSGYSWL 0   0 ITKGRNCYEYVDGKDTSWANWMR 2     1
YVNCARDEEEQNLVAFQYHRQIFYRTCRVVRPGCELLVWYGDEYSQELGIPWGSGWKSQLVaGR 1      2
DPKPKIQPCGSCSLAFSSQKILSQHVECSHPSQVLPRTSARDRVQPEDPCPGYQNRQQQYSDPHSWSNKPECQEVKERSKPLLKRIRLGRISRAFSSSPKGQMGSSRAHERMMEAGPSTGQKVNPEATGKLLIGAGVSRV
VK      VKYRSSGQGSKDRSSLTKHQRTHTGEKP    YVCGECGRDFSLKSDLIRHQRTHTGEKP YVCGECGRDFSLKSGLISHQRTHTGEKP YVCGECGRDFSQKSGLIRHQRTHTGEKP
YVCGECGRDFSLKSGLISHQRTHTGEKP YVCGECGRDFSQKSGLIRHQRTHTGEKP YVCGECGRDFSLKSGLITHQRTHTGEKP YVCGECGRDFSQKSNLITHQRTHTGEKP
YVCGECGRDFSRKSSYI.........
43      >PRDM7_susScr.  _9      laur    gene    GAS8+   Sus........     scrofa......    (pig).........  FP476134        unordered HTGS not
wgs misassembly or inversion; not in genome browser     0 MRPDRRPEESPDPAAGSTERKAA 0     0 ATDAFKDISIYFSKEEWTEMGEWEKIRYRNVKRNYEALTTI 1   2
GLRAPRPAFMCHRRQAIKPQVDDTEDSDEEWTPRQQ 1  2 VKPCRVAFRVEHNKHQK 0   0 SDSRVPLSNKSSLKELLTTAEVPETSGSEQAQEPVSPPGEASTSRRRSGQEL 1        2
ARRRKDTEARMYSLRERKGHAYQEVGEPQDDDYL 1    2 yCEKCQNFFIDSCAAHGPPTFVKDSAVDKGHPNRSALTLPPGLRIRPSGIPEAGLGVWNEAHDLPLGLHFGPYEGQVTEDEEAANSGYSWL 0 0
ITKGRNCYEYVDGKDKSWANWMR 2       1 YVNCARDDEEQNLVAFQYHRQIFYRTCRVVRPGCELLVWYGDEYSQELGIKWGSKWKKELTAGI 1    2
EPKPKIHPCPSCSLAFSSQRFLSQHVERSHPSQSLPRASARRGLQPEGPCPDNQQQQQPYPDPHSWDGTSESQDVKEGSKPFLERRRLRKTSRASSYAPEGQMRSSRVRERMTEEEPSAGQKVNPEDTGTLFTVAGES
        GILRVENRGYGPDSGLTRHPRTHTGEKP    HVCSECGRGFSVKSHLIRHQRTHTGEKP YVCRECGRGFSVKSHLIRHQRTHTGEKP YVCRECGRGFSVKSSLITHQRTHTGEKP
YVCRECGRGFSVKSHLIRHQRTHTGEKP YVCRECGRGFSEKSSLVTHQRTHTGEKP FVCRECGRGFSVKSSLVTHQRTHTGEKP YVCRECGRGFSVKSNFITHQRTHTGEKP
YVCRECGRGFSEKSSLVTHQRTHTGEKP YVCREGE.....................
44      >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
GIPRVPLSNKSSLKELSETAKLLNTSSPEQGQKSVSLPGKASTSGHHTRQKL 1  2 ELRRKDVEVKMYSLQERKGLAYQEVSEPQDDDYL 1  2 yCEK
QTFFIDSCTVHGPPTFVKDSEVDKGQPNHSALTLPPGLRIRTSSIPQAGLGVWN ASDLPLGLHFGPYKGQITEDEEAANSGYSCL 0        0 ITKGRNCYEYVDGKDkSWANWMR 2     1
YMNCARDDEEQS LVAFQYHRQIFYRTPGHQASCELLVWYGDEYSQELGIKWGSKWKSELTAGK 1      2 EPNPEIHPCPSCSL
AFSSQKFLSQHLEHNHPSQILPRISVREHFRPKDPCPGCQNQQQQQHSDPQRWNDRAKGQEGKERFKPLPKSIRQRRISRAFSTPCKGQTTCEGIVKEEPSAGSQKLNPEDTGKLFKGVGMTRIIR
VKYRGCGRGFNDRSHLSRHQRTHTGENP    YVCRECGRGFIHRTNLIIHQRTHTGEKP YVCRECGtGFIQRSNLSIHQRTHTGEKP YVCRECGRGFTQRSTLNEHQRTHTEEKP
YVCRECGRSFTRRSTLITHQRTHTGEKP YVCRECGRSFT................. KRSTWDPWVAQRFGACLWP.........
45      >PRDM7_felCat.  11      laur    gene    GAS8+   Felis......     catus.......    (cat).........  genome  two contigs GAS8 implied by
downstream CAD1 0 mSPLRFPEQSAERGSRKARWKPT 0     0 AKDAFKDISIYFSKEEWTEMGDWEKIRYRNVKRNYEALMTI 1   2 gLRAPRPAFMCHRRQAIKPQVDVTEDSDEEWTPRQQ 1
        2 VKPSWVASRVDQNKQHK 0   0 GTHRVPLSKESSLKDFSETAKLLNTSGSEQGQKPVSLPGEASTSGHHSRRKL 1        2 frRRKEIGVKMYSLRERKGFAYQEVSEPQDDDYL 1  2
yCEKCQNFFIDSCAVHGPPTFVKDNAVGKGHPNRSALTLPPGLRIRPSSIPEAGLGVWNEASDLPLGTHFGPYEGQITEDEEAANSGYSWL 0   0 ITKGRNCYEYVDGKDNSWANWMR 2     1
YVNCARDDEEQNLVAFQYHRQIFYRTCRVIRPGCELLVWYGDEYGQELGIKWGSKWKSELSTGK 1      2
EPQPDIHRCPSCSLAFSSQKFLSQHVECKHSSQSLPQISARKHFQPENPCPGDQNQQQQQHSDPHSWNDKAKCQEVKERSRPLLKSIKQRRISRAFSTPCKGQMGSSRVCEGMVEEGPSMGQNLNSEDTGKLFMGVGMSR
IVR     IKNRGCEQGFNDRSHFSRHQRTHKEEKP    SVCNERRDFSHKSALITHQRTHTGEKP YVCRECGRGFTQRSNLFRHQRTHTGEKP YVCRECGRGFTQRSDLFTHQRTHTGEKP
YVCRECGRGFTRRSNLFTHQRTHTGEKP YVCRECGRGFTRRSHLFTHQRTHTGEKP YVCRECGRGFTQRSNLFTHQRTHTGEKP YVCRECGRGFTQRSDLFRHQRTHTGEKP
YVCRECGRGFTQRSHLFTHQRTHTGEKP YVCRECGRGFTQRSNLFRHQRTHTGEKP YVCRECGRGFTWRSNLFTHQRTHTGEKP YVCRKDGQGFTNKLHL.SYQRT......
NVATTHSIPQL................
46      >PRDM7_ailMel.  _6      laur    gene    GAS8+   Ailuropoda.     melanoleuca.    (panda).......  GL193502        first three exons
from different contig   0 MSLNTSPEETPERDSGRTGWKPT 0     0 AKDAFKDISIYFSKEEWTEMGDWEKIRYRNVKRNYEALITI 1   2
GLRAPRPAFMCHRRQAIKPQVDDTEDSDEEWTPRRQ 1  2 VRPSWVAFRMEQSKHQR 0   0 GIPRAPLRNESSLKELSETAKLLNTSGSELGQKPVSLPGEASTSGHDSLQKL 1        2
GFRRKDVEVKMYSLRERKSLAYQEVSEPQDDDYL 1    2 yCEKCQNFFIDSCAVHGPPTFVKDSAVDKGQPNRSALTLPPGLRIRPSGIPQAGLGVWNEASDLPLGLHFGPYEGQITEDEEAANSGYSWL 0 0
ITKGRNCYEYVDGKDNSWANWMR 2       1 YVNCARDEEEQNLVAFQYHRQIFYRTCRVIRPGCELLVWYGDEYGQELGIKWGSKWKSELAAGK 1    2
EPKPEIHPCPSCSLAFSSQKFLSQHLEHNHPSQILSRKSASEHFQQEDPCPGHQNQQQQQHSDPHRWNDKAKGQEVKERFKPLLKSIRQRRISRAFSSPCKGQTRSSTVCEGMVEEEPSAGQKLNPEETGKLFMGVGMSG
IIR     VKYRGCGRDFSDRSHQSGHQRRHQ KKP    SVCKKVKREFSHKSVLITHQRTHTGEKP YVCRECGRGFTQRSNLIRHQRTHTGEKP YVCRECGRGFTQRSNLIRHQRTHTGEKP
YVCRECGRGFTQRSSLIRHQRTHTGEKP YVCRECGRGFTLRPNLIGHQRTHTEALP INYISTTKEQM................
47      >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 vQPSWVAFGVEQSKHQK 0   0
AMPRVPLSNESSLKELSVIANPLKASGSEQNQQPVFPPGKASASRQHSRRKL 1  2 eLRRKGVEVKMDSLRERMGRVYQEVSEPQDDDYL 1  2
yCEKCQNFFIDSCAAHGSPIFVKDSEVDIGHPNHSALTLPPGLRIGPSGIPEAGLGVWNEASNLPLGLLFGPYEGQVTEDEEAANSKYSwM 0   0 spKGETAEYV DGKDESRANWMR 2     1
YVNCARDDEDQNLVAFQFRRQIFYRTCRVIMPGCELLVWYGDEYGQGLGIKWGSKWKREFTAGR 1      2
EPKPEIHPCPSCSLAFSSRKFLSQHMKRSHPSQSLPGISARKHLQSKEPHPEDQSQQQQQQQHTDPCSWNDKAEGQEVKERSKPMLERNGQRKISRAFSKPPKGQMGSPRECERMMEAEPSTSQKVNPENTGKSSVGVGA
SRIVR    VKYGGCGHGFDDGSHFIRHQRTHSGEKP    FVCRECERGFNEKSSLTMHQRTHSGEKP FVCREC.EGFSVKSSLIRHQRTYSGEKP FVCRECEQGFNEKSSLTMHQRTHSGEKP
FFCRECEGFSVK.SSLIRHQRTHSGQKP FVCRECKRGFTQKSHLITHQRTHSGEKP FCRECER.GFTQKSHLIKHQRTHSGEKP FVCRECA.....................
48      >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 AKDAFKDISIYFSKEEWTEMGDWEKIRYRNVKRNYDALQAI
1       2 GLRAPRPAFMCRRRQAIKPQVDDSEDSDEEWTPRQQ 1        2 --- 0 0 AMPRVPLSNEPSLKELSVIANLLKASGSEQDQKPVFPPGKASASRQHSRQKL 1        2
GLRRKGVEVKMYSLRERTGRVYQEVSEPQDDDYL 1    2 yCEKCQNFFIDSCAAHGSPIFVKDSEVDIRHPNRSALTLPPGLRIGPSGIPEAGLGVWNEASDLPLGLLFGPYEGQVTEDEEAANSGYSWL 0 0
QGKGRNCYEYVDGKDESRANWMR 2       1 YVNCARDDEEQNLVAFQYHRQIFYRTCRVIRPGCELLVWYGDEYGQELGIKWGSKWKRELTAGR 1    2
EPKPAIHPCPSCSLAFSGQKFLSQHMKRSHPSQSLPGISARKHLQSKEPHPEDQSQQQHNDPRSWNDKAEGQEVKERSKPLLERNRQRKIFRAFSKPPKGQMGSPREYERMMEAEPSTSQKVNPENTGKSSVGVGASRIV
I       VKYGGCEHGFDDGSHLIMHQRTHSGEKP    FVCRECERGFSKKSNLITHQRTHSGEKP FVCRECERGFTRKSSLITHQRTHSGEKP FVCRECERGFTQKSHLITHQRTHSGEKP
FVCRECERGFSEKSSLIKHQRTHSGEKP FVCRECERGFTRKSSLITHQRTHSGEKP FVCRECERGFTQKSSLIKHQRTHSGEKP FVCRECERGFTQKSSLIKHQRTHSGEKP
FVCRECERGFTQKSSLIKHQRTHSGEKP FVCRECERGFTQKSSLITHQRTHSGEKP FVCRECERGFTQKSHLITHQRTHSGEKP FVCRECERGFSKKSNLITHQRTHSGEKP
FVCRECERGFTRKSLLITHQRTHSGEKP FVFRECERGFTQKSSLITHQRTHSGEKP FVCRECERGFTRKSYLITHQRTHSGEKP FVGRECE.....................
49      >PRDM7_myoLuc.  _6      laur    gene    gas8+   Myotis.....     lucifugus...    (bat).........  AAPE02062260    TGA stop codon; CpG
hotspot for R CGA; SXXRD implies missing KRAB no CAD1   0 --- 0         0 --- 1 2 --- 1 2 --- 0 0
AKSRAPLSNESSLKELSGTANLLTTSGSEQTQKTVPPPGEASTSGQHPRSKL 1  2 dLRRKEIEVKMYSLRERKCRVYQEISEPQDDDYL 1  2
YCEKCQNFFIDSCAVHGPPTFVKDSAVDKGHANRSALTLPPGLRIGPSGIPEAGLGVWNEECDLPVGLHYGPYEGQITEDEAIANSGYSWL 0   0 ITKGRNCYEYVDGKDTSQANWMR 2     1
YVNCARDDEEQNLVAFQYHRQIFYRTCRVVRKGCELLVWYGEEYGQELGIKWGSKWKTEPVAGR 1      2
EPKPEIHPCPSCSVAFSSQTFLSQHGKRNHPSEILPGAPAGNHLQSEEPGPERQNQQQQQQTGPHGWNDKAEGQEVKGRSKPLLKRIRQRGTSRASFKPPNRHMGSSSERERIREEEPSTGQNVNHKNTGKLFVGVKRSK
SVT     IKHGGCGQGFNDGSHIDTHQRTHSGEKP    YICRECGGFTHKSDL.IRHQRTHSQENP YVCRECGRGFRDRSTLITHQRTHSGEKP YVCRECGRGLTEKSTLITHQRTHSGEKP
YVCRECGRGFTRKSTLITHQRTHSGEKP  YVCRECGRGSRVKSNLIRHQRTHSGEK SGVCIEGE...................
50      >PRDM7_equCab.  _4      laur    gene    GAS8+   Equus......     caballus....    (horse).......  genome  missing front exons, pre-
terminal stop GAS8+- flanked right by EMR2-     0 --- 0         0 --- 1 2 --- 1 2 VKPSWVAFRVEQSKQQK 0   0
RMRTAPLSNESRLKELSGTAKLLKTSSSEQVQKPVSPLGEASSSEQHSRRKL 1  2 ELRRKEVGVKMYSLRERKGHAYQEVSEPQDDDYL 1  2
yCENCQNFFIDSCAAHGPPIFVKDSAVDKGHPNRSALTLPLGLRIRPSGIPEAGLGVWNEASDLPLGLHFGPYEGQITEDEEAANSGYSWL 0   0 ITKGRNCYEYVDGKDISWANWMR 2     1
YVNCARDDEEQNLVAFQYHRQIFYRTCRVVRPGCELLVWYGDEYGQELGIKWGSKWKRELTAGR 1      2
EPKLEIHPCPSCSLAFSSQKFLSQHVERNHPSQILPGTSARNHLQPEDPSPGDQNQQQQHSDPHSWKDKAHSQEVKERSKPLLKKIRQRRIPRAFSYPPKGQMENFRMRERIMEEKPSIGRKVNPEDTGKLFLEMRMSRN
VR      VQYGGCGRGFNDRASLIKHQRTHTGEKP    YVCRECEQGFTQKSSLIAHQRTHTGEKP YVCRECEQGFSEKSHLIRHQRTHTGEKP
YVCRECEQGFSVKSNLIRHQRTHTGEKL .FCREGK.....................
```

51 >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 GLRAARPAFMSHRRQAIKTQLDDTEESDEEWTPNQQ 1 2 VKSLRVAFRAEQSKHQK 0 0 GRSRTPISNESSSKELSGTRTLLNTKCTKQAQKPLFPPGEASTSGHYSKPKL 1 2 ELRRKEPEVKMYSLRERKGRAYQEVSEPQDDDYL 1 2 YCENCQNFFINKCSAHGSPIFVKDNAVAKGHSNRSALTLPHGLRIGPSGIPEAGLGIWNEASDLPLGLHFGPYEGQITNDEEAANSGYSWL 0 0 ITKGRNCYEYVDGVDESLANWMR 2 1 YVNCARDYEEQNLVAFQYHRQIFYRTCRIIKPGCELLVWYGDEYGQELGIKWGSKWKSELTADK 1 2 EPKPEIYPCPCCSLAFSNQKFLSRHVEHSHPSLILPGTSARTHPKSVNFCPGDQNQWQQHSDACNDKPDEPWNDKLENHKSKGRSKPLPKRMGQKRISTAFPNLRSSKMGSSNKHETIMDKINTGQKENPKDTYRVFAGI GMPRIIR DKHVTLRRSFTNRSSPLTHQRTHTGEKP YVCRECGRGFSQKSHLLTHQRTHTGEKP YVCRECGRGFTDRSSLLTHQRTHTGEKP YVCRECGRGFSLKSSLLRHQRTHTGEKP YVCRECGRGFSLKSSLLTHQRTHTGEKP YVCRECGRGFTDRSSLLTHQRTHTGEKP YVCRECGRGFSLKSSLLTHQRTHTGEKP YVCRECGRGFSRKSSLLRHQRTHTGEKP YVCES..... 52 >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 GTPKALLGNESSLKEVSGTAILLNTTGSEQAQKPVSSPGEASTSDQPSRWKL 1 2 EPRRNEVEVKMYNLRERKGLEYQEVSEPQDDDYL 1 2 yCEKCQNFFIDTCAVHGAPMFVKDSPVDRGHPNHSALTLPPGLRIGPSSIPKAGLGVWNEASELPLGLHFGPYEGQVTEDKEAANSGYSWL 0 0 ITKGKNCYEYVDGKDESWANWMR 2 1 YVNCARDEEEQNLVAFQYHRQIFYRTCRTIQPDCELLVWYGDEYGQELGIKWGSRWKKELTSGR 1 2 EPKPEIHPCPSCRLAFSSQKFLSQHMKHSHPSPPFPGTPERKYLQPEDPRPGGRRQQRSEQHMWSDKAEDPEAGDGSRLVFERTRRGCISKACSSLPKGQIGSSREGNRMMETKPSPGQKANPEDAEKLFLGVGTSRIAK VRCGECGQGFSQKSVLIRHQKTHSGEKP YVCGECGRGFSVKSVLIKHQRTHSGEKP YVCGECGRGFSVKSVLITHQRTHSGEKP YVCGECGRGFSVKSVLITHQRTHSGEKP YVCGECGRGFSQKSDLIKHQRTHSGEKP YSCRECGRGFSRKSVLITHQRTHSGEKP YVCGECGRGFSQKSNLITHQRTHSGEKP YVCGECGRGFSRKSVLITHQRTHSGEKP YVCGECGRGFSQKSNLITHQRTHSGEKP YVCGECGRGFSQKSDLITHQRTHSGEKP YVCRECGRGFSRKSNLITHQRTHSGEKP YVCRECRRGFSVKSALI..... GHGRRKCSKSAEPLHFPRVSRDQK.... 53 >PRDM9b_loxAfr _3 afro pseu noDet Loxodonta.. africana.... (elephant).... genome approx seq after frameshift correction 0 --- 0 0 --- 1 2 --- 1 2 --- 0 0 GTPKVLLSNESSLKEVSGTAILLSTMGSEQAQKPVSSPGEASTSDQPSRRKQ 1 2 EPRRKEVEVNMYSLRERKGLVYQEVGEPQDDDYL 1 2 yCEKCQNFFIHTCAVHGAPMFVKDSHVDRGHLNHSALTLPPGLRIGPSSIPEAGLRVR EVSEQLLGLHIGPYEGQVTEDkEAAHSGYSWL 0 0 ITKGRNCYKYVDGKDDPWANRMR 2 1 YVNCIQD KEQNLVAFQYHRQIFHWTCCTIRPGCELLVWYGDNYSQELGIKWGSR KKEL 1 2 EPKPEIHPCPSCPLAISSQKFLDQHTKHSHPSPPFPGTPERKHLQPEDPHPGGRRQQHSEQHLNDKAEDPETGDGSKPVFERARLVGGGAGGVSKVCSSLPKGQMGSSREGNRMMETEGQKVNPEDTEKLFLGVGISRLA K VRCGEYGQGFSQKSVLIRHQRTYSGEEH YVCGECGRGFSWKSQLTRHQRSHSWEKP YVCRECGGFSVKSTLI..... GTGEGNAATIHLHLPS..... 54 >PRDM7_loxAfr. _5 afro pseu GAS8+ Loxodonta.. africana.... (elephant).... genome scaffold_57 several frameshifts; ZNF540 opposite strand upstream of N-terminus 0 --- 0 0 --- 1 2 GLRASHPAFTCHCMQAIKAQMDDTEDSNEEQTPRQq 1 2 VRPSWVAFRMEQSKHQR 0 0 GMLRVPRSNESSLKNLSGTSIMLSRAGSEQAQKLVLPPGKASTSDEHSRQKP 1 2 EHRRKGVEVKMYSF ERKGLVYQEIS PQDDDYL 1 2 YCEKCQNFFIDTCESHGVPTFVKNSTTDSGHPNHLALTPSSGLRTRPSSIPKAWLRLWNKAFELLLGLPFSPCEGQVIEDEAVDNSGYSWL 0 0 --- 2 1 YVNGTQDEKEQNLVFFQYHRQIFYQTCYAVWPGCQLLVWYRDECGQELGIKWDNRGKKEFe 1 2 EPKPEAHPCPSCPLAFSSEKFLSQHMKHNHPSQSSPETPERKHLQPEDPHPGHQNQQQQQHSDPHRWNDKAEGQQTGDRSKPMFENIRQEVTSRAFSSLPKGQMVCSREGNRMMETEPSPGLKVNPEVTGKLFLGVESSR IAK VKYRGCGRDFSDRSHQSGHQRRHQ KKP SVCKKVKREFSHKSVLITHQRTHSGEKS YVCKESGRGFSAKSNLIRPRRTHTGEKP YVCGERGG.FSVSGLII.HQRAHSPEKP YVCREGRRGFGDKSSFIKHQRATLGEKS YVCKESGRGFS..... AKSNLIRPRRKKCRHDTTPHPQL..... 55 >PRDM7_echTel. _5 afro pseu noDet Echinops... telfairi.... (tenrec)..... genome 2 frameshifts plus stop codon 0 --- 0 0 --- 1 2 GLRAPRPAFMCHHRPAAKGQVEDSEDSDEEWTPRQR 1 2 --- 0 0 GMPGVSLRNESNLKVLSGTAILLTAAEPEQPH PGSPPGEATTSHEHLRQKV 1 2 epELRRRAVMMNSLRERKNLMYQEVSTPCDDNCL 1 2 YGERCHNFFIDTHIAHGATTFVKDS PMDRSNCSILPPGLRIGPSGIPEAGLGVWNEASELPLGLHFVPYEGQVTKDEAATNSGYSWM 0 0 ITKGRNCYEYVDGKDKSWANwMr 2 1 --- 1 2 EPKPEVNPCPSCPLALSSQQLKHSHPFQSLPGTPAEKHLQAEDFHPRGQKLHHFEHHIRNERAEGLETGDGSKPMLERTRLGKMSKTTYNSPKGQTRSSGETNRIREADLNPGQGVNAEDTRNLFLGIGISRIAK VRCRECGHGFSVKSSLITHQRIHTGEKP YVCSECGQGFSQKSVLIRHQRIHTGEKP YICRECDRGFSRKSHLIKHQRTHSGEKP YVCRECGQGFSQKSVLITHHRTHSGEKP YVCRECGRGFSQKSDLIKHERTHS.... 56 >PRDM7a_proCap 17 afro pseu noDet Procavia... capensis.... (hyrax)..... ABRQ01227339 two frameshift and three stop codons in exon 10 0 --- 0 0 AKDAFRDISIYFSKEEWAEMGEWEKSRYRNVKRNYEALVAI 1 2 GLRAPRPAFMCHRRQAIKAQVDNTEDSDEEWTPRQQ 1 2 AKPRSVASREELRKPQK 0 0 GTPKALLGNESSLKEVSGTAILLNTTGSEQAQKPVSSPGEASTSDQPSRWKL 1 2 EPRRKEAEVKRYNLREGTNPAYQEVGDTQDDDYL 1 2 yCEKYQKFCTDVCPAHGALAFLKDLSVERGHPKHSALTLPPGLRIGASGIPEAGLGVWSEASELPPGLHFGPCERQVTKDNEAANRGYLWP 0 0 ITKGRSCSLYMDRKDESRANWMR 2 1 YVRHAGDKEEQNLVAFQYHRQIFYRTCRPVQPGCELLVWPGAEDGQELGLQRGSRWKKELASQT 1 2 EARPEIHPCPSCPLAFSTPKFLSHHVKHSHPCQPFPGTLARRPLQPEDPHPGDRRQQHSEQPNWNDKAEGPEIGHVSRPVFEKTRQEGFSEARSSLPKGQMGRSREAERTTETQNSPGQKVNPEDTEILFLRGGISEIAK VKCGECGQGFSRKSHLIRHQRTHSGMKP YVCRECRRGFGVKSLLTRHQRTCSGMKP YVCRECGQGFRWKSHLIRHQRTHSGEKP FVCSECGRGFSVRSHLFTHQRTHSGEKP YVCKECGRGFSVKSYLTTHQRTHTGEKP YVCKECGRGFSWKSHLITHQRTHSGEKP YVCRQCGRGFSVQSHLIIHQRTHSGDKP YICRECGRDFTEKSSLIRHRRTHSGEKP YVCRDCG GFTRKSLLITHQRTHSGEKP YVYRECGRGFSCKSYLISHQKTHLGEKP YVCSDCGRGFSVKSQLVSHKRTHSGEKP FVCREC RGFSVKSSLISHQRTHSGEKP FVCRECGRGFSVKSSLIKHQRTHSGEKP YVCKECGRGFSQKSSLITHQRTHSGEKP YVCRECGRGFGLKSYLITHQRTHTGEKP YICRECG GFSVKSSLITDQRTHTGEKP YVCRECGRAFSKKSSLISHHRTHPAEAV YVHRECG..... 57 >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 GIRVFHPAFMIHPRKTIKAQMDDSEDSDEDWTARQQ 1 2 AKPPSVASREELRKPQK 0 0 GPSRAPLRIKSSLKRVSEPAIVWSTADSEQAQERVQKPVLSRREASASDQPLRRKV 1 2 EPRRHEAEDKRYSLRGGTGPACQEVGEPQDDDYL 1 2 yCEECRNFFIDTCVAHGTPVFIKDISVERGHPNRLALTLPTGLRIGPSSIPDAGLGVWNEASELPPGLHFGPCEGQVTEDEEAANSGYSWL 0 0 VTKGRSCFEYVDGKNEALANWMR 2 1 YVRRARDTEERNLVAFQYHRQIFYRTCCTVRPGCELLVWRGAEDSQALG SRRTMELTSQK 1 2 EARPEIHPCPSCPLAFSTQKFLSYHVNHSHSSEPFPGTHARRHLPREDPRPGYERDQRSEQHNWNDSTGGPERDVSRP VIERTWEGEISEACSSLPRGHMGRSREGERMAETQSSPGLKVTLAK VRWDEYGQGFGPKSHHITQQTKHSGKKP CVCKECG GFRVKSLLKSHQMTHSGEKP YVCRECGRGFSVKSTLITHQRTHSGEKP YVCRECGRGFSVKSFLISHQRTHSGEKP YVCRECGRGFSWKSGLITHQRTHTGEKR YVCRECGHGFNRPSRLIRHQRTHSGEQP YVCRECGHGFNRRSQLIRHQRTHTGEQP YVCRECGQGFSGKSGLNRHQRTHSGEKP YVYKECGRGFSVKSTLIKHQRGHSGEKP YVCKECGRGFSRNSGLITHQRTHSGEQP YVCRECGRGFNQKSGVISHQRIHSGEKP FVCGECGRRFSWQSNLITHQRTHSGEKP FVCRECGRGFSAKTSLINHQRIH GKKP YVCRDGG..... 58 >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 AQDAFRDISTYFSREEWAEMGRWEKLRYRNVKRNYEALLAI 1 2 GLRAPRPAFMCHRKQSIKPQVDDAEDSDEEWTPRQQ 1 2 --- 0 0 --- 1 2 EPRRKGIDVKMYSLRERKGLAYEEVSEPQDDDYL 1 2 yCEKCQNFFIDSCTVHGPPIFVKDSAVDKGHPNRSALTLPSGLRIGPSGIPEAGLGIWNEASDLPLGLHFGPYEGQVTEDEEAANSGYSWL 0 0 ITKGRNYYEYEDGKDKSWANWMR 2 1 YVNCAWDDKEQNLVAFQYHRQIFYRTCRTIRPGCELLVWYGDEYGQELGIKWGSKWKKEFMTGT 1 2 ELKPEIHPCPSCPLAFSSEKFLSQHVRRHHPSQSFPAACAREHFQPQNPRPRGEEQQQHSDQCGWKDKAEGQETENRPKPLFERIKPMGSPRAFYNPPRGQMRSSREGKRMMEIQPSQDQKMNSE RGQLFLGVGIFKTEV IKFGENRQDFSDKSDHTSHQRTHTGEKP YVCRECGRGFSNNSHLTRHQRTHTGVKP YVCRECGQGFSVKPALTKHQRTHTVEKP yVCSECG GFSVKSTLITHQRTHTGEKP CVCRECGRGFNNKPDLTKHQRTHTGEKS YVCRECG GFSVKSTLIIHQRTHTGEKP YVCRECGRGFSEKSNLTVHQRTHTGEKP YVCRECGRGFSEKSNLTVHQRTHTGEKP YVCRECGRSFSVKSTLITHQRTHTVEKP YVCMKSEVVVSNKSHLNSHRRMKCGHRT PPPPQL 59 >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 ycekcQNFFFENCAAHGPPTLLKDSAVGQGRPKHSALVLPPGLRLGPSGIPEAGLGVWNEASDLPLGLHFGPYEGQVTEDEEATNSGYSWL 0 0 ITKGRNCYEYVDGKDKSCANWMR 2 1 YVNCARDDEEQNLVAFQYHRQIFYRTCRAIRPGCELLVWYGDEYGQELGIKWGSKWKKELTAEK 1 2 GLKPEIHPCPSCPLAFSTEKFLSQHVQRNHPSQIFPVTYARKHLQPQDPRPGDQQQPQPHSDQCHCSDKAEDQETEKRSKPLFESTKQMGISRAYSSPPEGQMRSSREDKRTMEIEPSQDQKMNPEETRLFVGVGILKTA R IKCGEYGQGFSVKPNLTTHQRTHTEEKP YVCRECGRGFGQKPNLSRHQRTHTGEKP YVCRECGRGFG.....