

1 70

HomSap_1A6 (1) ATGGCCTGCCTCCTTCGCTCATTTTCAGAGAATTTCTGCAGGGGTTTTCTTCTT---AGCACTTTGGGGCA

PanTro_1A6 (1) ATGGCCTGCCTCCTTCGCGCATTTCAGAGAATTTCTGCAGGGGTTTTCTTCTT---AGCACTTTGGGGCA

PonAbe_1A6 (1) ATGGCCTGCCTCCTTCGTCGATTTCAGAGAATTTCTGCAGGGGTTTTCTTCTT---AGCACTTTGGGGCA

PapAnu_1A6 (1) ATGGCCTGCCTGCTTCGTCGATTTCAGAGAATTTCCGCAAGGGGTTTTCTTCTT---AGCACTTTGGGGCA

MacFas_1A6 (1) ATGGCCTGCCTGCTTCGTCGATTTCAGAGAATTTCCGCAAGGGGTTTTCTTCTT---AGCACTTTGGGGCA

AcjJub_1A6 (1) ATGGCCTGCCTCCCCATGGGTTTCAGAAAAGTTTCCCAAGGGGTTTTCTTCTT---AACGCTTTGGAAGTG

PanTig_1A6 (1) ATGGCCTG

PanOnc_1A6 (1) ATGGCCTG

PanUnc_1A6 (1) ATGGCCTG

PanLeo_1A6 (1) ATGGCCTG

PanPar_1A6 (1) ATGGCCTG

LeoGeo_1A6 (1) ATGGCCTGCCTCCCCCTGCCTTCAGAAAAGTTTCCGCAAGGGGTTTTCTTCTT---AGCGCTTTGGAAGTG

LeoTig_1A6 (1) ATGGCCTGCCTCCCCCTGCCTTCAGAAAAGTTTCCGCAAGGGGTTTTCTTCTT---AGCGCTTTGGAAGTG

LeoWie_1A6 (1) ATGGCCTGCCTCCCCCTGCCTTCAGAAAAGTTTCCGCAAGGGGTTTTCTTCTT---AGCGCTTTGGAAGTG

LynCan_1A6 (1) ATGGCCTGCCTCCCCATGCCTTCAGAAAAGTTTCCGCAAGGGGTTTTCTTCTT---AGCGCTTTGGAAGTG

LynRuf_1A6 (1) ATGGCCTGCCTCCCCATGCCTTCAGAAAAGTTTCCGCAAGGGGTTTTCTTCTT---AGCGCTTTGGAAGTG

ParTem_1A6 (1) ATGGCCTGCCTCCCCATGCCTTCAGAAAAGTTTCCGCAAGGGGTTTTCTTCTT---AGCGCTTTGGAAGTG

PumCon_1A6 (1) ATGGCCTGCCTCCCCATGCCTTCAGAAAAGTTTCCGCAAGGGGTTTTCTTCTT---AGCGCTTTGGAAGTG

PumCo2_1A6 (1) ATGGCCTGCCTCCCCATGCCTTCAGAAAAGTTTCCGCAAGGGGTTTTCTTCTT---AGCGCTTTGGAAGTG

FelCat_1A6 (1) ATGGCCTGCCTCCCCATGCCTTCAGAAAAGTTTCCGCAAGGGGTTTTCTTCTT---AGCGCTTTGGAAGTG

PriBen_1A6 (1) ATGGCCTGCCTCCCCATGCCTTCAGAAAAGTTTCCGCAAGGGGTTTTCTTCTT---AGCGCTTTGGAAGTG

CarAur_1A6 (1) ATGGCCTGCCTCCCCATGCCTTCAGAAAAGTTTCCGCAAGGGGTTTTCTTCTT---AGCGCTTTGGAAGTG

CarSer_1A6 (1) ATGGCCTGCCTCCCCATGCCTTCAGAAAAGTTTCCGCAAGGGGTTTTCTTCTT---AGCGCTTTGGAAGTG

CroCro_1A6 (1) ATGGCCTGCCTCCTCCGTGCATTTCAGAAAAGTTTCTGCAGGGGCTTCTTCTT---AGTGCTTTGGGGTG

ParBru_1A6 (1) ATGGCCTGCCTCCTCCGTGCATTTCAGAAAAGTTTCTGCAGGGGCTTCTTCTT---AGTGCTTTGGGGTG

ProCri_1A6 (1) -----

HyaHya_1A6 (1) ATGGCCTGCCTCCTCCGTGCATTTCAGAAAAGTTTCTGCAGGGGCTTCTTCTT---AGTGCTTTGGGGTG

BosTau_1A6 (1) ATGGCTTGCTTCTT-----TGGAGAGTTTCCGTGGCGGTTTTCTTCTT---AGCACTTTGGGGCT

OviAri_1A6 (1) ATGGCTTGCTTCTT---TTCTTCGACAGAGTTTCTGTGGCAGTTTTCTTCTT---AGCACTTTGGGGCT

SusScr_1A6 (1) ATGGCCTGCCTTCTCCGGGCGTTTTGGGCAAGTTTCTGCAGCGGTTCTCTCTC---AGCACTTTGGGGCA

MusMus_1A6a (1) ATGGCTTGCTTCTTCTCTGCTGCTCAGACACTTCTGCAGGGGTTTTCTTCTT---AGTGCTTTGGGGCT

MusMus_1A6b (1) ATGGCTTGCTTCTTCTCTGCTGCTCAGACACTTCTGCAGGGGTTTTCTTCTT---AGTGCTTTGGGGCT

RatNor_1A6 (1) ATGGCTTGCTTCTTCTCTGCTGCTC---GACTTCTGCAAGGCTTTCTTCTT---AGTGCTCTGGGGCT

OryCun_1A6 (1) ATGGCCTGCCTGCTTTCTGCACTCAGAGAGCGTCTGCGGGGTTCTTCTCTG---GGCACTCTGGGGCA

EquCab_1A6a (1) ATGGCCTGCCTTCTCCGTGCATTTTGGAGAGTTTCTGCAAGTGGTTTTCTTCTT---AGCATTGTGGGGCA

EquCab_1A6b (1) ATGGCCTGCCTTCTCCGTGCATTTTGGAGAGTTTCTGCAAGGGGTTTTCTTCTT---AGCATTGTGGGGCA

EquCab_1A6c (1) ATGGCCTGCCTTCTCTGTGCATTTTGGAGAGTTTCTGCAAGGGGTTTTCTTCTT---ATTGCTGTGGGGCA

MusNig_1A6 (1) ATGACCTGCCTCCTCCAGTTGTTTTGGAAAGTT-----TTCTTCTT---AGTGCTCTGGGGGG

MusPut_1A6 (1) ATGGCCTGCCTCCTCCAGTTGTTTTGGAAAGTT-----TTCTTCTT---AGTGCTCTGGGGGG

MirAng_1A6 (1) ATGGCCTGCCTCCTCCACATGTTTCAGAAAAGTT-----CTCCTCTT---AGTGCTCTGGGGCG

PhoVit_1A6 (1) ATGGCCTGCCTCCTCCACGTGTTTCAGAAAAGTT-----CTCTTCTT---AGTGCTCTGGGGCG

UrsMar_1A6 (1) -----

UrsThi_1A6 (1) -----

ProLot_1A6 (1) -----

CanFam_1A6 (1) ATGGCTCGCCTCCTTCATTGTTTCAAAAGGTG-----TTCTTCTT---AATGCTCTGGGGGG

CanRuf_1A6 (1) -----

ChrBra_1A6 (1) -----

VulVul_1A6 (1) -----

AilFul_1A6 (1) -----

ArcBin_1A6 (1) ATGGCCTGCCTCCTCCGCGCTTCAGAAAAGTTTCTGCNAGGATTTTCTTCTT---AGTGCTGTGGGGAG

CivCiv_1A6 (1) -----

HerJav_1A6 (1) ATGGCCTGCCTCCGCCATGCCTTCAGAAAAGTTTCTGCAGGGGTTTTCTTCTT---AGTGCTTTGGGGTG

GalGal_1A6 (1) ATGGCTCTTCTATTCTGTGTTTTACCCACGTACTGGGATATTTTTCTTCTTCTGTCATCTTTAATCT

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71 140

HomSap_1A6 (68) TGGTTGTAGGTGACAAGCTGCTGGTGGTCCCTCAGGACGGAAGCCACTGGCTTAGTATGAAGGATATAGT

PanTro_1A6 (68) TGGTTGTAGGTGACAAGCTGCTGGTGGTCCCTCAGGACGGAAGCCACTGGCTTAGTATGAAGGATATAGT

PonAbe_1A6 (68) TGGTTGTAGGTGACAAGCTGCTGGTGGTCCCTCAGGATGGAAGCCACTGGCTTAGTATGAAGGATATAGT

PapAnu_1A6 (68) TGGTTGTAGGTGACAAGCTGCTGGTGGTCCCTCAGGATGGAAGCCACTGGCTTAGTATGAAGGATATAGT

MacFas_1A6 (68) TGGTTGCAGGTGACAAGCTGCTGGTGGTCCCTCAGGATGGAAGCCACTGGCTTAGTATGAAGGATATAGT

AcjJub_1A6 (68) GGGGGNAGGNGACAAGCTGCTGGNGGTTCCNAGGANGGAAGCCCGGGCTCAGTCTGAAGGACGCACT

PanTig_1A6 (9) -----AGCCACGGGCTCAGTCTGAAGGACACAGT

PanOnc_1A6 (9) -----AGCCACGGGCTCAGTCTGAAGGACACAGT

PanUnc_1A6 (9) -----AGCCACGGGCTCAGTCTGAAGGACACAGT

PanLeo_1A6 (9) -----AGCCACGGGCTCAGTCTGAAGGACACAGT

PanPar_1A6 (9) -----AGCCACGGGCTCAGTCTGAAGGACACAGT

LeoGeo_1A6 (68) AGGTGGTAGGTGACAAGCTGCTGGTGGTCCCTCCGGATGGAAGCCACGGGCTCAGTCTGAAGGACACAGT

LeoTig_1A6 (68) AGGTGGTAGGTGACAAGCTGCTGGTGGTCCCTCCGGATGGAAGCCACGGGCTCAGTCTGAAGGACACAGT

LeoWie_1A6 (68) AGGTGGTAGGTGACAAGCTGCTGGTGGTCCCTCCGGATGGAAGCCACGGGCTCAGTCTGAAGGACACAGT

LynCan_1A6 (68) AGGTGGTAGGTGACAAGCTGCTGGTGGTCCCTCAGGATGGAAGCCACGGGCTCAGTCTGAAGGACACAGT

LynRuf_1A6 (68) AGGTGGTAGGTGACAAGCTGCTGGTGGTCCCTCAGGATGGAAGCCACGGGCTCAGTCTGAAGGACACAGT

ParTem_1A6 (68) AGGTGGTAGGTGACAAGCTGCTGGTGGTCCCTCAGGATGGAAGCCACGGGCTCAGTCTGAAGGACACAGT

PumCon_1A6 (68) AGGTGGTAGGTGACAAGCTGCTGGTGGTCCCTCAGGATGGAAGCCACGGGCTCAGTCTGAAGGACACAGT

PumCo2_1A6 (68) AGGTGGTAGGTGACAAGCTGCTGGTGGTCCCTCAGGATGGAAGCCACGGGCTCAGTCTGAAGGACACAGT

FelCat_1A6 (68) AGGTGGTAGGTGACAAGCTGCTGGTGGTCCCTCAGGATGGAAGCCACGGGCTCAGTCTGAAGGACACAGT

M6: bp9-108

PriBen_1A6 (68) AGGTGGTAGGTGACAAGCTGCTGGTGGTTCCTCAGGATGGAAGCCACGGGCTCAGTCTGAAGGACGCACT
 CarAur_1A6 (68) AGGTGGTAGGTGACAAGCTGCTGGTGGTTCCTCAGGATGGAAGCCACGGGCTCAGTCTGAAGGACGCACT
 CarSer_1A6 (68) AGGTGGTAGGTGACAAGCTGCTGGTGGTTCCTCAGGATGGAAGCCACGGGCTCAGTCTGAAGGACGCACT
 CroCro_1A6 (68) AGGTGGTAGGTGACAAGCTGCTGGTGGTTCCTCAGGATGGAAGCCACTGGCTCAGTATGAAGGAGATAGT
 ParBru_1A6 (68) AGGTGGTAGGTGACAAGCTGCTGGTGGTTCCTCAGGATGGAAGCCACTGGCTCAGTATGAAGGAGATAGT
 ProCri_1A6 (1) -----
 HyaHya_1A6 (68) AGGTGGTAGGTGACAAGCTGCTGGTGGTTCCTCAGGATGGAAGCCACTGGCTCAGTATGAAGGAGATAGT
 BosTau_1A6 (59) TCACCCCTGGGGGACAGGCTGCTGGTGGTCCCTCAGGATGGAAGCCACTGGCTCAGCATGAAGGACATCGT
 OviAri_1A6 (65) TCGCCCTGGGGGACAGGCTGCTGGTGGTCCCTCAGGATGGAAGCCACTGGCTCAGCATGAAGGACATCAC
 SusScr_1A6 (68) CGGTTGCAGGGGACAGGCTGCTGGTGGTCCCTCAGGATGGAAGCCACTGGCTCAGCATGAAGGACATCGT
 MusMus_1A6a (68) CAGTTCTAGGTGACAAGCTGCTGGTGGTCCCCCAGGATGGAAGCCACTGGCTTAGCATGAAGGAGATAGT
 MusMus_1A6b (68) CAGTTCTAGGTGACAAGCTGCTGGTGGTCCCCCAGGATGGAAGCCACTGGCTTAGCATGAAGGAGATAGT
 RatNor_1A6 (65) CAGTTCTAGGTGACAAGCTGCTGGTGGTCCCCCAGGATGGAAGCCACTGGCTTAGCATGAAGGAGATAGT
 OryCun_1A6 (68) CGGTGCTGGGTGACAGGCTGCTGGTGGTGGCCCAAGGATGGAAGCCACTGGCTTAGCATGACAGGACATAGT
 EquCab_1A6a (68) TGAGTGTAGGTGACAAGCTGCTGGTGGTCCCTCAGGATGGAAGCCACTGGCTCAGTATGAAGGACATAAT
 EquCab_1A6b (68) TGAGTGTAGGTGACAAGCTGCTGGTGGTCCCTCAGGACGGAAGCCACTGGCTCAGTATGAAGGACATCAT
 EquCab_1A6c (68) TGTTGTAGGTGACAAGCTGCTGGTGGTCCCTCAGGATGGAAGCCACTGGCTCAGTATGAAGGACATAAT
 MusNig_1A6 (56) AGGTGGTAGGTGACAGGCTGCTGGTGGTCCCTCAGGATGGAAGCCACTGGCTCAGTATGAAGGACATAAT
 MusPut_1A6 (56) AGGTGGTAGGTGACAGGCTGCTGGTGGTCCCTCAGGATGGAAGCCACTGGCTCAGTATGAAGGACATAAT
 MirAng_1A6 (56) GGGTTGTAGGTGACAAGCTGCTGGTGGTTCCTCAGGATGGAAGCCACTGGCTCAGTATGAAGGACATAAT
 PhoVit_1A6 (56) GGGTTGTAGGTGACAAGCTGCTGGTGGTCCCTCAGGATGGAAGCCACTGGCTCAGTATGAAGGACATAAT
 UrsMar_1A6 (1) -----ACTGGCTCAGTATGAAGGACATAAT
 UrsThi_1A6 (1) -----CTGGCTCAGTATGAAGGACATAAT
 ProLot_1A6 (1) -----
 CanFam_1A6 (56) AGGCTGTAGGTGACAAGCTTCTGGTGGTCCCTCAGGACGGAAGCCACTGGCTCAGTATGGAGAACATAAT
 CanRuf_1A6 (1) -----CTGGCTCAGTATGGAGAACATAAT
 ChrBra_1A6 (1) -----CTGGCTCAGTATGGAGAACATAAT
 VulVul_1A6 (1) -----CACTGGCTCAGTATGGAGAACATAAT
 AilFul_1A6 (1) -----
 ArcBin_1A6 (68) AGGTCGTATGTGACAAGCTGCTGGGGGTGCCTCAGGATGGAAGCCACTGGCTCAGTATGAAGGAGATAGT
 CivCiv_1A6 (1) -----
 HerJav_1A6 (68) AGGTGGTAGGTGACAAGCTGCTGGTGGTGCCTCAGGACGGAAGCCACTGGCTCAGTATGAAGGAGATAGT
 GalGal_1A6 (71) TTGCTGAATGTGGAAGATCCTGGTGATACCTCAGGATGGAAGTCATTGGCTCAGTATGCAACCACTAGT

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HomSap_1A6 (138) TGAGGTTCTCAGTGACCGGGGTCATGAGATTGTAGTGGTGGTGCCTGAAGTTAATTTGCTTTTGAAA---
 PanTro_1A6 (138) TGAGGTTCTCAGTGACCGGGGTCACGAGATTGTAGTGGTGGTGCCTGAAGTTAATTTGCTTTTGAAA---
 PonAbe_1A6 (138) TGAGGTTCTCAGTGACCGGGGTCATGACATTGTAGTGGTGGTGCCTGAAGTTAATTTGCTTTTGAAA---
 PapAnu_1A6 (138) TGAAGTTCTCAGTGACCGGGGTCATGACATTGTAGTGGTGGTGCCTGAAGTTAATTTGCTTTTGAAA---
 MacFas_1A6 (138) TGAAGTTCTCAGTGACCGGGGTCATGACATTGTAGTGGTGGTGCCTGAAGTTAATTTGCTTTTGAAA---
 AciJub_1A6 (138) TGAGCTTCTCAGTGAGAGGGGACATGACATGGTAGTGTGGTGTGTCAGAGGTCAATCTGCTTCTGAAG---
 PanTig_1A6 (38) TGAGCTTCTCAGTGAGAGGGGACATGACATGGTAGTGTGGTGTGTCAGAGGTCAATCTGCTTCTGAAG---
 PanOnc_1A6 (38) TGAGCTTCTCAGTGAGAGGGGACATGACATGGTAGTGTGGTGTGTCAGAGGTCAATCTGCTTCTGAAG---
 PanUnc_1A6 (38) TGAGCTTCTCAGTGAGAGGGGACATGACATGGTAGTGTGGTGTGTCAGAGGTCAATCTGCTTCTGAAG---
 PanLeo_1A6 (38) TGAGCTTCTCAGTGAGAGGGGACATGACATGGTAGTGTGGTGTGTCAGAGGTCAATCTGCTTCTGAAG---
 PanPar_1A6 (38) TGAGCTTCTCAGTGAGAGGGGACATGACATGGTAGTGTGGTGTGTCAGAGGTCAATCTGCTTCTGAAG---
 LeoGeo_1A6 (138) TGAGCTTCTCAGTGAGAGGGGACATGACATGGTAGTGTGGTGTGTCAGAGGTCAATCTGCTTCTGAAG---
 LeoTig_1A6 (138) TGAGCTTCTCAGTGAGAGGGGACATGACATGGTAGTGTGGTGTGTCAGAGGTCAATCTGCTTCTGAAG---
 LeoWie_1A6 (138) TGAGCTTCTCAGTGAGAGGGGACATGACATGGTAGTGTGGTGTGTCAGAGGTCAATCTGCTTCTGAAG---
 LynCan_1A6 (138) TGAGCTTCTCAGTGAGAGGGGACATGACATGGTAGTGTGGTGTGTCAGAGGTCAATCTGCTTCTGAAG---
 LynRuf_1A6 (138) TGAGCTTCTCAGTGAGAGGGGACATGACATGGTAGTGTGGTGTGTCAGAGGTCAATCTGCTTCTGAAG---
 ParTem_1A6 (138) TGAGCTTCTCAGTGAGAGGGGACATGACATGGTAGTGTGGTGTGTCAGAGGTCAATCTGCTTCTGAAG---
 PumCon_1A6 (138) TGAGCTTCTCAGTGAGAGGGGACATGACATGGTAGTGTGGTGTGTCAGAGGTCAATCTGCTTCTGAAG---
 PumCo2_1A6 (138) TGAGCTTCTCAGTGAGAGGGGACATGATGGTAGTGTGGTGTGTCAGAGGTCAATCTGCTTCTGAAG---
 FelCat_1A6 (138) TGAGCTTCTCAGTGAGAGGGGACATGACATGGTAGTGTGGTGTGTCAGAGGTCAATCTGCTTCTGAAG---
 PriBen_1A6 (138) TGAGCTTCTCAGTGAGAGGGGACATGACATGGTAGTGTGGTGTGTCAGAGGTCAATCTGCTTCTGAAG---
 CarAur_1A6 (138) TGAGCTTCTCAGTGAGAGGGGACATGACATGGTAGTGTGGTGTGTCAGAGGTCAATCTGCTTCTGAAG---
 CarSer_1A6 (138) TGAGCTTCTCAGTGAGAGGGGACATGACATGGTAGTGTGGTGTGTCAGAGGTCAATCTGCTTCTGAAG---
 CroCro_1A6 (138) TGAGTTCTCAGTGAGAGGGGACATGACATTGTAGTGTGGTGTGTCAGAGGTCAATCTGCTTCTGAAG---
 ParBru_1A6 (138) TGAGTTCTCAGTGAGAGGGGACATGACATTGTAGTGTGGTGTGTCAGAGGTCAATCTGCTTCTGAAG---
 ProCri_1A6 (1) -----TCTGCTTCTGAAG---
 HyaHya_1A6 (138) TGAGTTCTCAGTGAGAGGGGACATGACATTGTAGTGTGGTGTGTCAGAGGTCAATCTGCTTCTGAAG---
 BosTau_1A6 (129) TGAGCATCTCAGTGAGAGGGGACATGACATCGTGGTGGTGGTGCCTGAAGTCAACCTGCTCTCCAA---
 OviAri_1A6 (135) TGAACGTCTCAGTGAGAGGGGACATGACATCGTGGTGGTGGTGCCTGAAGTCAACCTGCTCTCCAA---
 SusScr_1A6 (138) TGTGCGGCTCAGTGAGAGGGGACATGACATCGTGGTGGTGGTGCCTGAAGTCAACCTGCTCTCCAA---
 MusMus_1A6a (138) AGAACATCTCAGTGAACGAGGACATGACATTATGGTCTAGTGCCAGAGTCAATTTGCTTTTGGGA---
 MusMus_1A6b (138) GGAGCATCTCAGTGAACGAGGACATGACATTGTGGTCTAGTGCCAGAGTCAATTTGCTTTTGGGA---
 RatNor_1A6 (135) GGAGCACCTCAGTGAACGCGGACACGACATTGTGGTCTAGTGCCAGAGTCAATTTGCTTTTGGGA---
 OryCun_1A6 (138) TGAGGCTCTTGGGGGACAGGGGACATGACATCGTGGTGTGGTGTGTCAGAGGTCAATTTGCTTTTGGGA---
 EquCab_1A6a (138) TGAGCCTCTCAGTGAGAGGGGACATGACATCGTGGTGTGGTGTGTCAGAGGTCAATTTGCTTTTGGGA---
 EquCab_1A6b (138) TGAGCCTCTCAGTGAGAGGGGACATGACATCGTGGTGTGGTGTGTCAGAGGTCAATTTGCTTTTGGGA---
 EquCab_1A6c (138) TGAGCCTCTCAGTGAGAGGGGACATGACATCGTGGTGTGGTGTGTCAGAGGTCAATTTGCTTTTGGGA---
 MusNig_1A6 (126) TGAGCTCCTCAGTGAGAGGGGACATGACATTGTGGTGTGGTGTGTCAGAGGTCAATTTGCTTTTGGGA---
 MusPut_1A6 (126) TGAGCTCCTCAGTGAGAGGGGACATGACATTGTGGTGTGGTGTGTCAGAGGTCAATTTGCTTTTGGGA---
 MirAng_1A6 (126) TGAGCTCCTCAGTGAGAGGGGACATGACATTGTGGTGTGGTGTGTCAGAGGTCAATTTGCTTTTGGGA---
 PhoVit_1A6 (126) TGAGCTCCTCAGTGAGAGGGGACATGACATTGTGGTGTGGTGTGTCAGAGGTCAATTTGCTTTTGGGA---
 UrsMar_1A6 (26) TGAGCTCCTCAGTGAGAGGGGACATGACATTGTGGTGTGGTGTGTCAGAGGTCAATTTGCTTTTGGGA---
 UrsThi_1A6 (25) TGAGCTCCTCAGTGAGAGGGGACATGACATTGTGGTGTGGTGTGTCAGAGGTCAATTTGCTTTTGGGA---

ProLot_1A6 (1) -----GGGCATGACTTTGTGGTGTGGTGCCCAAGCAATCTGCTTCGAAAT---
 CanFam_1A6 (126) TGAGCTCCTCAGTGAGAAGGGGCATGACATTGTGGTGTGGTGCCAGAAAGTCAATTTGCTTCTGAAG---
 CanRuf_1A6 (25) TGAGCTCCTCAGTGAGAAGGGGCATGACATTGTGGTGTGGTGCCAGAAAGTCAATTTGCTTCTGAAG---
 ChrBra_1A6 (25) TGAGCTCCTCAGTGAGAAGGGGCATGACATTGTGGTGTGGTGCCAGAAAGTCAATTTGCTTCTGAAG---
 VulVul_1A6 (27) TGAGCTCCTCAGTGAGAAGGGGCATGACATTGTGGTGTGGTGCCAGAAAGTCAATTTGCTTCTGAAG---
 AilFul_1A6 (1) -----TGCTGGTGTGAGAGGGCAATCTGCTTCTGAAG---
 ArcBin_1A6 (138) TGAGCACCTCAGTGAGAAGGGACATGATATTGTAGTGTGGCGCCAGAGGTCAATCTGATTCTGAAG---
 CivCiv_1A6 (1) -----ATCTGCTTCTGAAG---
 HerJav_1A6 (138) TGAGCTCCTCAGTGAGAAGGGACATGACCTTGTAGTGTGGTGCCAGAGGTCAATCTGCTTCTGAAG---
 GalGal_1A6 (141) AGGAAAACTCCAGCAAAATGGACATGATGTTGTGGTGTACCCTCATCAAGTTTGTATTATGAAGTCA

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HomSap_1A6 (205) ---GAATCCAAATACTACACAAGAAAAATCTATCCAGTGCCGTATGACCAAGAAGAGCTGAAGAACCCTT
 PanTro_1A6 (205) ---GAATCCAAATACTACACAAGAAAAATCTATCCAGTGCCGTATGACCAAGAAGAGCTGAAGAACCCTT
 PonAbe_1A6 (205) ---GAATCCAAATACTACACAAGAAAAATCTATCCAGTGCCGTATGACCAAGAAGAGCTGAAGAACCCTT
 PapAnu_1A6 (205) ---GAATCCAAATACTACACAAGAAAAATCTATCCAGTGCCGTATGACCAAGAAGAGCTGAAGAACCCTT
 MacFas_1A6 (205) ---GAATCCAAATACTACACAAGAAAAATCTATCCAGTGCCGTATGACCAAGAAGAGCTGAAGAACCCTT
 AciJub_1A6 (205) ---GAATCCAAACACTACACGAGAAAAATCTATCTAGTGCCATTGGACCGGGAAGAGCCGGAGCACCCTT
 PanTig_1A6 (105) ---GAATCCAAACACTACACGAGAAAAATCTATCCAGTGCCATTGACCGGGAAGAGCCGGAGCACCCTT
 PanOnc_1A6 (105) ---GAATCCAAACACTACACGAGAAAAATCTATCCAGTGCCATTGACCGGGAAGAGCCGGAGCACCCTT
 PanUnc_1A6 (105) ---GAATCCAAACACTACACGAGAAAAATCTATCCAGTGCCATTGACCGGGAAGAGCCGGAGCACCCTT
 PanLeo_1A6 (105) ---GAATCCAAACACTACACGAGAAAAATCTATCCAGTGCCATTGACCGGGAAGAGCCGGAGCACCCTT
 PanPar_1A6 (105) ---GAATCCAAACACTACACGAGAAAAATCTATCCAGTGCCATTGACCGGGAAGAGCCGGAGCACCCTT
 LeoGeo_1A6 (205) ---GAATCCAAACACTACACGAGAAAAATCTATCCAGTGCCATTGACCGGGAAGAGCCGGAGCACCCTT
 LeoTig_1A6 (205) ---GAATCCAAACACTACACGAGAAAAATCTATCCAGTGCCATTGACCGGGAAGAGCCGGAGCACCCTT
 LeoWie_1A6 (205) ---GAATCCAAACACTACCGGAGAAAAATCTATCCAGTGCCATTGACCGGGAAGAGCCGGAGCACCCTT
 LynCan_1A6 (205) ---GAATCCAAACACTACACGAGAAAAATCTATCCAGTGCCATTGACCGGGAAGAGCCGGAGCACCCTT
 LynRuf_1A6 (205) ---GAATCCAAACACTACACGAGAAAAATCTATCCAGTGCCATTGACCGGGAAGAGCCGGAGCACCCTT
 ParTem_1A6 (205) ---GAATCCAAACACTACACGAGAAAAATCTATCCAGTGCCATTGACCGGGAAGAGCCGGAGCACCCTT
 PumCon_1A6 (205) ---GAATCCAAACACTACACGAGAAAAATCTATCCAGTGCCATTGACCGGGAAGAGCCGGAGCACCCTT
 PumCo2_1A6 (205) ---GAATCCAAACACTACACGAGAAAAATCTATCCAGTGCCATTGACCGGGAAGAGCCGGAGCACCCTT
 FelCat_1A6 (205) ---GAATCCAAACACTACACGAGAAAAATCTATCCAGTGCCATTGACCGGGAAGAGCCGGAGCACCCTT
 PriBen_1A6 (205) ---GAATCCAAACACTACACGAGAAAAATCTATCCAGTGCCATTGACCGGGAAGAGCCGGAGCACCCTT
 CarAur_1A6 (205) ---GAATCCAAACACTACACGAGAAAAATCTATCCAGTGCCATTGACCGGGAAGAGCCGGAGCACCCTT
 CarSer_1A6 (205) ---GAATCCAAACACTACACGAGAAAAATCTATCCAGTGCCATTGACCGGGAAGAGCCGGAGCACCCTT
 CroCro_1A6 (205) ---GAATCCAAACACTACATGAGAAAAATCTATCCAGTGCCATTGACCGGGAAGAGCTGCAGAACCTT
 ParBru_1A6 (205) ---GAATCCAAACACTACGTGAGAAAAATCTATCCAGTGCCATTGACCGGGAAGAGCTGCAGAACCTT
 ProCri_1A6 (14) ---GAATCCAAACACTACATGAGAAAAATCTATCCAGTGCCATTGACCGGGAAGAGCTGCAGAACCTT
 Hyahya_1A6 (205) ---GAATCCAAACACTACGTGAGAAAAATCTATCCAGTGCCATTGACCGGGAAGAGCTGCAGAACCTT
 BosTau_1A6 (196) ---GAGTCCAAGCACTACACAAGGAAAAATCCACCAAGTGCCCTTCAACAGGAGGAGCTGGAAGCCCTT
 OviAri_1A6 (202) ---GAGTCCAAGCACTACACAAGGAAAAATCCACCAAGTGCCCTACGACCAAGAGGAGCTGGAAGCCCTT
 SusScr_1A6 (205) ---GAATCCAAATACTACACGAGAAAGATCTATCCGGTGCCCTACGACCAAGAGGAGCTGGAGGGCCCTT
 MusMus_1A6a (205) ---GAATCCAAATACTACAGGAGGAAAAATCTTCTCAGTTACCTACAGCCTAGAAGAACTGCAGAACCTT
 MusMus_1A6b (205) ---GAATCCAAATACTACAGGAGGAAAAATCTTCTCAGTTCCCTACAGCCTAGAAGAACTGCAGAACCTT
 RatNor_1A6 (202) ---GAATCCAAATACTACAGGAGGAAAAATCTTCCGGTCCCTTACAACTAGAAGAGTTCGGGAGCCCTT
 OryCun_1A6 (205) ---GAATCCAGGTTCTACACGAGGAGAAATCTATCCAGTGCCCTTACGACGAGGAGAGCTTACCGCTT
 EquCab_1A6a (205) ---GAATCGAAATACTACACAAGAAAGATCTATCCAGTGCCCTACGACGAGGAAAGAGTGGTGAGCCCTT
 EquCab_1A6b (205) ---GAATCTGAATACTACACAAGAAAGATCTATCCAGTGCCCTATGAAGAGGAAAGAGCTGATGAAGCCCTT
 EquCab_1A6c (205) ---GAATCCAAATACTACACAAGAAAGATCTATCCAGTGCCCTACGACGAGGAAAGAAATGGTGAGCCCTT
 MusNig_1A6 (193) ---GAGTCCAAGCACTACACAAGAAAAATCTATCCAGTGCCCTTCAACAGGAGGAGCTGGAGAATCGCTT
 MusPut_1A6 (193) ---GAGTCCAAGCACTACACAAGAAAAATCTATCCAGTGCCCTTCAACAGGAGGAGCTGGAGAATCGCTT
 MirAng_1A6 (193) ---GAATCCAAGCACTACACAAGAAAGAGCTATCCCGTGCCATTTCGATCAGAAAGAGCTGGAGAATCGCTT
 PhoVit_1A6 (193) ---GAATCCAAGCACTACACAAGAAAAATCTATCCAGTGCCCTTACGACGAGGAGAGCTGGAGAATCGCTT
 UrsMar_1A6 (93) ---GAATCCAAGCACTATGCGAGAAAAATCTATCCCGTGCCCTTACGACGAGGAGAGCTGGAGGCTCGCTT
 UrsThi_1A6 (92) ---GAATCCAAGCACTACGCGAGAAAAATCTATCCCGTGCCCTTACGACGAGGAGAGCTGGAGGCTCGCTT
 ProLot_1A6 (49) ---GAATCCTCGCACTACACGAGAAAGATCTATCCAGTGCCCTTTCGAGCGGAGGAGCTGGGGATCGCTT
 CanFam_1A6 (193) ---GAATCCAAACACTACACGAGACAAATCTACTCAGTGCCATTGCGCAGGAAAGAGTTGGAGAACCCTT
 CanRuf_1A6 (92) ---GAATCCAAACACTACACGAGACAAATCTACTCAGTGCCATTGCGCAGGAAAGAGTTGGAGAACCCTT
 ChrBra_1A6 (92) ---GAATCCAAACACTACACGAGACAAATCTACTCAGTGCCATTGCGCAGGAAAGAGTTGGAGAACCCTT
 VulVul_1A6 (94) ---GAATCCAAACACTACACGAGACAAATCTACTCAGTGCCATTGCGCAGGAAAGAGTTGGAGAACCCTT
 AilFul_1A6 (33) ---GAGTCCAAGCACTACACAAGGAAAAATCTATCCAGTGCCATTTCGACGAGGAAAGAGCTCGAGAATCGCTT
 ArcBin_1A6 (205) ---GAATCCAAACACTACACGAGAAAAATCTATCCAGTGCCATTGACCGGGAAGAGCTGGAGAACCCTT
 CivCiv_1A6 (15) ---GAATCCAAACACTACACGAGAAAAATCTATCCAGTGCCATTGACCGGGAAGAGCTGGAGAACCCTT
 HerJav_1A6 (205) ---GAATCCAAACACTACAGGAGAAAAATCTATCCAGTGCCATTGACCGGGAAGAGCTGCAGAACCTT
 GalGal_1A6 (211) AAGGAGCATCAGAAATATACAGTGAAAGTGATCGAATACCTTACGAAGAAGAACATTTACATCTTGTG

281

350

HomSap_1A6 (272) ACCAATCATTTGGAACAATCACTTTGCTGAGCGATCATTCCTAAGTCTCTCAGACAGAGTACAGGAA
 PanTro_1A6 (272) ACCAATCATTTGGAACAATCACTTTGCTGAGCGATCATTCCTGACTGCTCCTCAGACAGAGTACAGGAA
 PonAbe_1A6 (272) ACCAATCATTTGGAACAATCACTTTGCTGAGCGATCATTCCTGACTGCTCCTCAGACAGAGTACAGGAA
 PapAnu_1A6 (272) ACCAATTTGTTTGGAAACAATCACTTTGCTGAGCGATCATTCCTGACTGCTCCTCAGACAGAGTACAGGAA
 MacFas_1A6 (272) ACCAATTTGTTTGGAAACAATCACTTTGCTGAGCGATCATTCCTGACTGCTCCTCAGACAGAGTACAGGAA
 AciJub_1A6 (272) TCTGATCTTTTGGAAACAGTCACTTCGCTGAGAGGTGGCTCCTGAACCTGCTGTGAGGGAGGACAGGAA
 PanTig_1A6 (172) TCTGATCTTTTGGAAACAGTCACTTCGCTGAGAGGTGGCTCCTGAACCTGCTGTGCGGGAGGACAGGAA
 PanOnc_1A6 (172) TCTGATCTTTTGGAAACAGTCACTTCGCTGAGAGGTGGCTCCTGAACCTGCTGTGCGGGAGGACAGGAA
 PanUnc_1A6 (172) TCTGATCTTTTGGAAACAGTCACTTCGCTGAGAGGTGGCTCCTGAACCTGCTGTGCGGGAGGACAGGAA
 PanLeo_1A6 (172) TCTGATCTTTTGGAAACAGTCACTTCGCTGAGAGGTGGCTCCTGAACCTGCTGTGCGGGAGGACAGGAA
 PanPar_1A6 (172) TCTGATCTTTTGGAAACAGTCACTTCGCTGAGAGGTGGCTCCTGAACCTGCTGTGCGGGAGGACAGGAA

M1: bp274-276

LeoGeo_1A6 (272) TCTGATCTTTTGGAAATAGTCACTTCGCTGAGAGGTGGCTCCTGAACCCCTGCTGTGAGGGAGGACAGGAA
 LeoTig_1A6 (272) TCTGATCTTTTGGAAATAGTCACTTCGCTGAGAGGTGGCTCCTGAACCCCTGCTGTGAGGGAGGACAGGAA
 LeoWie_1A6 (272) TCTGATCTTTTGGAAATAGTCACTTCGCTGAGAGGTGGCTCCTGAACCCCTGCTGTGAGGGAGGACAGGAA
 LynCan_1A6 (272) TCTGATCTTTTGGAAACAGTCACTTCGCTGAGAGGTGGCTCCTGAACCCCTGCTGTGAGGGAGGACAGGAA
 LynRuf_1A6 (272) TCTGATCTTTTGGAAACAGTCACTTCGCTGAGAGGTGGCTCCTGAACCCCTGCTGTGAGGGAGGACAGGAA
 ParTem_1A6 (272) TCTGATCTTTTGGAAACAGTCACTTCGCTGAGAGGTGGCTCCTGAACCCCTGCTGTGAGGGAGGACAGGAA
 PumCon_1A6 (272) TCTGATCTTTTGGAAACAGTCACTTCGCTGAGAGGTGGCTCCTGAACCCCTGCTGTGAGGGAGGACAGGAA
 PumCo2_1A6 (272) TCTGATCTTTTGGAAACAGTCACTTCGCTGAGAGGTGGCTCCTGAACCCCTGCTGTGAGGGAGGACAGGAA
 FelCat_1A6 (272) TCTGATCTTTTGGAAACAGTCACTTCGCTGAGAGGTGGCTCCTGAACCCCTGCTGTGAGGGAGGACAGGAA
 PriBen_1A6 (272) TCTGATCTTTTGGAAACAGTCACTTCGCTGAGAGGTGGCTCCTGAACCCCTGCTGTGAGGGAGGACAGGAA
 CarAur_1A6 (272) TCTGATCTTTTGGAGATTGTCACTTCGCTGAGAGGTGGCTCCTGAACCCCTGCTGTGAGGGAGGACAGGAA
 CarSer_1A6 (272) TCTGATCTTTTGGAGATTGTCACTTCGCTGAGAGGTGGCTCCTGAACCCCTGCTGTGAGGGAGGACAGGAA
 CroCro_1A6 (272) TCCAATCTTTTGGAAACAATCACTTTGTGGAGAAAGGGCTCCTGAGCGCTGCTGTGATGGAGTACAGGAA
 ParBru_1A6 (272) TCTGATCTTTTGGAAAGCAATCACTTTGTGGAGAAAGGGCTCCTGAGCGCTGCTGTGATGGAGTACAGGAA
 ProCri_1A6 (81) TCCGATCTTTTGGAAACAATCACTTTGTGGAGAAAGGGCTCCTGAGCGCTGCTTTGATAGAGTACAGGAA
 HyaHya_1A6 (272) TCCGGTCTTTTGGAAAGCAATCACTTTGTGGAGAAAGGGCTCCTGAGCGCTGCTGTGATGGAGTACAGGAA
 BosTau_1A6 (263) ACCGCTCTTTTGGGAAACACCACTTTCTCCACGCTGGTTGGTGACTGCCCTGTGGTGGAGTACAGGAA
 OviAri_1A6 (269) ACCGTTCTTTTGGGAAACACCACTTTCTCCACGCTGGCTGGTGACTGCCCTATGGTGGAGTATAGGAA
 SusScr_1A6 (272) ACCGGTCTTTTGGAAAGAAACCACTTTTGGAGCGATGGTTGCTGAACGCCGCTCAGGTGGAGTACAGGAA
 MusMus_1A6a (272) TTCGCACCTTTGGAAACAACCACTTTCTCCCGTGCTCCCTGATGGGTCTCTAAGAGAGTACAGGAA
 MusMus_1A6b (272) TTCGCACCTTTGGACGCAACCACTTTGTTCTGGTGCCCTGATGGGTCTCTAAGAGAGTACAGGAA
 RatNor_1A6 (269) ATCGCTCTTTTGGGAACAACCACTTTGCTGCCAGTTCCCTGATGGCTCCTAAGAGAGTACAGGAA
 OryCun_1A6 (272) ATCGCACCTTTGGAGAAAGCACTTTACTGACAGGTCTGGCTGAGCGGCTCAGACGGAATACAGGAA
 EquCab_1A6a (272) ACCGCTCTTTTGGAAAGAATCACTTTGCTGAGAGATGGCTCCTAAATGCTGCTCAGACTGAGTATACAGGAA
 EquCab_1A6b (272) TCCGCTCTTTTGGAAAGAATCAATTCGCTGAGAGATGGCTCCTGGATGCTGCTCAGACTGAGTACAGGAA
 EquCab_1A6c (272) TCTGTTCTTTTGGCGACAATCACTTTGTTAAGAGATGGCTCCTGGATGCTGTTGAGACTGAGTACAGGAA
 MusNig_1A6 (260) ACCGCTCTTTTGGAAACAATCACTTTGCTGAGAGATGGCTCCTGAACGCTGCTCAGATGGAATACAGGAA
 MusPut_1A6 (260) ACCGCTCTTTTGGAAACAATCACTTTGCTGAGAGATGGCTCCTGAACGCTGCTCAGATGGAATACAGGAA
 MirAng_1A6 (260) ACCACTTTTTTGGAAACGATCACTTTGCTGAGAGATGGCTCCCGAACGCTGCTCAGATGGAGTACAGGAA
 PhoVit_1A6 (260) ACCACTCTTTTGGAAACAATCACTTTGCTGAGAGATGGCTCCTGAACGCTGCTCAGATGGAGTACAGGAA
 UrsMar_1A6 (160) ACCGCTCTTTTGGAAACAATCACTTTGCTGAGAGATGGCTCCTGAACGCCGCTCAAACGGAGTACAGGAA
 UrsThi_1A6 (159) ACCGCTCTTTTGGAAACAATCACTTTGCTGAGAGATGGCTCCTGAACGCCGCTCAAACGGAGTACAGGAA
 ProLot_1A6 (116) TCCGCTCTTTTGGAAACAATCACTTTGCTGAGAGATGGCTCCTGAACGCTGCTCAGGGGAGGACAGGAA
 CanFam_1A6 (260) ACCGCTCTTTTGGAAAGAATCACTTTGCTGAGAGATGGCTCCTGAACGCTGCTCAGATGGAGTACAGGAA
 CanRuf_1A6 (159) ACCGCTCTTTTGGAAAGAATCACTTTGCTGAGAGATGGCTCCTGAACGCTGCTCAGATGGAGTACAGGAA
 ChrBra_1A6 (159) ACCGCTCTTTTGGAAAGAATCACTTTGCTGAGAGATGGCTCCTGAACACTGCTCAGATGGAGTACAGGAA
 VulVul_1A6 (161) ACCGCTCTTTTGGAAAGAACCCTTTGCTGAGAGATGGCTCCTGAACGCTGCTCAGATGGAGTACAGGAA
 AilFul_1A6 (100) ACCGCTCTTTTGGAAACGCTGCTTTGCTGAGAGGTGGCTCCTGAATGCTGCTCAGACGAGTACAGGAA
 ArcBin_1A6 (272) TCCGAGCTTTTGGAAACAATCACTTTGCTGAGAGATGGCTCCTGAACGCTGCTGTGATGGAGTACAGGAA
 CivCiv_1A6 (82) TCCGAGCTTTTGGAAACAATCACTTTGCTGAGAGATGGCTCCTGAACGCTGCTGTGATGGAGTACAGGAA
 HerJav_1A6 (272) TCCGATCTTTTGGAAATAATCACTTTGCGGAGAGAGGGCTCCTGAGCGCCGCTCCGATGGAAATACAGGAA
 GalGal_1A6 (281) TCAAGTCATTTGTTAATGATCATTTTACTGAACAATCTTTATTGAATATTATTATTAATGATATCAAAA

M10: bp274-276

351
 HomSap_1A6 (342) TAACATGATTGTTATTGGCCTGTACTTCATCAACTGCCAGAGCCTCCTGCAGGACAG - GGACACCCGTGAA
 PanTro_1A6 (342) TAACATGATCGTTATTGGCCTGTACTTCATCAACTGCCAGAGCCTCCTGCAGGACAG - GGACACCCGTGAA
 PonAbe_1A6 (342) TAACATGATCGTTATTAGCCTGTACTTCATCAACTGCCAGAGCCTCCTGCAGGACAG - GGACACCCGTGAA
 PapAnu_1A6 (342) TAACATGGTCGTTATTGGCATGTACTTCATCAACTGCCAGAGCCTCCTGCAGGACGT - GGACACCCGTGAA
 MacFas_1A6 (342) TAACATGGTCGTTATTGGCATGTACTTCATCAACTGCCAGAGCCTCCTGCAGGACGT - GGGCACCCGTGAA
 AciJub_1A6 (342) TACCATGATTGTTACCGACACGTACTTCGCCAACCCTGCTAGAGCCTCCTGGAGGACTC - GCCACCTTGAG
 PanTig_1A6 (242) TACCATGATTGTTACCGACACGTACTTCGCCAACCCTGCTAGAGCCTCCTGGAGGACTC - GCCACCTTGAG
 PanOnc_1A6 (242) TACCATGATTGTTACCGACACGTACTTCGCCAACCCTGCTAGAGCCTCCTGGAGGACTC - GCCACCTTGAG
 PanUnc_1A6 (242) TACCATGATTGTTACCGACACGTACTTCGCCAACCCTGCTAGAGCCTCCTGGAGGACTC - GCCACCTTGAG
 PanLeo_1A6 (242) TACCATGATTGTTACCGACACGTACTTCGCCAACCCTGCTAGAGCCTCCTGGAGGACTC - GCCACCTTGAG
 PanPar_1A6 (242) TACCATGATTGTTACCGACACGTACTTCGCCAACCCTGCTAGAGCCTCCTGGAGGACTC - GCCACCTTGAG
 LeoGeo_1A6 (342) TACCGTGATTGTTACCGACACATATCTTCGCCAACCCTGCTAGAGCCTCCTGGAGGACTC - GCCACCTTGAG
 LeoTig_1A6 (342) TACCGTGATTGTTACCGACACATATCTTCGCCAACCCTGCTAGAGCCTCCTGGAGGACTC - GCCACCTTGAG
 LeoWie_1A6 (342) TACCGTGATTGTTACCGACACATATCTTCGCCAACCCTGCTAGAGCCTCCTGGAGGACTC - GCCACCTTGAG
 LynCan_1A6 (342) TACCATGATTGTTACCGACACATATCTTCGCCAACCCTGCTAGAGCCTCCTGGAGGACTC - GCCACCTTGAG
 LynRuf_1A6 (342) TACCATGATTGTTACCGACACATATCTTCGCCAACCCTGCTAGAGCCTCCTGGAGGACTC - GCCACCTTGAG
 ParTem_1A6 (342) TACCATGATTGTTACCGACACGTACTTCGCCAACCCTGCTAGAGCCTCCTGGAGGACTC - GCCACCTTGAG
 PumCon_1A6 (342) TACCATGATTGTTACCGAC - - - ACTTCGCCAACCCTGCTAGAGCCTCCTGGAGGACTC - GCCACCTTGAG
 PumCo2_1A6 (342) TACCATGATTGTTACCGAC - - - ACTTCGCCAACCCTGCTAGAGCCTCCTGGAGGACTC - GCCACCTTGAG
 FelCat_1A6 (342) TACCATGATTGTTACCGACACGTACTTCGCCAACCCTGCTAGAGCCTCCTGGAGGACTC - GCCACCTTGAG
 PriBen_1A6 (342) TACCATGATTGTTACCGACACGTACTTCGCCAACCCTGCTAGAGCCTCCTGGAGGACTC - GCCACCTTGAG
 CarAur_1A6 (342) TACCATGATTGTTACCGACACGTACTTCGCCAACCCTGCTAGAGCCTCCTGGAGGACTC - GCCACCTTGAG
 CarSer_1A6 (342) TACCATGATCGTTACCNACACGTACTTCGCCGACCGCTAGAGCCTCCTGGAGGACTC - GCCACCTTGAG
 CroCro_1A6 (342) TAGCATGATTATCTTGACATGTGGTTACCAACTGCCAGAGCCTCCTGGGGGACTC - CGCCACCCGTGAG
 ParBru_1A6 (342) TAGCATGATTATCCTTGACATGTGGTTACCAACTGCCAGAGCCTCCTGGGGGACTC - CGCCACCCGTGAG
 ProCri_1A6 (151) TAGCATGATTATCTTGACATGTGGTTACCAACTGCCAGAGCCTCCTGGGGGACTC - CACAACCCGTGAG
 HyaHya_1A6 (342) TAGCATGATTATCCTTGACATGTGGTTACCAACTGCCAGAGCCTCCTGGGGGACTC - CGCCACCCGTGAG
 BosTau_1A6 (333) CAACATGATTGTCATCAATATGTACTTTCAACTGCCAGAGTCTCCTGAGGCCTC - AGACACCCGTGCG
 OviAri_1A6 (339) CAACATGATCGTCATCAACATGTACTTTCTCAACTGCCAGAGTCTCCTGAGGCCTC - GGGAAACCCGTGCG
 SusScr_1A6 (342) TAACATGATTGTGATCAACATGTATTTCTCACCCTGCCAGAGCCTCCTGAGGGAGCG - CGCCACCCGTGAG
 MusMus_1A6a (342) CAACATGATTGTCGTGGACATGTTCTTTTCAACTGCCAGAGCCTCCTGAAGGACTC - TGCCACCCGTGAG
 MusMus_1A6b (342) AGCATGCTTTTACATTTGGAGATGTTCTTTTCAACTGCCAGAGCCTCCTGAAGGACTC - TGCCACCCGTGAG
 RatNor_1A6 (339) CAACATGATTGTGATGACATGTGCTTTTCAAGTGCCAGAGCCTCCTGAAGGACTC - GGCCACCCGTGAG
 OryCun_1A6 (342) TAACATGGTTGTGATTGACATGTACTTCATCAACTGCCAGAGCCTGCTGAGACACGG - CGACACCTTGAG

M2: bp379-381

M3: bp399

M7: bp361-364

EquCab_1A6a (342) TAACATGATCGTTATCAACATGTACTTCACCAACTGCCAGAGCCTCCTGAACCACTC - TGAGACCCTGAG
 EquCab_1A6b (342) TACCATGATCGTTATCCACATGTACTTCACCAACTGCCAGAGCCTCCTGAACCACTC - TGAGACCCTGAG
 EquCab_1A6c (342) TACCATGGTGTTATGGAGCTGTGCTTCTTCAACTGCCAGAGCCTCCTGAACCACTC - TGAGACCCTGAG
 MusNig_1A6 (330) TAGCATGATTGTTATTGACATGTATTTACCACCTGCCAGAGCCTCCTGGAGGACAC - AGCCACCCTGTG
 MusPut_1A6 (330) TAGCATGATTGTTATTGACATGTATTTACCACCTGCCAGAGCCTCCTGGAGGACAC - AGCCACCCTGAG
 MirAng_1A6 (330) TAGCATGATGGTTATTGACATGTACTTCACCAACTGCCAGAGCCTCCTGGAGGACCC - GGGCACCCTGAG
 PhoVit_1A6 (330) TAGCATGATGGTTATTGACATGTACTTCACCAACTGCCAGAGCCTCCTGGAGGACTC - GGGCACCCTGAG
 UrsMar_1A6 (230) TAACATGATTGTTATTGACATGTACTTCACCAACTGCCAGAGCCTCCTGGAGGACGC - GGGCACCCTGAG
 UrsThi_1A6 (229) TAACATGATTGTTATTGACATGTACTTCACCAACTGCCAGAGCCTCCTGGAGGACGC - GGGCACCCTGAG
 ProLot_1A6 (186) CAACATGATCGGTATTGACATGTACTTCACCAACTGCCAGAGCCTCCTGGAGGACTC - GGGCACCCTGAG
 CanFam_1A6 (330) TAGCATGATTGTTATTGACATGTACTTCACCAACTGCCAGAGCCTCCTGGAGGACTC - GGGCACCCTGAG
 CanRuf_1A6 (229) TAGCATGATTGTTATTGACATGTACTTCACCAACTGCCAGAGCCTCCTGGAGGACTC - GGGCACCCTGAG
 ChrBra_1A6 (229) TAGCATGATTGTTATTGACATGTACTTCACCAACTGCCAGAGCCTCCTGGAGGACTC - GGGCACCCTGAG
 VulVul_1A6 (231) TAACATGATTGTTATTGACATGTACTTCACCAACTGCCAGAGCCTCCTGGAGGACTC - GGGCACCCTGAG
 AilFul_1A6 (170) TAACATGATCGTTATTGACATGTATTTACCACCTGCCAGAGCCTCCTGGAGGACTT - GGGCACCCTGAG
 ArcBin_1A6 (342) CACCATGATTATTTCTGGACATGTGTTTACCAGCTGCCAGAGCCTCCTGGAGGACTC - CGCCACCCTGAG
 CivCiv_1A6 (152) CACCATGATTGTTCTTGGACATGTATTTACCACCTGCCAGAGCCTCCTGGAGGACTC - CGCCACCCTGAG
 HerJav_1A6 (342) TACCATGATTGTTATTGACATGTACTTCACCAACTGCCAGAGCCTCCTGGAGGACCC - CGCCACCCTGAG
 GalGal_1A6 (351) CATTATAGAAATTTCCAGGTTTTTTTACCACCTGTGAGAGCCTGTTGCACAAAC - AGAAATGATGCA

M11: bp398-399

421
 HomSap_1A6 (411) CTTCTTTAAGGAGAGCAAGTTTGATGCTCTTTTACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCT
 PanTro_1A6 (411) CTTCTTTAAGGAGAGCAAGTTTGATGCTCTTTTACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCT
 PanAbe_1A6 (411) CTTCTCAAGGAGAGCAAGTTTCGATGCTCTTTTACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCT
 PapAnu_1A6 (411) CTTCTCAAGGAGAGCAAGTTTCGATGCTCTTTTACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCT
 MacFas_1A6 (411) CTTCTCAAGGAGAGCAAGTTTCGATGCTCTTTTACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCT
 Acijub_1A6 (410) TTTCTCAGGGAGAGCAAGTTTCGACACCCTCTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCA
 PanTig_1A6 (310) TTTCTCAGGGAGAGCAAGTTTCGACACCCTCTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCA
 PanOnc_1A6 (310) TTTCTCAGGGAGAGCAAGTTTCGACACCCTCTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCA
 PanUnc_1A6 (310) TTTCTCAGGGAGAGCAAGTTTCGACACCCTCTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCA
 PanLeo_1A6 (310) TTTCTCAGGGAGAGCAAGTTTCGACACCCTCTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCA
 PanPar_1A6 (310) TTTCTCAGGGAGAGCAAGTTTCGACACCCTCTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCA
 LeoGeo_1A6 (410) TTTCTCAGGGAGAGCAAGTTTCGACACCCTCTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCA
 LeoTig_1A6 (410) TTTCTCAGGGAGAGCAAGTTTCGACACCCTCTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCA
 LeoWie_1A6 (410) TTTCTCAGGGAGAGCAAGTTTCGACACCCTCTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCA
 LynCan_1A6 (410) TTTCTCAGGGAGAGCAAGTTTCGACACCCTCTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCA
 LynRuf_1A6 (410) TTTCTCAGGGAGAGCAAGTTTCGACACCCTCTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCA
 ParTem_1A6 (410) TTTCTCAGGGAGAGCAAGTTTCGACACCCTCTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCA
 PumCon_1A6 (406) TTTCTCAGGGAGAGCAAGTTTCGACACCCTCTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCA
 PumCo2_1A6 (406) TTTCTCAGGGAGAGCAAGTTTCGACACCCTCTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCA
 FelCat_1A6 (410) TTTCTCAGGGAGAGCAAGTTTCGACACCCTCTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCA
 PriBen_1A6 (410) TTTCTCAGGGAGAGCAAGTTTCGACACCCTCTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCA
 CarAur_1A6 (410) TTTCTCAGGGAGAGCAAGTTTCGACACCCTCTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCA
 CarSer_1A6 (410) TTTCTCAGGGAGAGCAAGTTTCGACACCCTCTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCA
 CroCro_1A6 (411) TTTCTCAGGGAGAGCAAGTTTCGACACCCTCTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCA
 ParBru_1A6 (411) CTTCTCAAGGAGAGCAAAATTCGATGCTCTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCA
 ProCri_1A6 (220) TTTCTCAGGGAGAGCAAAATTCGACATCCTCTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCA
 Hyahya_1A6 (411) CTTCTCAAGGAGAGCAAAATTCGATGCTCTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCA
 BosTau_1A6 (402) CTTCTCCGGGAGAGCAAGTTTCGACGCCCTGTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCC
 OviAri_1A6 (408) CTTCTCCGGGAGAGCAAGTTTCGATGCCCTGTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCC
 SusScr_1A6 (411) CTTCTCCGGGAGGCAAGTTTCGATGCCCTGTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCC
 MusMus_1A6a (411) CTTCTCAGGGAGAGCAAGTTTGATGCTCTGTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCT
 MusMus_1A6b (411) CTTCTCAGGGAGAGCAAGTTTGATGCTCTGTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCT
 RatNor_1A6 (408) CTTCTCAGGGAGAGCAAGTTTGATGCTCTGTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCT
 OryCun_1A6 (411) TTTCTCAGGGAGAGCAAGTTTCGATGCCCTTTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCT
 EquCab_1A6a (411) CTTCTCAGGGAGAGCAAGTTTCGATGCCCTTTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCT
 EquCab_1A6b (411) CTTCTCAGGGAGAGCAAGTTTCGATGCCCTTTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCT
 EquCab_1A6c (411) TTTCTCAGGGAGAGCAAGTTTCGATGCCCTTTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCT
 MusNig_1A6 (399) TCTCTCAGGGAGAGCAAGTTTCGATGCCCTTTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCT
 MusPut_1A6 (399) TGTCTCAGGGAGAGCAAGTTTCGATGCCCTTTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCT
 MirAng_1A6 (400) TGTCTCAGGGAGAGCAAGTTTCGATGCCCTTTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCT
 PhoVit_1A6 (399) TGTCTCAGGGAGAGCAAGTTTCGATGCCCTTTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCT
 UrsMar_1A6 (299) CGTCTCCGGAAGAGCAAGTTTCGATGCCCTTTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCT
 UrsThi_1A6 (298) CGTCTCCGGAAGAGCAAGTTTCGATGCCCTTTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCT
 ProLot_1A6 (255) CGTCTCAGGGAGAGCAAGTTTCGATGCCCTTTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCT
 CanFam_1A6 (399) TGTCTCAGGCAGAGCAAGTTTCGATGCCCTTTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCT
 CanRuf_1A6 (298) TGTCTCAGGCAGAGCAAGTTTCGATGCCCTTTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCT
 ChrBra_1A6 (298) TGTCTCAGGCAGAGCAAGTTTCGATGCCCTTTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCT
 VulVul_1A6 (300) TGTCTCAGGCAGAGCAAGTTTCGATGCCCTTTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCT
 AilFul_1A6 (239) TGTCTCAGGGAGAGCAAGTTTCGATGCCCTTTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCT
 ArcBin_1A6 (411) TTTCTCAGGGAGAGCAAGTTTCGACGCCCTCTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCA
 CivCiv_1A6 (221) TTTCTCAGGGAGAGCAAGTTTCGACGCCCTCTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCA
 HerJav_1A6 (411) CTTCTCCGGGAGAGCAAGTTTCGACGCCCTCTTTCACAGACCCAGCCTTACCCTGTGGGGTGATCCTGGCT
 GalGal_1A6 (420) GTATTTGAGAAAGAGCAAAATTTGACGTTGTTTTCACAGATCCAATTCGATGTGTGGAGCAATACTTGCT

491
 HomSap_1A6 (481) GAGTATTTGGGCTACCATCTGTGTACCTCTTCAGGGGTTTTCCGTGTTCCCTGGAGCATACATTACGCA
 PanTro_1A6 (481) GAGTATTTGGGCTACCATCTGTGTACCTCTTCAGGGGTTTTCCGTGTTCCCTGGAGCATACATTACGCA

560

PonAbe_1A6 (481) GAGTATTTGGGCTACCTCCGTGTACCTCTTCAGGGGTTTTCCGTGTTCCCTCGAGCATACATTACGCA
PapAnu_1A6 (481) GAGTATTTGGGCTACCTCCGTGTACCTCTTCAGGGGTTTTCCGTGTTCCCTGGAGCATACATTACGCA
MacFas_1A6 (481) GAGTATTTGGGCTACCTCCGTGTACCTCTTCAGGGGTTTTCCGTGTTCCCTGGAGCATACATTACGCA
AciJub_1A6 (480) GAGTACCTAGGCTGCCCTCCATGTATCTCTTCAGGGGCTTCCACGCTCCCTGGGGCAGCGATACGCC
PanTig_1A6 (380) GAGTACCTAGGCTGCCCTCCATGTATCTCTTCAGGGGCTTCCACGCTCCCTGGGGCAGCGATACGCC
PanOnc_1A6 (380) GAGTACCTAGGCTGCCCTCCATGTATCTCTTCAGGGGCTTCCACGCTCCCTGGGGCAGCGATACGCC
PanUnc_1A6 (380) GAGTACCTAGGCTGCCCTCCATGTATCTCTTCAGGGGCTTCCACGCTCCCTGGGGCAGCGATACGCC
PanLeo_1A6 (380) GAGTACCTAGGCTGCCCTCCATGTATCTCTTCAGGGGCTTCCACGCTCCCTGGGGCAGCGATACGCC
PanPar_1A6 (380) GAGTACCTAGGCTGCCCTCCATGTATCTCTTCAGGGGCTTCCACGCTCCCTGGGGCAGCGATACGCC
LeoGeo_1A6 (480) GAGTACCTAGGCTGCCCTCCATGTATCTCTTCAGGGGCTTCCACGCTCCCTGGGGCAGCGATACGCC
LeoTig_1A6 (480) GAGTACCTAGGCTGCCCTCCATGTATCTCTTCAGGGGCTTCCACGCTCCCTGGGGCAGCGATACGCC
LeoWie_1A6 (480) GAGTACCTAGGCTGCCCTCCATGTATCTCTTCAGGGGCTTCCATGCTCCCTGGGGCAGCGATACGCC
LynCan_1A6 (480) GAGTACCTAGGCTGCCCTCCATGTATCTTTTCAGGGGCTTCCACGCTCCCTGGGGCAGCGATACGCC
LynRuf_1A6 (480) GAGTACCTAGGCTGCCCTCCATGTATCTTTTCAGGGGCTTCCACGCTCCCTGGGGCAGCGATACGCC
ParTem_1A6 (480) GAGTACCTAGGCTGCCCTCCATGTATCTTTTCAGGGGCTTCCACGCTCCCTGGGGCAGCGATACGCC
PumCon_1A6 (476) GAGTACCTAGGCTGCCCTCCATGTATCTCTTCAGGGGCTTCCACGCTCCCTGGGGCAGCGATACGCC
PumCo2_1A6 (476) GAGTACCTAGGCTGCCCTCCATGTATCTCTTCAGGGGCTTCCACGCTCCCTGGGGCAGCGATACGCC
FelCat_1A6 (480) GAGTACCTAGGCTGCCCTCCATGTATCTCTTCAGGGGCTTCCACGCTCCCTGGGGCAGCGATACGCC
PriBen_1A6 (480) GAGTACCTAGGCTGCCCTCCATGTATCTCTTCAGGGGCTTCCACGCTCCCTGGGGCAGCGATACGCC
CarAur_1A6 (480) GAGTACCTAGGCTGCCCTCCATGTATCTCTTCAGGGGCTTCCACGCTCCCTGGGGCAGCGATACGCC
CarSer_1A6 (480) GAGTACCTAGGCTGCCCTCCATGTATCTCTTCAGGGGCTTCCACGCTCCCTGGGGCAGCGATACGCC
CroCro_1A6 (481) GAGTACCTGGGCTGCCCTCCGTATATCTCTTCAGGGGCTTCCATGCTCCCTGGAGCAGCGATACGCA
ParBru_1A6 (481) GAGTACCTGGGCTGCCCTCCGTATATCTCTTCAGGGGCTTCCATGCTCCCTGGAGCAGCTGATACGCA
ParCri_1A6 (290) GAGTACCTGGGCTGCCCTCCGTATATCTCTTCAGGGGCTTCCATGCTCCCTGGAGCAGCGATACGCA
HyaHya_1A6 (481) GAGTACCTGGGCTGCCCTCCGTATATCTCTTCAGGGGCTTCCATGCTCCCTGGAGCAGCTGATACGCA
BosTau_1A6 (472) GAGTACCTGAACCTGCCCTCCGTGTATCTCTTCAGGGGCTTCCCTGTGCCCTGGAGAACACTTTACCA
OviAri_1A6 (478) GAGTACCTGAACCTGCCCTCCGTGTATCTCTTCAGGGGCTTCCCTGTGCCCTGGAGAACACTTTACCA
SusScr_1A6 (481) GAGTACCTGGGCTGCCCTCCGTGTACCTCTTCAGGGGCTTCCCTGTGCCCTGGAGAACACTTTACCA
MusMus_1A6a (481) GAGTATCTCAACCTGCCCTCTGTCTACCTCTTCAGAGGTTTCCATGCTCTCTGGAACACATGCTTGGTC
MusMus_1A6b (481) GAGTATCTCAACCTGCCCTCTGTCTACCTCTTCAGAGGTTTCCATGCTCTCTGGAACACATGCTTGGTC
RatNor_1A6 (478) GAGTATCTCAAGCTGCCCTCCATCTACCTCTTCAGAGGTTTCCATGCTCTCTGGAACACATGCTTGGTC
OryCun_1A6 (481) GAGTACCTGGGCTGCCCTCCGTGTACCTGTTTCAGGGGCTTCCCTGTTCCCTGGAGCATGGGTTTGGCG
EquCab_1A6a (481) GACTACCTGGGCTGCCCTCCGTGTACCTCTTCAGGGGCTTCCCTGTTCCCTGGAGTTTGCCTTCACTA
EquCab_1A6b (481) GAGTACCTGGGCTGCCCTCCGTGTACCTCTTCAGGGGCTTCCATGTTCCCTGGAGTATGCCTTACCA
EquCab_1A6c (481) GAGTACCTGGGCTGCCCTCTGTGTACCTCTTCAGGGGTTTCCATGTTCCCTGGAGTATGCATTACCA
MusNig_1A6 (469) GAGTACCTGGGCTGCCCTCCGTGTACCTCTTCAGGGGCTTCCATGCTCCCTGGAGCATACCATGAGCA
MusPut_1A6 (469) GAGTACCTGGGCTGCCCTCCGTGTACCTCTTCAGGGGCTTCCATGCTCCCTGGAGCATACCATGAGCA
MirAng_1A6 (470) GAGTACCTGAACCTGCCCTCCGTGTACCTCTTCAGGGGCTTCCATGCTCCCTGGAGCATATGATGAGCA
PhoVit_1A6 (469) GAGTACCTGGGCTGCCCTCCGTGTACCTCTTCAGGGGCTTCCATGCTCCCTGGAGCATATGATGAGCA
UrsMar_1A6 (369) GAGTACCTGGGCTGCCCTCCGTGTACCTCTTCAGGGGCTTCCATGCTCCCTGGAGCATACCATGAGCA
ProLot_1A6 (325) GAGTACCTGGGCTGCCCTCCGTGTACCTCTTCAGGGGTTTCCCTGCTCCCTGGAGCATGCCATGAGCA
CanFam_1A6 (469) GAGTACCTGGGCTGCCCTCCGTGTACCTCTTCAGGGGCTTCCATGCTCCCTGGAGCATACTATACGCA
CanRuf_1A6 (368) GAGTACCTGGGCTGCCCTCCGTGTACCTCTTCAGGGGCTTCCATGCTCCCTGGAGCATACTATACGCA
ChrBra_1A6 (368) GAGTACCTGGGCTGCCCTCCGTGTACCTCTTCAGGGGCTTCCATGCTCCCTGGAGCATACTATACGCA
VulVul_1A6 (370) GAGTACCTGGGCTGCCCTCCGTGTACCTCTTCAGGGGCTTCCATGCTCCCTGGAGCATACTATACGCA
AilFul_1A6 (309) GAGTACCTGGGCTGCCCTCCGTATACCTCTTCAGGGGTTTCCATGCTCCCTGGAGCATGCGATGAGCA
ArBin_1A6 (481) GAGTACCTGGGCTGCCCTCCGTGTACCTCTTCAGGGGCTTCCCTGCTCCCTGGAGCAGCGATACGCA
CivCiv_1A6 (291) GAGTACCTGGGCTGCCCTCTGTGTATCTCTTCAGGGGCTTCCATGCTCCCTGGAGCAGCGATACGCA
HerJav_1A6 (481) GAGTACCTGGGCTGCCCTCTGTGTATCTCTTCAGGGGCTTCCCTGCTCCCTGGAGCAGCGATACGCA
GalGal_1A6 (490) GATTATCTTTTCAGTTCTCTGTCTACTTCTTCGAGGATTTCCTTGTGGTATGATTCAAAGCTACCC

561

630

HomSap_1A6 (551) GAAGCCCAAGCCCTGTGTCTACATTCCAGGTTGCTACACAAAGTTTTTCAGACCACATGACTTTTTCCCA
PanTro_1A6 (551) GAAGCCCAAGCCCTGTGTCTACATTCCAGGTTGCTACACAAAGTTTTTCAGACCACATGACTTTTTCCCA
PonAbe_1A6 (551) GAAGCCCAAGCCCTGTGTCTACATTCCAGGTTGCTACACAAAGTTTTTCAGACCACATGACTTTTTCCCA
PapAnu_1A6 (551) GAAGCCCAAAACCCTGTGTCTATATTTCCAGGTTGCTACACAAAGTTTTTCAGACCACATGACTTTTTCCCA
MacFas_1A6 (551) GAAGCCCAAAACCCTGTGTCTATATTTCCAGGTTGCTACACAAAGTTTTTCAGACCACATGACTTTTTCCCA
AciJub_1A6 (550) AGAGCCCAAAACCCGATCCTACATTCCAGATGCTACACTCAGTTCTCAGACCAGGATGACCTTCCCCCA
PanTig_1A6 (450) AGAGCCCGAACCCGATCCTACATTCCAGATGCTACACTCAGTTCTCAGACCAGGATGACCTTCCCCCA
PanOnc_1A6 (450) AGAGCCCGAACCCGATCCTACATTCCAGATGCTACACTCAGTTCTCAGACCAGGATGACCTTCCCCCA
PanUnc_1A6 (450) AGAGCCCGAACCCGATCCTACATTCCAGATGCTACACTCAGTTCTCAGACCAGGATGACCTTCCCCCA
PanLeo_1A6 (450) AGAGCCCGAACCCGATCCTACATTCCAGATGCTACACTCAGTTCTCAGACCAGGATGACCTTCCCCCA
PanPar_1A6 (450) AGAGCCCGAACCCGATCCTACATTCCAGATGCTACACTCAGTTCTCAGACCAGGATGACCTTCCCCCA
LeoGeo_1A6 (550) AGAGCCCAAAACCCTGCATCCTACATTCCAGATGCTACACTCAGTTCTCAGACCAGGATGACCTTCCCCCA
LeoTig_1A6 (550) AGAGCCCAAAACCCTGCATCCTACATTCCAGATGCTACACTCAGTTCTCAGACCAGGATGACCTTCCCCCA
LeoWie_1A6 (550) AGAGCCCAAAACCCTGCATCCTACATTCCAGATGCTACACTCAGTTCTCAGACCAGGATGACCTTCCCCCA
LynCan_1A6 (550) AGAGCCCAAAACCCGATCCTACATTCCAGATGCTACACTCAGTTCTCAGACCAGGATGACCTTCCCCCA
LynRuf_1A6 (550) AGAGCCCGAACCCGATCCTACATTCCAGATGCTACACTCAGTTCTCAGACCAGGATGACCTTCCCCCA
ParTem_1A6 (550) AGAGCCCAAAACCCGATCCTACATTCCAGATGCTACACTCAGTTCTCAGACCAGGATGACCTTCCCCCA
PumCon_1A6 (546) AGAGCCCAAAACCCGATCCTACATTCCAGATGCTATACTCAGTTCTCAGACCAGGATGACCTTCCCCCA
PumCo2_1A6 (546) AGAGCCCAAAACCCTGCATCCTACATTCCAGATGCTATACTCAGTTCTCAGACCAGGATGACCTTCCCCCA
FelCat_1A6 (550) AGAGCCCAAAACCCGATCCTACATTCCAGATGCTACACTCAGTTCTCAGACCAGGATGACCTTCCCCCA
PriBen_1A6 (550) AGAGCCCAAAACCCGATCCTACATTCCAGATGCTACACTCAGTTCTCAGACCAGGATGACCTTCCCCCA
CarAur_1A6 (550) AGAGCCCAAAACCCGATCCTACATTCCAGATGCTACACTCAGTTCTCAGACCAGGATGACCTTCCCCCA
CarSer_1A6 (550) AGAGCCCAAAACCCGATCCTACATTCCAGATGCTACACTCAGTTCTCAGACCAGGATGACCTTCCCCCA
CroCro_1A6 (551) GAAGCCCAAAACCCTGGGTCCTACATTCCAGATGCTACACTCAGTTCTCAGACCAGGATGACCTTCCCCCA
ParBru_1A6 (551) GAAGCCCAAAACCCTGGGTCCTACATTCCAGATGCTACACTCAGTTCTCAGACCAGGATGACCTTCCCCCA

ProCri_1A6 (360) GAAGCCCAAACCTGGGTCTACATTTCCAGATGCTACACTCAGTTCTCAGACCGGATGACCTTCCCCCA
HyaHya_1A6 (551) GAAGCCCAAACCTGGGTCTACATTTCCAGATGCTACACTCAGTTCTCAGACCGGATGACCTTCCCCCA
BosTau_1A6 (542) GGACTCCGAGCCCTTGTCTACGTCCAGGTACTACACTCAGTTCTCAGACCAAGATGACCTTCCCTCCA
OviAri_1A6 (548) GGACTCCAAGCCCTTGTCTACGTCCCAAGGTACTACACTCAGTTTTCAGACAAGATGACCTTCCCTCCA
SusScr_1A6 (551) GGACCCCAAGCCCCACGTCTACGTCCCAAGGTACTACACTCGCTTCTCCGACCGGATGACCTTCCCCCA
MusMus_1A6a (551) AAAGCCCAAGCCCTGTGTCTATGTGCCAGATTCTACACAAATTCAGACCACATGACGTTTCCCCCA
MusMus_1A6b (551) AAAGCCCAAGCCCTGTGTCTATGTGCCAGATTCTACACAAATTCAGACCACATGACGTTTCCCCCA
RatNor_1A6 (548) AAAGCCCAAGCCCGTATCCTATGTTCCAGATTCTACACAAATTCAGACCACATGACATTTCCCCCA
OryCun_1A6 (551) GAAGCCCAACCCGGTGTCTACATCCCCCGGTGCTACACAAAGTTCTCCGACCGATGAGCTTCCCCCA
EquCab_1A6a (551) GAAGTCCAAACCCGGTGTCTACGTTCACATGCTACACCAAGTTCTCAGACCAGATGACATTTCCCCCA
EquCab_1A6b (551) GAAGCCCAACCCGGTGTCTACACTCCAGGTGCTACACCAAGTTCTCAGACAGGATGATTTTCCCCCA
EquCab_1A6c (551) GAAGCCCAACCCAGTGTCTACACTCCAGGTGCTATACCAAGTTCTCAGACAGGATGACATTTCCCCCA
MusNig_1A6 (539) GAAGCCCAACCCGTGTGTCCACATTCACAGATGCTACACTCAGTTCTCAGACCAGATGACGTTCCCCCA
MusPut_1A6 (539) GAAGCCCAACCCGTGTGTCCACATTCACAGATGCTACACTCAGTTCTCAGACCAGATGACGTTCCCCCA
MirAng_1A6 (540) GGAGCCCAACCCGTGTGTCCATATTCACAGATGCTACACTCAGTTCTCAGACCAGATGACGTTCCCCCA
PhoVit_1A6 (539) GGAGCCCAACCCGTGTGTCCACATTCACAGTGTCTACACTCAGTTCTCAGACCAGATGACGTTCCCCCA
UrsMar_1A6 (439) GGAGCCCGAACCCCGTGTCTACATTCACAGATGCTACACTCAGTTCTCAAACCGGATGACATTTCCCCCA
UrsThi_1A6 (438) GGAGCCCGAACCCCGTGTCTACATTCACAGATGCTACACTCAGTTCTCAAACCGGATGACATTTCCCCCA
ProLot_1A6 (395) GGACCCCGAACCCCGTGTCTACATTCACAGATGCTACACTCAGTTCTCAAACCGGATGACGTTCCCCCA
CanFam_1A6 (539) GGAGCCCAACCCGTGTGTCCATTCACAGGTGCTATACTCAGTTCTCAGACAAGATGACATTTCCCCCA
CanRuf_1A6 (438) GGAGCCCAACCCGTGTGTCTACATTCACAGGTGCTATACTCAGTTCTCAGACAAGATGACATTTCCCCCA
ChrBra_1A6 (438) GGAGCCCAACCCGTGTGTCTACATTCACAGGTGCTATACTCAGTTCTCAGACAAGATGACATTTCTCTCA
VulVul_1A6 (440) GGAGCCCAACCCGTGTGTCTACATTCACAGGTGCTATACTCAGTTCTCAGACAAGATGACATTTCCCCCA
AilFul_1A6 (379) GGAGTCCAAACCCCGTGTCTACAGATGCTACACTCAGTTCTCAGACCAGATGACGTTCCCCCA
ArcBin_1A6 (551) GGAGCCCAACCCGTGTGTCTACGTTCACAGATGCTACACTAAGTTCTCAGACCGGATGACCTTCCCCCA
CivCiv_1A6 (361) GGAGCCCAACCCGTGTGTCCACATTCACAGGTGCTACACTCAGTTCTCAGACCGGATGACCTTCCCCCA
HerJav_1A6 (551) GGAGCCCAACCCGTGTGTCTACAGATGCTACACTCAGTTCTCAGACCAGGATGACCTTCCCCCA
GalGal_1A6 (560) AGTGTCCAAGCCCTCTTCTTATGTTCCAGGCTCTTCTCTAAATAATTGATAGCATGACATTTGCTCA

631 700
HomSap_1A6 (621) ACGAGTGGCCAACCTCCTGTGTAATTTGTTGGAGCCCTATCTATTTTATTGTCTGTTTTCAAAGTATGAA
PanTro_1A6 (621) ACGAGTGGCCAACCTCCTGTGTAATTTGTTGGAGCCCTATCTATTTTATTGTCTGTTTTCAAAGTATGAA
PonAbe_1A6 (621) ACGAGTGGCCAACCTCCTGTGTAATTTGTTGGAGCCATATCTATTTTATTGTCTGTTTTCAAAGTATGAA
PapAnu_1A6 (621) ACGAGTGGCCAACCTCCTCGTTAATTTGTTGGAGCCCTATCTATTTTATTGTCTGTTTTCAAAGTACGAC
MacFas_1A6 (621) ACGAGTGGCCAACCTCCTCGTTAATTTGTTGGAGCCCTATCTATTTTATTGTCTGTTTTCAAAGTACGAT
AciJub_1A6 (620) ACGGGTGGCCAACCTACCTCGTTCTGTTACTTGGAGACCTA ----- CCTTTGTATTCAAAGTATGAA
PanTig_1A6 (519) ACGGGTGGCCAACCTACCTCGTTCTTACTTGGAGACCTA ----- CCTTCGTATTCAAAGTATGAA
PanOnc_1A6 (520) ACGGGTGGCCAACCTACCTCGTTCTTACTTGGAGACCTA ----- CCTTCGTATTCAAAGTATGAA
PanUnc_1A6 (520) ACGGGTGGCCAACCTACCTCGTTCTTACTTGGAGACCTA ----- CCTTCGTATTCAAAGTATGAA
PanLeo_1A6 (520) ACGGGTGGCCAACCTACCTCGTTCTTACTTGGAGACCTA ----- CCTTCATATTCAAAGTATGAA
PanPar_1A6 (520) ACGGGTGGCCAACCTACCTCGTTCTTACTTGGAGACCTA ----- CCTTCGTATTCAAAGTATGAA
LeoGeo_1A6 (620) ACGGGTGGCCAACCTACCTCGTTCTTACTTGGAGACCTA ----- CCTTCGTATTCAAAGTATGAA
LeoTig_1A6 (620) ACGGGTGGCCAACCTACCTCGTTCTTACTTGGAGACCTA ----- CCTTCGTATTCAAAGTATGAA
LeoWie_1A6 (620) ACGGGTGGCCAACCTACCTCGTTCTTACTTGGAGACCTA ----- CCTTCGTATTCAAAGTATGAA
LynCan_1A6 (620) ATGGGTGGCCAACCTACCTCGTTCTTACTTGGAGACCTA ----- CCTTCGTATTCAAAGTATGAA
LynRuf_1A6 (620) GTGGGTGGCCAACCTACCTCGTTCTTACTTGGAGACCTA ----- CCTTCGTATTCAAAGTATGAA
ParTem_1A6 (620) ACGGGTGGCCAACCTATCTGTTCCTTACTTGGAGACCTA ----- CCTTCGTATTCAAAGTATGAA
PumCon_1A6 (616) ACGGGTGGCCAACCTACCTCGTTCTGTTACTTGGAGGCTA ----- CCTTCGTATTCAAAGTATGAA
PumCo2_1A6 (616) ACGGGTGGCCAACCTACCTCGTTCTGTTACTTGGAGGCTA ----- CCTTCGTATTCAAAGTATGAA
FelCat_1A6 (620) ACGGGTGGCCAACCTACCTCGTTCTGTTACTTGGAGACCTA ----- CCTTCGTATTCAAAGTATGAA
PriBen_1A6 (620) ACGGGTGGCCAACCTACCTCGTTCTGTTACTTGGAGACCTA ----- CCTTCGTATTCAAAGTATGAA
CarAur_1A6 (620) ACGGGTGGCCAACCTCCCTCGTTCTTACTTGGAGACCTA ----- CCTTCGTATTCAAAGTATGAA
CarSer_1A6 (620) ACGGGTGGCCAACCTCCCTCGTTCTTACTTGGAGACCTA ----- CCTTCGTATTCAAAGTATGAA
CroCro_1A6 (621) ACGGGTGGCCAACCTACCTCGTTAGTTACTTGGAGACCTATTTATTCTACCTTCTGTATTCAAAGTATGAA
ParBru_1A6 (621) ACGGGTGGCCAACCTACCTCGTTAGTTACTTGGAGACCTATTTATTCTACCTTCTATATTCAAAGTATGAA
ProCri_1A6 (430) ACGGGTGGTCAACTACCTCGTTAGTTACTTGGAGACCTATTTATTCTACCTTCTGTATTCAAAGTACGAA
HyaHya_1A6 (621) ACGGGTGGCCAACCTACCTCGTTAGTTACTTGGAGACCTATTTATTCTACCTTCTATATTCAAAGTATGAA
BosTau_1A6 (612) AAGGGTGGGCAATTCCTGGTGAACCTACCTGGAGAACATTCTGCTCTACGCGTGTATTCAAAGTACGAA
OviAri_1A6 (618) AAGGGTGGGCAACTTCCTGGTGAATACCTGGAGAACATTTTGTCTATGCGCTGTATTCAAAGTACGAA
SusScr_1A6 (621) ACGGGTGGGCAACTTCCTTACTAGGATCTTGGAGAATATCCTCCTTGACCTGTGTATTAAGTACGAA
MusMus_1A6a (621) ACGGGTGGGCAACTTCATTGTTAAACATCTTGGAAAACCTACCTATATTATTGTCTGTATTCAAAGTATGAA
MusMus_1A6b (621) ACGGGTGGGCAACTTCATTGTTAAACATCTTGGAAAACCTACCTATATTATTGTCTGTATTCAAAGTATGAA
RatNor_1A6 (618) ACGGGTGGGCAACTTCATTGTTAAACATCTTGGAGAACCTACCTTTATCATTGTCTGTACTCAAAGTATGAG
OryCun_1A6 (621) GCGCGTGGTCAACTTCCTCGTTAACTTGTGGAGGTCCCTCTATTTTACTGTCTGTATTCAAAGTATGAG
EquCab_1A6a (621) ACGTGTGGGCAACTTCCTCGTTAATTACTTGAAGGACTACCTATTTTACTGTCTGTATTCAAAGTATGAA
EquCab_1A6b (621) ACGTGTGGGCAACTTCCTCGTTAATTACTTGGAGGACTACCTATTTTACTGTCTGTATTCAAAGTATGAA
EquCab_1A6c (621) ACGTGTGGGCAACTTCCTCGTTAATTACTTGGAGAACTCCTATTTTACTGTCTGTATTCAAAGTATGAA
MusNig_1A6 (609) ACGGGTGGGCAACTACCTCGTTAATTACTTGGAGACCTATCTGTTCCACTGTCTGTACTCGAAGTACGAA
MusPut_1A6 (609) ACGGGTGGGCAACTACCTCGTTAATTACTTGGAGACCTATCTGTTCCACTGTCTGTACTCGAAGTACGAA
MirAng_1A6 (610) ACGGGTGGGCAACTACCTCGTTAATTACTTGGAGACCTATCTGTTCAAAGTATGAA
PhoVit_1A6 (609) ACGGGTGGGCAACTACCTCGTTAATTCTTGGAGACCTATCTGTTCTGCTGCTGTATTCAAAGTATGAA
UrsMar_1A6 (509) AAGGGTGGGCAACTACCTCGTTAATTACTTGGAGACCTATCTGTTCTACTGTCTGTATTCAAAGTATGAA
UrsThi_1A6 (508) AAGGGTGGGCAACTACCTCGTTAATTACTTGGAGACCTATCTGTTCTACTGTCTGTATTCAAAGTATGAA
ProLot_1A6 (465) ACGGGTGGGCAACTACCTGTTAATTACTTGGAGACCTATCTGTTCCACTGTCTGTACTCAAAGTACGAA
CanFam_1A6 (609) ACGGGTGGGCAACTACCTCGTTAATTACTTGGAGACCTACCTGTTCTACTGTCTGTATTCAAAGTACGAA
CanRuf_1A6 (508) ACGGGTGGGCAACTACCTGTTAATTACTTGGAGACCTACCTGTTCTACTGTCTGTATTCAAAGTACGAA
ChrBra_1A6 (508) ACGGGTGGGCAACTACCTCGTTAATTACTTGGAGACCTACCTGTTCTACTGTCTGTATTCAAAGTACGAA
VulVul_1A6 (510) ACGGGTGGGCAACTACCTCGTTAATTACTTGGAGACCTACCTGTTCTACTGTCTGTATTCAAAGTACGAA

M4: bp660-669

M12: bp667-669

AilFul_1A6 (449) ACGGGTGGCCAACCTCCTCGTTAATTACTTAGAGACCTACCTGTTCTACTGTCTGACTCAAAGTACGAA
 ArcBin_1A6 (621) GCGGGTGGCCAACCTACCTCGTTAATAACTTGGAGACCTATATATCCACCTTCTGTATTCAAAGTATGAA
 CivCiv_1A6 (431) GCGGGTGGCCAACCTACCTCGTTAATAACTTGGAGACCTATATATTTTACCTTCTGTATTCAAAGTATGAA
 HerJav_1A6 (621) ACGGGTGGCCAACCTACCTGTTAGTTACTTGGAGACCTACATATTCTACCTTCTGTATTCAAAGTATGAA
 GalGal_1A6 (630) ACGCATGAAAAACATGCTGGTCAGTATACTGGAGCTTGTCTTACTGTGACGCTTTTACTACTCAGTTTGAA

701

770

HomSap_1A6 (691) --GAACCTCGCATCAGCTGTCCTCAAGAGAGATGTGGATATAATCACCTTATATCAGAAGGTCTCTGTTTG
 PanTro_1A6 (691) --GAACCTCGCATCAGCTGTCCTCAAGAGAGATGTGGATATAATCACCTTATATCAGAAGGTCTCTGTTTG
 PonAbe_1A6 (691) --GAACCTGTCATCAGCTGTCCTCAAGAGAGATGTGGATATAATCACCTTATATCAGAAGGTCTCTATTTTG
 PapAnu_1A6 (691) --GAACCTGTCATCAGCTGTCCTCAAGAGAGATGTGGATGTAATCACCTTGTATCAGAAGGTCTCTGTTTG
 MacFas_1A6 (691) --GAACCTGTCATCAGCTGTCCTCAAGAGAGATGTGGATGTAATCACCTTATATCAGAAGGTCTCTGTTTG
 AciJub_1A6 (680) --GACCTTGTCATCCAATATCCTCAAGAGAGATGTGCNCTTACCCACCTTGTATCGGAAGGGCTCCGCTG
 PanTig_1A6 (579) --GACCTGTCATCCAATATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCGCTG
 PanOnc_1A6 (580) --GACCTGTCATCCAATATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCGCTG
 PanUnc_1A6 (580) --GACCTGTCATCCAATATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCGCTG
 PanLeo_1A6 (580) --GACCTGTCATCCAATATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCGCTG
 PanPar_1A6 (580) --GACCTGTCATCCAATATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCGCTG
 LeoGeo_1A6 (680) --GACCTGTCATCCAATATCCTCAAGAGAGATGTGCACCTTACTCGCCTTGTATCGGAAGGGCTCCGCTG
 LeoTig_1A6 (680) --GACCTGTCATCCAATATCCTCAAGAGAGATGTGCACCTTACTCGCCTTGTATCGGAAGGGCTCCGCTG
 LeoWie_1A6 (680) --GACCTGTCATCCAATATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCGCTG
 LynCan_1A6 (680) --GACCTGTCATCCAATATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCGCTG
 LynRuf_1A6 (680) --GACCTGTCATCCAATATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCGCTG
 ParTem_1A6 (680) --GACCTGTCATCCAATATCCTCAAGAGAGATGTGCACCTTATCCACCTTGTATCGGAAGGGCTCCATTTG
 PumCon_1A6 (676) --GACCTGTCATCCAATATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCGCTG
 PumCo2_1A6 (676) --GACCTGTCATCCAATATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCGCTG
 FelCat_1A6 (680) --GGCCTTGTCATCCAATATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCGCTG
 PriBen_1A6 (680) --GGCCTTGTCATCCAATATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCGCTG
 CarAur_1A6 (680) --GACCTGTCATCCAATATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCGCTG
 CarSer_1A6 (680) **TG**GACCTGTCATCCAATATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCGCTG **M8: bp691-692**
 CroCro_1A6 (691) --GACCTGTCATCCAATATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCATTTG
 ParBru_1A6 (691) --GACCTGTCATCCAATATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCATTTG
 ProCri_1A6 (500) --GACCTGTCATCCAATATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCATTTG
 Hyahya_1A6 (691) --GACCTGTCATCCAATATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCATTTG
 BosTau_1A6 (682) --GACCTGGCAGGGGAAGTCTTGGGAGACAGGTGCACCTTGCCGGCCTTGTATCGGAAGGGCTCCATTTG
 OviAri_1A6 (688) --GACCTGGCAGGGGAAGTCTTGGGAGACAGGTGCACCTTGCCGGCCTTGTATCGGAAGGGCTCCATTTG
 SusScr_1A6 (691) --GACCTGTCATCCAATATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCATTTG
 MusMus_1A6a (691) --ATCATTGCTCAGACCTCCTCAAGAGAGATGTGCCCTACCTTCTTACACACAGAA--TTCTCTGTG
 MusMus_1A6b (691) --ATCATTGCTCAGACCTCCTCAAGAGAGATGTGCCCTACCTTCTTACACACAGAA--TTCTCTGTG
 RatNor_1A6 (688) --ATCCTTGCTCAGACCTCCTCAAGAGAGATGTGCCCTACCTTCTTACACACAGAA--TTCTCTGTG
 OryCun_1A6 (691) --GACCTGGCAGTGAAGTCTCCTCAAGAGAGATGTGCACCTTACCCACCTTATTCGAAGGGCTCCGCTG
 EquCab_1A6a (691) --GACCTCACATGGAATGTTCTCAAGAGAGATGTGCACCTTACCCAGCTTATATCGGAAGGGCTCCATTTG
 EquCab_1A6b (691) --GACCTTGTCATGGAATCTTCTCAAGAGAGATGTGCACCTTACCTGCTTATATCAGAAGGGCTCCATTTG
 EquCab_1A6c (691) --GAACCTGTCATCATATCCTCAAGAGAGATGTGCACCTTACCCGCTTATATCAGAAGGGCTCCATTTG
 MusNig_1A6 (679) --GACCTCGCTCCAACATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCATTTG
 MusPut_1A6 (679) --GACCTCGCTCCAACATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCATTTG
 MirAng_1A6 (680) --GACCTCCCTCCAATATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCGTTTG
 PhoVit_1A6 (679) --GACCTCACCTCCAATATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCATTTG
 UrsMar_1A6 (579) --GACCTTGCTCCAACATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCATTTG
 UrsThi_1A6 (578) --GACCTTGCTCCAACATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCATTTG
 ProLot_1A6 (535) --GACCTGCTCCGTCATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCATTTG
 CanFam_1A6 (679) --GACCTTGTCATCCAATATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCATTTG
 CanRuf_1A6 (578) --GACCTTGTCATCCAATATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCATTTG
 ChrBra_1A6 (578) --GACCTTGTCATCCAATATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCATTTG
 VulVul_1A6 (580) --GACCTTGTCATCCAATATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCATTTG
 AilFul_1A6 (519) --GACCTGCTCCAATATCCTCAAGAGAGATGTGCACCTTACCCACCTTGTATCGGAAGGGCTCCGCTG
 ArcBin_1A6 (691) --GACCTGTCATCCAATATGCTCAAGAGAGATGTGCACCTTGCCACCTTGTATCGGAAGGGCTCCCTTTG
 CivCiv_1A6 (501) --GACCTGTCATCCAATATCCTCAAGAGAGATGTGACTTACCCGCTTGTATCGGAAGGGCTCCCTTTG
 HerJav_1A6 (691) --GACCTGTCATCCAATATCCTCAAGAGAGATGTGGACTTACCCACCTTGTATCGGAAGGGCTCCATTTG
 GalGal_1A6 (700) --GAACCTGTCATATGAGATTTTGCAAAAGAAAGTGACAGCTACAGACCTTCTAAGCCATGGATCTGTCTG

771

840

HomSap_1A6 (759) GCTGTTA-AGATATGACCTTGTGCTTGAATATCCTAGGCCGGTCATGCCAACATGGTCTTCATTGGAGG
 PanTro_1A6 (759) GCTGTTA-AGATATGACCTTGTGCTTGAATATCCTAGGCCGGTCATGCCAACATGGTCTTCATTGGAGG
 PonAbe_1A6 (759) GCTGTTA-AGATATGACCTTGTGCTTGAATATCCTAGGCCAGTCATGCCAACATGGTCTTCATTGGAGG
 PapAnu_1A6 (759) GCTGTTA-AGATATGACCTTGTACTTGAATATCCTAGGCCAGTCATGCCAACATGGTCTTCATTGGAGG
 MacFas_1A6 (759) GCTGTTA-AGATATGACCTTGTACTTGAATATCCTAGGCCAGTCATGCCAACATGGTCTTCATTGGAGG
 AciJub_1A6 (748) GCTGTTA-CGATACGACTTGTGTTTCAAGTATCCAGACCAAGTCATGCCAACATGGTCTTCATTGGAGG
 PanTig_1A6 (647) GCTGTTA-CGATACGACTTGTGTTTCAAGTATCCAGACCAAGTCATGCCAACATGGTCTTCATTGGAGG
 PanOnc_1A6 (648) GCTGTTA-CGATACGACTTGTGTTTCAAGTATCCAGACCAAGTCATGCCAACATGGTCTTCATTGGAGG **M9: bp768-769**
 PanUnc_1A6 (648) GCTGTTA-TGATACGACTTGTGTTTCAAGTATCCAGACCAAGTCATGCCAACATGGTCTTCATTGGAGG
 PanLeo_1A6 (648) GCTGTTA-CGATACGACTTGTGTTTCAAGTATCCAGACCAAGTCATGCCAACATGGTCTTCATTGGAGG
 PanPar_1A6 (648) GCTGTTA-CGATACGACTTGTGTTTCAAGTATCCAGACCAAGTCATGCCAACATGGTCTTCATTGGAGG
 LeoGeo_1A6 (748) GCTGTTA-CGATACGACTTGTGTTTCAAGTATCCAGACCAAGTCATGCCAACATGGTCTTCATTGGAGG
 LeoTig_1A6 (748) GCTGTTA-CGATACGACTTGTGTTTCAAGTATCCAGACCAAGTCATGCCAACATGGTCTTCATTGGAGG
 LeoWie_1A6 (748) GCTGTTA-CGATACGACTTGTGTTTCAAGTATCCAGACCAAGTCATGCCAACATGGTCTTCATTGGAGG
 LynCan_1A6 (748) GCTGTTA-CGATACGACTTGTGTTTCAAGTATCCAGACCAAGTCATGCCAACATGGTCTTCATTGGAGG
 LynRuf_1A6 (748) GCTGTTA-CGATACGACTTGTGTTTCAAGTATCCAGACCAAGTCATGCCAACATGGTCTTCATTGGAGG

ParTem_1A6	(748)	GCTGTGA-CGATACGACTTTGTTGTTTCGAGTATCCCAGACCAAGTCATGCCCAACATGGTTTTTCATTGGAGG	
PumCon_1A6	(744)	GCCGTGA-CGATACGACTTTGTTGTTTCGAGTATCCCAGACCAAGTCATGCCCAACATGGTTTTTCATTGGAGG	
PumCo2_1A6	(744)	GCTGTGA-CGATACGACTTTGTTGTTTCGAGTATCCCAGACCAAGTCATGCCCAACATGGTTTTTCATTGGAGG	
FelCat_1A6	(748)	GCTGTGA-CAATACGACTTTGTTGTTTCGAGTATCCCAGACCAAGTCATGCCCAACATGGTTTTTCATTGGAGG	
PriBen_1A6	(748)	GCTGTGA-CAATACGACTTTGTTGTTTCGAGTATCCCAGACCAAGTCATGCCCAACATGGTTTTTCATTGGAGG	M5: bp827
CarAur_1A6	(748)	GCTGTGA-CGATACGACTTTGTTGTTTCGAGTATCCCAGACCAAGTCATGCCCAACATGGTTTTTCATTGGAGG	
CarSer_1A6	(750)	GCTGTGA-CGATACGACTTTGTTGTTTCGAGTATCCCAGACCAAGTCATGCCCAACATGGTTTTTCATTGGAGG	
CroCro_1A6	(759)	GCTGTGA-AGATATGACTTTGTTGTTTCGAGTATCCCAGACCAAGTCATGCCCAACATGGTTTTTCATTGGAGG	
ParBru_1A6	(759)	GCTGTGA-AGATACGACTTTGTTGTTTCGAGTATCCCAGACCAAGTCATGCCCAACATGGTTTTTCATTGGAGG	
ProCri_1A6	(568)	GCTGTTG-AGATACGACTTTGTTGTTTCGAGTATCCCAGACCAAGTCATGCCCAACATGGT-TTCATCGGAGA	
HyaHya_1A6	(759)	GCTGTGA-AGATACGACTTTGTTGTTTCGAGTATCCCAGACCAAGTCATGCCCAACATGGTTTTTCATTGGAGG	
BosTau_1A6	(750)	GCTGTGA-AGATACGACTTTGTTGTTTCGAGTATCCCAGACCAAGTCATGCCCAACATGGTCTTCATCGGAGG	
OviAri_1A6	(756)	GCTGCTA-AGATACGACTTTGTTGTTTCGAGTATCCCAGACCAAGTCATGCCCAACATGGTCTTCATCGGAGG	
SusScr_1A6	(759)	GCTGATG-AGATACGACTTTGTTGTTTCGAGTATCCCAGACCAAGTCATGCCCAACATGGTCTTCATTGGAGG	
MusMus_1A6a	(756)	GCTGTGA-CGGTACGATTTTGTGTTTCGAATATCCCAGGCCGGTCATGCCCAACATGATCTTCTTAGGAGG	
MusMus_1A6b	(756)	GCTGTGA-CGGTACGATTTTGTGTTTCGAATATCCCAGGCCGGTCATGCCCAACATGATCTTCTTAGGAGG	
RatNor_1A6	(753)	GCTGTGA-CGGTATGATTTTGTGTTTCGAATATCCCAGGCCGGTCATGCCCAACATGATCTTCTTAGGAGG	
OryCun_1A6	(759)	GCTGCTA-AGATACGACTTTGTTGTTTCGAGTATCCCAGGCCGGTCATGCCCAACATGGTGCTCATTGGCGG	
EquCab_1A6a	(759)	GCTGTGA-AGATACGACTTTGTTGTTTCGAGTATCCAAGACCAAGTCATGCCCAACATGGTCTTCATTGGAGG	
EquCab_1A6b	(759)	GCTGTGA-AGATATGACTTTGTTGTTTCGAGTATCCAAGACCAAGTCATGCCCAACATGGTCTTCATTGGCGG	
EquCab_1A6c	(759)	GTTGTGA-AGATACGACTTTGCTGTTTCGAGTATCCAAGACCAAGTCATGCCCAAGCATGGTCTTCATTGGAGG	
MusNig_1A6	(747)	GCTCTTA-AGATATGACTTTGTTGTTTCGAATATCCCAGACCGGTCATGCCTAACATGGTTTTTCGTTGGAGG	
MusPut_1A6	(747)	GCTCTTA-AGATATGACTTTGTTGTTTCGAATATCCCAGACCGGTCATGCCTAACATGGTTTTTCGTTGGAGG	
MirAng_1A6	(748)	GCTCTTA-----	
PhoVit_1A6	(747)	GCTCTTA-CAATACGATTT-----	
UrsMar_1A6	(647)	GCTCTTA-CAATACGACTT-----	
UrsThi_1A6	(646)	GCTCTTA-CAATACGACTTT-----	
ProLot_1A6	(603)	GCTCTTA-CAATACAACCTTTGTGCTCAAAA-----	
CanFam_1A6	(747)	GCTGTGA-AGATATGACTTTGTTGTTTCGAGTATCCCAGACCAAGTCATGCCCAACATGGTTTTTCATTGGAGG	
CanRuf_1A6	(646)	GCTCTTA-CAATACGACTTT-----	
ChrBra_1A6	(646)	GCTCTTA-CAATACGA-----	
VulVul_1A6	(648)	GCTCTTA-CAATACGACTTT-----	
AilFul_1A6	(587)	GTTGCTA-AGATACGACTTTGTTGTTTCGAGTATCCCAGACCGGTCATGCCCAACATGGTTTTTCATTGGAGG	
ArcBin_1A6	(759)	GCTCTTA-CAATACGACTTTGTTGTTTCGAGTATCCCAGACCAAGTCATGCCCAACATGGTCTTCATTGGAGG	
CivCiv_1A6	(569)	GCTGTGA-AGATATGACTTTGTTGTTTCGAGTATCCCAGACCAAGTCATGCCCAACATGGTTTTTCATTGGAGG	
HerJav_1A6	(759)	GCTGTGA-AGATATGACTTTGTTGTTTCGAGTATCCCAGACCAAGTCATGCCCAACATGGTTTTTC-----	
GalGal_1A6	(768)	GCTCATG-AGATATGATTTTGTGTTTCGAATTCCTCAAGACCAACAATGCCCAACATGGTTTTTCATTGGAGG	

		841	874
HomSap_1A6	(828)	TATCAACTGTAAGAAGAGGAAAGACTTGTCTCAG	
PanTro_1A6	(828)	TATCAACTGTAAGAAGAGGAAAGACTTGTCTCAC	
PonAbe_1A6	(828)	TACCAACTGTAAGAAGAGGAAAGACTTGTCTCAG	
PapAnu_1A6	(828)	TACCAACTGTAAGAAGAGGAAAGACCTGTCTGAG	
MacFas_1A6	(828)	TACCAACTGTAAGAAGAGGAAAGACCTGTCTGAG	
AcjJub_1A6	(817)	GACCAACTGCAAGGAAAAGGGAGTCTGTCTCAG	
PanTig_1A6	(716)	GACCAATTGCAAGGAAAAGGGAGTCTGTCTCAG	
PanOnc_1A6	(718)	GACCAATTGCAAGGAAAAGGGAGTCTGTCTCAG	
PanUnc_1A6	(717)	GATGAATTGCAAGGAAAAGGGAGTCTGTCTCAG	
PanLeo_1A6	(717)	GACCAATTGCAAGGAAAAGGGAGTCTGTCTCAG	
PanPar_1A6	(717)	GACCAATTGCAAGGAAAAGGGAGTCTGTCTCAG	
LeoGeo_1A6	(817)	GACCAACTGCAAGGAAAAGGGAGTCTGTCTCAG	
LeoTig_1A6	(817)	GACCAACTGCAAGGAAAAGGGAGTCTGTCTCAG	
LeoWie_1A6	(817)	GACCAACTGCAAGGAAAAGGGAGTCTGTCTCAG	
LynCan_1A6	(817)	GACCAACTGCAAGGAAAAGGGAGTCTGTCTCAG	
LynRuf_1A6	(817)	GACCAACTGCAAGGAAAAGGGAGTCTGTCTCAG	
ParTem_1A6	(817)	GGCCAAGTCAAGGAAAAGGGAGTCTGTCTCAG	
PumCon_1A6	(813)	GACCAACTGCAAGGAAAAGGGAGTCAAGTCTCAG	
PumCo2_1A6	(813)	GACCAACTGCAAGGAAAAGGGAGTCTGTCTCAG	
FelCat_1A6	(816)	GACCAACCTCAAGGAAAAGGGAGTCTGTCTCAG	
PriBen_1A6	(816)	GACCAACCTCAAGGAAAAGGGAGTCTGTCTCAG	
CarAur_1A6	(817)	GACCAACTGCAAGGAAAAGGGAGTCTGTCTCAG	
CarSer_1A6	(819)	GACCAACTGCAAGGAAAAGGGAGTCTGTCTCAG	
CroCro_1A6	(828)	GACCAACTGCAAGGAAAAGGGAGTCTGTCTCAG	
ParBru_1A6	(828)	GACCAACTGCAAGGAAAAGGGAGTCTGTCTCAG	
ProCri_1A6	(636)	CCA-----	
HyaHya_1A6	(828)	GACCAACTGCAAGGAAAAGGGAGTC-----	
BosTau_1A6	(819)	GTCCAGCTGCAAGAAACAGGGCGTCTGTCTCAG	
OviAri_1A6	(825)	GTCAGCTGCCAAGAAACAAGGCATCTGCCCTCGG	
SusScr_1A6	(828)	GACCAACTGCAAGGAAAAGGGAGTCTGTCTCAG	
MusMus_1A6a	(825)	GATCAACTGTAAGAAGGAAAGGAAAGTGAAGTCTCAG	
MusMus_1A6b	(825)	GATCAACTGTAAGAAGGAAAGGAAAGTGAAGTCTCAG	
RatNor_1A6	(822)	GACCAACTGCAAGGAAAGGAAAGGAAAGTGTCTCAG	
OryCun_1A6	(828)	GATCAACTGCAAGGAAAGCGGAGTCTGTCTCAG	
EquCab_1A6a	(828)	GGTCAACTGCAAGGAAAGGAAAGGAAAGTGCCTCAG	
EquCab_1A6b	(828)	GGTCAACTGCAAGGAAAGGAAAGGAAAGTGCCTCAG	
EquCab_1A6c	(828)	GGTCAACTGCAAGGAAAGGAAAGGAAAGTGCCTCAG	
MusNig_1A6	(816)	GAGCAATTGCAAGGAAAGGAGGGGCTGTCTCAG	
MusPut_1A6	(816)	GAGCAATTGCAAGGAAAGTGGGGCTGTCTCAG	

MirAng_1A6	(755)	-----
PhoVit_1A6	(765)	-----
UrsMar_1A6	(665)	-----
UrsThi_1A6	(665)	-----
ProLot_1A6	(632)	-----
CanFam_1A6	(816)	GACCAACTGCAAGATGAAGGGAGTCCTGCCTCAG
CanRuf_1A6	(665)	-----
ChrBra_1A6	(661)	-----
VulVul_1A6	(667)	-----
AilFul_1A6	(656)	GACCAACTGCAAGAAGAAGGGAGTCCTGTCT---
ArcBin_1A6	(828)	GACCAACTGCAAGGAAAAGGGAGTCCTG-----
CivCiv_1A6	(638)	GACCAACTGCAAGAAAAAGGGAGTCCTGTCTCAG
HerJav_1A6	(820)	-----
GalGal_1A6	(837)	GATAAACTGTGCTCAGAAGAACAAGCTGTCTCAG