

Gene: PALB2 - Sequence: NG_007406.1
 Transcript: NM_024675.3 - Protein: NP_078951.2
 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: 5001 | End: 5248 | Length: 247

```

. . . . .
aacgccgaccaggcctcaaagggacgcaggggttgaaagaggaggatacatatctggacc

. . . . .
cgcgccacggtctcgatgtactcagacttgttgtagagcagctcgcccaactccatggccg

. . . . .
ccgcctccttccctcagccccggatcctgtcagagtcagtcggtcagtccttcagagatt

. . . . .
ccggctacttccggccgctcctccacttccgctccagggtggcccactgggactcatcgac

. . . . .
agcgcggtctccttttaggcggcctcgtccactgctcggccgtctacggctgcgcgtgc

|-199      |-189      |-179      |-169      |-159      |-149
GCAGGCCGAATGGTGGATTTAATTGGCCGAGTTTAGGGCGCGCTTGGCCCGCGTGGGTC

|-139      |-129      |-119      |-109      |-99       |-89
AGCTGATCGCGCACTGAGGGTGCGATCCCGGGCTCCCCATTCCTTCCTGGGGCGCCTCCC

|-79       |-69       |-59       |-49       |-39       |-29
CGGCCCAGGGCCAACTGGGTCCCGGTGTCGGCAGGCCTGGGGTCGGCGACGGCTGCTCTT

|-19       |-9        |1         |11        |21        |31
TTCGTTCTGTCGCCTGCCCGATGGACGAGCCTCCCGGGAAGCCCCTCAGCTGTGAGGAGA
      M D E P P G K P L S C E E K
      |1                               |11

|41
AGGAAAAGgtgccgggggtgcgggaagggcggacgcaggactctgaccccgctttccag
E K

```

ggttttaggcctggctttgtgtcctcggcagtcgagggcagcagtatcatctgaccacc
ccctcctcttagggctgagggggcacagaaaatgaaaatgtggaaatagcgtgggtgtca
cgtggtggcgtttaaagaacaaatttcattacagtagcagcgattaataacaatgtgtaa
cagtttgtagataaagctgtatcgacacccttgctcctccccctcccacaccctcaatc
tttacttc

Exon 2 | Start: 8229 | End: 8288 | Length: 59
BE AWARE: Flanking intron is shared with the following exon

```
. . . . .
gtctaacctagatTTGGAGAAGGACCTAGAAGTCTATCCCAGGGAAATAAAAATCTAAGC
. . . . .
taaggTTTGAGGAATCAGTAGGAATTGGCAAAGGAAGGACATGTTCCAGATGATAGGAAC
. . . . .
aggTTATGCAAAGATCCTGAAATGGTCAGAGCTTGGTGCTTTTTGAGAACCAAAAGTAGA
. . . . .
TTGTTATGGACCAGTGCTACTCCCTGCCTCTTGCCAAGGGACCCGCAAGCACTGCATC
. . . . .
ccttccctctgactccacctttccacttgcccagTATTGTTGGTGTTTTCTTCTTCCAG
|51      |61      |71      |81      |91      |101
TTAAAGGAGAAATTAGCATTCTTGAAAAGGGAATACAGCAAGACACTAGCCCGCCTTCAG
L  K  E  K  L  A  F  L  K  R  E  Y  S  K  T  L  A  R  L  Q
      |21                                |31
. . . . .
gtaagtgaatcgtattctcaaattaaggTGTtatagtacaaacaatttaaaaacagtt
```

Exon 3 | Start: 8406 | End: 8508 | Length: 102
 BE AWARE: Flanking intron is shared with the previous exon

.
 cttgactctataaaactttaagaaaacgtattttctggggctgtttttgtctcctctagC
 R

111	121	131	141	151	161
GTGCCCAAAGAGCTGAAAAGATTAAGCATTCTATTAAGAAAACAGTAGAAGAACAAGATT					
A	Q	R	A	E	K
			I	K	H
			S	I	K
			K	T	V
				E	E
				Q	D
				C	
		41		51	

171	181	191	201	211	.	.	.
GTTTGTCTCAGCAGGATCTCTCACC GCAGCTAAAACACTCAGgtaaatctagaccattca							
L	S	Q	Q	D	L	S	P
					Q	L	K
					H	S	E
		61				71	

.
 cttatgcctgctttattattcatttcccaggtatattttggctattgttctttttcccac

.
 agtgtgaagataatgactagcaatagacgctttaattttaattttaattttaattttatt

.
 tttttgagacagagtctcactctttgttaccaggctggagtgcagtggcacaatcttgg

.
 ctcactacaacctccaactcccaggctcaagtgattctcgtgcctcagcctcctgagtag

.
 ctgggactacaggcacgtgcactaccacacctgactaattgt

Exon 4 | Start: 10024 | End: 11496 | Length: 1472

.
tcagaacttttaaaaaatatgtacagtatggagtatgtacagttcctttacatactccatc

.
agatagtagaagtagtcaacaccttgaacacattcctcctaaaggtaacagtgaccttac

.
tactcacagcctaaaaaataggtttatttcacctgtaaattcatctgcctgaatgaaatg

.
tcactgattctttcttaaaataaatgtttagtagtatttatataataaggttaaaaatga

.
gtatTTTTTgttttattttataagaaaaatataagttatatacatTTTTTcctcctcag

 |221 |231 |241 |251 |261 |271
AACCTAAAAATAAAATATGTGTTTATGACAAGTTACACATCAAAACCCATCTTGATGAAG
 P K N K I C V Y D K L H I K T H L D E E
 |81 |91

 |281 |291 |301 |311 |321 |331
AAACTGGAGAAAAGACATCTATCACACTTGATGTTGGGCCTGAGTCCTTTAACCCTGGAG
 T G E K T S I T L D V G P E S F N P G D
 |101 |111

 |341 |351 |361 |371 |381 |391
ATGGCCCAGGAGGATTACCTATACAAAGAACAGATGACACCCAAGAACATTTTCCCCACA
 G P G G L P I Q R T D D T Q E H F P H R
 |121 |131

 |401 |411 |421 |431 |441 |451
GGGTCAGTGACCCTAGTGGTGAGCAAAAGCAGAAGCTGCCAAGCAGAAGAAAGAAGCAGC
 V S D P S G E Q K Q K L P S R R K K Q Q
 |141 |151

 |461 |471 |481 |491 |501 |511
AGAAGAGGACATTTATTTTACAGGAGAGAGACTGTGTCTTTGGCACTGATTCACCTCAGAT
 K R T F I S Q E R D C V F G T D S L R L
 |161 |171

521	531	541	551	561	571
TGTCTGGGAAAAGACTAAAGGAACAGGAAGAAATCAGTAGCAAAAATCCTGCTAGATCAC					
S	G	K	R	L	K
E	Q	E	E	I	S
S	S	K	N	P	A
R	S	P			
		181			191
581	591	601	611	621	631
CAGTAACTGAAATAAGAACTCACCTTTTAAAGTCTTAAATCTGAACTTCCAGATTCTCCAG					
V	T	E	I	R	T
H	L	L	S	L	K
S	E	L	P	D	S
P	E				
		201			211
641	651	661	671	681	691
AACCAGTTACAGAAATTAATGAAGACAGTGTATTAATTCCACCAACTGCCCAACCAGAAA					
P	V	T	E	I	N
E	D	S	V	L	I
P	P	T	A	Q	P
E	K				
		221			231
701	711	721	731	741	751
AAGGTGTTGATACATTCCCTAAGAAGACCTAATTTACCAGGGCGACTACAGTTCCTTTAC					
G	V	D	T	F	L
R	R	P	N	F	T
R	A	T	T	V	P
L	Q				
		241			251
761	771	781	791	801	811
AGACTCTATCAGATAGCGGTAGTAGTCAGCACCTTGAACACATTCCCTCCTAAAGGTAGCA					
T	L	S	D	S	G
S	S	Q	H	L	E
H	I	P	P	K	G
S					
		261			271
821	831	841	851	861	871
GTGAACTTACTACTCACGACCTAAAAACATTAGATTTACTTCACCTGTAAGTTTGGAGG					
E	L	T	T	H	D
L	K	N	I	R	F
T	S	P	V	S	L
E	A				
		281			291
881	891	901	911	921	931
CACAAAGGCAAAAAATGACTGTCTCTACAGATAACCTCCTTGTAATAAAGCTATAAGTA					
Q	G	K	K	M	T
V	S	T	D	N	L
L	V	N	K	A	I
S	K				
		301			311
941	951	961	971	981	991
AAAGTGGCCAACTGCCACAAAGTTCTAATTTAGAGGCAAATATTTTCATGTTCTCTAAATG					
S	G	Q	L	P	T
S	S	N	L	E	A
N	I	S	C	S	L
N	E				
		321			331
1001	1011	1021	1031	1041	1051
AACTCACCTACAATAACTTACCAGCAAATGAAAACCAAACTTAAAAGAACAAAATCAAA					
L	T	Y	N	N	L
P	A	N	E	N	Q
N	L	K	E	Q	N
Q	T				
		341			351

1061	1071	1081	1091	1101	1111
CAGAGAAATCTTTAAAAATCTCCAGTGACACTCTTGATGGCAGGAATGAAAATCTTCAGG					
E	K	S	L	K	S
P	S	D	T	L	D
G	R	N	E	N	L
Q	E				
			361		
371					
1121	1131	1141	1151	1161	1171
AAAGTGAGATTCTAAGTCAACCTAAGAGTCTTAGCCTGGAAGCAACCTCTCCTCTTTCTG					
S	E	I	L	S	Q
P	K	S	L	S	L
E	A	T	S	P	L
S	A				
			381		
391					
1181	1191	1201	1211	1221	1231
CAGAAAAACATTCTTGACAGTGCCTGAAGGCCTTCTGTTTCCTGCAGAATATTATGTTA					
E	K	H	S	C	T
V	P	E	G	L	L
F	P	A	E	Y	Y
V	R				
			401		
411					
1241	1251	1261	1271	1281	1291
GAACAACACGAAGCATGTCCAATTGCCAGAGGAAAGTAGCCGTGGAGGCTGTCATTGAGA					
T	T	R	S	M	S
N	C	Q	R	K	V
A	V	E	A	V	I
Q	S				
			421		
431					
1301	1311	1321	1331	1341	1351
GTCATTTGGATGTCAAGAAAAAAGGGTTTAAAAATAAAAAATAAGGATGCAAGTAAAAATT					
H	L	D	V	K	K
K	G	F	K	N	K
N	K	D	A	S	K
N	L				
			441		
451					
1361	1371	1381	1391	1401	1411
TAAACCTTTCCAATGAGGAACTGACCAAAGTGAAATTAGGATGTCTGGCACATGCACAG					
N	L	S	N	E	E
T	D	Q	S	E	I
R	M	S	G	T	C
T	G				
			461		
471					
1421	1431	1441	1451	1461	1471
GACAACCAAGTTCAAGAACCCTCTCAGAACTTCTCTCATTAAGTAAAGTCAGCTCTCCCG					
Q	P	S	S	R	T
S	Q	K	L	L	S
L	T	K	V	S	S
P	A				
			481		
491					
1481	1491	1501	1511	1521	1531
CTGGGCCCCACTGAAGATAATGACTTGTCTAGGAAGGCAGTTGCCCAAGCACCTGGTAGAA					
G	P	T	E	D	N
D	L	S	R	K	A
V	A	Q	A	P	G
R	R				
			501		
511					
1541	1551	1561	1571	1581	1591
GATACACAGGAAAAAGAAAAATCAGCCTGCACCCCAGCATCAGATCATTGTGAACCACTTT					
Y	T	G	K	R	K
S	A	C	T	P	A
S	D	H	C	E	P
L	L				
			521		
531					

1601	1611	1621	1631	1641	1651
TGCCAACCTTCTAGCCTGTCGATTGTTAACAGGTCCAAGGAAGAAGTCACCTCACACAAAT					
P	T	S	S	L	S
				I	V
				N	R
				S	K
				E	E
				V	T
				S	H
				K	Y
			541		551

1661	1671	1681
ATCAGCACGAAAAATTATTTATTCAAGTGAAAGgtaaatcaagatgtggttgatgatgat							
Q	H	E	K	L	F	I	Q
						V	K
						G	
						561	

.
gatgatgatgatgaaagttaacaattactatgtgctggcacttccttttctttcttttc

.
taaaaagtgacagggccaagtgtggtggcttacgtctgtaatcccagcactttgggaggc

.
tgaggaacagagtgagaccctggctcaaaaaatttaataaataaataaataaataaat

.
aaataaataaataaaaaataaagagacaggggctcactgttgtccaggctggagtgccgtg

.
gtgcagcctctatctcctgggctcaaagtgtcc

Exon 5 | Start: 15889 | End: 16718 | Length: 829

.
tgaccggtgtttgaacccttcgccaagtttctgagtcatggatgggaaaagtaatgaac
.
atTTTTtagtatatttgagtttagaagctcactctttggtgggtattacatttaagaatg
.
gtttaacatgtttctttgataggacttcattgtaaacattaagttcattctggggaaatt
.
aagggttcattaaaaatgtttcttttaaacttaggagatcctattctctttgtcatcagtga
.
aacagattgtctgttttgttgggtttgttactattttgtgacttatttttcttcttttag

|1691 |1701 |1711 |1721 |1731 |1741
GGAAGAAAAGTCGTCATCAAAAAGAGGATTCCCTTTCTTGGAGTAATAGTGCTTATTTAT
K K S R H Q K E D S L S W S N S A Y L S
|571 |581

|1751 |1761 |1771 |1781 |1791 |1801
CCTTGGATGATGATGCTTTCACGGCTCCATTTTCATAGGGATGGAATGCTGAGTTTAAAGC
L D D D A F T A P F H R D G M L S L K Q
|591 |601

|1811 |1821 |1831 |1841 |1851 |1861
AACTACTGTCTTTTCTCAGTATCACAGACTTTCAGTTACCTGATGAAGACTTTGGACCTC
L L S F L S I T D F Q L P D E D F G P L
|611 |621

|1871 |1881 |1891 |1901 |1911 |1921
TTAAGCTTGAAAAAGTGAAGTCCTGCTCAGAAAAACCAGTGGAGCCCTTTGAGTCAAAAA
K L E K V K S C S E K P V E P F E S K M
|631 |641

|1931 |1941 |1951 |1961 |1971 |1981
TGTTTGGAGAGAGACATCTTAAAGAGGGAAGCTGTATTTTTCCAGAGGAAGTGAAGTCTTA
F G E R H L K E G S C I F P E E L S P K
|651 |661

1991	2001	2011	2021	2031	2041
AACGCATGGATACAGAAATGGAGGACTTAGAAGAGGACCTTATTGTTCTACCAGGAAAAT					
R	M	D	T	E	M
			D	L	E
			E	D	L
			I	V	L
			P	G	K
			S		
			671		681
2051	2061	2071	2081	2091	2101
CACATCCCAAAAGGCCAAACTCGCAAAGCCAGCATACAAAGACGGGCCTTTCTTCATCCA					
H	P	K	R	P	N
		S	Q	S	Q
		H	T	K	T
		G	L	S	S
		S	S	S	I
		691			701
2111	2121	2131	2141	2151	2161
TATTACTTTATACTCCTTTAAATACGGTTGCGCCTGATGATAATGACAGGCCTACCACAG					
L	L	Y	T	P	L
		N	T	V	A
		P	D	D	N
		D	R	P	T
		711			721
2171	2181	2191	2201	2211	2221
ACATGTGTTACCTGCTTTCCCATCTTAGGTACTACTCCAGCCTTTGGCCCTCAAGGCT					
M	C	S	P	A	F
		P	I	L	G
		T	T	P	A
		F	G	P	Q
		731			741
2231	2241	2251	2261	2271	2281
CCTATGAAAAAGCATCTACAGAAGTTGCTGGACGAACTTGCTGCACACCCCAACTTGCTC					
Y	E	K	A	S	T
		E	V	A	G
		R	T	C	C
		751			761
2291	2301	2311	2321	2331	2341
ATTTGAAAGACTCAGTCTGTCTTGCCAGTGATACTAAACAATTCGACAGTTCAGGCAGCC					
L	K	D	S	V	C
		L	A	S	D
		T	K	Q	F
		771			781
2351	2361	2371	2381	2391	2401
CAGCAAAACCACATACCACCCTGCAAGTGTGAGGCAGGCAAGGACAACCTACCTGTGACT					
A	K	P	H	T	T
		L	Q	V	S
		G	R	Q	G
		791			801
2411	2421	2431	2441	2451	2461
GTGACTCTGTCCCGCCAGGAACACCTCCACCCATTGAGTCATTCACTTTTAAAGAAAATC					
D	S	V	P	P	G
		T	P	P	P
		I	E	S	F
		811			821
2471	2481	2491	2501	2511	.
AGCTCTGTAGAAACACATGCCAGGAGCTGCATAAACATTCCGTCGAACAGgtacaatcca					
L	C	R	N	T	C
		Q	E	L	H
		K	H	S	V
		831			

tttcctctgtgaaat t t t t c t c t g a a g g a a t g a a a t g c c t t a g t g a a t g t a a a c a g c a t g a
c t t g c t t g c g c a t t g g g c c t t c c a c g t t t a a g a a t g g t t t g a c g t g t t t c t t t g a t a t g a
t t t c a t t g t a a t c a t t a a g t t c a t t c t g g g g a a a t t a a g g t t c a t t a a a a t g t t t c t t t
a a a t a t g g g a g g t c c t a t t c t c t t t g t t a t c a g t g a a a c a g t t t g c a t t t g g a g c t t t g c
t g c t g t t a t a a g a g g a a a t a a g a c a a t a c g a a g t a g a c a t t t t g a t g a g

Exon 6 | Start: 17083 | End: 17154 | Length: 71

.
gcatgacttgcttgcgcatcgggcctccacgtttaagaatggtttgacgtgtttccttg

.
atatgatttcattgtaatcattaagttcattctggggaaattaagggttcattaaaatgtt

.
tcttttaaataatgggaggtcctattctctttgttatcagtgaaacagtttgcatcgttgag

.
ctttgctgctgttataagaggaaataaagacaatacgaagtagacattttgatgagtggtg

.
taatgcaggcagacattatacataaagtgtagactaatgatgtgacttttgttttcacag

 |2521 |2531 |2541 |2551 |2561 |2571
ACTGAAACAGCAGAGCTTCCTGCTTCTGATAGCATAAACCCAGGCAACCTACAATTGGTT
T E T A E L P A S D S I N P G N L Q L V
 |841 |851

 |2581
TCAGAGTTAAAGgtcagaagaatattctcttccagtggtctcgtgtcttacatatgaaaac
S E L K
 |861

.
tttaatgaactgaaaagaattcagtcatatagcttcttggttctttaataactattaaagat

.
attggtaaacagattcagaaaaacagatttggttggttatttttcccaatatttacctc

.
tgtttatgttttgagctctcctcttaaagtttctatgccaacctattggcaagaacaact

.
taggctaagtaactgaacttcattgtctaaatctaagttaggagctgggcacggtggctc

. . . .
accctataatc

Exon 7 | Start: 19961 | End: 20122 | Length: 161

```
. . . . .
gtaagccgagattgcaccactgcactccagcctgggtgataaaagtgagactcagtcctcaa

. . . . .
aaacaccccaaaaattaaaattaataaaaataaaaaataaaaatctttcatgatgtaag

. . . . .
tttgataggcatttttttaggtacataagaaccacaaagctctttcttttcacctgcata

. . . . .
agacttaaattttacatacctactgtttcattgaattataattcatcactttgcatactt

. . . . .
atgctttgcataaaacagcactcgagtgccactttaacagaactgttgccattgtgtcag

      |2591      |2601      |2611      |2621      |2631      |2641
AATCCTTCAGGTTCCGTAGATGTGAGTGCCATGTTTTGGGAAAGAGCCGTTGT
N P S G S C S V D V S A M F W E R A G C
                        |871                        |881

      |2651      |2661      |2671      |2681      |2691      |2701
AAAGAGCCATGTATCATAACTGCTTGCGAAGATGTAGTTTCTCTTTGGAAAGCTCTGGAT
K E P C I I T A C E D V V S L W K A L D
                        |891                        |901

      |2711      |2721      |2731      |2741      . . .
GCTTGGCAGTGGGAAAACTTTATACCTGGCACTTCGCAGAGgtaagtgggaatctcgag
A W Q W E K L Y T W H F A E
                        |911

. . . . .
ctgaaagagatctttgcagccatttgcttgataatgtagatgggcagcttaccaaaattg

. . . . .
ggagctatgaccatgcaaggcagaacagagatgagggttttttccaacattttattatg

. . . . .
aaaagtttcaaacatccagaaaagttgtatagtgagcacccatatacccaccattctaga

. . . . .
ctctaccattaacatcctgctttgttcgctttatcacaaatttttgtttgtttggttgag

. . . . .
acaggggtctcactctgtcatgcaggctggagtgcagtggcat
```

Exon 8 | Start: 22264 | End: 22349 | Length: 85

```
. . . . .
tatacttttaaagtggctgcataaatattctttacattcacatgccaaaatataaccaatt

. . . . .
attcccctattggttagaattataccttg cattaggtaaatgctcagtaagcactattatg

. . . . .
ctattatgcatatagtttatttagatttacagctaataaaaaagagttttctgagccttca

. . . . .
aatgatgaaaattatccttg tacagtgagaatacaaaaagaatgtgataaattttggaaaa

. . . . .
tctggattaaacaaaaatgaaacaaccaagcataatttttggctgctttgttttatttag

|2751      |2761      |2771      |2781      |2791      |2801
GTTCCAGTATTACAGATAGTTCCAGTGCCTGATGTGTATAATCTCGTGTGTGTAGCTTTG
V P V L Q I V P V P D V Y N L V C V A L
|921                      |931

|2811      |2821      |2831      . . . . .
GGAAATTTGGAAATCAGAGAGATCAGgtatgtaattcccaaggagtgatttgtttttcct
G N L E I R E I R
|941

. . . . .
tcatcctttgtctctgtcagctggttttaagtgcaggtaataacctaggcttgagtcttga

. . . . .
aagaatctgaaagatctaaagagagagagatttgtttaaaaaaaaaatcaatagaatgaca

. . . . .
tccttgactgaagtttctattttaaagtgaacctaggctggcgagtggtcacgcct

. . . . .
gtaatcccagcactttgggaggccaaggaaggtggatcaactgaggtcaggagtttgaga

. . . . .
ccagcctggccaacatggtgaaactg
```

Exon 9 | Start: 23228 | End: 23389 | Length: 161

.
ggagttcgagaccagcctgaccaacatggtgaaaccccgctctctacaaaaatacagaaaa

.
attagccagggtgtggtggtgcgcacctataatcccagctactcaggagggtgaggcagga

.
cagtcgcttgaacctgggaggcagagttgcagtgagccaagattgtgccactgcactcca

.
gcctaggcgacagagcaagactctgtctcaaaaaaaaaaaaaaaaaaaaaagtgaacctag

.
tcctttaataattaaaagggttactcctcacatcacccatttttccttatatttggttag

 |2841 |2851 |2861 |2871 |2881 |2891
GGCATTGTTTTGTTTCCTCTGATGATGAAAAGTAAAAAGCAAGTACTACTGAAGTCTGGAAA
A L F C S S D D E S E K Q V L L K S G N
 |951 |961

 |2901 |2911 |2921 |2931 |2941 |2951
TATAAAAGCTGTGCTTGGCCTGACAAAGAGGAGGCTAGTTAGTAGCAGTGGGACCCTTTC
I K A V L G L T K R R L V S S S G T L S
 |971 |981

 |2961 |2971 |2981 |2991 . . .
TGATCAACAAGTAGAAGTCATGACGTTTGCAGAAAGATGGAGGgtaagaaaagcattgatt
D Q Q V E V M T F A E D G G
 |991

.
gatttttaactattagatgaagaatgattttatcacagggttcagagaaagttgggtaac

.
taggatctcgtttttctgtgctgggggtgtaataaagcatgtaccgcatcaacactagg

.
ttatgacatagaagcaggttagtgagggtggaagccagacatgtcagggatgaagtcaaag

.
aagggtgagaggctcagcaaatgtagtttgttcttcagtcttcttgaaatctgtgtgtccc

.
ttaaatgttagaaaatacctctgctgggcacagtggctcatgc

Exon 10 | Start: 24880 | End: 24996 | Length: 116

```
. . . . .
ttagatggtgatgcaattcattgagataggaatgcagaaagaaacaaaaggtttatagaa

. . . . .
aaagttaacaagtttaattttgaatataatgaattcgagggtgcttgccagcatatctaggt

. . . . .
agatattatgaaagtaatatatgttcattgtagaaagtttagtatacacgttttctgggt

. . . . .
tagatTTTTTTTcctgatattaggttagtttatattatgcagttcaacaatgcggagaa

. . . . .
gggctacctagagactgctttagtgcaggactgacttttcatactgtttaattacag

      |3001      |3011      |3021      |3031      |3041      |3051
AGGCAAAGAAAACCAATTTTGTGATGCCCCCTGAGGAGACTATACTAACTTTTGCTGAGGT
  G  K  E  N  Q  F  L  M  P  P  E  E  T  I  L  T  F  A  E  V
      |1001                                |1011

      |3061      |3071      |3081      |3091      |3101      |3111
CCAAGGGATGCAAGAAGCTCTGCTTGGTACTACTATTATGAACAACATTGTTATTTGgta
  Q  G  M  Q  E  A  L  L  G  T  T  I  M  N  N  I  V  I  W
      |1021                                |1031

. . . . .
agctttccctctaggctcctcagttccctcatctgtagtatgaggatataacctctaatttt

. . . . .
acagggttggtgtgaagattaaataagagagtatgtgtaaacatgattgtggttttgtgt

. . . . .
tgctgttggtgtgtttttgtgtgttttgagacagagtcctccttatcaccaggtgg

. . . . .
gagtacagtggatgatctcggctcactgcaacctctgcctcctggattcaagtgattct

. . . . .
cctgcctcagcctcccgagtagctgggattataggcatgtgccaccacaccagcta
```


Exon 11 | Start: 32267 | End: 32354 | Length: 87

.
catgtgcctgatttcaataccaggttgaatgagatgatggaaccttcctcatggaatttg

.
gagagatttatccctaggggcattgtagatttaataaggaactatcaaataaac

.
tattggcaaaaattaacccacagttctacttttacctaaatctatgactaaagaaaactaa

.
ggagctcttagtccccctgggcacctcctaagacatgctatgatgaataagaaaata

.
ttttctgaatactggttgggaagaatgtgatcagcttatttattttgttatctaag

 |3121 |3131 |3141 |3151 |3161 |3171
GAATTTAAAACTGGTCAACTCCTGAAAAAGATGCACATTGATGATTCTTACCAAGCTTC
 N L K T G Q L L K K M H I D D S Y Q A S
 |1041 |1051

 |3181 |3191 |3201.
AGTCTGTACAAAGCCTATTCTGAAATGgtaagtaatgactggctgggaccactttgtgt
 V C H K A Y S E M
 |1061

.
gttactgttggctctcatgaagtgaagagcagtaagtcataagcagtaatgaacaaaccttc

.
cccggtggcatcttttttcaaaattggatagcaatgttgtcctttcttgaaatttaggat

.
gaaaataagtgttggtagcagtgattgcttggtaattttctggctgtaggacctgagggc

.
aaatattttatttctagctgtggatttgaactgagaactattatgcctgttatcagacttg

.
actcccagccacattgccatgtttaagt

Exon 12 | Start: 38346 | End: 38494 | Length: 148

.
gaggctgaggtgggaggatcccttgaggccaggtgttcaacaacagcctgggtaacacag

.
gaaggccttgctctctaaaaaaaaaagaagaacaagaagccagaagtcagtcagtcagtc

.
aataatctcaacagttccttagacggcagggaaaaaaatcaagccagtggttaaattcctgg

.
atacttcagagcctatcggtcattgctttaattgtttggtttttgtctctgccagatctt

.
tatttttcctgacatactcttgacagtcatttgggatatttatttttctccgaaattag

 |3211 |3221 |3231 |3241 |3251 |3261
GGGCTTCTCTTTATTGTCCTGAGTCATCCCTGTGCCAAAGAGAGTGAGTCGTTGCCAAGC
G L L F I V L S H P C A K E S E S L R S
 |1071 |1081

 |3271 |3281 |3291 |3301 |3311 |3321
CCTGTGTTTCAGCTCATTGTGATTAACCCTAAGACGACTCTCAGCGTGGGTGTGATGCTG
P V F Q L I V I N P K T T L S V G V M L
 |1091 |1101

 |3331 |3341
TACTGTCTTCTCCAGGGCAGGCTGGCAGgcaagtggtgcataactgctactctatgggtg
Y C L P P G Q A G R
 |1111

.
ggacattctgaaaggcactgtgcaaacacaaaaactagatatttttgtgtcacttagaag

.
aatggaaaacatgaaatactatatatcatgataggaatattcagaagtaggatgaagatt

.
agtggacttgagtcacacccagattccctgcatcctgatctctactagtatggggttat

.
atagggtttttaatagtggtttattcaagccctgttttttcccctaaggtaaataattttggc

.
agcacatggtggatcatgcctgtaatccc

Exon 13 | Start: 42689 | End: 43196 | Length: 507

```
. . . . .
gacactgagttgggactgagtttggccagagtgatggagagtggaaggaaggccactgtg

. . . . .
cgccagccttcaattgctacaagatgcatcagagagattggcaggaactggacatgtgat

. . . . .
tctgtccaaaactgcaacacaatagccaacagacctctaaggctacaaatgtaggcattc

. . . . .
atagttacagggattttttgttcctgttgctggttttgggaacatggttttgacctttttt

. . . . .
ttttttttaattgttttttggatatgtaatctgaattatatcttctttgtatgctatcag

|3351      |3361      |3371      |3381      |3391      |3401
GTCCTGGAAGGTGACGTGAAAGATCACTGTGCAGCAGCAATCTTGACTTCTGGAACAAT
 F L E G D V K D H C A A A I L T S G T I
      |1121                      |1131

|3411      |3421      |3431      |3441      |3451      |3461
TGCCATTTGGGACTTACTTCTCGGTCAGTGTACTGCCCTCCTCCCACCTGTCTCTGACCA
 A I W D L L L G Q C T A L L P P V S D Q
      |1141                      |1151

|3471      |3481      |3491      |3501      |3511      |3521
ACATTGGTCTTTTGTGAAATGGTCGGGTACAGACTCTCATTTGCTGGCTGGACAAAAAGA
 H W S F V K W S G T D S H L L A G Q K D
      |1161                      |1171

|3531      |3541      |3551      |3561      |*11      |*21
TGGAAATATATTTGTATACCACTATTTCATAAGTTAGGGTAAAGTGAAAACACAATTTTCT
 G N I F V Y H Y S *
      |1181

|*31      |*41      |*51      |*61      |*71      |*81
GGATATATTGGGCCTCTTAGTATTTTTTGGAGTTTTTAAATATAAAGGAGAATATCTGAAT

|*91      |*101     |*111     |*121     |*131     |*141
GACACTTAAAAATGATTGCTTGTATGTCCAGACAGACTTATTTTTTATTCTAATGATGG
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|*151      |*161      |*171      |*181      |*191      |*201
TAGCACCACCTGATCTTGGATGTACATTTATGTATACTTTGAGAAAAAGGGTTTTAGGTTG

|*211      |*221      |*231      |*241      |*251      |*261
ATTTTGTAAATTTCCCACATTTGTACATGTGCTTTTAAAGGTGTACATAAAGCTTCAAAT

|*271      |*281      |*291      .      .      .      .      .      .
GGCAATAAATATTTATTTTATACATTctgcttggcatgttattgtttcccattctttca

.      .      .      .      .      .      .      .      .      .
agatcatttgcagaagcaagaactaattattatacaaccaggatatttaataatcaatagtct

.      .      .      .      .      .      .      .      .      .
ttgcctagtaagtgtaaatttcagttcagttaacttactacactaatatgcaatatactt

.      .      .      .      .      .      .      .      .      .
tttgctgctatttgaataactttatttttacatacactaaaataaaaatgaaacctacta

.      .      .      .      .      .      .      .      .      .
aaatatcctaatttagggatactcttactctttttcattctcatgcatctttcatgccag

.      .      .      .      .      .
tgctgcattatcactagagtcacctttt

```

LRG Parser: Version: 1.1, Version Date: 11/02/2015
Reader: Version: 1, Version Date: 11/02/2015
Writer: Version: 1, Version Date: 11/02/2015
Control: Version: 1, Version Date: 11/02/2015