

Gene: MSH6 - Sequence: NG\_007111.1  
 Transcript: NM\_000179.2 - Protein: NP\_000170.1  
 Date : February 26, 2015

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

Exon 1 | Start: 4936 | End: 5347 | Length: 411

```

. . . . .
gccggggcgggtgcgcgccccgctgttccgcttccgctccagagaggcagggtttccg

. . . . .
agcctgctagccccgcggccgcaactaaccgccgggtcggagtgttccggcccgccagcc

. . . . .
ccgcggcgtgagggaaggggagctcagcagttccccgcgcggggcccaggcgtcggcggc

. . . . .
agggcgggcccctcaccgccagcgtgccagccccgccctaccaccagtgtgccagccc

. . . . .
cgcccttccccacgtcgccgcgcgccccggggcggggcctggcgcgcaccgccgcgcac

|-149    |-139    |-129    |-119    |-109    |-99
GGCGAGGCGCCTGTTGATTGGCCACTGGGGCCCGGGTTCCTCCGGCGGAGCGCGCCTCCC

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

|-29     |-19     |-9      |1       |11      |21
GACAGAACGGTTGGGCCTTGCCGGCTGTCGGTATGTCGCGACAGAGCACCTGTACAGCT
                               M S R Q S T L Y S F
                               |1

|31       |41       |51       |61       |71       |81
TCTTCCCAAGTCTCCGGCGCTGAGTGATGCCAACAAGGCTCGGCCAGGGCCTCACGCG
F P K S P A L S D A N K A S A R A S R E
|11       |21

|91       |101      |111      |121      |131      |141
AAGGCGGCCGTGCCGCCGCTGCCCCGGGGCCTCTCCTTCCCAGGCGGGGATGCGGCCT
G G R A A A A P G A S P S P G G D A A W

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|31                                |41

|151      |161      |171      |181      |191      |201
GGAGCGAGGCTGGGCCTGGGCCCAGGCCCTTGGCGCGCTCCGCGTCACCGCCCAAGGCGA
S E A G P G P R P L A R S A S P P K A K
|51                                |61

|211      |221      |231      |241      |251      .
AGAACCTCAACGGAGGGCTGCGGAGATCGGTAGCGCCTGCTGCCCCACCAGgtagcggg
N L N G G L R R S V A P A A P T S
|71                                |81

. . . . .
gtgggggtgggggtcgaaggcgggggcatagcggcggggcgcttggaaccggcgagggga

. . . . .
ggctcgcacagggggttgggggggtgcacggcctggccctgggctcggaggaggcggggc

. . . . .
cgcagagtggcttgaatgagtgacgggggtcgagtctggagcatttgggggtgtagcttg

. . . . .
taaacagggtcggaggagagaggctgtgcaggaagagggtgcaggggagacgcggagag

. . . . .
ttcgggccttttggagggaggagacgcgtcccgcaggtgggggtgctgggc

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Exon 2 | Start: 12781 | End: 12977 | Length: 196

```
. . . . .
ttcctgccatcagcattatacctaaattctgccatgggttttaactttgattctgagaa

. . . . .
agtttctcaccctaataacataactatatttggtgtgtcttcatagttaaataatgcatt

. . . . .
atgatatcagcttgcatatcttttttaaatgacttgaatatctgactttaaaattattc

. . . . .
tagaatttctgtgcttcaatattaatgccagaagacttgaattgtttattttaggttaa

. . . . .
ctgcctttaaggaaacttgaccaaataactaagttatgtatttccttttggaacag

|261      |271      |281      |291      |301      |311
TTGTGACTTCTCACCAGGAGATTTGGTTTGGGCCAAGATGGAGGGTTACCCCTGGTGGCC
 C D F S P G D L V W A K M E G Y P W W P
      |91                      |101

|321      |331      |341      |351      |361      |371
TTGTCTGGTTTACAACCACCCCTTTGATGGAACATTCATCCGCGAGAAAGGGAAATCAGT
 C L V Y N H P F D G T F I R E K G K S V
      |111                      |121

|381      |391      |401      |411      |421      |431
CCGTGTTTCATGTACAGTTTTTTTGATGACAGCCCAACAAGGGGCTGGGTAGCAAAAGGCT
 R V H V Q F F D D S P T R G W V S K R L
      |131                      |141

|441      |451      . . . . .
TTTAAAGCCATATACAGgtaagagtcactactgccatgtgtgtgtgtttgtgtgtgtg
 L K P Y T G
      |151

. . . . .
tgtgtgtgtgagagaaacagacagacagcagacttttttctatatgatgaaattaagt

. . . . .
tattttacccagtaaattgcaaggggtggcagttgtgaaagcttctggcatgggaaagg

. . . . .
gatgtaacatgggtcttttagctgggtttgtttgtggaatggaatttttatttctgtccttt
```

. . . . .  
gagtgacttacagcaatattatacccttaataagggtaaactaaactgtcccccatctt

. . . .  
gaagggtccaagagaaa

Exon 3 | Start: 17748 | End: 17917 | Length: 169

```
. . . . .
tagctgggactacaggcgacaccaccacctggctaatttttgatTTTTTTTTTggg

. . . . .
agagatgggggtttcaccacattgccaggctggtcctgaattcctgacctcaagtagtcc

. . . . .
gcccacctaagcctcccaaagtgtgggattacaggcgtgagccaccacacctggcatat

. . . . .
atatattttaagatagagatgggggttgctatgttgccaggctggtcctgaactgctgg

. . . . .
gattacaggcgtgagcctctgcaccggcccttattgtttataaatacatTTTcttcttag

      |461      |471      |481      |491      |501      |511
GTTCAAAATCAAAGGAAGCCCAGAAGGGAGGTCATTTTACAGTGCAAAGCCTGAAATAC
  S  K  S  K  E  A  Q  K  G  G  H  F  Y  S  A  K  P  E  I  L
                        |161                                |171

      |521      |531      |541      |551      |561      |571
TGAGAGCAATGCAACGTGCAGATGAAGCCTTAAATAAAGACAAGATTAAGAGGCTTGAAT
  R  A  M  Q  R  A  D  E  A  L  N  K  D  K  I  K  R  L  E  L
                        |181                                |191

      |581      |591      |601      |611      |621      . . .
TGGCAGTTTGTGTATGAGCCCTCAGAGCCAGAAGAGGAAGAAGAGATGGAGgtgggacacg
  A  V  C  D  E  P  S  E  P  E  E  E  E  E  M  E
                        |201

. . . . .
gcaagcattcagttgttatttatgttaggggtgatgggggaagaaagggggagggtgtatt

. . . . .
aacaagataccttgTTTTatatatgtgtgtgtatatgtattattttattatacatcatg

. . . . .
catacttctgtagttccctggactgtaggataagttagggtacttagaatctcaacagct

. . . . .
agcatcgTTTTtacttaggttttcaagcctactggcagggtgaagcaagaggtagtaccat

. . . . .
tttggtgaagaagtagagagctagggacagtaaagatggagtaatatatat
```

Exon 4 | Start: 20465 | End: 23009 | Length: 2544

. . . . .  
aaacgtgtttaatacacctacccaccgaatattgtagcttgggcgtagcctaacctatc  
. . . . .  
tcagacgtgctcagaacactttaatgtagcctaaagttgggcaagatcatctaacacaa  
. . . . .  
agcctattttataataaggaattgcctatctcatgtaattcatcgaatactgtactaaaa  
. . . . .  
atgaaaaacagtggctgcacgggtaccattataaagtcaaaaaatcataagttgaactgt  
. . . . .  
cttacattatgggttttccaaattttgatttgtttttaaatactctttccttgccctggcag

      |631      |641      |651      |661      |671      |681  
GTAGGCACAACCTTACGTAACAGATAAGAGTGAAGAAGATAATGAAATTGAGAGTGAAGAG  
V G T T Y V T D K S E E D N E I E S E E  
      |211                  |221

      |691      |701      |711      |721      |731      |741  
GAAGTACAGCCTAAGACACAAGGATCTAGGCGAAGTAGCCGCCAAATAAAAAACGAAGG  
E V Q P K T Q G S R R S S R Q I K K R R  
      |231                  |241

      |751      |761      |771      |781      |791      |801  
GTCATATCAGATTCTGAGAGTGACATTGGTGGCTCTGATGTGGAATTTAAGCCAGACACT  
V I S D S E S D I G G S D V E F K P D T  
      |251                  |261

      |811      |821      |831      |841      |851      |861  
AAGGAGGAAGGAAGCAGTGATGAAATAAGCAGTGGAGTGGGGGATAGTGAGAGTGAAGGC  
K E E G S S D E I S S G V G D S E S E G  
      |271                  |281

      |871      |881      |891      |901      |911      |921  
CTGAACAGCCCTGTCAAAGTTGCTCGAAAGCGGAAGAGAATGGTGACTGGAAATGGCTCT  
L N S P V K V A R K R K R M V T G N G S  
      |291                  |301

      |931      |941      |951      |961      |971      |981  
CTTAAAAGGAAAAGCTCTAGGAAGGAAACGCCCTCAGCCACCAAACAAGCAACTAGCATT  
L K R K S S R K E T P S A T K Q A T S I  
      |311                  |321

991	1001	1011	1021	1031	1041
TCATCAGAAACCAAGAATACTTTGAGAGCTTTCTCTGCCCTCAAAATTCTGAATCCCAA					
S	S	E	T	K	N
T	L	R	A	F	S
A	P	Q	N	S	E
S	S	Q			
331		341			
1051	1061	1071	1081	1091	1101
GCCCACGTTAGTGGAGGTGGTGATGACAGTAGTCGCCCTACTGTTTGGTATCATGAAACT					
A	H	V	S	G	G
G	D	D	S	S	R
P	T	V	W	Y	H
E	T				
351		361			
1111	1121	1131	1141	1151	1161
TTAGAATGGCTTAAGGAGGAAAAGAGAAGAGATGAGCACAGGAGGAGCCTGATCACCCC					
L	E	W	L	K	E
E	K	R	R	D	E
H	R	R	R	P	D
H	P				
371		381			
1171	1181	1191	1201	1211	1221
GATTTTGATGCATCTACACTCTATGTGCCTGAGGATTTCCCTCAATTCTGTACTCCTGGG					
D	F	D	A	S	T
L	Y	V	P	E	D
F	L	N	S	C	T
P	G				
391		401			
1231	1241	1251	1261	1271	1281
ATGAGGAAGTGGTGGCAGATTAAGTCTCAGAACTTTGATCTTGTCTCATCTGTTACAAGGTG					
M	R	K	W	W	Q
I	K	S	Q	N	F
D	L	V	I	C	Y
K	V				
411		421			
1291	1301	1311	1321	1331	1341
GGGAAATTTTATGAGCTGTACCACATGGATGCTCTTATTGGAGTCAGTGAAGTGGGGCTG					
G	K	F	Y	E	L
Y	H	M	D	A	L
I	G	V	S	E	L
G	L				
431		441			
1351	1361	1371	1381	1391	1401
GTATTCATGAAAGGCAACTGGGCCATTCTGGCTTTCCTGAAATTGCATTGGCCGTAT					
V	F	M	K	G	N
W	A	H	S	G	F
P	E	I	A	F	G
R	Y				
451		461			
1411	1421	1431	1441	1451	1461
TCAGATTCCCTGGTGCAGAAGGGCTATAAAGTAGCACGAGTGAACAGACTGAGACTCCA					
S	D	S	L	V	Q
K	G	Y	K	V	A
R	V	E	Q	T	E
T	P				
471		481			
1471	1481	1491	1501	1511	1521
GAAATGATGGAGGCACGATGTAGAAAGATGGCACATATATCCAAGTATGATAGAGTGGTG					
E	M	M	E	A	R
C	R	K	M	A	H
I	S	K	Y	D	R
V	V				
491		501			

1531	1541	1551	1561	1571	1581
AGGAGGGAGATCTGTAGGATCATTACCAAGGGTACACAGACTTACAGTGTGCTGGAAGGT					
R	R	E	I	C	R
I	I	T	K	G	T
Q	T	Y	S	V	L
E	G				
511			521		
1591	1601	1611	1621	1631	1641
GATCCCTCTGAGAACTACAGTAAGTATCTTCTTAGCCTCAAAGAAAAAGAGGAAGATTCT					
D	P	S	E	N	Y
S	K	Y	L	L	S
L	K	E	K	E	E
D	S				
531			541		
1651	1661	1671	1681	1691	1701
TCTGGCCATACTCGTGCATATGGTGTGTGCTTTGTTGATACTTCACTGGGAAAGTTTTTC					
S	G	H	T	R	A
Y	G	V	C	F	V
D	T	S	L	G	K
F	F				
551			561		
1711	1721	1731	1741	1751	1761
ATAGGTCAGTTTTTCAGATGATCGCCATTGTTTCGAGATTTAGGACTCTAGTGGCACACTAT					
I	G	Q	F	S	D
D	R	H	C	S	R
F	R	T	L	V	A
H	Y				
571			581		
1771	1781	1791	1801	1811	1821
CCCCCAGTACAAGTTTTATTTGAAAAAGGAAATCTCTCAAAGGAAACTAAAAACAATTCTA					
P	P	V	Q	V	L
F	E	K	G	N	L
S	K	E	T	K	T
I	L				
591			601		
1831	1841	1851	1861	1871	1881
AAGAGTTCATTGTCCTGTTCTCTTCAGGAAGGTCTGATACCCGGCTCCCAGTTTTGGGAT					
K	S	S	L	S	C
S	L	Q	E	G	L
I	P	G	S	Q	F
W	D				
611			621		
1891	1901	1911	1921	1931	1941
GCATCCAAAACCTTTGAGAACTCTCCTTGAGGAAGAATATTTTAGGGAAAAGCTAAGTGAT					
A	S	K	T	L	R
T	L	L	E	E	E
Y	F	R	E	K	L
S	D				
631			641		
1951	1961	1971	1981	1991	2001
GGCATTGGGGTGATGTTACCCCAGGTGCTTAAAGGTATGACTTCAGAGTCTGATTCCATT					
G	I	G	V	M	L
P	Q	V	L	K	G
M	T	S	E	S	D
S	I				
651			661		
2011	2021	2031	2041	2051	2061
GGGTTGACACCAGGAGAGAAAAAGTGAATTGGCCCTCTCTGCTCTAGGTGGTTGTGTCTTC					
G	L	T	P	G	E
K	S	E	L	A	L
S	A	L	G	G	C
V	F				
671			681		
2071	2081	2091	2101	2111	2121



TACCTCAAAAAATGCCTTATTGATCAGGAGCTTTTATCAATGGCTAATTTTGAAGAATAT  
Y L K K C L I D Q E L L S M A N F E E Y  
|691 |701  
|2131 |2141 |2151 |2161 |2171 |2181  
ATTCCCTTGGATTCTGACACAGTCAGCACTACAAGATCTGGTGCTATCTTCACCAAAGCC  
I P L D S D T V S T T R S G A I F T K A  
|711 |721  
|2191 |2201 |2211 |2221 |2231 |2241  
TATCAACGAATGGTGCTAGATGCAGTGACATTAAACAACCTGGAGATTTTCTGAATGGA  
Y Q R M V L D A V T L N N L E I F L N G  
|731 |741  
|2251 |2261 |2271 |2281 |2291 |2301  
ACAAATGGTTCTACTGAAGGAACCCTACTAGAGAGGGTTGATACTTGCCATACTCCTTTT  
T N G S T E G T L L E R V D T C H T P F  
|751 |761  
|2311 |2321 |2331 |2341 |2351 |2361  
GGTAAGCGGCTCCTAAAGCAATGGCTTTGTGCCCCACTCTGTAACCATTATGCTATTAAT  
G K R L L K Q W L C A P L C N H Y A I N  
|771 |781  
|2371 |2381 |2391 |2401 |2411 |2421  
GATCGTCTAGATGCCATAGAAGACCTCATGGTTGTGCCTGACAAAATCTCCGAAGTTGTA  
D R L D A I E D L M V V P D K I S E V V  
|791 |801  
|2431 |2441 |2451 |2461 |2471 |2481  
GAGCTTCTAAAGAAGCTTCCAGATCTTGAGAGGCTACTCAGTAAAATTCATAATGTTGGG  
E L L K K L P D L E R L L S K I H N V G  
|811 |821  
|2491 |2501 |2511 |2521 |2531 |2541  
TCTCCCCTGAAGAGTCAGAACCACCCAGACAGCAGGGCTATAATGTATGAAGAACTACA  
S P L K S Q N H P D S R A I M Y E E T T  
|831 |841  
|2551 |2561 |2571 |2581 |2591 |2601  
TACAGCAAGAAGAAGATTATTGATTTTCTTTCTGCTCTGGAAGGATTCAAAGTAATGTGT  
Y S K K K I I D F L S A L E G F K V M C  
|851 |861  
|2611 |2621 |2631 |2641 |2651 |2661  
AAAATTATAGGGATCATGGAAGAAGTTGCTGATGGTTTTAAGTCTAAAATCCTTAAGCAG

K I I G I M E E V A D G F K S K I L K Q  
 |871 |881  
  
 |2671 |2681 |2691 |2701 |2711 |2721  
 GTCATCTCTCTGCAGACAAAAATCCTGAAGGTCGTTTTCTGATTGACTGTAGAATTG  
 V I S L Q T K N P E G R F P D L T V E L  
 |891 |901  
  
 |2731 |2741 |2751 |2761 |2771 |2781  
 AACCGATGGGATACAGCCTTTGACCATGAAAAGGCTCGAAAGACTGGACTTATTACTCCC  
 N R W D T A F D H E K A R K T G L I T P  
 |911 |921  
  
 |2791 |2801 |2811 |2821 |2831 |2841  
 AAAGCAGGCTTTGACTCTGATTATGACCAAGCTCTTGCTGACATAAGAGAAAATGAACAG  
 K A G F D S D Y D Q A L A D I R E N E Q  
 |931 |941  
  
 |2851 |2861 |2871 |2881 |2891 |2901  
 AGCCTCCTGGAATACCTAGAGAAACAGCGCAACAGAATTGGCTGTAGGACCATAGTCTAT  
 S L L E Y L E K Q R N R I G C R T I V Y  
 |951 |961  
  
 |2911 |2921 |2931 |2941 |2951 |2961  
 TGGGGGATTGGTAGGAACCGTTACCAGCTGGAAATTCCTGAGAATTTCACTACTCGCAAT  
 W G I G R N R Y Q L E I P E N F T T R N  
 |971 |981  
  
 |2971 |2981 |2991 |3001 |3011 |3021  
 TTGCCAGAAGAATACGAGTTGAAATCTACCAAGAAGGGCTGTAAACGATACTGGACCAAA  
 L P E E Y E L K S T K K G C K R Y W T K  
 |991 |1001  
  
 |3031 |3041 |3051 |3061 |3071 |3081  
 ACTATTGAAAAAGAAGTTGGCTAATCTCATAAATGCTGAAGAACGGAGGGATGTATCATTG  
 T I E K K L A N L I N A E E R R D V S L  
 |1011 |1021  
  
 |3091 |3101 |3111 |3121 |3131 |3141  
 AAGGACTGCATGCGGCGACTGTTCTATAACTTTGATAAAAAATTACAAGGACTGGCAGTCT  
 K D C M R R L F Y N F D K N Y K D W Q S  
 |1031 |1041  
  
 |3151 |3161 |3171 . . . . .  
 GCTGTAGAGTGTATCGCAGTGTGGtaagactttgaacaagcttggttctcaggctttga  
 A V E C I A V L D

|1051

. . . . .  
taagtagtgctgtttgccagctgtatatattatccctaaaaataagtaataaggtatatatg  
. . . . .  
gtacatatatttgacatgcatatacatatttgcatcctgactaggctgcccacagcaattt  
. . . . .  
aagttacttgaaactcgcttttatcttagtagccctttggcctttcttcagtttttttt  
. . . . .  
tttttttttttttttggagacatggctcttgctctgttgcccaggctagaatatggtgaca  
. . . . .  
caaccatggctactgcagcctcgac

Exon 5 | Start: 25274 | End: 25539 | Length: 265

. . . . .  
gttggtcaggctggtcctgaactgctgacctcgtgaactctgccgcctaggcctcctga

. . . . .  
agtgctgggattacaggcgtgagccaccgtgcctggcctctgctctatcttttagctttc

. . . . .  
ccttggcacttctatggtccagatgtagaggtaagtattttgatgggggagatcgttg

. . . . .  
gactgtaattgaaagtatgtcttataatgaaatgtgttatataaagaagacctataaaa

. . . . .  
cacttaggctgataaaacccccaaacgatgaagcctcacttttaccctctcttttaacag

          |3181      |3191      |3201      |3211      |3221      |3231  
ATGTTTTACTGTGCCTGGCTAACTATAGTCGAGGGGGTGATGGTCCTATGTGTCGCCAG  
  V  L  L  C  L  A  N  Y  S  R  G  G  D  G  P  M  C  R  P  V  
          |1061                          |1071

          |3241      |3251      |3261      |3271      |3281      |3291  
TAATTCTGTGCGGAAGATACCCCCCTTCTTAGAGCTTAAAGGATCAGCCATCCTT  
  I  L  L  P  E  D  T  P  P  F  L  E  L  K  G  S  R  H  P  C  
          |1081                          |1091

          |3301      |3311      |3321      |3331      |3341      |3351  
GCATTACGAAGACTTTTTTTGGAGATGATTTTATTCTAATGACATTCTAATAGGCTGTG  
  I  T  K  T  F  F  G  D  D  F  I  P  N  D  I  L  I  G  C  E  
          |1101                          |1111

          |3361      |3371      |3381      |3391      |3401      |3411  
AGGAAGAGGAGCAGGAAAAATGGCAAAGCCTATTGTGTGCTTGTTACTGGACCAAATATGG  
  E  E  E  Q  E  N  G  K  A  Y  C  V  L  V  T  G  P  N  M  G  
          |1121                          |1131

          |3421      |3431      .      .      .      .      .  
GGGGCAAGTCTACGCTTATGAGACAGgtaactgattcttaaagttttgttatcagaaagt  
  G  K  S  T  L  M  R  Q  
          |1141

. . . . .  
catttgtgacattaggaataacatacttaggtgatcattttccaaacacagttacataaa

. . . . .

agtcagccagtgacttaataggaagcaaagggaattactccctgtgttataaaattgag

. . . . .  
aattatatttagctgaaacatcgatgcttaatgttaaggggaatatatgttaaaaagggg

. . . . .  
aaggaggtcagtcattcaggtcatgaggccctttgacttgaattcatttcctcagaaggt

. . . . .  
aggtatattcatagtgaacaaaaata

Exon 6 | Start: 26764 | End: 26881 | Length: 117

```
. . . . .
agtagttttaagagctcctaggtgattctattctggccagcgttgagaatcactagggt

. . . . .
agtgggttggttaagcaggctctgatgttttaaggccaggtgaggccctatgcctcttgt

. . . . .
ctctcttagcctcaactttctccatgtagcaaatggatttcagaacagaaccaacgtac

. . . . .
atgtgattgtgaaagttgttttagagtgacctcttacgtaagggttcataagaaaga

. . . . .
caaaagtttatgaaactgttactaccagtcataaaagaccttttcctccctcattcacag

|3441      |3451      |3461      |3471      |3481      |3491
GCTGGCTTATTAGCTGTAATGGCCCAGATGGGTTGTTACGTCCTGCTGAAGTGTGCAGG
A G L L A V M A Q M G C Y V P A E V C R
|1151                                |1161

|3501      |3511      |3521      |3531      |3541      |3551
CTCACACCAATTGATAGAGTGTTTACTAGACTTGGTGCCTCAGACAGAATAATGTCAGgt
L T P I D R V F T R L G A S D R I M S G
|1171                                |1181

. . . . .
gagttttttgtttccacttaagttctcattcagtcatttagatgtgataaaagatatatt

. . . . .
gcttcttgatatgagccttttaaatctaataatttgatttttctgggtgttactttaaaaa

. . . . .
catcactttttaagaactgcatagtctctctctctttttttttttttttgagatggagtgtt

. . . . .
ccctcttggtgcccaagctggagtgcaatggcacgatcttggctcactgcaacctctgct

. . . . .
tcaggttcaagtgattctcctgcctcagcctctcgagtagctgggattacaggcgca
```

Exon 7 | Start: 27472 | End: 27561 | Length: 89

```
. . . . .
tacaggcgcatgccatcacgcccagctaattttttgtatttttagtagaagcggggttc

. . . . .
accatgttaggctggtctcttaactcctgacctcaggtgatctgcttgccctcggcctccc

. . . . .
aaagtgctgggattacaggcgtgagccaccgtgcccgccaataattgcatagtctctta

. . . . .
atgagatttaatcttttataccaatatgtgtagctcatgatagctatataacctagaaga

. . . . .
tgaatttatgtaatatgatttgcaaatgagtattcatttgatgtttttttttttaag

      |3561      |3571      |3581      |3591      |3601      |3611
GTGAAAGTACATTTTTGTTGAATTAAGTGAAACTGCCAGCATACTCATGCATGCAACAG
  E  S  T  F  F  V  E  L  S  E  T  A  S  I  L  M  H  A  T  A
                |1191                                |1201

      |3621      |3631      |3641      . . . . .
CACATTCTCTGGTGCTTGTGGATGAATTAGgtaagacattaaacttctcatttgaagact
  H  S  L  V  L  V  D  E  L  G
                |1211

. . . . .
atctatcttaaaaacatttgtacaaataactatttttatagaagattatctgaagtacat

. . . . .
ttaaacaatatgaatgttttttagagcacgcactcaccattgtggcacagaccgatagttg

. . . . .
gagataaaaagggtgatattgtgaaagggtttttgattaccattaattattaggccttacac

. . . . .
tgtttagttgtaataaaacatttgttatactacgggggatgagaacactaataggaggact

. . . . .
caggaagtttatgaccttgagcgatactgt
```

Exon 8 | Start: 28058 | End: 28212 | Length: 154  
 BE AWARE: Flanking intron is shared with the following exon

```

. . . . .
attagccttacactgttttagttgtaataaaacatttgttatactacggggatgagaaca
. . . . .
ctaataggaggactcaggaagtttatgaccttgagcgatactgtattttctttaaaagaa
. . . . .
acctcactcccatgggctgctaagcagactcgtgtagctaaacaaggcctatttataga
. . . . .
atgcttttagacgtggatgtactaaccgatgttgcttttctgtcctagcattttgtttt
. . . . .
aattcctttttgttttaattcctttgagttacttccttatgcatattttactttaacag

      |3651      |3661      |3671      |3681      |3691      |3701
GAAGAGGTACTGCAACATTTGATGGGACGGCAATAGCAAATGCAGTTGTTAAAGAACTTG
  R  G  T  A  T  F  D  G  T  A  I  A  N  A  V  V  K  E  L  A
                |1221                                |1231

      |3711      |3721      |3731      |3741      |3751      |3761
CTGAGACTATAAAATGTCGTACATTATTTTCAACTCACTACCATTTCATTAGTAGAAGATT
  E  T  I  K  C  R  T  L  F  S  T  H  Y  H  S  L  V  E  D  Y
                |1241                                |1251

      |3771      |3781      |3791      |3801.      .      .      .
ATTCTCAAATGTTGCTGTGCGCCTAGGACATATGgtatgtgcaaattgttttttccac
  S  Q  N  V  A  V  R  L  G  H  M
                |1261

. . . . .
aaattcgggttttttgagaggg

```



Exon 9 | Start: 28306 | End: 28505 | Length: 199  
 BE AWARE: Flanking intron is shared with the previous exon

```

. . . . . |3811
cacttctcttgctagcacatgtatcgctaataatctttctttcttaagGCATGCATGGTAG
                                     A C M V E
                                     |1271

      |3821      |3831      |3841      |3851      |3861      |3871
AAAATGAATGTGAAGACCCAGCCAGGAGACTATTACGTTCTCTATAAATTCATTAAGG
  N E C E D P S Q E T I T F L Y K F I K G
                        |1281                        |1291

      |3881      |3891      |3901      |3911      |3921      |3931
GAGCTTGTCTTAAAGCTATGGCTTAAATGCAGCAAGGCTTGCTAATCTCCAGAGGAAG
  A C P K S Y G F N A A R L A N L P E E V
                        |1301                        |1311

      |3941      |3951      |3961      |3971      |3981      |3991
TTATTCAAAGGGACATAGAAAAGCAAGAGAATTTGAGAAGATGAATCAGTCACTACGAT
  I Q K G H R K A R E F E K M N Q S L R L
                        |1321                        |1331

      |4001.      . . . . .
TATTTTCGtaactaactaactataatggaattataactaactgaccttaagtttcaaaga
  F R

. . . . .
aacagtaaaaggggaagggatgatgcactatgaaaaacaaaaaactttttttttttt

. . . . .
tttttaattttaagggaagtttgctggctagtgaagggtcaactgtagatgctgaagct

. . . . .
gtccataaattgctgactttgattaaggaattatagactgactacattggaagctttgag

. . . . .
ttgacttctgacaaaggtggtaaattcagacaacattatgatctaataaactttatttt

. . .
taaaaat

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Exon 10 | Start: 28633 | End: 28807 | Length: 174  
 BE AWARE: Flanking intron is shared with the previous exon

```

. . . . .
aggggaagggatgatgcactatgaaaaacaaaaaactttttttttttttttttaatt

.          |4011      |4021      |4031      |4041      |4051
ttaagGGAAGTTTGCCTGGCTAGTGAAAGGTCAACTGTAGATGCTGAAGCTGTCCATAAA
      E V C L A S E R S T V D A E A V H K
                |1341                      |1351

      |4061      |4071      |4081      |*11      |*21      |*31
TTGCTGACTTTTGATTAAGGAATTATAGACTGACTACATTGGAAGCTTTGAGTTGACTTCT
L L T L I K E L *
                |1361

      |*41      |*51      |*61      |*71      |*81      |*91
GACAAAGGTGGTAAATTCAGACAACATTATGATCTAATAAACTTTATTTTTTAAAAATGA

. . . . .
ccatttttccattttctttctaggaattaaacccttttaattcttatctaccttctaca

. . . . .
taatggttattgaatactccacaatatattaagtctagatgttatggtacatgcatacac

. . . . .
tttcaggctgttttataccactgtcaccaatacacataaatgggggaggaaaagctatg

. . . . .
aaactgtatagggtgtatatatacttgtctcagcttaatgcaggaaattggtttaattt

. . . . .
ccagcagttttgtctaaactgttcaaaaaaactatgaacagagttcaaatacaggact

```

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