

1 >PRDM9\_homSap. 13 prim gene CDH12 Homo..... sapiens..... (human)..... NM\_020227 chr5 10 exon size 18,301 bp KRAB  
SSXR SET C2H2 0 MSPERSQESPEEDTERTERKPM 0 0 VKDAFKDISIYFTKEEWAEMGDWETRYRNVKRNALITI 1 2 GLRATRFAPMCHRRQAIAKLQVDDTSDSEEWTPRQ 1 2  
VKPFWMAFRGEQSKHQK 0 0 GMPKASFNNESLKLSELTANLNASGSEQAQKVPSPGPEASTSGQHSRLK 1 2 ELRKKETEGKMSYLRERKHAYKEVSEPODDYL 1 2  
YVNCARDDEQNVAFOYHRQIFRYTRCVIRPGCELLVWYDEYQELGKIGKWSKWKELMAGR 1 2  
EKPEIHPSPCLLAFSSQKFLSQHVERNHSSQNFPGPSARKLQLENPCPDQNOEQYSDPDRSCNDKTGQEKERSKLLNKTRQWREISRAFSSPPKQMGMSRVGKRIMEESRTGQKVPNGTGLKLVGVGISRIAK  
VKYCEGCGFSVSKSDVITHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWQSVLLTHQRTHTGKPK YVRCRCGRGFSRSQSVLLTHQRTHTGKPK YVRCRCGRGFSRSQSVLLTHQRTHTGKPK  
YVRCRCGRGFSWQSVLLTHQRTHTGKPK YVRCRCGRGFSWQSVLLTHQRTHTGKPK YVRCRCGRGFSRSQSVLLTHQRTHTGKPK YVRCRCGRGFSRSQSVLLTHQRTHTGKPK YVRCRCGRGFSRSQSVLLTHQRTHTGKPK  
YVRCRCGRGFSRSQSVLLTHQRTHTGKPK YVRCRCGRGFSRSQSVLLTHQRTHTGKPK YVRCRCGRGFSRSQSVLLTHQRTHTGKPK YVRCRCGRGFSRSQSVLLTHQRTHTGKPK YVRCRCGRGFSRSQSVLLTHQRTHTGKPK  
2 >PRDM9\_panTro. 19 prim gene CDH12 Pan..... troglodytes. (chimp)..... G166820 chr5 frag assembly glitch in mid  
C2H2 0 MSPERSQESPEEDTERTERKPM 0 0 VKDAFKDISIYFTKEEWAEMGDWgKTRRYRiVMKNYALITI 1 2 GLRATRFAPMCHRRQAIAKLQVDDTSDSEEWTPRQ 1 2  
VKPFWMAFRGEQSKHQK 0 0 GMPKASFNNESLKLSELTANLNASGSEQAQKVPSPGPEASTSGQHSRLK 1 2 ELRKKETEGKMSYLRERKHAYKEVSEPODDYL 1 2  
yCEM0NFFIDSCAAHGPPPTFKDSAVDKGHNPNSALSPLPGLRIGPSGIPQAGLVWNEASDPLGLHFGYGRITDEEAANNYSWL 0 0 ITKGRNCEYVVDGKDKSWANWR 2 1  
YVNCARDDEQNVAFOYHRQIFRYTRCVIRPGCELLVWYDEYQELGKIGKWSKWKELMAGR 1 2  
EKPEIHPSPCLLAFSSQKFLSQHVERNHSSQNFPGPSARKLQLENPCPDQNOEQYSDPDRSCNDKTGQEKERSKLLNKTRQWREISRAFSSPPKQMGMSRVGKRIMEESRTGQKVPNGTGLKLVGVGISRIAK  
VKYCEGCGFSVSKSDVITHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK  
YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK  
YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK  
3 >PRDM9\_gorGor. -- prim gene cdh12 Gorilla..... gorilla..... CABD02290264 chr5 several contigs needed,  
most of ZNF domain missing 0 MSPERSQESPEEDTERTERKPM 0 0 VKDAFKDISIYFTKEEWAEMGDWETRYRNVKRNALITI 1 2 GLRATRFAPMCHRRQAIAKLQVDDTSDSEEWTPRQ 1 2  
2 VKPFWMAFRGEQSKHQK 0 0 GMPKASFNNESLKLSELTANLNASGSEQAQKVPSPGPEASTSGQHSRLK 1 2 ELRKKETEGKMSYLRERKHAYKEVSEPODDYL 1 2  
yCEM0NFFIDSCAAHGPPPTFKDSAVDKGHNPNSALSPLPGLRIGPSGIPQAGLVWNEASDPLGLHFGYGRITDEEAANNYSWL 0 0 ITKGRNCEYVVDGKDKSWANWR 2 1  
YVNCARDDEQNVAFOYHRQIFRYTRCVIRPGCELLVWYDEYQELGKIGKWSKWKELMAGR 1 2  
EKPEIHPSPCLLAFSSQKFLSQHVERNHSSQNFPGPSARKLQLENPCPDQNOEQYSDPDRSCNDKTGQEKERSKLLNKTRQWREISRAFSSPPKQMGMSRVGKRIMEESRTGQKVPNGTGLKLVGVGISRIAK  
VKYCEGCGFSVSKSDVITHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK  
YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK  
4 >PRDM9\_ponAbe. 10 prim gene CDH12 Pongo..... abelii..... (orangutan)... XR\_093432 chr5 frameshift extra  
penultimate ZNF 0 MSPERSQESPEEDTERTERKPM 0 0 VKDAFKDISIYFTKEEWAEMGDWETRYRNVKRNALITI 1 2 GLRATRFAPMCHRRQAIAKLQVDDTSDSEEWTPRQ 1 2  
2 VKPFWMAFRGEQSKHQK 0 0 GMPKASFNNESLKLSELTANLNASGSEQAQKVPSPGPEASTSGQHSRLK 1 2 ELRKKETEGKMSYLRERKHAYKEVSEPODDYL 1 2  
YVNCARDDEQNVAFOYHRQIFRYTRCVIRPGCELLVWYDEYQELGKIGKWSKWKELMAGR 1 2  
YVNCARDDEQNVAFOYHRQIFRYTRCVIRPGCELLVWYDEYQELGKIGKWSKWKELMAGR 1 2  
EKPEIHPSPCLLAFSSQKFLSQHVERNHSSQNFPGPSARKLQLENPCPDQNOEQYSDPDRSCNDKTGQEKERSKLLNKTRQWREISRAFSSPPKQMGMSRVGKRIMEESRTGQKVPNGTGLKLVGVGISRIAK  
VKYCEGCGFSVSKSDVITHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK  
YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK  
YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK  
5 >PRDM9\_nomLeu. 10 prim gene cdh12 Nomascus... leucogenys.. (gibbon)..... ADFV01015315 ADFV01015319 no CDH  
but best blastn favors PRDM9 0 MSPERSQESPEEDTERTERKPM 0 0 VKDAFKDISIYFTKEEWAEMGDWETRYRNVKRNALITI 1 2 GLRATRFAPMCHRRQAIAKLQVDDTSDSEEWTPRQ 1 2  
2 --- 0 --- 1 2 --- 1 2 AAGPPTFKIDSTVGGKHPNRSALSPLPGLRIGPSGIPQAGLVWNEASDPLGLHFGYGRITDEEAANNYSWL 0 0  
ITKGRNCEYVVDGKDKSWANWR 2 1 --- 1 2  
EKPEIHPSPCLLAFSSQKFLSQHVARNHSSQNFPGPSARKLQLENPCPDQNOEQYSDPDRSCNDKTGQEKERSKLLNKTRQWREISRAFSSPPKQMGMSRVGKRIMEESRTGQKVPNGTGLKLVGVGISRIAE  
VKYCEGCGFSVSKSDVITHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK  
YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK  
6 >PRDM9\_macMul. 9 prim gene CDH12 Macaca..... mulatta..... (rhesus)..... XM\_001083675 chr6 exon 4 lost to Ns 0  
MSPERSQESPEEDTERTERKPT 0 0 VKDAFKDISIYFTKEEWAEMGDWETRYRNVKRNALITI 1 2 GLRATRFAPMCHRRQAIAKLQVDDTSDSEEWTPRQ 1 2 --- 0 0  
GMPKASFNNESLKLSELTANLNASGSEQAQKVPSPGPEASTSGQHSRLK 1 2 ELRKKETEGKMSYLRERKHAYKEVSEPODDYL 1 2  
YVNCARDDEQNVAFOYHRQIFRYTRCVIRPGCELLVWYDEYQELGKIGKWSKWKELMAGR 1 2  
EKPEIHPSPCLLAFSSQKFLSQHVARNHSSQNFPGPSARKLQLENPCPDQNOEQYSDPDRSCNDKTGQEKERSKLLNKTRQWREISRAFSSPPKQMGMSRVGKRIMEESRTGQKVPNGTGLKLVGVGISRIAK  
VKYCEGCGFSVSKSDVITHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK  
YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK  
7 >PRDM9\_papHam. 11 prim gene cdh12 Papio..... hamadryas... (baboon)..... genome contigs scattered 0 --- 0  
0 --- 1 2 --- 1 2 VKPFWMAFRGEQSKHQK 0 0 EMPKTSFNNESLKLSELTANLNASGSEQAQKVPSPGPEASTSGQHSRLK 1 2 ELRKKETEGKMSYLRERKHAYKEVSEPODDYL 1 2  
yCEM0NFFIDSCAAHGPPPTFKDSAVDKGHNPNSALSPLPGLRIGPSGIPQAGLVWNEASDPLGLHFGYGRITDEEAANNYSWL 0 0 ITKGRNCEYVVDGKDKSWANWR 2 1 --- 1 2  
EKPEIHPSPCLLAFSSQKFLSQHVARNHSSQNFPGPSARKLQLENPCPDQNOEQYSDPDRSCNDKTGQEKERSKLLNKTRQWREISRAFSSPPKQMGMSRVGKRIMEESRTGQKVPNGTGLKLVGVGISRIAK  
VKYCEGCGFSVSKSDVITHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK  
YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK  
YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK  
8 >PRDM7\_homSap. 3 prim gene GAS8+ Homo..... sapiens..... (human)..... genome chr16 TUBB3+ DEFB+ AFG3L1+ DBND1- GAS8+  
PRDM7- 92% id 0 MSPERSQESPEEDTERTERKPM 0 0 VKDAFKDISIYFTKEEWAEMGDWETRYRNVKRNALITI 1 2 GLRATRFAPMCHRRQAIAKLQVDDTSDSEEWTPRQ 1 2  
VKPFWMAFRGEQSKHQK 0 0 GMPKASFNNESLKLSELTANLNASGSEQAQKVPSPGPEASTSGQHSRLK 1 2 ELRKKETEGKMSYLRERKHAYKEVSEPODDYL 1 2  
YVNCARDDEQNVAFOYHRQIFRYTRCVIRPGCELLVWYDEYQELGKIGKWSKWKELMAGR 1 2  
EKPEIHPSPCLLAFSSQKFLSQHVARNHSSQNFPGPSARKLQLENPCPDQNOEQYSDPDRSCNDKTGQEKERSKLLNKTRQWREISRAFSSPPKQMGMSRVGKRIMEESRTGQKVPNGTGLKLVGVGISRIAK  
VKYCEGCGFSVSKSDVITHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK  
YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK  
9 >PRDM7\_panTro. 2 prim pseu GAS8+ Pan..... troglodytes. (chimp)..... genome chr16 0 MSPERSQESPEEDTERTERKPM 0  
0 VKDAFKDISIYFTKEEWAEMGDWETRYRNVKRNALITI 1 2 GLRATRFAPMCHRRQAIAKLQVDDTSDSEEWTPRQ 1 2 VKPFWMAFRGEQSKHQK 0 0  
GMPKASFNNESLKLSELTANLNASGSEQAQKVPSPGPEASTSGQHSRLK 1 2 ELRKKETEGKMSYLRERKHAYKEVSEPODDYL 1 2  
YVNCARDDEQNVAFOYHRQIFRYTRCVIRPGCELLVWYDEYQELGKIGKWSKWKELMAGR 1 2  
EKPEIHPSPCLLAFSSQKFLSQHVARNHSSQNFPGPSARKLQLENPCPDQNOEQYSDPDRSCNDKTGQEKERSKLLNKTRQWREISRAFSSPPKQMGMSRVGKRIMEESRTGQKVPNGTGLKLVGVGISRIAK  
VKYCEGCGFSVSKSDVITHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK  
YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK  
10 >PRDM7\_gorGor. 3 prim pseu GAS8+ Gorilla..... gorilla..... (gorilla)..... genome chr15730 numerous frameshifts in  
terminal ZNF domain 0 MSPERSQESPEEDTERTERKPM 0 0 VKDAFKDISIYFTKEEWAEMGDWETRYRNVKRNALITI 1 2 GLRATRFAPMCHRRQAIAKLQVDDTSDSEEWTPRQ 1 2  
2 --- 0 0 GMPKASFNNESLKLSELTANLNASGSEQAQKVPSPGPEASTSGQHSRLK 1 2 ELRKKETEGKMSYLRERKHAYKEVSEPODDYL 1 2  
YVNCARDDEQNVAFOYHRQIFRYTRCVIRPGCELLVWYDEYQELGKIGKWSKWKELMAGR 1 2  
EKPEIHPSPCLLAFSSQKFLSQHVARNHSSQNFPGPSARKLQLENPCPDQNOEQYSDPDRSCNDKTGQEKERSKLLNKTRQWREISRAFSSPPKQMGMSRVGKRIMEESRTGQKVPNGTGLKLVGVGISRIAK  
VKYCEGCGFSVSKSDVITHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK  
YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK  
11 >PRDM7\_ponAbe. 4 prim gene GAS8+ Pongo..... abelii..... (orangutan)... genome chr16 0 MSPERSQESPEEDTERTERKPT 0  
0 VKDAFKDISIYFTKEEWAEMGDWETRYRNVKRNALITI 1 2 GLRATRFAPMCHRRQAIAKLQVDDTSDSEEWTPRQ 1 2 VKPFWMAFRGEQSKHQK 0 0  
GMPKASFNNESLKLSELTANLNASGSEQAQKVPSPGPEASTSGQHSRLK 1 2 ELRKKETEGKMSYLRERKHAYKEVSEPODDYL 1 2  
YVNCARDDEQNVAFOYHRQIFRYTRCVIRPGCELLVWYDEYQELGKIGKWSKWKELMAGR 1 2  
EKPEIHPSPCLLAFSSQKFLSQHVARNHSSQNFPGPSARKLQLENPCPDQNOEQYSDPDRSCNDKTGQEKERSKLLNKTRQWREISRAFSSPPKQMGMSRVGKRIMEESRTGQKVPNGTGLKLVGVGISRIAK  
VKYCEGCGFSVSKSDVITHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK  
YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK  
12 >PRDM7\_nomLeu. 5 prim pseu gas8+ Nomascus... leucogenys.. (gibbon)..... ADFV01125891 synteny implied by non-coding  
0 --- 0 --- 1 2 --- 1 2 IKSPMAVVRVEQSKHQK 0 0 GMPKASFNNESLKLSELTANLNASGSEQAQKVPSPGPEASTSGQHSRLK 1 2 ELRKKETEGKMSYLRERKHAYKEVSEPODDYL 1 2  
ERKGHAYKEVSEPODDYL 1 2 yCEM0NFFIDSCAAHGPPPTFKDSAVDKGHNPNSALSPLPGLRIGPSGIPQAGLVWNEASDPLGLHFGYGRITDEEAANNYSWL 0 0 ITKGRNCEYVVDGKDKSWANWR 2 1  
1 YVNCARDDEQNVAFOYHRQIFRYTRCVIRPGCELLVWYDEYQELGKIGKWSKWKELMAGR 1 2  
EKPEIHPSPCLLAFSSQKFLSQHVARNHSSQNFPGPSARKLQLENPCPDQNOEQYSDPDRSCNDKTGQEKERSKLLNKTRQWREISRAFSSPPKQMGMSRVGKRIMEESRTGQKVPNGTGLKLVGVGISRIAK  
VKYCEGCGFSVSKSDVITHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK  
YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK  
13 >PRDM7\_macMul. 2 prim pseu GAS8+ Macaca..... mulatta..... (rhesus)..... genome chr20 frameshifts exon 5 and 10, exon 10  
a to aa restorers frame 0 --- 0 --- 1 2 --- 1 2 VKPFWMAFRGEQSKHQK 0 0 EMPKTSFNNESLKLSELTANLNASGSEQAQKVPSPGPEASTSGQHSRLK 1 2  
ELRKKETEGKMSYLRERKHAYKEVSEPODDYL 1 2 YVNCARDDEQNVAFOYHRQIFRYTRCVIRPGCELLVWYDEYQELGKIGKWSKWKELMAGR 1 2  
ITKGRNCEYVVDGKDKSWANWR 2 1 --- 1 2  
EKPEIHPSPCLLAFSSQKFLSQHVARNHSSQNFPGPSARKLQLENPCPDQNOEQYSDPDRSCNDKTGQEKERSKLLNKTRQWREISRAFSSPPKQMGMSRVGKRIMEESRTGQKVPNGTGLKLVGVGISRIAK  
VKYCEGCGFSVSKSDVITHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK  
YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK  
14 >PRDM7\_papHam. 2 prim pseu gas8+ Papio..... hamadryas... (baboon)..... genome contigs scattered 0  
MSPERSQESPEEDTERTERKPM 0 0 VKDAFKDISIYFTKEEWAEMGDWETRYRNVKRNALITI 1 2 GLRATRFAPMCHRRQAIAKLQVDDTSDSEEWTPRQ 1 2 VKPFWMAFRGEQSKHQK 0 0  
GMPKASFNNESLKLSELTANLNASGSEQAQKVPSPGPEASTSGQHSRLK 1 2 ELRKKETEGKMSYLRERKHAYKEVSEPODDYL 1 2  
YVNCARDDEQNVAFOYHRQIFRYTRCVIRPGCELLVWYDEYQELGKIGKWSKWKELMAGR 1 2  
EKPEIHPSPCLLAFSSQKFLSQHVARNHSSQNFPGPSARKLQLENPCPDQNOEQYSDPDRSCNDKTGQEKERSKLLNKTRQWREISRAFSSPPKQMGMSRVGKRIMEESRTGQKVPNGTGLKLVGVGISRIAK  
VKYCEGCGFSVSKSDVITHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK  
YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK YVRCRCGRGFSWKSLLHSHQRTHTGKPK  
15 >PRDM7\_calJac. 12 prim gene GAS8+ Callithrix. jacchus..... (marmoset).... XR\_090591 chr20 one frameshift in repeat

area chr20 terminus 0 MSPERSQEESEPGDTRTEQKPM 0 0 VKDAFKDISMYFSKEEWAEMGDWETRYRNMKNRYNALITI 1 2 GLRATRPAPMCHRRQAIAKLQVDDTDESDDEWTPRQ 1  
2 VKPMPAFMVRVGSQKHQK 0 0 GMPKASFGNSSLKLSGTANLVNTSGPEQAQKPVSPGEASTSGHRSRLK 1 2 ELRRKDETEKMYSLRERKGLAYKEVSEPPDDYDL 1 2  
YCEICQNFIDSCAAGHPPTFKVDSAVDKGHPNHAALSLPGLRIGSPGIPQAGLVWNEASDLPLGLHFGYEGQITDEDEEAANSYSWL 0 0 ITKGRNCEYVVDGDKDSANWNR 2 1  
YNCARDDEQNVAFOYHRQIFRYTRCVIRPGCELLVWYDEYQELGKIGWSKWKELMAGR 1 2  
ESKPEIHPCCSLAFSSQKFLSHVHNRHNSQNFPGTSTRKLLQENPCPGKQEEQOYFPCNSNDKTGQETKERSKLLNIRTQWEMARAFSNPPKQMGSSRVEERMEESRTGQKVPNPVDTGKLVFVGVISRIAK  
AYGECGQSDKRSLSVSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
16 >PRM7\_micMur. 8 prim gene gas8+ Microcebus. murinus..... (lemur)..... ABCD01433247 weak coverage 0  
MSPEKQSEESPEEDTERTKRPM 0 0 VKDAFKDISMYFSKEEWAEMGDWETRYRNMKNRYNALITI 1 2 GLRATRPAPMCHRRQAIAKLQVDDTDESDDEWTPRQ 1 2 VKPMPAFMVRVGSQKHQK 0  
0 GMPKASFGNSSLKLSGTANLVNTSGPEQAQKPVSPGEASTSGHRSRLK 1 2 ELRRKDETEKMYSLRERKGLAYKEVSEPPDDYDL 1 2  
YCEICQNFIDSCAAGHPPTFKVDSAVDKGHPNHAALSLPGLRIGSPGIPQAGLVWNEASDLPLGLHFGYEGQITDEDEEAANSYSWL 0 0 ITKGRNCEYVVDGDKDSANWNR 2 1  
YNCARDDEQNVAFOYHRQIFRYTRCVIRPGCELLVWYDEYQELGKIGWSKWKELMAGR 1 2  
YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
17 >PRM7\_otoGar. 7 prim gene GAS8+ Otolemur... garnettii..... (galago)..... genome good coverage 0  
MSPEKQSEESPEEDTERTKRPM 0 0 VKDAFKDISMYFSKEEWAEMGDWETRYRNMKNRYNALITI 1 2 GLRATRPAPMCHRRQAIAKLQVDDTDESDDEWTPRQ 1 2 VKPMPAFMVRVGSQKHQK 0  
0 ILKCMFLSNMMLKELSGASPLPNISSGEOHQHMSSPREASTSGHRSRLK 1 2 DLRIKETEVMYSLRERKGLAYKEVSEPPDDYDL 1 2  
YCEICQNFIDSCAAGHPPTFKVDSAVDKGHPNHAALSLPGLRIGSPGIPQAGLVWNEASDLPLGLHFGYEGQITDEDEEAANSYSWL 0 0 ITKGRNCEYVVDGDKDSANWNR 2 1  
YNCARDDEQNVAFOYHRQIFRYTRCVIRPGCELLVWYDEYQELGKIGWSKWKELMAGR 1 2  
YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
18 >PRM7\_tarSyr. -- prim pseu gas8+ Tarsius.... syrichta.... (tarsier)..... ABR011082008 double frameshift in exon 5  
ABRT01049286 0 --- 0 --- 1 2 GLRATRPAPMCHRRQAIAKLQVDDTDESDDEWTPRQ 1 2  
2 EFRKKEIEVMYSLRERKDCAYKEVSEPPDDYDL 1 2 YCEICQNFIDSCAAGHPPTFKVDSAVDKGHPNHAALSLPGLRIGSPGIPQAGLVWNEASDLPLGLHFGYEGQITDEDEEAANSYSWL 0 0  
ITKGRNCEYVVDGDKDSANWNR 2 1 YNCARDDEQNVAFOYHRQIFRYTRCVIRPGCELLVWYDEYQELGKIGWSKWKELMAGR 1 2 --- --- ---  
19 >PRM9\_oryCun. 8 glir gene other Oryctolagus cuniculus..... (rabbit)..... genome ON161 exon 2 ttt to tt restores frame;  
ZNF717+ DCAF4+ YAP1+ PRD9+ qTer 0 MSAAPAEPSFGADAGQARQPE 0 0 VQAFRDISIYFSKEEWAEMGDWETRYRNMKNRYNALITI 1 2  
GLRATRPAPMCHRRQAIAKLQVDDTDESDDEWTPRQ 1 2 VKPMPAFMVRVGSQKHQK 0 0 GMPRLPVMNSSLKELSGIANLLNTTSGEEDQKPSFPFKETRTSGHRSRLK 1 2  
GLRRKNEIYVMYSLRERKDCAYKEVSEPPDDYDL 1 2 YCEICQNFIDSCAAGHPPTFKVDSAVDKGHPNHAALSLPGLRIGSPGIPQAGLVWNEASDLPLGLHFGYEGQITDEDEEAANSYSWL 0 0  
ITKGRNCEYVVDGDKDSANWNR 2 1 YNCARDDEQNVAFOYHRQIFRYTRCVIRPGCELLVWYDEYQELGKIGWSKWKELMAGR 1 2  
YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
20 >PRM7\_oryCun. 4 glir gene other Oryctolagus cuniculus.... (rabbit)..... genome synteny novel 0 --- 0 --- 1  
2 GLRATRPAPMCHRRQAIAKLQVDDTDESDDEWTPRQ 1 2 VKPMPAFMVRVGSQKHQK 0 0 GMPRLPVMNSSLKELSGIANLLNTTSGEEDQKPSFPFKETRTSGHRSRLK 1 2  
GLRRKNEIYVMYSLRERKDCAYKEVSEPPDDYDL 1 2 YCEICQNFIDSCAAGHPPTFKVDSAVDKGHPNHAALSLPGLRIGSPGIPQAGLVWNEASDLPLGLHFGYEGQITDEDEEAANSYSWL 0 0  
ITKGRNCEYVVDGDKDSANWNR 2 1 YNCARDDEQNVAFOYHRQIFRYTRCVIRPGCELLVWYDEYQELGKIGWSKWKELMAGR 1 2  
YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
21 >PRM7\_ochPri. -- glir gene noDet Ochotona.... princeps.... (pika)..... AAY201312269 dubious fragment, no orthologous  
terminal exon 0 --- 0 --- 1 2 --- 1 2 --- 0 --- 1 2 --- 1 2 YCEICQNFIDSCAAGHPPTFKVDSAVDKGHPNHAALSLPGLRIGSPGIPQAGLVWNEASDLPLGLHFGYEGQITDEDEEAANSYSWL 0  
GPHRSVLSPLSGLRIGSPGIPQAGLVWNEASDLPLGLHFGYEGQITDEDEEAANSYSWL 0 0 ITKGRNCEYVVDGDKDSANWNR 2 1  
YNCARDDEQNVAFOYHRQIFRYTRCVIRPGCELLVWYDEYQELGKIGWSKWKELMAGR 1 2 --- --- ---  
22 >PRM7\_ratNor. 10 glir gene PCD2 Rattus.... norvegicus.. (rat)..... NM\_001108903 chr1 FM103467 single transcript  
from body fat 0 MNTNKPENSTEGDAGLEWPKK 0 0 VKDAFKDISMYFSKEEWAEMGDWETRYRNMKNRYNALITI 1 2 GLRATRPAPMCHRRQAIAKLQVDDTDESDDEWTPRQ 1 2  
VSSPWPVFRVKSQK 0 0 ETPRMLSDKRSVKEVFNENLLTSGEHAQKPVSPGEASTSGHRSRLK 1 2 ELRRKDETEKMYSLRERKGLAYKEVSEPPDDYDL 1 2  
YCEICQNFIDSCAAGHPPTFKVDSAVDKGHPNHAALSLPGLRIGSPGIPQAGLVWNEASDLPLGLHFGYEGQITDEDEEAANSYSWL 0 0 ITKGRNCEYVVDGDKDSANWNR 2 1  
YNCARDDEQNVAFOYHRQIFRYTRCVIRPGCELLVWYDEYQELGKIGWSKWKELMAGR 1 2  
ELRTEIHPCLLCSLAFSSQKFLSHVHNRHNSQNFPGTSTRKLLQENPCPGKQEEQOYFPCNSNDKTGQETKERSKLLNIRTQWEMARAFSNPPKQMGSSRVEERMEESRTGQKVPNPVDTGKLVFVGVISRIAK  
SIERQCGQYFSDKSNVNEHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
23 >PRM7\_musMus. 12 glir gene PCD2 Mus..... musculus.... (mouse)..... NM\_144809 chr17 CN72348 eight  
transcripts, four from retina 0 MNTNKPENSTEGDAGLEWPKK 0 0 VKDAFKDISMYFSKEEWAEMGDWETRYRNMKNRYNALITI 1 2 GLRATRPAPMCHRRQAIAKLQVDDTDESDDEWTPRQ 1 2  
2 VSPWPVFRVKSQK 0 0 ESSRMPFSGESNVKEGSIENLLTSGEHAQKPVSPGEASTSGHRSRLK 1 2 ELRRKDETEKMYSLRERKGLAYKEVSEPPDDYDL 1 2  
YCEICQNFIDSCAAGHPPTFKVDSAVDKGHPNHAALSLPGLRIGSPGIPQAGLVWNEASDLPLGLHFGYEGQITDEDEEAANSYSWL 0 0 ITKGRNCEYVVDGDKDSANWNR 2 1  
YNCARDDEQNVAFOYHRQIFRYTRCVIRPGCELLVWYDEYQELGKIGWSKWKELMAGR 1 2  
ELRTEIHPCLLCSLAFSSQKFLSHVHNRHNSQNFPGTSTRKLLQENPCPGKQEEQOYFPCNSNDKTGQETKERSKLLNIRTQWEMARAFSNPPKQMGSSRVEERMEESRTGQKVPNPVDTGKLVFVGVISRIAK  
SIERQCGQYFSDKSNVNEHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
24 >PRM7\_musMol. 11 glir gene noDet Mus..... molossinus.. (wild mouse).. GU216230 full length deposit 0  
MNTNKPENSTEGDAGLEWPKK 0 0 VKDAFKDISMYFSKEEWAEMGDWETRYRNMKNRYNALITI 1 2 GLRATRPAPMCHRRQAIAKLQVDDTDESDDEWTPRQ 1 2 VSPWPVFRVKSQK 0  
0 ESSRMPFSGESNVKEGSIENLLTSGEHAQKPVSPGEASTSGHRSRLK 1 2 ELRRKDETEKMYSLRERKGLAYKEVSEPPDDYDL 1 2  
YCEICQNFIDSCAAGHPPTFKVDSAVDKGHPNHAALSLPGLRIGSPGIPQAGLVWNEASDLPLGLHFGYEGQITDEDEEAANSYSWL 0 0 ITKGRNCEYVVDGDKDSANWNR 2 1  
YNCARDDEQNVAFOYHRQIFRYTRCVIRPGCELLVWYDEYQELGKIGWSKWKELMAGR 1 2  
ELRTEIHPCLLCSLAFSSQKFLSHVHNRHNSQNFPGTSTRKLLQENPCPGKQEEQOYFPCNSNDKTGQETKERSKLLNIRTQWEMARAFSNPPKQMGSSRVEERMEESRTGQKVPNPVDTGKLVFVGVISRIAK  
SIERQCGQYFSDKSNVNEHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
25 >PRM7\_dipOrd. -- glir gene noDet Dipodomys.. ordii..... (kangaroo rat) genome dubious fragment, no orthologous  
terminal exon 0 --- 0 --- 1 2 GLRATRPAPMCHRRQAIAKLQVDDTDESDDEWTPRQ 1 2  
2 YCEICQNFIDSCAAGHPPTFKVDSAVDKGHPNHAALSLPGLRIGSPGIPQAGLVWNEASDLPLGLHFGYEGQITDEDEEAANSYSWL 0 0 ITKGRNCEYVVDGDKDSANWNR 2 1  
YNCARDDEQNVAFOYHRQIFRYTRCVIRPGCELLVWYDEYQELGKIGWSKWKELMAGR 1 2  
YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
26 >PRM7\_speTri. -- glir gene noDet Spermophilu tridecemline (squirrel).... AAQ001308561 plus exon by exon traces  
0 --- 0 --- 1 2 GFRATRPAPMCHRRQAIAKLQVDDTDESDDEWTPRQ 1 2  
2 ELRTEIHPCLLCSLAFSSQKFLSHVHNRHNSQNFPGTSTRKLLQENPCPGKQEEQOYFPCNSNDKTGQETKERSKLLNIRTQWEMARAFSNPPKQMGSSRVEERMEESRTGQKVPNPVDTGKLVFVGVISRIAK  
SIERQCGQYFSDKSNVNEHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
27 >PRM9a\_bosTau 7 laur gene noDet Bos..... taurus..... (cattle)..... NW\_003053109 chr1 0  
MSQNSPEERTKAGDGRTEWKL 0 0 AKDAFKDISMYFSKEEWAEMGDWETRYRNMKNRYNALITI 1 2 GLRATRPAPMCHRRQAIAKLQVDDTDESDDEWTPRQ 1 2 GKSRRKAFMEHRKHQK 0  
0 GKSRRKAFMEHRKHQK 0 2 ELRRKDETEKMYSLRERKGLAYKEVSEPPDDYDL 1 2  
YCEICQNFIDSCAAGHPPTFKVDSAVDKGHPNHAALSLPGLRIGSPGIPQAGLVWNEASDLPLGLHFGYEGQITDEDEEAANSYSWL 0 0 ITKGRNCEYVVDGDKDSANWNR 2 1  
YNCARDDEQNVAFOYHRQIFRYTRCVIRPGCELLVWYDEYQELGKIGWSKWKELMAGR 1 2  
YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
28 >PRM9b\_bosTau 5 laur gene noDet Bos..... taurus..... (cattle)..... DAA02065087 plus exon by exon traces  
exon 2 KRAB SXXRD SET C2H2 0 MSPRNPENSTEGDAGLEWPKK 0 0 AKDAFKDISMYFSKEEWAEMGDWETRYRNMKNRYNALITI 1 2 GFRATRPAPMCHRRQAIAKLQVDDTDESDDEWTPRQ 1 2  
2 GKSRRKAFMEHRKHQK 0 2 ELRRKDETEKMYSLRERKGLAYKEVSEPPDDYDL 1 2  
YCEICQNFIDSCAAGHPPTFKVDSAVDKGHPNHAALSLPGLRIGSPGIPQAGLVWNEASDLPLGLHFGYEGQITDEDEEAANSYSWL 0 0 VTKGRNCEYVVDGDKDSANWNR 2 1  
YNCARDDEQNVAFOYHRQIFRYTRCVIRPGCELLVWYDEYQELGKIGWSKWKELMAGR 1 2  
YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
29 >PRM9c\_bosTau 4 laur gene noDet Bos..... taurus..... (cattle)..... XM\_002699750 chr5 G0353654 4-cell embryo  
transcript no zinc domain despite 43k bp 0 MSPRNPENSTEGDAGLEWPKK 0 0 AKDAFKDISMYFSKEEWAEMGDWETRYRNMKNRYNALITI 1 2 GFRATRPAPMCHRRQAIAKLQVDDTDESDDEWTPRQ 1 2  
2 GKSRRKAFMEHRKHQK 0 2 ELRRKDETEKMYSLRERKGLAYKEVSEPPDDYDL 1 2  
YCEICQNFIDSCAAGHPPTFKVDSAVDKGHPNHAALSLPGLRIGSPGIPQAGLVWNEASDLPLGLHFGYEGQITDEDEEAANSYSWL 0 0 VTKGRNCEYVVDGDKDSANWNR 2 1  
YNCARDDEQNVAFOYHRQIFRYTRCVIRPGCELLVWYDEYQELGKIGWSKWKELMAGR 1 2  
YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP YVCRCEGRGFSQKSLLSHQRTHTGKEP  
30 >PRM9d\_bosTau 9 laur gene noDet Bos..... taurus..... (cattle)..... genome chrX proximal tandem 0  
MRPNTSPEESTERDAGTEWKL 0 0 AKDAFKDISMYFSKEEWAEMGDWETRYRNMKNRYNALITI 1 2 GFRATRPAPMCHRRQAIAKLQVDDTDESDDEWTPRQ 1 2 GKLSSMAFVREHNKHQK 0  
0 TMSRAPLSKELPGLAALLKTSKGAQKLVPPGKARTPQHPQRV 1 2 ELRRKDETEKMYSLRERKGLAYKEVSEPPDDYDL 1 2

YCECQSFIDSCAAHGPPFVKDCAVEKGHANRSALTLPGLSIRESSIPFAGLVWNEVSDPLGLHFGPYEGQITDDEEAANSYGSWL 0 0 ITKRRNCYEVVDGKDTSLANWNR 2 1  
YVNCARDEQNVAQYHQIFVYTCQVVRPCELLVWYDGYDGLIKRRESSRKLSELAGR 1 2  
EPKPKIYPCASCLLSSQKFLSQQVORRHPSQILLRPSIDGLHQEPEDPCGQSQNRYSDPHSLSDKPEGPERKERPHLLKPKLIRKPRKSTASSYPPKQMGSGVEHMERTEEPSTSKLNPEDTGLKFMAGVSGIVR  
VNYGDHEGQSKDSSLI THEKHTHTEGPK YVCECGSFSNRSKDLTKHRTHTGPK YACGCGRFSFKNLI THKRTHTGPK YVCECGRFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK  
YVCECGRFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK  
31 >PROM9e\_bosTau\_9 laur gene noDet Bos..... taurus..... (cattle)..... genome chrX distal tandem 0  
MRPNRPEESTEGDAGRTEKMP 0 0 AKDAFKDISYFKEEWEEMGEWEKIRYRNKRNVEALITL 1 2 GFRAAPAFMHRRQVVKPQVDDTDESEEWTPRQ 1 2 GKPSMAFRVRSKHQ 0  
0 GMSRAPLINESKLLPGAALKLTSKGAQKLVPPPKARTPEQHPQKV 1 2 ERRRKEQVVKYSLRERKGVYQVSEPPDDYDL 1 2  
YCECQSFIDSCAAHGPPFVKDCAVEKGHANRSALTLPGLSIRESSIPFAGLVWNEVSDPLGLHFGPYEGQITDDEEAANSYGSWL 0 0 ITKRRNCYEVVDGKDTSLANWNR 2 1  
YVNCARDEQNVAQYHQIFVYTCQVVRPCELLVWYDGYDGLIKRRESSRKLSELAGR 1 2  
EPKPKIYPCASCLLSSQKFLSQQVORRHPSQILLRPSIDGLHQEPEDPCGQSQNRYSDPHSLSDKPEGPERKERPHLLKPKLIRKPRKSTASSYPPKQMGSGVEHMERTEEPSTSKLNPEDTGLKFMAGVSGIVR  
VNYGDHEGQSKDSSLI THEKHTHTEGPK YVCECGSFSNRSKDLTKHRTHTGPK YACGCGRFSFKNLI THKRTHTGPK YVCECGRFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK  
YVCECGRFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK  
32 >PROM9e\_oviAri\_ -- laur gene noDet Ovis..... aries..... (sheep)..... genome chr 18 cow has PDM7 pseudogene; sheep  
GAS8 is on sheep chr14 0 --- 0 0 0 1 2 GLRAP PFMYHRQVVKPQVDDTDESEEWTPRQ 1 2 --- 0 --- 1 2 ELRRKETEEMKYSLQRKKGIMYQVSEPPDDYDL 1 2  
2 YCEKQNF IDSCAAHGPPFVKDCAVEKGHANRSALTLPGLSIRESSIPFAGLVWNEVSDPLGLHFGPYEGQITDDEEAANSYGSWL 0 0 ITKRRNCYEVVDGKDTSLANWNR 2 1  
TCWVVRPCELLVWYDGYDGLIKRRESSRKLSELAGR 1 2 --- --- ---  
33 >PROM9d\_oviAri\_ -- laur gene noDet Ovis..... aries..... (sheep)..... genome chr1 near end chr1 0 --- 0  
0 --- 1 2 GLRATRLAFMHHRQVVKPQVDDTDESEEWTPRQ 1 2 --- 0 --- 1 2 --- 0 0 ITKRRNCYEVVDGKDTSLANWNR 2 1  
YVNCARDEQNVAQYHQIFVYTCQVVRPCELLVWYDGYDGLIKRRESSRKLSELAGR 1 2 --- --- ---  
34 >PROM9c\_oviAri\_4 laur p seu noDet Ovis..... aries..... (sheep)..... genome chr5 middle of 108,514,869 bp 0 --- 0  
0 --- 1 2 GLRATRLAFMHHRQVVKPQVDDTDESEEWTPRQ 1 2 --- 0 0 GMSKALVSNKSKLMPGASGLKTRGPKAQIIPVAPREPSTEQHPQKV 1 2 --- 1 2  
HGLPTLVKDCAVEKGHANRSALTLPGLSIRESSIPFAGLVWNEVSDPLGLHFGPYEGQITDDEEAANSYGSWL 0 0 --- 2 1 YVNGAQD KEQNLVAFLTRHQIFY  
TCWVVRPCELLVWYDGYDGLIKRRESSRKLSELAGR 1 2  
PMSKSLAFSSQKFLSQQVORRHPSQILLRPSIDGLHQEPEDPCGQSQNRYSDPHSLSDKPEGPERKERPHLLKPKLIRKPRKSTASSYPPKQMGSGVEHMERTEEPSTSKLNPEDTGLKFMAGVSGIVR  
VNYGDHEGQSKDSSLI THEKHTHTEGPK YVCECGSFSNRSKDLTKHRTHTGPK YACGCGRFSFKNLI THKRTHTGPK YVCECGRFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK  
35 >PROM9b\_oviAri\_2 laur p seu noDet Ovis..... aries..... (sheep)..... genome chrX not tandem: 62 mbp separation  
0 MSPNRSPEESTEGDAGRTEKMP 0 0 AKDAFKDISYFKEEWEEMGEWEKIRYRNKRNVEALITL 1 2 GFRAQPAFMHHRQVVKPQVDDTDESEEWTPRQ 1 2 GKPSMAFRVRSKHQ 0  
0 GMSRAPLINESKLLPGAALKLTSKGAQKLVPPPKARTPEQHPQKV 1 2 ELRRKETEEMKYSLQRKKGIMYQVSEPPDDYDL 1 2  
YCECQSFIDSCAAHGPPFVKDCAVEKGHANRSALTLPGLSIRESSIPFAGLVWNEVSDPLGLHFGPYEGQITDDEEAANSYGSWL 0 0 ITKRRNCYEVVDGKDTSLANWNR 2 1  
YVNCARDEQNVAQYHQIFVYTCQVVRPCELLVWYDGYDGLIKRRESSRKLSELAGR 1 2  
EPKPKIYPCASCLLSSQKFLSQQVORRHPSQILLRPSIDGLHQEPEDPCGQSQNRYSDPHSLSDKPEGPERKERPHLLKPKLIRKPRKSTASSYPPKQMGSGVEHMERTEEPSTSKLNPEDTGLKFMAGVSGIVR  
VNYGDHEGQSKDSSLI THEKHTHTEGPK YVCECGSFSNRSKDLTKHRTHTGPK YACGCGRFSFKNLI THKRTHTGPK YVCECGRFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK  
YVCECGRFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK  
36 >PROM9a\_oviAri\_9 laur gene noDet Ovis..... aries..... (sheep)..... genome chrX not tandem 0  
MSPNRSPEESTEGDAGRTEKMP 0 0 AKDAFKDISYFKEEWEEMGEWEKIRYRNKRNVEALITL 1 2 GFRAQPAFMHHRQVVKPQVDDTDESEEWTPRQ 1 2 GKPSMAFRVRSKHQ 0  
0 GMSRAPLINESKLLPGAALKLTSKGAQKLVPPPKARTPEQHPQKV 1 2 ELRRKETEEMKYSLQRKKGIMYQVSEPPDDYDL 1 2  
YCECQSFIDSCAAHGPPFVKDCAVEKGHANRSALTLPGLSIRESSIPFAGLVWNEVSDPLGLHFGPYEGQITDDEEAANSYGSWL 0 0 ITKRRNCYEVVDGKDTSLANWNR 2 1  
YVNCARDEQNVAQYHQIFVYTCQVVRPCELLVWYDGYDGLIKRRESSRKLSELAGR 1 2  
EPKPKIYPCASCLLSSQKFLSQQVORRHPSQILLRPSIDGLHQEPEDPCGQSQNRYSDPHSLSDKPEGPERKERPHLLKPKLIRKPRKSTASSYPPKQMGSGVEHMERTEEPSTSKLNPEDTGLKFMAGVSGIVR  
VNYGDHEGQSKDSSLI THEKHTHTEGPK YVCECGSFSNRSKDLTKHRTHTGPK YACGCGRFSFKNLI THKRTHTGPK YVCECGRFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK  
YVCECGRFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK  
37 >PROM9d\_munMun\_4 laur gene noDet Muntiacus... muntjac..... (muntjac)..... AC216498 frameshift exon 9 no syntenic  
loci; identities: 92% 89% 90%  
0 MRPNRSPEESTEGDAGRTEKMP 0 0 AKDAFKDISYFKEEWEEMGEWEKIRYRNKRNVEALITL 1 2 GFRAQPAFMHHRQVVKPQVDDTDESEEWTPRQ 1 2 GKPSMAFRVRSKHQ 0  
0 GMSRAPLINESKLLPGAALKLTSKGAQKLVPPPKARTPEQHPQKV 1 2 ELRRKETEEMKYSLQRKKGIMYQVSEPPDDYDL 1 2  
YCECQSFIDSCAAHGPPFVKDCAVEKGHANRSALTLPGLSIRESSIPFAGLVWNEVSDPLGLHFGPYEGQITDDEEAANSYGSWL 0 0 ITKRRNCYEVVDGKDTSLANWNR 2 1  
YVNCARDEQNVAQYHQIFVYTCQVVRPCELLVWYDGYDGLIKRRESSRKLSELAGR 1 2  
EPKPKIYPCASCLLSSQKFLSQQVORRHPSQILLRPSIDGLHQEPEDPCGQSQNRYSDPHSLSDKPEGPERKERPHLLKPKLIRKPRKSTASSYPPKQMGSGVEHMERTEEPSTSKLNPEDTGLKFMAGVSGIVR  
VNYGDHEGQSKDSSLI THEKHTHTEGPK YVCECGSFSNRSKDLTKHRTHTGPK YACGCGRFSFKNLI THKRTHTGPK YVCECGRFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK  
YVCECGRFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK  
38 >PROM9c\_munMun\_15 laur gene noDet Muntiacus... muntjac..... (muntjac)..... AC154919 no syntenic loci AC204173 99%  
identical 0 MRPNRSPEESTEGDAGRTEKMP 0 0 AKDAFKDISYFKEEWEEMGEWEKIRYRNKRNVEALITL 1 2 GFRAQPAFMHHRQVVKPQVDDTDESEEWTPRQ 1 2  
0 GMSRAPLINESKLLPGAALKLTSKGAQKLVPPPKARTPEQHPQKV 1 2 ELRRKETEEMKYSLQRKKGIMYQVSEPPDDYDL 1 2  
YCECQSFIDSCAAHGPPFVKDCAVEKGHANRSALTLPGLSIRESSIPFAGLVWNEVSDPLGLHFGPYEGQITDDEEAANSYGSWL 0 0 ITKRRNCYEVVDGKDTSLANWNR 2 1  
YVNCARDEQNVAQYHQIFVYTCQVVRPCELLVWYDGYDGLIKRRESSRKLSELAGR 1 2  
EPKPKIYPCASCLLSSQKFLSQQVORRHPSQILLRPSIDGLHQEPEDPCGQSQNRYSDPHSLSDKPEGPERKERPHLLKPKLIRKPRKSTASSYPPKQMGSGVEHMERTEEPSTSKLNPEDTGLKFMAGVSGIVR  
VNYGDHEGQSKDSSLI THEKHTHTEGPK YVCECGSFSNRSKDLTKHRTHTGPK YACGCGRFSFKNLI THKRTHTGPK YVCECGRFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK  
YVCECGRFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK  
39 >PROM9b\_munMun\_13 laur gene noDet Muntiacus... muntjac..... (muntjac)..... AC218859 no syntenic loci 0  
MRPNRSPEESTEGDAGRTEKMP 0 0 AKDAFKDISYFKEEWEEMGEWEKIRYRNKRNVEALITL 1 2 GFRAQPAFMHHRQVVKPQVDDTDESEEWTPRQ 1 2 GKPSMAFRVRSKHQ 0  
0 GMSRAPLINESKLLPGAALKLTSKGAQKLVPPPKARTPEQHPQKV 1 2 ELRRKETEEMKYSLQRKKGIMYQVSEPPDDYDL 1 2  
YCECQSFIDSCAAHGPPFVKDCAVEKGHANRSALTLPGLSIRESSIPFAGLVWNEVSDPLGLHFGPYEGQITDDEEAANSYGSWL 0 0 ITKRRNCYEVVDGKDTSLANWNR 2 1  
YVNCARDEQNVAQYHQIFVYTCQVVRPCELLVWYDGYDGLIKRRESSRKLSELAGR 1 2  
EPKPKIYPCASCLLSSQKFLSQQVORRHPSQILLRPSIDGLHQEPEDPCGQSQNRYSDPHSLSDKPEGPERKERPHLLKPKLIRKPRKSTASSYPPKQMGSGVEHMERTEEPSTSKLNPEDTGLKFMAGVSGIVR  
VNYGDHEGQSKDSSLI THEKHTHTEGPK YVCECGSFSNRSKDLTKHRTHTGPK YACGCGRFSFKNLI THKRTHTGPK YVCECGRFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK  
YVCECGRFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK  
40 >PROM9a\_munMun\_7 laur gene noDet Muntiacus... muntjac..... (muntjac)..... AC225653 unordered contigs htgs; no  
synteny tag stop instead of aag K 0 MRPNRSPEESTEGDAGRTEKMP 0 0 AKDAFKDISYFKEEWEEMGEWEKIRYRNKRNVEALITL 1 2 GFRAQPAFMHHRQVVKPQVDDTDESEEWTPRQ 1 2  
0 GMSRAPLINESKLLPGAALKLTSKGAQKLVPPPKARTPEQHPQKV 1 2 ELRRKETEEMKYSLQRKKGIMYQVSEPPDDYDL 1 2  
YCECQSFIDSCAAHGPPFVKDCAVEKGHANRSALTLPGLSIRESSIPFAGLVWNEVSDPLGLHFGPYEGQITDDEEAANSYGSWL 0 0 ITKRRNCYEVVDGKDTSLANWNR 2 1  
YVNCARDEQNVAQYHQIFVYTCQVVRPCELLVWYDGYDGLIKRRESSRKLSELAGR 1 2  
EPKPKIYPCASCLLSSQKFLSQQVORRHPSQILLRPSIDGLHQEPEDPCGQSQNRYSDPHSLSDKPEGPERKERPHLLKPKLIRKPRKSTASSYPPKQMGSGVEHMERTEEPSTSKLNPEDTGLKFMAGVSGIVR  
VNYGDHEGQSKDSSLI THEKHTHTEGPK YVCECGSFSNRSKDLTKHRTHTGPK YACGCGRFSFKNLI THKRTHTGPK YVCECGRFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK  
YVCECGRFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK  
41 >PROM7\_bosTau\_ -- laur p seu GAS8+ Bos..... taurus..... (cattle)..... genome missing C2H2 0  
MSPNRSPEESTEGDAGRTEKMP 0 0 AKDAFKDISYFKEEWEEMGEWEKIRYRNKRNVEALITL 1 2 --- 1 2 --- 0 --- 1 2 --- 1 2 --- 1 2 --- 1 2 --- 1 2  
--- --- ---  
42 >PROM7\_turTur\_9 laur gene gas8+ Turciops... truncatus... (dolphin)..... ABRN01441536 no useful synteny 0  
MSTRDPEDSTEGDAGRTEKMP 0 0 AKDAFKDISYFKEEWEEMGEWEKIRYRNKRNVEALITL 1 2 GLRAPAFMHRRQVVKPQVDDTDESEEWTPRQ 1 2 VKPSMAFRVRSKHQ 0  
0 AVPPVPLNESLKLPGAALKLTSKGAQKLVPPPKARTPEQHPQKV 1 2 ERRRKEQVVKYSLRERKGVYQVSEPPDDYDL 1 2  
YCECQSFIDSCAAHGPPFVKDCAVEKGHANRSALTLPGLSIRESSIPFAGLVWNEVSDPLGLHFGPYEGQITDDEEAANSYGSWL 0 0 ITKRRNCYEVVDGKDTSLANWNR 2 1  
YVNCARDEQNVAQYHQIFVYTCQVVRPCELLVWYDGYDGLIKRRESSRKLSELAGR 1 2  
DPKPKIYPCASCLLSSQKFLSQQVORRHPSQILLRPSIDGLHQEPEDPCGQSQNRYSDPHSLSDKPEGPERKERPHLLKPKLIRKPRKSTASSYPPKQMGSGVEHMERTEEPSTSKLNPEDTGLKFMAGVSGIVR  
VNYGDHEGQSKDSSLI THEKHTHTEGPK YVCECGSFSNRSKDLTKHRTHTGPK YACGCGRFSFKNLI THKRTHTGPK YVCECGRFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK  
YVCECGRFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK  
43 >PROM7\_susScr\_9 laur gene GAS8+ Sus..... scrofa..... (pig)..... PF476134 unordered HTGS not wgs  
misassembly or inversion; not in genome browser 0 MRPNRSPEESTEGDAGRTEKMP 0 0 AKDAFKDISYFKEEWEEMGEWEKIRYRNKRNVEALITL 1 2  
0 GMSRAPLINESKLLPGAALKLTSKGAQKLVPPPKARTPEQHPQKV 1 2 ELRRKETEEMKYSLQRKKGIMYQVSEPPDDYDL 1 2  
YCECQSFIDSCAAHGPPFVKDCAVEKGHANRSALTLPGLSIRESSIPFAGLVWNEVSDPLGLHFGPYEGQITDDEEAANSYGSWL 0 0 ITKRRNCYEVVDGKDTSLANWNR 2 1  
YVNCARDEQNVAQYHQIFVYTCQVVRPCELLVWYDGYDGLIKRRESSRKLSELAGR 1 2  
EPKPKIYPCASCLLSSQKFLSQQVORRHPSQILLRPSIDGLHQEPEDPCGQSQNRYSDPHSLSDKPEGPERKERPHLLKPKLIRKPRKSTASSYPPKQMGSGVEHMERTEEPSTSKLNPEDTGLKFMAGVSGIVR  
VNYGDHEGQSKDSSLI THEKHTHTEGPK YVCECGSFSNRSKDLTKHRTHTGPK YACGCGRFSFKNLI THKRTHTGPK YVCECGRFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK  
YVCECGRFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK  
44 >PROM7\_canFam\_5 laur p seu GAS8+ Canis..... familiaris..... (dog)..... genome frameshift fixed to 6 ZNF; synteny MNS1  
K1F1B intervening CHD3 oddity 0 --- 0 0 0 1 2 VKPSMAFRVRSKHQ 0 0 GIPRVPLSNKSKLSEKLETAKLNTSPGQKASVPLGKASTSGHTRQKL 1 2  
2 ELRRKETEEMKYSLQRKKGIMYQVSEPPDDYDL 1 2 YCEK QTFIDSCAAHGPPFVKDCAVEKGHANRSALTLPGLSIRESSIPFAGLVWNEVSDPLGLHFGPYEGQITDDEEAANSYGSWL 0 0  
ITKRRNCYEVVDGKDTSLANWNR 2 1  
YVNCARDEQNVAQYHQIFVYTCQVVRPCELLVWYDGYDGLIKRRESSRKLSELAGR 1 2  
EPKPKIYPCASCLLSSQKFLSQQVORRHPSQILLRPSIDGLHQEPEDPCGQSQNRYSDPHSLSDKPEGPERKERPHLLKPKLIRKPRKSTASSYPPKQMGSGVEHMERTEEPSTSKLNPEDTGLKFMAGVSGIVR  
VNYGDHEGQSKDSSLI THEKHTHTEGPK YVCECGSFSNRSKDLTKHRTHTGPK YACGCGRFSFKNLI THKRTHTGPK YVCECGRFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK  
YVCECGRFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK  
45 >PROM7\_felCat\_11 laur gene GAS8+ Felis..... catus..... (cat)..... genome two contigs GAS8 implied by downstream  
cads 0 MSPNRSPEESTEGDAGRTEKMP 0 0 AKDAFKDISYFKEEWEEMGEWEKIRYRNKRNVEALITL 1 2 GLRAPAFMHRRQVVKPQVDDTDESEEWTPRQ 1 2  
0 GMSRAPLINESKLLPGAALKLTSKGAQKLVPPPKARTPEQHPQKV 1 2 ELRRKETEEMKYSLQRKKGIMYQVSEPPDDYDL 1 2  
YCECQSFIDSCAAHGPPFVKDCAVEKGHANRSALTLPGLSIRESSIPFAGLVWNEVSDPLGLHFGPYEGQITDDEEAANSYGSWL 0 0 ITKRRNCYEVVDGKDTSLANWNR 2 1  
YVNCARDEQNVAQYHQIFVYTCQVVRPCELLVWYDGYDGLIKRRESSRKLSELAGR 1 2  
EPKPKIYPCASCLLSSQKFLSQQVORRHPSQILLRPSIDGLHQEPEDPCGQSQNRYSDPHSLSDKPEGPERKERPHLLKPKLIRKPRKSTASSYPPKQMGSGVEHMERTEEPSTSKLNPEDTGLKFMAGVSGIVR  
VNYGDHEGQSKDSSLI THEKHTHTEGPK YVCECGSFSNRSKDLTKHRTHTGPK YACGCGRFSFKNLI THKRTHTGPK YVCECGRFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK  
YVCECGRFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK YVCECGSFSFKNLI THKRTHTGPK

EPQPDHRCPCSLAFSSQKFLSHQVCEKSSQSLPQISARKHFQENPCFQDQNOQQQHSDDPHWNDKAKQEVKERSRPLLSKIKORRISRAFSTPCQGMGSSRVCEGMVEEFGPMGQNLNSEDTKGLFMVGMRSRVR  
IKNRGCEGNDNRSHFHSRHTHEKEPK SVNCFRFRDFSHKSALITHQRTHTGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
46 >PRDM7\_ailMel. 6 laur gene GAS8+ Ailurodopa. melanoleuca. (panda)..... GL193502 first three exons from different  
contig 0 MSLNTSPEETPERDSRGTGWKPT 0 0 AKDAFKDISIYFSKEEWTMGGWKEKIRYRNRYEALIT 1 2 GLRAPRPAFMCRRRAIKQAVDQVDDTDSDEWTPRQ 1 2  
VRP5WAFVFMGQSKHOR 0 0 GIPRALPRLNSSLKELSETAKLLNTSGSELGQKPVSLPEGASSTGHSDSLQKL 1 2 GFRKRDVEVKMYSRLERKSLAYQEVSEPDQDYL 1 2  
YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
EPKPEIHPCCSCLAFSSQKFLSHQVCEKSSQSLPQISARKHFQENPCFQDQNOQQQHSDDPHWNDKAKQEVKERSRPLLSKIKORRISRAFSTPCQGMGSSRVCEGMVEEFGPMGQNLNSEDTKGLFMVGMRSRVR  
VKYRGCRDPSDRSHQSGHORRHK KKP SVCKVKREFSHKSVLITHQRTHTGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
47 >PRDM9\_pteVam. 15 laur pseu noDet Pteropus... vampyrus... (bat)..... ABRP01232219 frameshift ttt to ttt fixed in  
last zinc finger; no blastx synteny 0 --- 0 0 --- 1 2 --- 1 2 --- 0 0 AMRPRVPLSNESLKLSESVIANPLKASGSENOQVFPFGKASASRQHSRKL 1  
2 eLRKRGVEVMDSLRERMGVYQEVSEPDQDYL 1 2 YCKCNQFFIDSCAAGHSPFVVDKSEVDIHPHNSALTLPLGLRIGPSPGPEAGLVWNEASDLPLGLHFGPYEGQVTEDEEAANSKYSWM 0 0  
spKGETAEYV DGDKESRANWNR 2 1 YVNCARDEEQLNVAFOYHRQIFRYTRCTRVKPCGELLVWYDGYEQLGKWSKWKRELTAGR 1 2  
EPKPEIHPCCSCLAFSSQKFLSHQVCEKSSQSLPQISARKHFQENPCFQDQNOQQQHSDDPHWNDKAKQEVKERSRPLLSKIKORRISRAFSTPCQGMGSSRVCEGMVEEFGPMGQNLNSEDTKGLFMVGMRSRVR  
VYGGCGHGDGSHIRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
48 >PRDM7\_pteVam. 7 laur gene GAS8+ Pteropus... vampyrus... (bat)..... ABRP01250178 4 distal exons of GAS8+; unique  
G sweep in zinc finger; 15 ZNF dotplot no CAD1 0 MRPRSPPEAEPDGRTRTKCPK 0 0 AKDAFKDISIYFSKEEWTMGGWKEKIRYRNRYEALIT 1 2  
GLRAPRPAFMCRRRAIKQAVDQVDDTDSDEWTPRQ 1 2 --- 0 0 AMRPRVPLSNESLKLSESVIANPLKASGSENOQVFPFGKASASRQHSRKL 1 2  
2 YCKCNQFFIDSCAAGHSPFVVDKSEVDIHPHNSALTLPLGLRIGPSPGPEAGLVWNEASDLPLGLHFGPYEGQVTEDEEAANSKYSWM 0 0 GQKGRNCEYVDGKDESANWNR 2 1  
YVNCARDEEQLNVAFOYHRQIFRYTRCTRVKPCGELLVWYDGYEQLGKWSKWKRELTAGR 1 2  
EPKPEIHPCCSCLAFSSQKFLSHQVCEKSSQSLPQISARKHFQENPCFQDQNOQQQHSDDPHWNDKAKQEVKERSRPLLSKIKORRISRAFSTPCQGMGSSRVCEGMVEEFGPMGQNLNSEDTKGLFMVGMRSRVR  
VYGGCGHGDGSHIRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
49 >PRDM7\_myoLuc. 6 laur gene gas8+ Myotis.... lucifugus... (bat)..... AAP02062260 TGA stop codon; CpG hotspot for  
R CGA; SYXRD implies missing KRAB no CAD1 0 --- 0 0 --- 1 2 --- 0 0 AKSRAPLSNSSLKELSGTANLLTSSGSEQTKVTPPPEAGSSTQGHFPRKL 1  
2 dLRKREIVKMSYLRERKGRVQIYSEPDQDYL 1 2 YCKCNQFFIDSCAAGHSPFVVDKSEVDIHPHNSALTLPLGLRIGPSPGPEAGLVWNEASDLPLGLHFGPYEGQVTEDEEAANSKYSWM 0 0  
ITKGRNCEYVDGKDESANWNR 2 1 YVNCARDEEQLNVAFOYHRQIFRYTRCTRVKPCGELLVWYDGYEQLGKWSKWKRELTAGR 1 2  
EPKPEIHPCCSCLAFSSQKFLSHQVCEKSSQSLPQISARKHFQENPCFQDQNOQQQHSDDPHWNDKAKQEVKERSRPLLSKIKORRISRAFSTPCQGMGSSRVCEGMVEEFGPMGQNLNSEDTKGLFMVGMRSRVR  
VYGGCGHGDGSHIRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
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 --- 2 2 VPSWVAFVGEOSKHOK 0 0 RMRTAPLSNSSLKELSGTANLLTSSGSEQTKVTPPPEAGSSTQGHFPRKL 1  
2 ITKGRNCEYVDGKDESANWNR 2 1 YVNCARDEEQLNVAFOYHRQIFRYTRCTRVKPCGELLVWYDGYEQLGKWSKWKRELTAGR 1 2  
EPKPEIHPCCSCLAFSSQKFLSHQVCEKSSQSLPQISARKHFQENPCFQDQNOQQQHSDDPHWNDKAKQEVKERSRPLLSKIKORRISRAFSTPCQGMGSSRVCEGMVEEFGPMGQNLNSEDTKGLFMVGMRSRVR  
VYGGCGHGDGSHIRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
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 MSLNPAEMTQTKGKARLMLKPM 0 0 SKDAFKDISIYFSKEEWTMGGWKEKIRYRNRYEALIT 1 2  
GLRAPRPAFMCRRRAIKQAVDQVDDTDSDEWTPRQ 1 2 VKSRLVAFRAEQSKHOK 0 0 GRSRTISNSSLKELSGTANLLTSSGSEQTKVTPPPEAGSSTQGHFPRKL 1  
2 ELRKRREIVKMSYLRERKGRVQIYSEPDQDYL 1 2 YCKCNQFFIDSCAAGHSPFVVDKSEVDIHPHNSALTLPLGLRIGPSPGPEAGLVWNEASDLPLGLHFGPYEGQVTEDEEAANSKYSWM 0 0  
ITKGRNCEYVDGKDESANWNR 2 1 YVNCARDEEQLNVAFOYHRQIFRYTRCTRVKPCGELLVWYDGYEQLGKWSKWKRELTAGR 1 2  
EPKPEIHPCCSCLAFSSQKFLSHQVCEKSSQSLPQISARKHFQENPCFQDQNOQQQHSDDPHWNDKAKQEVKERSRPLLSKIKORRISRAFSTPCQGMGSSRVCEGMVEEFGPMGQNLNSEDTKGLFMVGMRSRVR  
DKHVTLRSLFTNRSSLTHTHTGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
52 >PRDM9a\_loxAfr. 12 afro gene noDet Loxodonta.... africana.... (elephant).... genome chr 153 novel synteny THEG+ MIER2+  
PAP2C PRDM9- ZNF699- 0 MSPARAANKNPRGVDGAGRTPT 0 0 AKTDFRDISIYFSKEEWTMGGWKEKIRYRNRYEALIT 1 2 GLRAPRPAFMCRRRAIKQAVDQVDDTDSDEWTPRQ 1  
2 VKP5VASRAEQSKHOR 0 0 GTPKALLGNSSLKELVSGTALLTSSGSEQTKVTPPPEAGSSTQGHFPRKL 1 2 EPRRKEVEVMYSLRERKGLYQEVSEPDQDYL 1 2  
YCKCNQFFIDSCAAGHSPFVVDKSEVDIHPHNSALTLPLGLRIGPSPGPEAGLVWNEASDLPLGLHFGPYEGQVTEDEEAANSKYSWM 0 0 ITKGRNCEYVDGKDESANWNR 2 1  
YVNCARDEEQLNVAFOYHRQIFRYTRCTRVKPCGELLVWYDGYEQLGKWSKWKRELTAGR 1 2  
EPKPEIHPCCSCLAFSSQKFLSHQVCEKSSQSLPQISARKHFQENPCFQDQNOQQQHSDDPHWNDKAKQEVKERSRPLLSKIKORRISRAFSTPCQGMGSSRVCEGMVEEFGPMGQNLNSEDTKGLFMVGMRSRVR  
VRCGCGGFSQKSVLIRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
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 GTPKALLGNSSLKELVSGTALLTSSGSEQTKVTPPPEAGSSTQGHFPRKL 1 2 EPRRKEVEVMYSLRERKGLYQEVSEPDQDYL 1 2  
YCKCNQFFIDSCAAGHSPFVVDKSEVDIHPHNSALTLPLGLRIGPSPGPEAGLVWNEASDLPLGLHFGPYEGQVTEDEEAANSKYSWM 0 0 ITKGRNCEYVDGKDESANWNR 2 1 YVNCIQD  
KEQNLVAFQYHRQIFRYTRCTRVKPCGELLVWYDGYEQLGKWSKWKRELTAGR 1 2  
EPKPEIHPCCSCLAFSSQKFLSHQVCEKSSQSLPQISARKHFQENPCFQDQNOQQQHSDDPHWNDKAKQEVKERSRPLLSKIKORRISRAFSTPCQGMGSSRVCEGMVEEFGPMGQNLNSEDTKGLFMVGMRSRVR  
VRCGCGGFSQKSVLIRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
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 --- 1 2 --- 0 0 GTPKALLGNSSLKELVSGTALLTSSGSEQTKVTPPPEAGSSTQGHFPRKL 1 2  
GMLRVPRLNSSLKELVSGTALLTSSGSEQTKVTPPPEAGSSTQGHFPRKL 1 2 EPRRKEVEVMYSLRERKGLYQEVSEPDQDYL 1 2  
YCKCNQFFIDSCAAGHSPFVVDKSEVDIHPHNSALTLPLGLRIGPSPGPEAGLVWNEASDLPLGLHFGPYEGQVTEDEEAANSKYSWM 0 0 --- 1 2  
YVNCIQDKEQNLVAFQYHRQIFRYTRCTRVKPCGELLVWYDGYEQLGKWSKWKRELTAGR 1 2  
EPKPEIHPCCSCLAFSSQKFLSHQVCEKSSQSLPQISARKHFQENPCFQDQNOQQQHSDDPHWNDKAKQEVKERSRPLLSKIKORRISRAFSTPCQGMGSSRVCEGMVEEFGPMGQNLNSEDTKGLFMVGMRSRVR  
VKYRGCRDPSDRSHQSGHORRHK KKP SVCKVKREFSHKSVLITHQRTHTGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
55 >PRDM7\_echTel. 5 afro pseu noDet Echinops... telfairi... (tenrec).... genome 2 frameshifts plus stop codon 0 --- 0  
0 --- 1 2 GLRAPRPAFMCRRRAIKQAVDQVDDTDSDEWTPRQ 1 2 --- 0 0 GMPVSLRNLKVLGSLTALLTSSGSEQTKVTPPPEAGSSTQGHFPRKL 1 2  
epELRRRAVMNLSRERKMLYQEVSTPCDNC 1 2 YGERCHNFIPTDIAHAGATTVFKDS PMDRSNCISILPGLRIGPSPGPEAGLVWNEASDLPLGLHFGPYEGQVTEDEEAANSKYSWM 0 0  
ITKGRNCEYVDGKDESANWNR 2 1 --- 1 2  
EPKPEIHPCCSCLAFSSQKFLSHQVCEKSSQSLPQISARKHFQENPCFQDQNOQQQHSDDPHWNDKAKQEVKERSRPLLSKIKORRISRAFSTPCQGMGSSRVCEGMVEEFGPMGQNLNSEDTKGLFMVGMRSRVR  
VRCGCGGFSQKSVLIRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
56 >PRDM7\_proCap. 13 afro gene noDet Procapia.... capensis.... (hyrax).... ABR01392668 CpG stop in ZNF1, frameshift  
exon 5 c to cc, blastn favors PDM9 0 MSPTNAEWSFGDGTASMGTKPK 0 0 AKDAFKDISIYFSKEEWTMGGWKEKIRYRNRYEALIT 1 2  
GIRVFPFAMHPRKTIKAQMDSEDSDEWTPRQ 1 2 AKP5VASRAEQSKHOR 0 0 GSPRAPRLKSSLRVSEPAIIVWSTADSEQAQEVQKPVASASDQLRRK 1 2  
EPRRHEADKRYSLRGGTGAQVGEQDQDYL 1 2 YCKCNQFFIDSCAAGHSPFVVDKSEVDIHPHNSALTLPLGLRIGPSPGPEAGLVWNEASDLPLGLHFGPYEGQVTEDEEAANSKYSWM 0 0  
VTKGRSCEYVDGKDESANWNR 2 1 YVNCARDEEQLNVAFOYHRQIFRYTRCTRVKPCGELLVWYDGYEQLGKWSKWKRELTAGR 1 2  
EPKPEIHPCCSCLAFSSQKFLSHQVCEKSSQSLPQISARKHFQENPCFQDQNOQQQHSDDPHWNDKAKQEVKERSRPLLSKIKORRISRAFSTPCQGMGSSRVCEGMVEEFGPMGQNLNSEDTKGLFMVGMRSRVR  
VRWDEYGGGFGSHIHTQRTHTGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
57 >PRDM7\_dasNov. 9 xena pseu TRAPP Dasypus.... novemcinctus (armadillo)... AAGV020462211 plus exon-by-exon traces, no  
GAS8 but facing TRAPP3, frameshifts, tandem ZNF fragment 0 --- 0 0 AQAADRISTYFSREWEAEMGRWELRYRNRYEALIT 1 2  
GLRAPRPAFMCRRRAIKQAVDQVDDTDSDEWTPRQ 1 2 --- 0 0 --- 1 2 EPRRKEVEVMYSLRERKGLYQEVSEPDQDYL 1 2  
YCKCNQFFIDSCAAGHSPFVVDKSEVDIHPHNSALTLPLGLRIGPSPGPEAGLVWNEASDLPLGLHFGPYEGQVTEDEEAANSKYSWM 0 0 ITKGRNCEYVDGKDESANWNR 2 1  
YVNCARDEEQLNVAFOYHRQIFRYTRCTRVKPCGELLVWYDGYEQLGKWSKWKRELTAGR 1 2  
EPKPEIHPCCSCLAFSSQKFLSHQVCEKSSQSLPQISARKHFQENPCFQDQNOQQQHSDDPHWNDKAKQEVKERSRPLLSKIKORRISRAFSTPCQGMGSSRVCEGMVEEFGPMGQNLNSEDTKGLFMVGMRSRVR  
IKFENRQDSDSHSTHTHTGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
58 >PRDM7\_choHof. 2 xena gene noDet Choleopus.... hoffmanni.... (sloth).... ABVD0189361 fragmentary gene with  
indeterminate synteny 0 --- 0 0 --- 1 2 --- 1 2 --- 0 0 YCKCNQFFIDSCAAGHSPFVVDKSEVDIHPHNSALTLPLGLRIGPSPGPEAGLVWNEASDLPLGLHFGPYEGQVTEDEEAANSKYSWM 0 0  
YVNCARDEEQLNVAFOYHRQIFRYTRCTRVKPCGELLVWYDGYEQLGKWSKWKRELTAGR 1 2  
EPKPEIHPCCSCLAFSSQKFLSHQVCEKSSQSLPQISARKHFQENPCFQDQNOQQQHSDDPHWNDKAKQEVKERSRPLLSKIKORRISRAFSTPCQGMGSSRVCEGMVEEFGPMGQNLNSEDTKGLFMVGMRSRVR  
IKGEGYGGFSVKNLTHQRTHTGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK  
YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK YVRCRCGRGTQRSNLRHQRTHGKEK