

Gene: BRCA1 - Sequence: NG_005905.2
 Transcript: NM_007294.3 - Protein: NP_009225.1
 LRG: LRG_292t1 - Date : Friday 5th February, 2016

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: 92501 | End: 92713 | Length: 212

```

. . . . .
tacttatatttaccgaaactggagacctccattagggcggaaagagtgggggattgggac

. . . . .
ctcttcttacgactgctttggacaataggtagcgattctgaccttcgtacagcaattact

. . . . .
gtgatgcaataagccgcaactggaagagtagaggctagagggcaggcactttatggcaaa

. . . . .
ctcaggtagaattcttcctcttccgtctctttcctttacgtcatccgggggcagactgg

. . . . .
gtggccaatccagagccccgagagacgcttggtctcttctgtccctcccatcctctgatt

|-229      |-219      |-209      |-199      |-189      |-179
GTACCTTGATTTCGTATTCTGAGAGGCTGCTGCTTAGCGGTAGCCCCTTGTTTCCGTGG

|-169      |-159      |-149      |-139      |-129      |-119
CAACGAAAAAGCGCGGGAATTACAGATAAATTAAACTGCGACTGCGCGGCGTGAGCTCG

|-109      |-99       |-89       |-79       |-69       |-59
CTGAGACTTCCTGGACGGGGGACAGGCTGTGGGGTTTCTCAGATAACTGGGCCCCTGCGC

|-49       |-39       |-29
TCAGGAGGCCTTCACCCTCTGCTCTGGGTAAAGgtagtagagtcccggaaggacagg

. . . . .
gggccaagtgatgctctggggtactggcgtgggagagtggatttccgaagctgacagat

. . . . .
gggtattctttgacgggggtaggggcggaacctgagaggcgtaaggcgttgtgaaccct

```

.
ggggaggggggcagttttaggtcgcgaggggaagcgctgaggatcaggaagggggcactg

.
agtgtccgtgggggaatcctcgtgataggaactggaatatgccttgagggggacactatg

.
tctttaaaaacgtcggctggtcatgaggtcagg

Exon 2 | Start: 93869 | End: 93967 | Length: 98

```
. . . . .
aggctaccaccacctacccggtcagtcactcctctgtagctttctctttcttggagaaag

. . . . .
gaaaagaccaaggggttgagcaaatatgtgaaaaattcagaatttatgttgtctaata

. . . . .
tacaaaaagcaacttctagaatctttaaaaataaaggacgttggtcattagttctttggtt

. . . . .
tgtattattctaaaaccttccaaatcttaaatcttatttttaaaatgataaaatgaa

. . . . .
gttggtcattttataaaccttttaaaagatatatatatgtttttctaattgtgttaaag

|-19      |-9      |1      |11      |21      |31      |41
TTCATTGGAACAGAAAGAAATGGATTATCTGCTCTTCGCGTTGAAGAAGTACAAAATGT
          M D L S A L R V E E V Q N V
          |1                      |11

          |51      |61      |71
CATTAATGCTATGCAGAAAATCTTAGAGTGTCCCATCTGgtaagtcagcacaagagtgtg
I N A M Q K I L E C P I C
          |21

. . . . .
ttaatttgggattcctatgattatctcctatgcaaataacagaattgaccttacatact

. . . . .
agggaagaaaagacatgtctagtaagattaggctattgtaattgctgattttcttaactg

. . . . .
aagaactttaaaaatatagaaaatgattccttggttctccatccactctgcctctccact

. . . . .
cctctccttttcaacacaaatcctgtggtccgggaaagacagggactctgtcttgattgg

. . . . .
ttctgcactggggcaggaatctagtttagattaactggc
```

Exon 3 | Start: 102205 | End: 102258 | Length: 53

```
. . . . .
aattcgtacgaactattatcaactaatcttttaaagtctgatgatagtatagagtattga
. . . . .
agggatcaatataattctgttttgatatctgaaagctcactgaaggaaggaatcgtattc
. . . . .
tctgctgtattctcagttcctgacacagcagacatttaataaatattgaacgaacttgag
. . . . .
gccttatgttgactcagtcataacagctcaaagttgaacttattcactaagaatagcttt
. . . . .
atttttaataaattattgagcctcatttattttcttttctccccctaccctgctag
|81      |91      |101      |111      |121      |131      .
TCTGGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACCACATATTTGCAAgtagt
 L  E  L  I  K  E  P  V  S  T  K  C  D  H  I  F  C  K
      |31                      |41
. . . . .
ttgaatgtgttatgtggctccattattagcttttgttttgtccttcataaccagaaa
. . . . .
cacctaactttatagaagctttactttcttcaattaagtgagaacgaaaaatccaactcc
. . . . .
atttcattctttctcagagagtatatagttatcaaaagttggttgtaatcatagttcctg
. . . . .
gtaaagtttgacatatattatcttttttttttttttgagacaaagtctcgctctgtcg
. . . . .
cccaggctggagtgagtgcatgatcttggctcactgcaacctccgcccccg
```

Exon 4 | Start: 111451 | End: 111528 | Length: 77

```
. . . . .
tatgaatatatcattaaatatgccatattaactttttattaagttttatgtgatcataaca

. . . . .
gtaagccatatgcatgtaagttcagttttcatagatcattgcttatgtagtttaggtttt

. . . . .
tgcttatgcagcatccaaaaacaattaggaaactattgcttgtaattcacctgccattac

. . . . .
tttttaaatggctcttaagggcagttgtgagattatctttcatggctatttgcccttttg

. . . . .
agtattctttctacaaaaggaagtaaattaaattgttctttctttctttataatttatag

      |141      |151      |161      |171      |181      |191
ATTTTGCA TGCTGAACTTCTCAACCAGAAGAAAGGGCCTTCACAGTGTCTTTATGTAA
  F  C  M  L  K  L  L  N  Q  K  K  G  P  S  Q  C  P  L  C  K
                |51                      |61

      |201      |211      . . . . .
GAATGATATAACCAAAAGgtatataatttggtaatgatgctaggttgaagcaaccacag
  N  D  I  T  K  R
                |71

. . . . .
taggaaaaagtagaaattatttaataacatagcgttcctataaaaccattcatcagaaaa

. . . . .
atttataaaagagtttttagcacacagtaaattatttccaaagttattttcctgaaagtt

. . . . .
ttatgggacatctgccttatacaggtattagaaacttactgcctttctctaattgcttcta

. . . . .
gtgtaaaaacttgcagacttatgtaaagtagggctgtatcgccgtgccccattgtctgt

. . . . .
taatcttgtttttatatt
```

Exon 5 | Start: 113028 | End: 113116 | Length: 88

.
aaattaaacaaaaaaaaaagtactctagttttctatgcaatgcattatatctgctgtgga

.
tttagggcagtattatatcagataattttaggcatttggtaggcttaaataatgaatgacaaa

.
aagttactaaatcactgccatcacacggtttatacagatgtcaatgatgtattgattata

.
gagggttttctactgttgctgcatcttatttttatttgtttacatgtcttttcttatttta

.
gtgtccttaaaaggttgataatcacttgctgagtggtgtttctcaacaatttaatttcag

 |221 |231 |241 |251 |261 |271
GAGCCTACAAGAAAAGTACGAGATTTAGTCAACTTGTGAAGAGCTATTGAAAAATCATTG
S L Q E S T R F S Q L V E E L L K I I C
 |81 |91

 |281 |291 |301
TGCTTTTCAGCTTGACACAGGTTTGGAGTgtaagtggtgaatatccaagaatgacactc
A F Q L D T G L E Y
 |101

.
aagtgctgtccatgaaaactcaggaagtttgacaaattactttctatgacgtggtgataa

.
gaccttttagtctaggttaatttttagttctgtatctgtaatctatttttaaaaaattact

.
cccactgggtctcacaccttattttatcaatcgtaagggtgcacatttttcacatcttaaca

.
tctctgaaattgggaacattttactattgagggtgtgtcatttgtttaatttggtgtgctt

.
tctttcttagtgatacagaaaataatagt

Exon 6 | Start: 113723 | End: 113862 | Length: 139

.
tacattgttggtgtcttagctttagtgaaatacagtattgataggcaaatttcttagtgt

.
taaggtagaaaacaaggactctaaataactttgatggctctgtgtatttgtttttgtttcc

.
taggagtagaaatttccagttgattttttaaaatttgatttttaaaaaaatcacaggtaa

.
ccttaatgcattgtcttaacacaacaaagagcatatagggttctcttggtttctttg

.
attataattcatatatttttctctaactgcaaacataatgttttcccttgatttttacag

 |311 |321 |331 |341 |351 |361
ATGCAAAACAGCTATAATTTTGCAAAAAAGGAAAAATAACTCTCCTGAACATCTAAAAGATG
 A N S Y N F A K K E N N S P E H L K D E
 |111 |121

 |371 |381 |391 |401 |411 |421
AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG
 V S I I Q S M G Y R N R A K R L L Q S E
 |131 |141

 |431 |441
AACCCGAAAAATCCTTCCTTGgtaaaaccatttgttttcttcttcttcttcttcttctt
 P E N P S L

.
cttttttttttctttttttttttgagatggagtccttgctctgtggcccaggctagaagc

.
agtcctcctgccttagcccccttagtagctgggattacaggcacgcgccaccatgccagg

.
ctaatttttgatttttagtagagacggggtttcatcatgttgccaggctggtctcgaa

.
ctcctaacctcagtgatccaccacctcggctcccaaattgctgggattacaggtgtg

.
agccactgtgcccggcggt

Exon 7 | Start: 118104 | End: 118209 | Length: 105

```
. . . . .
actactactattattttgtagagactgggtctcactctgttgcttatgctggctcttgaac

. . . . .
tcctggcctcaagcagtcctgctccagcctcccaaagtgctgggattataggcatgagct

. . . . .
accgctcccagccccagacatttttagtggtgtaaattcctgggcattttttccaggcatca

. . . . .
tacatgtagctgactgatgatggtaattttatgtccatgggtgcaagtttctcttc

. . . . .
aggaggaaaagcacagaactggccaacaattgcttgactgttctttaccatactgtttag

      |451      |461      |471      |481      |491      |501
CAGGAAACCACTCTCAGTGTCCAACCTCTTAACCTTGGAACCTGTGAGAACTCTGAGGACA
Q E T S L S V Q L S N L G T V R T L R T
      |151                      |161

      |511      |521      |531      |541      . .
AAGCAGCGGATACAAACCTCAAAAGACGTCTGTCTACATTGAATTGGGtaagggtctcagg
K Q R I Q P Q K T S V Y I E L G
      |171                      |181

. . . . .
ttttttaagtatttaataataattgctggattccttatcttatagttttgcaaaaatct

. . . . .
tggtcataatttgatattgtggttaggcagctttgggaagtgaattttatgagccctatgg

. . . . .
tgagttataaaaaatgtaaaagacgcagttccacctgaagaatcttactttaaaagg

. . . . .
gagcaaaagaggccaggcatggtggctcacacctgtaatcccagcactttgggaggccaa

. . . . .
agtgggtggatcacctgaggtcgggagttcgagaccagcctagcca
```


Exon 8 | Start: 120695 | End: 120740 | Length: 45

```
. . . . .
tagaaacgggggtctcactttgttggccaggctggtcttgaactcctaacctcaaataat

. . . . .
ccaccatctcggcctcctcaagtgtgggattacaggtgagagccactgtgcctggcga

. . . . .
agcccatgcctttaaccacttctctgtattacatactagcttaactagcattgtacctgc

. . . . .
cacagtagatgctcagtaaataatttctagttgaatatctgtttttcaacaagtacatttt

. . . . .
tttaacccttttaattaagaaaacttttattgatttatttttgggggaaatttttag

    |551      |561      |571      |581      |591      . .
GATCTGATTCTTCTGAAGATACCGTTAATAAGGCAACTTATTGCAGgtgagtcaaagaga
  S  D  S  S  E  D  T  V  N  K  A  T  Y  C  S
                        |191

. . . . .
acctttgtctatgaagctggtattttcctatttagttaatattaaggattgatgtttctc

. . . . .
tctttttaaaaatattttaacttttatttttaggttcagggatgtatgtgcagtttggtat

. . . . .
ataggtaaacacacgacttgggatttggtgtatagattttttcatcatccgggtactaa

. . . . .
gcataccccacagttttttgtttgctttcttctgaatttctccctcttcccaccttctc

. . . . .
ccctcaagtaggctggtgttttctccagactagaatcatggtattgg
```

Exon 9 | Start: 122062 | End: 122138 | Length: 76

.
gtatttttagtagagatggggtttcaccatgttggccaggctggtcttgaactcatgacc

.
tcaagtgggtccaccgcctcagcctcccaaagtgctggaattacaggcttgagccaccgt

.
gccagcaaccatttcatttcaactagaagtttctaaaggagagagcagctttcactaac

.
taaataagattggtcagctttctgtaatcgaaagagctaaaatgtttgatcttggtcatt

.
tgacagttctgcatacatgtaactagtgtttcttattaggactctgtcttttccctatag

 |601 |611 |621 |631 |641 |651
TGTGGGAGATCAAGAATTGTTACAAATCACCCCTCAAGGAACCAGGGATGAAATCAGTTT
V G D Q E L L Q I T P Q G T R D E I S L
 |201 |211

 |661
GGATTCTGCAAAAAGGgtaatggcaaagtttgccaacttaacaggcactgaaaagagag
D S A K K A
 |221

.
tgggtagatacagtactgtaattagattattctgaagaccatttgggacctttacaaccc

.
acaaaatctcttggcagagtttagagtatcattctctgtcaaatgtcgtggtatggtctga

.
tagatttaaattggtactagactaatgtacctataataaaccttctgtaactgattgttg

.
ccctttcgttttttttttgtttgtttgtttgttttttttgagatgggggtctcactctg

.
ttgccaggctggagtg

Exon 10 | Start: 123124 | End: 126549 | Length: 3425
 BE AWARE: Flanking intron is shared with the following exon

```

. . . . .
agttttctgatggccaatctgcttttaattcactccttagacgttagagaaataggtgtgg
. . . . .
tttctgcatagggaaaattctgaaattaaaaatttaatggatcctaagtggaaataatct
. . . . .
aggtaaataggaattaaatgaaagagtatgagctacatcttcagtatacttggtagttta
. . . . .
tgagggttagtttctctaatatagccagttggttgatttccacctccaaggtgtatgaagt
. . . . .
atgtatttttttaatgacaattcagtttttgagtaccttggtatttttgtatatatttcag

|671      |681      |691      |701      |711      |721
CTGCTTGTGAATTTCTGAGACGGATGTAACAAATACTGAACATCATCAACCCAGTAATA
  A C E F S E T D V T N T E H H Q P S N N
                        |231                        |241

|731      |741      |751      |761      |771      |781
ATGATTTGAACACCACTGAGAAGCGTGCAGCTGAGAGGCATCCAGAAAAGTATCAGGGTA
  D L N T T E K R A A E R H P E K Y Q G S
                        |251                        |261

|791      |801      |811      |821      |831      |841
GTTCTGTTTCAAACCTTGCATGTGGAGCCATGTGGCACAAATACTCATGCCAGCTCATTAC
  S V S N L H V E P C G T N T H A S S L Q
                        |271                        |281

|851      |861      |871      |881      |891      |901
AGCATGAGAACAGCAGTTTATTACTCACTAAAGACAGAATGAATGTAGAAAAGGCTGAAT
  H E N S S L L L T K D R M N V E K A E F
                        |291                        |301

|911      |921      |931      |941      |951      |961
TCTGTAATAAAAGCAAACAGCCTGGCTTAGCAAGGAGCCAACATAACAGATGGGCTGGAA
  C N K S K Q P G L A R S Q H N R W A G S
                        |311                        |321

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971	981	991	1001	1011	1021
GTAAGGAAACATGTAATGATAGGCGGACTCCCAGCACAGAAAAAAGGTAGATCTGAATG					
K	E	T	C	N	D
			R	R	T
			P	S	T
			E	K	K
			V	D	L
			N	A	
		331			341

1031	1041	1051	1061	1071	1081
CTGATCCCCTGTGTGAGAGAAAAGAATGGAATAAGCAGAAACTGCCATGCTCAGAGAATC					
D	P	L	C	E	R
			K	E	W
			N	K	Q
			K	L	P
			C	S	E
			N	P	
		351			361

1091	1101	1111	1121	1131	1141
CTAGAGATACTGAAGATGTTCTTGGATAACACTAAATAGCAGCATTCAGAAAGTTAATG					
R	D	T	E	D	V
			P	W	I
			T	L	N
			S	S	I
			Q	K	V
			N	E	
		371			381

1151	1161	1171	1181	1191	1201
AGTGGTTTTCAGAAAGTGATGAACTGTTAGGTTCTGATGACTCACATGATGGGGAGTCTG					
W	F	S	R	S	D
			E	L	L
			G	S	D
			D	S	H
			D	G	E
			S	E	
		391			401

1211	1221	1231	1241	1251	1261
AATCAAATGCCAAAGTAGCTGATGTATTGGACGTTCTAAATGAGGTAGATGAATATTCTG					
S	N	A	K	V	A
			D	V	L
			D	V	L
			N	E	V
			D	E	Y
			S	G	
		411			421

1271	1281	1291	1301	1311	1321
GTTCTTCAGAGAAAATAGACTTACTGGCCAGTGATCCTCATGAGGCTTTAATATGTAAAA					
S	S	E	K	I	D
			L	A	S
			D	P	H
			E	A	L
			I	C	K
			S		
		431			441

1331	1341	1351	1361	1371	1381
GTGAAAGAGTTCACTCCAAATCAGTAGAGAGTAATATTGAAGACAAAATATTTGGGAAAA					
E	R	V	H	S	K
			S	V	E
			S	N	I
			E	D	K
			I	F	G
			K	T	
		451			461

1391	1401	1411	1421	1431	1441
CCTATCGGAAGAAGGCAAGCCTCCCCAACTTAAGCCATGTAAGTAAAAATCTAATTATAG					
Y	R	K	K	A	S
			L	P	N
			L	S	H
			V	T	E
			N	L	I
			I	I	G
		471			481

1451	1461	1471	1481	1491	1501
GAGCATTGTGTTACTGAGCCACAGATAATACAAGAGCGTCCCCTCACAAATAAATTAAAGC					
A	F	V	T	E	P
			Q	I	I
			Q	E	R
			P	L	T
			N	K	L
			K	R	
		491			501

1511	1521	1531	1541	1551	1561
GTAAAAGGAGACCTACATCAGGCCTTCATCCTGAGGATTTTATCAAGAAAGCAGATTTGG					
K	R	R	P	T	S
		G	L	H	P
			E	D	F
			I	K	K
			A	D	L
					A
		511			521
1571	1581	1591	1601	1611	1621
CAGTTCAAAAAGACTCCTGAAATGATAAATCAGGGAACCTAACCAACGGAGCAGAATGGTC					
V	Q	K	T	P	E
		M	I	N	Q
			G	T	N
			Q	T	E
				Q	N
					G
					Q
		531			541
1631	1641	1651	1661	1671	1681
AAGTGATGAATATTACTAATAGTGGTCATGAGAATAAAACAAAAGGTGATTCTATTTCAGA					
V	M	N	I	T	N
		S	G	H	E
			N	K	T
			K	G	D
				S	I
				Q	N
		551			561
1691	1701	1711	1721	1731	1741
ATGAGAAAAATCCTAACCCAATAGAATCACTCGAAAAAGAATCTGCTTTCAAACGAAAG					
E	K	N	P	N	P
		I	E	S	L
			E	K	E
			S	A	F
				K	T
				K	A
		571			581
1751	1761	1771	1781	1791	1801
CTGAACCTATAAGCAGCAGTATAAGCAATATGGAACCTCGAATTAAATATCCACAATTCAA					
E	P	I	S	S	S
		I	S	N	M
			E	L	E
			L	N	I
				H	N
				S	K
		591			601
1811	1821	1831	1841	1851	1861
AAGCACCTAAAAAGAATAGGCTGAGGAGGAAGTCTTCTACCAGGCATATTCATGCGCTTG					
A	P	K	K	N	R
		L	R	R	K
			S	S	T
			R	H	I
				H	A
				L	E
		611			621
1871	1881	1891	1901	1911	1921
AACTAGTAGTCAGTAGAAATCTAAGCCACCTAATTGTACTGAATTGCAAATTGATAGTT					
L	V	V	S	R	N
		L	S	P	P
			N	C	T
			E	L	Q
				I	D
				S	C
		631			641
1931	1941	1951	1961	1971	1981
GTTCTAGCAGTGAAGAGATAAAGAAAAAAAAGTACAACCAATGCCAGTCAGGCACAGCA					
S	S	S	E	E	I
		K	K	K	K
			Y	N	Q
			M	P	V
				R	H
				S	R
		651			661
1991	2001	2011	2021	2031	2041
GAAACCTACAACCTCATGGAAGGTAAAGAACCTGCAACTGGAGCCAAGAAGAGTAACAAGC					
N	L	Q	L	M	E
		G	K	E	P
			A	T	G
			A	K	K
				S	N
				K	P
		671			681

2051	2061	2071	2081	2091	2101
CAATGAACAGACAAGTAAAAGACATGACAGCGATACTTTCCCAGAGCTGAAGTTAACAA					
N	E	Q	T	S	K
			R	H	D
			S	D	T
			F	P	E
			L	K	L
			T	N	
		691			701
2111	2121	2131	2141	2151	2161
ATGCACCTGGTTCTTTTACTAAGTGTTCAAATACCAAGTGAAGTTAAAGAATTTGTCAATC					
A	P	G	S	F	T
			K	C	S
			N	T	S
			E	L	K
			E	F	V
			N	P	
		711			721
2171	2181	2191	2201	2211	2221
CTAGCCTTCCAAGAGAAGAAAAAGAAGAGAACTAGAAACAGTTAAAGTGTCTAATAATG					
S	L	P	R	E	E
			K	E	E
			K	L	E
			T	V	K
			V	S	N
			N	A	
		731			741
2231	2241	2251	2261	2271	2281
CTGAAGACCCCAAAGATCTCATGTTAAGTGGAGAAAGGGTTTTGCAAAGTAAAGATCTG					
E	D	P	K	D	L
			M	L	S
			G	E	R
			V	L	Q
			T	E	R
			S	V	
		751			761
2291	2301	2311	2321	2331	2341
TAGAGAGTAGCAGTATTTTATTGGTACCTGGTACTGATTATGGCACTCAGGAAAGTATCT					
E	S	S	S	I	S
			L	V	P
			G	T	D
			Y	G	T
			Q	E	S
			I	S	
		771			781
2351	2361	2371	2381	2391	2401
CGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACAGAACCAAAATAAATGTGTGAGTC					
L	L	E	V	S	T
			L	G	K
			A	K	T
			E	P	N
			K	C	V
			S	Q	
		791			801
2411	2421	2431	2441	2451	2461
AGTGTGCAGCATTTGAAAACCCCAAGGGACTAATTCATGGTTGTTCCAAAGATAATAGAA					
C	A	A	F	E	N
			P	K	G
			L	I	H
			G	C	S
			K	D	N
			R	N	
		811			821
2471	2481	2491	2501	2511	2521
ATGACACAGAAGGCTTTAAGTATCCATTGGGACATGAAGTTAACCACAGTCGGGAAACAA					
D	T	E	G	F	K
			Y	P	L
			G	H	E
			V	N	H
			S	R	E
			T	S	
		831			841
2531	2541	2551	2561	2571	2581
GCATAGAAATGGAAGAAAGTGAAGTTGATGCTCAGTATTTGCAGAATACATTCAAGGTTT					
I	E	M	E	E	S
			E	L	D
			A	Q	Y
			L	Q	N
			T	F	K
			V	S	
		851			861

2591	2601	2611	2621	2631	2641
CAAAGCGCCAGTCATTTGCTCCGTTTTCAAATCCAGGAAATGCAGAAGAGGAATGTGCAA					
K	R	Q	S	F	A
	P	F	S	N	P
			G	N	A
				E	E
				E	C
					A
					T
		871			881
2651	2661	2671	2681	2691	2701
CATTCTCTGCCCACTCTGGGTCCTTAAAGAAACAAAGTCCAAAAGTCACTTTTGAATGTG					
F	S	A	H	S	G
	S	L	K	K	Q
			S	P	K
				V	T
				F	E
					C
					E
		891			901
2711	2721	2731	2741	2751	2761
AACAAAAGGAAGAAAATCAAGGAAAGAATGAGTCTAATATCAAGCCTGTACAGACAGTTA					
Q	K	E	E	N	Q
	G	K	N	E	S
			N	I	K
				P	V
				Q	T
					V
					N
		911			921
2771	2781	2791	2801	2811	2821
ATATCACTGCAGGCTTTCCTGTGGTTGGTCAGAAAGATAAGCCAGTTGATAATGCCAAAT					
I	T	A	G	F	P
	V	V	G	Q	K
			D	K	P
				V	D
				N	A
					K
					C
		931			941
2831	2841	2851	2861	2871	2881
GTAGTATCAAAGGAGGCTCTAGGTTTTGTCTATCATCTCAGTTCAGAGGCAACGAAACTG					
S	I	K	G	G	S
	R	F	C	L	S
			S	Q	F
				R	G
				N	E
					T
					G
		951			961
2891	2901	2911	2921	2931	2941
GACTCATTACTCCAAATAAACATGGACTTTTACAAAACCCATATCGTATACCACCACTTT					
L	I	T	P	N	K
	H	G	L	L	Q
			N	P	Y
				R	I
				P	P
					L
					F
		971			981
2951	2961	2971	2981	2991	3001
TTCCCATCAAGTCATTTGTTAAACTAAATGTAAGAAAAATCTGCTAGAGGAAAACTTTG					
P	I	K	S	F	V
	K	T	K	C	K
			K	N	L
				L	E
				E	N
					F
					E
		991			1001
3011	3021	3031	3041	3051	3061
AGGAACATTCAATGTCACCTGAAAGAGAAATGGGAAATGAGAACATTCCAAGTACAGTGA					
E	H	S	M	S	P
	E	R	E	M	G
			N	E	N
				I	P
				S	T
					V
					S
		1011			1021
3071	3081	3091	3101	3111	3121
GCACAATTAGCCGTAATAACATTAGAGAAAATGTTTTTAAAGAAGCCAGCTCAAGCAATA					
T	I	S	R	N	N
			I	R	E
			N	V	F
				K	E
				A	S
					S
					S
					N
					I
		1031			1041

3131	3141	3151	3161	3171	3181
TTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAATAGGTTCCA					
N E V G S S T N E V G S S I N E I G S S					
				1051	1061
3191	3201	3211	3221	3231	3241
GTGATGAAAACATTCAAGCAGAACTAGGTAGAAACAGAGGGCCAAAATTGAATGCTATGC					
D E N I Q A E L G R N R G P K L N A M L					
				1071	1081
3251	3261	3271	3281	3291	3301
TTAGATTAGGGGTTTGTCAACCTGAGGTCTATAAACAAAGTCTTCCTGGAAGTAATTGTA					
R L G V L Q P E V Y K Q S L P G S N C K					
				1091	1101
3311	3321	3331	3341	3351	3361
AGCATCCTGAAATAAAAAAGCAAGAATATGAAGAAGTAGTTCAGACTGTTAATACAGATT					
H P E I K K Q E Y E E V V Q T V N T D F					
				1111	1121
3371	3381	3391	3401	3411	3421
TCTCTCCATATCTGATTTTCAGATAAAGTCTAGAACAGCCTATGGGAAGTAGTCATGCATCTC					
S P Y L I S D N L E Q P M G S S H A S Q					
				1131	1141
3431	3441	3451	3461	3471	3481
AGGTTTGTCTGAGACACCTGATGACCTGTAGATGATGGTGAAATAAAGGAAGATACTA					
V C S E T P D D L L D D G E I K E D T S					
				1151	1161
3491	3501	3511	3521	3531	3541
GTTTTGCTGAAAATGACATTAAGGAAAGTTCTGCTGTTTTAGCAAAAGCGTCCAGAAAG					
F A E N D I K E S S A V F S K S V Q K G					
				1171	1181
3551	3561	3571	3581	3591	3601
GAGAGCTTAGCAGGAGTCCTAGCCCTTTCACCCATACACATTTGGCTCAGGGTTACCGAA					
E L S R S P S P F T H T H L A Q G Y R R					
				1191	1201
3611	3621	3631	3641	3651	3661
GAGGGGCCAAGAAATTAGAGTCTCAGAAGAGAAGTCTATCTAGTGAGGATGAAGAGCTTC					
G A K K L E S S E E N L S S E D E E L P					
				1211	1221

.
gctaggacgtcatctttgactgaatg

Exon 11 | Start: 126952 | End: 127040 | Length: 88
 BE AWARE: Flanking intron is shared with the previous exon

```

. . . . .
agctttaacatcctaattactggtggacttacttctggtttcattttataaaagcaaadc
. . . . .
caggtgtcccaaagcaaggaatttaatcattttgtgtgacatgaaagtaaaccagtcct
. . . . .
gccaatgagaagaaaaagacacagcaagttgcagcgtttatagtctgcttttacatctga
. . . . .
. . . . . |4101 |4111 |4121 |4131
acctctgtttttgttatttaagGTGAAGCAGCATCTGGGTGTGAGAGTGAAACAAGCGTC
                        E A A S G C E S E T S V
                        |1371

. . . . .
TCTGAAGACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAACCACTCAGgtaaaaagc
S E D C S G L S S Q S D I L T T Q
|1381 |1391

. . . . .
gtgtgtgtgtgtgcacatgcgtgtgtgtggtgtcctttgcattcagtagtatgtatccca
. . . . .
cattcttaggtttgctgacatcatctctttgaattaatggcacaattgtttgtggttcac
. . . . .
tgtctccttaaattagactgtaagcaccttgatggaactcatactaccttttatttcaca
. . . . .
cacacgcacacgcgcacacacagcctacacatacactgcctagctcattgtagcatacta
. . . . .
aatactgatttttaataagtaaaccttcgaaaccatttgctaatacc

```

Exon 12 | Start: 135409 | End: 135580 | Length: 171

```
. . . . .
tattttttcactccctagcttttaaagaaaataaccaacttcaaaaggacatcacataa

. . . . .
catcaagtctatttgggggaatttgaggatttttccctcactaacatcatttggaata

. . . . .
atthcatgggcattaattgcatgaatgtggttagattaaaagggtgttcagctagaacttg

. . . . .
tagttccatactaggtgatttcaattcctgtgctaaaattaatttgatgatataatttc

. . . . .
atthaatggaaagcttctcaaagtatttcatthttcttggtgccatttatcgthtttgaag

      |4191      |4201      |4211      |4221      |4231      |4241
CAGAGGGATACCATGCAACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACTAGAA
Q R D T M      Q H N L I K L Q Q E M A E L E
              |1401                      |1411

      |4251      |4261      |4271      |4281      |4291      |4301
GCTGTGTTAGAACAGCATGGGAGCCAGCCTTCTAACAGCTACCCTTCCATCATAAGTGAC
A V L E Q      H G S Q P S N S Y P S I I S D
              |1421                      |1431

      |4311      |4321      |4331      |4341      |4351      .
TCTTCTGCCCTTGAGGACCTGCGAAATCCAGAACAAAGCACATCAGAAAAAGgtgtgtat
S S A L E D L R N P E Q S T S E K A
              |1441                      |1451

. . . . .
tgttggccaaactgatatcttaagcaaaattctttccttcccctttatctccttctga

. . . . .
agagtaaggacctagctccaacattttatgatccttgctcagcacatgggtaattatgga

. . . . .
gccttggttcttgtccctgctcacaactaatataaccagtcagagggacccaaggcagtca

. . . . .
ttcatgtgtcatctgagtacctacaacaagtagatgctatggggagcccatggaagata
```

.
catggtataacaacatagctcttgctctattggaagctaagtggaatgggaga

Exon 13 | Start: 141370 | End: 141496 | Length: 126

```
. . . . .
tcaggccaaggaatatagatttttttttcagccttgctcagctgggtgtctttattt

. . . . .
actctgtcttaaagtggtccttttattatcattatttttttaatcattgaattccatt

. . . . .
tggtgctagcatctgtctgttgcttgcttggtttataaaattctgcctgatatacttg

. . . . .
tttaaaaaccaatttggtgatcatagattgatgcttttgaaaaaatcagtattctaacc

. . . . .
tgaattatcactatcagaacaaagcagtaaagtagatttgttttctcattccatttaaag

      |4361      |4371      |4381      |4391      |4401      |4411
CAGTATTAAC TTCACAGAAAAGTAGTGAATACCCTATAAGCCAGAATCCAGAAGGCCTTT
  V  L  T  S  Q  K  S  S  E  Y  P  I  S  Q  N  P  E  G  L  S
                        |1461                        |1471

      |4421      |4431      |4441      |4451      |4461      |4471
CTGCTGACAAGTTTGAGGTGTCTGCAGATAGTTCTACCAGTAAAAATAAAGAACCAGGAG
  A  D  K  F  E  V  S  A  D  S  S  T  S  K  N  K  E  P  G  V
                        |1481                        |1491

      |4481
TGGAAGGtaagaaacatcaatgtaaagatgctgtggtatctgacatctttatttatatt
  E  R

. . . . .
gaactctgattgttaatttttttcaccatactttctccagttttttgcatacaggcattt

. . . . .
atacacttttattgctctaggatacttcttttgtttaacacctatataggttttttgaacc

. . . . .
tataacataagctacaacatgagaaatgtgcggttagatagatatgtcccttctgaaggt

. . . . .
cagaaaaaatataatggaggtaaaacctgaacaagcttggaactgatggtagacttct

. .
tcaaggc
```

Exon 14 | Start: 143463 | End: 143653 | Length: 190

.
agcctcccgagtagctgagattacaggcgccagccaccacacccagctactgacctgctt

.
ttaaacagctgggagatatggtgcctcagaccaaccaaccccatgttatatgtcaaccc

.
tgacatatggcaggcaacatgaatccagacttctaggctgtcttgcgggctcttttttg

.
ccagtcatttctgatctctctgacatgagctgtttcatttatgctttggctgccagcaa

.
gtatgatttgtcctttcacaattggtggcgatggttttctccttcatttatctttctag

4491	4501	4511	4521	4531	4541
GTCATCCCTTCTAAATGCCCATCATTAGATGATAGGTGGTACATGCACAGTTGCTCTGG					
S S P S K C P S L D D R W Y M H S C S G					
1501				1511	

4551	4561	4571	4581	4591	4601
GAGTCTTCAGAATAGAACTACCCATCTCAAGAGGAGCTCATTAAGGTTGTTGATGTGGA					
S L Q N R N Y P S Q E E L I K V V D V E					
1521				1531	

4611	4621	4631	4641	4651	4661
GGAGCAACAGCTGGAAGAGTCTGGGCCACACGATTTGACGGAACATCTTACTTGCCAAG					
E Q Q L E E S G P H D L T E T S Y L P R					
1541				1551	

4671
GCAAGATCTAG	gtaatatatttcattctgctgtattggaacaaacactttgattttactctga
Q D L E	

.
atcctacataaagatatattctggttaaccaacttttagatgtactagtctatcatggacac

.
ttttgttatacttaattaagcccacttttagaaaaatagctcaagtgttaatcaaggttta

.
cttgaaaattattgaaactgttaatccatctatatattttaattaatggtttaactaatgat

.
tttgaggatgagggagtcttggtgtactctaaatgtattatttcaggccaggcatagtgg

. . .
ctcacgcctgt

Exon 15 | Start: 146746 | End: 147056 | Length: 310

```
. . . . .
tctaaaattatactattcctatgactaaacctttgcatatatcttttatctccctaggat

. . . . .
atatttctaaaactagcattgttgactgaaagtgtaaatacgtgttaaggtgtttgctac

. . . . .
ataatgccatatttccttttaggaaactaagctactttggattccaccaacactgtat

. . . . .
tcatgtaccatttttctcttaacctactttattggctcttttaattcttaacagagac

. . . . .
cagaactttgtaattcaacattcatcgttggtgtgtaaattaaacttctcccattcctttcag

      |4681      |4691      |4701      |4711      |4721      |4731
AGGGAACCCCTTACCTGGAATCTGGAATCAGCCTCTTCTCTGATGACCCTGAATCTGATC
  G  T  P  Y  L  E  S  G  I  S  L  F  S  D  D  P  E  S  D  P
      |1561                                |1571

      |4741      |4751      |4761      |4771      |4781      |4791
CTTCTGAAGACAGAGCCCCAGAGTCAGCTCGTGTGGCAACATACCATCTTCAACCTCTG
  S  E  D  R  A  P  E  S  A  R  V  G  N  I  P  S  S  T  S  A
      |1581                                |1591

      |4801      |4811      |4821      |4831      |4841      |4851
CATTGAAAGTTCCCAATTGAAAGTTGCAGAATCTGCCAGAGTCCAGCTGCTGCTCATA
  L  K  V  P  Q  L  K  V  A  E  S  A  Q  S  P  A  A  A  H  T
      |1601                                |1611

      |4861      |4871      |4881      |4891      |4901      |4911
CTACTGATACTGCTGGGTATAATGCAATGGAAGAAAGTGTGAGCAGGGAGAAGCCAGAAT
  T  D  T  A  G  Y  N  A  M  E  E  S  V  S  R  E  K  P  E  L
      |1621                                |1631

      |4921      |4931      |4941      |4951      |4961      |4971
TGACAGCTTCAACAGAAAGGGTCAACAAAAGAATGTCCATGGTGGTGTCTGGCCTGACCC
  T  A  S  T  E  R  V  N  K  R  M  S  M  V  V  S  G  L  T  P
      |1641                                |1651
```

```

      |4981      . . . . .
CAGAAGAATTTgtgagtgatccatatgtatctccctaataagacttaacaacatt
      E  E  F
      |1661

. . . . .
ctggaaagagttttatgtaggtattgtcaattaataacctagaggaagaatctagaaa

. . . . .
caatcacagttctgtgtaatttaatttcgattactaatttctgaaaatttagatctagat

. . . . .
aaagctatagtggtgattatttatgtatatattacttgagaaaataattattaaatatta

. . . . .
gtggaaaagctatactttgggtatgatataggactttcgaattggaattttcctttctat

. . . . .
ctgtaaaagca

```

Exon 16 | Start: 150289 | End: 150376 | Length: 87

```
. . . . .
gagacttcaggtgtcttagaattttttaaatgtacccttctgagaaaaacagagactta
. . . . .
aagctaggataactgggtattctatttttttttttttttttttttacctccagcctgggt
. . . . .
gacagagcaagactctgtctaaaaaaaaaaaaaaaaaattcactttaaatagttccagg
. . . . .
acacgtgtagaacgtgcaggattgctacataggtaaacatatgccatggtggaataacta
. . . . .
gtattctgagctgtgtgctagaggtaactcatgataatggaatatttgatttaatttcag
      |4991      |5001      |5011      |5021      |5031      |5041
ATGCTCGTGTAACAAGTTTGCCAGAAAACACCACATCACTTTAACTAATCTAATTACTGAA
M L V Y K F A R K H H I T L T N L I T E
                        |1671                        |1681

      |5051      |5061      |5071      . . . . .
GAGACTACTCATGTTGTTATGAAAACAGgtataccaagaacctttacagaataccttgca
E T T H V V M K T D
                        |1691

. . . . .
tctgctgcataaaaccacatgaggcgaggcacggtggcgcatgcctgtaatcgcagcact
. . . . .
ttgggaggccgaggcgggcagatcacgagattaggagatcgagaccatcctggccagcat
. . . . .
ggtgaaaccccgctctctactaaaaataaaaaattagctgggtgtggtcgcgtgcgcct
. . . . .
gtagtcccagctactcgtgaggctgaggcaggagaatcacttgaaccggggagatggagg
. . . . .
ttgcagtgagccgagatcatgccactgc
```

Exon 17 | Start: 154033 | End: 154110 | Length: 77
 BE AWARE: Flanking intron is shared with the following exon

.
 tataatggagatctatagctagccttggcgtctagaagatgggtgttgagaagagggagt

 ggacagatatttcctctggtcttaacttcatatcagcctcccctagacttccaaatatcc

 atacctgctggttataattagtgggtgttttcagcctctgattctgtcaccaggggtttta

 gaatcataaatccagattgatcttgggagtgtaaaaaactgaggctcttttagcttcttag

 gagagcacttcctgattttgttttcaacttctaatacctttgagtgtttttcattctgcag

5081	5091	5101	5111	5121	5131
ATGCTGAGTTTGTGTGTGAACGGACACTGAAATATTTTCTAGGAATTGCGGGAGGAAAAT					
A E F V C E R T L K Y F L G I A G G K W					
	1701				1711

5141	5151
GGGTAGTTAGCTATTCTGtaagtataataactatttctcccctcctccctttaacacctc								
V V S Y F W								

.
 agaattgcatttttacacctaacgtttaacacctaagggttttctgatgctgagtctga

 gttacaaaaggctctttaattgtaataactaaactacttttatctttaatatcactttgtt

 cagataagctggtgatgctgggaaaatgggtctcttttataactaataggacctaacttg

 ctccctagcaatgtagcatatgagctag

Exon 18 | Start: 154611 | End: 154651 | Length: 40
 BE AWARE: Flanking intron is shared with the previous exon

```

. . . . .
ggatttatttaatagtcggcaggaatccatgtgcagcaggcaaacttataatgtttaaat
. . . . .
taaacatcaactctgtctccagaaggaaactgctgctacaagccttattaaagggtgtg
. . . . .
gcttttagagggaaggacctctcctctgtcattcttcctgtgctcttttgtgaatcgtga
. . . . .
cctctctatctccgtgaaaagagcacgttcttctgctgtatgtaacctgtcttttctatg
. . . . .
. . . . .
atctcttttagGGGTGACCCAGTCTATTAAAGAAAGAAAAATGCTGAATGAGgtaagtact
      |5161      |5171      |5181      |5191      .
      V T Q S I K E R K M L N E
      |1721      |1731
. . . . .
tgatgttacaaactaaccagagatattcattcagtcatatagttaaaaatgtatttgctt
. . . . .
ccttccatcaatgcaccactttccttaacaatgcacaaattttccatgataatgaggatc
. . . . .
atcaagaattatgcaggcctgcactgtggctcatacctataatcccagcgctttgggagg
. . . . .
ctgaggcgcttggtacacctgatgtcgggagttcaagaccagcctgaccaacatggagaa
. . . . .
accccgtttctactaaaaatacaaaattagccgggcttggtggcacttgcc

```

Exon 19 | Start: 160849 | End: 160932 | Length: 83

```
. . . . .
gcattcaaaagattctcctgcctcagcctcccaagtagctgggattacaggtgcctgcc
. . . . .
ccacgccaactaatttttgtatttttagtagagatgaggtttcaccatgttggtcaga
. . . . .
ctggtgtcgaactcctgacctcaagtgatctgcctgcctcagtctccaaagtgctagga
. . . . .
ttacaggggtgagccactgcgcctggcctgaatgccttaaatatgacgtgtctgtccac
. . . . .
ttccattgaaggaagcttctcttctcttatcctgatgggttggtttggtttctttcag
      |5201      |5211      |5221      |5231      |5241      |5251
CATGATTTTGAAGTCAGAGGAGATGTGGTCAATGGAAGAAACCACCAAGGTCCAAAGCGA
H D F E V R G D V V N G R N H Q G P K R
                        |1741                        |1751

      |5261      |5271      . . . . .
GCAAGAGAATCCCAGGACAGAAAGgtaaagctccctccctcaagttgacaaaaatctcac
A R E S Q D R K

. . . . .
cccaccactctgtattccactcccctttgcagagatgggccgcttcattttgtaagactt
. . . . .
attacatacatcacagtgctagatactttcacacaggttcttttttctactcttccatcc
. . . . .
caaccacataaataagtattgtctctactttatgaatgataaaactaagagatttagaga
. . . . .
ggctgtgtaatttggattcccgctctcgggttcagatcttagctgataagtggaagagctg
. . . . .
ggactttaagcagatgagaatcta
```

Exon 20 | Start: 166867 | End: 166921 | Length: 54

```
. . . . .
cttggcctgattggtgacaaaagtgagatgctcagtccttgaatgacaaagaatgcctgt

. . . . .
agagtgcagggtcaactacatatgcacttcaagaagatcttctgaaatccagtagtggtct

. . . . .
ggacattggactgcttgctccctgggaagtagcagcagaaatcatcaggtggtgaacagaa

. . . . .
gaaaaagaaaagctcttcctttttgaaagtctgttttttgaataaaagccaatattcttt

. . . . .
tataactagattttccttctctccattcccctgtccctctctcttcctctcttctccag

    |5281    |5291    |5301    |5311    |5321    |5331 .
ATCTTCAGGGGGCTAGAAATCTGTTGCTATGGGCCCTTCACCAACATGCCCACAGgtaag
I  F  R  G  L  E  I  C  C  Y  G  P  F  T  N  M  P  T  D
    |1761                                |1771

. . . . .
agcctgggagaaccccagagttccagcaccagcctttgtcttacatagtggagtattata

. . . . .
agcaagatcccacgatgggggttcctcagattgctgaaatggttagaggctattctatt

. . . . .
tctctaccactctccaaacaaaacagcacctaaatgttatcctatggcaaaaaaaaacta

. . . . .
taccttgcccccttctcaagagcatgaagggtggttaatagttaggattcagtatgttat

. . . . .
gtgttcagatggcggttgagctgctgtagtgccaacatgtagtgagaaaaatc
```

Exon 21 | Start: 168790 | End: 168863 | Length: 73

.
attaatggaaattagatctttgattttttttctttcaagcattttatttgagagactat

.
caaaccttataccaagtggccttatggagactgataaccagagtacatggcatatcagtg

.
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 |5341 |5351 |5361 |5371 |5381 |5391
ATCAACTGGAATGGATGGTACAGCTGTGTGGTGCTTCTGTGGTGAAGGAGCTTTCATCAT
 Q L E W M V Q L C G A S V V K E L S S F
 |1781 |1791

 |5401
TCACCCTTGGCACAgtaagtattgggtgccctgtcagagaggaggacacaatattctct
 T L G T
 |1801

.
cctgtgagcaagactggcacctgtcagtccttatggatgccctactgtagcctcagaag

.
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.
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.
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. . . .
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Exon 22 | Start: 170281 | End: 170341 | Length: 60

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.
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 |5411 |5421 |5431 |5441 |5451 |5461
GGTGTCCACCCAATTGTGGTTGTGCAGCCAGATGCCTGGACAGAGGACAATGGCTTCCAT
G V H P I V V V Q P D A W T E D N G F H
 |1811 |1821

.
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A

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Exon 23 | Start: 172182 | End: 173689 | Length: 1507

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|5471      |5481      |5491      |5501      |5511      |5521
CAATTGGGCAGATGTGTGAGGCACCTGTGGTGACCCGAGAGTGGGTGTTGGACAGTGTAG
I G Q M C E A P V V T R E W V L D S V A
|1831      |1841

|5531      |5541      |5551      |5561      |5571      |5581
CACTCTACCAGTGCCAGGAGCTGGACACCTACCTGATACCCAGATCCCCACAGCCACT
L Y Q C Q E L D T Y L I P Q I P H S H Y
|1851      |1861

|5591      |*11      |*21      |*31      |*41      |*51
ACTGACTGCAGCCAGCCACAGGTACAGAGCCACAGGACCCCAAGAATGAGCTTACAAAGT
*

|*61      |*71      |*81      |*91      |*101     |*111
GGCCTTTCCAGGCCCTGGGAGCTCCTCTCACTCTTCAGTCCTTCTACTGTCCTGGCTACT

|*121     |*131     |*141     |*151     |*161     |*171
AAATATTTTATGTACATCAGCCTGAAAAGGACTTCTGGCTATGCAAGGGTCCCTTAAAGA

|*181     |*191     |*201     |*211     |*221     |*231
TTTTCTGCTTGAAGTCTCCCTTGAAATCTGCCATGAGCACAAAATTATGGTAATTTTC

|*241     |*251     |*261     |*271     |*281     |*291
ACCTGAGAAGATTTTAAAACCATTTAAACGCCACCAATTGAGCAAGATGCTGATTCATTA
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*301	*311	*321	*331	*341	*351
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*361	*371	*381	*391	*401	*411
GGCTTGGCCTCAAGAGAATAGCTGGTTTCCCTAAGTTTACTTCTCTAAAACCTGTGTTC					
*421	*431	*441	*451	*461	*471
ACAAAGGCAGAGAGTCAGACCCTTCAATGGAAGGAGAGTGCTTGGGATCGATTATGTGAC					
*481	*491	*501	*511	*521	*531
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*541	*551	*561	*571	*581	*591
ATTCTGAGGCAGGTATTAGAAATGAAAAGGAAACTTGAAACCTGGGCATGGTGGCTCACG					
*601	*611	*621	*631	*641	*651
CCTGTAATCCCAGCACTTTGGGAGGCCAAGGTGGGCAGATCACTGGAGGTCAGGAGTTTCG					
*661	*671	*681	*691	*701	*711
AAACCAGCCTGGCCAACATGGTGAAACCCCATCTCTACTAAAAATACAGAAATTAGCCGG					
*721	*731	*741	*751	*761	*771
TCATGGTGGTGGACACCTGTAATCCCAGCTACTCAGGTGGCTAAGGCAGGAGAATCACTT					
*781	*791	*801	*811	*821	*831
CAGCCCGGGAGGTGGAGGTTGCAGTGAGCCAAGATCATACCACGGCACTCCAGCCTGGGT					
*841	*851	*861	*871	*881	*891
GACAGTGAGACTGTGGCTCAAAAAAAAAAAAAAAAAAGGAAAATGAACTAGAAGAGAT					
*901	*911	*921	*931	*941	*951
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*961	*971	*981	*991	*1001	*1011
GATTTTCAAGAACCGGTTTCCAAAGACAGTCTTCTAATTCCTCATTAGTAATAAGTAAAA					
*1021	*1031	*1041	*1051	*1061	*1071
TGTTTATTGTTGTAGCTCTGGTATATAATCCATTCCTCTTAAAAATATAAGACCTCTGGCA					
*1081	*1091	*1101	*1111	*1121	*1131
TGAATATTTTATATCTATAAAATGACAGATCCCACCAGGAAGGAAGCTGTTGCTTTCTTT					
*1141	*1151	*1161	*1171	*1181	*1191
GAGGTGATTTTTTCTTTGCTCCCTGTTGCTGAAACCATACAGCTTCATAAATAATTTT					

|*1201 |*1211 |*1221 |*1231 |*1241 |*1251
 GCTTGCTGAAGGAAGAAAAAGTGTTCATTAACCCATTATCCAGGACTGTTTATAGCT

|*1261 |*1271 |*1281 |*1291 |*1301 |*1311
 GTTGGAAGGACTAGGTCTTCCTAGCCCCCAGTGTGCAAGGGCAGTGAAGACTTGATT

|*1321 |*1331 |*1341 |*1351 |*1361 |*1371
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|*1381
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LRG Parser: Version: 1.3, Version Date: 11/02/2015
Reader: Version: 1.3, Version Date: 11/02/2015
Writer: Version: 1.3, Version Date: 11/02/2015
Control: Version: 1.3, Version Date: 11/02/2015