```
2.0
                                                40
L1PA1 : GGGGGGAGGAGCCAAGATGGCCGAATAGGAACAGCTCCGGTC
                                                          42
L1PA2 : GGGGGGAGGAGCCAAGATGGCCGAATAGGAACAGCTCCGGTC
                                                          42
L1PA3 : GGGGGGAGGAGCCAAGATGGCCGAATAGGAACAGCTCCGGTC
                                                          42
                                                          42
L1PA4 : GGGGGGAGGAGCCAAGATGGCCGAATAGGAACAGCTCCGGTC
L1PA5 : GGGGGGAGGAGCCAAGATGGCCGAATAGGAACAGCTCCGGTC
                                                          42
L1PA6 : -----CCAAGATGGCCGAATAGGAACAGCTCCGGTC
                                                          31
        gggggaggagCCAAGATGGCCGAATAGGAACAGCTCCGGTC
                         60
                                              80
L1PA1 : TACAGCTCCCAGCGTGAGCGACGCAGAAGACGG-TGATTTCT
                                                          83
L1PA2 : TACAGCTCCCAGCGTGAGCGACGCAGAAGACGGGTGATTTCT
                                                          84
L1PA3 : TACAGCTCCCAGCGTGAGCGACGCAGAAGACGGGTGATTTCT
                                                          84
L1PA4 : TACAGCTCCCAGCGTGAGCGACGCAGAAGACGGGTGATTTCT
                                                          84
L1PA5 : TACAGCTCCCAGCGTGAGCGACGCAGAAGACGGGTGATTTCT
                                                          84
L1PA6 : TGCAGCTCCCAGCGTGATCGACGCAGAAGACGGGTGATTTCT
                                                          73
        TaCAGCTCCCAGCGTGAgCGACGCAGAAGACGGgTGATTTCT
                      100
                                           120
L1PA1 : GCATTTCCATCTGAGGTACCGGGTTCATCTCACTAGGGAGTG
                                                        125
        GCATTTCCA<mark>T</mark>CTGAGGTACC<mark>G</mark>GGTTCATCTCA<mark>C</mark>T<mark>A</mark>GG<mark>GAGT</mark>G
                                                         126
L1PA2:
L1PA3 : GCATTTCCATCTGAGGTACCGGGTTCATCTCACTAGGGAGTG
                                                         126
L1PA4 : GCATTTCCAACTGAGGTACCGGGTTCATCTCACTGGGGAGTG :
                                                        126
L1PA5 : GCATTTCCAACTGAGGTACCGGGTTCATCTCACTGGGGGCTTG
                                                         126
L1PA6 : GCATTTCCAACTGAGGTACCTGGTTCATCTCATTGGGACTGG :
                                                         115
        GCATTTCCA CTGAGGTACCGGGTTCATCTCACT GGg tG
                    140
                                         160
L1PA1 : CCAGACAGTGGGCGCAGGCCCAGTGTGTGT-GCGCACCGTGCG
                                                        166
L1PA2 : CCAGACAGTGGGCGCAGGTCAGTGGGTGC-GCGCACCGTGCG
                                                        167
L1PA3 : CCAGACAGTGGGCGCAGGACAGTGGGTGCAGCGCACCGTGCG
                                                        168
L1PA4 : CCAGACAGTGGGTGCAGGACAGTGGGTGCAGCGCACCGTGCG
                                                         168
L1PA5 : TCAGACAGTGGGTGCAGGACAGTGGGTGCAGCCCACCGAGCG
                                                        168
L1PA6 : TTGGACAGTGGGTGCAG-----CCCACGGAGGG
                                                        143
         caGACAGTGGG GCAGg cagtg gtg gC CACcG GcG
                  180
                                       200
L1PA1 : CGAGCCGAAGCAGGGCGAGGCATTGCCTCACCTGGGAAGCGC
                                                         208
L1PA2 : CGAGCCGAAGCAGGGCGAGGCATTGCCTCACTTGGGAAGCGC
                                                         209
L1PA3 : CGAGCCGAAGCAGGCCGAGGCATTGCCTCACTCGGGAAGCGC
                                                        210
L1PA4 : TGAGCCGAAGCAGGGCGAGGCATTGCCTCACCCGGGGAAGCGC
                                                        210
L1PA5 : TGAGCCAAAGCAGGGCGAGGCATTGCCTCACCCGGGAAGCGC
                                                        210
L1PA6 : TGAGCCGAAGCAGGGCGGGGCATCGCCTCACCTGGGAAGCGC
                                                        185
         GAGCCGAAGCAGGCGAGGCATtGCCTCAC GGGAAGCGC
```

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220
                                    240
L1PA1 : AAGGGGTCAGGGAGTTCCCTTTCCGAGTCAAAGAAAGGGGGTG :
                                                        250
L1PA2 : AAGGGGTCAGGGAGTTCCCTTTCCGAGTCAAAGAAAGGGGTG :
                                                        251
L1PA3 : AAGGGGTCAGGGAGTTCCCTTTCCTAGTCAAAGAAAGGGGTG
                                                         252
L1PA4 : AAGGGGTCAGGGAATTCCCTTTCCTAGTCAAAGAAAGGGGTG :
                                                         252
L1PA5 : AAGGGGTCAGGGAATTCCCTTTCCTAGCCAAGGGAAGCTGTG :
                                                         252
L1PA6 : AAGGGGTCGGGGATTTCCCTTTCCTAGCCAAGGGAAGCCGTG :
                                                         227
        AAGGGGTCaGGGA TTCCCTTTCC AG CAA G AAG
             260
                                  280
L1PA1 : ACGGACG-CACCTGGAAAATCGGGTCACTCCCACCCGAATAT :
                                                         291
L1PA2 : ACGGACG-CACCTGGAAAATCGGGTCACTCCCACCCGAATAT :
                                                         292
L1PA3 : ACAGACGGCACCTGGAAAATCGGGTCACTCCCACCCTAATAC :
                                                         294
L1PA4 : ACAGACGCCACCTGGAAAATCGGGTCACTCCCACCCTAATAC :
                                                         294
L1PA5 : ACAGAC<mark>GC</mark>ACCTGGAAAATCGGGTCACTCCCACCCTAATAC :
                                                         294
L1PA6 : ACAGACTGTACCTGGAAAAACGGGACACTCCCGCCCAAAATAC :
                                                         269
        AC GACG cACCTGGAAAAtCGGGtCACTCCCaCCC AATA
           300
                                320
L1PA1 : TGCGCTTTTCAGACCGGCTTAAGAAACGGCGCACCACGAGAC :
                                                        333
L1PA2 : TGCGCTTTTCCGACGGCGCTTAAAAAACGGCGCACCACGAGAT :
                                                         334
L1PA3 : TGCGCTTTTCCGACGGCTTAAAAAACGGCACACCAGGAGAT :
                                                         336
L1PA4 : TGCGCTTTTCCAACGGCGCTTAACAAACGGCACACCAGGAGAT :
                                                        336
L1PA5 : TGCGCTTTTCCAATGGTCTTAGCAAACGGCACACCAGGAGAT : L1PA6 : TGCGCTTTTCCAATGGTCTTAGCAAACGGCAGACCAGGAGAT :
                                                        336
                                                         311
        TGCGCTTTTCc A qG CTTA AAACGGC cACCA GAGAt
         340
                              360
L1PA1 : TATATCCCACACCTGGCTCGGAGGGTCCTACGCCCACGGAAT :
                                                         375
L1PA2 : TATATCCCGCACCTGGCTCGGAGGGTCCTACGCCCACGGAGT :
                                                        376
L1PA3 : TATATCCCGCACCTGGCTCGGAGGGTCCTACGCCCACGGAGT :
                                                        378
L1PA4 : TATATCCCGCACCTGGCTCGGAGGGTCCTACGCCCACGGAGC :
                                                         378
L1PA5 : TATATCCCGCGCCCTGGCTCGGAGGGTCCCACGCCCACGGAGC :
                                                        378
L1PA6 : TATATCCCGTGCCTGGCTCGGCGGGTCCCACGCCCATGGAGC :
                                                        353
        TATATCCCgc CCTGGCTCGGaGGGTCC ACGCCCAcGGAg
                            400
L1PA1 : CTCGCTGATTGCTAGCACAGCAGTCTGAGATCAAACTGCAAG :
                                                        417
L1PA2 : CTCGCTGATTGCTAGCACAGCAGTCTGAGATCAAACTGCAAG :
                                                        418
L1PA3 : CTCGCTGATTGCTAGCACAGCAGTCTGAGATCAAACTGCAAG :
                                                        420
L1PA4 : CTCGCTCATTGCTAGCACAGCAGTCTGAGATCAAACTGCAAG :
                                                        420
L1PA5 : CTCGCTCATTGCTAGCACAGCAGTCTGAGATCGAAACTGCAAG :
                                                        420
L1PA6 : CTTGCTCACTGCTAGCGCAGCAGTCTGAGATCCACCTGCAAG :
                                                        395
        CTcGCT AtTGCTAGCaCAGCAGTCTGAGATC AaCTGCAAG
```

		*	440		*	460		
L1PA1	:	GCGGCAACGAG	GC <mark>T</mark> GGGGGAG	GGGCG <mark>C</mark> CC	CGCCATTG(CCCAGG	:	459
L1PA2	:	GCGGCAGCGAG					:	460
L1PA3		GCGGCAGCGAG					•	462
L1PA4	:	GCGGCAGCGAG					:	462
L1PA5	:	GCGGCAGCGAG					•	462
	•	GCAGCAGCCTG					•	437
L1PA6	•						:	437
		GCgGCAgCgaG	ULLUUUUUU		.gccarrig	C AGG		
		*	480	*	E (0.0		
L1PA1	_	CTTGCTTAGGT						501
	•						•	
L1PA2	:	CTTGCTTAGGT					:	502
L1PA3	:	CTTGCTTAGGT					:	504
L1PA4	:	CTTG <mark>AG</mark> TAGGT					:	504
L1PA5	:	CTTG <mark>AG</mark> TAGGT					:	504
L1PA6	:	CTTG <mark>AG</mark> TAGGT					:	479
		CTTG TAGGT	AAACAAAG a	GCCgGGAA	GCTCGAA	CTGGGT		
		*	520	*	540			
L1PA1	:	GGAGCCCACC <mark>A</mark>					:	543
L1PA2	:	GGAGCCCACC <mark>A</mark>	CAGCTCA <mark>AGG</mark> 2	AGGCCTGC	C <mark>TGCCTC</mark>	ГGТАG <mark>G</mark>	:	544
L1PA3	:	GGAGCCCACC <mark>A</mark>	CAGCTCA <mark>AGG</mark>	AGGCCTGC	C <mark>TGCCTC</mark>	rgtag <mark>g</mark>	:	546
L1PA4	:	GGAGCCCACC <mark>A</mark>	CAGCTCA <mark>AGG</mark>	AGGCCTGC	CTGCCTC:	ГGТАG <mark>А</mark>	:	546
L1PA5	:	GGAGCCCACC <mark>G</mark>	CAGCTCA <mark>AGG</mark>	AGGCCTGC	CTGCCTC:	rgtag <mark>a</mark>	:	546
L1PA6	:	GGAGCCCACC <mark>G</mark>					:	520
		GGAGCCCACC						
			3 3					
		*	560	*	580			
L1PA1	:	CTCCACCTCTG	GGGGCAGGGC	A <mark>C</mark> AG <mark>A</mark> CAA	ACAAAA <mark>A</mark> (G <mark>A</mark> CAGC	:	585
L1PA2	:	CTCCACCTCTG	GGGGCAGGGC2	ACAGACAA	ACAAAA <mark>A</mark> (G <mark>A</mark> CAGC	:	586
L1PA3	:	CTCCACCTCTG	GGGGCAGGGC	ACAGACAA	ACAAAA <mark>A</mark> (GACAGC	:	588
L1PA4	•	CTCCACCTCTG					•	588
L1PA5	•	CTCCACCTCTG						588
L1PA6	:	CTCCACCTCTG				G <mark>G</mark> CAGC	:	561
штттто	•	CTCCACCTCTG					•	301
		010011001010	000001100001	.1 110 Car.		3 01100		
		* 60	0	*	620	*		
L1PA1		AG <mark>T</mark> AAC <mark>C</mark> TCTG		ГСТСССТС		GCT <mark>T</mark> TG	•	627
L1PA2	•	AGTAACCTCTG					•	628
L1PA3	:	AGTAACCTCTG AGTAACCTCTG					•	630
L1PA3	:	AGTAACCTCTG AGTAACCTCTG					•	630
	•	AGAAACCTCTG					:	630
L1PA5	:						•	
L1PA6	:	AGAAACTTCTG					:	603
		AG AACcTCTG	CAGAC'I''I'AAa	tGTCCCTG	TCTGACA(JCT'tTG		

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640
                                 660
L1PA1 : AAGAGAGCCAGTGTTCTCCCAGCACGCAGCTCGGAGATCTGAG : 669
L1PA2 : AAGAGAGCAGGTTCTCCCAGCACGCAGCTGGAGATCTGAG : 670
L1PA3 : AAGAGAGCAGGTTCTCCCAGCACGCAGCTGGAGATCTGAG : 672
L1PA4 : AAGAGAGTAGTGGTTCTCCCAGCACG<mark>CAGCTG</mark>GAGATCTGAG : 672
L1PA5 : AAGAGAGTAGTGGTTCTCCCAGCACG<mark>GAGT</mark>TTGAGATCTGAG : 672
L1PA6 : AAGAGAGCCAGTGTTCTCCCAGCACGCTGTTTTGAGCCTCTGAG : 645
       AAGAGAG AGTGGTTCTCCCAGCACG aG T GAGATCTGAG
            680
                              700
L1PA1 : AACGGGCAGACTGCCTCCTCAAGTGGGTCCCTGACTCCTGAC :
                                                    711
L1PA2 : AACGGGCAGACTGCCTCCTCAAGTGGGTCCCTGACCCTGAC :
                                                    712
L1PA3 : AACGGGCAGACTGCCTCCTCAAGTGGGTCCCTGACCCCTGAC
                                                    714
L1PA4 : AACGG-CAGACTGCCTCCTCAAGTGGGTCCCTGACCCCGAC :
                                                    713
L1PA5 : AACGGACAGACTGCCTCCAAGTGGGTCCCTGACCCC---- : 710
L1PA6 : AACGGACAGACTGCCTCCAAGTGGGTCCCTGCC---- : 680
       AACGG CAGACTGCCTCCTCAAGTGGGTCCCTGaC cc
          720
                            740
L1PA1 : CCCCGAGCAGCCTAACTGGGAGGCACCCCCAGCAGGGGGCAC : 753
L1PA2 : CCCCGAGCAGCCTAACTGGGAGGCACCCCCCAGCAGGGGGCAC : 754
L1PA3 : CCCCGAGCAGCCTAACTGGGAGGCACCCCCCAGTAGGGGCAG :
                                                    756
L1PA4 : C--CAAGTAGCCTAACTGGGAGGCACCCCCAGTAGGGGCAG : 753
L1PA5 : ---CGAGTAGCCTAACTGGGAGGCACCCCCCAGTAGGGGCAG : 749
L1PA6 : ---CGTGTAGCCTAACTGGGAGACACCTCCCAGTAGGGGCCA :
                                                    719
          CgaG AGCCTAACTGGGAGGCACCCCCAG AGGGGCa
        760
                           780
L1PA1 : ACTGACACCTCACACGGCAGGGTATTCC----- : 781
L1PA2 : ACTGACACCTCACACGGCAGGGTATTCC----- : 782
L1PA3 : ACTGACACCTCACACGGCCGGGTACTCCTCTGAGACAAAACT : 798
L1PA4 : ACTGACACCTCACACGGCCGGGTACTCCTCTGAGACAAAACT : 795
L1PA5 : ACTGACACCTCACACGGCCGGGTACCCCTCTGAGACGAAACT : 791
L1PA6 : ACTGACACCTCATACAGGTGGGTGCCCCTCTGGGACGAAGCT : 761
       ACTGACACCTCAcACGGC GGGTa CC
L1PA1 : -----: :
L1PA2 : ----- :
L1PA3 : TCCAGAGGAACGATCAGACAGCAGCATTCGCGGTTCACCAAA : 840
L1PA4 : TCCAGAGGAACGATCAGGCAGCATTTGCGGTTCACCAAT : 837
L1PA5 : TCCAGAGGAACGATCAGGCAGCAACATTTGCGGTTCACCAAT : 833
L1PA6 : TCCAGAGGAAGGATCAGGCAGCATG-----CAAT : 790
```

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860
                                           880
L1PA1 : -----
L1PA2 : -----::
L1PA3 : ATCCGCTGTTCTGCAGCCACCGCTGCTGATACCCAGGCAAAC :
                                                   882
L1PA4 : ATCCGCTGTTCTGCAGCCACCGCTGCTGATACCCAGGCAAAC :
                                                   879
L1PA5 : ATTCGCTGTTCTGCAGCCTCCGCTGCTGATACCCAGGCAAAC : 875
L1PA6 : ATTTGCTGTTCTGCAGCCTCTGCTGGTGATACCCAGGCAAAC :
                                                   832
                      900
                                         920
L1PA1 : -
                               -----AACAGACCTGCA
                                                   793
L1PA2 : -----AACAGACCTGCA
                                                   794
L1PA3: AGGGTCTGGAGTGGACCTCTAGCAAACTCCAACAGACCTGCA
                                                   924
L1PA4: AGGGTCTGGAGTGGACCTCCAGCAAACTCCAACAGACCTGCA
                                                   921
L1PA5 : AGGGTCTGGAGTGGACCTCCAGCAAACTCCAACAGACCTGCA
                                                   917
L1PA6 : AGGGTCTGGAGTGGACCTCCAGCAAACTCCAACAGACCTGCA :
                                                   874
                                    AACAGACCTGCA
                    940
                                       960
L1PA1 : GCTGAGGG<mark>T</mark>CCTGTCTGTTAGAAGGAAAACTAACAA<mark>C</mark>CAGAA
                                                   835
L1PA2 :
       GCTGAGGG<mark>T</mark>CCTG<mark>T</mark>CTGTTAGAAGGAAAACTAACAA<mark>A</mark>CAGAA
                                                   836
L1PA3 : GCTGAGGG<mark>T</mark>CCTGTTAGAAGGAAAACTAACAA<mark>A</mark>CAGAA :
                                                   966
L1PA4 : GCTGAGGGTCCTGACTGTTAGAAGGAAAACTAACAAACAGAA :
                                                   963
L1PA5 : GCTGAGGGTCCTGACTGTTAGAAGGAAAACTAACAAACAGAA :
                                                  959
L1PA6 : GCTGAGGGACCTGACTGTTAGAAGGAAAACTAACAAACAGAA :
                                                   916
       GCTGAGGGtCCTG CTGTTAGAAGGAAAACTAACAAaCAGAA
                  980
                                    1000
L1PA1 : AGGA------CATCTACACCGAA
                                                   852
L1PA2 : AGGA------CATCCACCAAAA
                                                   853
L1PA3 : AGGA-----CATCCACACCAAA :
                                                   983
L1PA4 : AGGA------CATCCACACAAA
                                                   980
L1PA5 : AGGA-----CATCCACACCAAA : 976
L1PA6 : AGGAATAGCATCAACAACAAAAAGGACATCCACCCAAA : 958
       AGGA
                                   CATCcACACCaAA
               1020
                                  1040
L1PA1 : AACCCATCTGTACATCACCATCATCAAAGACCAAAAGTAGAT
                                                : 894
                                                : 895
L1PA2 : AACCCATCTGTACATCACCATCATCAAAGACCAAAAGTAGAT
L1PA3 : AACCCATCTGTACATCACCATCATCAAAGACCAAAAGTAGAT : 1025
L1PA4 : AACCCATCTGTACGTCACCATCATCAAAGACCAAAGGTAGAT : 1022
L1PA5 : ACCCCATCTGTACGTCACCATCATCAAAGACCAAAGGTAGAT : 1018
L1PA6 : ACCCCATCTGTAGGTCACCAACATCAAAGACCAAAGGTAGAT : 1000
       A CCCATCTGTAC TCACCAtCATCAAAGACCAAA GTAGAT
```

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1060
                                   1080
L1PA1 : AAAACCACAAAGATGGGGAAAAAACAGAACAGAAAAACTGGA : 936
L1PA2 : AAAACCACAAAGATGGGGAAAAAACAGAACAGAAAAACTGGA : 937
L1PA3 : AAAACCACAAAGATGGGGAAAAAACAGAGCAGAAAAACTGGA : 1067
L1PA4 : AAAACCACAAAGATGGGGAAAAAACAGAGCAGAAAAACTGGA : 1064
L1PA5 : AAAACCACAAAGATGGGGAAAAAACAGAGCAGAAAAGCTGAA : 1060
L1PA6 : AAAACCACAAAGATGGGGA<mark>G</mark>AAA<mark>C</mark>CAGA<mark>G</mark>CAGAAAA<mark>G</mark>CTG<mark>A</mark>A : 1042
        AAAACCACAAAGATGGGGAAAAAACAGA CAGAAAA CTG A
            1100
                                 1120
L1PA1 : AACTCTAAAACGCAGAGCGCCTCTCCTCCAAAGGAACGC :
                                                       978
L1PA2 : AACTCTAAAAAAGCAGAGCGCCTCTCCTCCTAAAGGAACGC : 979
L1PA3 : AACTCTAAAAAAGCAGAGCGCCTCTCCTCCTAAAGGAACGC : 1109
L1PA4 : AACTCTAAAAATCAGAGCGCCTCTCCTCCTCCAAAGGAACGC : 1106
L1PA5 : AATTCTAAAAATCAGAGCGCCTCTCCTCCTCCAAAGGAACGC : 1102
L1PA6 : AATTCTAAAAACCAGAGCGCCTCTTCTCCTCCAAAGGATTGC : 1084
        AA TCTAAAAa CAGAGCGCCTCTCCTCCTCCAAAGGAacGC
          1140
                              1160
L1PA1 : AGTTCCTCACCAGCAACAGAACAAAGCTGGATGGAGAATGAT : 1020
L1PA2 : AGTTCCTCACCAGCAACGGAACAAAGCTGGATGGAGAATGAC : 1021
L1PA3 : AGTTCCTCACCAGCAACGGAACAAAGCTGGATGGAGAATGAC : 1151
L1PA4 : AGCTCCTCACCAGCAACGGAACAAAGCTGGATGGAGAATGAC : 1148
L1PA5 : AGCTCCTCACCAGCAACGGAACAAAGCTGGATGGAGAATGAC : 1144
L1PA6 : AGCTCCTCGCCAGCAACGGAACAAAGCTGGACGGAGAATGAC : 1126
        AG TCCTCaCCAGCAACqGAACAAAGCTGGAtGGAGAATGAC
        1180
                                                 12
                            1200
L1PA1 : TTTGACGAGCTGAGAGAGAGGCTTCAGACGATC----- : 1055
L1PA2 : TTTGACGAGCTGAGAGAAGAAGGCTTCAGACGATC----- : 1056
L1PA3 : TTTGACGAGTTGAGAGAAGAAGGCTTCAGACGATC----- : 1186
L1PA4 : TTTGACGAGTTGAGAGAAGAAGGCTTCAGACGATC----- : 1183
L1PA5 : TTTGACGAGTTGAGAGAGAGGCTTCAGACGATC----- : 1179
L1PA6 : TTTGACGAG<mark>T</mark>TGACAGAAGTAGGCTTCAGAAGGTCGGTAATA : 1168
        TTTGACGAG TGAGAGAAGAAGGCTTCAGACGATC
                           1240
                                               1260
L1PA1 : --AAATTACTCTGAGCTACGGGAGGACATTCAAACCAAAGGC : 1095
L1PA2 : --AAATTACTCTGAGCTACGGGAGGACATTCAAACCAAAGGC : 1096
L1PA3 : --AAACTACTCCGAGCTACAGGAGGAAATTCAAACCAAAGGC : 1226
L1PA4 : --AAACTACTCCGAGCTAAAGGAGGAAGTTCGAACCAATGGC : 1223
L1PA5 : --AAACTTCTCCGAGCTAAAGGAGGAAGTTCGAACCCATCGC : 1219
L1PA6 : ACAAACTTCTCCGAGCTAAAGGAGGATGTTCAAAACCCATCGC : 1210
          AAA T CTC GAGCTA GGAGGA TTC AACC A GC
```

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1280
                                                  1300
L1PA1 : AAAGAAGTTGAAAACTTTGAAAAAAATTTAGAAGAATGTATA : 1137
L1PA2 : AAAGAAGTTGAAAAACTTTGAAAAAAATTTAGAAGAATGTATA : 1138
L1PA3 : AAAGAAGTTAAAAACTTTGAAAAAATTTAGACGAATGTATA
                                                         : 1268
L1PA4 : AAAGAAGTTAAAAACTTTGAAAAAAATTAGACGAATGGCTA : 1265
L1PA5 : AAAGAAGCTAAAAACCTTGAAAAAAGATTAGACGAATGGCTA : 1261
L1PA6 : AAGGAAGCTAAAAACCTTGAAAAAAGATTAGACGAATGGCTA : 1252
         AAaGAAG T AAAAC TTGAAAAAA TTAGA GAATG
                         1320
                                               1340
L1PA1 : ACTAGAATAACCAATACAGAGAAGTGCTTAAAGGAGCTGATG : 1179
L1PA2 : ACTAGAATAACCAATACAGAGAAGTGCTTAAAGGAGCTGATG : 1180
L1PA3 : ACTAGAATAACCAATACAGAGAAGTGCTTAAAGGAGCTGATG : 1310
L1PA4 : ACTAGAATAACCAATGCAGAGAAGTCCTTAAAGGACCTGATG : 1307
L1PA5 : ACTAGAATAACCAGTGTAGAGAAGTCCTTAAATGACCTGATG : 1303
L1PA6 : ACTAGAATAAACAGTGTAGAGAAGACCTTAAATGACCTGATG : 1294
         ACTAGAATAACCA T AGAGAAGt CTTAAA GA CTGATG
                      1360
                                             1380
L1PA1 : GAGCTGAAAACCA<mark>A</mark>GGC<mark>T</mark>CGAGAACTACGTGA<mark>AGA</mark>ATGCA<mark>G</mark>A : 1221
L1PA2 : GAGCTGAAAACCA<mark>A</mark>GGC<mark>T</mark>CGAGAACTACGTGA<mark>A</mark>GATGCA<mark>G</mark>A : 1222
L1PA3 : GAGCTGAAAACCA<mark>A</mark>GGC<mark>T</mark>CGAGAACTACGTGA<mark>A</mark>GAATGCA<mark>G</mark>A : 1352
L1PA4 : GAGCTGAAAACCAAGGCACGAGAACTACGTGACGAATGCACA : 1349
L1PA5 : GAGCTGAAAACCA<mark>T</mark>GGC<mark>A</mark>CGAGAACTACGTGA<mark>C</mark>G<mark>A</mark>ATGCA<mark>C</mark>A : 1345
L1PA6 : GAGCTGAAAACCA<mark>T</mark>GGC<mark>A</mark>CGAGAACTACGTGA<mark>C</mark>GCATGCA<mark>C</mark>A : 1336
         GAGCTGAAAACCA GGC CGAGAACTACGTGA GAATGCA A
                    1400
                                           1420
L1PA1 : AGCCTCAGGAGCCGATGCGATCAACTGGAAGAAAGGGTATCA : 1263
L1PA2 : AGCCTCAGGAGCCGATGCGATCAACTGGAAGAAGGGTATCA : 1264
L1PA3 : AGCCTCAGGAGCCGATGCGATCAACTGGAAGAAAGGGTATCA : 1394
                                                         : 1391
L1PA4 : AGCCTCAGTAGCCGATGCGATCAACTGGAAGAAAGGGTATCA
L1PA5 : AGCTTCAGTAGCCGATTCGATCAACTGGAAGAAGGGTATCA : 1387
L1PA6 : AGCTTCAATAGCCGATTCGATCAAGTGGAAGAAAGGGTATCA : 1378
         AGC TCAG AGCCGAT CGATCAAcTGGAAGAAAGGGTATCA
                  1440
                                         1460
L1PA1 : GCAATGGAAGATGAAATGAAATGAAGCGAGAAGGGAAG : 1305
L1PA2 : GCAATGGAAGATGAAATGAAATGAAGCGAGAAGGGAAG : 1306
L1PA3 : GTGATGGAAGATGAAATGAAGCGAGAAGGGAAG : 1436
L1PA4 : GTGATGGAAGATGAAATGAAATGAAGCGAGAAGAGAAG : 1433
L1PA5 : GTGATTGAAGATCAAATGAAATGAAGCGAGAAGAGAAG : 1429
L1PA6 : GTGATTGAAGATCAAATTAATGAAATAAAGCGAGAAGACAAG : 1420
         G AT GAAGAT AAATGAATGAAATGAAGCGAGAAG GAAG
```

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1480
                                  1500
        TTTAGAGAAAAAAGA<mark>A</mark>TAAAAAGAAATGA<mark>G</mark>CAAAGCCTCCAA : 1347
L1PA2 : TTTAGAGAAAAAAGAATAAAAAGAAATGAGCAAAGCCTCCAA : 1348
L1PA3 : TTTAGAGAAAAAAGAATAAAAAGAAATGAACAAAGCCTCCAA
                                                   : 1478
L1PA4 : TTTAGAGAAAAAAGAATAAAAAGAAATGAACAAAGCCTCCAA
                                                   : 1475
L1PA6 : TTTAGAGAAAAAGAGTAAAAAGAAATGAACAAAGCCTCCAA
                                                   : 1462
        TTTAGAGAAAAAGAATAAAAAGAAATGA CAAAGCCTCCAA
            1520
                                1540
        GAAATATGGGACTATGTGAAAAGACCAAATCTACGT<mark>C</mark>TGATT : 1389
L1PA1 :
L1PA2 : GAAATATGGGACTATGTGAAAAGACCAAATCTACGTCTGATT
                                                   : 1390
L1PA3 : GAAATATGGGACTATGTGAAAAGACCAAATCTACGTCTGATT
                                                   : 1520
L1PA4 : GAAATATGGGACTATGTGAAAAGACCAAATCTACGTCTGATT
                                                   : 1517
L1PA5 : GAAATATGGGACTATGTGAAAAGACCAAATCTACGTCTGATT
                                                   : 1513
L1PA6 : GAAATATGGGACTATGTGAAAAGACCAAATCTACGTTTGATT : 1504
        GAAATATGGGACTATGTGAAAAGACCAAATCTACGTcTGATT
          1560
                              1580
L1PA1 : GGTGTACCTGAAAGTGATGTGGAGAATGGAACCAAGTTGGAA : 1431
        GGTGTACCTGAAAGTGA<mark>T</mark>G<mark>G</mark>GGAGAATGGAACCAAGTTGGAA
                                                   : 1432
L1PA2:
L1PA3 : GGTGTACCTGAAAGTGACGGGGGAGAATGGAACCAAGTTGGAA : 1562
L1PA4 : GGTGTACCTGAAAGTGACGGGGAGAATGGAACCAAGTTGGAA : 1559
L1PA5 : GGTGTACCTGAAAGTGACGGGGGAGAATGGAACCAAGTTGGAA : 1555
L1PA6 : GGTGTACCTGAAAGTGACGGGGGAGAATGGAACCAAGTTGGAA : 1546
        GGTGTACCTGAAAGTGA GGGGAGAATGGAACCAAGTTGGAA
        1600
                            1620
                                                16
L1PA1 : AACACTCTGCAGGATATTATCCAGGAGAACTTCCCCAATCTA : 1473
L1PA2 : AACACTCTGCAGGATATTATCCAGGAGAACTTCCCCAATCTA : 1474
L1PA3 : AACACTCTGCAGGATATTATCCAGGAGAACTTCCCCAATCTA : 1604
L1PA4 : AACACTCTGCAGGATATTATCCAGGAGAACTTCCCCAATCTA : 1601
L1PA5 : AACACTCTGCAGGATATTATCCAGGAGAACTTCCCCAACCTA : 1597
L1PA6 : AACACTCTTCAGGATATTATCCAGGAGAACTTCCCCAACCTA : 1588
        AACACTCTqCAGGATATTATCCAGGAGAACTTCCCCAA CTA
                          1660
L1PA1 : GCAAGGCAGGCCAACGTTCAGATTCAGGAAATACAGAGAACG : 1515
L1PA2 : GCAAGGCAGGCCAACGTTCAGATTCAGGAAATACAGAGAACG : 1516
L1PA3 : GCAAGGCAGGCCAACGTTCAGATTCAGGAAATACAGAGAACG : 1646
L1PA4 : GCAAGGCAGGCCAACGTTCAAATTCAGGAAATACAGAGAACG : 1643
L1PA5 : GCAAGGCAGGCCAACGTTCAAATTCAGGAAATACAGAGAACG : 1639
L1PA6 : GCAAGGCAGGCCAACATTCAAATTCAGGAAATACAGAGAACA : 1630
        GCAAGGCAGGCCAACGTTCA ATTCAGGAAATACAGAGAACG
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1700
                                             1720
L1PA1 : CCACAAAGATACTCCTCGAGAAGAGCAACTCCAAGACACATA : 1557
L1PA2 : CCACAAAGATACTCCTCGAGAAGAGCAACTCCAAGACACATA
                                                    : 1558
L1PA3 : CCACAAAGATACTCCTCGAGAAGAGCAACTCCAAGACACATA
                                                    : 1688
L1PA4 : CCACAAAGATACTCCTCGAGAAGAGCAACTCCAAGACACATA
                                                    : 1685
L1PA5 : CCACAAAGATACTCCTCGAGAAGAGCAACTCCAAGACACATA
                                                    : 1681
L1PA6 : CCACAAAGATACTCCTCGAGAAGACAACCCCCAAGACACATA
                                                    : 1672
        CCACAAAGATACTCCTCGAGAAGAGCAACtCCAAGACACATA
                       1740
                                           1760
        ATTGTCAGATTCACCAA<mark>A</mark>GTTGAAATGAAGGAAAAAATGTTA : 1599
L1PA1 :
L1PA2 : ATTGTCAGATTCACCAAAGTTGAAATGAAGGAAAAAATGTTA
                                                    : 1600
L1PA3 : ATTGTCAGATTCACCAAAGTTGAAATGAAGGAAAAAATGTTA
                                                    : 1730
L1PA4 : ATTGTCAGATTCACCAAAGTTGAAATGAAGGAAAAAATGTTA
                                                    : 1727
L1PA5 : ATTGTCAGATTCACCAAAGTTGAAATGAAGGAAAAAATGTTA
                                                    : 1723
L1PA6 : ATTGTCAGATTCACCAAGGTTGAAATGAAGGAAAAAATGTTA : 1714
        ATTGTCAGATTCACCAAaGTTGAAATGAAGGAAAAAATGTTA
                    1780
                                         1800
L1PA1 : AGGGCAGCCAGAGAGAAAGGTCGGGTTACCCTCAAAGGAAAG : 1641
        <u>AGGGCAGCCA</u>GAGAGAAAGGTCGGGTTACCC<mark>T</mark>CAAAGG<mark>G</mark>AAG
                                                    : 1642
L1PA2:
L1PA3 : AGGGCAGCCAGAGAGAAAGGTCGGGTTACCCACAAAGGGAAG : 1772
L1PA4 : AGGGCAGCCAGAGAGAGAGGTCGGGTTACCCACAAAGGGAAG : 1769
L1PA5 : AGGGCAGCCAGAGAGAGAGGTCGGGTTACCCACAAAGGGAAG : 1765
L1PA6 : AGGGCAGCCAGAGAGAGAGGTCGGGTTACCCACAAAGGGAAG : 1756
        AGGGCAGCCAGAGAGAAAGGTCGGGTTACCC CAAAGGGAAG
                  1820
                                       1840
L1PA1 : CCCATCAGACTAACAGCGGATCTCTCGGCCAGAAACCCCTACAA : 1683
L1PA2 : CCCATCAGACTAACAGCGGATCTCTCGGCCAGAAACCCTACAA : 1684
L1PA3 : CCCATCAGACTAACAGCGGATCTCTCGGCAGAAACTCTACAA : 1814
                                                    : 1811
L1PA4 : CCCATCAGACTAACAGCGGATCTCTCGGCAGAAACTCTACAA
L1PA5 : CCCATCAGACTAACAGCGGATCTCTCGGCAGAAACTCTACAA : 1807
L1PA6 : CCCATCAGACTAACAGCGGATCTCTCAGCAGAAACCCTACAA : 1798
        CCCATCAGACTAACAGCGGATCTCTCGGCAGAAAC CTACAA
                1860
                                     1880
        GCCAGAAGAGAGTGGGGGCCAATATTCAACATTCTTAAAGAA : 1725
L1PA1 :
                                                    : 1726
L1PA2 : GCCAGAAGAGAGTGGGGGCCAATATTCAACATTCTTAAAGAA
L1PA3 : GCCAGAAGAGAGTGGGGGCCAATATTCAACATTCTTAAAGAA : 1856
L1PA4 : GCCAGAAGAGAGTGGGGGCCAATATTCAACATTCTTAAAGAA : 1853
        GCCAGAAGAGAGTGGGGGCCAATATTCAACATTCTTAAAGAA
L1PA5:
                                                    : 1849
L1PA6 : GCCAGAAGAGAGTGGGGGCCAATATTCAACATTCTTAAAGAA : 1840
        GCCAGAAGAGAGTGGGGGCCAATATTCAACATTCTTAAAGAA
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1900
                                     1920
L1PA1 : AAGAATTTTCAACCCAGAATTTCATATCCAGCCAAACTAAGC
                                                      : 1767
L1PA2 : AAGAATTTTCAACCCAGAATTTCATATCCAGCCAAACTAAGC
                                                      : 1768
L1PA3 : AAGAATTTTCAACCCAGAATTTCATATCCAGCCAAACTAAGC
                                                       : 1898
L1PA4: AAGAATTTTCAACCCAGAATTTCATATCCAGCCAAACTAAGC
                                                      : 1895
                                                      : 1891
L1PA5 : AAGAATTTTCAACCCAGAATTTCATATCCAGCCAAACTAAGC
L1PA6 : AAGAATTTTCAACCCAGAATTTCATATCCAGCCAAACTAAGC
                                                      : 1882
        AAGAATTTTCAACCCAGAATTTCATATCCAGCCAAACTAAGC
             1940
                                  1960
        TTCATAAGTGAAGGAGAAATAAAAT<mark>A</mark>CTTTA<mark>T</mark>AGACAAGCAA : 1809
L1PA1:
L1PA2 : TTCATAAGTGAAGGAGAAATAAAAT<mark>A</mark>CTTTA<mark>C</mark>AGACAAGCAA
                                                      : 1810
L1PA3 : TTCATAAGTGAAGGAGAAATAAAATACTTTACAGACAAGCAA : 1940
        TTCATAAGTGAAGGAGAAATAAAAT<mark>A</mark>CTTTA<mark>C</mark>AGACAAGCAA
L1PA4 :
                                                      : 1937
L1PA5 : TTCATAAGTGAAGGAGAAATAAAATCCTTTACAGACAAGCAA : 1933
L1PA6 : TTCATAAGTGAAGGAGAAATAAAATCCTTTACAGACAAGCAA : 1924
        TTCATAAGTGAAGGAGAAATAAAAT CTTTAcAGACAAGCAA
           1980
                                2000
L1PA1 : ATGTTGAGAGATTTTGTCACCACCAGGCCTGCCCTAAAAAGAG : 1851
L1PA2 :
        ATG<mark>C</mark>TGAGAGATTTTGTCACCACCAGGCCTGCC<mark>C</mark>TA<mark>A</mark>AAGAG
                                                      : 1852
L1PA3 : ATGCTGAGAGATTTTGTCACCACCAGGCCTGCCCTAAAAAGAG : 1982
L1PA4 : ATGCTGAGAGATTTTGTCACCACCAGGCCTGCCCTAAAAAGAG : 1979
L1PA5 : ATGCTGAGAGATTTTGTCACCACCAGGCCTGCCCTACAAGAG : 1975
L1PA6 : ATGCTGAGAGATTTTGTCACCACCAGGCCTGCCTTACAAGAG : 1966
        ATGCTGAGAGATTTTGTCACCACCAGGCCTGCCCTA AAGAG
         2020
                                                    20
                              2040
L1PA1 : CTCCTGAAGGAAGCGCTAAACATGGAAAGGAACAACCGGTAC
                                                      : 1893
L1PA2 : CTCCTGAAGGAAGCGCTAAACATGGAAAGGAACAACCGGTAC
                                                      : 1894
        CTCCTGAAGGAAGC<mark>G</mark>CTAAACATGGAAAGGAACAACCGGTAC
L1PA3 :
                                                      : 2024
L1PA4 : CTCCTGAAGGAAGCGCTAAACATGGAAAGGAACAACCGGTAC
                                                      : 2021
L1PA5 : CTCCTGAAGGAAGCCCCTAAACATGGAAAGGAACAACCGGTAC
                                                      : 2017
L1PA6 : CTCCTGAAGGAAGCACTAAACATGGAAAGGAACAACCGGTAC : 2008
        CTCCTGAAGGAAGCGCTAAACATGGAAAGGAACAACCGGTAC
                            2080
L1PA1 : CAGCCGCTGCAAAATCATGCCAAAATGTAAAGACCATCGAGA : 1935
L1PA2 : CAGCCGCTGCAAAATCATGCCAAAATGTAAAGACCATCGAGA : 1936
L1PA3 : CAGCCACTGCAAAATCATGCCAAATTGTAAAGACCATCGAGG : 2066
L1PA4 : CAGCCACTGCAAAAACATGCCAAATTGTAAAGACCATCGAGG : 2063
L1PA5 : CAGCCACTGCAAAAACATGCCAAATTGTAAAGACCATCGATG : 2059
L1PA6 : CAGCCACTGCAAAAACATGCCAAATTGTAAAGACCATCGATG : 2050
        CAGCC CTGCAAAA CATGCCAAA TGTAAAGACCATCGA
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2140
                         2120
L1PA1 : CTAGGAAGAAACTGCATCAACTAA<mark>T</mark>GAGCAAAAT<mark>C</mark>ACCAGCT
                                                     : 1977
L1PA2 : CTAGGAAGAAACTGCATCAACTAACGAGCAAAATCACCAGCT
                                                     : 1978
L1PA3 : CTAGGAAGAACTGCATCAACTAACGAGCAAAATAACCAGCT
                                                     : 2108
L1PA4 : CTAGGAAGAAACTGCATCAACTAACGAGCAAAATAACCAGCT
                                                     : 2105
L1PA5 : CTAGGAAGAAACTGCATCAACTAA<mark>C</mark>GAGCAAAAT<mark>A</mark>ACCAGCT
                                                     : 2101
L1PA6 : CTAGGAAGAACTGCATCAACTAA<mark>C</mark>GGGCAAAAT<mark>A</mark>ACCAGCT
                                                     : 2092
        CTAGGAAGAACTGCATCAACTAACGAGCAAAAT ACCAGCT
                       2160
                                            2180
L1PA1 : AACATCATAATGACAGGATCAAATTCACACATAACAATATTA
                                                     : 2019
L1PA2 : AACATCATAATGACAGGATCAAATTCACACATAACAATATTA
                                                     : 2020
L1PA3 : AACATCATAATGACAGGATCAAATTCACACATAACAATATTA
                                                     : 2150
L1PA4 : AACATCATAATGACAGGATCAAATTCACACATAACAATATTA
                                                     : 2147
L1PA5 : AACATCATAATGACAGGATCAAATTCACACATAACAATATTA
                                                     : 2143
L1PA6: AACATCATAATGACAGGATCAAATTCACACATAACAATATTA: 2134
        AACATCATAATGACAGGATCAAATTCACACATAACAATATTA
                     2200
                                          2220
L1PA1 : ACTTTAAATATAAATGGACTAAATTCTGCAATTAAAAGACAC
                                                     : 2061
                                                     : 2062
L1PA2 : ACTTTAAATGTAAATGGACTAAATGCTCCAATTAAAAGACAC
L1PA3 : ACTTTAAATGTAAATGGACTAAATGCTCCAATTAAAAGACAC
                                                     : 2192
L1PA4 : ACCTTAAATGTAAATGGGCTAAATGCTCCAATTAAAAGACAC
L1PA5 : ACCTTAAATGTAAATGGGCTAAATGCTCCAATTAAAAGACAC
                                                     : 2185
L1PA6 : ACCTTAAATGTAAATGGGCTAAATGCCCCCAATTAAAAGACAC : 2176
        AC TTAAATGTAAATGG CTAAATGCtcCAATTAAAAGACAC
                   2240
                                        2260
L1PA1 : AGACTGGCAAGTTGGATAAAGAGTCAAGACCCATCAGTGTGC
                                                     : 2103
L1PA2 : AGACTGGCAAATTGGATAAAGAGTCAAGACCCATCAGTGTGC
                                                     : 2104
L1PA3 : AGACTGGCAAATTGGATAAAGAGTCAAGACCCATCAGTGTGC
                                                     : 2234
L1PA4: AGACTGGCAAATTGGATAAAGAGTCAAGACCCATCAGTGTGC
                                                     : 2231
L1PA5 : AGACTGGCAAATTGGATAAAGAGTCAAGACCCATCAGTGTGC
                                                     : 2227
                                                     : 2218
L1PA6 : AGACTGGCAAATTGGATAAAGAGTCAAGACCCATCAGTGTGC
        AGACTGGCAAaTTGGATAAAGAGTCAAGACCCATCAGTGTGC
                 2280
                                      2300
        TGTATTCAGGA<mark>A</mark>ACCCATCTCACGTGCAGAGACACACATAGG
                                                     : 2145
L1PA1 :
                                                     : 2146
L1PA2 : TGTATTCAGGAAACCCATCTCACGTGCAGAGACACACATAGG
L1PA3 : TGTATTCAGGAAACCCATCTCACGTGCAGAGACACACATAGG
                                                     : 2276
L1PA4 : TGTATTCAGGAAACCCATCTCACGTGCAGAGACACACATAGG
                                                     : 2273
L1PA5 : TGTATTCAGGAGACCCATCTCACGTGCAGAGACACACATAGG
                                                     : 2269
L1PA6 : TGTATTCAGGAGACCCATCTCACGTGCAGAGACACACATAGG : 2260
        TGTATTCAGGA ACCCATCTCACGTGCAGAGACACACATAGG
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2320
                                  2340
L1PA1 : CTCAAAATAAAAGGATGGAGGAAGATCTACCAAGCCAATGGA : 2187
L1PA2 : CTCAAAATAAAAGGATGGAGGAAGATCTACCAAGCAAATGGA : 2188
L1PA3 : CTCAAAATAAAAAGGATGGAGGAAGATCTACCAAGCAAATGGA
                                                   : 2318
L1PA4 : CTCAAAATAAAGGGATGGAGGAAGATCTACCAAGCAAATGGA
                                                   : 2315
L1PA5 : CTCAAAATAAAGGGATGGAGGAAGATCTACCAAGCAAATGGA
                                                   : 2311
L1PA6 : CTCAAAATAAAGGGGATGGAGGAAGATCTACCAAGCAAATGGA
                                                   : 2302
        CTCAAAATAAA GGATGGAGGAAGATCTACCAAGCAAATGGA
            2360
                                2380
L1PA1 : AAACAAAAAAAGGCAGGGGTTGCAATCCTAGTCTCTGATAAA : 2229
L1PA2 : AAACAAAAAAGGCAGGGGTTGCAATCCTAGTCTCTGATAAA
                                                   : 2230
L1PA3 : AAACAAAAAAAGGCAGGGGTTGCAATCCTAGTCTCTGATAAA : 2360
L1PA4 : AAACAAAAAAAGGCCAGGGGTTGCAATCCTAGTCTCTGATAAA
                                                   : 2357
L1PA5 : AAACAAAAAAAGGCAGGGGTTGCAATCCTAGTCTCTGATAAA : 2353
L1PA6 : AAGCAAAAAAAAGCAGGGGTTGCAATCCTAGTCTCTGATAAA : 2344
        AAaCAAAAAAAGGCAGGGGTTGCAATCCTAGTCTCTGATAAA
          2400
                              2420
L1PA1 : ACAGACTTTAAACCAACAAAGATCAAAAGAGACAAAGAAGGC : 2271
L1PA2 : ACAGACTTTAAACCAACAAGATCAAAAGAGACAAAGAGGC
                                                   : 2272
                                                   : 2402
L1PA3 : ACAGACTTTAAACCAACAAGATCAAAAGAGACAAAGAGAGGC
L1PA4 : ACAGACTTTAAACCAACAAGATCAAAAGAGACAAAGAGGC
L1PA5 : ACAGACTTTAAACCAACAAGATCAAAAGAGACAAAGAGAGGC
                                                   : 2395
L1PA6 : ACAGACTTTAAACCAACAAAGATCAAAAGAGACAAAGAAGCC
                                                   : 2386
        ACAGACTTTAAACCAACAAAGATCAAAAGAGACAAAGAAGCC
        2440
                                                 24
                            2460
L1PA1 : CATTACATAATGGTAAAGGGATCAATTCAACAAGAGGGGAGCTA
                                                   : 2313
L1PA2 : CATTACATAATGGTAAAGGGATCAATTCAACAAGAAGAGGCTA
L1PA3 : CATTACATAATGGTAAAGGGATCAATTCAACAAGAAGAAGACTA
                                                   : 2444
                                                   : 2441
L1PA4 : CATTACATAATGGTAAAGGGATCAATTCAACAAGAAGAGGCTA
L1PA5 : CATTACATAATGGTAAAGGGATCAATTCAACAAGAAGAGGGCTA
                                                   : 2437
L1PA6 : CATTACATAATGGTAAAGGGATCAATTCAACAAGAAGAGCTA : 2428
        CATTACATAATGGTAAAGGGATCAATTCAACAAGAAGAGCTA
                          2500
L1PA1 : ACTATCCTAAATATTTATGCACCCAATACAGGAGCACCCAGA : 2355
L1PA2 : ACTATCCTAAATATATATGCACCCAATACAGGAGCACCCAGA : 2356
L1PA3 : ACTATCCTAAATATATATGCACCCAATACAGGAGCACCCAGA : 2486
L1PA4 : ACTATCCTAAATATATATGCACCCAATACAGGAGCACCCAGA : 2483
L1PA5 : ACTATCCTAAATATATATGCACCCAATACAGGAGCACCCAGA : 2479
L1PA6 : ACTATCCTAAATATATATGCACCCAATACAGGAGCACCCAGA : 2470
        ACTATCCTAAATATaTATGCACCCAATACAGGAGCACCCAGA
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2540
                                              2560
L1PA1 : TTCATAAAGCAAGTCCTCAGTGACCTACAAAGAGACTTAGAC
                                                    : 2397
                                                     : 2398
L1PA2 : TTCATAAAGCAAGTCCTGAGTGACCTACAAAGAGACTTAGAC
L1PA3 : TTCATAAAGCAAGTCCTGAGTGACCTACAAAGAGACTTAGAC
                                                     : 2528
L1PA4 : TTCATAAAGCAAGTCCTTAGTGACCTACAAAGAGACTTAGAC
                                                    : 2525
L1PA5 : TTCATAAAGCAAGTCCTTAGAGAGACCTACAAAGAGACTTAGAC
                                                    : 2521
L1PA6 : TTCATAAAGCAAGTCCTTAGAGAGACCTACAAAGAGACTTAGAC
                                                    : 2512
        TTCATAAAGCAAGTCCT AG GACCTACAAAGAGACTTAGAC
                       2580
                                            2600
        TCCCACACA<mark>T</mark>TAATAATGGGAGACTTTAACACCCCACTGTCA
L1PA1 :
                                                    : 2439
L1PA2 : TCCCACACATTAATAATGGGAGACTTTAACACCCCACTGTCA
                                                    : 2440
L1PA3 : TCCCACACAATAATAATGGGAGACTTTAACACCCCACTGTCA
                                                    : 2570
L1PA4 : TCCCACACAATAATAATGGGAGACTTTAACACCCCACTGTCA
                                                    : 2567
L1PA5 : TCCCACACAATAATAATGGGAGACTTTAACACCCCACTGTCA
                                                    : 2563
L1PA6 : TCCCACACAATAATAATGGGAGACTTTAACACCCCACTGTCA : 2554
        TCCCACACA TAATAATGGGAGACTTTAACACCCCACTGTCA
                     2620
                                         2640
L1PA1 : ACATTAGACAGATCAACGAGACAGAAAGTCAACAAGGATACC
                                                    : 2481
                                                    : 2482
L1PA2:
          ATTAGACAGATCAACGAGACAGAA<mark>A</mark>GT<mark>C</mark>AACAAGGATA<mark>C</mark>
L1PA3 : ACATTAGACAGATCAACGAGACAGAAAGTTAACAAGGATACC
                                                    : 2612
L1PA4 : ACATTAGACAGATCAACGAGACAGAAAGTTAACAAGGATATC : 2609
L1PA5 : ACATTAGACAGATCAACGAGACAGAAAGTTAACAAGGATATC : 2605
L1PA6 : ATATTAGACAGATCAACGAGACAGAAGGTTAACAAGGATATC : 2596
        ACATTAGACAGATCAACGAGACAGAAAGT AACAAGGATA C
                  2660
                                       2680
L1PA1 : CAGGAATTGAACTCAGCTCTGCACCAAGCAGACCTAATAGAC
                                                    : 2523
L1PA2 : CAGGAATTGAACTCAGCTCTGCACCAAGCGGACCTAATAGAC
                                                    : 2524
L1PA3 : CAGGAATTGAACTCAGCTCTGCACCAAGCGGACCTAATAGAC
                                                    : 2654
L1PA4 : CAGGAATTGAACTCAGCTCTGCACCAAGCGGACCTAATAGAC
                                                    : 2651
L1PA5 : CAGGAATTGAACTCAGCTCTGCACCAAGCGGACCTAATAGAC
                                                    : 2647
L1PA6 : CAGGACTTGAACTCAGCTCTGCACCAAGCGGACCTAATAGAC : 2638
        CAGGAaTTGAACTCAGCTCTGCACCAAGCGGACCTAATAGAC
                2700
                                     2720
L1PA1: ATCTACAGAACTCTCCACCCCAAATCAACAGAATATACATTT : 2565
L1PA2 : ATCTACAGAACTCTCCACCCCAAATCAACAGAATATACATTT : 2566
L1PA3 : ATCTACAGAACTCTCCACCCCAAATCAACAGAATATACATTT : 2696
L1PA4 : ATCTACAGAACTCTCCACCCCAAATCAACAGAATATACATTC : 2693
        ATCTACAGAACTCTCCACCCCAAATCAACAGAATATACATTC : 2689
L1PA5:
L1PA6 : ATCTACAGAACTCTCCACCCCAAATCAACAGAATATACATTC : 2680
        ATCTACAGAACTCTCCACCCCAAATCAACAGAATATACATT
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2740
                                   2760
L1PA1 : TTTTCAGCACCACACCCTATTCCAAAATTGACCACATA : 2607
L1PA2 : TTTTCAGCACCACACCCTATTCCAAAATTGACCACATA : 2608
L1PA3 : TTTTCAGCACCACACCCTATTCCAAAATTGACCACATA
                                                   : 2738
L1PA4 : TTTTCAGCACCACACCCTATTCCAAAATTGACCACATA : 2735
L1PA5 : TTCTCAGCACCACATCACACTTATTCCAAAATTGACCACATA : 2731
L1PA6 : TTCTCAGCACCACATCGCACTTATTCCAAAATTGACCACATA
                                                   : 2722
        TT TCAGCACCACA CaCAC TATTCCAAAATTGACCACATA
            2780
                                2800
L1PA1 : GTTGGAAGTAAAGCTCTCCTCAGCAAATGTAAAAGAACAGAA : 2649
L1PA2 : CTTGGAAGTAAAGCTCTCCTCAGCAAATGTAAAAGAACAGAA : 2650
L1PA3 : GTTGGAAGTAAAGCTCTCCTCAGCAAATGTAAAAGAACAGAA : 2780
L1PA4 : GTTGGAAGTAAAGCACTCCTCAGCAAATGTAAAAGAACAGAA : 2777
L1PA5 : GTTGGAAGTAAAGCACTCCTCAGCAAATGTAAAAGAACAGAA : 2773
L1PA6 : ATTGGAAGTAAAGCACTCCTCAGCAAATGTAAAAGAACAGAA : 2764
         TTGGAAGTAAAGC CTCCTCAGCAAATGTAAAAGAACAGAA
          2820
                              2840
L1PA1 : ATTATAACAAACTATCTCTCAGACCACAGTGCAATCAAACTA : 2691
                                                   : 2692
L1PA2 : ATTATAACAAACTATCTCTCAGACCACAGTGCAATCAAACTA
L1PA3 : ATTATAACAAACTGTCTCTCAGACCACAGTGCAATCAAACTA : 2822
L1PA4 : ATTATAACAAACTGTCTCTCAGACCACAGTGCAATCAAACTA : 2819
L1PA5 : ATTATAACAAACTGTCTCTCAGACCACAGTGCAATCAAACTA : 2815
L1PA6 : ATCACAACAAACTGTCTCTCAGACCACAGTGCAATCAAATTA : 2806
        ATTATAACAAACT TCTCTCAGACCACAGTGCAATCAAACTA
                                                 29
        2860
                            2880
L1PA1 : GAACTCAGGATTAAGAA<mark>T</mark>CTCACTCAAA<mark>G</mark>CCGC<mark>T</mark>CAACTACA : 2733
L1PA2 : GAACTCAGGATTAAGAATCTCACTCAAAACCGCTCAACTACA : 2734
L1PA3 : GAACTCAGGATTAAGAAACTCACTCAAAACCGCTCAACTACA : 2864
L1PA4 : GAACTCAGGATTAAGAAACTCACTCAAAACCGCTCAACTACA : 2861
L1PA5 : GAACTCAGGATTAAGAAACTCACTCAAAACCGCTCAACTACA : 2857
L1PA6 : GAACTCAGGATTAAGAAACTCACTCAAAACCGCACAACTACA : 2848
        GAACTCAGGATTAAGAA CTCACTCAAAACCGCtCAACTACA
                          2920
                                               2940
L1PA1 : TGGAAACTGAACAACCTGCTCCTGAATGACTACTGGGTACAT : 2775
                                                   : 2776
L1PA2 : TGGAAACTGAACAACCTGCTCCTGAATGACTACTGGGTACAT
L1PA3 : TGGAAACTGAACAACCTGCTCCTGAATGACTACTGGGTACAT : 2906
L1PA4 : TGGAAACTGAACAACCTGCTCCTGAATGACTACTGGGTACAT : 2903
L1PA5 : TGGAAACTGAACAACCTGCTCCTGAATGACTACTGGGTACAT
                                                   : 2899
L1PA6 : TGGAAACTGAACACCTGCTCCTGAATGACTACTGGGTAAAT : 2890
        TGGAAACTGAACAACCTGCTCCTGAATGACTACTGGGTACAT
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2960
                                              2980
L1PA1 : AACGAAATGAAGGCAGAAATAAAGATGTTCTTTGAAACCAAC
L1PA2 : AACGAAATGAAGGCAGAAATAAAGATGTTCTTTGAAACCAAC
                                                     : 2818
L1PA3 : AACGAAATGAAGGCAGAAATAAAGATGTTCTTTGAAACCAAC
                                                      : 2948
                                                     : 2945
L1PA4 : AACGAAATGAAGGCAGAAATAAAGATGTTCTTTGAAACCAAC
L1PA5 : AACGAAATGAAGGCAGAAATAAAGATGTTCTTTGAAACCAAC : 2941
L1PA6 : AACGAAATGAAGGCAGAAATAAAGATGTTCTTTGAAACCAAT : 2932
        AACGAAATGAAGGCAGAAATAAAGATGTTCTTTGAAACCAAc
                       3000
                                            3020
L1PA1 : GAGAACAAAGACACAATACCAGAATCTCTGGGACGCATTC : 2859
L1PA2 : GAGAACAAGACACACACAGAATCTCTGGGGACGCATTC : 2860
L1PA3 : GAGAACAAAGACACACACAGAATCTCTGGGGACGCATTC : 2990
L1PA4 : GAGAACAAAGACACAACATACCAGAATCTCTGGGACGCATTC : 2987
L1PA5 : GAGAACAAAGACACAACATACCAGAATCTCTGGGACGCATTT : 2983
L1PA6 : GAGAACAAAGACACAGTACCAGAATCTCTGGGACACATTT : 2974
        GAGAACAAAGACACaACaTACCAGAATCTCTGGGACqCATT
                     3040
                                          3060
L1PA1 : AAAGCAGTGTGTAGAGGGAAATTTATAGCACTAAATGCCTAC
                                                     : 2901
                                                     : 2902
L1PA2:
        AAAGCAGTGTGTAGAGGGAAATTTATAGCACTAAATGCC<mark>C</mark>AC
L1PA3 : AAAGCAGTGTGTAGAGGGAAATTTATAGCACTAAATGCCCCAC
                                                     : 3032
L1PA4 : AAAGCAGTGTGTAGAGGGGAAATTTATAGCACTAAATGCCCCAC
L1PA5 : AAAGCAGTGTGTAGAGGGAAATTTATAGCACTAAATGCCCAC
                                                     : 3025
L1PA6 : AAAGCAGTGTGTAGAGGGAAATTTATAGCACTAAATGCCCCAC
                                                     : 3016
        AAAGCAGTGTGTAGAGGGAAATTTATAGCACTAAATGCCcAC
                   3080
                                        3100
L1PA1 : AAGAGAAAGCAGGAAAGATC<mark>C</mark>AAAAT<mark>T</mark>GACACCCTAACATCA
                                                     : 2943
L1PA2 : AAGAGAAAGCAGGAAAGATCCAAAAATTGACACCCTAACATCA
                                                     : 2944
L1PA3 : AAGAGAAAGCAGGAAAGATCCAAAAATTGACACCCTAACATCA
                                                     : 3074
L1PA4 : AAGAGAAAGCAGGAAAGATCTAAAATTGACACCCTAACATCA
                                                     : 3071
L1PA5 : AAGAGAAAGCAGGAAAGATCTAAAATTGACACCCTAACATCA
                                                     : 3067
L1PA6 : AAGAGAAAGCAGGAAAGATCTAAAAATCGACACCCTAACATCA : 3058
        AAGAGAAAGCAGGAAAGATC AAAATtGACACCCTAACATCA
                 3120
                                      3140
L1PA1 : CAATTAAAAGAACTAGAAAAGCAAGAGCAAACACATTCAAAA : 2985
                                                     : 2986
L1PA2 : CAATTAAAAGAACTAGAAAAAGCAAGAGCAAACACATTCAAAA
L1PA3 : CAATTAAAAGAACTAGAAAAGCAAGAGCAAACACATTCAAAA : 3116
L1PA4 : CAATTAAAAGAACTAGAGAAGCAAGAGCAAACACATTCAAAA : 3113
        CAATTAAAAGAACTAGA<mark>G</mark>AAGCAAGAGCAAACA<mark>C</mark>ATTCAAAA
L1PA5:
                                                     : 3109
L1PA6 : CAATTAAAAGAACTAGA<mark>G</mark>AAGCAAGAGCAAACA<mark>A</mark>ATTCAAAA : 3100
        CAATTAAAAGAACTAGA AAGCAAGAGCAAACACATTCAAAA
```

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3160
                                   3180
L1PA1 : GCTAGCAGAAGGCAAGAATAACTAAAATCAGAGCAGAACTG : 3027
L1PA2 : GCTAGCAGAAGGCAAGAAATAACTAAAAATCAGAGCAGAACTG
                                                    : 3028
                                                    : 3158
L1PA3 : GCTAGCAGAAGGCAAGAATAACTAAAATCAGAGCAGAACTG
L1PA4 : GCTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAACTG
                                                    : 3155
L1PA5 : GCTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAACTG
                                                    : 3151
L1PA6 : GCTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAACTG
                                                    : 3142
        GCTAGCAGAAGGCAAGAATAACTAA ATCAGAGCAGAACTG
            3200
                                 3220
L1PA1 : AAGGAAATAGAGACACAAAAAACCCTTCAAAAAATCAATGAA : 3069
L1PA2 : AAGGAAATAGAGACACAAAAAACCCTTCAAAAAATTAATGAA : 3070
L1PA3 : AAGGAAATAGAGACACAAAAAACCCTTCAAAAAATTAATGAA : 3200
L1PA4 : AAGGAAATAGAGACACAAAAAACCCTTCAAAAAATCAATGAA
                                                    : 3197
L1PA5 : AAGGAGATAGAGACACAAAAAACCCTTCAAAAAATCAATGAA : 3193
L1PA6 : AAGGAGATAGAGACACAAAAAACCCTTCAAAAAATCAATGAA : 3184
        AAGGA ATAGAGACACAAAAAACCCTTCAAAAAAT AATGAA
          3240
                               3260
L1PA1 : TCCAGGAGCTGGTTTTTTGAAAGGATCAACAAAATTGATAGA
                                                    : 3111
                                                    : 3112
        TCCAGGAGCTGGTTTTTTGAAA<mark>G</mark>GATCAACAAAATTGATAGA
L1PA2:
L1PA3 : TCCAGGAGCTGGTTTTTTGAAAGGATCAACAAAATTGATAGA
                                                    : 3242
L1PA4 : TCCAGGAGCTGGTTTTTTGAAAAGATCAACAAAATTGATAGA : 3239
L1PA5 : TCCAGGAGCTGGTTTTTTGAAAAAGATCAACAAAATTGATAGA
                                                    : 3235
L1PA6 : TCCAGGAGCTGGTTTTTTGAAAAAGATCAACAAAATTGATAGA : 3226
        TCCAGGAGCTGGTTTTTTGAAA GATCAACAAAATTGATAGA
        3280
                                                 33
                             3300
L1PA1 : CCGCTAGCAAGACTAATAAAGAAAAAAGAGAAGAAAAAAA : 3153
L1PA2 : CCGCTAGCAAGACTAATAAAGAAAAAAGAGAAGAAAAAAA : 3154
L1PA3 :
        CC<mark>G</mark>CTAGCAAGACTAATAAAGAA<mark>G</mark>AAAAGAGAGAAGAATCAA
                                                    : 3284
                                                    : 3281
L1PA4 : CCGCTAGCAAGACTAATAAAGAAGAGAGAAGAAGAATCAA
L1PA5 : CCGCTAGCAAGACTAATAAAGAAGAAAAGAGAAGAAAACAA : 3277
L1PA6 : CCACTAGCAAGACTAATAAAGAAGAAAAGAGAAGAAATCAA : 3268
        CCGCTAGCAAGACTAATAAAGAA AAAAGAGAGAAGAATCAA
                          3340
L1PA1 : ATAGACACAATAAAAATGATAAAGGGGATATCACCACCGAT : 3195
L1PA2 : ATAGACACAATAAAAAATGATAAAGGGGATATCACCACCGAT
                                                    : 3196
L1PA3 : ATAGACGCAATAAAAAATGATAAAGGGGATATCACCACCGAT
                                                    : 3326
L1PA4 : ATAGACGCAATAAAAAATGATAAAGGGGATATCACCACCGAT
                                                    : 3323
L1PA5 : ATAGACGCAATAAAAAATGATAAAGGGGATATCACCACCGAT
                                                    : 3319
L1PA6 : ATAGACGCAATAAAAAATGATAAAGGGGATATCACCACCGAT : 3310
        ATAGAC CAATAAAAAATGATAAAGGGGGATATCACCACCGAT
```

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3380
                                             3400
L1PA1 : CCCACAGAAATACAAACTACCATCAGAGAATACTACAAACAC
                                                   : 3237
L1PA2 : CCCACAGAAATACAAACTACCATCAGAGAATACTACAAACAC
                                                    : 3238
L1PA3 : CCCACAGAAATACAAACTACCATCAGAGAATACTACAAACAC
                                                    : 3368
L1PA4 : CCCACAGAAATACAAACTACCATCAGAGAATACTATAAACAC
                                                    : 3365
L1PA5 : CCCACAGAAATACAAACTACCATCAGAGAATACTATAAACAC
                                                   : 3361
L1PA6 : CCCACAGAAATACAAACTACCATCAGAGAATACTATAAAACAC
                                                    : 3352
        CCCACAGAAATACAAACTACCATCAGAGAATACTA AAACAC
                      3420
                                           3440
        CTCTA<mark>C</mark>GCAAATAAACTAGAAAATCTAGAAGAAATGGATA<mark>C</mark>A : 3279
L1PA1 :
L1PA2 : CTCTACGCAAATAAACTAGAAAATCTAGAAGAAATGGATAAA : 3280
L1PA3 : CTCTACGCAAATAAACTAGAAAATCTAGAAGAAATGGATAAA
                                                   : 3410
L1PA4 : CTCTACGCAAATAAACTAGAAAATCTAGAAGAAATGGATAAA
                                                    : 3407
L1PA5 : CTCTACGCAAATAAACTAGAAAATCTAGAAGAAATGGATAAA : 3403
L1PA6 : CTCTATGCAAATAAACTAGAAAATCTAGAAGAAATGGATAAA : 3394
        CTCTAcGCAAATAAACTAGAAAATCTAGAAGAAATGGATAaA
                    3460
                                         3480
L1PA1 : TTCCTCGACACATACACTCTCCCCAAGACTAAACCAGGAAGAA : 3321
                                                    : 3322
        TTCCT<mark>C</mark>GACACATACAC<mark>T</mark>CTCCCAAGACTAAACCAGGAAGAA
L1PA2:
L1PA3 : TTCCTCGACACATACACCCCTCCCAAGACTAAACCAGGAAGAA : 3452
L1PA4 : TTCCTCGACACATACACCCTCCCAAGACTAAACCAGGAAGAA : 3449
L1PA5 : TTCCTGGACACATACACCCTCCCAAGACTAAACCAGGAAGAA : 3445
L1PA6 : TTCCTGGACACATACACCCCTCCCAAGACTAAACCAGGAAGAA : 3436
        TTCCT GACACATACAC CTCCCAAGACTAAACCAGGAAGAA
                  3500
                                       3520
L1PA1 : GTTGAATCTCTGAATCGACCAATAACAGGCTCTGAAATTGTG
                                                   : 3363
L1PA2 : GTTGAATCTCTGAATAGACCAATAACAGGATCTGAAATTGTG
                                                   : 3364
L1PA3 : GTTGAATCTCTGAATAGACCAATAACAGGCTCTGAAATTGTG : 3494
L1PA4 : GTTGAATCTCTGAATAGACCAATAACAGGCTCTGAAATTGAG
                                                   : 3491
L1PA5 : GTTGAATCCCTGAATAGACCAATAACAGGCTCTGAAATTGAG : 3487
L1PA6 : GTTGAATCTCTGAATAGACCAATAACAGGCTCTGAAATTGAG : 3478
        GTTGAATCtCTGAATaGACCAATAACAGGcTCTGAAATTG G
                3540
                                     3560
L1PA1 : GCAATAATCAATAGTTTTACCAACCAAAAAGAGTCCAGGACCA
                                                   : 3405
                                                   : 3406
L1PA2 : GCAATAATCAATAGCTTACCAACCAAAAAGAGTCCAGGACCA
L1PA3 : GCAATAATCAATAGCTTACCAACCAAAAAGAGTCCAGGACCA : 3536
L1PA4 : GCAATAATTAATAGCTTACCAACCAAAAAAAAGTCCAGGACCA : 3533
: 3529
L1PA6 : GCAATAATTAATAG<mark>CC</mark>TACCAACCAAAAAAAAAAGTCCAGGACCA : 3520
        GCAATAAT AATAGCTTACCAACCAAAAA AGTCCAGGACCA
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3580
                                    3600
L1PA1 : GATGGATTCACAGCCGAATTCTACCAGAGGTACAAGGAGGAA : 3447
L1PA2 : GATGGATTCACAGCCGAATTCTACCAGAGGTACAAGGAGGAA : 3448
L1PA3 : GATGGATTCACAGCCGAATTCTACCAGAGGTACAAGGAGGAA : 3578
L1PA4 : GATGGATTCACAGCCGAATTCTACCAGAGGTACAAGGAGGAG : 3575
L1PA5 : GATGGATTCACAGCCGAATTCTACCAGAGGTACAAGGAGGAG : 3571
L1PA6 : GACGGATTCACAGCCGAATTCTACCAGAGGTACAAAGAGGAG : 3562
        GAtGGATTCACAGCCGAATTCTACCAGAGGTACAAGGAGGA
            3620
                                  3640
        CTGGTACCATTCCTTCTGAAACTATTCCAATCAATAGAAAAA : 3489
L1PA1 :
L1PA2 : CTGGTACCATTCCTTCTGAAACTATTCCAATCAATAGAAAAA : 3490
L1PA3 : CTGGTACCATTCCTTCTGAAACTATTCCAATCAATAGAAAAA : 3620
L1PA4 : CTGGTACCATTCCTTCTGAAACTATTCCAATCAATAGAAAAA
                                                     : 3617
L1PA5 : CTGGTACCATTCCTTCTGAAACTATTCCAATCAATAGAAAAA : 3613
L1PA6 : CTGGTACCATTCCTTCTGAAACTATTCCAATCAATAGAAAAA : 3604
        CTGGTACCATTCCTTCTGAAACTATTCCAATCAATAGAAAAA
          3660
                        *
                                3680
L1PA1 : GAGGGAATCCTCCCTAACTCATTTTATGAGGCCAGCATCATT : 3531
L1PA2 :
        GAGGGAATCCTCCCTAACTCATTTTATGAGGCCAGCATCATT : 3532
L1PA3 : GAGGGAATCCTCCCTAACTCATTTTATGAGGCCAGCATCATC : 3662
L1PA4 : GAGGGAATCCTCCCTAACTCATTTTATGAGGCCAGCATCATC : 3659
L1PA5 : GAGGGAATCCTCCCTAACTCATTTTATGAGGCCAGCATCATC : 3655
L1PA6 : GAGGGAATCCTCCCTAACTCATTTTATGAGGCCAGCATCATC : 3646
        GAGGGAATCCTCCCTAACTCATTTTATGAGGCCAGCATCAT
        3700
                                                   37
                              3720
L1PA1 : CTGATACCAAAGCC<mark>G</mark>GGCAGAGACACAAC<mark>C</mark>AAAAAAGAGAAAT
                                                     : 3573
L1PA2 : CTGATACCAAAGCCGGGCAGAGACACCAAAAAAAGAGAAT : 3574
L1PA3 : CTGATACCAAAGCCGGGCAGAGACACCCAAACCAAAAAAAGAGAAT
                                                     : 3704
L1PA4 : CTGATACCAAAGCC<mark>G</mark>GGCAGAGACACAAC<mark>A</mark>AAAAAAGAGAAAT
                                                     : 3701
L1PA5 : CTGATACCAAAGCCGGGCAGAGACACAACAAAAAAAAGAGAAT
                                                     : 3697
L1PA6 : CTGATACCAAAGCCTGGCAGAGACACAACAAAAAAAGAGAAT : 3688
        CTGATACCAAAGCCGGGCAGAGACACAAC AAAAAAGAGAAT
                           3760
        TTTAGACCAATATCCTTGATGAACATTGATGCAAAAATCCTC : 3615
L1PA1 :
                                                     : 3616
L1PA2 : TTTAGACCAATATCCTTGATGAACATTGATGCAAAAATCCTC
L1PA3 : TTTAGACCAATATCCTTGATGAACATTGATGCAAAAATCCTC
                                                     : 3746
L1PA4 : TTTAGACCAATATCCCTGATGAACATTGATGCAAAAATCCTC
                                                     : 3743
        TTTAGACCAATATCC<mark>C</mark>TGATGAACAT<mark>C</mark>GATGC<mark>A</mark>AAAATCCTC
L1PA5:
                                                     : 3739
L1PA6 : TTTAGACCAATATCCCTGATGAACATCGATGCGAAAATCCTC
                                                     : 3730
        TTTAGACCAATATCC TGATGAACAT GATGCAAAAATCCTC
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3800
                                               3820
L1PA1 : AATAAAATACTGGCAAACCGAATCCAGCAGCACATCAAAAAG
                                                      : 3657
                                                      : 3658
L1PA2 : AATAAAATACTGGCAAACCGAATCCAGCAGCACATCAAAAAG
L1PA3 : AATAAAATACTGGCAAACCGAATCCAGCAGCACATCAAAAAG
                                                      : 3788
L1PA4 : AATAAAATACTGGCAAACCGAATCCAGCAGCACATCAAAAAG
                                                      : 3785
L1PA5 : AATAAAATACTGGCAAACCGAATCCAGCAGCACATCAAAAAG
                                                      : 3781
L1PA6 : AATAAAATACTGGCAAACCGAATCCAGCAGCACATCAAAAAG
                                                      : 3772
        AATAAAATACTGGCAAACCGAATCCAGCAGCACATCAAAAAG
                       3840
                                             3860
        CTTATCCACCATGATCAAGT<mark>G</mark>GGCTTCATCCCTGGGATGCAA : 3699
L1PA1 :
L1PA2 : CTTATCCACCATGATCAAGTGGGCTTCATCCCTGGGATGCAA
                                                      : 3700
L1PA3 : CTTATCCACCATGATCAAGTGGGCTTCATCCCTGGGATGCAA
                                                      : 3830
        CTTATCCACCATGATCAAGT<mark>G</mark>GGCTTCATCCCTGGGATGCAA
L1PA4 :
                                                      : 3827
L1PA5 : CTTATCCACCATGATCAAGTGGGCTTCATCCCTGGGATGCAA
                                                      : 3823
L1PA6 : CTTATCCACCATGATCAAGTCGGCTTCATCCCTGGGATGCAA : 3814
        CTTATCCACCATGATCAAGTqGGCTTCATCCCTGGGATGCAA
                     3880
                                           3900
L1PA1 : GGCTGGTTCAATATACGCAAATCAATAAATGTAATCCAGCAT
                                                      : 3741
L1PA2 :
        GGCTGGTTCAA<mark>T</mark>ATACGCAAATCAATAAA<mark>T</mark>GTAATCCA<mark>G</mark>CA<mark>T : 3742</mark>
L1PA3 : GGCTGGTTCAATATACGCAAATCAATAAATGTAATCCAGCAT : 3872
L1PA4 : GGCTGGTTCAACATACGCAAATCAATAAATGTAATCCAGCAT : 3869
L1PA5 : GGCTGGTTCAACATACGCAAATCAATAAATGTAATCCAGCAT : 3865
L1PA6 : GGCTGGTTCAACATACGCAAATCAATAAACGTAATCCATCAC : 3856
        GGCTGGTTCAA ATACGCAAATCAATAAAtGTAATCCAqCAt
                   3920
                                        3940
L1PA1 : ATAAACAGAGCCAAAAGCCACATGATTATCTCAATA : 3783
L1PA2 : ATAAACAGAGCCAAAAAACCACATGATTATCTCAATA
                                                      : 3784
L1PA3 : ATAAACAGA<mark>A</mark>CCAA<mark>A</mark>GACAAAAACCACATGATTATCTCAATA
                                                      : 3914
L1PA4 : ATAAACAGAACCAAAGACCACATGATTATCTCAATA
                                                      : 3911
L1PA5 : ATAAACAGAACCAAAGACCACATGATTATCTCAATA
                                                      : 3907
L1PA6 : ATAAACAGAACCAATGACAAAAACCACATGATTATCTCAATA : 3898
        ATAAACAGA CCAAaGACAAAAACCACATGATTATCTCAATA
                 3960
                                      3980
L1PA1 : GATGCAGAAAAAGCCTTTGACAAAATTCAACAACCCTTCATG
                                                      : 3825
L1PA2 : GATGCAGAAAAAGCCTTTGACAAAAATTCAACAACCCTTCATG
                                                      : 3826
L1PA3 : GATGCAGAAAAGGCCTTTGACAAAATTCAACAACCCTTCATG
                                                      : 3956
L1PA4 : GATGCAGAAAAGGCCTTTGACAAAATTCAACAACCCTTCATG
                                                      : 3953
        GATGCAGAAAA<mark>G</mark>GCCTTTGACAAAATTCAACA<mark>G</mark>CCCTTCATG
L1PA5:
                                                      : 3949
L1PA6 : GATGCAGAAAAGGCCTTTGACAAAATTCAACAGCCCTTCATG
                                                      : 3940
        GATGCAGAAAA GCCTTTGACAAAATTCAACA CCCTTCATG
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4000
                                     4020
L1PA1 : CTAAAAACTCTCAATAAATTAGGTATTGATGGGACGTATTTC : 3867
L1PA2 : CTAAAAACTCTCAATAAATTTAGGTATTGATGGGACGTATTTC
                                                       : 3868
L1PA3 : CTAAAAACTCTCAATAAA<mark>T</mark>TAGGTATTGATGG<mark>G</mark>ACGTAT<mark>C</mark>TC
                                                       : 3998
L1PA4 : CTAAAAACTCTCAATAAATTAGGTATTGATGGGACGTATCTC
                                                       : 3995
L1PA5 : CTAAAAACTCTCAATAAA<mark>T</mark>TAGGTATTGATGG<mark>G</mark>ACGTAT<mark>C</mark>TC
                                                       : 3991
L1PA6 : CTAAAAACTCTCAATAAACTTAGGTATTGATGGAACGTATCTC
                                                       : 3982
        CTAAAAACTCTCAATAAAtTAGGTATTGATGGGACGTAT TC
             4040
                                   4060
L1PA1 : AAAATAATAAGAGCTATCTATGACAAACCCACAGCCAATATC : 3909
L1PA2 : AAAATAATAAGAGCTATCTATGACAAACCCACAGCCAATATC
                                                       : 3910
L1PA3 : AAAATAATAAGAGCTAT<mark>C</mark>TATGACAAACCCACAGCCAATATC : 4040
L1PA4 : AAAATAATAAGAGCTATCTATGACAAACCCACAGCCAATATC
                                                       : 4037
L1PA5 : AAAATAATAAGAGCTATCTATGACAAACCCACAGCCAATATC
                                                       : 4033
L1PA6 : AAAATAATAAGAGCTATTTATGACAAACCCACAGCCAATATC : 4024
        AAAATAATAAGAGCTATCTATGACAAACCCACAGCCAATATC
           4080
                                4100
L1PA1 : ATACTGAATGGGCAAAAACTGGAAGCATTCCCTTTGAAAACC : 3951
L1PA2 : ATACTGAATGGGCAAAAACTGGAAGCATTCCCTTTGAAAAC<mark>T</mark> : 3952
L1PA3 : ATACTGAATGGGCAAAAACTGGAAGCATTCCCTTTGAAAAC<mark>T : 408</mark>2
L1PA4 : ATACTGAATGGGCAAAAACTGGAAGCATTCCCTTTGAAAACT : 4079
L1PA5 : ATACTGAATGGGCAAAAACTGGAAGCATTCCCTTTGAAAACT : 4075
L1PA6 : ATACTGAATGGGCAAAAACTGGAAGCATTCCCTTTGAAAACT : 4066
        ATACTGAATGGGCAAAAACTGGAAGCATTCCCTTTGAAAACt
        4120
                              4140
L1PA1 : GGCACAAGACAGGGATGCCCTCTCTCACCGCTCCTATTCAAC : 3993
L1PA2 : GGCACAAGACAGGGATGCCCTCTCTCACCACCACTCTTCAAC
                                                       : 3994
L1PA3 : GGCACAAGACAGGGGATGCCCTCTCTCACCACTCTTCAAC
                                                       : 4124
                                                       : 4121
L1PA4 : GGCACAAGACAGGGATGCCCTCTCTCACCACTCCTATTCAAC
L1PA5 : GGCACAAGACAGGGATGCCCTCTCTCACCACCACTCTTCAAC
                                                       : 4117
L1PA6 : GGCACAAGACAAGGATGCCCTCTCTCACCACTCTCTCAAC : 4108
        GGCACAAGACAGGGATGCCCTCTCTCACCaCTCCTATTCAAC
                            4180
L1PA1 : ATAGTGTTGGAAGTTCTGGCCAGGGCAATCAGGCAGGAGAAG : 4035
L1PA2 : ATAGTGTTGGAAGTTCTGGCCAGGGCAATTAGGCAGGAGAAG : 4036
L1PA3 : ATAGTGTTGGAAGTTCTGGCCAGGGCAATTAGGCAGGAGAAG : 4166
L1PA4 : ATAGTGTTGGAAGTTCTGGCCAGGGCAATCAGGCAGGAGAAG : 4163
L1PA5 : ATAGTGTTGGAAGTTCTGGCCAGGGCAAT<mark>C</mark>AGGCA<mark>G</mark>GAGAA<mark>A : 4159</mark>
L1PA6 : ATAGTGTTGGAAGTTCTGGCCAGGGCAATCAGGCAAGAGAAA : 4150
        ATAGTGTTGGAAGTTCTGGCCAGGGCAAT AGGCAGGAGAA
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4220
                                              4240
L1PA1 : GAAATAAAGGGTATTCAATTAGGAAAAGAGGAAGTCAAATTG
                                                     : 4077
L1PA2 : GAAATAAAGGGTATTCAATTAGGAAAAGAGGAAGTCAAATTG
                                                      : 4078
L1PA3 : GAAATAAAGGGTATTCAATTAGGAAAAGAGGAAGTCAAATTG
                                                      : 4208
L1PA4 : GAAATAAAGGGTATTCAATTAGGAAAAGAGGAAGTCAAATTG
                                                      : 4205
                                                      : 4201
L1PA5 : GAAATAAAGGGTATTCAATTAGGAAAAGAGGAAGTCAAATTG
L1PA6 : GAAATAAAGGGTATTCAATTAGGAAAAGAGGAAGTCAAATTG
                                                      : 4192
        GAAATAAAGGGTATTCAATTAGGAAAAGAGGAAGTCAAATTG
                       4260
                                             4280
        TCCCTGTTTGCAGA<mark>C</mark>GACATGATTGT<mark>T</mark>TAT<mark>C</mark>TAGAAAACCCC
L1PA1 :
                                                     : 4119
L1PA2 : TCCCTGTTTGCAGACGACGACATGATTGTATATCTAGAAAACCCC
                                                     : 4120
L1PA3 : TCCCTGTTTGCAGACGACATGATTGTATATCTAGAAAACCCC
                                                     : 4250
L1PA4 :
        TCCCTGTTTGCAGA<mark>C</mark>GACATGATTGT<mark>A</mark>TAT<mark>C</mark>TAGAAAACCCC
                                                     : 4247
L1PA5 : TCCCTGTTTGCAGACGACATGATTGTATATCTAGAAAACCCC
                                                     : 4243
L1PA6 : TCCCTGTTTGCAGATGACATGATTGTATATTTAGAAAACCCC : 4234
        TCCCTGTTTGCAGAcGACATGATTGTaTATcTAGAAAACCCC
                     4300
                                          4320
L1PA1 : ATCGTCTCAGCCCAAAATCTCCTTAAGCTGATAAGCAACTTC
                                                     : 4161
L1PA2 :
                                                      : 4162
        AT<mark>TG</mark>TCTCAGCCCAAAATCTCCTTAAGCTGATAAGCAACTTC
                                                      : 4292
L1PA3 : ATTGTCTCAGCCCAAAATCTCCTTAAGCTGATAAGCAACTTC
L1PA4: ATTGTCTCAGCCCAAAATCTCCTTAAGCTGATAAGCAACTTC
                                                      : 4289
L1PA5 : ATCGTCTCAGCCCAAAATCTCCTTAAGCTGATAAGCAACTTC
                                                      : 4285
                                                     : 4276
L1PA6 : ATCATCTCAGCCCAAAATCTCCTTAAGCTGATAAGCAACTTC
        AT GTCTCAGCCCAAAATCTCCTTAAGCTGATAAGCAACTTC
                   4340
                                        4360
L1PA1 : AGCAAAGTCTCAGGATACAAAATCAATGTACAAAAATCACAA : 4203
L1PA2 : AGCAAAGTCTCAGGATACAAAATCAATGTACAAAAATCACAA
                                                     : 4204
L1PA3 : AGCAAAGTCTCAGGATACAAAATCAATGTACAAAAATCACAA
                                                     : 4334
                                                     : 4331
L1PA4 : AGCAAAGTCTCAGGATACAAAATCAATGTGCAAAAATCACAA
L1PA5 : AGCAAAGTCTCAGGATACAAAATCAATGTGCAAAAATCACAA
                                                     : 4327
L1PA6 : AGCAAAGTCTCAGGATACAAAATCAATGTGCAAAAATCACAA : 4318
        AGCAAAGTCTCAGGATACAAAATCAATGT CAAAAATCACAA
                 4380
                                      4400
L1PA1 : GCATTCTTATACACCAACAACAGACAAACAGAGAGCCAAATC
                                                     : 4245
L1PA2 : GCATTCTTATACACCAACAACAGACAAACAGAGAGCCAAATC
                                                     : 4246
L1PA3 : GCATTCTTATACACCAATAACAGACAAACAGAGAGCCAAATC
                                                     : 4376
L1PA4 : GCATTCTTATACACCAATAACAGACAAACAGAGAGCCAAATC
                                                     : 4373
L1PA5 : GCATTCTTATACACCAATAACAGACAAACAGAGAGCCAAATC
                                                      : 4369
L1PA6 : GCATTCCTATACACCAATAACAGACAAACAGAGAGCCAAATC
                                                     : 4360
        GCATTCTTATACACCAA AACAGACAAACAGAGAGCCAAATC
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4420
                                    4440
L1PA1 : ATGGGTGAACTCCCATTCACAATTGCTTCAAAGAGAAATAAAA : 4287
L1PA2 : ATGAGTGAACTCCCATTCACAATTGCTTCAAAGAGAAATAAAA : 4288
L1PA3 : ATGAGTGAACTCCCATTCACAATTGCTTCAAAGAGAATAAAA
                                                     : 4418
L1PA4: ATGAGTGAACTCCCATTCACAATTGCTTCAAAGAGAATAAAA
                                                     : 4415
L1PA5 : ATGAGTGAACTCCCATTCACAATTGCTTCAAAGAGAATAAAA
                                                     : 4411
L1PA6 : ATGAGTGAACTCCCATTCACAATTGCTACAAAGAGAATAAAA
                                                     : 4402
        ATGaGTGAACTCCCATTCACAATTGCTtCAAAGAGAATAAAA
            4460
                                  4480
        TACCTAGGAATCCAACTTACAAGGGATGTGAAGGACCTCTTC
                                                     : 4329
L1PA1:
L1PA2: TACCTAGGAATCCAACTTACAAGGGATGTGAAGGACCTCTTC
                                                     : 4330
L1PA3: TACCTAGGAATCCAACTTACAAGGGATGTGAAGGACCTCTTC
                                                     : 4460
        TACCTAGGAATCCAACTTACAAGGGATGTGAAGGACCTCTTC
L1PA4:
                                                     : 4457
L1PA5 : TACCTAGGAATCCAACTTACAAGGGATGTGAAGGACCTCTTC
                                                     : 4453
L1PA6: TACCTAGGAATCCAACTTACAAGGGATGTGAAGGACCTCTTC: 4444
        TACCTAGGAATCCAACTTACAAGGGATGTGAAGGACCTCTTC
          4500
                               4520
L1PA1 : AAGGAGAACTACAAACCACTGCTCAAGGAAATAAAAGAGGAG : 4371
        aaggagaactacaaaccactgctcaa<mark>g</mark>gaaataaaagaggat : 4372
L1PA2:
L1PA3 : AAGGAGAACTACAAACCACTGCTCAA<mark>T</mark>GAAATAAAAGAGGAT : 4502
L1PA4 : AAGGAGAACTACAAACCACTGCTCAATGAAATAAAAGAGGGAT : 4499
L1PA5 : AAGGAGAACTACAAACCACTGCTCAA<mark>T</mark>GAAATAAAAGAGGA<mark>C</mark> : 4495
L1PA6 : AAGGAGAACTACAAACCACTGCTCAA<mark>T</mark>GAAATAAAAGAGGA<mark>C : 4486</mark>
        AAGGAGAACTACAAACCACTGCTCAA GAAATAAAAGAGGA
        4540
                             4560
                                                   45
L1PA1 : ACAAACAAATGGAAGAACATTCCATGCTCATGGGTAGGAAGA : 4413
L1PA2 : ACAAACAAATGGAAGAACATTCCATGCTCATGGGTAGGAAGA : 4414
L1PA3 : ACAAACAAATGGAAGAACATTCCATGCTCATGGGTAGGAAGA : 4544
L1PA4 : ACAAACAAATGGAAGAACATTCCATGCTCATGGGTAGGAAGA : 4541
L1PA5 : ACAAACAAATGGAAGAACATTCCATGCTCATGGATAGGAAGA : 4537
L1PA6 : ACAAACAAATGGAAGAACATTCCATGCTCATGGATAGGAAGA : 4528
        ACAAACAAATGGAAGAACATTCCATGCTCATGG TAGGAAGA
                           4600
L1PA1 : ATCAATATCGTGAAAATGGCCATACTGCCCAAGGTAATTTAC : 4455
L1PA2 : ATCAATATCGTGAAAATGGCCATACTGCCCAAGGTAATTTAC : 4456
L1PA3: ATCAATATCGTGAAAATGGCCATACTGCCCAAGGTAATTTAT: 4586
L1PA4 : ATCAATATCGTGAAAATGGCCATACTGCCCAAGGTAATTTAT : 4583
L1PA5:
        ATCAATATCGTGAAAATGGCCATACTGCCCAAGGTAATTTA<mark>T</mark> : 4579
L1PA6 : ATCAATATCGTGAAAATGGCCATACTGCCCAAGGTAATTTA<mark>T</mark> : 4570
        ATCAATATCGTGAAAATGGCCATACTGCCCAAGGTAATTTA
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4640
                                              4660
L1PA1 : AGATTCAATGCCATCCCCATCAAGCTACCAATGACTTTCTTC
                                                     : 4497
L1PA2 : AGATTCAATGCCATCCCCATCAAGCTACCAATGACTTTCTTC
                                                     : 4498
L1PA3 : AGATTCAATGCCATCCCCATCAAGCTACCAATGACTTTCTTC
                                                     : 4628
L1PA4: AGATTCAATGCCATCCCCATCAAGCTACCAATGACTTTCTTC
                                                     : 4625
                                                     : 4621
L1PA5 : AGATTCAATGCCATCCCCATCAAGCTACCAATGACTTTCTTC
                                                     : 4612
L1PA6 : AGATTCAATGCCATCCCCATCAAGCTACCAATGACTTTCTTC
        AGATTCAATGCCATCCCCATCAAGCTACCAATGACTTTCTTC
                       4680
                                            4700
L1PA1 : ACAGAATTGGAAAAACTACTTTAAAGTTCATATGGAACCAA
                                                    : 4539
L1PA2 : ACAGAATTGGAAAAAACTACTTTAAAGTTCATATGGAACCAA
                                                     : 4540
L1PA3 : ACAGAATTGGAAAAAACTACTTTAAAGTTCATATGGAACCAA
                                                    : 4670
                                                     : 4667
L1PA4 :
        ACAGAATTGGAAAAAACTACTTTAAAGTTCATATGGAACCAA
L1PA5 : ACAGAATTGGAAAAAACTACTTTAAAGTTCATATGGAACCAA
                                                    : 4663
L1PA6 : ACAGAATTGGAAAAACTACTTTAAAGTTCATATGGAACCAA : 4654
        ACAGAATTGGAAAAACTACTTTAAAGTTCATATGGAACCAA
                     4720
                                          4740
L1PA1 : AAAAGAGCCCGCAT<mark>T</mark>GCCAAG<mark>T</mark>CAATCCTAAGCCAAAAGAAC
                                                    : 4581
L1PA2 :
        AAAAGAGCCCGCAT<mark>C</mark>GCCAAG<mark>T</mark>CAATCCTAAGCCAAAAGAAC
                                                     : 4582
                                                     : 4712
L1PA3 : AAAAGAGCCCGCATCGCCAAGTCAATCCTAAGCCAAAAGAAC
L1PA4 : AAAAGAGCCCGCATCGCCAAGTCAATCCTAAGCCAAAAGAAC
                                                     : 4709
L1PA5 : AAAAGAGCCCGCATCGCCAAGACAATCCTAAGCCAAAAGAAC
                                                     : 4705
L1PA6 : AAAAGAGCCCGCATTGCCAAGACAATCCTAAGCCAAAAGAAC
                                                    : 4696
        AAAAGAGCCCGCAT GCCAAG CAATCCTAAGCCAAAAGAAC
                  4760
                                       4780
L1PA1 : AAAGCTGGAGGCATCACACTACCTGACTTCAAACTATACTAC
                                                    : 4623
L1PA2 : AAAGCTGGAGGCATCACACTACCTGACTTCAAACTATACTAC
                                                     : 4624
L1PA3 : AAAGCTGGAGGCATCACACTACCTGACTTCAAACTATACTAC
                                                     : 4754
L1PA4 : AAAGCTGGAGGCATCACACTACCTGACTTCAAACTATACTAC
                                                     : 4751
L1PA5 : AAAGCTGGAGGCATCACACTACCTGACTTCAAACTATACTAC
                                                     : 4747
                                                    : 4738
L1PA6 : AAAGCTGGAGGCATCACGCTACCTGACTTCAAACTATACTAC
        AAAGCTGGAGGCATCACACTACCTGACTTCAAACTATACTAC
                4800
                                     4820
L1PA1 : AAGGCTACAGTAACCAAAACAGCATGGTACTGGTACCAAAAC
                                                    : 4665
L1PA2 : AAGGCTACAGTAACCAAAACAGCATGGTACTGGTACCAAAAC
                                                     : 4666
L1PA3 : AAGGCTACAGTAACCAAAACAGCATGGTACTGGTACCAAAAC
                                                     : 4796
                                                     : 4793
L1PA4 : AAGGCTACAGTAACCAAAACAGCATGGTACTGGTACCAAAAC
L1PA5:
        AAGGCTACAGTAACCAAAACAGCATGGTACTGGTACCAAAAC
                                                     : 4789
                                                    : 4780
L1PA6 : AAGGCTACAGTAACCAAAACAGCATGGTACTGGTACCAAAAC
        AAGGCTACAGTAACCAAAACAGCATGGTACTGGTACCAAAAC
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4840
                                  4860
L1PA1 : AGAGATATAGATCAATGGAACAGAACAGAGCCCTCAGAAATA : 4707
L1PA2 : AGAGATATAGATCAATGGAACAGAACAGAGCCCTCAGAAATA : 4708
                                                   : 4838
L1PA3 : AGAGATATAGATCAATGGAACAGAACAGAGCCCTCAGAAATA
L1PA4 : AGAGATATAGACCAATGGAACAGAACAGAGCCCTCAGAAATA : 4835
L1PA5 : AGAGATATAGACCAATGGAACAGAACAGAGCCCTCAGAAATA : 4831
L1PA6 : AGAGATATAGACCAATGGAACAGAACAGAGGCCTCAGAAATA
                                                   : 4822
        AGAGATATAGA CAATGGAACAGAACAGAGCCCTCAGAAATA
            4880
                                4900
L1PA1 : ATGCCGCATATCTACAACTATCTGATCTTTGACAAACCTGAG : 4749
L1PA2 : ACGCCGCATATCTACAACTATCTGATCTTTGACAAACCTGAG : 4750
L1PA3 : ACGCCGCATATCTACAACTATCTGATCTTTGACAAACCTGAG : 4880
L1PA4 : ACGCCGCATATCTACAACTATCTGATCTTTGACAAACCTGAC : 4877
L1PA5 : ACGCCGCACATCTACAACCATCTGATCTTTGACAAACCTGAC : 4873
L1PA6 : ACGCCACACATCTACAACCATCTGATCTTTGACAAACCTGAC : 4864
        ACGCCCCA ATCTACAAC ATCTGATCTTTGACAAACCTGA
          4920
                              4940
L1PA1 : AAAAACAAGCAATGGGGAAAGGATTCCCTATTTAATAAATGG : 4791
L1PA2 : AAAAACAAGCAATGGGGAAAGGATTCCCTATTTAATAAATGG
                                                   : 4792
L1PA3 : AAAAACAAGCAATGGGGAAAGGATTCCCTATTTAATAAATGG
                                                   : 4922
L1PA4 : AAAAACAAGCAATGGGGAAAGGATTCCCTATTTAATAAATGG : 4919
L1PA5 : AAAAACAAGAAATGGGGAAAGGATTCCCTATTTAATAAATGG : 4915
L1PA6 : AAAAACAAGAAATGGGGAAAGGATTCCCTATTTAATAAATGG : 4906
        AAAAACAAG AATGGGGAAAGGATTCCCTATTTAATAAATGG
        4960
                                                 50
                            4980
L1PA1: TGCTGGGAAAACTGGCTAGCCATATGTAGAAAGCTGAAACTG: 4833
L1PA2: TGCTGGGAAAACTGGCTAGCCATATGTAGAAAGCTGAAACTG: 4834
L1PA3: TGCTGGGAAAACTGGCTAGCCATATGTAGAAAGCTGAAACTG
                                                   : 4964
                                                   : 4961
L1PA4: TGCTGGGAAAACTGGCTAGCCATATGTAGAAAGCTGAAACTG
L1PA5 : TGCTGGGAAAACTGGCTAGCCATATGTAGAAAGCTGAAACTG : 4957
L1PA6: TGCTGGGAAAACTGGCTAGCCATATGTAGAAAGCTGAAACTG: 4948
        TGCTGGGAAAACTGGCTAGCCATATGTAGAAAGCTGAAACTG
                          5020
L1PA1 : GATCCCTTCCTTACACCTTATACAAAAATCAATTCAAGATGG : 4875
L1PA2 : GATCCCTTCCTTACACCTTATACAAAAATCAATTCAAGATGG : 4876
L1PA3 : GATCCCTTCCTTACACCTTATACAAAAATTAATTCAAGATGG : 5006
L1PA4 : GATCCCTTCCTTACACCTTATACAAAAATTAATTCAAGATGG : 5003
L1PA5:
        GATCCCTTCCTTACACCTTATACAAAAAT<mark>T</mark>AATTCAAGATGG : 4999
L1PA6 : GATCCCTTCCTTACACCTTATACAAAAATTAATTCAAGATGG : 4990
        GATCCCTTCCTTACACCTTATACAAAAAT AATTCAAGATGG
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5060
                                               5080
L1PA1 : ATTAAAGATTTAAACGTTAAACCTAAAAACCATAAAAACCCTA : 4917
L1PA2 : ATTAAAGACTTAAACGTTAGACCTAAAAACCATAAAAACCCTA
                                                      : 4918
L1PA3 : ATTAAAGACTTAAACGTTAGACCTAAAAACCATAAAAACCCTA
                                                      : 5048
L1PA4 : ATTAAAGACTTAAACGTTAGACCTAAAACCATAAAAACCCTA
                                                      : 5045
L1PA5 : ATTAAAGACTTAAACGTTAGACCTAAAAACCATAAAAACCCTA
                                                      : 5041
L1PA6 : ATTAAAGA<mark>C</mark>TTAAA<mark>T</mark>GTTA<mark>G</mark>ACCTAAAAACCATAAAAACCCTA
                                                      : 5032
        ATTAAAGACTTAAACGTTAGACCTAAAAACCATAAAAACCCTA
                       5100
                                             5120
L1PA1 : GAAGAAACCTAGGCATTCAGGACATAGGCGTGGGC
                                                      : 4959
L1PA2 : GAAGAAACCTAGGCATTCAGGACATAGGCATGGGC
                                                      : 4960
L1PA3 : GAAGAAAACCTAGGCA<mark>T</mark>TACCATTCAGGACATAGGC<mark>A</mark>TGGGC
                                                      : 5090
L1PA4 : GAAGAAAACCTAGGCAATACCATTCAGGACATAGGCATGGGC
                                                      : 5087
L1PA5 : GAAGAAAACCTAGGCAATACCATTCAGGACATAGGCATGGGC
                                                      : 5083
L1PA6 : GAAGAAACCTAGGCAATACCATTCAGGACATAGGCATGGGC : 5074
        GAAGAAACCTAGGCA TACCATTCAGGACATAGGCaTGGGC
                     5140
                                           5160
L1PA1 : AAGGACTTCATGTCCAAAACACCAAAAGCAATGGCAACAAAA : 5001
        AAGGACTTCATG<mark>T</mark>C<mark>T</mark>AAAACACCAAAAGCAATGGCAACAAAA
                                                      : 5002
L1PA2:
L1PA3 : AAGGACTTCATGTCTAAAACACCAAAAGCAATGGCAACAAAA
                                                      : 5132
L1PA4 : AAGGACTTCATGTCTAAAACACCAAAAGCAATGGCAACAAAA : 5129
L1PA5 : AAGGACTTCATGTCTAAAACACCAAAAGCAATGGCAACAAAA
                                                      : 5125
L1PA6 : AAGGACTTCATG<mark>ACT</mark>AAAACACCAAAAGCAATGGCAACAAAA : 5116
        AAGGACTTCATGtCtAAAACACCAAAAGCAATGGCAACAAAA
                   5180
                                        5200
L1PA1 : GCCAAAATTGACAAATGGGATCTAATTAAACTAAAGAGCTTC
                                                      : 5043
L1PA2 : GCCAAAATTGACAAATGGGATCTAATTAAACTAAAGAGCTTC
                                                      : 5044
L1PA3 : GCCAAAATTGACAAATGGGATCTAATTAAACTAAAGAGCTTC
                                                      : 5174
                                                      : 5171
L1PA4 : GCCAAAAT<mark>T</mark>GACAAATGGGATCTAATTAAACTAAAGAGCTTC
L1PA5 : GCCAAAATTGACAAATGGGATCTAATTAAACTAAAGAGCTTC
                                                      : 5167
                                                      : 5158
L1PA6 : GCCAAAATAGACAAATGGGATCTAATTAAACTAAAGAGCTTC
        GCCAAAATtGACAAATGGGATCTAATTAAACTAAAGAGCTTC
                 5220
                                      5240
        TGCACAGCAAAAGAAACTACCATCAGAGTGAACAGGCAACCT
L1PA1 :
                                                      : 5085
                                                      : 5086
L1PA2 : TGCACAGCAAAAGAAACTACCATCAGAGTGAACAGGCAACCT
L1PA3 : TGCACAGCAAAAGAAACTACCATCAGAGTGAACAGGCAACCT
                                                      : 5216
L1PA4 : TGCACAGCAAAAGAAACTACCATCAGAGTGAACAGGCAACCT
                                                      : 5213
L1PA5:
        TGCACAGCAAAAGAAACTACCATCAGAGTGAACAGGCAACCT
                                                      : 5209
                                                      : 5200
L1PA6 : TGCACAGCAAAAGAAACTACCATCAGAGTGAACAGGCAACCT
        TGCACAGCAAAAGAAACTACCATCAGAGTGAACAGGCAACCT
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5260
                                    5280
L1PA1 : ACAACATGGGAGAAAATTTTTGCAACCTACTCATCTGACAAA : 5127
L1PA2 : ACAAAATGGGAGAAAATTTTCGCAACCTACTCATCTGACAAA
                                                     : 5128
L1PA3 : ACAAAATGGGAGAAAATTTTCGCAACCTACTCATCTGACAAA
                                                     : 5258
L1PA4 : ACAAATGGGAGAAAATTTTCGCAACCTACTCATCTGACAAA
                                                     : 5255
L1PA5 : ACAGAATGGGAGAAAATTTTCGCAATCTACTCATCTGACAAA
                                                     : 5251
L1PA6 : ACA<mark>GA</mark>ATGGGAGAAAATTTT<mark>T</mark>GCAA<mark>T</mark>CTAC<mark>C</mark>CATCTGACAAA
                                                     : 5242
        ACA aATGGGAGAAAATTTT GCAA CTACtCATCTGACAAA
                                  5320
            5300
        GGGCTAATATCCAGAATCTACAA<mark>T</mark>GAACT<mark>C</mark>AAACAAATTTAC
L1PA1 :
                                                     : 5169
L1PA2 : GGGCTAATATCCAGAATCTACAATGAACTCAAACAAATTTAC
                                                     : 5170
L1PA3 : GGGCTAATATCCAGAATCTACAA<mark>T</mark>GAACT<mark>C</mark>AAACAAATTTAC
                                                     : 5300
L1PA4 : GGGCTAATATCCAGAATCTACAATGAACTCAAACAAATTTAC
                                                     : 5297
L1PA5 : GGGCTAATATCCAGAATCTACAAAGAACTCAAACAAATTTAC
                                                     : 5293
L1PA6 : GGGCTAATATCCAGAATCTACAAAGAACTTAAACAAATTTAC : 5284
        GGGCTAATATCCAGAATCTACAA GAACTCAAACAAATTTAC
          5340
                                5360
L1PA1 : AAGAAAAAAAAAACAACCCCATCAAAAAGTGGGCCGAAGGAC : 5211
L1PA2 : AAGAAAAAAAAAAACCCCATCAAAAAGTGGGCCGAAGGAC : 5212
L1PA3 : AAGAAAAAAACAACCCCATCAAAAAGTGGGCCGAAGGAC : 5342
L1PA4 : AAGAAAAAAACAACCCCATCAAAAAGTGGGCGAAGGAT : 5339
L1PA5 : AAGAAAAAAAAAAACCCCATCAAAAAGTGGGCCGAAGGAT : 5335
L1PA6 : AAGAAAAAAAAACAACCCCATCAAAAAGTGGGCAAAGGAT : 5326
        AAGAAAAAACAAACCCCCATCAAAAAGTGGGCGAAGGA
        5380
                                                   54
                             5400
L1PA1 : ATGAACAGACACTTCTCAAAAGAAGACATTTATGCAGCCAAA : 5253
L1PA2 : ATGAACAGACACTTCTCAAAAGAAGACATTTATGCAGCCAAA : 5254
L1PA3 : ATGAACAGACACTTCTCAAAAGAAGACATTTATGCAGCCAAA : 5384
L1PA4 : ATGAACAGACACTTCTCAAAAGAAGACATTTATGCAGCCAAA : 5381
L1PA5 : ATGAACAGACACTTCTCAAAAGAAGACATTTATGCAGCCAAC : 5377
L1PA6 : ATGAACAGACACTTCTCAAAAGAAGACATTTATGCAGCCAAC : 5368
        ATGAACAGACACTTCTCAAAAGAAGACATTTATGCAGCCAA
                           5440
L1PA1 : AAACACATGAAGAAATGCTCATCATCACTGGCCATCAGAGAA : 5295
L1PA2 : AAACACATGAAAAAATGCTCATCATCACTGGCCATCAGAGAA : 5296
L1PA3 : AAACACATGAAAAAATGCTCATCATCACTGGCCATCAGAGAA : 5426
L1PA4 : AAACACATGAAAAAATGCTCATCATCACTGGCCATCAGAGAA : 5423
L1PA5 : AGACACATGAAAAAATGCTCATCATCACTGGCCATCAGAGAA : 5419
L1PA6 : AGACACATGAAAAAATGCTCATCATCACTGGTCATCAGAGAA : 5410
        A ACACATGAAaAATGCTCATCATCACTGGcCATCAGAGAA
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5480
                                               5500
L1PA1 : ATGCAAATCAAAACCAC<mark>T</mark>ATGAGATA<mark>T</mark>CATCTCACACCAGTT
                                                      : 5337
                                                       : 5338
L1PA2 : ATGCAAATCAAAACCACAATGAGATACCATCTCACACCAGTT
L1PA3 : ATGCAAATCAAAACCACAATGAGATACCATCTCACACCAGTT
                                                       : 5468
L1PA4 : ATGCAAATCAAAACCACAATGAGATACCATCTCACACCAGTT
                                                      : 5465
L1PA5 : ATGCAAATCAAAACCACAATGAGATACCATCTCACACCAGTT
                                                      : 5461
L1PA6 : ATGCAAATCAAAACCACAATGAGATACCATCTCACACCAGTT
                                                       : 5452
        ATGCAAATCAAAACCACaATGAGATAcCATCTCACACCAGTT
                        5520
                                             5540
L1PA1 : AGAATGGCAATCATTAAAAAGTCAGGAAACAACAGGTGCTGG
                                                      : 5379
L1PA2 : AGAATGGCAATCATTAAAAAGTCAGGAAACAACAGGTGCTGG
                                                      : 5380
L1PA3 : AGAATGGCAATCATTAAAAAGTCAGGAAACAACAGGTGCTGG
                                                      : 5510
L1PA4 : AGAATGGCGATCATTAAAAAGTCAGGAAACAACAGGTGCTGG
                                                      : 5507
L1PA5 : AGAATGGCGATCATTAAAAAGTCAGGAAACAACAGGTGCTGG
                                                      : 5503
L1PA6 : AGAATGGCGATCATTAAAAAGTCAGGAAACAACAGATGCTGG : 5494
        AGAATGGC ATCATTAAAAAGTCAGGAAACAACAGGTGCTGG
                     5560
                                           5580
L1PA1 : AGAGGATGCGGAGAAATAGGAACACTTTTACACTGTTGGTGG
                                                      : 5421
                                                       : 5422
L1PA2:
        AGAGGATG<mark>T</mark>GGAGAAATAGGAAC<mark>A</mark>CTTTTACACTGTTGGTGG
L1PA3 : AGAGGATGTGGAGAAATAGGAACACTTTTACACTGTTGGTGG
                                                      : 5552
L1PA4 : AGAGGATGTGGAGAAATAGGAACACTTTTACACTGTTGGTGG
L1PA5 : AGAGGATGTGGAGAAATAGGAACACTTTTACACTGTTGGTGG
                                                      : 5545
L1PA6 : AGAGGATG<mark>T</mark>GGAGAAATAGGAAC<mark>G</mark>CTTTTACACTGTTGGTGG
                                                      : 5536
        AGAGGATGtGGAGAAATAGGAACaCTTTTACACTGTTGGTGG
                   5600
                                         5620
L1PA1 : GACTGTAAACTAGTTCAACCATTGTGGAAGTCAGTGTGGCGA : 5463
L1PA2 : GACTGTAAACTAGTTCAACCATTGTGGAAGTCAGTGTGGCGA
                                                      : 5464
                                                      : 5594
L1PA3 : GACTGTAAACTAGTTCAACCATTGTGGAAGTCAGTGTGGCGA
                                                      : 5591
L1PA4 : GACTGTAAACTAGTTCAACCATTGTGGAAGTCAGTGTGGCGA
L1PA5 : GACTGTAAACTAGTTCAACCATTGTGGAAGACAGTGTGGCGA
                                                      : 5587
L1PA6 : GAGTGTAAACTAGTTCAACCATTGTGGAAGACAGTGTGGCGA : 5578
        GACTGTAAACTAGTTCAACCATTGTGGAAG CAGTGTGGCGA
                 5640
                                       5660
        TTCCTCA<mark>G</mark>GGATCTAGAACTAGAAATACCATTTGACCCAGC<mark>C</mark>
                                                      : 5505
L1PA1:
                                                      : 5506
L1PA2 : TTCCTCAGGGATCTAGAACTAGAAATACCATTTGACCCAGCC
L1PA3: TTCCTCAGGGATCTAGAACTAGAAATACCATTTGACCCAGCC
                                                      : 5636
                                                      : 5633
L1PA4 : TTCCTCAGGGATCTAGAACTAGAAATACCATTTGACCCAGCC
        TTCCTCA<mark>A</mark>GGATCTAGAACTAGAAATACCATTTGACCCAGC<mark>C</mark>
L1PA5:
                                                      : 5629
L1PA6 : TTCCTCAAGGATCTAGAACTAGAAATACCATTTGACCCAGCA : 5620
        TTCCTCA GGATCTAGAACTAGAAATACCATTTGACCCAGCC
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5680
                                    5700
L1PA1 : ATCCCATTACTGGGTATATACCCAAATGAGTATAAATCATGC
                                                     : 5547
L1PA2 : ATCCCATTACTGGGTATATACCCAAATGACTATAAATCATGC
                                                     : 5548
L1PA3 : ATCCCATTACTGGGTATATACCCAAAGGACTATAAATCATGC
                                                      : 5678
L1PA4 : ATCCCATTACTGGGTATATACCCAAAGGATTATAAATCATGC
                                                     : 5675
L1PA5 : ATCCCATTACTGGGTATATACCCAAAGGATTATAAATCATGC
                                                     : 5671
L1PA6 : ATCCCATTACTGGGTATATACCCAAAGGATTATAAATCATGC
                                                     : 5662
        ATCCCATTACTGGGTATATACCCAAA GA TATAAATCATGC
             5720
                                  5740
        T<mark>G</mark>CTATAAAGACACATGCACACGTATGTTTATTGCGGCA<mark>C</mark>TA
L1PA1 :
                                                     : 5589
L1PA2 : TGCTATAAAGACACATGCACACGTATGTTTATTGCGGCATTA
                                                     : 5590
L1PA3 : TGCTATAAAGACACATGCACACGTATGTTTATTGCGGCACTA
                                                     : 5720
        T<mark>G</mark>CTATAAAGACACATGCACACGTATGTTTATTGCGGCA<mark>C</mark>TA
                                                     : 5717
L1PA4 :
L1PA5 : TGCTATAAAGACACATGCACACGTATGTTTATTGCGGCACTA
                                                     : 5713
L1PA6 : TACTATAAAGACACATGCACACGTATGTTTATTGCGGCACTA : 5704
        TGCTATAAAGACACATGCACACGTATGTTTATTGCGGCAcTA
          5760
                                5780
L1PA1: TTCACAATAGCAAAGACTTGGAACCAACCCAAATGTCCAACA
                                                     : 5631
L1PA2 :
        TTCACAATAGCAAAGACTTGGAACCAACCCAAATGTCCA<mark>A</mark>CA
                                                     : 5632
                                                     : 5762
L1PA3 : TTCACAATAGCAAAGACTTGGAACCAACCCAAATGTCCAACA
L1PA4 : TTCACAATAGCAAAGACTTGGAACCAACCCAAATGTCCAACA : 5759
L1PA5 : TTCACAATAGCAAAGACTTGGAACCAAACCCAAATGTCCATCA : 5755
L1PA6 : TTCACAATAGCAAAGACTTGGAACCAACCCAAATGTCCATCA : 5746
        TTCACAATAGCAAAGACTTGGAACCAACCCAAATGTCCA CA
        5800
                             5820
                                                   58
        ATGATAGACTGGATTAAGAAAATGTGGCACATATACACCATG
L1PA1 :
                                                     : 5673
L1PA2: ATGATAGACTGGATTAAGAAAATGTGGCACATATACACCATG
                                                     : 5674
L1PA3: ATGATAGACTGGATTAAGAAAATGTGGCACATATACACCATG
                                                      : 5804
                                                     : 5801
L1PA4: ATGATAGACTGGATTAAGAAAATGTGGCACATATACACCATG
L1PA5 : ATGATAGACTGGATTAAGAAAATGTGGCACATATACACCATG
                                                     : 5797
L1PA6: ATGATAGACTGGATTAAGAAAATGTGGCACATATACACCATG: 5788
        ATGATAGACTGGATTAAGAAAATGTGGCACATATACACCATG
                           5860
L1PA1 : GAATACTATGCAGCCATAAAAAATGATGAGTTCATATCCTTT
                                                     : 5715
L1PA2 : GAATACTATGCAGCCATAAAAAATGATGAGTTCATGTCCTTT
                                                     : 5716
L1PA3 : GAATACTATGCAGCCATAAAAAATGATGAGTTCATGTCCTTT
                                                     : 5846
L1PA4 : GAATACTATGCAGCCATAAAAAATGATGAGTTCATGTCCTTT
                                                     : 5843
L1PA5:
        GAATACTATGCAGCCATAAAAAA<mark>T</mark>GATGAGTTCAT<mark>G</mark>TCCTTT
                                                     : 5839
L1PA6 : GAATACTATGCAGCCATAAAAAAGGGATGAGTTCATGTCCTTT
                                                     : 5830
        GAATACTATGCAGCCATAAAAAAtGATGAGTTCATGTCCTTT
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5900
                                              5920
L1PA1 : GTAGGGACATGGATGAAATTGGAAACCATCATTCTCAGTAAA : 5757
L1PA2 : GTAGGGACATGGATGAAATTGGAAATCATCATCTCAGTAAA : 5758
L1PA3 : GTAGGGACATGGATGAAATTGGAAATCATCATTCTCAGTAAA
                                                     : 5888
L1PA4 : GTAGGGACATGGATGAAGCTGGAAACCATCATTCTCAGCAAA
                                                     : 5885
L1PA5 : GTAGGGACATGGATGAAGCTGGAAACCATCATTCTCAGCAAA : 5881
L1PA6 : GCAGGGACATGGATGAAGCTGGAAACCATCATTCTCAGCAAA
                                                     : 5872
        Gtagggacatggatgaa tggaaa catcattctcag aaa
                       5940
                                            5960
L1PA1 : CTATCGCAAGAACAAAAACCAAACACCGCATATTCTCACTC
                                                     : 5799
L1PA2 : CTATCGCAAGAACAAAAACCAAACACCGCATATTCTCACTC
                                                     : 5800
L1PA3 : CTATCGCAAGAACAAAAACCAAACACCGCATATTCTCACTC
                                                     : 5930
L1PA4 : CTATCGCAAGGACAAAAACCAAACACCGCATGTTCTCACTC
                                                     : 5927
L1PA5 : CTATCGCAAGGACAAAAAACCAAACACCGCATGTTCTCACTC
                                                     : 5923
L1PA6 : CTATCGCAAGGACAGAAACCAAACCCGCATGTTCTCACTC : 5914
        CTATCGCAAG ACAAAAACCAAACACCGCAT TTCTCACTC
                     5980
                                          6000
L1PA1 : ATAGGTGGGAATTGAACAATGAGATCACATGGACACAGGAAG : 5841
L1PA2 : ATAGGTGGGAATTGAACAATGAGA<mark>T</mark>CACATGGACACAGG<mark>AA</mark>G
                                                     : 5842
L1PA3 : ATAGGTGGGAATTGAACAATGAGAACACATGGACACAGGAAG : 5972
L1PA4 : ATAGGTGGGAATTGAACAATGAGAACACATGGACACAGGAAG : 5969
L1PA5 : ATAGGTGGGAATTGAACAATGAGAACTTTGGACACAGGAAG : 5965
L1PA6 : ATAGGTGGGAATTGAACAATGAGAACACTTGGACACAGGGCG : 5956
        ATAGGTGGGAATTGAACAATGAGA CAC TGGACACAGGaaG
                   6020
                                        6040
L1PA1 : GGGAATATCACACTCTGGGGACTGTGGTGGGGTCGGGGGGAGG : 5883
L1PA3 : GGGAACATCACACTCTGGGGACTGTTGTGGGGGTGGGGGGGAGG : 6014
L1PA4 : GGGAACATCACACACTGGGGACTGTTGTGGGGGTGGGGGGAGG : 6011
L1PA5 : GGGAACATCACACCGGGGCCTGTTGTGGGGGTGGGGGGAGG : 6007
L1PA6 : GGGAACATCACACACCGGGGCCCTGTCAGGGGGGTGGGGGGCTG : 5998
        GGGAA ATCACAC C GGGG CTGT gtGGGGTgGGGGGAgG
                 6060
                                      6080
L1PA1 : GGGGAGGGATAGCATT<mark>G</mark>GGAGA<mark>T</mark>ATACCTAATGCTA<mark>G</mark>ATGAC
                                                     : 5925
                                                     : 5926
L1PA2 : GGGGAGGGATAGCATTGGGGAGATATACCTAATGCTAGGATGAC
L1PA3 : GGGGAGGGATAGCATTAGGAGATATACCTAATGCTAAATGAC
                                                     : 6056
                                                     : 6053
L1PA4 : GGGGAGGGATAGCATT<mark>A</mark>GGAGA<mark>T</mark>ATACCTAATG<mark>C</mark>TA<mark>A</mark>ATGAC
L1PA5 : GGGGAGGGATAGCATT<mark>A</mark>GGAGA<mark>T</mark>ATACCTAATG—TA<mark>A</mark>ATGAC
                                                     : 6048
L1PA6 : GGGGAGGGATAGCATTAGGAGAATACCTAATG-TAAATGAC : 6039
        GGGGAGGGATAGCATT GGAGATATACCTAATG TA ATGAC
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6100
                                  6120
L1PA1 : ACATTAGTGGGTGCAGCGCACCAGCATGCACATGTATACAT : 5967
L1PA2 : GAGTTAGTGGGTGCAGCGCACCAGCATGGCACATGTATACAT : 5968
L1PA3 : GAGTTAATGGGTGCAGCACACCAGCATGGCACATGTATACAT
                                                  : 6098
L1PA4 : GAGTTAATGGGTGCAGCACACACACATGGCACATGTATACAT : 6095
L1PA5 : GAGTTAATGGGTGCAGCACACCAACATGGCACATGTATACAT : 6090
L1PA6 : GAGTT-GTGGGTGCAGCAAACCAACATGGCACATGTATACCT : 6080
        qaqTTa TGGGTGCAGC cACCA CATGGCACATGTATACaT
            6140
                                6160
L1PA1 : ATGTAACTGAACTGCACAATGTGCACATGTACCCTAAAACTT : 6009
L1PA2 : ATGTAACTAACCTGCACAATGTGCACATGTACCCTAAAACTT
                                                  : 6010
L1PA3 : ATGTAACTGAACTGCACATTGTGCACATGTACCCTAAAACTT : 6140
L1PA4 : ATGTAACAAACCTGCACGTTGTGCACATGTACCCTAAAACTT : 6137
L1PA5 : ATGTAACAAACCTGCACGTTGTGCACATGTACCCTAGAACTT : 6132
L1PA6 : ATGTAACAAACCTGCACGTTGTGCACATGTACCCTAGAACTT : 6122
       ATGTAAC AACCTGCAC TGTGCACATGTACCCTA AACTT
          6180
L1PA1 : AGAGTATAAT---- : 6019
L1PA2 : AAAGTATAAT----- : 6020
L1PA3 : AAAGTATAAT---- : 6150
L1PA4 : AAAGTATAAT---- : 6147
L1PA5 : AAAGTATAAT----- : 6142
L1PA6 : AAAGTATAATTAAAAAAA : 6140
       AaAGTATAAT
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