

Gene: MECP2 - Sequence: NG_007107.2
 Transcript: NM_004992.3 - Protein: NP_004983.1
 Date : March 2, 2015

1st line: Base numbering. Full stops for intronic +/- 5, 10, 15...
 2nd line: Base sequence. lower case Introns, upper case Exons
 3rd line: Amino acid sequence. Printed on FIRST base of codon
 4th line: Amino acid numbering. Numbered on 1st and increments of 10

Exon 1 | Start: 44391 | End: 44518 | Length: 127

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.      .      .      .      .      .      .      .      .      .      .
ctaaaccagtcctccgcgccaagccgcctcttttccccaacgacggccgaaagcagc

.      .      .      .      .      .      .      .      .      .      .
caatcaacagctggaggggtccgcccccttttccctggccgaaatggacaggaaatctcg

.      .      .      .      .      .      .      .      .      .      .
ccaattgacggcatcgccgctgagacctccccctcccccgctcctccccgtcccagccccg

.      .      .      .      .      .      .      .      .      .      .
gccatcacagccaatgacgggcgggctcgagcggcgccgagggcggggcgcgggcgcgcg

.      .      .      .      .      .      .      .      .      .      .
aggtgcagcagcgcgcgggccggccaagagggcgggcgcgacgtcgggcgtgcggggtc

      | -219      | -209      | -199      | -189      | -179      | -169
CCGGCGTCGGCGGCGCGCGCTCCCTCCTCTCGGAGAGAGGGCTGTGGTAAAAGCCGTC

      | -159      | -149      | -139      | -129      | -119      | -109
CGGAAAAATGGCCGCCGCCGCCGCCGCCGCGCCGAGCGGAGGAGGAGGAGGAGGCGAGGAG

      | -99
GAGAGACTgtgagtgggaccgccgtggccgcggggcggggacccttgccggggggcggggg

.      .      .      .      .      .      .      .      .      .      .
tcagggcgggacgtggcggggaggggcccgcggggtcggacgacacggctggcggatg

.      .      .      .      .      .      .      .      .      .      .
gcgtccctcctctctaccctccccctcccgccgcccgggtggcgactctccctcggcc

.      .      .      .      .      .      .      .      .      .      .
cgtcaccgcgtgctcggggtgaccgtcctcggcgggcctccctggagccgccttcgcct

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gacgcccctcttcctcccgccctcgacgcgcaccccgcccccgccccgcgggcgcc

tgtcgccg

Exon 2 | Start: 49814 | End: 49937 | Length: 123

```
. . . . .
agaagaaatacttgccagaaatcgccactcatgggtatgcttttgtagtgtcgaagtgtcc

. . . . .
cctagaggtgacaaggcttgtgatagtgttgattctaacaagcatgaatctttcctttat

. . . . .
ttagcactgtgtgttacgtgccagtaatttgagcttatcctttgtttctagctaggta

. . . . .
agctgggaaatagcctagtactttgtctatgtgtttatcttcaaaatgtcccaaatagcc

. . . . .
ctgggaaaaaggctcgtgcagctcaatgggggctttcaacttacaattttctttgttttag

      |-89      |-79      |-69      |-59      |-49      |-39
GCTCCATAAAAAATACAGACTCACCAGTTCCTTGCTTTGATGTGACATGTGACTCCCCAGAA

      |-29      |-19      |-9       |1       |11       |21
TACACCTTGCTTCTGTAGACCAGCTCCAACAGGATTCCATGGTAGCTGGGATGTTAGGGC
                      M V A G M L G L
                      |1

. . . . .
TCAGGtaagtaaccttccttttttttttttagtatatgtcctggtttgccatctgttt
R

. . . . .
tttttttttttaaaaaaaaaaaaaaaaaaggaaaagaggaaaaaaatatactactcttgga

. . . . .
agtataaaagtaccccaaagactaaagacataactgtgccaaactgtgcatataataaa

. . . . .
aaaaagtcacttcctgagccctgaaagggtcagtgtgtgtagggttacttggtcgccaca

. . . . .
gcgtgatctgggggcgggcgtcagattagagccggaactggtgatctgcaacttcagttc

.
acct
```

Exon 3 | Start: 109571 | End: 109921 | Length: 350

.
gccgcagtggttccgctcagaggaaagggctctgattctcctgcagtgctaggagacttg
.
tgggtggccacagtgacaggtcaggcacaccggccagcaccacccacagcccaaattccta
.
aagaaatatttgggtcccagcttggcccagatctctgttgtcctggggaaggacatcaag
.
atctgagtgatatgatggcctggggccttgcatgtggtgggggtccaagcctgcctctgct
.
cacttgttctgcagactggcatgttctctgtgatacttacatacttgtttaacacttcag

|31 |41 |51 |61 |71 |81
GGAAGAAAAGTCAGAAGACCAGGACCTCCAGGGCCTCAAGGACAAACCCCTCAAGTTTAA
E E K S E D Q D L Q G L K D K P L K F K
|11 |21

|91 |101 |111 |121 |131 |141
AAAGGTGAAGAAAGATAAGAAAGAAGAGAAAGAGGGCAAGCATGAGCCCGTGCAGCCATC
K V K K D K K E E K E G K H E P V Q P S
|31 |41

|151 |161 |171 |181 |191 |201
AGCCCACCACTCTGCTGAGCCCGCAGAGGCAGGCAAAGCAGAGACATCAGAAGGGTCAGG
A H H S A E P A E A G K A E T S E G S G
|51 |61

|211 |221 |231 |241 |251 |261
CTCCGCCCCGGCTGTGCCGGAAGCTTCTGCCTCCCCCAAACAGCGGCGCTCCATCATCCG
S A P A V P E A S A S P K Q R R S I I R
|71 |81

|271 |281 |291 |301 |311 |321
TGACCGGGGACCCATGTATGATGACCCACCCTGCCTGAAGGCTGGACACGGAAGCTTAA
D R G P M Y D D P T L P E G W T R K L K
|91 |101

331	341	351	361	371	.
GCAAAGGAAATCTGGCCGCTCTGCTGGGAAGTATGATGTGTATTTGATCAAgttaagtaag					
Q	R	K	S	G	R
					S
					A
					G
					K
					Y
					D
					V
					Y
					L
					I
					N
111			121		

.
agcaactcctatctctacagggcagggagggcagggacaaggatccctcatggagcagga											
.
aaatgtatgtgccaggggtggggtcggggggaacataaacaatgaacactgagaccaggt											
.
gtgcttgaaatgaccgtgtacagaggtcgctgccctgagtgggaagttctcaaggtagca											
.
ggccctctatcctctccacacctcaagtctttatctggggatggaatagctgcggaagca											
.
gaggaacttgagagctaggggttcagaggggtgaagaagcatgtttcagt											

Exon 4 | Start: 110678 | End: 120315 | Length: 9637

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. . . . .
gttctagatggtgactcaggcccaggcaccaaccagcagaatgggcctcagcctgacaac

. . . . .
ccttctgtaccaggcctgactctttggttgctgaactttggagaggcctgggggggtcag

. . . . .
cggcaggcagacgagtgagtggctttggtgacaggctcctcaggggcagccaggcagtggtg

. . . . .
actctcgttcaatagtaacgtttgtcagagcgttgtcaccaccatccgctctgccctatc

. . . . .
tctgacattgctatggagagcctctaattgttccttgtgtctttctgtttgtccccacag

      |381      |391      |401      |411      |421      |431
TCCCCAGGGAAAAGCCTTTCGCTCTAAAGTGGAGTTGATTGCGTACTTCGAAAAGGTAGG
P  Q  G  K  A  F  R  S  K  V  E  L  I  A  Y  F  E  K  V  G
      |131                        |141

      |441      |451      |461      |471      |481      |491
CGACACATCCCTGGACCCTAATGATTTTGACTTCACGGTAACTGGGAGAGGGAGCCCCCTC
D  T  S  L  D  P  N  D  F  D  F  T  V  T  G  R  G  S  P  S
      |151                        |161

      |501      |511      |521      |531      |541      |551
CCGGCGAGAGCAGAAACCACCTAAGAAGCCCAAATCTCCCAAAGCTCCAGGAAGTGGCAG
R  R  E  Q  K  P  P  K  K  P  K  S  P  K  A  P  G  T  G  R
      |171                        |181

      |561      |571      |581      |591      |601      |611
AGGCCGGGGACGCCCCAAAGGGAGCGGCACCACGAGACCCAAGGCGGCCACGTGAGAGGG
G  R  G  R  P  K  G  S  G  T  T  R  P  K  A  A  T  S  E  G
      |191                        |201

      |621      |631      |641      |651      |661      |671
TGTGCAGGTGAAAAGGGTCCTGGAGAAAAGTCCTGGGAAGCTCCTTGTCAAGATGCCTTT
V  Q  V  K  R  V  L  E  K  S  P  G  K  L  L  V  K  M  P  F
      |211                        |221
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681	691	701	711	721	731
TCAAAC TTCGCCAGGGGGCAAGGCTGAGGGGGGTGGGGCCACCACATCCACCCAGGTCAT					
Q	T	S	P	G	G
				K	A
				E	G
				G	G
				A	T
				T	S
				T	Q
				V	M
	231			241	
741	751	761	771	781	791
GGTGATCAAACGCCCCGGCAGGAAGCGAAAAGCTGAGGCCGACCCTCAGGCCATTCCCAA					
V	I	K	R	P	G
				R	K
				R	K
				A	E
				A	D
				P	Q
				A	I
				P	K
	251			261	
801	811	821	831	841	851
GAAACGGGGCCGAAAGCCGGGGAGTGTGGTGGCAGCCGCTGCCGCCGAGGCCAAAAAGAA					
K	R	G	R	K	P
				G	S
				V	V
				A	A
				A	A
				A	E
				A	K
				K	K
	271			281	
861	871	881	891	901	911
AGCCGTGAAGGAGTCTTCTATCCGATCTGTGCAGGAGACCGTACTCCCCATCAAGAAGCG					
A	V	K	E	S	S
				I	R
				S	V
				Q	E
				T	V
				L	P
				I	K
				K	R
	291			301	
921	931	941	951	961	971
CAAGACCCGGGAGACGGTCAGCATCGAGGTCAAGGAAGTGGTGAAGCCCCTGCTGGTGTG					
K	T	R	E	T	V
				S	I
				E	V
				K	E
				V	V
				K	P
				L	L
				V	S
	311			321	
981	991	1001	1011	1021	1031
CACCTCGGTGAGAAGAGCGGGAAAGGACTGAAGACCTGTAAGAGCCCTGGGCGGAAAAG					
T	L	G	E	K	S
				G	K
				L	K
				T	C
				K	S
				P	G
				R	K
				S	
	331			341	
1041	1051	1061	1071	1081	1091
CAAGGAGAGCAGCCCCAAGGGGCGCAGCAGCAGCGCCTCCTACCCCCCAAGAAGGAGCA					
K	E	S	S	P	K
				G	R
				S	S
				S	A
				S	S
				P	P
				K	K
				E	H
	351			361	
1101	1111	1121	1131	1141	1151
CCACCACCATCACCACCACTCAGAGTCCCCAAAGGCCCCCGTGCCACTGCTCCCACCCCT					
H	H	H	H	H	H
				S	E
				S	P
				K	A
				P	V
				P	L
				L	P
				P	L
	371			381	
1161	1171	1181	1191	1201	1211
GCCCCACCTCCACCTGAGCCCGAGAGCTCCGAGGACCCACCAGCCCCCTGAGCCCCA					
P	P	P	P	P	E
				P	E
				S	S
				E	D
				P	T
				S	P
				P	P
				E	P
				Q	
	391			401	

*481	*491	*501	*511	*521	*531
TGTGAGGCAGGAGAGACAGTTGGATTCTTTAGAGAAGATGGATATGACCAGTGGCTATGG					
*541	*551	*561	*571	*581	*591
CCTGTGCGATCCCACCCGTGGTGGCTCAAGTCTGGCCCCACACCAGCCCCAATCCAAAAC					
*601	*611	*621	*631	*641	*651
TGGCAAGGACGCTTCACAGGACAGGAAAAGTGGCACCTGTCTGCTCCAGCTCTGGCATGGC					
*661	*671	*681	*691	*701	*711
TAGGAGGGGGGAGTCCCTTGAACACTGTTGGTGTAGACTGGCCTGAACCACAGGAGAGGAT					
*721	*731	*741	*751	*761	*771
GGCCAGGGTGAGGTGGCATGGTCCATTCTCAAGGGACGTCTCCAACGGGTGGCGCTAG					
*781	*791	*801	*811	*821	*831
AGGCCATGGAGGCAGTAGGACAAGGTGCAGGCAGGCTGGCCTGGGGTCAGGCCGGGCAGA					
*841	*851	*861	*871	*881	*891
GCACAGCGGGGTGAGAGGGATTCCCTAATCACTCAGAGCAGTCTGTGACTTAGTGACAGG					
*901	*911	*921	*931	*941	*951
GGAGGGGGCAAAGGGGGAGGAGAAGAAAATGTTCTTCCAGTTACTTTCCAATTCTCCTTT					
*961	*971	*981	*991	*1001	*1011
AGGGACAGCTTAGAATTATTTGCACTATTGAGTCTTCATGTTCCCACTTCAAAACAAACA					
*1021	*1031	*1041	*1051	*1061	*1071
GATGCTCTGAGAGCAAACCTGGCTTGAATTGGTGACATTTAGTCCCTCAAGCCACCAGATG					
*1081	*1091	*1101	*1111	*1121	*1131
TGACAGTGTTGAGAACTACCTGGATTTGTATATATACCTGCGCTTGTTTTAAAGTGGGCT					
*1141	*1151	*1161	*1171	*1181	*1191
CAGCACATAGGGTTCCACGAAGCTCCGAAACTCTAAGTGTTTGCTGCAATTTTATAAGG					
*1201	*1211	*1221	*1231	*1241	*1251
ACTTCCTGATTGGTTTCTCTTCTCCCCTTCCATTTCTGCCTTTTGTTTCATTTATCCTTT					
*1261	*1271	*1281	*1291	*1301	*1311
CACTTCTTTCCCTTCCCTCCGTCCTCCTCCTTAGTTCATCCCTTCTCTTCCAGGCAGC					
*1321	*1331	*1341	*1351	*1361	*1371
CGCGGTGCCCCAACCACTTGTCTGGCTCCAGTCCCCAGAACTCTGCCTGCCCTTTGTCCT					

*1381	*1391	*1401	*1411	*1421	*1431
CCTGCTGCCAGTACCAGCCCCACCCTGTTTTGAGCCCTGAGGAGGCCTTGGGCTCTGCTG					
*1441	*1451	*1461	*1471	*1481	*1491
AGTCCGACCTGGCCTGTCTGTGAAGAGCAAGAGAGCAGCAAGGTCTTGCTCTCCTAGGTA					
*1501	*1511	*1521	*1531	*1541	*1551
GCCCCCTCTTCCCTGGTAAGAAAAAGCAAAAGGCATTTCCACCCTGAACAACGAGCCTT					
*1561	*1571	*1581	*1591	*1601	*1611
TTCACCTTCTACTCTAGAGAAGTGGACTGGAGGAGCTGGGCCCCGATTTGGTAGTTGAGG					
*1621	*1631	*1641	*1651	*1661	*1671
AAAGCACAGAGGCCTCCTGTGGCCTGCCAGTCATCGAGTGGCCCAACAGGGGGCTCCATGC					
*1681	*1691	*1701	*1711	*1721	*1731
CAGCCGACCTTGACCTCACTCAGAAGTCCAGAGTCTAGCGTAGTGCAGCAGGGCAGTAGC					
*1741	*1751	*1761	*1771	*1781	*1791
GGTACCAATGCAGAACTCCCAAGACCCGAGCTGGGACCAGTACCTGGGTCCCCAGCCCTT					
*1801	*1811	*1821	*1831	*1841	*1851
CCTCTGCTCCCCCTTTTCCCTCGGAGTTCTTCTTGAATGGCAATGTTTTGCTTTTGCTCG					
*1861	*1871	*1881	*1891	*1901	*1911
ATGCAGACAGGGGGCCAGAACACCACACATTTCACTGTCTGTCTGGTCCATAGCTGTGGT					
*1921	*1931	*1941	*1951	*1961	*1971
GTAGGGGCTTAGAGGCATGGGCTTGCTGTGGGTTTTTAATTGATCAGTTTTTCATGTGGGA					
*1981	*1991	*2001	*2011	*2021	*2031
TCCCATCTTTTTAACCTCTGTTTCAGGAAGTCCTTATCTAGCTGCATATCTTCATCATATT					
*2041	*2051	*2061	*2071	*2081	*2091
GGTATATCCTTTTCTGTGTTTACAGAGATGTCTCTTATATCTAAATCTGTCCAACCTGAGA					
*2101	*2111	*2121	*2131	*2141	*2151
AGTACCTTATCAAAGTAGCAAATGAGACAGCAGTCTTATGCTTCCAGAAACACCCACAGG					
*2161	*2171	*2181	*2191	*2201	*2211
CATGTCCCATGTGAGCTGCTGCCATGAACTGTCAAGTGTGTGTTGTCTTGTGTATTTTCA					
*2221	*2231	*2241	*2251	*2261	*2271
TTATTGTCCCTGGCTTCCTTACTATGGTGTAAATCATGAAGGAGTGAAACATCATAGAAAC					

*2281	*2291	*2301	*2311	*2321	*2331
TGTCTAGCACTTCCTTGCCAGTCTTTAGTGATCAGGAACCATAGTTGACAGTTCCAATCA					
*2341	*2351	*2361	*2371	*2381	*2391
GTAGCTTAAGAAAAAACCGTGTTTGTCTCTTCTGGAATGGTTAGAAAGTGAGGGAGTTTGC					
*2401	*2411	*2421	*2431	*2441	*2451
CCCGTTCTGTTTGTAGAGTCTCATAGTTGGACTTTCTAGCATATATGTGTCCATTTTCCTT					
*2461	*2471	*2481	*2491	*2501	*2511
ATGCTGTAAAAGCAAGTCCTGCAACCAAACCTCCCATCAGCCCAATCCCTGATCCCTGATC					
*2521	*2531	*2541	*2551	*2561	*2571
CCTTCCACCTGCTCTGCTGATGACCCCCCAGCTTCACTTCTGACTCTTCCCCAGGAAGG					
*2581	*2591	*2601	*2611	*2621	*2631
GAAGGGGGGTCAGAAGAGAGGGTGAGTCCTCCAGAACTCTTCCTCCAAGGACAGAAGGCT					
*2641	*2651	*2661	*2671	*2681	*2691
CCTGCCCCCATAGTGGCCTCGAACTCCTGGCACTACCAAAGGACACTTATCCACGAGAGC					
*2701	*2711	*2721	*2731	*2741	*2751
GCAGCATCCGACCAGGTTGTCACTGAGAAGATGTTTATTTTGGTCAGTTGGGTTTTTATG					
*2761	*2771	*2781	*2791	*2801	*2811
TATTATACTTAGTCAAATGTAATGTGGCTTCTGGAATCATTGTCCAGAGCTGCTTCCCCG					
*2821	*2831	*2841	*2851	*2861	*2871
TCACCTGGGCGTCATCTGGTCCTGGTAAGAGGAGTGCGTGGCCCACCAGGCCCCCTGTC					
*2881	*2891	*2901	*2911	*2921	*2931
ACCCATGACAGTTCATTTCAGGGCCGATGGGGCAGTCGTGGTTGGGAACACAGCATTTCAA					
*2941	*2951	*2961	*2971	*2981	*2991
GCGTCACTTTATTTTCAATTCGGGCCCCACCTGCAGCTCCCTCAAAGAGGCAGTTGCCAGC					
*3001	*3011	*3021	*3031	*3041	*3051
CTCTTTCCCTTCCAGTTTATTCCAGAGCTGCCAGTGGGGCCTGAGGCTCCTTAGGGTTTT					
*3061	*3071	*3081	*3091	*3101	*3111
CTCTCTATTTCCCCCTTTCTTCCTCATTCCTCGTCTTTCCCAAAGGCATCACGAGTCAG					
*3121	*3131	*3141	*3151	*3161	*3171
TCGCCTTTCAGCAGGCAGCCTTGGCGGTTTATCGCCCTGGCAGGCAGGGGCCCTGCAGCT					

*3181	*3191	*3201	*3211	*3221	*3231
CTCATGCTGCCCCTGCCTTGGGGTCAGGTTGACAGGAGGTTGGAGGGAAAGCCTTAAGCT					
*3241	*3251	*3261	*3271	*3281	*3291
GCAGGATTCTCACCAGCTGTGTCCGGCCAGTTTTGGGGTGTGACCTCAATTTCAATTTT					
*3301	*3311	*3321	*3331	*3341	*3351
GTCTGTACTTGAACATTATGAAGATGGGGGCCTCTTTCAGTGAATTTGTGAACAGCAGAA					
*3361	*3371	*3381	*3391	*3401	*3411
TTGACCGACAGCTTTCAGTACCCATGGGGCTAGGTCATTAAGGCCACATCCACAGTCTC					
*3421	*3431	*3441	*3451	*3461	*3471
CCCCACCTTGTTCAGTTGTTAGTTACTACCTCCTCTCCTGACAATACTGTATGTCGTC					
*3481	*3491	*3501	*3511	*3521	*3531
GAGCTCCCCCAGGTCTACCCCTCCCGGCCCTGCCTGCTGGTGGGCTTGTTCATAGCCAGT					
*3541	*3551	*3561	*3571	*3581	*3591
GGGATTGCCGGTCTTGACAGCTCAGTGAGCTGGAGATACTTGGTCACAGCCAGGCGCTAG					
*3601	*3611	*3621	*3631	*3641	*3651
CACAGCTCCCTTCTGTTGATGCTGTATTCCCATATCAAAAGACACAGGGGACACCCAGAA					
*3661	*3671	*3681	*3691	*3701	*3711
ACGCCACATCCCCCAATCCATCAGTGCCAAACTAGCCAACGGCCCCAGCTTCTCAGCTCG					
*3721	*3731	*3741	*3751	*3761	*3771
CTGGATGGCGGAAGCTGCTACTCGTGAGCGCCAGTGCGGGTGCAGACAATCTTCTGTTGG					
*3781	*3791	*3801	*3811	*3821	*3831
GTGGCATCATTCAGGCCCCAAGCATGAACAGTGCACCTGGGACAGGGAGCAGCCCCAAA					
*3841	*3851	*3861	*3871	*3881	*3891
TTGTCACCTGCTTCTCTGCCCAGCTTTTCATTGCTGTGACAGTGATGGCGAAAGAGGGTA					
*3901	*3911	*3921	*3931	*3941	*3951
ATAACCAGACACAAACTGCCAAGTTGGGTGGAGAAAGGAGTTTCTTTAGCTGACAGAATC					
*3961	*3971	*3981	*3991	*4001	*4011
TCTGAATTTTAAATCACTTAGTAAGCGGCTCAAGCCCAGGAGGGAGCAGAGGGATACGAG					
*4021	*4031	*4041	*4051	*4061	*4071
CGGAGTCCCCTGCGCGGGACCATCTGGAATTGGTTTAGCCCAAGTGGAGCCTGACAGCCA					

*4081	*4091	*4101	*4111	*4121	*4131
GAACTCTGTGTCCCCGCTAACCACAGCTCCTTTTCCAGAGCATTCCAGTCAGGCTCTC					
*4141	*4151	*4161	*4171	*4181	*4191
TGGGCTGACTGGGCCAGGGGAGGTTACAGGTACCAGTTCTTTAAGAAGATCTTTGGGCAT					
*4201	*4211	*4221	*4231	*4241	*4251
ATACATTTTTAGCCTGTGTCATTGCCCAAATGGATTCCCTGTTTCAAGTTCACACCTGCA					
*4261	*4271	*4281	*4291	*4301	*4311
GATTCTAGGACCTGTGTCCTAGACTTCAGGGAGTCAGCTGTTTCTAGAGTTCCTACCATG					
*4321	*4331	*4341	*4351	*4361	*4371
GAGTGGGTCTGGAGGACCTGCCCGGTGGGGGGGCAGAGCCCTGCTCCCTCCGGGTCTTCC					
*4381	*4391	*4401	*4411	*4421	*4431
TACTCTTCTCTGCTCTGACGGGATTTGTTGATTCTCTCCATTTTGGTGTCTTTCTCTT					
*4441	*4451	*4461	*4471	*4481	*4491
TTAGATATTGTATCAATCTTTAGAAAAGGCATAGTCTACTTGTATAAAATCGTTAGGATA					
*4501	*4511	*4521	*4531	*4541	*4551
CTGCCTCCCCCAGGGTCTAAAATTACATATTAGAGGGGAAAAGCTGAACACTGAAGTCAG					
*4561	*4571	*4581	*4591	*4601	*4611
TTCTCAACAATTTAGAAGGAAAACCTAGAAAACATTTGGCAGAAAATTACATTTTCGATGT					
*4621	*4631	*4641	*4651	*4661	*4671
TTTTGAATGAATACGAGCAAGCTTTTACAACAGTGCTGATCTAAAAATACTTAGCACTTG					
*4681	*4691	*4701	*4711	*4721	*4731
GCCTGAGATGCCTGGTGAGCATTACAGGCAAGGGGAATCTGGAGGTAGCCGACCTGAGGA					
*4741	*4751	*4761	*4771	*4781	*4791
CATGGCTTCTGAACCTGTCTTTTGGGAGTGGTATGGAAGGTGGAGCGTTCACCAGTGACC					
*4801	*4811	*4821	*4831	*4841	*4851
TGGAAGGCCCAGCACCACCCTCCTTCCCACTCTTCTCATCTTGACAGAGCCTGCCCCAGC					
*4861	*4871	*4881	*4891	*4901	*4911
GCTGACGTGTCAGGAAAACACCCAGGGAAGTCTAGGAAGGCACTTCTGCCTGAGGGGCAGCC					
*4921	*4931	*4941	*4951	*4961	*4971
TGCCTTGCCCACTCCTGCTCTGCTCGCCTCGGATCAGCTGAGCCTTCTGAGCTGGCCTCT					

*4981	*4991	*5001	*5011	*5021	*5031
CACTGCCTCCCCAAGGCCCCCTGCCTGCCCTGTCAGGAGGCAGAAGGAAGCAGGTGTGAG					
*5041	*5051	*5061	*5071	*5081	*5091
GGCAGTGCAAGGAGGGAGCACAAACCCCAGCTCCCGCTCCGGGCTCCGACTTGTGCACAG					
*5101	*5111	*5121	*5131	*5141	*5151
GCAGAGCCCAGACCCTGGAGGAAATCCTACCTTTGAATTCAAGAACATTTGGGGAATTTG					
*5161	*5171	*5181	*5191	*5201	*5211
GAAATCTCTTTGCCCCCAAACCCCATTTCTGTCTACCTTTAATCAGGTCCTGCTCAGCA					
*5221	*5231	*5241	*5251	*5261	*5271
GTGAGAGCAGATGAGGTGAAAAGGCCAAGAGGTTTGGCTCCTGCCCACTGATAGCCCCTC					
*5281	*5291	*5301	*5311	*5321	*5331
TCCCCGAGTGTTTGTGTGTCAAGTGGCAAAGCTGTTCTTCCTGGTGACCCTGATTATAT					
*5341	*5351	*5361	*5371	*5381	*5391
CCAGTAACACATAGACTGTGCGCATAGGCCTGCTTTGTCTCCTCTATCCTGGGCTTTTGT					
*5401	*5411	*5421	*5431	*5441	*5451
TTTGCTTTTGTAGTTTGTCTTTGTCTTTCTGTCCCTTTTATTTAACGCACCGACTAGAC					
*5461	*5471	*5481	*5491	*5501	*5511
ACACAAAGCAGTTGAATTTTATATATATATCTGTATATTGCACAATTATAAACTCATTT					
*5521	*5531	*5541	*5551	*5561	*5571
TGCTTGTGGCTCCACACACACAAAAAAGACCTGTTAAAATTATACCTGTTGCTTAATTA					
*5581	*5591	*5601	*5611	*5621	*5631
CAATATTTCTGATAACCATAGCATAGGACAAGGAAAAATAAAAAAGAAAAAAGAAAA					
*5641	*5651	*5661	*5671	*5681	*5691
AAAAACGACAAATCTGTCTGCTGGTCACTTCTTCTGTCCAAGCAGATTCTGTTGCTTTTC					
*5701	*5711	*5721	*5731	*5741	*5751
CTCGCTTCTTTCAAGGGCTTTCTGTGCCAGGTGAAGGAGGCTCCAGGCAGCACCCAGGT					
*5761	*5771	*5781	*5791	*5801	*5811
TTTGCACTCTTGTCTTCTCCCGTGCTTGTGAAAGAGGTCCCAAGTTCTGGGTGCAGGAGC					
*5821	*5831	*5841	*5851	*5861	*5871
GCTCCCTTGACCTGCTGAAGTCCGGAACGTAGTCGGCACAGCCTGGTCGCCTTCCACCTC					

*5881	*5891	*5901	*5911	*5921	*5931
TGGGAGCTGGAGTCCACTGGGGTGGCCTGACTCCCCAGTCCCCTTCCCCTGACCTGGTC					
*5941	*5951	*5961	*5971	*5981	*5991
AGGGTGAGCCCATGTGGAGTCAGCCTCGCAGGCCTCCCTGCCAGTAGGGTCCGAGTGTGT					
*6001	*6011	*6021	*6031	*6041	*6051
TTCATCCTTCCCCTCTGTCGAGCCTGGGGGCTGGAGCGGAGACGGGAGGCCTGGCCTGT					
*6061	*6071	*6081	*6091	*6101	*6111
CTCGGAACCTGTGAGCTGCACCAGGTAGAACGCCAGGGACCCAGAATCATGTGCGTCAG					
*6121	*6131	*6141	*6151	*6161	*6171
TCCAAGGGGTCCCCTCCAGGAGTAGTGAAGACTCCAGAAATGTCCCTTTCTTCTCCCCCA					
*6181	*6191	*6201	*6211	*6221	*6231
TCCTACGAGTAATTGCATTTGCTTTTGTAATTCTTAATGAGCAATATCTGCTAGAGAGTT					
*6241	*6251	*6261	*6271	*6281	*6291
TAGCTGTAAACAGTTCTTTTTGATCATCTTTTTTAATAATTAGAAACACCAAAAAAATCC					
*6301	*6311	*6321	*6331	*6341	*6351
AGAAACTTGTCTTCCAAAGCAGAGAGCATTATAATCACCAGGGCCAAAAGCTTCCCTCC					
*6361	*6371	*6381	*6391	*6401	*6411
CTGCTGTCAATTGCTTCTTCTGAGGCCTGAATCCAAAAGAAAAACAGCCATAGGCCCTTTC					
*6421	*6431	*6441	*6451	*6461	*6471
AGTGCCCGGGCTACCCGTGAGCCCTTCGGAGGACCAGGGCTGGGGCAGCCTCTGGGCCCA					
*6481	*6491	*6501	*6511	*6521	*6531
CATCCGGGGCCAGCTCCGGCGTGTGTTTCAGTGTTAGCAGTGGGTCATGATGCTCTTTCCC					
*6541	*6551	*6561	*6571	*6581	*6591
ACCCAGCCTGGGATAGGGGCAGAGGAGGCGAGGAGGCCGTTGCCGCTGATGTTTGGCCGT					
*6601	*6611	*6621	*6631	*6641	*6651
GAACAGGTGGGTGTCTGCGTGCGTCCACGTGCGTGTTTTCTGACTGACATGAAATCGACG					
*6661	*6671	*6681	*6691	*6701	*6711
CCCGAGTTAGCCTCACCCGGTGACCTCTAGCCCTGCCCGGATGGAGCGGGGCCACCCGG					
*6721	*6731	*6741	*6751	*6761	*6771
TTCACTGTTTCTGGGGAGCTGGACAGTGGAGTGCAAAAGGCTTGCAGAACTGAAGCCTG					

*6781	*6791	*6801	*6811	*6821	*6831
CTCCTTCCCTTGCTACCACGGCCTCCTTTCCGTTTGATTTGTCACTGCTTCAATCAATAA					
*6841	*6851	*6861	*6871	*6881	*6891
CAGCCGCTCCAGAGTCAGTAGTCAATGAATATATGACCAAATATCACCAGGACTGTTACT					
*6901	*6911	*6921	*6931	*6941	*6951
CAATGTGTGCCGAGCCCTTGCCCATGCTGGGCTCCCGTGTATCTGGACACTGTAACGTGT					
*6961	*6971	*6981	*6991	*7001	*7011
GCTGTGTTTGCTCCCCCTCCCCTTCTTTGCCCTTTACTTGTCTTTCTGGGGTTTTT					
*7021	*7031	*7041	*7051	*7061	*7071
CTGTTTGGGTTTGGTTTGGTTTTATTTCTCCTTTTGTGTTCCAAACATGAGGTTCTCTC					
*7081	*7091	*7101	*7111	*7121	*7131
TACTGGTCCTCTTAAGTGTGGTGTGAGGCTTATATTTGTGTAATTTTTGGTGGGTGAAA					
*7141	*7151	*7161	*7171	*7181	*7191
GGAATTTTGCTAAGTAAATCTTCTGTGTTTGAAGTGAAGTCTGTATTGTAACATGTT					
*7201	*7211	*7221	*7231	*7241	*7251
TAAAGTAATTGTTCCAGAGACAAATATTTCTAGACACTTTTTCTTTACAAACAAAAGCAT					
*7261	*7271	*7281	*7291	*7301	*7311
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*7321	*7331	*7341	*7351	*7361	*7371
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*7381	*7391	*7401	*7411	*7421	*7431
GCCGAATAGCTGATGTGTTGCCACTTTCCAAGTCACTGCAAAACCAGGTTTTGTTCCGCC					
*7441	*7451	*7461	*7471	*7481	*7491
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*7501	*7511	*7521	*7531	*7541	*7551
AAGGAAAGGCAAGATTGATGTTTCCTTGAGGGGAGCCAGGAGGGGATGTGTGTGTGCAGA					
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GCTGAAGAGCTGGGGAGAATGGGGCTGGGCCCCACCAAGCAGGAGGCTGGGACGCTCTGC					
*7621	*7631	*7641	*7651	*7661	*7671
TGTGGGCACAGGTCAGGCTAATGTTGGCAGATGCAGCTCTTCCTGGACAGGCCAGGTGGT					

*7681	*7691	*7701	*7711	*7721	*7731
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*7741	*7751	*7761	*7771	*7781	*7791
TCCCACCCCATCCTCCAGGGCTCAACACTGTGACATCTCTATTCCCCACCCTCCCCTTCC					
*7801	*7811	*7821	*7831	*7841	*7851
CAGGGCAATAAAATGACCATGGAGGGGGCTTGCACTCTCTTGGCTGTCACCCGATCGCCA					
*7861	*7871	*7881	*7891	*7901	*7911
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*7921	*7931	*7941	*7951	*7961	*7971
AGCCATTACCCTCATTAGGCATGGTTTTGGGCTCCCAAAACACCTGACAGCCCCCTCCCTC					
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CTCTGAGAGGCGGAGAGTGCTGACTGTAGTGACCATTGCATGCCGGGTGCAGCATCTGGA					
*8041	*8051	*8061	*8071	*8081	*8091
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