

a. DNA sequence alignment.

		*	20	*	40	*	60	*	80	
P.coatneyi_CM002856.1	:	ATGAAGT	GCAACGGCT	CCTTGCTAGT	CTACTTAGCGCA	ATACTCAGCGCT	ACGAAAGCTTTGATACG	AAATGGGAACAA	:	80
Pknowlesi_NC_011906.1	:	ATGAAGT	GCAACGGCT	CCTTGCTAGT	CTACTTAGCGCA	ATACTCAGCGC	CACGAAAGCTTTGATACG	AAATGGGAACAA	:	80
Pinui_NW_008481888.1	:	ATGAAGT	GCAACACGG	CCTTGCTAGT	CTACTTAGCGCA	ATACTCAGCGCT	GCAAAAGCTTTGATACG	AAATGGGAACAC	:	80
Pfragile_NW_012192586.1	:	ATGAAGT	ATAACGCCAC	CCTTGCTTGT	CTACTTAGCGCA	ATAATTGAGCGCT	GGGAAAGCTTTGATACG	AAATGGGAACAA	:	80
Pcynomolgi_BAEJ01000249	:	ATGAAGT	GCAACGCCG	CCTTGCTAGT	CTACTTAGCGCAT	TACTCAGCGCT	TGCAACGCTTTGATACG	AAATGGGAACAA	:	80
Brazil-I_AFMK01000508.1_A	:	ATGAAGT	GCAACGCC	CCTTGCTAGT	CTACTTAGCGCACT	TACTCAGCGCT	TGCGAAGCTTTGATACG	GAATGGGAACAA	:	80
VCG-I	:	ATGAAGT	GCAACGCC	CCTTGCTAGT	CTACTTAGCGCACT	TACTCAGCGCT	TGCGAAGCTTTGATACG	GAATGGGAACAA	:	80
Sal-1_PVX_088910	:	ATGAAGT	GCAACGCC	CCTTGCTAGT	CTACTTAGCGCACT	TACTCAGCGCT	TGCGAAGCTTTGATACG	GAATGGGAACAA	:	80
Mauritania_I_AFNIO1000333	:	ATGAAGT	GCAACGCC	CCTTGCTAGT	CTACTTAGCGCACT	TACTCAGCGCT	TGCGAAGCTTTGATACG	GAATGGGAACAA	:	80
NKorean_AFNJ01000531	:	ATGAAGT	GCAACGCC	CCTTGCTAGT	CTACTTAGCGCACT	TACTCAGCGCT	TGCGAAGCTTTGATACG	GAATGGGAACAA	:	80
India-VII_AFBK01000586_AFBK01000587	:	ATGAAGT	GCAACGCC	CCTTGCTAGT	CTACTTAGCGCACT	TACTCAGCGCT	TGCGAAGCTTTGATACG	GAATGGGAACAA	:	80
		ATGAAGTgcAACgcc	CCTTGCTAgTcCTACTTAGCGCA	TAcTcAGCGCt	cgAAcGCTTTGATACG	AATGG	AACAA			

		*	100	*	120	*	140	*	160	
P.coatneyi_CM002856.1	:	TCCGCAGGCATTAGTTCCG	GAAAAAGAGCGATGACT	CCAGTGGGGGC	CAGAACAAC	CCCTCCCGT	GACAAACCAAGACACGT	:	160	
Pknowlesi_NC_011906.1	:	TCCGCAGGCATTAGTTCCG	GAAATAGTCTGTGACCCGAATGC	GGGGC	CAGAACAAC	AACGTCCACT	GACAAACCAAGACACAT	:	160	
Pinui_NW_008481888.1	:	TACGCAGGCATTAGTTCCG	GAAAAAGAGCAATGACCCGAGTGGGGGC	CAGAACAAC	CCCTCCCGT	GACAAACCAAGACACTT	:	160		
Pfragile_NW_012192586.1	:	TACGCAGGCCTTAGTTCCCT	GAAAAATGGCGCTGACCCCTAGTGGGGGC	CAGAACAAC	CCCTCCCGT	GAAAAACCAAGATACCT	:	160		
Pcynomolgi_BAEJ01000249	:	TACGCAGGCATTAGTTCCG	GAAAAAGAGCGCTGACCCGAGTGGGGGC	CAGAACAAC	CCCTCCCGT	GATAACCAAGACACGT	:	160		
Brazil-I_AFMK01000508.1_A	:	CCCGCAGGCATTAGTTCCCT	GAAAAAGGGCGCTGACCCGAGTGGGGGC	CAGAACAAC	CGCTCCCGG	GAAAAACCAAGACACGT	:	160		
VCG-I	:	CCCGCAGGCATTAGTTCCCT	GAAAAAGGGCGCTGACCCGAGTGGGGGC	CAGAACAAC	CGCTCCCGG	GAAAAACCAAGACACGT	:	160		
Sal-1_PVX_088910	:	CCCGCAGGCATTAGTTCCCT	GAAAAAGGGCGCTGACCCGAGTGGGGGC	CAGAACAAC	CGCTCCCGG	GAAAAACCAAGACACGT	:	160		
Mauritania_I_AFNIO1000333	:	CCCGCAGGCATTAGTTCCCT	GAAAAAGGGCGCTGACCCGAGTGGGGGC	CAGAACAAC	CGCTCCCGG	GAAAAACCAAGACACGT	:	160		
NKorean_AFNJ01000531	:	CCCGCAGGCATTAGTTCCCT	GAAAAAGGGCGCTGACCCGAGTGGGGGC	CAGAACAAC	CGCTCCCGG	GAAAAACCAAGACACGT	:	160		
India-VII_AFBK01000586_AFBK01000587	:	CCCGCAGGCATTAGTTCCCT	GAAAAAGGGCGCTGACCCGAGTGGGGGC	CAGAACAAC	CGCTCCCGG	GAAAAACCAAGACACGT	:	160		
		CGCAGGCATTAGTTCC	GAAaAg	Gcg	TGACcCgAgTGgGGGc	CAGAACAACc	cTCCgG	GA	AACCAAGAcACgT	

		*	180	*	200	*	220	*	240	
P.coatneyi_CM002856.1	:	GCGAAATTCAAAGATGGCG	GAAGAAATGATGGA	AAAAATGCTGAAC	GAAAAAGAT	GTGTTTAC	CTCCATCATGGAACCT	:	240	
Pknowlesi_NC_011906.1	:	GTGAAATTCAAAGATGGCC	GAGAAATGATGGA	AAAAATGATGAAA	GAAAAAGACGT	GTGTTTAC	CTCCATTATGGAACCT	:	240	
Pinui_NW_008481888.1	:	GTGAAATTCAAAGATGGCC	CAAGAAATGATGGA	AAAAATGATGAAA	GAAAAAGACGT	GTGTTTAC	CTCCATCATGGAACCC	:	240	
Pfragile_NW_012192586.1	:	GCGAACTTCAAAGATGGCT	GAAAGAAATGATGG	AAAAATGATGAAA	GAAAAAGACCT	GTGTTTAC	CTCCATTATGGAACCT	:	240	
Pcynomolgi_BAEJ01000249	:	CTGAAATTCAAAGATGGCC	GAGAAATGATGGA	AAAAATGATGAAA	GAAAAAGACAT	GTGTTTAC	CTCCATCATGGAACCT	:	240	
Brazil-I_AFMK01000508.1_A	:	GCGAAATTCAAAGATGGCC	GAGAAATGATGGA	AAAAATGATGAA	GAAAAAGACGT	GTGTTTAC	CTCCATCATGGAACCT	:	240	
VCG-I	:	GCGAAATTCAAAGATGGCC	GAGAAATGATGGA	AAAAATGATGAA	GAAAAAGACGT	GTGTTTAC	CTCCATCATGGAACCT	:	240	
Sal-1_PVX_088910	:	GCGAAATTCAAAGATGGCC	GAGAAATGATGGA	AAAAATGATGAA	GAAAAAGACGT	GTGTTTAC	CTCCATCATGGAACCT	:	240	
Mauritania_I_AFNIO1000333	:	GCGAAATTCAAAGATGGCC	GAGAAATGATGGA	AAAAATGATGAA	GAAAAAGACGT	GTGTTTAC	CTCCATCATGGAACCT	:	240	
NKorean_AFNJ01000531	:	GCGAAATTCAAAGATGGCC	GAGAAATGATGGA	AAAAATGATGAA	GAAAAAGACGT	GTGTTTAC	CTCCATCATGGAACCT	:	240	
India-VII_AFBK01000586_AFBK01000587	:	GCGAAATTCAAAGATGGCC	GAGAAATGATGGA	AAAAATGATGAA	GAAAAAGACGT	GTGTTTAC	CTCCATCATGGAACCT	:	240	
		G	GAAaTTCAAaAGATGGCCg	AAGAAATGATGGa	AAAAATGaTGAA	GAAAAAGAcg	GTGTTTAg	CCTCCATc	ATGGAACCT	

		*	260	*	280	*	300	*	320	
P.coatneyi_CM002856.1	:		CTCCAGAGCAAATTAA	CGATGATCA	CTCTGTTC	CAAAACT	AAAAATATACGAAC	GTTTGTCTTCA	GAAAAGGACAAAAC	: 320
Pknowlesi_NC_011906.1	:		CTCCAGAGCAAATTAA	CGATGATCGC	CTCTGTTC	TAAAT	GAAATATACAAAT	TATTTGTCTTCA	GAAAAGGACAAAAC	: 320
Pinui_NW_008481888.1	:		CTCCAGAGCAAATTAG	CCGACGATCAC	CTCTGTTC	CAGAGT	AAAAATATA	GAACATTTGTCTTCA	GAAAAGGACAAATAA	: 320
Pfragile_NW_012192586.1	:		CTCCAGAGCAAATTAT	CCGACAATCAT	CTCTGTTC	CAACAGT	GAAATATACGAAC	ATTTGTCTTCA	GAAAAGGATAAAAC	: 320
Pcynomolgi_BAEJ01000249	:		CTCCAGAGCAAATTAC	CGACGATCAC	CTCTGTTC	CAAAACT	GAAATATACGAAC	ATTTGTCTTCA	GAAAAGGACAAAAC	: 320
Brazil-I_AFBK01000508.1_A	:		CTCCAGAGCAAATTAA	CGACGATCAT	CTCTGTTC	CAAAAT	GAAATATACGAAC	ATTTGTCTTCA	GAAAAGGACAAAAC	: 320
VCG-I	:		CTCCAGAGCAAATTAA	CGACGATCAT	CTCTGTTC	CAAAAT	GAAATATACGAAC	ATTTGTCTTCA	GAAAAGGACAAAAC	: 320
Sal-1_PVX_088910	:		CTCCAGAGCAAATTAA	CTGACGATCAT	CTCTGTTC	CAAAAT	GAAATATACGAAC	ATTTGTCTTCA	GAAAAGGACAAAAC	: 320
Mauritania_I_AFNIO1000333	:		CTCCAGAGCAAATTAA	CGACGATCAT	CTCTGTTC	CAAAAT	GAAATATACGAAC	ATTTGTCTTCA	GAAAAGGACAAAAC	: 320
NKorean_AFNJO1000531	:		CTCCAGAGCAAATTAA	CGACGATCAT	CTCTGTTC	CAAAAT	GAAATATACGAAC	ATTTGTCTTCA	GAAAAGGACAAAAC	: 320
India-VII_AFBK01000586_AFBK01000587	:		CTCCAGAGCAAATTAA	CGACGATCAT	CTCTGTTC	CAAAAT	GAAATATACGAAC	ATTTGTCTTCA	GAAAAGGACAAAAC	: 320
			CTCCAGAGCAAATTA	CcGAcgATCa	CT	TGTTCAaaa	TgAAATATACgAAca	TTTGTCTTCA	GAAAAGGAcAAaAc	

		*	340	*	360	*	380	*	400	
P.coatneyi_CM002856.1	:		TCCCTTGACCTTCC	CTGCACAAGTCCG	GAGTACGAAA	AATTAATTCAG	CAATTTACTTAT	CAAAAAGTTAT	TGCAACTCCA	: 400
Pknowlesi_NC_011906.1	:		TCCCTTGACCTTCC	ATGCACAAGTCC	CAATACGAACA	AATTAATTCAG	CAATTTACTTATA	AAAAAGTTAT	TGCAACTCCA	: 400
Pinui_NW_008481888.1	:		TCCCTTGACCTTCC	CTGCACAAGTCCG	GAGTACGAACA	AATTAATTCACGA	ATTTACTTATA	AAAAAGTTAT	TGCAATTC	: 400
Pfragile_NW_012192586.1	:		TCCCTTGACCTTCC	CTGCACAAGTCCG	CAGTACGAACA	AATTAATTCACCA	CTTTACTTATA	AAAAAGTTCT	CTGTAACCTC	: 400
Pcynomolgi_BAEJ01000249	:		TCCCTTGACCTTACC	CTGCACAAGTCCG	CAGTACGAACA	AATTAATTCACA	CTTTACTTATA	AAAAAGTTAT	TGCAACTCC	: 400
Brazil-I_AFBK01000508.1_A	:		TCCCTTGACCTTCC	CTGCACAAGTCCG	CAGTACGAACAG	CTAATTCATCG	CTTCACTTATA	AAAAAGTTCT	TGCAACTCCA	: 400
VCG-I	:		TCCCTTGACCTTCC	CTGCACAAGTCCG	CAGTACGAACAG	CTAATTCATCG	CTTCACTTATA	AAAAAGTTCT	TGCAACTCCA	: 400
Sal-1_PVX_088910	:		TCCCTTGACCTTCC	CTGCACAAGTCCG	CAGTACGAACAG	CTAATTCATCG	CTTCACTTATA	AAAAAGTTCT	TGCAACTCCA	: 400
Mauritania_I_AFNIO1000333	:		TCCCTTGACCTTCC	CTGCACAAGTCCG	CAGTACGAACAG	CTAATTCATCG	CTTCACTTATA	AAAAAGTTCT	TGCAACTCCA	: 400
NKorean_AFNJO1000531	:		TCCCTTGACCTTCC	CTGCACAAGTCCG	CAGTACGAACAG	CTAATTCATCG	CTTCACTTATA	AAAAAGTTCT	TGCAACTCCA	: 400
India-VII_AFBK01000586_AFBK01000587	:		TCCCTTGACCTTCC	CTGCACAAGTCCG	CAGTACGAACAG	CTAATTCATCG	CTTCACTTATA	AAAAAGTTCT	TGCAACTCCA	: 400
			TcCCTTGACCTTcCC	cTGcACAAGTCCG	cAgTACGAACa	TAATTCa	c	TT ACTTATAa	AAAAAGTT TGcAAcTCca	

		*	420	*	440	*	460	*	480	
P.coatneyi_CM002856.1	:		AGGTGGCCTTTAG	CAACGTGTTGCT	GAAATCCTTCAT	CGATAA	GAAGAA	CGAAGAAAA	CACATTCAAC	CGCATCATACAG : 480
Pknowlesi_NC_011906.1	:		AGGTGGCCTTTAG	CAACGTGTTGCT	GAAATCCTTCAT	CGATAA	GAAGAA	CGAAGAAAA	CACATTTAAC	CGCATCATACAG : 480
Pinui_NW_008481888.1	:		AGGTGGCCTTTAG	CAACGTGTTGCT	CAAATCGTTTCAT	CGATAA	GAAGAA	CGAAGAAAA	CACATTTAAC	ACGATCATACAG : 480
Pfragile_NW_012192586.1	:		AA GTGGCCTTTA	CAACGTGTTGCT	CAAATCCTTCAT	CAATAA	GAAGAA	CGAAGAAAA	CACATTTAAC	ACGATCATACAG : 480
Pcynomolgi_BAEJ01000249	:		AGGTGGCCTTTAG	CAACGTGTTGCT	CAAATCCTTCAT	CAATAA	GAAGAA	CGAAGAAAA	TACATTTAAT	ACGATCATACAG : 480
Brazil-I_AFBK01000508.1_A	:		AGGTGGCCTTTAG	CAACGTCTTGCT	CAAATCCTTCAT	CGATAA	GAAGAA	CGAAGAAAA	CACATTTAAC	ACGATCATACAG : 480
VCG-I	:		AGGTGGCCTTTAG	CAACGTCTTGCT	CAAATCCTTCAT	CGATAA	GAAGAA	CGAAGAAAA	CACATTTAAC	ACGATCATACAG : 480
Sal-1_PVX_088910	:		AGGTGGCCTTTAG	CAACGTCTTGCT	CAAATCCTTCAT	CGATAA	GAAGAA	CGAAGAAAA	CACATTTAAC	ACGATCATACAG : 480
Mauritania_I_AFNIO1000333	:		AGGTGGCCTTTAG	CAACGTCTTGCT	CAAATCCTTCAT	CGATAA	GAAGAA	CGAAGAAAA	CACATTTAAC	ACGATCATACAG : 480
NKorean_AFNJO1000531	:		AGGTGGCCTTTAG	CAACGTCTTGCT	CAAATCCTTCAT	CGATAA	GAAGAA	CGAAGAAAA	CACATTTAAC	ACGATCATACAG : 480
India-VII_AFBK01000586_AFBK01000587	:		AGGTGGCCTTTAG	CAACGTCTTGCT	CAAATCCTTCAT	CGATAA	GAAGAA	CGAAGAAAA	CACATTTAAC	ACGATCATACAG : 480
			AgGTGGCCTTtAg	cAACGT	TTGCTcAAATC	cCTTCATCg	ATAAaAA	AA	GAAGAAAAc	ACATTtAAcaCGATcATAcAg

		*	500	*	520	*	540	*	560	
P.coatneyi_CM002856.1	:	AATTACAAA	AGTTCTGTCCACTTGTATTGATGAAGATTTTGAAGGATATTTACAAATGCATCTATAGAAATTATTCTCCGACAT	:	560					
Pknowlesi_NC_011906.1	:	AATTACAAA	AGTTTGTCCACTTGTATTGATGAAGATTTTGAAGGACATTTATAATGCATCCATAGAGTTATTCTCCGATCT	:	560					
Pinui_NW_008481888.1	:	AATTACAAA	AGTTCTGTCCACTTGTATTGATGCAGATTTTGAAGGACATTTATAGTCATCCATACAGTTATTCTCCGACCT	:	560					
Pfragile_NW_012192586.1	:	AATTACAAA	ATTCTGTCCACTTGTATTGATGAAGATTTTGAAGGACATTTATGATGCCGCCATACAGTTATTCTCCGACAT	:	560					
Pcynomolgi_BAEJ01000249	:	AATTACAAA	CTTCTGTCCACTTGTATTGATGAAGATTTTGAAGGACATTTATAATGCATCCATAGATTATTCTCCGATAT	:	560					
Brazil-I_AFBK01000508.1_A	:	AATTACAAA	AGTTCTGTCCACTTGCATTGACGATGATTTTGAAGGACATTTATAATGCATCCATAGAGTTATTCTCCGACAT	:	560					
VCG-I	:	AATTACAAA	AGTTCTGTCCACTTGCATTGACGATGATTTTGAAGGACATTTATAATGCATCCATAGAGTTATTCTCCGACAT	:	560					
Sal-1_PVX_088910	:	AATTACAAA	AGTTCTGTCCACTTGCATTGACGATGATTTTGAAGGACATTTATAATGCATCCATAGAGTTATTCTCCGACAT	:	560					
Mauritania_I_AFNIO1000333	:	AATTACAAA	AGTTCTGTCCACTTGCATTGACGATGATTTTGAAGGACATTTATAATGCATCCATAGAGTTATTCTCCGACAT	:	560					
NKorean_AFNJ01000531	:	AATTACAAA	AGTTCTGTCCACTTGCATTGACGATGATTTTGAAGGACATTTATAATGCATCCATAGAGTTATTCTCCGACAT	:	560					
India-VII_AFBK01000586_AFBK01000587	:	AATTACAAA	AGTTCTGTCCACTTGCATTGACGATGATTTTGAAGGACATTTATAATGCATCCATAGAGTTATTCTCCGACAT	:	560					
		AATTACAAA	gTtCTGTCCACTTG ATTGA Ga GATTTTGAAGGAcATTTAtaaTGCATCcATAgAgTtATTtCTCCGAcAT							

		*	580	*	600	*	620	*	640	
P.coatneyi_CM002856.1	:	TAGAAGCTCCGTCACAGAAATCACG	GAAAAGTTGTGGTCCAAAAATATGATCGATGTTTTAAAAACAAGAGAGCAACCCA	:	640					
Pknowlesi_NC_011906.1	:	TAGAACA	CTGTGTCAGAGAAATTACGGAAAAATTGTGGTCCAAAAATATGATCGAGTTTTTAAAAACAAGAGAGCAACCCA	:	640					
Pinui_NW_008481888.1	:	TAGAAGCCCGTCACAGAAATCTCG	GAAAGTTGTGGTCCAAAGAAATATGATCGATGTTTTTAAAGACAAGAGAGGAAACCA	:	640					
Pfragile_NW_012192586.1	:	TAGAGTG	TCGTCACAGAAATCACAGAAAAGCTGTGGTCTAAAAATATGATCGACGTTTTTAAAGACAAGAGAGCAAAACCA	:	640					
Pcynomolgi_BAEJ01000249	:	TAGAACC	TCGTCACGGAATCACG	GAAAAGTTGTGGTCCAAAAATATGATCGAGGTTTTTAAAGCAAGAGAGCAAAACCA	:	640				
Brazil-I_AFBK01000508.1_A	:	AAGAACC	TCGTCACAGAAATTACCG	GAAAAGTTGTGGTCCAAAAATATGATCGAAGTTTTTAAAGACAAGAGAGCAAAACCA	:	640				
VCG-I	:	AAGAACC	TCGTCACAGAAATTACCG	GAAAAGTTGTGGTCCAAAAATATGATCGAAGTTTTTAAAGACAAGAGAGCAAAACCA	:	640				
Sal-1_PVX_088910	:	AAGAACC	TCGTCACAGAAATTACCG	GAAAAGTTGTGGTCCAAAAATATGATCGAAGTTTTTAAAGACAAGAGAGCAAAACCA	:	640				
Mauritania_I_AFNIO1000333	:	AAGAACC	TCGTCACAGAAATTACCG	GAAAAGTTGTGGTCCAAAAATATGATCGAAGTTTTTAAAGACAAGAGAGCAAAACCA	:	640				
NKorean_AFNJ01000531	:	AAGAACC	TCGTCACAGAAATTACCG	GAAAAGTTGTGGTCCAAAAATATGATCGAAGTTTTTAAAGACAAGAGAGCAAAACCA	:	640				
India-VII_AFBK01000586_AFBK01000587	:	AAGAACC	TCGTCACAGAAATTACCG	GAAAAGTTGTGGTCCAAAAATATGATCGAAGTTTTTAAAGACAAGAGAGCAAAACCA	:	640				
		AGAa	ctCcGTCaCaGAAAT aC GAAAagtTGTGGTCCAAAATATGATCGA GTTTTTAAAGaCAAGAGAGCAAAcCa							

		*	660	*	680	*	700	*	720	
P.coatneyi_CM002856.1	:	TTGCAGGC	ATTTTATGTGAGTTAAGAAACGGAAACAAATCTCCCTAGTATCAAAACAGTTTGTCTATGAAAATTTTGGG	:	720					
Pknowlesi_NC_011906.1	:	TTGCAGGC	ATTTTATGTGAGTTAAGAAACGGAAATAAATCTACCTAGTATCAAAATAGTTTGTCTATGAAAATTTTGGG	:	720					
Pinui_NW_008481888.1	:	TTACAGGC	ATTTTATGTGAGTTAAGAAAGGGAAATAAATCTACTCTAGTATCGAACAGTTTTCCTATGACAAATTTTGGG	:	720					
Pfragile_NW_012192586.1	:	TTGCAGGC	ATTTTATGTGAGTTACGAAATGGAAATAAATCAACCTAGTATCAAAACAGTTTGTCTATGAAAATTTTGGG	:	720					
Pcynomolgi_BAEJ01000249	:	TTGCAGGC	ATTTTATGTGAGTTAAGAAACGGAAATAAATCTACCTAGTATCAACAGTTTGTCTATGAAAATTTTGGG	:	720					
Brazil-I_AFBK01000508.1_A	:	TTGCAGGC	ATTTTATGTGAGTTAAGAAATGGAAATAAATCTCCCTAGTATCGAACAGTTTTCCTATGAAAATTTTGGG	:	720					
VCG-I	:	TTGCAGGC	ATTTTATGTGAGTTAAGAAATGGAAATAAATCTCCCTAGTATCGAACAGTTTTCCTATGAAAATTTTGGG	:	720					
Sal-1_PVX_088910	:	TTGCAGGC	ATTTTATGTGAGTTAAGAAATGGAAATAAATCTCCCTAGTATCGAACAGTTTTCCTATGAAAATTTTGGG	:	720					
Mauritania_I_AFNIO1000333	:	TTGCAGGC	ATTTTATGTGAGTTAAGAAATGGAAATAAATCTCCCTAGTATCGAACAGTTTTCCTATGAAAATTTTGGG	:	720					
NKorean_AFNJ01000531	:	TTGCAGGC	ATTTTATGTGAGTTAAGAAATGGAAATAAATCTCCCTAGTATCGAACAGTTTTCCTATGAAAATTTTGGG	:	720					
India-VII_AFBK01000586_AFBK01000587	:	TTGCAGGC	ATTTTATGTGAGTTAAGAAATGGAAATAAATCTCCCTAGTATCGAACAGTTTTCCTATGAAAATTTTGGG	:	720					
		TtGcAGGc	ATTTTATGTGAGTTAaGAAA GGAAAtAAtTcT CcCTAGTATC AAcAGTTT TC TATGAAATTTTGGa							

		*	740	*	760	*	780	*	800	
P.coatneyi_CM002856.1	:	ATC	CCTCAAGGTTAATTATGAAAGC	CTTAATGA	ACCAGGCGTATAAAGC	TTTTCAGACTACTATT	CATACTTT	CCC	GCTTT	: 800
Pknowlesi_NC_011906.1	:	ATC	CCTTAAAGTGAATTATGAAAGC	CTTAATAA	ACCAGGCGTATAAAGC	TTTTCAGACTACTATT	CTTACTTT	CCC	GGCTT	: 800
Pinui_NW_008481888.1	:	ATC	CCTCAAGGTTAATTATGAAAGC	TTACTAA	ACCAGGCGTATGTCG	CAATTTTTCAGACTACTATT	CATTTCTTT	CCC	CTTTT	: 800
Pfragile_NW_012192586.1	:	ATC	CCTCAAGGTTAATTATGAAAGC	TTAATGA	ACCAGGCGTACAAGC	CAATTTTTCAGACTACTATT	CATACTTT	CCCC	AATTT	: 800
Pcynomolgi_BAEJ01000249	:	ATC	CCTCAAGGTTAATTATGAAAGC	TTACTAA	ACCAGGCGTATGCGGC	TTTTCAGACTACTATT	CATACTTT	CCC	GCTTT	: 800
Brazil-I_AFBK01000508.1_A	:	ATT	CTCAAGGTTAATTATGAGGC	ATTACTAA	ACCAGGCGTATGCGGC	TTTTCAGACTACTATT	CATACTTT	CCC	GCTTT	: 800
VCG-I	:	ATT	CTCAAGGTTAATTATGAGGC	ATTACTAA	ACCAGGCGTATGCGGC	TTTTCAGACTACTATT	CATACTTT	CCC	GCTTT	: 800
Sal-1_PVX_088910	:	ATT	CTCAAGGTTAATTATGAGGC	ATTACTAA	ACCAGGCGTATGCGGC	TTTTCAGACTACTATT	CATACTTT	CCC	GCTTT	: 800
Mauritania_I_AFNIO1000333	:	ATT	CTCAAGGTTAATTATGAGGC	ATTACTAA	ACCAGGCGTATGCGGC	TTTTCAGACTACTATT	CATACTTT	CCC	GCTTT	: 800
NKorean_AFNJ01000531	:	ATT	CTCAAGGTTAATTATGAGGC	ATTACTAA	ACCAGGCGTATGCGGC	TTTTCAGACTACTATT	CATACTTT	CCC	GCTTT	: 800
India-VII_AFBK01000586_AFBK01000587	:	ATT	CTCAAGGTTAATTATGAGGC	ATTACTAA	ACCAGGCGTATGCGGC	TTTTCAGACTACTATT	CATACTTT	CCC	GCTTT	: 800
		AT	CTCAAGGTTAATTATGA	Gg	TTA	TaAACCAGGCGTat	gGC	TTTTCAGACTACTATT	CaTacTTtCCCgctTT	

		*	820	*	840	*	860	*	880	
P.coatneyi_CM002856.1	:	TGCC	ATTAAATTTT	AGAAAAGG	AGGTTCTG	TCGAGCGA	TTGGTCGCTAT	CCATGAAAG	TTGACCAACTACAGGACGA	: 880
Pknowlesi_NC_011906.1	:	TGCC	ATTAGACTTT	TAGAAAAG	CATGGGTT	GGTCGAGCGG	TTGGTCGCTAT	CCATGAAAG	TTGACCAACTACAGGACGA	: 880
Pinui_NW_008481888.1	:	TGCC	ATTGCGCTTT	GTTAGAAA	ATGGCGGATT	GGTCGAGCGA	TTGGTCGCTAT	CCATGAGAA	TTGACCAACTACAGGACGA	: 880
Pfragile_NW_012192586.1	:	TGCC	ATTAAATTTT	GGAGAAAG	GTTGGGTT	GGTCGAGCGG	TTGGTCGCTAT	CCATGAGAG	TTGACCAACTACAGGACGA	: 880
Pcynomolgi_BAEJ01000249	:	TGCC	ATTAAATTTT	GTTAGAAA	AGGCGGGTT	GGTCGAGCGG	TTGGTCGCTAT	CCATGAGAG	TTTAAACCAACTACAGGACCA	: 880
Brazil-I_AFBK01000508.1_A	:	TGCC	ATTAGCATGTT	AGAAAAGG	CAGGGTT	GGTCGACCGG	TTGGTCGCTAT	CCATGAGAG	TTTGACCAACTACAGGACGA	: 880
VCG-I	:	TGCC	ATTAGCATGTT	AGAAAAGG	CAGGGTT	GGTCGACCGG	TTGGTCGCTAT	CCATGAGAG	TTTGACCAACTACAGGACGA	: 880
Sal-1_PVX_088910	:	TGCC	ATTAGCATGTT	AGAAAAGG	CAGGGTT	GGTCGACCGG	TTGGTCGCTAT	CCATGAGAG	TTTGACCAACTACAGGACGA	: 880
Mauritania_I_AFNIO1000333	:	TGCC	ATTAGCATGTT	AGAAAAGG	CAGGGTT	GGTCGACCGG	TTGGTCGCTAT	CCATGAGAG	TTTGACCAACTACAGGACGA	: 880
NKorean_AFNJ01000531	:	TGCC	ATTAGCATGTT	AGAAAAGG	CAGGGTT	GGTCGACCGG	TTGGTCGCTAT	CCATGAGAG	TTTGACCAACTACAGGACGA	: 880
India-VII_AFBK01000586_AFBK01000587	:	TGCC	ATTAGCATGTT	AGAAAAGG	CAGGGTT	GGTCGACCGG	TTGGTCGCTAT	CCATGAGAG	TTTGACCAACTACAGGACGA	: 880
		TGCC	ATta	TgTTaGAaAAgGg	GGgTTgGTCGA	CG	TTGGTCGC	ATCCATGAgAgcTTg	ACCAACTACAGGACgA	

		*	900	*	920	*	940	*	960	
P.coatneyi_CM002856.1	:	AAA	ATATTCTCAAGA	AGATCAAT	GAGAAGTCCAAAA	ATGAGGTCTGA	AATAACGAGG	ATATTATGC	ACAGCTTGAGCAGT	: 960
Pknowlesi_NC_011906.1	:	AAA	ATATTCTCAAGA	AGATCAAT	GAGAAGTCCAAAA	ATGAGGTCTGA	AATAATGAGG	ATATTATGC	ACAGCTTGAGCAGT	: 960
Pinui_NW_008481888.1	:	AAA	ATATTCTCAAGA	AGATCAAT	GAGAAGTCCAAAA	ATGAGGTCTGA	AATAACGAGG	ATATTATGC	ACAGCTTGAGCAGT	: 960
Pfragile_NW_012192586.1	:	AAA	ATATTCTCCAG	AAAATCAAT	GAGAAGTCCAAAA	ATGAAATCCTGA	AATAACGAGG	ATATTATGC	ACAGCTTGAGCAGT	: 960
Pcynomolgi_BAEJ01000249	:	AAA	ATATTCTCAAGA	AGATCAAT	GAGAAGTCCAAAA	ATGAGGTCTGA	AATAATGGG	ATATTATGC	ACAGCTTGAGCAGT	: 960
Brazil-I_AFBK01000508.1_A	:	AAA	ATATTCTCAAGA	AGATCAAT	GAGAAGTCCAAAA	ATGAGGTCTGA	AATAATGA	AAAATTTAT	GCACAGCTTGAGCAGT	: 960
VCG-I	:	AAA	ATATTCTCAAGA	AGATCAAT	GAGAAGTCCAAAA	ATGAGGTCTGA	AATAATGA	AAAATTTAT	GCACAGCTTGAGCAGT	: 960
Sal-1_PVX_088910	:	AAA	ATATTCTCAAGA	AGATCAAT	GAGAAGTCCAAAA	ATGAGGTCTGA	AATAATGA	AAAATTTAT	GCACAGCTTGAGCAGT	: 960
Mauritania_I_AFNIO1000333	:	AAA	ATATTCTCAAGA	AGATCAAT	GAGAAGTCCAAAA	ATGAGGTCTGA	AATAATGA	AAAATTTAT	GCACAGCTTGAGCAGT	: 960
NKorean_AFNJ01000531	:	AAA	ATATTCTCAAGA	AGATCAAT	GAGAAGTCCAAAA	ATGAGGTCTGA	AATAATGA	AAAATTTAT	GCACAGCTTGAGCAGT	: 960
India-VII_AFBK01000586_AFBK01000587	:	AAA	ATATTCTCAAGA	AGATCAAT	GAGAAGTCCAAAA	ATGAGGTCTGA	AATAATGA	AAAATTTAT	GCACAGCTTGAGCAGT	: 960
		g	AAATATTCTCa	AGAAgATCAAT	GAgAAGTCCAAAA	ATGAgGTCTT	AATAA	Ga	GA	ATTATGCACAGCTTGAGCAGT

		*	980	*	1000	*	1020	*	1040	
P.coatneyi_CM002856.1	:	TACAAGCACC	ATGCCGGGGG	CACACGTGG	CTCTTGTCAGT	CCAGAGGTGT	GAGCCAAAGTTAC	CGAAGGCCTC	CTGAG	: 1040
Pknowlesi_NC_011906.1	:	TATAAGCACC	ATGCCGGGGG	TACTCGTGG	CTCTTATGCA	GTACAGAGGT	GTGGGCCAACTT	TCAAGGCG	GCCTCAG	: 1040
Pinui_NW_008481888.1	:	TACAAGCACC	ATGCCACGGG	TACGCGTGG	CTCTTCCTGC	AGTCCAGAGG	GTGTGGCCAA	AGTTACCA	ACACACG	: 1040
Pfragile_NW_012192586.1	:	TACAAGCACC	GTGCCGGG	ACTACGCGT	GCTTCTTCCT	GCAGTCCAG	AGGTGCGCA	AACTTTAC	AAAAGTC	: 1040
Pcynomolgi_BAEJ01000249	:	TACAAGCACC	ATGCTGGGGG	CACGCGTGG	CTCTTCCTGC	AGTCCAGAG	TTGGCGCGC	GAAGTTAG	CGAAGGC	: 1040
Brazil-I_AFBK01000508.1_A	:	TACAAGCACC	ATGCCGGGGG	CACGCGTGG	GCCTTCCTGC	AGTCCAGAG	ATGTGCGC	GAAGTTAC	CGCAAGG	: 1040
VCG-I	:	TACAAGCACC	ATGCCGGGGG	CACGCGTGG	GCCTTCCTGC	AGTCCAGAG	ATGTGCGC	GAAGTTAC	CGCAAGG	: 1040
Sal-1_PVX_088910	:	TACAAGCACC	ATGCCGGGGG	CACGCGTGG	GCCTTCCTGC	AGTCCAGAG	ATGTGCGC	GAAGTTAC	CGCAAGG	: 1040
Mauritania_I_AFNIO1000333	:	TACAAGCACC	ATGCCGGGGG	CACGCGTGG	GCCTTCCTGC	AGTCCAGAG	ATGTGCGC	GAAGTTAC	CGCAAGG	: 1040
NKorean_AFNJO1000531	:	TACAAGCACC	ATGCCGGGGG	CACGCGTGG	GCCTTCCTGC	AGTCCAGAG	ATGTGCGC	GAAGTTAC	CGCAAGG	: 1040
India-VII_AFBK01000586_AFBK01000587	:	TACAAGCACC	ATGCCGGGGG	CACGCGTGG	GCCTTCCTGC	AGTCCAGAG	ATGTGCGC	GAAGTTAC	CGCAAGG	: 1040
		TAcAAGCACC	atGccgGgG	ACgCGTGGc	CCTTCcTGCA	GtCAGTcCAGAG	TGtGcgC	AagTTacg	Aagg ga gTgAg	

		*	1060	*	1080	*	1100	*	1120		
P.coatneyi_CM002856.1	:	CGTTCGAC	GAGAAGGGT	GACCCCTC	CTCCACCG	CGGGG	GGCAACCAAAGCG	AAACATGGG	CACGGCGG	CCCCAAC	: 1116
Pknowlesi_NC_011906.1	:	CGTTGACG	GAGAAGGGT	TGGCCAG	CAGATTG	CTCCCGCG	GTGGCAACCAAAGCG	AAACATGG	CTCGCG	CGGGTCC	: 1120
Pinui_NW_008481888.1	:	CGTTGACC	GAGAAGGGCG	ATCAGAC	CGCCACCG	CGGGG	GGCAACCAAAGCG	AAACCTG	CCCGCG	CGGTCCCC	: 1117
Pfragile_NW_012192586.1	:	GTTTGACG	GAG-----	ACCTCCAC	CACGGGG	GGCAACCAAAGCG	AAACATGG	CGCTG	CGGGCG	CCCTAAC	: 1105
Pcynomolgi_BAEJ01000249	:	CGTTGACG	GAGAAGGGT	TGACCA	AGATGCC	ACCACAGGG	GGCAACCAAAGCG	AAACATGG	CGCGCG	CGGCCCC	: 1117
Brazil-I_AFBK01000508.1_A	:	CGTTGATG	GAGAAGGGCG	ACCGGG	CCACCACCG	CGGGG	GGCAACCAAAGCG	AAAGCGT	GGCTG	CGGGCG	: 1117
VCG-I	:	CGTTGATG	GAGAAGGGCG	ACCGGG	CCACCACCG	CGGGG	GGCAACCAAAGCG	AAAGCGT	GGCTG	CGGGCG	: 1117
Sal-1_PVX_088910	:	CGTTGATG	GAGAAGGGCG	ACCGGG	CCACCACCG	CGGGG	GGCAACCAAAGCG	AAAGCGT	GGCTG	CGGGCG	: 1117
Mauritania_I_AFNIO1000333	:	CGTTGATG	GAGAAGGGCG	ACCGGG	CCACCACCG	CGGGG	GGCAACCAAAGCG	AAAGCGT	GGCTG	CGGGCG	: 1117
NKorean_AFNJO1000531	:	CGTTGATG	GAGAAGGGCG	ACCGGG	CCACCACCG	CGGGG	GGCAACCAAAGCG	AAAGCGT	GGCTG	CGGGCG	: 1117
India-VII_AFBK01000586_AFBK01000587	:	CGTTGATG	GAGAAGGGCG	ACCGGG	CCACCACCG	CGGGG	GGCAACCAAAGCG	AAAGCGT	GGCTG	CGGGCG	: 1117
		cGTtGA	gAGaaggg	gacc g	cc ccaCC	CgGgG	GGCAACcAAAGCG	cAA C TGgc	gCgGCGG	ccCC AAgg	

		*	1140	*	1160	*	1180	*	1200		
P.coatneyi_CM002856.1	:	-----	-----	-----	ACGGTTCC	TGCTAC	CAACACGG	CTGCTG	CTACCA	CTGCTACT	: 1158
Pknowlesi_NC_011906.1	:	ATTCTC	CCCTACA	ATG-----	GCTGCT	CCCTCC	ACCGAC	ACTGTT	ACTAACA	ACATGG	: 1179
Pinui_NW_008481888.1	:	ATGACG	CGCCTAC	TAGGGTT	GCTTCT	TCTCCCGG	CCCTGCT	GCTTTT	CCCAAC	ACGCTT	: 1197
Pfragile_NW_012192586.1	:	ATTCGGG	CCCTAC	CACCGCTG	CTGCTG	CAAAACAG	TGCTGCT	TCCCCA	AAACAG	CTGCTG	: 1185
Pcynomolgi_BAEJ01000249	:	ATGCGAG	CCCTAC	CACG---	GCTGCT	TCCAACG	CTGCTG	CTTCCC	CGAC	ACTACT	: 1194
Brazil-I_AFBK01000508.1_A	:	ATGCGGG	CCCA	ACCGTG	-----	GCTGCT	CCTAAC	ACTGCT	GCTAC	GCTCAAAA	: 1170
VCG-I	:	ATGCGGG	CCCA	ACCGTG	-----	GCTGCT	CCTAAC	ACTGCT	GCTAC	GCTCAAAA	: 1170
Sal-1_PVX_088910	:	ATGCGGG	CCCA	ACCGTG	-----	GCTGCT	CCTAAC	ACTGCT	GCTAC	GCTCAAAA	: 1170
Mauritania_I_AFNIO1000333	:	ATGCGGG	CCCA	ACCGTG	-----	GCTGCT	CCTAAC	ACTGCT	GCTAC	GCTCAAAA	: 1170
NKorean_AFNJO1000531	:	ATGCGGG	CCCA	ACCGTG	-----	GCTGCT	CCTAAC	ACTGCT	GCTAC	GCTCAAAA	: 1170
India-VII_AFBK01000586_AFBK01000587	:	ATGCGGG	CCCA	ACCGTG	-----	GCTGCT	CCTAAC	ACTGCT	GCTAC	GCTCAAAA	: 1170
		at c	ccc ac	g		gCt ctCC	acAC g	gCt c	ca ac	gct	

		*	1220	*	1240	*	1260	*	1280	
P.coatneyi_CM002856.1	:	ACTACGAACACGGCAACTAATACCAACACGGCA	-----	ACTAATACCAACACGGCTACT	---	AATAC	:	1217		
Pknowlesi_NC_011906.1	:	ACTACAACCGCGCCTGCTACTGCCAACATGGCTGCTCCTTCCACCAACACTGCTACTGCCAACATGGCTGCT	---	CCTTC	:	1256				
Pinui_NW_008481888.1	:	AACGCTACTGCTGCTTCCAACGCTACTGCTGCTTCCAACGCTACTGCTGCTTCCAACGCTACTGAT	-----	GCTTC	:	1268				
Pfragile_NW_012192586.1	:	ACCAGC	-----	GCTTC	:	1196				
Pcynomolgi_BAEJ01000249	:	ACCGTGCTGCGAACACCGCTGCTGCTCCGAACACTGCTTCTGCTTCCAACGCTGCTGCTACTCCCAACCCCTGCT		GCTGC	:	1274				
Brazil-I_AFMK01000508.1_A	:	-----		GCTTC	:	1175				
VCG-I	:	-----		GCTTC	:	1175				
Sal-1_PVX_088910	:	-----		GCTTC	:	1175				
Mauritania_I_AFNIO1000333	:	-----		GCTTC	:	1175				
NKorean_AFNJ01000531	:	-----		GCTTC	:	1175				
India-VII_AFBK01000586_AFBK01000587	:	-----		GCTTC	:	1175				

gcTtC

		*	1300	*	1320	*	1340	*	1360	
P.coatneyi_CM002856.1	:	CAACAGTGCAGCTACTACCAACACGGCCGCT	-----	ACTACCAACACGGCCGCTACTACCAACACGA	:	1279				
Pknowlesi_NC_011906.1	:	CACCAACACTGCTACTGCCAACATGGCTGCTCCTTCCACCGACACTGTA		ACTACCAACATGGCTACCACTACAACCGTGC	:	1336				
Pinui_NW_008481888.1	:	CAACGCTACTGCTGCTTCCAACCCCTGCTGCT			:	1300				
Pfragile_NW_012192586.1	:	CAACGATACTAATGCTTCTCCCCACACGAAT			:	1228				
Pcynomolgi_BAEJ01000249	:	TCCGAACACTGCTGCTACTCCCAACTCTGCT			:	1306				
Brazil-I_AFMK01000508.1_A	:	CCCCAACCGCGGCTGCTACTAACA		CTGCTGCT	:	1207				
VCG-I	:	CCCCAACCGCGGCTGCTACTAACA		CTGCTGCT	:	1207				
Sal-1_PVX_088910	:	CCCCAACCGCGGCTGCTACTAACA		CTGCTGCT	:	1207				
Mauritania_I_AFNIO1000333	:	CCCCAACCGCGGCTGCTACTAACA		CTGCTGCT	:	1207				
NKorean_AFNJ01000531	:	CCCCAACCGCGGCTGCTACTAACA		CTGCTGCT	:	1207				
India-VII_AFBK01000586_AFBK01000587	:	CCCCAACCGCGGCTGCTACTAACA		CTGCTGCT	:	1207				

c caa C gcTgCT C aaCa gCtgct

		*	1380	*	1400	*	1420	*	1440	
P.coatneyi_CM002856.1	:	CCGCTACTACCACTGTAGCTACTTC		CCCTGAACACC	-----	CCCCTGTACGGCACCAGOTCC	:	1338		
Pknowlesi_NC_011906.1	:	CTGCTACTGCCAACACGGCTGCTTC		CCCTGACACTAA		TACTGATTCTTCTACTTAC		CCCCTGTATGGCAAGGAATCC	:	1413
Pinui_NW_008481888.1	:	CTGCCAACACTGCTGCT	---	ACTTCCCAA	---	CTGAGCAAC	-----	CCCCTGTATGGCATCAGOTCC	:	1356
Pfragile_NW_012192586.1	:	CTTCCAAAGAGGGTGCTTCCACCAGTCC	---	CTGAGCAAC	-----	CCCCTGTACGGCACCCTGOTAC	:	1287		
Pcynomolgi_BAEJ01000249	:	CCCCAACGCTGCTGCT	---	ACTTCCCA	---	CTGAGCAAC	-----	CCCCTGTACGACAGAGOTCC	:	1362
Brazil-I_AFMK01000508.1_A	:	CCCCAACATGGGTGCT	---	ACCTCCCG	---	CTGAGCAAC	-----	CCCCTGTACGGCACCAGOTCC	:	1263
VCG-I	:	CCCCAACATGGGTGCT	---	ACCTCCCG	---	CTGAGCAAC	-----	CCCCTGTACGGCACCAGOTCC	:	1263
Sal-1_PVX_088910	:	CCCCAACATGGGTGCT	---	ACCTCCCG	---	CTGAGCAAC	-----	CCCCTGTACGGCACCAGOTCC	:	1263
Mauritania_I_AFNIO1000333	:	CCCCAACATGGGTGCT	---	ACCTCCCG	---	CTGAGCAAC	-----	CCCCTGTACGGCACCAGOTCC	:	1263
NKorean_AFNJ01000531	:	CCCCAACATGGGTGCT	---	ACCTCCCG	---	CTGAGCAAC	-----	CCCCTGTACGGCACCAGOTCC	:	1263
India-VII_AFBK01000586_AFBK01000587	:	CCCCAACATGGGTGCT	---	ACCTCCCG	---	CTGAGCAAC	-----	CCCCTGTACGGCACCAGOTCC	:	1263

C CcAac g tgc aC tccCc ctgAgcaac CCCCTGTAcGgCAccagcTcC

		*	1700	*	1720	*	1740	*	1760		
P.coatneyi_CM002856.1	:		GACGCCAAATG		TATTGCAAGAAAAG		CTAGTTAATGGCCAGCTAAT		TAGAAAAC	TCGACTTAAAGG	TCGCACGGAGGA : 1658
Pknowlesi_NC_011906.1	:		GACGCCAGAAATG		TATTGCAAGAAAAA		CTAGTTAATGGCCAGTTAAT		TAGAAAAA	CAACGATTTAAAGG	TCAGACAGAGGA : 1733
Pinui_NW_008481888.1	:		GACGCCAAATC		TATTGCAACAAAAG		CTAGTTAATGGCAAGCTAAT		TGAAACCT	TCGATATAAGG	TTTCGACGGAGGA : 1676
Pfragile_NW_012192586.1	:		GACGCCAAATTT		TATTGCAAGAAAAT		CTAGTTAATGGCCAGCTACT		TACAAACCT	CTGATTTTCAGGCAT	TCGCACGAGGA : 1607
Pcynomolgi_BAEJ01000249	:		GACGCCAAATCT		TATTGCAAGAAAGTC		CTAGTTAATGGTCAGCTAGT		TCGAAACCT	TCGATTTAAGCG	TCGCACGGAGGA : 1682
Brazil-I_AFBK01000508.1_A	:		GACGCCAAGACCT		TATTGCAAGAAAGCC		CTAGTTAATGGCCAGCTAAT		TCGAAACCT	TCAGATTTAAAC	TCGCGGACGGAGGA : 1583
VCG-I	:		GACGCCAAGACCT		TATTGCAAGAAAGCC		CTAGTTAATGGCCAGCTAAT		TCGAAACCT	TCAGATTTAAAC	TCGCGGACGGAGGA : 1583
Sal-1_PVX_088910	:		GACGCCAAGACCT		TATTGCAAGAAAGCC		CTAGTTAATGGCCAGCTAAT		TCGAAACCT	TCAGATTTAAAC	TCGCGGACGGAGGA : 1583
Mauritania_I_AFNIO1000333	:		GACGCCAAGACCT		TATTGCAAGAAAGCC		CTAGTTAATGGCCAGCTAAT		TCGAAACCT	TCAGATTTAAAC	TCGCGGACGGAGGA : 1583
NKorean_AFNJ01000531	:		GACGCCAAGACCT		TATTGCAAGAAAGCC		CTAGTTAATGGCCAGCTAAT		TCGAAACCT	TCAGATTTAAAC	TCGCGGACGGAGGA : 1583
India-VII_AFBK01000586_AFBK01000587	:		GACGCCAAGACCT		TATTGCAAGAAAGCC		CTAGTTAATGGCCAGCTAAT		TCGAAACCT	TCAGATTTAAAC	TCGCGGACGGAGGA : 1583
			GACGCCAa A		TATTGCAAgAAA		CTAGTTAATGGccAGcTAaT		gAAAcCtc	GAttTaAa Gc	gcGacgGAGGA

		*	1780	*	1800	*	1820	*	1840	
P.coatneyi_CM002856.1	:		AGAAGACATGATAAC		CGAGTTTTCCAGCAAG		TACAATTTATTCTACGAA		AGGCTGAAATGGAG	GAGTTGCGGAAATTG : 1738
Pknowlesi_NC_011906.1	:		AGAAGATATGATAAAC		GAAATTTTCCAGTAAG		TACAATTTATTCTATGAA		AGGCTTAACATGGAG	GAGTTGCGGAAATTG : 1813
Pinui_NW_008481888.1	:		AGAAGACCTGATAAC		CGAGTTTTCCAGCAAG		TACAATTTATTCTACGAA		AGGCTGAACATGGA	GAGTTGCGGAAATTG : 1756
Pfragile_NW_012192586.1	:		AGAAGATCTGATAAAC		GAAATTTTCCAGCAAA		TACAATTTATTCTACGAA		AGGCTTGAAGCTGGA	GAGTTGCGGAAATTG : 1687
Pcynomolgi_BAEJ01000249	:		AGAAGATCTGATAAAC		GAGTTTTTCCAGCAAG		TACAATTTATTCTACGAA		AGGCTGAAATGGAG	GAGTTGCGGAAATTG : 1762
Brazil-I_AFBK01000508.1_A	:		AGACGACCTCATAAAC		GAGTTTTTCCAGCAG		TACAATTTATTCTACGAC		AGGCTCAAGCTGGAG	GAGTTGCGGAAATTG : 1663
VCG-I	:		AGACGACCTCATAAAC		GAGTTTTTCCAGCAG		TACAATTTATTCTACGAC		AGGCTCAAGCTGGAG	GAGTTGCGGAAATTG : 1663
Sal-1_PVX_088910	:		AGACGACCTCATAAAC		GAGTTTTTCCAGCAG		TACAATTTATTCTACGAC		AGGCTCAAGCTGGAG	GAGTTGCGGAAATTG : 1663
Mauritania_I_AFNIO1000333	:		AGACGACCTCATAAAC		GAGTTTTTCCAGCAG		TACAATTTATTCTACGAC		AGGCTCAAGCTGGAG	GAGTTGCGGAAATTG : 1663
NKorean_AFNJ01000531	:		AGACGACCTCATAAAC		GAGTTTTTCCAGCAG		TACAATTTATTCTACGAC		AGGCTCAAGCTGGAG	GAGTTGCGGAAATTG : 1663
India-VII_AFBK01000586_AFBK01000587	:		AGACGACCTCATAAAC		GAGTTTTTCCAGCAG		TACAATTTATTCTACGAC		AGGCTCAAGCTGGAG	GAGTTGCGGAAATTG : 1663
			AGA GA cT		ATAAacGAgTTTTCCAGcA		gTACAATTTATTCTAcGA		AgGcT AAgcTGGAg	GAGTTGCGcGAAATTG

		*	1860	*	1880	*	1900	*	1920		
P.coatneyi_CM002856.1	:		AACAGAACAGGAAAG		CGGTCGAAGAATT		CGAAGGGAAGTCTGTC		CGTGCTGCAGGT	CGGCAACTCGCAGAAT	TGGTCCAGAC : 1818
Pknowlesi_NC_011906.1	:		AACAGGACAGAAAA		TCGGTAAGAATT		CCGAAGGGCAACTTGT		CTGTGTTGGAGGT	GCGCAACTCCGAGAAT	TGTCCTCCGAC : 1893
Pinui_NW_008481888.1	:		AACAGAACAA		GAAAGCTATCAAGAATT		CGAAGGGCAGCCTGTC		CGTGCTGCAGGT	CGGCAACTCGCAAAAT	AGTCTCCGAC : 1836
Pfragile_NW_012192586.1	:		AACAGAACAGGAAAG		CGGTCGAAGAATT		CGAAGGGTAGCCTGTC		CGTGCTGCAGGT	CGGCAACTCGCAGAAT	TGTACCCAC : 1767
Pcynomolgi_BAEJ01000249	:		AACAGAACAGGAAAG		CGGTCGAAGAATT		CGAAGGGCAGCCTGTC		CGTGCTGCAGGT	CGGCAACTCGCAGAAT	TGTCCAGAC : 1842
Brazil-I_AFBK01000508.1_A	:		AACAGAACAGGAAAG		CGGTCGAAGAATT		CGAAGGGCACCTGTC		CGTGCTGCAGGT	CGGCAACTCGCAGAAC	CCCCCGAC : 1743
VCG-I	:		AACAGAACAGGAAAG		CGGTCGAAGAATT		CGAAGGGCACCTGTC		CGTGCTGCAGGT	CGGCAACTCGCAGAAC	CCCCCGAC : 1743
Sal-1_PVX_088910	:		AACAGAACAGGAAAG		CGGTCGAAGAATT		CGAAGGGCACCTGTC		CGTGCTGCAGGT	CGGCAACTCGCAGAAC	CCCCCGAC : 1743
Mauritania_I_AFNIO1000333	:		AACAGAACAGGAAAG		CGGTCGAAGAATT		CGAAGGGCACCTGTC		CGTGCTGCAGGT	CGGCAACTCGCAGAAC	CCCCCGAC : 1743
NKorean_AFNJ01000531	:		AACAGAACAGGAAAG		CGGTCGAAGAATT		CGAAGGGCACCTGTC		CGTGCTGCAGGT	CGGCAACTCGCAGAAC	CCCCCGAC : 1743
India-VII_AFBK01000586_AFBK01000587	:		AACAGAACAGGAAAG		CGGTCGAAGAATT		CGAAGGGCACCTGTC		CGTGCTGCAGGT	CGGCAACTCGCAGAAC	CCCCCGAC : 1743
			AACAGaACAggAAAgCgcTc		AAGAATtCgAAGGGcA		ccTgTCCgTGcTGgAGGTcg		CAAcTCgCAgAA g	cCcgAC	

		*	2180	*	2200	*	2220	*	2240		
P.coatneyi_CM002856.1	:	-----								:	-
Pknowlesi_NC_011906.1	:	-----								:	-
Pinui_NW_008481888.1	:	-----								:	-
Pfragile_NW_012192586.1	:	-----AG								:	1808
Pcynomolgi_BAEJ01000249	:	-----AACAAACGCAAATGGGAACAACGCAA								:	1907
Brazil-I_AFBK01000508.1_A	:	GCAAATGCAAACCTCGCAAATGCAAACCTCGCAAATGCAAACCTCGCAAACGCAAACGCCGCAAACGCAAACGCCGCTAA	:	1955							
VCG-I	:	GCAAATGCAAACCTCGCAAATGCAAACCTCGCAAATGCAAACCTCGCAAACGCAAACGCCGCAAACGCAAACGCCGCTAA	:	2063							
Sal-1_PVX_088910	:	GCAAATGCAAACCTCGCAAATGCAAACCTCGCAAATGCAAACCTCGCAAACGCAAACGCCGCAAACGCAAACGCCGCTAA	:	2063							
Mauritania_I_AFNIO1000333	:	-----GCAAACGCAAACGCCGCAAACGCAAACGCCGCTAA								:	1817
NKorean_AFNJ01000531	:	-----								:	-
India-VII_AFBK01000586_AFBK01000587	:	-----								:	-

		*	2260	*	2280	*	2300	*	2320		
P.coatneyi_CM002856.1	:	-----AACGCCCAAATGGAAACGGCGCAAATGTAAATGCTCAAAATGAA								:	1918
Pknowlesi_NC_011906.1	:	-----AACACATGAATGGA-----GCTA								:	1951
Pinui_NW_008481888.1	:	-----AACGCGCAAATGGAA								:	1891
Pfragile_NW_012192586.1	:	CGGACATGCGGCAAATGAC	:	1843							
Pcynomolgi_BAEJ01000249	:	TGGAAACAAACGCAAATGGA	:	1942							
Brazil-I_AFBK01000508.1_A	:	TGCAAACGCCGCAAATGGG	:	1990							
VCG-I	:	TGCAAACGCCGCAAATGGG	:	2098							
Sal-1_PVX_088910	:	TGCAAACGCCGCAAATGGG	:	2098							
Mauritania_I_AFNIO1000333	:	TGCAAACGCCGCAAATGGG	:	1852							
NKorean_AFNJ01000531	:	-----AACGCCCAAATAGCA								:	1953
India-VII_AFBK01000586_AFBK01000587	:	-----AACGCCCAAATAGCA								:	1901

aacgcc caaat g A

		*	2340	*	2360	*	2380	*	2400	
P.coatneyi_CM002856.1	:	ACAACGGAAGCGCTCCCCCTCATCGTAGTGGTAGGGGACGAGCTCGGAGAAAAAACCGAGATATCATCAAAAAAAT	:	1998						
Pknowlesi_NC_011906.1	:	ACAACGGAAGCGCTCCCTCCCTCATCGTAGTAGTAAGGACGATCTCGCTGAAAAAACCTGATGACATCATCAAAAAAAT	:	2031						
Pinui_NW_008481888.1	:	ACAACGGAAGCGCTCCCCCTCATCGTAGTGGTAGGGGCGATCTCGCGAAAAAACCGAGGACATCATCAAGAACAAAT	:	1971						
Pfragile_NW_012192586.1	:	ATGACNNN-----	:	1848						
Pcynomolgi_BAEJ01000249	:	ACAACGGAAGCGGATCCCCCTCATCGTAGTGGTAGGGGCGATCTCGCGAAAAAACCTGACGACATCATCAAGAACAAAT	:	2022						
Brazil-I_AFBK01000508.1_A	:	ACAACGGAAGCGGATCCCCCTCATCGTAGTGGTAGGGGCGATCTCGCGAAAAAACCGAGGACATCATCAAGAACAAAC	:	2070						
VCG-I	:	ACAACGGAAGCGGATCCCCCTCATCGTAGTGGTAGGGGCGATCTCGCGAAAAAACCGAGGACATCATCAAGAACAAAC	:	2178						
Sal-1_PVX_088910	:	ACAACGGAAGCGGATCCCCCTCATCGTAGTGGTAGGGGCGATCTCGCGAAAAAACCGAGGACATCATCAAGAACAAAC	:	2178						
Mauritania_I_AFNIO1000333	:	ACAACGGAAGCGGATCCCCCTCATCGTAGTGGTAGGGGCGATCTCGCGAAAAAACCGAGGACATCATCAAGAACAAAC	:	1932						
NKorean_AFNJ01000531	:	ACAACGGAAGCGGATCCCCCTCATCGTAGTGGTAGGGGCGATCTCGCGAAAAAACCGAGGACATCATCAAGAACAAAC	:	2033						
India-VII_AFBK01000586_AFBK01000587	:	ACAACGGAAGCGGATCCCCCTCATCGTAGTGGTAGGGGCGATCTTGGCGAAAAAACCGAGGACATCATCAAGAACAAAC	:	1981						

AcaACGgaagcgc tccccctcatcgtagtggtagggg cgatctcgg gaaaaaac ga gacatcatcaa aa aa

		*	2420	*	2440	*	2460	*	2480		
P.coatneyi_CM002856.1	:	GTGGACGTGG	AAG	CCTTGACAGCCGACGTGGAACAAGCCTTT	CAAAA	GCT	TCGAATACCAAAGTGGAAAGT	TTCTCT	TGCAAA	: 2078	
Pknowlesi_NC_011906.1	:	GTGGAC	CTGGAAT	CCTT	AAAAGCCGACGTGGAACAAGCCTTTA	GAAAC	TCGAATACCAAAGTGGAAAGT	TTCTCGGCAAA		: 2111	
Pinui_NW_008481888.1	:	GTGGACGTGG	CAAC	CCTTGACAG	AAAG	CGTGGAACAAGCCTTTA	AAAACTC	TCATGG	AAGTGGAAAGT	: 2051	
Pfragile_NW_012192586.1	:	-----								:	-
Pcynomolgi_BAEJ01000249	:	GTGGACGTGG	CAG	CCTTGG	CAGCCGACGTGGAACAAGCCTTTA	GAAAC	TCGAAT	TGAAAAGTGGAAAG	CTTCTCGGCAAA	: 2102	
Brazil-I_AFMK01000508.1_A	:	GTGGACGTGG	CAG	CCTTGACAGCCGACGTGGAACAAGCCTTTA	AAAACTC	GAAT	TGCAGAGTGGAAAG	CTTCTCGGCAAA		: 2150	
VCG-I	:	GTGGACGTGG	CAG	CCTTGACAGCCGACGTGGAACAAGCCTTTA	AAAACTC	GAAT	TGCAGAGTGGAAAG	CTTCTCGGCAAA		: 2258	
Sal-1_PVX_088910	:	GTGGACGTGG	CAG	CCTTGACAGCCGACGTGGAACAAGCCTTTA	AAAACTC	GAAT	TGCAGAGTGGAAAG	CTTCTCGGCAAA		: 2258	
Mauritania_I_AFNI01000333	:	GTGGACGTGG	CAG	CCTTGACAGCCGACGTGGAACAAGCCTTTA	AAAACTC	GAAT	TGCAGAGTGGAAAG	CTTCTCGGCAAA		: 2012	
NKorean_AFNJ01000531	:	GTGGACGTGG	CAG	CCTTGACAGCCGACGTGGAACAAGCCTTTA	AAAACTC	GAAT	TGCAGAGTGGAAAG	CTTCTCGGCAAA		: 2113	
India-VII_AFBK01000586_AFBK01000587	:	GTGGACGTGG	CAG	CCTTGACAGCCGACGTGGAACAAGCCTTTA	AAAACTC	GAAT	TGCAGAGTGGAAAG	CTTCTCGGCAAA		: 2061	
		gtggacgtgg a ccttgacagccgacgtggaacaagccttta aaac tcgaat a agtggaaag ttctcggcaaa									

		*	2500	*	2520	*			
P.coatneyi_CM002856.1	:	CTTATCT	CACGC	CTGGTTCTCCTCTC	TCCATTGCGTT	GCTCT	TATTCATTT	GT : 2133	
Pknowlesi_NC_011906.1	:	CTTATCT	CACGC	CTGGTTCTCCT	ATCC	TCCATTGCGTT	AGTCCTATTCATTT	GT : 2166	
Pinui_NW_008481888.1	:	CTTATCG	CACGC	CTGGTTCTCCTCTC	T	TCCATTGCT	TAACTCCTATTCATTT	GT : 2106	
Pfragile_NW_012192586.1	:	-----						:	-
Pcynomolgi_BAEJ01000249	:	CTTATCG	CACGC	CTGGTTCTCCTCTC	T	TCCATTGCGTT	ACTCCTATTCATTT	TT : 2157	
Brazil-I_AFMK01000508.1_A	:	CTTATCG	CACGC	CTGGTTCTCCTCTC	T	TCCATTGCGTT	GCTCCTATTCATTT	TT : 2205	
VCG-I	:	CTTATCG	CACGC	CTGGTTCTCCTCTC	T	TCCATTGCGTT	GCTCCTATTCATTT	TT : 2313	
Sal-1_PVX_088910	:	CTTATCG	CACGC	CTGGTTCTCCTCTC	T	TCCATTGCGTT	GCTCCTATTCATTT	TT : 2313	
Mauritania_I_AFNI01000333	:	CTTATCG	CACGC	CTGGTTCTCCTCTC	T	TCCATTGCGTT	GCTCCTATTCATTT	TT : 2067	
NKorean_AFNJ01000531	:	CTTATCG	CACGC	CTGGTTCTCCTCTC	T	TCCATTGCGTT	GCTCCTATTCATTT	TT : 2168	
India-VII_AFBK01000586_AFBK01000587	:	CTTATCG	CACGC	CTGGTTCTCCTCTC	T	TCCATTGCGTT	GCTCCTATTCATTT	TT : 2116	
		cttatc cacgc ctggttctcctctc tccattgcgtt ctcctattcattt t							

b. Deduced amino acid alignment.

		*	20	*	40	*	60	*	80																																																																	
P.coatneyi_CM002856.1	:	MK	NGS	LLV	LLS	AIL	SAT	NAL	IR	NG	NN	EQ	AL	V	PE	K	S	D	S	S	G	G	Q	N	K	P	S	C	D	N	Q	D	T	C	E	I	Q	K	M	A	E	E	M	M	E	K	M	V	N	E	K	D	V	F	T	S	I	M	E	P	L	:	81											
Pknowlesi_NC_011906.1	:	MK	NGS	LLV	LLS	AIL	SAT	NAL	IR	NG	NN	EQ	AL	V	P	D	N	S	G	D	E	N	A	G	O	N	K	T	S	S	D	N	Q	D	T	C	E	I	Q	K	M	A	E	E	M	M	E	K	M	M	E	K	D	V	F	S	S	I	M	E	P	L	:	81										
Pinui_NW_008481888.1	:	MK	NT	ALL	V	LLS	AIL	S	A	N	A	L	I	R	N	G	N	T	T	Q	A	L	V	P	E	K	S	N	D	P	S	G	G	Q	N	N	P	S	C	D	N	R	E	T	C	E	I	Q	M	A	Q	E	M	M	E	K	M	M	E	K	D	V	F	S	S	I	M	E	P	L	:	81		
Pfragile_NW_012192586.1	:	MK	YN	AT	LL	V	LLS	AIL	S	A	G	K	A	L	I	R	N	G	N	T	Q	A	L	V	P	E	N	G	G	D	P	S	G	G	Q	N	N	P	S	C	E	N	Q	D	T	C	E	V	Q	K	M	A	E	E	M	M	E	K	M	M	E	K	D	V	F	S	S	I	M	E	P	L	:	81
Pcynomolgi_BAEJ01000249	:	MK	CN	A	ALL	V	LLS	AIL	S	A	N	A	L	I	R	N	G	N	T	Q	A	L	V	P	E	K	S	G	D	P	S	G	G	Q	N	N	P	S	C	D	N	Q	D	T	C	E	I	Q	K	M	A	E	E	M	M	E	K	M	M	E	K	D	M	F	S	S	I	M	E	P	L	:	81	
Brazil-I_AFMK01000508.1_A	:	MK	CN	AS	LL	V	LLS	AIL	S	A	N	A	L	I	R	N	G	N	N	Q	A	L	V	P	E	K	G	A	D	P	S	G	G	Q	N	N	R	S	C	E	N	Q	D	T	C	E	I	Q	K	M	A	E	E	M	M	E	K	M	M	E	K	D	V	F	S	S	I	M	E	P	L	:	81	
VCG-I	:	MK	CN	AS	LL	V	LLS	AIL	S	A	N	A	L	I	R	N	G	N	N	Q	A	L	V	P	E	K	G	A	D	P	S	G	G	Q	N	N	R	S	C	E	N	Q	D	T	C	E	I	Q	K	M	A	E	E	M	M	E	K	M	M	E	K	D	V	F	S	S	I	M	E	P	L	:	81	
Sal-1_PVX_088910	:	MK	CN	AS	LL	V	LLS	AIL	S	A	N	A	L	I	R	N	G	N	N	Q	A	L	V	P	E	K	G	A	D	P	S	G	G	Q	N	N	R	S	C	E	N	Q	D	T	C	E	I	Q	K	M	A	E	E	M	M	E	K	M	M	E	K	D	V	F	S	S	I	M	E	P	L	:	81	
Mauritania_I_AFNI01000333	:	MK	CN	AS	LL	V	LLS	AIL	S	A	N	A	L	I	R	N	G	N	N	Q	A	L	V	P	E	K	G	A	D	P	S	G	G	Q	N	N	R	S	C	E	N	Q	D	T	C	E	I	Q	K	M	A	E	E	M	M	E	K	M	M	E	K	D	V	F	S	S	I	M	E	P	L	:	81	
N.Korean_AFNJ01000531	:	MK	CN	AS	LL	V	LLS	AIL	S	A	N	A	L	I	R	N	G	N	N	Q	A	L	V	P	E	K	G	A	D	P	S	G	G	Q	N	N	R	S	C	E	N	Q	D	T	C	E	I	Q	K	M	A	E	E	M	M	E	K	M	M	E	K	D	V	F	S	S	I	M	E	P	L	:	81	
India-VII_AFBK01000586_AFBK01000587	:	MK	CN	AS	LL	V	LLS	AIL	S	A	N	A	L	I	R	N	G	N	N	Q	A	L	V	P	E	K	G	A	D	P	S	G	G	Q	N	N	R	S	C	E	N	Q	D	T	C	E	I	Q	K	M	A	E	E	M	M	E	K	M	M	E	K	D	V	F	S	S	I	M	E	P	L	:	81	

MKcN LLVLLSA6LSA nALIRNGNn QALVPek DpsgGQnN Sg NqdTCE6QkMA2EMMeKM6kEKD6F3SIMEPL

		*	100	*	120	*	140	*	160																																																																												
P.coatneyi_CM002856.1	:	Q	S	K	L	T	D	D	H	L	C	S	K	L	K	Y	T	N	V	C	L	H	E	K	D	K	T	P	L	T	F	P	C	T	S	P	E	Y	E	K	L	I	Q	O	F	T	Y	Q	K	L	C	N	S	K	V	A	F	S	N	V	L	L	K	S	F	I	D	K	K	N	E	E	N	T	F	N	A	I	I	Q	N	Y	:	162	
Pknowlesi_NC_011906.1	:	Q	S	K	L	T	D	D	R	L	C	S	K	M	K	Y	T	N	I	C	L	H	E	K	D	K	T	P	L	T	F	P	C	T	N	P	Q	Y	E	Q	L	I	Q	O	F	T	Y	K	K	L	C	N	S	K	V	A	F	S	N	V	L	L	K	S	F	I	D	K	K	N	E	E	N	T	F	N	A	I	I	Q	N	Y	:	162	
Pinui_NW_008481888.1	:	Q	S	K	L	A	D	D	H	L	C	S	E	V	K	Y	T	N	I	C	L	H	E	K	D	N	S	L	T	F	P	C	T	S	P	E	Y	E	Q	L	I	H	E	F	T	Y	K	K	L	C	N	S	K	V	A	F	S	N	V	L	L	K	S	F	I	D	K	K	N	E	E	N	T	F	N	T	I	I	E	N	Y	:	162		
Pfragile_NW_012192586.1	:	Q	S	K	L	S	D	N	H	L	C	S	T	V	K	Y	T	N	I	C	L	H	E	K	D	K	T	P	L	T	F	P	C	T	S	P	Q	Y	E	Q	L	I	H	E	F	T	Y	K	K	L	C	N	S	K	V	A	F	S	N	V	L	L	K	S	F	I	N	K	N	E	E	N	T	F	N	T	I	I	Q	N	Y	:	162		
Pcynomolgi_BAEJ01000249	:	Q	S	K	L	P	D	D	H	L	C	S	K	L	K	Y	T	N	I	C	L	H	E	K	D	K	T	P	L	T	F	P	C	T	S	P	Q	Y	E	Q	L	I	H	E	F	T	Y	K	K	L	C	N	S	K	V	A	F	S	N	V	L	L	K	S	F	I	N	K	N	E	E	N	T	F	N	T	I	I	Q	N	Y	:	162		
Brazil-I_AFMK01000508.1_A	:	Q	S	K	L	T	D	D	H	L	C	S	K	M	K	Y	T	N	I	C	L	H	E	K	D	K	T	P	L	T	F	P	C	T	S	P	Q	Y	E	Q	L	I	H	R	E	F	T	Y	K	K	L	C	N	S	K	V	A	F	S	N	V	L	L	K	S	F	I	D	K	K	N	E	E	N	T	F	N	T	I	I	Q	N	Y	:	162
VCG-I	:	Q	S	K	L	T	D	D	H	L	C	S	K	M	K	Y	T	N	I	C	L	H	E	K	D	K	T	P	L	T	F	P	C	T	S	P	Q	Y	E	Q	L	I	H	R	E	F	T	Y	K	K	L	C	N	S	K	V	A	F	S	N	V	L	L	K	S	F	I	D	K	K	N	E	E	N	T	F	N	T	I	I	Q	N	Y	:	162
Sal-1_PVX_088910	:	Q	S	K	L	T	D	D	H	L	C	S	K	M	K	Y	T	N	I	C	L	H	E	K	D	K	T	P	L	T	F	P	C	T	S	P	Q	Y	E	Q	L	I	H	R	E	F	T	Y	K	K	L	C	N	S	K	V	A	F	S	N	V	L	L	K	S	F	I	D	K	K	N	E	E	N	T	F	N	T	I	I	Q	N	Y	:	162
Mauritania_I_AFNI01000333	:	Q	S	K	L	T	D	D	H	L	C	S	K	M	K	Y	T	N	I	C	L	H	E	K	D	K	T	P	L	T	F	P	C	T	S	P	Q	Y	E	Q	L	I	H	R	E	F	T	Y	K	K	L	C	N	S	K	V	A	F	S	N	V	L	L	K	S	F	I	D	K	K	N	E	E	N	T	F	N	T	I	I	Q	N	Y	:	162
N.Korean_AFNJ01000531	:	Q	S	K	L	T	D	D	H	L	C	S	K	M	K	Y	T	N	I	C	L	H	E	K	D	K	T	P	L	T	F	P	C	T	S	P	Q	Y	E	Q	L	I	H	R	E	F	T	Y	K	K	L	C	N	S	K	V	A	F	S	N	V	L	L	K	S	F	I	D	K	K	N	E	E	N	T	F	N	T	I	I	Q	N	Y	:	162
India-VII_AFBK01000586_AFBK01000587	:	Q	S	K	L	T	D	D	H	L	C	S	K	M	K	Y	T	N	I	C	L	H	E	K	D	K	T	P	L	T	F	P	C	T	S	P	Q	Y	E	Q	L	I	H	R	E	F	T	Y	K	K	L	C	N	S	K	V	A	F	S	N	V	L	L	K	S	F	I	D	K	K	N	E	E	N	T	F	N	T	I	I	Q	N	Y	:	162

QSKL DlhLCSk6KYtN6CLhEKDktpLTfPCTsP2YEqlI FTYkKLCNSkVAFsNVLLKSFilKkNEENTFNtII2NY

		*	180	*	200	*	220	*	240																																																																											
P.coatneyi_CM002856.1	:	K	V	L	S	T	C	I	D	E	D	L	K	D	I	Y	N	A	S	I	E	L	F	S	D	I	R	S	S	V	T	E	I	T	E	K	L	W	S	K	N	M	I	D	V	L	K	T	R	E	Q	T	I	A	G	I	L	C	E	L	R	N	G	N	N	S	P	L	V	S	N	S	L	S	Y	E	N	F	G	I	L	K	:	243
Pknowlesi_NC_011906.1	:	K	V	L	S	T	C	I	D	E	D	L	K	D	I	Y	N	A	S	I	E	L	F	S	D	L	R	T	S	V	R	E	I	T	E	K	L	W	S	K	N	M	I	E	V	L	K	T	R	E	Q	T	I	A	G	I	L	C	E	L	R	N	G	N	N	S	T	L	V	S	N	S	L	S	Y	E	N	F	G	I	L	K	:	243
Pinui_NW_008481888.1	:	K	V	L	S	T	C	I	D	A	D	L	K	D	I	Y	S	A	S	I	Q	L	F	S	D	L	R	S	A	V	T	E	I	S	E	R	L	W	S	K	N	M	I	D	V	L	K	T	R	E	E	T	I	T	G	I	L	C	E	L	R	K	G	N	N	S	T	L	V	S	N	S	E	S	Y	D	N	F	G	I	L	K	:	243
Pfragile_NW_012192586.1	:	K	I	L	S	T	C	I	D	E	D	L	K	D	I	Y	D	A	S	I	Q	L	F	S	D	I	R	V	S	V	T	E	I	T	E	K	L	W	S	K	N	M	I	D	V	L	K	T	R	E	Q	T	I	A	G	I	L	C	E	L	R	N	G	N	K	S	T	L	V	S	N	S	L	S	Y	E	N	F	G	I	L	K	:	243
Pcynomolgi_BAEJ01000249	:	K	L	L	S	T	C	I	D	E	D	L	K	D	I	Y	N	A	S	I	D	L	F	S	D	I	R	T	S	V	T	E	I	T	E	K	L	W	S	K	N	M	I	E	V	L	K	T	R	E	Q	T	I	A	G	I	L	C	E	L	R	N	G	N	N	S	P	L	V	S	N	S	E	S	Y	E	N	F	G	I	L	K	:	243
Brazil-I_AFMK01000508.1_A	:	K	V	L	S	T	C	I	D	D	L	K	D																																																																							

		*	260	*	280	*	300	*	320	
P.coatneyi_CM002856.1	:	VNYE	ALMNQAYKAFSDYYSYFP	FAIK	LEKGGFVERL	VAIHESLTNYR	TKNILKKINEKSKNEVLN	NNE	IMHSLSSYKHH	: 324
Pknowlesi_NC_011906.1	:	VNYE	GLINQAYKAFSDYYSYFP	FAIR	LLEKDGIVERL	VAIHESLTNYR	TRNILKKINEKSKNEVLN	NNE	IMHSLSSYKHH	: 324
Pinui_NW_008481888.1	:	VNYE	GLLNQAYVAFSDYYSFF	FLFAMRLLEN	GGIVERL	VAIHEKLTNYR	TRNILKKINDKSKNEVLN	NNE	IMHSLSSYKHH	: 324
Pfragile_NW_012192586.1	:	VNYE	GLMNQAYKAFSDYYSYFP	FAIK	LEKGGIVERL	VAIHESLTNYR	TKNILKKINEKSKNEVLN	NNE	IMHSLSSYKHH	: 324
Pcynomolgi_BAEJ01000249	:	VNYE	GLLNQAYAFSDYYSYFP	FAIK	LEKGGIVERL	VAIHESLTNYR	TRNILKKINEKSKNEVLN	NNE	IMHSLSSYKHH	: 324
Brazil-I_AFMK01000508.1_A	:	VNYE	GLLNQAYAFSDYYSYFP	FAIS	MLEKGGIVDRL	VAIHESLTNYR	TRNILKKINEKSKNEVLN	NNE	IMHSLSSYKHH	: 324
VCG-I	:	VNYE	GLLNQAYAFSDYYSYFP	FAIS	MLEKGGIVDRL	VAIHESLTNYR	TRNILKKINEKSKNEVLN	NNE	IMHSLSSYKHH	: 324
Sal-1_PVX_088910	:	VNYE	GLLNQAYAFSDYYSYFP	FAIS	MLEKGGIVDRL	VAIHESLTNYR	TRNILKKINEKSKNEVLN	NNE	IMHSLSSYKHH	: 324
Mauritania_I_AFNIO1000333	:	VNYE	GLLNQAYAFSDYYSYFP	FAIS	MLEKGGIVDRL	VAIHESLTNYR	TRNILKKINEKSKNEVLN	NNE	IMHSLSSYKHH	: 324
N.Korean_AFNJ01000531	:	VNYE	GLLNQAYAFSDYYSYFP	FAIS	MLEKGGIVDRL	VAIHESLTNYR	TRNILKKINEKSKNEVLN	NNE	IMHSLSSYKHH	: 324
India-VII_AFBK01000586_AFBK01000587	:	VNYE	GLLNQAYAFSDYYSYFP	FAIS	MLEKGGIVDRL	VAIHESLTNYR	TRNILKKINEKSKNEVLN	NNE	IMHSLSSYKHH	: 324
		VNYE	gLG6NQAY AFSDYYS5FP	aFA6	6LEkgG1V	RLVAIHESLTNYR	T4NIlkKINeKSKNEVLN	Ne	IMHSLSSYKHH	

		*	340	*	360	*	380	*	400		
P.coatneyi_CM002856.1	:	AGGTRGS	FVQSRGVS	VTQGVLSVDEKGD	PPSS	TAG-GNQSAN	MMATAAPN	-----	TVEATNTAAAT	TATTTNTA : 391	
Pknowlesi_NC_011906.1	:	AGGTRGS	FMQYRGV	GLSKGGLSVDEKGG	QQIASAV	GNQSAN	MMVAPAPK	DSSPTM-----	AAPSTDTVTNNM	ATTTTAP : 398	
Pinui_NW_008481888.1	:	ATGTRGS	FLQSRGVR	QVINSVSDQKGD	QTATAG	GNESEN	VPAAVPKDDAP	TRVASPGPAA	FPNTVASNPT	AVSNATAA : 404	
Pfragile_NW_012192586.1	:	AGGTRGS	FLQSRGAHNV	LKVVDKVD	-----	TSITG	GNQSAN	MAAAAPNNSG	PTTAAAA	NSAASPNTAAT	TNTAATTS : 397
Pcynomolgi_BAEJ01000249	:	AGGTRGS	FLQSRVAREV	RQGDVSVDEKGD	QTATAG	GNQSAN	MAAAAPK	DASPTT-AAS	NAAASPDTTA	ANTAAANTAAAN : 403	
Brazil-I_AFMK01000508.1_A	:	AGGTRGA	FLQSRDVREVT	QGDVSVDEKGD	RATTAG	GNQSA	SVAAAAAPK	DAGPTV-----	AAPNTAAT	LKTA----- : 390	
VCG-I	:	AGGTRGA	FLQSRDVREVT	QGDVSVDEKGD	RATTAG	GNQSA	SVAAAAAPK	DAGPTV-----	AAPNTAAT	LKTA----- : 390	
Sal-1_PVX_088910	:	AGGTRGA	FLQSRDVREVT	QGDVSVDEKGD	RATTAG	GNQSA	SVAAAAAPK	DAGPTV-----	AAPNTAAT	LKTA----- : 390	
Mauritania_I_AFNIO1000333	:	AGGTRGA	FLQSRDVREVT	QGDVSVDEKGD	RATTAG	GNQSA	SVAAAAAPK	DAGPTV-----	AAPNTGAT	LKTA----- : 390	
N.Korean_AFNJ01000531	:	AGGTRGA	FLQSRDVREVT	QGDVSVDEKGD	RATTAG	GNQSA	SVAAAAAPK	DAGPTV-----	AAPNTAAT	LKTA----- : 390	
India-VII_AFBK01000586_AFBK01000587	:	AGGTRGA	FLQSRDVREVT	QGDVSVDEKGD	RATTAG	GNQSA	SVAAAAAPK	DAGPTV-----	AAPNTAAT	LKTA----- : 390	
		AggTRG	F6QsR v	6 g 6sVD2kgd	t g	GN2Sa	6aaaaPk	pt	a P T a	ta	

		*	420	*	440	*	460	*	480	
P.coatneyi_CM002856.1	:	TNTNTA	-----	TNTNTAT	NTNSAAT	TNTAA	-----	TTNTAAT	TNTTATTSVA	TSELNT-----
Pknowlesi_NC_011906.1	:	ATANMA	APSTNTAT	ATANMAA	-----	PSTNTAT	ANMAAPST	DTVTTN	MMATTTT	VPATANTAASE
Pinui_NW_008481888.1	:	SNATAA	SNATAAS	NATD	-----	ASNATAA	SNPAA	-----	PPNTAA	TSQ-LSN-----
Pfragile_NW_012192586.1	:	-----	-----	ASN	DTNAS	PHTN	-----	TSNE	CASTSP-LSN	-----
Pcynomolgi_BAEJ01000249	:	TAAAPNT	ASASNA	AATPNPA	-----	AAPNTAAT	PNPAA	-----	TPNAAA	TSP-LST-----
Brazil-I_AFMK01000508.1_A	:	-----	-----	ASP	NAAA	TNTAA	-----	PPN	MGA-TSP-LSN	-----
VCG-I	:	-----	-----	ASP	NAAA	TNTAA	-----	PPN	MGA-TSP-LSN	-----
Sal-1_PVX_088910	:	-----	-----	ASP	NAAA	TNTAA	-----	PPN	MGA-TSP-LSN	-----
Mauritania_I_AFNIO1000333	:	-----	-----	ASP	NAAA	TNTAA	-----	PPN	MGA-TSP-LSN	-----
N.Korean_AFNJ01000531	:	-----	-----	ASP	NAAA	TNTAA	-----	PPN	MGA-TSP-LSN	-----
India-VII_AFBK01000586_AFBK01000587	:	-----	-----	ASP	NAAA	TNTAA	-----	PPN	MGA-TSP-LSN	-----
				a	aa n aa			n a tSp	l3n	PLYgtss1 KDV

	*	500	*	520	*	540	*	560		
P.coatneyi_CM002856.1	:	VVLVRDLLKNTNIIKFEKNEPTSQIDDEGIKKLIESSFFDLSDNTMLMRLLIKPQAAIILFI		IQSFIMMTPSPTRDAKMYCK	:	533				
Pknowlesi_NC_011906.1	:	VVLVRDLLKDTNIIKFEKNEPTSQIDDEGIKKLIESSFFDLSDNTMLMRLLIKPQASILFI		IQSFIMMTPSPTRDARMYCK	:	558				
Pinui_NW_008481888.1	:	VVLVRDLLKNTNIIKFDKDEPTSQMDDEGIKKLIESSFFDLSDNTMLMOLLIKPQAAMLF		IQSFIMMTPSPTRDAKTYCN	:	539				
Pfragile_NW_012192586.1	:	VVLIRDLLKNTNIIKFEKDEPTQIDDEGIKKLIESSFFDLSDNTMLMRLLIKPQAAIILFI		IQSFIMMTPSPTRDAKTYCK	:	516				
Pcynomolgi_BAEJ01000249	:	VVLVRDLLKNTNIIKFEKDEPTSQIDDEGIKKLIESSFFDLSDNTMLMRLLIKPQAAIILFI		IQSFIMMTPSPTRDAKTYCK	:	541				
Brazil-I_AFBK01000508.1_A	:	AVLVRDLLKNTNIIKFENNEPTSQMDDEEIKKLIESSFFDLSDNTMLMRLLIKPQAAIILFI		IESFIMMTPSPTRDAKTYCK	:	508				
VCG-I	:	AVLVRDLLKNTNIIKFENNEPTSQMDDEEIKKLIESSFFDLSDNTMLMRLLIKPQAAIILFI		IESFIMMTPSPTRDAKTYCK	:	508				
Sal-1_PVX_088910	:	AVLVRDLLKNTNIIKFENNEPTSQMDDEEIKKLIESSFFDLSDNTMLMRLLIKPQAAIILFI		IESFIMMTPSPTRDAKTYCK	:	508				
Mauritania_I_AFNIO1000333	:	AVLVRDLLKNTNIIKFENNEPTSQMDDEEIKKLIESSFFDLSDNTMLMRLLIKPQAAIILFI		IESFIMMTPSPTRDAKTYCK	:	508				
N.Korean_AFNJO1000531	:	AVLVRDLLKNTNIIKFENNEPTSQMDDEEIKKLIESSFFDLSDNTMLMRLLIKPQAAIILFI		IESFIMMTPSPTRDAKTYCK	:	508				
India-VII_AFBK01000586_AFBK01000587	:	AVLVRDLLKNTNIIKFENNEPTSQMDDEEIKKLIESSFFDLSDNTMLMRLLIKPQAAIILFI		IESFIMMTPSPTRDAKTYCK	:	508				
		VL6RDLLK1TNIIKFe		1EPtsQ6DdE		IKKLIESSFFDLSDNTMLMrL6IKPQAa6L		II2SFIMMTPSPTRDA4		Yck

	*	580	*	600	*	620	*	640										
P.coatneyi_CM002856.1	:	KKLVNGQLIENSDIKAAATEEEDMITEFSSKYNLFYERLKLEELREIEQNRKALKNSKGSLSVLQVNSQNGPDGKEANGSG							: 614									
Pknowlesi_NC_011906.1	:	KKLVNGQLIENNDIKAAATEEEDMINEFSSKYNLFYERLKMEELREIEQDRKSLKNSKGNLSVLEVRNSQNGPDGKEVNGSG							: 639									
Pinui_NW_008481888.1	:	KSLVNGKLIETSDIKASTEEEDLITEFSSKYNLFYEKLMEELREIEENKKAIKNSKGSLSVLEVANSQNSPDGKRVNGSG							: 620									
Pfragile_NW_012192586.1	:	KNLVNGQLVQTSDFSDAHEEEDLINEFSSKYNLFYERLKLEELREIEQNRKALKNAKGSLSVLQVNSQNGTHCNGVNOGG							: 597									
Pcynomolgi_BAEJ01000249	:	KVLVNGQLVETSDLSAAATEEEDLINEFSSKYNLFYERLKLEELREIEQNRKALKNSKGSLSVLEVNSQNGPDGSGMNGSG							: 622									
Brazil-I_AFBK01000508.1_A	:	KALVNGQLIETSDINAAATEEEDLINEFSSRYNLFYERLKLEELREIEQNRKALKNSKGTLSVLEVANSQNA PDGKCVNGSG							: 589									
VCG-I	:	KALVNGQLIETSDINAAATEEEDLINEFSSRYNLFYERLKLEELREIEQNRKALKNSKGTLSVLEVANSQNA PDGKCVNGSG							: 589									
Sal-1_PVX_088910	:	KALVNGQLIETSDINAAATEEEDLINEFSSRYNLFYERLKLEELREIEQNRKALKNSKGTLSVLEVANSQNA PDGKCVNGSG							: 589									
Mauritania_I_AFNIO1000333	:	KALVNGQLIETSDINATTEEEDLINEFSSRYNLFYERLKLEELREIEQNRKALKNSKGTLSVLEVANSQNA PDGKCVNGSG							: 589									
N.Korean_AFNJO1000531	:	KALVNGQLIETSDINAAATEEEDLINEFSSRYNLFYERLKLEELREIEQNRKALKNSKGTLSVLEVANSQNA PDGKCVNGSG							: 589									
India-VII_AFBK01000586_AFBK01000587	:	KALVNGQLIETSDINAAATEEEDLINEFSSRYNLFYERLKLEELREIEQNRKALKNSKGTLSVLEVANSQNA PDGKCVNGSG							: 589									
		K		LVNGqL62tsD		a		tEE		D6InEFSS4YNLFYE4LK6EELREIE214Ka6KNsKG		LSVL2V		NSQN		pdGk		vNgsG

	*	660	*	680	*	700	*	720	
P.coatneyi_CM002856.1	:	NAANG-----							: 619
Pknowlesi_NC_011906.1	:	DAANG-----							: 644
Pinui_NW_008481888.1	:	NDANG-----							: 625
Pfragile_NW_012192586.1	:	HAANE-----							: 602
Pcynomolgi_BAEJ01000249	:	NAANG-----							: 627
Brazil-I_AFBK01000508.1_A	:	NAANANAANANAANANAANANAANGNLANANLANAN-----							: 634
VCG-I	:	NAANANAANANAANANAANANAANGNLANANLANANANAANADAANANAANANAANANAANANLANANLANANLANANLANAN							: 670
Sal-1_PVX_088910	:	NAANANAANANAANANAANANAANGNLANANLANANANAANADAANANAANANAANANAANANLANANLANANLANANLANAN							: 670
Mauritania_I_AFNIO1000333	:	NAANA-----							: 594
N.Korean_AFNJO1000531	:	NAANANAANANAANANAANANAANX--XNANLANANAANANAANANAANANAANANAANG-----							: 645
India-VII_AFBK01000586_AFBK01000587	:	NAANANAANANAANANAANANAANXNLANANLANANAA-----							: 628
		aAN							

		*	740	*	760	*	780	*	800	*	
P.coatneyi_CM002856.1	:	-----	NAQNGNGANVNAQNE	----	NA	PN	GNNGSASPLIVVVGDELGEKTD	----	DI	IK	NVDVEALTADV : 676
Pknowlesi_NC_011906.1	:	-----	NNMNG	----	----	GNNGSAS	SLIVVVRDDIAEKTDDIIKNNVDIESTKADV : 687	----	----	----	
Pinui_NW_008481888.1	:	-----	-----	----	NA	AN	GNNGSGSPLLVVVGADLGEKTE	----	DI	IK	NNVDAATLTEGV : 667
Pfragile_NW_012192586.1	:	-----	SGHAAND	----	-----	NA	HAAND	----	----	----	----- : 616
Pcynomolgi_BAEJ01000249	:	-----	NNANGNNANGNNANG	----	NA	AN	GNNGSGSPLIAVVGADLGEKTD	----	DI	IK	NNVDVAATAADV : 684
Brazil-I_AFMK01000508.1_A	:	LANANLANANAANANAANANAANG	----	NA	PN	SNNGSGSPLIVVVGADLGEKTE	----	DI	IK	NNVDVAALTADV : 700	
VCG-I	:	LANANLANANAANANAANANAANG	----	NA	PN	SNNGSGSPLIVVVGADLGEKTE	----	DI	IK	NNVDVAALTADV : 736	
Sal-1_PVX_088910	:	LANANLANANAANANAANANAANG	----	NA	PN	SNNGSGSPLIVVVGADLGEKTE	----	DI	IK	NNVDVAALTADV : 736	
Mauritania_I_AFNI01000333	:	-----	ANANAANANAANANAANG	----	NA	PN	SNNGSGSPLIVVVGADLGEKTE	----	DI	IK	NNVDVAALTADV : 654
N.Korean_AFNJ01000531	:	-----	-----	----	NA	PN	SNNGSGSPLIVVVGADLGEKTE	----	DI	IK	NNVDVAALTADV : 687
India-VII_AFBK01000586_AFBK01000587	:	-----	-----	----	NA	PN	SNNGSGSPLIVVVGADLGEKTE	----	DI	IK	NNVDVAALTADV : 670
							na n Nlgs spl vvvvg dlgekt diiknnvd				1 adv

			820	*	840	
P.coatneyi_CM002856.1	:	EQAFK	SEFY	QSGSFSANL	SHALVLLSSIALLLF	IC : 711
Pknowlesi_NC_011906.1	:	EQAFR	NFEY	QSGSFSANL	SHALVLLSSIALVLF	IC : 722
Pinui_NW_008481888.1	:	EQAFK	NLSLE	GSFSANL	SHALVLLSSIALLLF	IC : 702
Pfragile_NW_012192586.1	:	-----	-----	-----	-----	-
Pcynomolgi_BAEJ01000249	:	EQAFR	NLEL	KSGSFSANL	SHALVLLSSIALLLF	IF : 719
Brazil-I_AFMK01000508.1_A	:	EQAFK	NLEL	QSGSFSANL	SHALVLLSSIALLLF	IF : 735
VCG-I	:	EQAFK	NLEL	QSGSFSANL	SHALVLLSSIALLLF	IF : 771
Sal-1_PVX_088910	:	EQAFK	NLEL	QSGSFSANL	SHALVLLSSIALLLF	IF : 771
Mauritania_I_AFNI01000333	:	EQAFK	NLEL	QSGSFSANL	SHALVLLSSIALLLF	IF : 689
N.Korean_AFNJ01000531	:	EQAFK	NLEL	QSGSFSANL	SHALVLLSSIALLLF	IF : 722
India-VII_AFBK01000586_AFBK01000587	:	EQAFK	NLEL	QSGSFSANL	SHALVLLSSIALLLF	IF : 705
		eqaf	n e	sgsfsanl	shalvllssial lfi	