

		20		40		60	
MdPME2	ATGGCCAAA	TCAAAGAGTT	TTTAGCCAGA	ATGTCCGAAT	CAGGCCAAAA	ATTATCCACA	AACAAGAAGA 70
MDP245813_cds_GDR	ATGGCCAAAC	TCAAAGAGTT	TTTAGCCAGA	ATGTCCGAAT	CAGGCCAAAA	ATTATCCACA	AACAAGAAGA 70
MDP222620_cds_GDR	ATGGCCAAA	TCAAAGAGTT	TTTAGCCAAA	ATGTCCGAAT	CGGGCAAAACA	AATATCCACA	AACAAGAAAC 70
AryANE_v1_00021521	-----	-----	-----	-----	-----	-----	-
		80		100		120	
MdPME2	ACAAGAAGCT	CTTCATATCC	CTTTTCGCAA	CCATCCTACT	CGTGGGCGCC	GTCATCGGCA	TTGTCACCGG 140
MDP245813_cds_GDR	ACAAGAAGCT	CTTCATATCC	CTTTTCGCAA	CCATCCTACT	CGTGGGCGCC	GTCATCGGCA	TTGTCACCGG 140
MDP222620_cds_GDR	ACAAGAAGCT	CTTCATATCC	CTTTTCGCAA	CCATCCTACT	AGTCGGCGCC	ATCGTCGGCA	TTGTCACCGG 140
AryANE_v1_00021521	-----	-----	-----	-----	-----	-----	-
		160		180		200	
MdPME2	AGTAAAGTCC	TCCAAAAACA	ACTCCGACGA	CGAAACCATC	GAGGCCTCCC	ACGCCATAGT	CAAATCCTCA 210
MDP245813_cds_GDR	AGTAAAGTCC	TCCAAAAACA	ACTCCGACGA	CGAAACCATC	GAGGCCTCCC	ACGCCATAGT	CAAATCCTCA 210
MDP222620_cds_GDR	AGTCAAGTCC	TCCAAAAACA	ACTCCGACGA	CGAAACCAAC	GAGGCCTCCC	ACGCCATAGT	CAAATCCTCA 210
AryANE_v1_00021521	-----	-----	-----	-----	-----	-----	-
		220		240		260	
MdPME2	TGCAGCTCCA	CCCTCTACCC	TGATCTGTGC	TTTTCAACTC	TTGCCCTTCA	CCCGGAAGCC	TCCAAAAAGG 280
MDP245813_cds_GDR	TGCAGCTCCA	CCCTCTACCC	TGATCTGTGC	TTTTCAACTC	TTGCCCTTCA	CCCGGAAGCC	TCCAAAAAGG 280
MDP222620_cds_GDR	TGCAGCTCCA	CCCTCTACCC	TGAACTGTGC	TTTTCCACTC	TTGCACCTCA	CCCGGAAGCC	GCCAAAAAGG 280
AryANE_v1_00021521	-----	-----	-----	-----	-----	-----	-
		300		320		340	
MdPME2	TTTCGAGCCA	GAAGGACGTG	ATAGAATTGT	CACTGAACAT	CACGACCACG	GCGGTGCAGC	ACATCTTCTT 350
MDP245813_cds_GDR	TTTCGAGCCA	GAAGGACGTG	ATAGAATTGT	CACCTGAACAT	CACGACCACG	GCGGTGCAGC	ACATCTTCTT 350
MDP222620_cds_GDR	TTTCGAGCCA	GAAGGACGTG	ATAGAATTGT	CATTGAACAT	CACGACCAAG	GCGGTTCAGC	ACAACCTTCTT 350
AryANE_v1_00021521	-----	-----	-----	-----	-----	-----	-
		360		380		400	
MdPME2	CACCGTCTGAG	AAGCTGCTGA	AGTCCAGGAA	GAACAAGCTC	ACTAAGCGTG	AGAAGGGGCG	TCTCCACGAC 420
MDP245813_cds_GDR	CACYGTCTGAG	AAGCTGCTGA	AGTCCAGGAA	GAACAAGCTC	ACTAAGCGTG	AGAAGGGGCG	TCTCCACGAC 420
MDP222620_cds_GDR	CACTGTCTGAG	AAGCTGCTGA	AGTCCAGGAA	GAATAAGCTC	ACTAAGCGTG	AGAAGGGGCG	TCTTCACGAC 420
AryANE_v1_00021521	-----	-----	-----	-----	-----	-----	-
		440		460		480	
MdPME2	TGTTTGAGAGA	CCATTGACGA	AACCCCTCGAC	GAGCTCCACG	AGGCTGTGCGA	GGATCTCCAT	GAGTACCCCA 490
MDP245813_cds_GDR	TGTTTGAGAGA	CCATTGACGA	AACCCCTCGAC	GAGCTCCACG	AGGCTGTGCGA	GGATCTCCAT	GAGTACCCCA 490
MDP222620_cds_GDR	TGTTTGAGAGA	CCATTGATGA	AACCTCTCGAC	GAGCTTCACG	ATGCTGTGGA	GGACCTCCAT	GAGTACCCCA 490
AryANE_v1_00021521	-----	-----	-----	-----	-----	-----	-
		500		520		540	
MdPME2	ATAACAAGAC	TTTGGTTTCA	CATGCTGATG	ACCTTAAAC	TTTGCTAAGC	TCCGCCATTA	CCAACCAAGA 560
MDP245813_cds_GDR	ATAACAAGAC	TTTGGTTTCA	CATGCTGATG	ACCTTAAAC	TTTGMTAAGC	TCCGCCATTA	CCAACCAAGA 560
MDP222620_cds_GDR	ATAAGAAGAC	TTTGACTCAG	CATGCGGATG	ACCTAAAAAC	TTTGATCAGC	TCCGCCATTA	CCAACCAAGA 560
AryANE_v1_00021521	-----	-----	-----	-----	-----	-----	-
		580		600		620	
MdPME2	AACTTGCTTT	AATGGGTTCT	CTCATGATGG	AGGTGATAAG	AAAGTTAGGA	AAGTTTTGTT	GGCTGGTGAG 630
MDP245813_cds_GDR	AACTTGCTTT	AATGGGTTCT	CTCATGATGG	AGGTGATAAG	AAAGTTAGGA	AAGTTTTGTT	GGCTGGTGAG 630
MDP222620_cds_GDR	AACTTGCTTT	GCTGGGTTCT	CGCACGATGA	TGCTGATAAA	AAAGTTAGGA	AAGTTTTTTT	GGCGGGTCTAG 630
AryANE_v1_00021521	-----	-----	-----	-----	-----	-----	-
		640		660		680	
MdPME2	-----	-----	-----	-----	-----	GAACACATA	GAAAAATTGT 649
MDP245813_cds_GDR	ACCGTCRATA	TYTCTKTTAA	CACCGATATT	TRAACAATTG	CGGTCACTCA	GGAACACATA	GAAAAATTGT 700
MDP222620_cds_GDR	-----	-----	-----	-----	-----	GTGCACGTA	GAAAAATTGT 649
AryANE_v1_00021521	-----	-----	-----	-----	-----	-----	-
		720		740		760	
MdPME2	GCAGTAATGT	ACTGGCCATG	ATCAAGAACA	TGACCGATAC	CGACATTGCA	AACGAGATGA	AAATGAATGT 719
MDP245813_cds_GDR	GCAGTAATGT	ACTGGCCATG	ATCAAGAACA	TGACCGATAC	CGACATTGCA	AACGAGATGA	AAATGAATGT 770
MDP222620_cds_GDR	GCAGTAATGC	GCTGGCCATG	ATCAAGAACA	TGACCGATAC	CGACATTGCA	AACGAGATGA	AAACGAATGT 719
AryANE_v1_00021521	-----	-----	-----	-----	-----	-----	-
		780		800		820	
MdPME2	GAACCGAAAA	CTCAAGGAGA	ATATGGTGGA	CGAGCACGGG	TGGCCGGAGT	GGCTGTCGGT	GGCGGACAGG 789
MDP245813_cds_GDR	GAACCGAAAA	CTCAAGGAGA	ATATGGTGGA	CGAGCACGGG	TGGCCGGAGT	GGCTGTCGGT	GGCGGACAGG 840
MDP222620_cds_GDR	GAACCGAAAG	CTGAAGGAGG	ATGTGGTGGA	CGAGCATGGG	TGGCCGGAGT	GGCTGTCGGT	GGCAGACAGG 789
AryANE_v1_00021521	-----	-----	-----	-----	-----	-----	-
		860		880		900	
MdPME2	CGACTGCTGC	AGTCGTCTTC	TGTCACGCCG	AATGTGGTGG	TGGCAGCAGA	CGGCACTGGG	AACTACAAGA 859
MDP245813_cds_GDR	CGACTGCTGC	AGTCGTCTTC	TGTCACGCCG	AATGTGGTGG	TGGCAGCAGA	CGGCACTGGG	AACTACAAGA 910
MDP222620_cds_GDR	CGACTGCTGC	AGTCGTCTTC	TGTCACACCA	AATGTGGTGG	TGGCAGCAGA	CGGGAGTGGG	AACTACAAGA 859
AryANE_v1_00021521	-----	-----	-----	-----	-----	-----	-
		920		940		960	
MdPME2	CGGTGTCGGA	AGCGGTGGCT	GCTGCCCCAG	AGAAGAGTAG	TAGCAGATAC	GTGATTAATA	TAAAGGCGGG 929
MDP245813_cds_GDR	CGGTGTCGGA	AGCGGTGGCT	GCTGCCCCAG	AGAAGAGTAG	TAGCAGATAC	GTGATTAATA	TAAAGGCGGG 980
MDP222620_cds_GDR	CGGTGTCGGC	TGCGGTGGCT	GCCGCCCCGG	AGAAGAGCAG	TAAAAGATAT	GTGATTAGAA	TAAAGGCGGG 929
AryANE_v1_00021521	-----	-----	-----	-----	-----	-----	-
		1 000		1 020		1 040	
MdPME2	GATTTATAGA	GAAAAATGTTG	ACGTGCCAAA	GAAAAAGACC	AACATTATGT	TTTTGGGAGA	TGGGAGGGTA 999
MDP245813_cds_GDR	GATTTATAGA	GAAAAATGTTG	ACGTGCCAAA	GAAAAAGACC	AACATTATGT	TTTTGGGAGA	TGGGAGGGTA 1050
MDP222620_cds_GDR	GGTTTATAGA	GAAAAATGTTG	ACGTGCCGAA	GAAAAAGACC	AACATTATGT	TTATGGGAGA	TGGGAGAAAA 999
AryANE_v1_00021521	-----	-----	-----	-----	-----	-----	-
		1 060		1 080		1 100	
MdPME2	AACACCATCA	TCACTGCTAG	TAGAAATGTC	GTCGATGGCA	GCACAACCTT	CAACTCAGCC	ACAGTTGC -- 1067
MDP245813_cds_GDR	AACACCATCA	TCACTGCTAG	TAGAAATGTC	GTCGATGGCA	GCACAACCTT	CAACTCAGCC	ACAGTTGC -- 1118
MDP222620_cds_GDR	AACACTATCA	TCACTGCTAG	TAAAAATGTG	GTCGATGGCA	GCACAACCTT	CAACTCGGCC	ACAGTTGTGA 1069
AryANE_v1_00021521	-----	-----	AAAATGTG	GTCGATGGCA	GCACAACCTT	CAACTCGGCC	ACAGTTGTGA 48

		1 140		1 160		1 180		
MdPME2	TGCG-GT-TG	G- - - TGAGA	AGTTTCTAGC	CCGAGACATA	ACATTCCAAA	ACACAGCAGG	CCCATCAAAG	1131
MDP245813_cds_GDR	TGCG-GT-TG	G- - - TGAGA	AGTTTCTAGC	CCGAGACATA	ACATTCCAAA	ACACAGCAGG	CCCATCAAAG	1182
MDP222620_cds_GDR	TGTATGTATG	TACMTTGAGG	ATTTTTT- - -	TCGGAWTCT	- C- TTTTGGA	TCTTAG- - - -	- - - - -	1119
AryANE_v1_00021521	TGTATGTATG	TA- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	60
		1 200		1 220		1 240		1 260
MdPME2	CACCAAGCTG	TTGCCCTAAG	AGTTGGGTCC	GATCTCTCAG	CATTCTACCG	CTGCGACATT	CTTGCGTACC	1201
MDP245813_cds_GDR	CACCAAGCTG	TTGCCCTAAG	AGTTGGGTCC	GATCTCTCAG	CATTCTACCG	CTGCGACATT	CTTGCGTACC	1252
MDP222620_cds_GDR	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	1119
AryANE_v1_00021521	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	60
		1 280		1 300		1 320		
MdPME2	AAGACTCGCT	CTACGTGCAC	TCGAATCGCC	AGTTTTTTGA	AGGCTGCTTG	GTAGCCGGAA	CAGTTGACTT	1271
MDP245813_cds_GDR	AAGACTCGCT	CTACGTGCAC	TCGAATCGCC	AGTTTTTTGA	AGGCTGCTTG	GTAGCCGGAA	CAGTTGACTT	1322
MDP222620_cds_GDR	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	1119
AryANE_v1_00021521	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	60
		1 340		1 360		1 380		1 400
MdPME2	CATCTTCGGC	AATGCTGCTG	TCGTGTTACA	AAATTGTGAC	ATCCATGCAA	GAAAACCTGA	TTCGGGCCAG	1341
MDP245813_cds_GDR	CATCTTCGGC	AATGCTGCTG	TCGTGTTACA	AAATTGTGAC	ATCCATGCAA	GAAAACCTGA	TTCGGGCCAG	1392
MDP222620_cds_GDR	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	1119
AryANE_v1_00021521	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	60
		1 420		1 440		1 460		
MdPME2	AAGAACATGG	TCACTGCACA	AGGTAGAACT	GACCCGAATC	AAAACACCGG	CATCGTGATC	CAAAAATCGA	1411
MDP245813_cds_GDR	AAGAACATGG	TCACTGCACA	AGGTAGAACT	GACCCGAATC	AAAACACCGG	CATCGTGATC	CAAAAATCGA	1462
MDP222620_cds_GDR	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	1119
AryANE_v1_00021521	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	60
		1 480		1 500		1 520		1 540
MdPME2	GAATCGGGCG	CACTTCCGAC	TTGCAAGCCT	CAAAGAGCAG	CTTCAAAACG	TTTTTGGGGA	GGCCATGGAA	1481
MDP245813_cds_GDR	GAATCGGGCG	CACTTCCGAC	TTGCAAGCCT	CAAAGAGCAG	CTTCAAAACG	TTTTTGGGGA	GGCCATGGAA	1532
MDP222620_cds_GDR	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	1119
AryANE_v1_00021521	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	60
		1 560		1 580		1 600		
MdPME2	GGAGTATTCA	AGGACTGTGA	TCATGCAGTC	GAGTATAACT	GATATCATTG	ACCCTGCTGG	ATGGCATGAG	1551
MDP245813_cds_GDR	GGAGTATTCA	AGGACTGTGA	TCATGCAGTC	GAGTATAACT	GATATCATTG	ACCCTGCTGG	ATGGCATGAG	1602
MDP222620_cds_GDR	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	1119
AryANE_v1_00021521	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	60
		1 620		1 640		1 660		1 680
MdPME2	TGGTCTGGCA	CTTTTGCCCT	CGACACTTTG	TTTTATGGAG	AGTATGCTAA	CACTGGGGCA	GGCGCTGGGA	1621
MDP245813_cds_GDR	TGGTCTGGCA	CTTTTGCCCT	CGACACTTTG	TTTTATGGAG	AGTATGCTAA	CACTGGGGCA	GGCGCTGGGA	1672
MDP222620_cds_GDR	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	1119
AryANE_v1_00021521	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	60
		1 700		1 720		1 740		
MdPME2	CTGCAAACAG	GGTGACGTGG	AAGGGGTTTA	AGGTAATTAC	AAGTCCCACT	GAGGCTGAGG	CGTATACGCC	1691
MDP245813_cds_GDR	CTGCAAACAG	GGTGACGTGG	AAGGGGTTTA	AGGTAATTAC	AAGTCCCACT	GAGGCTGAGG	CGTATACGCC	1742
MDP222620_cds_GDR	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	1119
AryANE_v1_00021521	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	60
		1 760		1 780		1 800		
MdPME2	GGGCAACTTT	ATTGCTGGTG	GTAGTTGGTT	GAGTTCTACC	GGTTTTCCAT	TTTCTCTTGC	GCTGTAA	1758
MDP245813_cds_GDR	GGGCAACTTT	ATTGCTGGTG	GTAGTTGGTT	GAGTTCTACC	GGTTTTCCAT	TTTCTCTTGC	GCTGTAA	1809
MDP222620_cds_GDR	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	1119
AryANE_v1_00021521	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	60