Legend:
Borders of exons involved at junction points are indicated before each BLAST alignment.
Arrows indicate beginning/ end of BLAST alignments.
Chromosome location of each partner gene is indicated.
Gene descriptions are provided (Entrez gene, UniProtKB/Swiss-Prot databases).

Chimeras sequences

PRKAA1-TTC33

```
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Sanger sequencing (forward and reverse)

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Pcr band          51 GTCTACAGTTATACCAAGTGGATAGTAGAACTTATCTACTGGATTTCCGT    100

EMBOSS_001       101 AGTATTGATGAATGGCTTCCTTTGGGTGGAAGAGGAAAATTGGTGAGAAG    150
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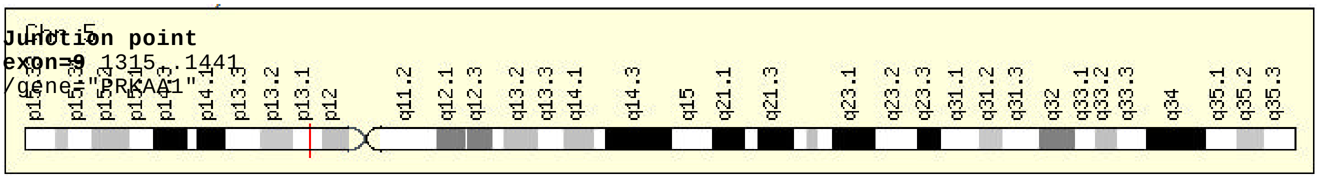
5’ partner: PRKAA1



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BLAST vs mRNA

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linked to NM_006251.5Genome view with mapviewer linked to NM_006251.5 Homo sapiens protein kinase, AMP-
activated, alpha 1 catalytic subunit (PRKAA1), transcript variant 1, mRNA
Length=5085
GENE ID: 5562 PRKAA1 | protein kinase, AMP-activated, alpha 1 catalytic subunit [Homo sapiens]
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Identities = 629/629 (100%), Gaps = 0/629 (0%)

Strand=Plus/Plus

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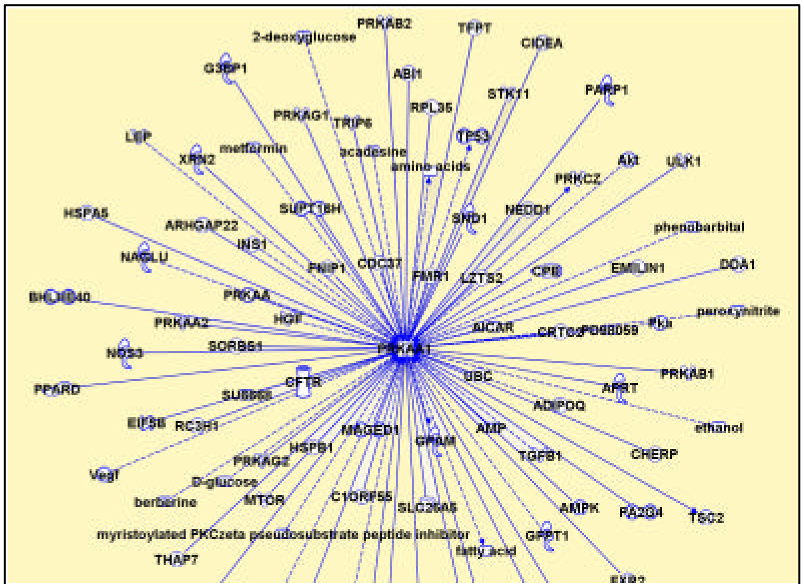
PRKAA1 interaction network.

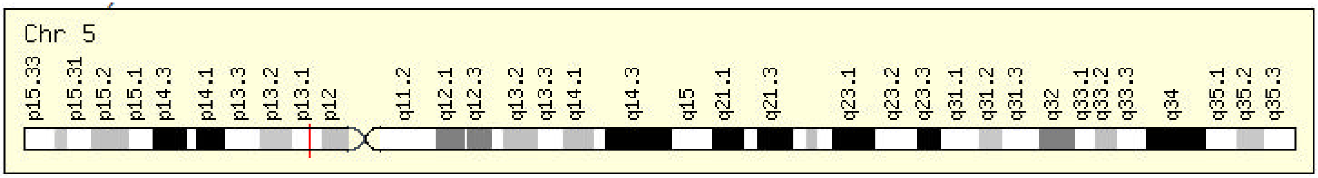
Protein kinase, AMP-activated, alpha 1 catalytic sub-unit (AMPK1). Major interactions are with AMP, p53, AKT, mTOR, TGFB1 and cell cycle regulatory proteins.



Summary for PRKAA1

PKA belongs to Ser/Thr protein kinases. It is the catalytic subunit of the cAMP-activated protein kinase (AMPK). AMPK is a cellular energy sensor conserved in all eukaryotic cells. The kinase activity of AMPK is activated by the stimuli that increase cell AMP/ATP ratio. AMPK regulates key metabolic enzymes through phosphorylation. It protects cells from stress that causes ATP depletion by switching-off ATP-consuming biosynthetic pathways. PKA regulates fatty acid synthesis by phosphorylation of acetyl-CoA carboxylase. It also regulates cholesterol synthesis via phosphorylation and inactivation of hormone-sensitive lipase and hydroxymethylglutaryl-CoA reductase.

3’ partner: TTC33



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BLAST vs mRNA

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linked to NM_012382.2Genome view with mapviewer linked to NM_012382.2 Homo sapiens tetratricopeptide
repeat domain 33 (TTC33), mRNA
Length=5519
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Score =  741 bits (401),  Expect = 0.0
Identities = 492/530 (93%), Gaps = 30/530 (5%)

Strand=Plus/Plus

                ↓
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Query  692   AGCAGTTTGAAGCTGAAGCTGCTGATGAGAAGGATGTAGTTGACAACGATGAA-AGAACT  750
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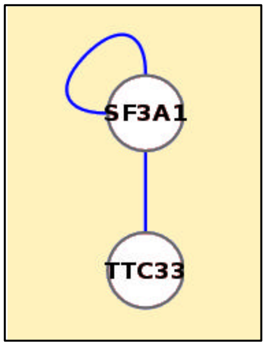
TTC33 interaction network.



Summary for TTC33
Tetratricopeptide repeat protein 33. Size: 262 amino acids; 29411 Da Secondary accessions: B2R6G0 O95105.

SAMM50-PARVB

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Sanger sequencing (forward and reverse)

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RDBC0852_G11.    620 GACAGTGAGTGACCTGCAGGAAGAAGGCAAGAATGCCATCAACTCACCG     101
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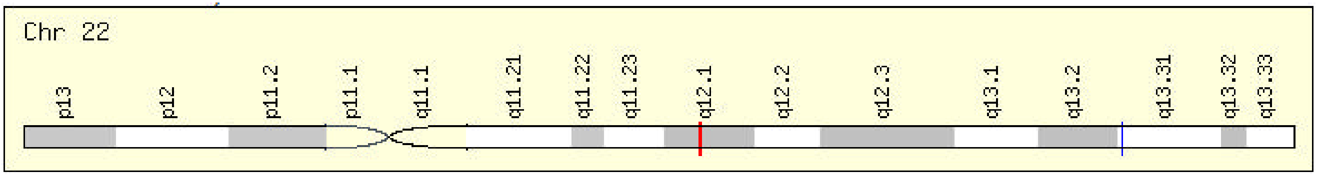
5’ partner: SAMM50



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BLAST vs mRNA

>ref|NM_015380.4| UniGene info linked to NM_015380.4GEO profiles info linked to NM_015380.4Gene info linked to NM_015380.4Genome view with mapviewer linked to NM_015380.4 Homo sapiens sorting and assembly machinery component 50 homolog (S. cerevisiae) (SAMM50), mRNA
Length=1773
GENE ID: 25813 SAMM50 | sorting and assembly machinery component 50 homolog (S. cerevisiae) [Homo sapiens]
Score = 1129 bits (611), Expect = 0.0
Identities = 617/620 (99%), Gaps = 0/620 (0%)

Strand=Plus/Plus

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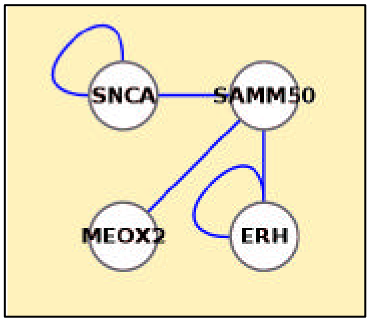
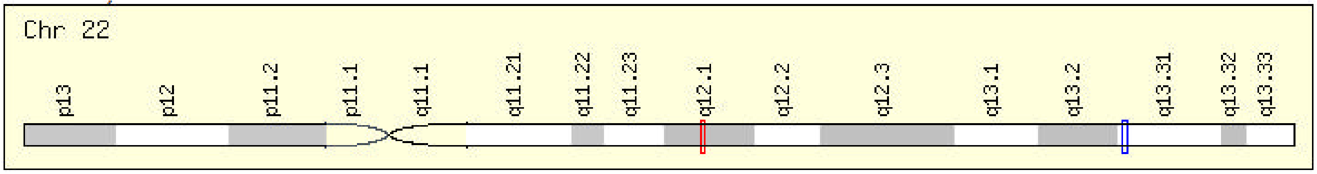
SAMM50 interaction network.



Summary for SAMM50
SAMM50 is a component of the sorting and assembly machinery (SAM) complex of the outer mitochondrial membrane. The SAM complex has a role in integrating beta-barrel proteins into the outer mitochondrial membrane.

3’ partner: PARVB



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BLAST vs mRNA

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Length=1808
GENE ID: 29780 PARVB | parvin, beta [Homo sapiens]
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Identities = 471/514 (92%), Gaps = 30/514 (5%)

Strand=Plus/Plus

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               ↓
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Sbjct  378   CCCCACTTCCAAGGAAGACCCCAAGTTCAAGGAACTGGTCAAGGTCCTCCTCGACTGGAT  437

Query  802   TAATGACGTGCTGGTGGAGGAGAGGATCATTGTGAAGCAGCTGGAGGAAGACCTGTATGA  861
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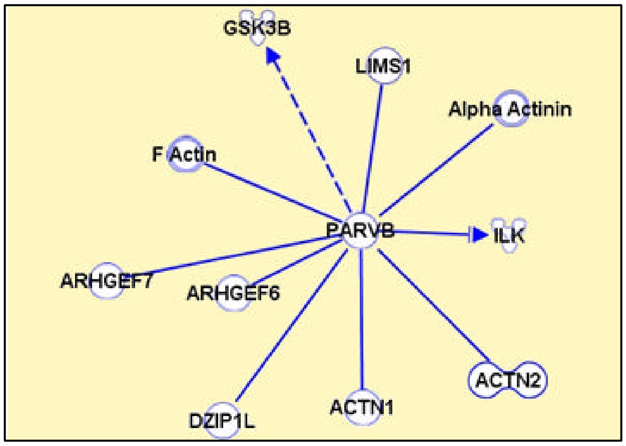
PARVB interaction network.
Beta parvin is involved in integrin linked kinase signaling. It directly interacts with ILK, ACTIN, ALPHA ACTININ and other proteins.



Summary for PARVB
Members of the parvin family, including PARVB, are actin-binding proteins associated with focal contacts. It probably has a role in the regulation of cell adhesion and cytoskeleton organization.

URB1-C21orf45

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Sanger sequencing (forward and reverse)

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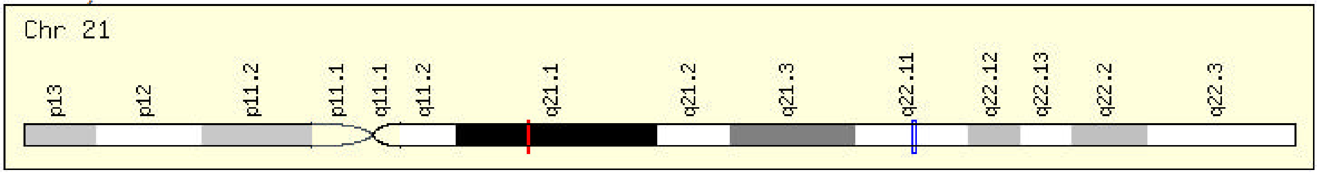
5’ partner: URB1



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BLAST vs mRNA

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>ref|NM_014825.2| UniGene info linked to NM_014825.2GEO profiles info linked to NM_014825.2Gene info
linked to NM_014825.2Genome view with mapviewer linked to NM_014825.2Download subject sequence
NM_014825 spanning the HSP Homo sapiens URB1 ribosome biogenesis 1 homolog (S. cerevisiae)
(URB1), mRNA
Length=10808
GENE ID: 9875 URB1 | URB1 ribosome biogenesis 1 homolog (S. cerevisiae) [Homo sapiens]
Score =  322 bits (174),  Expect = 7e-87
Identities = 176/177 (99%), Gaps = 0/177 (0%)

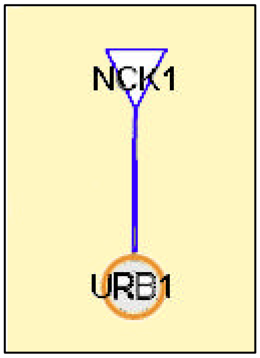
Strand=Plus/Plus

Query  1     ATAGCCGGCTCTGTGGGGCTGAGGGGCTGGCAGGGCCTGTGCAGGAGGTGGCCTGCCTGT  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6551  ATAGCCGGCTCTGTGGGGCTGAGGGGCTGGCAGGGCCTGTGCAGGAGGTGGCCTGCCTGT  6610

Query  61    TCAATACGGTCATGCTGCAGCTGGTGGCTGCCCAGGGCCGGGCAGGGAGCCCTTTCCACC  120
             |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  6611  TCAATACGGTCATGCTGCAGCTGGTGGCTGCCCAGGGCCGGGCAGGGAGCCCCTTCCACC  6670

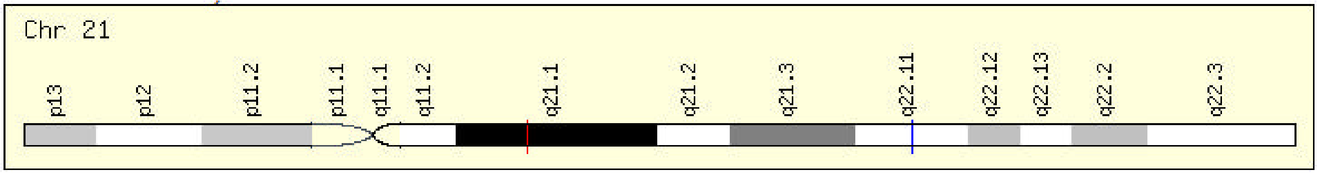
Query  121   CGGCCATGGAAGCCCTCTCCCTGTCTTCTCTGAGTGAGAAGGATGAAGCCACACAAG  177
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6671  CGGCCATGGAAGCCCTCTCCCTGTCTTCTCTGAGTGAGAAGGATGAAGCCACACAAG  6727
                                                                     ↑
```

URB1 interaction network.



Summary for URB1
Nucleolar pre-ribosomal-associated protein 1. Subcellular location: Nucleus, nucleolus. Secondary accessions: Q96NX1 Q9NYQ1.

3’ partner: C21orf45



Junction point
exon=2 386..452
/gene="MIS18A"
/gene_synonym="B28; C21orf45; C21orf46; FASP1; hMis18alpha; MIS18alpha"

BLAST vs mRNA

```
>ref|NM_018944.2| UniGene info linked to NM_018944.2GEO profiles info linked to NM_018944.2Gene info
linked to NM_018944.2Genome view with mapviewer linked to NM_018944.2 Homo sapiens MIS18 kinetochore
protein homolog A (S. pombe) (MIS18A), mRNA
Length=1587
GENE ID: 54069 MIS18A | MIS18 kinetochore protein homolog A (S. pombe) [Homo sapiens]
Score =  826 bits (447),  Expect = 0.0
Identities = 451/453 (99%), Gaps = 0/453 (0%)
```

```
Strand=Plus/Plus

                ↓
Query  178  GTGTTTCCTGTAATGTTTCTGTGGATAAGGAACAGAAGCTATCCAAACGTGAAAAGGAAA  237
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  386  GTGTTTCCTGTAATGTTTCTGTGGATAAGGAACAGAAGCTATCCAAACGTGAAAAGGAAA  445

Query  238  ATGGTTGCGTCCTTGAGACTTTGTGCTGCGCGGGGTGCTCACTCAATCTTGGCTACGTGT  297
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  446  ATGGTTGCGTCCTTGAGACTTTGTGCTGCGCGGGGTGCTCACTCAATCTTGGCTACGTGT  505

Query  298  ACAGATGCACGCCCAAGAATCTTGATTACAAGAGAGACTTGTTTTGCCTCAGTGTTGAAG  357
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  506  ACAGATGCACGCCCAAGAATCTTGATTACAAGAGAGACTTGTTTTGCCTCAGTGTTGAAG  565

Query  358  CCATTGAAAGTTATGTTTTAGGGTCCTCTGAAAAGCAAATTGTGTCAGAAGATAAAGAGC  417
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  566  CCATTGAAAGTTATGTTTTAGGGTCCTCTGAAAAGCAAATTGTGTCAGAAGATAAAGAGC  625

Query  418  TTTTTAATCTTGAAAGCAGAGTTGAAATAGAAAAGTTTCTAACACAGATGGAAGATGTCT  477
            |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  626  TTTTTAATCTTGAAAGCAGAGTTGAAATAGAAAAGTCTCTAACACAGATGGAAGATGTCT  685

Query  478  TGAAAGCATTACAAATGAAGCTGTGGGAGGCCGAATCCAAATTGTCCTTTCCCACTTGTA  537
            |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  686  TGAAAGCATTACAAATGAAGCTGTGGGAGGCCGAATCCAAATTGTCCTTTGCCACTTGTA  745

Query  538  AAAGCTGAACTCTAGTCTGTGTCCTCCATTCTGCCCCCGCCCTTCCTCCCCTTATTTGTT  597
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  746  AAAGCTGAACTCTAGTCTGTGTCCTCCATTCTGCCCCCGCCCTTCCTCCCCTTATTTGTT  805

Query  598  AAATGAAGCAACATAGTGAGACGTCGTCTCTAC  630
            |||||||||||||||||||||||||||||||||
Sbjct  806  AAATGAAGCAACATAGTGAGACGTCGTCTCTAC  838
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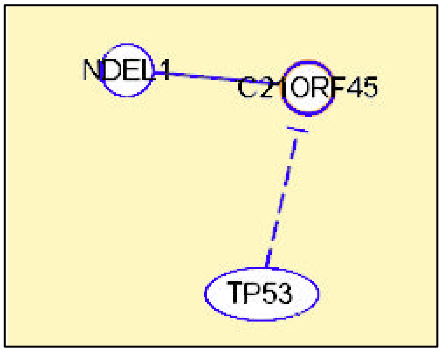
C21ORF45 interaction network.
It indirectly interacts with p53.



Summary for C21ORF45
MS18A_HUMAN, Q9NYP9. Protein Mis18-alpha. Subunit: Homodimer, and heterodimer with MIS18B. Identified in a complex containing MIS18A, MIS18B, MIS18BP1, RBBP7 and RBBP4. Subcellular location: nucleus. It associates with centromeres in interphase cells, from late anaphase to G1 phase. It is not detected on centromeres during earlier phases of mitosis and is associated with chromatin.

CTBS-GNG5

```
TGAATCTGTCTGAGGATCATGTTTGTACCATTGCAAAAGTCCCTTTCCGGGGGGCTCCTTGTAGTGACGCTGCAGGACGTCAGGTGCCCTACAAAACGATCA
GAAGCAAATAAATAGTTCTATTTCTGGAAACCTATGGGATAAAGATCAGCGGGCTCCTTATTATAACTATAAAGTTTCCCAGGCAGCTGCAGACTTGAAACA
TTCTGTCTGCAGAATGCTCAACATGACCCTCTGCTGACTGGAGTATCTTCAAGTACAAATCCCTTCAGACCCCAGAAAGTCTGTTCCTTTTTGTAGTAAAAT
AATCTTTCAAAGGTTTCCCAAACCACTCCTTATGATCCAGTGAATATTCAAGAGAGCTACATTTGAAGCCTGTACAAAAGCTTATCCCTGTAACACATGTGC
ATAATATACAAACTTTTACTTTCGTCAGTCCTTAACATCTACCTCTCTGAATTTTCATGAATTTCTATTTCACAAGGGTAATTGTTTTATATACACTGGCAG
AGCATACAATAAAACTTAGTATGAAACTTT
```

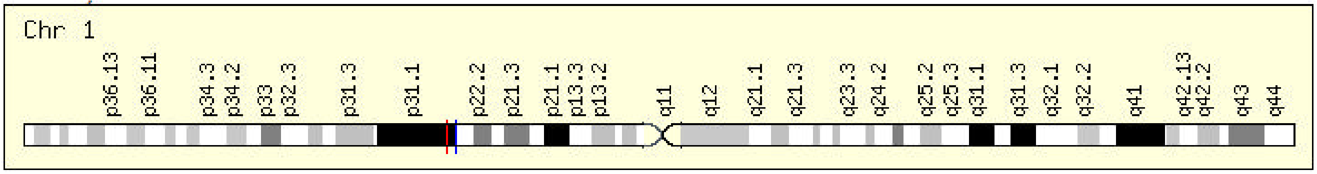
Sanger sequencing (forward and reverse)

```
EMBOSS_001         1 -CCTACAAAACGATCATGAAGCAAATAAATAGTTCTATTTCTGGAAACCT     49
                      |||||||||||||||||||||||||||||||||||||||||||||||||
PCR band           1 TCCTACAAAACGATCATGAAGCAAATAAATAGTTCTATTTCTGGAAACCT     50

EMBOSS_001        50 ATGGGATAAAGATCAGCGGGCTCCTTATTATAACTATAAAGTTTCCCAGG     99
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
PCR band          51 ATGGGATAAAGATCAGCGGGCTCCTTATTATAACTATAAAGTTTCCCAGG    100

EMBOSS_001       100 CAGCTGCAGACTTGAAACAGTTCTGTCTGCAGAATGCTCAACATGACC    147
                     ||||||||||||||||||||||||||||||||||||||||||||||||
PCR band         101 CAGCTGCAGACTTGAAACAGTTCTGTCTGCAGAATGCTCAACATGACC    148
```

5' partner: CTBS



Junction point
exon=6 861..1022
/gene="CTBS"
/gene_synonym="CTB"

BLAST vs mRNA

```
>ref|NM_004388.2| UniGene info linked to NM_004388.2GEO profiles info linked to NM_004388.2Gene info
linked to NM_004388.2Genome view with mapviewer linked to NM_004388.2 Homo sapiens chitobiase, di-N-
acetyl- (CTBS), mRNA
Length=3152
GENE ID: 1486 CTBS | chitobiase, di-N-acetyl- [Homo sapiens]
Score =  327 bits (177),  Expect = 1e-88
Identities = 177/177 (100%), Gaps = 0/177 (0%)

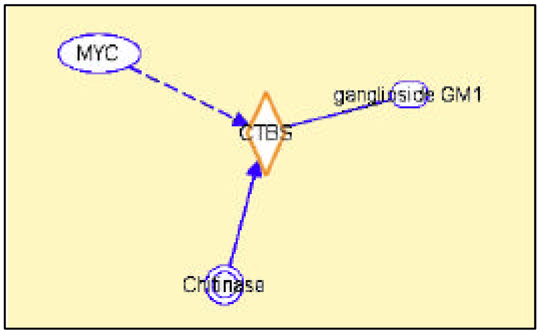
Strand=Plus/Plus

Query  1     TGAATCTGTCTGAGGATCATGTTTGTACCATTGCAAAAGTCCCTTTCCGGGGGGCTCCTT  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  847   TGAATCTGTCTGAGGATCATGTTTGTACCATTGCAAAAGTCCCTTTCCGGGGGGCTCCTT  906

Query  61    GTAGTGACGCTGCAGGACGTCAGGTGCCCTACAAAACGATCATGAAGCAAATAAATAGTT  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  907   GTAGTGACGCTGCAGGACGTCAGGTGCCCTACAAAACGATCATGAAGCAAATAAATAGTT  966

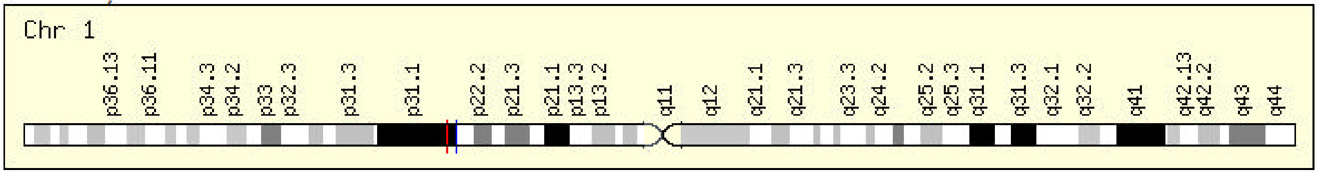
Query  121   CTATTTCTGGAAACCTATGGGATAAAGATCAGCGGGCTCCTTATTATAACTATAAAG  177
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  967   CTATTTCTGGAAACCTATGGGATAAAGATCAGCGGGCTCCTTATTATAACTATAAAG  1023
                                                                    ↑
```

CTBS interaction network.



Summary for CTBS
Chitobiase is a lysosomal glycosidase involved in degradation of asparagine-linked oligosaccharides on glycoproteins. It is also involved on hydrolyzation of N-acetyl-beta-D-glucosamine (1-4)N-acetylglucosamine chitobiose from the reducing end of the bond. This requires prior cleavage by glycosyl-asparaginase.

3' partner: GNG5



Junction point
exon=3 436..580
/gene="GNG5"
/gene_synonym="FLJ92393"

BLAST vs mRNA

```
>ref|NM_005274.2| UniGene info linked to NM_005274.2GEO profiles info linked to NM_005274.2Gene info
linked to NM_005274.2Genome view with mapviewer linked to NM_005274.2 Homo sapiens guanine nucleotide
binding protein (G protein), gamma 5 (GNG5), mRNA
Length=823
```

```
GENE ID: 2787 GNG5 | guanine nucleotide binding protein (G protein), gamma 5 [Homo sapiens]
Score =  682 bits (369),  Expect = 0.0
Identities = 371/372 (99%), Gaps = 0/372 (0%)

Strand=Plus/Plus

              ↓
Query  174  AAAGTTTCCCAGGCAGCTGCAGACTTGAAACAGTTCTGTCTGCAGAATGCTCAACATGAC  233
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  433  AAAGTTTCCCAGGCAGCTGCAGACTTGAAACAGTTCTGTCTGCAGAATGCTCAACATGAC  492

Query  234  CCTCTGCTGACTGGAGTATCTTCAAGTACAAATCCCTTCAGACCCCAGAAAGTCTGTTCC  293
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  493  CCTCTGCTGACTGGAGTATCTTCAAGTACAAATCCCTTCAGACCCCAGAAAGTCTGTTCC  552

Query  294  TTTTTGTAGTAAAATGAATCTTTCAAAGGTTTCCCAAACCACTCCTTATGATCCAGTGAA  353
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  553  TTTTTGTAGTAAAATGAATCTTTCAAAGGTTTCCCAAACCACTCCTTATGATCCAGTGAA  612

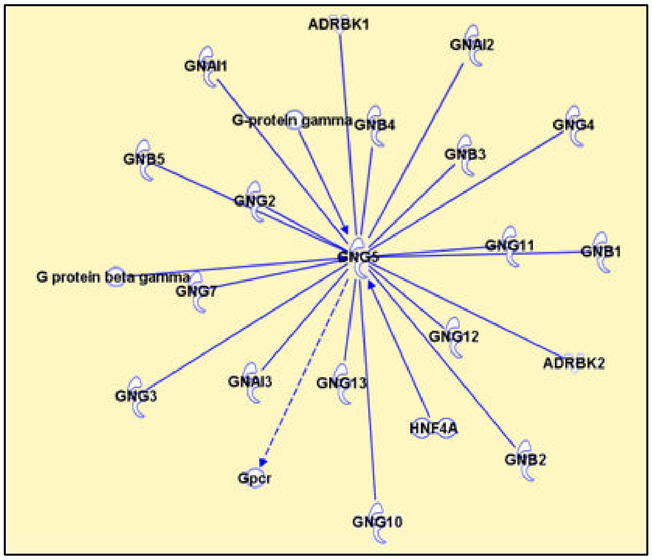
Query  354  TATTCAAGAGAGCTACATTTGAAGCCTGTACAAAAGCTTATCCCTGTAACACATGTGCCA  413
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  613  TATTCAAGAGAGCTACATTTGAAGCCTGTACAAAAGCTTATCCCTGTAACACATGTGCCA  672

Query  414  TAATATACAAACTTTTACTTTCGTCAGTCCTTAACATCTACCTCTCTGAATTTTCATGAA  473
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  673  TAATATACAAACTTCTACTTTCGTCAGTCCTTAACATCTACCTCTCTGAATTTTCATGAA  732

Query  474  TTTCTATTTCACAAGGGTAATTGTTTTATATACACTGGCAGCAGCATACAATAAAACTTA  533
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  733  TTTCTATTTCACAAGGGTAATTGTTTTATATACACTGGCAGCAGCATACAATAAAACTTA  792

Query  534  GTATGAAACTTT  545
            ||||||||||||
Sbjct  793  GTATGAAACTTT  804
```

GNG5 interaction network.



Summary for GNG5

G proteins are trimeric proteins that regulate flow of information from cell surface receptors to internal metabolic effectors. Interactions of a G protein with its activated receptor promotes exchange of GTP for GDP (alpha subunit). The alpha-GTP complex dissociates from the beta-gamma heterodimer so as to interact with and regulate effector molecules. G proteins are involved as modulators or transducers in transmembrane signaling systems. The beta and gamma chains are required for the GTPase activity, for replacement of GDP by GTP, and for G protein-effector interactions.

CHD2- CHMP1A

```
CTACTAGTAGATAGGACTCTTGGTTTGGACATACTACATGGATCAGTAAATACCTGGGCACAGGACTTCAAAGCAAACACAGATTCCCCCTCCCCCTTAATA
TTAAGAATTAAAAGATGATGAGAAATAAGGACAAAAGCCAAGAGGAGGACAGTTCGCTACACAGCAATGCATCGAGGTGACCAAGAATATGGCCCAGGTGAC
AAAGCCCTGGACAAGGCCCTGAGCACCATGGACCTGCAGAAGGTCTCCTCAGTGATGGACAGGTTCGAGCAGCAGGTGCAGAACCTGGACGTCCATACATCG
TGATGGAGGACTCCATGAGCTCGGCCACCACCCTGACCACGCCGCAGGAGCAGGTGGACAGCCTCATCATGCAGATCGCCGAGGAGAATGGCCTGGAGGTGC
GGACCAGCTCAGCCAGCTGCCCGAGGGCGCCTCTGCCGTGGGCGAGAGCTCTGTGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTTGGCCGCCTTGAGGAA
TAGCCGTGCCCCGCCGGTGTGCACCGCCTCTGCCCCGTGATGTGCTGGAAGGCTCCTGTCCTCTCCCCACCGCGTCTTGCCTTTGTGCTGACCCCGCGGGGC
GCGGCCGGCAGCCACTCTGCGTCTCTCACCTGCCAGGCCTGCGTGGCCTTAGGGTTGTTCCTGTTCTTTTAGGTTGGGCGGTGGGTCTGTGTCCTGGTGTTG
GTTTCTGCAAATTTCTGGGGGTGATTTCTGTGACTCTGGGCCCACAGCGGGGAGGCCAAGAAGGGCCCTGTGGACTTTCACCCAGCACTGTGGGGGCCTTCA
ACTCTGGGGCAGCAGACATGCTGCTTCCCATCAGCAGAGGGGGTCAGGCCTGCCCTGTTGCCAAACAACTCCTTGAGGCCTCTCCGCACCAACTCATCGGGC
GGAGGTCTCACCCATGTTGGACGACATAGCCCTAGGAGGACACCACAGGTCTAGTGTGGCTTGGGGGATGTCAGGTCACTAAGCGTTCTGGGTGTATTCAAT
ACATCCTTCCTTCTTCAAATTACTTTCAAGAG
```

Sanger sequencing (forward and reverse)

```
EMBOSS_001        51 TACCTGGGCACAGGACTTCAAAGCAAACACAGATTCCCCCTCCCCCTTAA    100
                                                     ||||||||||||||||||
PCR band           1                                 ATTCCCCCTCCCCCTTAA     18

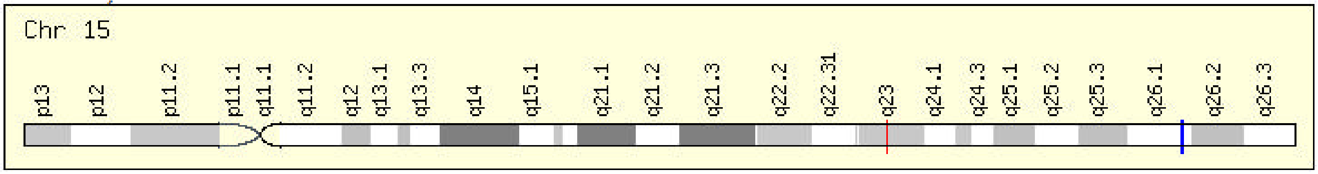
EMBOSS_001       101 TATTTAAGAATTAAAAGATGATGAGAAATAAGGACAAAAGCCAAGAGGAG    150
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
PCR band          19 TATTTAAGAATTAAAAGATGATGAGAAATAAGGACAAAAGCCAAGAGGAG     68

EMBOSS_001       151 GACAGTTCGCTACACAGCAATGCATCGAGGTGACCAAGAATATGGCCCAG    200
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
PCR band          69 GACAGTTCGCTACACAGCAATGCATCGAGGTGACCAAGAATATGGCCCAG    118

EMBOSS_001       201 GTGACCAAAGCCCTGGACAAGGCCCTGAGCACCATGGACCTGCAGAAGGT    250
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
PCR band         119 GTGACCAAAGCCCTGGACAAGGCCCTGAGCACCATGGACCTGCAGAAGGT    168

EMBOSS_001       251 CTCCTCAGTGATGGACAGGTTCGAGCAGCAGGTGCAGAACCTGGACGTCC    300
                     |||||||||||||||||||||||||||
PCR band         169 CTCCTCAGTGATGGACAGGTTCGAGCA                           195
```

5’ partner: CHD2



Junction point
exon=2 505..637
/gene="CHD2"
/gene_synonym="DKFZp547I1315; DKFZp686E01200;
DKFZp781D1727; FLJ38614"

BLAST vs mRNA

```
>ref|NM_001271.3| Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2),
transcript variant 1, mRNA
Length=9374
GENE ID: 1106 CHD2| chromodomain helicase DNA binding protein 2 [Homo sapiens]
Score =  324 bits (358),  Expect = 3e-91
Identities = 179/179 (100%), Gaps = 0/179 (0%)

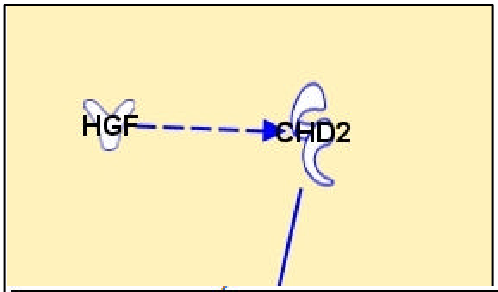
Strand=Plus/Plus

Query  1     CTACTAGTAGATAGGACTCTTGGTTTGGACATACTACATGGATCAGTAAATACCTGGGCA  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  459   CTACTAGTAGATAGGACTCTTGGTTTGGACATACTACATGGATCAGTAAATACCTGGGCA  518

Query  61    CAGGACTTCAAAGCAAACACAGATTCCCCCTCCCCCTTAATATTTAAGAATTAAAAGATG  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  519   CAGGACTTCAAAGCAAACACAGATTCCCCCTCCCCCTTAATATTTAAGAATTAAAAGATG  578

Query  121   ATGAGAAATAAGGACAAAAGCCAAGAGGAGGACAGTTCGCTACACAGCAATGCATCGAG  179
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  579   ATGAGAAATAAGGACAAAAGCCAAGAGGAGGACAGTTCGCTACACAGCAATGCATCGAG  637
                                                                     ↑
```

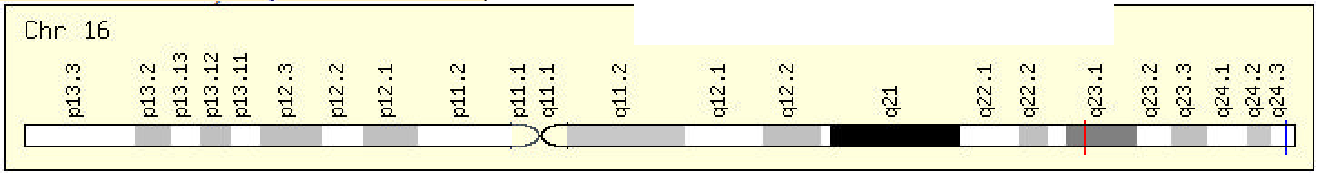
CHD2 interaction network.



Summary for CHD2

The CHD family of proteins is characterized by the presence of chromo (chromatin organization modifier) and SNF2-related helicase/ATPase domains. CHD domains modify gene expression by altering chromatin structure and access of the transcriptional apparatus to target DNA sites. HGF regulates cell growth, and cell motility and modulates CHD2 activity.

3’ partn



```
Junction point
exon=5 366..494
/gene="CHMP1A"
/gene_synonym="CHMP1; KIAA0047; PCOLN3; PRSM1"

BLAST vs mRNA

>ref|NM_001083314.1| Homo sapiens chromatin modifying protein 1A (CHMP1A), transcript
variant 1, mRNA
Length=2353
GENE ID: 5119 CHMP1A| chromatin modifying protein 1A [Homo sapiens]
Score = 1292 bits (1432),  Expect = 0.0
Identities = 814/878 (92%), Gaps = 14/878 (1%)

Strand=Plus/Plus

                ↓

Query  179   GGTGACCAAGAATATGGCCCAGGTGACCAAAGCCCTGGACAAGGCCCTGAGCACCATGGA  238
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  365   GGTGACCAAGAATATGGCCCAGGTGACCAAAGCCCTGGACAAGGCCCTGAGCACCATGGA  424

Query  239   CCTGCAGAAGGTCTCCTCAGTGATGGACAGGTTCGAGCAGCAGGTGCAGAACCTGGACGT  298
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  425   CCTGCAGAAGGTCTCCTCAGTGATGGACAGGTTCGAGCAGCAGGTGCAGAACCTGGACGT  484

Query  299   CCATACATCGGTGATGGAGGACTCCATGAGCTCGGCCACCACCCTGACCACGCCGCAGGA  358
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  485   CCATACATCGGTGATGGAGGACTCCATGAGCTCGGCCACCACCCTGACCACGCCGCAGGA  544

Query  359   GCAGGTGGACAGCCTCATCATGCAGATCGCCGAGGAGAATGGCCTGGAGGTGCTGGACCA  418
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  545   GCAGGTGGACAGCCTCATCATGCAGATCGCCGAGGAGAATGGCCTGGAGGTGCTGGACCA  604

Query  419   GCTCAGCCAGCTGCCCGAGGGCGCCTCTGCCGTGGGCGAGAGCTCTGTnnnnnnnnnnnn  478
             ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  605   GCTCAGCCAGCTGCCCGAGGGCGCCTCTGCCGTGGGCGAGAGCTCTGTGCGCAGCCAGGA  664

Query  479   nnnnnnnnnnnnnnnnnnnnTGGCCGCCTTGAGGAACTAGCCGTGCCCCGCCGGTGTGCA  538
                                 ||||||||||||||||||||||||||||||||||||||||
Sbjct  665   GGACCAGCTGTCACGGAGGTTGGCCGCCTTGAGGAACTAGCCGTGCCCCGCCGGTGTGCA  724

Query  539   CCGCCTCTGCCCCGTGATGTGCTGGAAGGCTCCTGTCCTCTCCCCACCGCGTCTTGCCTT  598
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  725   CCGCCTCTGCCCCGTGATGTGCTGGAAGGCTCCTGTCCTCTCCCCACCGCGTCTTGCCTT  784

Query  599   TGTGCTGACCCCGCGGGGCTGCGGCCGGCAGCCACTCTGCGTCTCTCACCTGCCAGGCCT  658
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  785   TGTGCTGACCCCGCGGGGCTGCGGCCGGCAGCCACTCTGCGTCTCTCACCTGCCAGGCCT  844

Query  659   GCGTGGCCTTAGGGTTGTTCCTGTTCTTTTAGGTTGGGCGGTGGGTCTGTGTCCTGGTGT  718
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  845   GCGTGGCCTTAGGGTTGTTCCTGTTCTTTTAGGTTGGGCGGTGGGTCTGTGTCCTGGTGT  904

Query  719   TGAGTTTCTGCAAATTTCTGGGGGTGATTTCTGTGACTCTGGGCCCACAGCGGGGAGGCC  778
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  905   TGAGTTTCTGCAAATTTCTGGGGGTGATTTCTGTGACTCTGGGCCCACAGCGGGGAGGCC  964

Query  779   AAGAAGGGCCCTGTGGACTTTCACCCAGCACTGTGGGGGCCTTCAGACTCTGGGGCAGCA  838
             |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  965   AAGAGGGGCCCTGTGGACTTTCACCCAGCACTGTGGGGGCCTTCAGACTCTGGGGCAGCA  1024

Query  839   GACATGCTGCTTCCCATCAG-CAGAGGGGGTCAGGCCTGCCCTGTTGCCAAACAACTCCT  897
             |||||||||||||||||||| |||||||||||||| |||||||||||||||||||||||
```

```
Sbjct  1025  GACATGCTGCTTCCCATCAGCCAGAGGGGGTCAGGGCTGCCCTGTTGCCAAACAACTCCC  1084

Query  898   TGAGGCCTCTCCGCACCAACTCATCGGGCAGGAGGTCTCACCCATGTTGGAC-GACATAG  956
             |||||||||||||||||| |||| ||||||||||||| || ||||| ||||| |||||||
Sbjct  1085  TGAGGCCTCTCCGCACCACCTCAGCGGGCAGGAGGTCCCA-CCATG-TGGACAGACATAG  1142

Query  957   CCCTAGGAGGACACCACAGGTCTAGTGTGGCTTGGGGGATGTCAGGT--CACTAAGC---  1011
             ||| |||||| ||||||||||||| ||||   |||||||||||||||  |||  | |
Sbjct  1143  CCCAAGGAGG-CACCACAGGTCTA-TGTGTGCTGGGGGATGTCAGGTGCCACCCAACGCT  1200

Query  1012  GTTCTGGGTGTATT--CAATGACATCCTTCCTTCTTCA  1047
             || ||||  |||||  ||||||||||| |||| || ||
Sbjct  1201  GTCCTGGTGGTATTTACAATGACATCC-TCCTCCTCCA  1237
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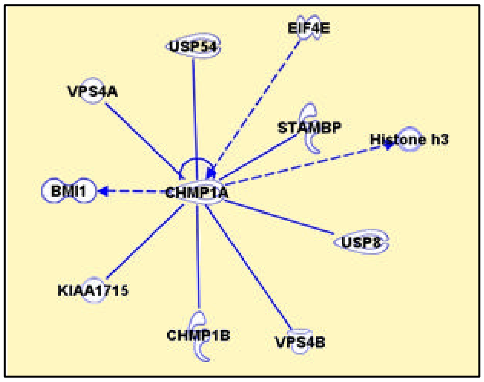
CHMP1A interaction network.



Summary for CHMP1A

CHMP1A a member of the CHMP/Chmp family. CHMP1A is a component of endosomal sorting transport complex III (ESCRT-III) which is involved in multivesicular bodies (MVBs) formation and sorting of endosomal cargo proteins into MVBs. The MVB pathway appears to require the sequential function of ESCRT-O, -I,-II and -III complexes. ESCRT-III proteins mostly dissociate from the invaginating membrane before the ILV is released. The ESCRT machinery also functions in topologically equivalent membrane fission events, such as the terminal stages of cytokinesis and the budding of enveloped viruses (HIV-1). Involved in recruiting VPS4A and/or VPS4B to the midbody of dividing cells. May also be involved in chromosome condensation. Targets the Polycomb group (PcG) protein BMI1/PCGF4 to regions of condensed chromatin.

P2RX5-TAX1BP3

```
TTGGCTCACATCTGGGCCAGGGCTGCTGGGGATGCCGGAGCAGCAGGAGCTGCAGGAGCCACCCGAGGCGAAGCGTGGAAGCAGCAGTCAGAAGGGGAACGG
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CGACCAGGATCCTTCCCAGAATCCCTTCTCTGAAGACAAGACGGACAAGGGTATTTATGTCACACGGGTGTCTGAAGGAGGCCCTGCTGAAATCGCTGGGCT
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TCCCTTCTCCCATCCCTGGCCTGGGGCCTCTGGGACCGGCTTTCTCTCCTGGACACCGAGGATTGGAAATAAAGGCCCTGGAGCTGAGTAGTAGCCCAGTCT
CTGTGACCACAGGCTCACGTCCGACCCTGCTGCTTGGCCACAGCAGTGGCTGGGGCAAGTGGGAACCACTACCTCTTGGGGACCCCCAAAAGCCTGGGAAA
```

Sanger sequencing (reverse)

```
EMBOSS_001         2 GTCAGAAGGGGAACGGATCTGTGTGCCCACAGCTCCTGGAGCCCCACAGC     51
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
PCR band           2 GTCAGAAGGGGAACGGATCTGTGTGCCCACAGCTCCTGGAGCCCCACAGC     51

EMBOSS_001        52 AAAGAGTTGAAATTCACAAGCTGCGTCAAGGTGAGAACTTAATCCTGGGT    101
                     |||||||||||| |||||||||||||||||||||||||||||||||||||
PCR band          52 AAAGAGTTGAAATTCACAAGCTGCGTCAAGGTGAGAACTTAATCCTGGGT    101

EMBOSS_001       102 TTCAGCATTGGAGGTGGAAT    151
                     ||||||||||||||||||||
PCR band         102 TTCAGCATTGGAGGTGGAAT    151
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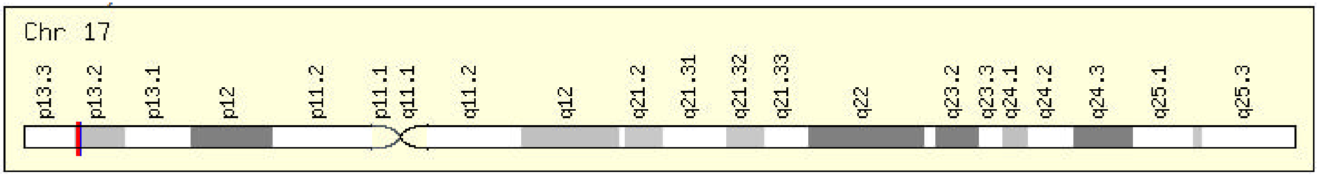
5' partner: P2RX5



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Junction point
exon=11 1392..1586
/gene="P2RX5"
/gene_synonym="LRH-1; MGC47755; P2X5; P2X5R"
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BLAST vs mRNA

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>ref|NM_001204520.1| Gene info linked to NM_001204520.1 Homo sapiens purinergic receptor P2X, ligand-
gated ion channel, 5 (P2RX5), transcript variant 5, mRNA
Length=2269
GENE ID: 5026 P2RX5 | purinergic receptor P2X, ligand-gated ion channel, 5 [Homo sapiens]
Score =  244 bits (132),  Expect = 2e-63
Identities = 132/132 (100%), Gaps = 0/132 (0%)

Strand=Plus/Plus

Query  4     GCTCACATCTGGGCCAGGGCTGCTGGGGATGCCGGAGCAGCAGGAGCTGCAGGAGCCACC  63
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1455  GCTCACATCTGGGCCAGGGCTGCTGGGGATGCCGGAGCAGCAGGAGCTGCAGGAGCCACC  1514

Query  64    CGAGGCGAAGCGTGGAAGCAGCAGTCAGAAGGGGAACGGATCTGTGTGCCCACAGCTCCT  123
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1515  CGAGGCGAAGCGTGGAAGCAGCAGTCAGAAGGGGAACGGATCTGTGTGCCCACAGCTCCT  1574

Query  124   GGAGCCCCACAG  135
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Sbjct  1575  GGAGCCCCACAG  1586
                        ↑
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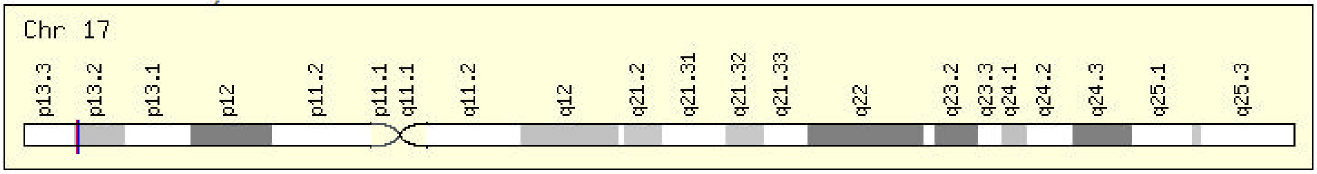
3' partner: TAX1BP3



Junction point
exon=2 193..312
/gene="TAX1BP3"
/gene_synonym="TIP-1"

BLAST vs mRNA

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>ref|NM_014604.3| Gene info linked to NM_014604.3 Homo sapiens Tax1 (human T-cell leukemia virus type
I) binding protein 3 (TAX1BP3), transcript variant 1, mRNA
Length=1398
GENE ID: 30851 TAX1BP3 | Tax1 (human T-cell leukemia virus type I) binding protein 3 [Homo sapiens]
Score = 1218 bits (659),  Expect = 0.0
Identities = 680/689 (99%), Gaps = 6/689 (0%)

Strand=Plus/Plus

            ↓
Query  135  GCAAAGAGTTGAAATTCACAAGCTGCGTCAAGGTGAGAACTTAATCCTGGGTTTCAGCAT  194
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  192  GCAAAGAGTTGAAATTCACAAGCTGCGTCAAGGTGAGAACTTAATCCTGGGTTTCAGCAT  251

Query  195  TGGAGGTGGAATCGACCAGGATCCTTCCCAGAATCCCTTCTCTGAAGACAAGACGGACAA  254
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  252  TGGAGGTGGAATCGACCAGGATCCTTCCCAGAATCCCTTCTCTGAAGACAAGACGGACAA  311

Query  255  GGGTATTTATGTCACACGGGTGTCTGAAGGAGGCCCTGCTGAAATCGCTGGGCTGCAGAT  314
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  312  GGGTATTTATGTCACACGGGTGTCTGAAGGAGGCCCTGCTGAAATCGCTGGGCTGCAGAT  371

Query  315  TGGAGACAAGATCATGCAGGTGAACGGCTGGGACATGACCATGGTCACACACGACCAGGC  374
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  372  TGGAGACAAGATCATGCAGGTGAACGGCTGGGACATGACCATGGTCACACACGACCAGGC  431

Query  375  CCGCAAGCGGCTCACCAAGCGCTCGGAGGAGGTGGTGCGTCTGCTGGTGACGCGGCAGTC  434
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  432  CCGCAAGCGGCTCACCAAGCGCTCGGAGGAGGTGGTGCGTCTGCTGGTGACGCGGCAGTC  491

Query  435  GCTGCAGAAGGCCGTGCAGCAGTCCATGCTGTCCTAGCAGCCACCACCATCTGCGACTCC  494
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  492  GCTGCAGAAGGCCGTGCAGCAGTCCATGCTGTCCTAGCAGCCACCACCATCTGCGACTCC  551

Query  495  TGCCTGCCGCCTCTCTGTACAGTAACGCCACTTCCACACTCTGTCCCCATCTGGCTTCTG  554
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  552  TGCCTGCCGCCTCTCTGTACAGTAACGCCACTTCCACACTCTGTCCCCATCTGGCTTCTG  611

Query  555  CTGACCGCTGGGCCCCAGCTCAGAAGGGCTATAGCTGGTCCCAGAGGCCTGGCCTGGCCT  614
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  612  CTGACCGCTGGGCCCCAGCTCAGAAGGGCTATAGCTGGTCCCAGAGGCCTGGCCTGGCCT  671
```

NXPH1-TXNL4A

```
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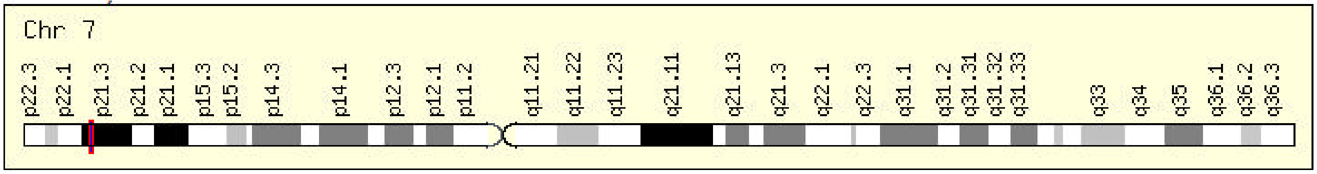
5’ partner: NXPH1



Junction point
exon=2 802..965
/gene="NXPH1"
/gene_synonym="Nbla00697; NPH1"

BLAST vs mRNA

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>ref|NM_152745.2| UniGene infoGeoGene info Homo sapiens neurexophilin 1 (NXPH1), mRNA
Length=2931
GENE ID: 30010 NXPH1 | neurexophilin 1 [Homo sapiens]
Score =  720 bits (798),  Expect = 0.0
Identities = 399/399 (100%), Gaps = 0/399 (0%)

Strand=Plus/Plus

Query  5    CAACTGTGCCAAGCCTTGGCTCCCGCGAACCAATCCTGAGCGCGACCCGGGCACTGGGAC  64
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  569  CAACTGTGCCAAGCCTTGGCTCCCGCGAACCAATCCTGAGCGCGACCCGGGCACTGGGAC  628

Query  65   GGCGACTCCGCCAAAGCTGGACGAGGCAGCCGGACCCGTCTGCGCTCGAGCATGGAGACG  124
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  629  GGCGACTCCGCCAAAGCTGGACGAGGCAGCCGGACCCGTCTGCGCTCGAGCATGGAGACG  688

Query  125  GAGCGCCTGGGAGGGCACGTCCGGGGCGCTGGAGACGCCAGGCCCGAGTAGCTTCTCCAT  184
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  689  GAGCGCCTGGGAGGGCACGTCCGGGGCGCTGGAGACGCCAGGCCCGAGTAGCTTCTCCAT  748

Query  185  GGAGCCTGCCCAGAGCGGTCCCTTCTCGCAGGATTCGCCCCAAGTCCTGTGCGGCTGCTG  244
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  749  GGAGCCTGCCCAGAGCGGTCCCTTCTCGCAGGATTCGCCCCAAGTCCTGTGCGGCTGCTG  808

Query  245  AGAGCGCTCCTTGCTCTGTAAAGTGGATGTCAGGTGGATCTATGTTTCTGAAGGAACAAA  304
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  809  AGAGCGCTCCTTGCTCTGTAAAGTGGATGTCAGGTGGATCTATGTTTCTGAAGGAACAAA  868

Query  305  GACTCAAAGAAGGCACCGCCAAGGAAGTTTGAGACGCGGGAGAATGCAGGCTGCGTGCTG  364
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  869  GACTCAAAGAAGGCACCGCCAAGGAAGTTTGAGACGCGGGAGAATGCAGGCTGCGTGCTG  928

Query  365  GTACGTGCTTTTCCTCCTGCAGCCCACCGTCTACTTGGT  403
            |||||||||||||||||||||||||||||||||||||||
Sbjct  929  GTACGTGCTTTTCCTCCTGCAGCCCACCGTCTACTTGGT  967
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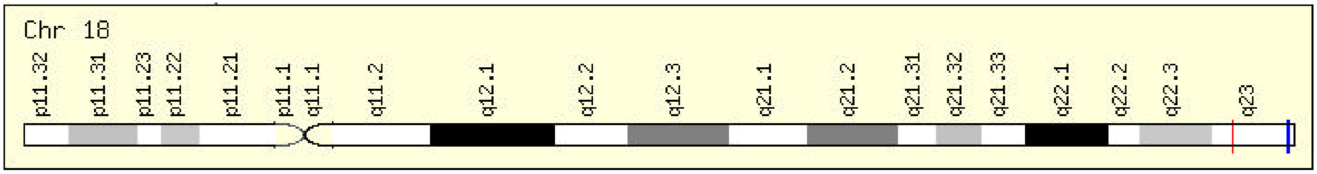
3’ partner: TXNL4A



Junction point
exon=2 294..397

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/gene="TXNL4A"
/gene_synonym="DIB1; DIM1; HsT161; TXNL4; U5-15kD"
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BLAST vs mRNA

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>ref|NM_006701.2| Homo sapiens thioredoxin-like 4A (TXNL4A), mRNA
Length=1415
Score =  654 bits (724),  Expect = 0.0
Identities = 375/381 (98%), Gaps = 2/381 (0%)

Strand=Plus/Plus

          ↓
Query  401  GGTTAAAAATTTTGCAGTTATTTATCTTGTGGATATTACAGAAGTGCCTGACTTCAACAA  460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  293  GGTTAAAAATTTTGCAGTTATTTATCTTGTGGATATTACAGAAGTGCCTGACTTCAACAA  352

Query  461  AATGTATGAGTTATACGATCCATGTACTGTCATGTTTTTCTTCAGGAACAAGCACATCAT  520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  353  AATGTATGAGTTATACGATCCATGTACTGTCATGTTTTTCTTCAGGAACAAGCACATCAT  412

Query  521  GATTGACTTGGGGACTGGCAACAACAACAAGATTAACTGGGCCATGGAGGACAAGCAGGA  580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  413  GATTGACTTGGGGACTGGCAACAACAACAAGATTAACTGGGCCATGGAGGACAAGCAGGA  472

Query  581  GATGGTGGACATCATCGAGACGGTGTACCGCGGGGCCCGCAAAGGCCGCGGCCTGGTGGT  640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  473  GATGGTGGACATCATCGAGACGGTGTACCGCGGGGCCCGCAAAGGCCGCGGCCTGGTGGT  532

Query  641  GTCCCCCAAGGACTACTCCACCAAGTACCGCTACTGAGGCGCCCTCAGTCTGCGCGGATA  700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  533  GTCCCCCAAGGACTACTCCACCAAGTACCGCTACTGAGGCGCCCTCAGTCTGCGCGGATA  592

Query  701  AATGTCGTGGAGACCTTTTTGTATAGAAACATATTTAAGCTATTTAAAGCCTTTGG-AAA  759
             |||||||||||| ||||||||||| ||||| | ||||||||||||||||||||||| |||
Sbjct  593  AATGTCGTGGAGCCCTTTTTGTATGGAAACGT-TTTAAGCTATTTAAAGCCTTTGGAAAA  651

Query  760  TACAGGAAGCTCCCGGGCTGG  780
             ||||||||||||| |||||||
Sbjct  652  TACAGGAAGCTCCAGGGCTGG  672
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KIAA1704- ITGB3BP

```
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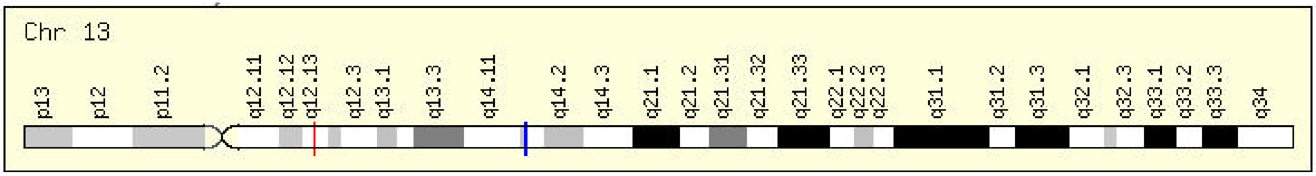
5’ partner: KIAA1704



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Junction point
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/gene_synonym="AD029; bA245H20.2; LSR7; RP11-245H20.2"
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BLAST vs mRNA

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Length=1431
Score =  527 bits (584),  Expect = 2e-153
Identities = 292/292 (100%), Gaps = 0/292 (0%)

Strand=Plus/Plus
```

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Query  5     CAGTAAGAAAGATGAAGAACATATATTATCAGGAAGAGATAAGAGACTGGCTGAGCAGGT  64
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  835   CAGTAAGAAAGATGAAGAACATATATTATCAGGAAGAGATAAGAGACTGGCTGAGCAGGT  894

Query  65    ATCTTCATACAATGAATCAAAAAGATCAGAATCTCTTATGGACATACATCATAAAAAGTT  124
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  895   ATCTTCATACAATGAATCAAAAAGATCAGAATCTCTTATGGACATACATCATAAAAAGTT  954

Query  125   AAAGAGTAAGGCTGCTGAAGACAAAAATAAGCCTCAAGAGAGAATACCATTTGACCGTGA  184
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  955   AAAGAGTAAGGCTGCTGAAGACAAAAATAAGCCTCAAGAGAGAATACCATTTGACCGTGA  1014

Query  185   TAAAGATCTCAAGGTTAATCGGTTTGATGAAGCTCAGAAAAAAGCCCTAATaaaaaaaTC  244
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1015  TAAAGATCTCAAGGTTAATCGGTTTGATGAAGCTCAGAAAAAAGCCCTAATAAAAAAATC  1074

Query  245   TAGAGAACTAAACACCAGATTTTCACACGGCAAAGGCAATATGTTTTTATAA  296
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1075  TAGAGAACTAAACACCAGATTTTCACACGGCAAAGGCAATATGTTTTTATAA  1126
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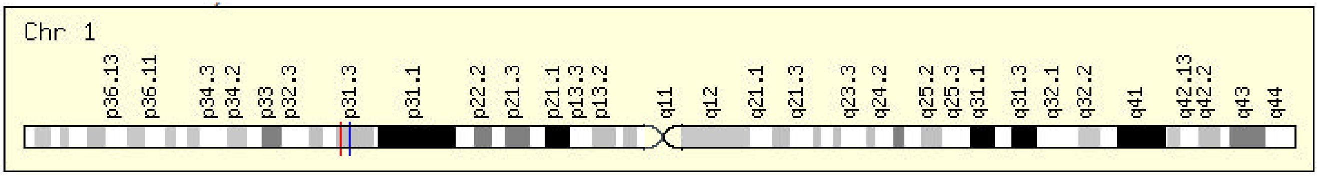
3’ partner: ITGB3BP



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Junction point
exon=5 286..364
/gene="ITGB3BP"
/gene_synonym="CENP-R; CENPR; HSU37139; NRIF3; TAP20"

BLAST vs mRNA

>ref|NM_014288.3| Homo sapiens integrin beta 3 binding protein (beta3-endonexin) (ITGB3BP), mRNA
Length=892
Score =  241 bits (266),  Expect = 3e-67
Identities = 135/136 (99%), Gaps = 0/136 (0%)

Strand=Plus/Plus

                      ↓
Query  293  ATAAATTCATGATGTTGCTATCAAAAGTTGAGAAATTGTCAGAAGAAATCATGGAGATAA  352
            || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  282  ATGAATTCATGATGTTGCTATCAAAAGTTGAGAAATTGTCAGAAGAAATCATGGAGATAA  341

Query  353  TGCAAAATTTAAGTAGTATACAGGCTTTGGAGGGCAGTAGAGAGCTTGAAAATCTCATTG  412
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  342  TGCAAAATTTAAGTAGTATACAGGCTTTGGAGGGCAGTAGAGAGCTTGAAAATCTCATTG  401

Query  413  GAATCTCCTGTGCATC  428
            ||||||||||||||||
Sbjct  402  GAATCTCCTGTGCATC  417
```

DHX8 -ADK

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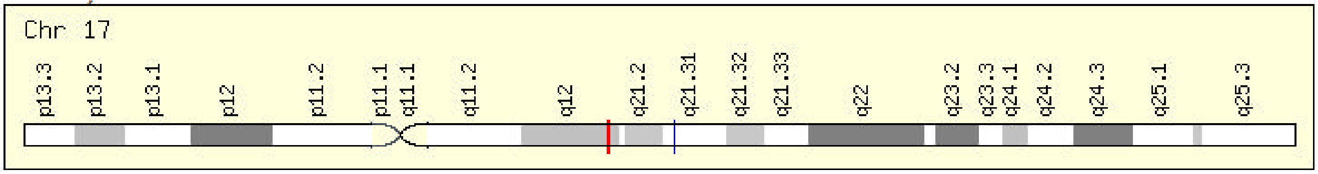
5’ partner: DHX8



Junction point
exon=3 308..380
/gene="DHX8"
/gene_synonym="DDX8; HRH1; PRP22; PRPF22"

BLAST vs mRNA

```
>ref|NM_004941.1| Homo sapiens DEAH (Asp-Glu-Ala-His) box polypeptide 8 (DHX8), mRNA
Length=4201
Gene id: 4826690 ATP-dependent RNA helicase DHX8
Score =  542 bits (600),  Expect = 2e-157
Identities = 300/300 (100%), Gaps = 0/300 (0%)

Strand=Plus/Plus

Query  2    TGGCTGTAGCCATGGCGGGAGCCTTAATCGGGTCGGAGCCAGGCCCCGCGGAAGAACTTG  61
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  81   TGGCTGTAGCCATGGCGGGAGCCTTAATCGGGTCGGAGCCAGGCCCCGCGGAAGAACTTG  140

Query  62   CCAAACTCGAGTACCTGTCTTTGGTGTCAAAGGTTTGCACTGAGCTGGACAATCACTTGG  121
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  141  CCAAACTCGAGTACCTGTCTTTGGTGTCAAAGGTTTGCACTGAGCTGGACAATCACTTGG  200

Query  122  GGATCAACGACAAGGACCTTGCTGAATTTGTGATCAGTCTTGCTGAGAAAAATACCACCT  181
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  201  GGATCAACGACAAGGACCTTGCTGAATTTGTGATCAGTCTTGCTGAGAAAAATACCACCT  260

Query  182  TTGATACTTTTAAGGCTTCTCTCGTCAAAAATGGTGCAGAATTTACGGATTCTCTTATTA  241
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  261  TTGATACTTTTAAGGCTTCTCTCGTCAAAAATGGTGCAGAATTTACGGATTCTCTTATTA  320

Query  242  GTAACTTGCTGCGTCTCATACAAACCATGCGGCCTCCAGCGAAGCCTTCCACTAGCAAAG  301
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  321  GTAACTTGCTGCGTCTCATACAAACCATGCGGCCTCCAGCGAAGCCTTCCACTAGCAAAG  380
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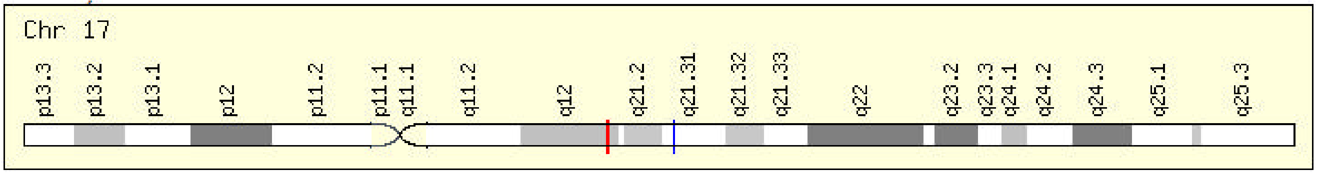
3’ partner: ADK



Junction point
exon=12 1037..2018
/gene="ADK"
/gene_synonym="AK"

BLAST vs mRNA

```
>ref|NM_006721.2| Homo sapiens adenosine kinase (ADK), transcript variant ADK-long, mRNA
Length=2018
GENE ID: 132 ADK| adenosine kinase [Homo sapiens]
Score = 1088 bits (1206),  Expect = 0.0
Identities = 667/713 (93%), Gaps = 41/713 (5%)


Strand=Plus/Plus

               ↓
Query  300   AGGTTTTCTGTCTCAACTGGTCTCTGACAAGCCTCTGACTGAATGTATCCGTGCTGGCCA  359
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1035  AGGTTTTCTGTCTCAACTGGTCTCTGACAAGCCTCTGACTGAATGTATCCGTGCTGGCCA  1094

Query  360   CTATGCAGCAAGCATCATAATTAGACGGACTGGCTGCACCTTTCCTGAGAAGCCAGACTT  419
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1095  CTATGCAGCAAGCATCATAATTAGACGGACTGGCTGCACCTTTCCTGAGAAGCCAGACTT  1154
```

```
Query  420   CCACTGATGGAAGAGCTGAAAACACAAGCCCAGGAGTGCAGACACTGCCCTAATTGCTTC  479
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1155  CCACTGATGGAAGAGCTGAAAACACAAGCCCAGGAGTGCAGACACTGCCCTAATTGCTTC  1214

Query  480   CTGAGAATTCCCATATTAATAAAGAAGAAAATTATCTGCCATTTTTTCCTACTATAATAA  539
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1215  CTGAGAATTCCCATATTAATAAAGAAGAAAATTATCTGCCATTTTTTCCTACTATAATAA  1274

Query  540   TGCTGAATCTTAATTTAGAGGGTACAAGGGTATGGTAATGCTTGTAGAATCTTTATTATC  599
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1275  TGCTGAATCTTAATTTAGAGGGTACAAGGGTATGGTAATGCTTGTAGAATCTTTATTATC  1334

Query  600   TCAACAATCTAAAAAATGATGTTTATTTCCATAGTTTGATAGTGCCACTTAAATGCCAAT  659
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1335  TCAACAATCTAAAAAATGATGTTTATTTCCATAGTTTGATAGTGCCACTTAAATGCCAAT  1394

Query  660   TAAACAAGAATATAACATTTCAATAGAAATTTTTATTTCATTTTCAATTACTTTGTA---  716
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1395  TAAACAAGAATATAACATTTCAATAGAAATTTTTATTTCATTTTCAATTACTTTGTAAAT  1454

Query  717   --------------------------------TACATTTCTGCTTTGAATGCAGATGCAA  744
                                             ||||||||||||||||||||||||||||
Sbjct  1455  TCGTGTGTATTTAGTACACTGATTTGTTTTTTTACATTTCTGCTTTGAATGCAGATGCAA  1514

Query  745   ATTTTAATATAATAGATTTTTTAATGAATTAATCTTAACATAGTAATCTTTAGCTTTTTA  804
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1515  --TTTAATATAATAGATTTTTTAATGAATTAATCTTAACATAGTAATCTTTAGCTTTTTA  1572

Query  805   TACAAATATATTTAATTTAGGAGTATATGTGTGTCTATACACACACATACATAAATATAC  864
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1573  TACAAATATATTTAATTTAGGAGTATATGTGTGTCTATACACACACATACATAAATATAC  1632

Query  865   CACATATACA-CTGATAGTCAAATAGGGTACAGAAATTTTATCTTGTCAA-TATGCC-AA  921
             |||||||||| |||||||||||||| |||||||||||||||||||||||| |||||| ||
Sbjct  1633  CACATATACACCTGATAGTCAAATAAGGTACAGAAATTTTATCTTGTCAATTATGCCAAA  1692

Query  922   TTATCTCTTTAATGTGCACTCCAACATGTAAT-AACTTTGGATATTTAAAAAA  973
             | ||||||||||||||||||| |||||||||| ||||||||||| ||||| ||
Sbjct  1693  TAATCTCTTTAATGTGCACTCAAACATGTAATAAACTTTGGATAATTAAATAA  1745
```

PPIL1-KIAA1614

```
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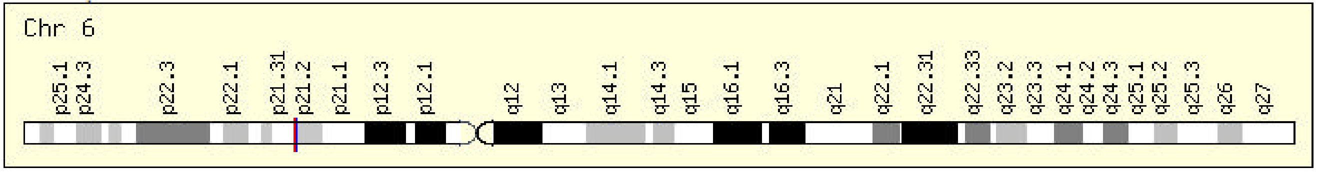
5' partner: PPIL1



```
Junction point
exon=2 309..463
/gene="PPIL1"
/gene_synonym="CGI-124; CYPL1; hCyPX; MGC678; PPIase"

BLAST vs mRNA

>ref|NM_016059.4| Homo sapiens peptidylprolyl isomerase (cyclophilin)-like 1 (PPIL1), mRNA
Length=1750
GENE ID: 51645 PPIL1| peptidylprolyl isomerase (cyclophilin)-like 1 [Homo sapiens]
Score =  437 bits (484),  Expect = 3e-126
Identities = 242/242 (100%), Gaps = 0/242 (0%)

Strand=Plus/Plus
```

```
Query  12   CTAGACAAGCATTCCGCCGCCGGCTTCGCTATGGCGGCAATTCCCCCAGATTCCTGGCAG  71
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  223  CTAGACAAGCATTCCGCCGCCGGCTTCGCTATGGCGGCAATTCCCCCAGATTCCTGGCAG  282
```

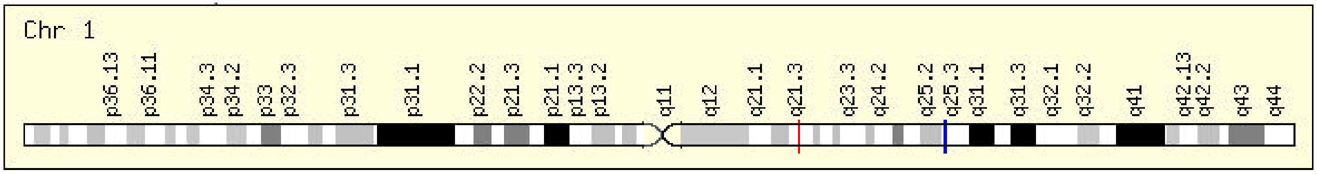
```
Query  72   CCACCCAACGTTTACTTGGAGACCAGCATGGGAATCATTGTGCTGGAGCTGTACTGGAAG  131
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  283  CCACCCAACGTTTACTTGGAGACCAGCATGGGAATCATTGTGCTGGAGCTGTACTGGAAG  342

Query  132  CATGCTCCAAAGACCTGTAAGAACTTTGCTGAGTTGGCTCGTCGAGGTTACTACAATGGC  191
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  343  CATGCTCCAAAGACCTGTAAGAACTTTGCTGAGTTGGCTCGTCGAGGTTACTACAATGGC  402

Query  192  ACAAAATTCCACAGAATTATCAAAGACTTCATGATCCAAGGAGGTGACCCAACAGGGACA  251
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  403  ACAAAATTCCACAGAATTATCAAAGACTTCATGATCCAAGGAGGTGACCCAACAGGGACA  462

Query  252  GG  253
            ||
Sbjct  463  GG  464
             ↑
```

3' partner: KIAA1614



Junction point
exon=6 2829..2985
/gene="KIAA1614"
/gene_synonym="RP11-46A10.3"

BLAST vs mRNA

```
>ref|NM_020950.1| Homo sapiens KIAA1614 (KIAA1614), mRNA
Length=4155
GENE ID: 57710 KIAA1614| KIAA1614 [Homo sapiens]
Score = 1238 bits (1372),  Expect = 0.0
Identities = 712/724 (98%), Gaps = 4/724 (0%)

Strand=Plus/Plus
```

```
               ↓
Query  252   GGAGGACCCCAGGGCTTTCTTGGCTCAGCAGATGTTGCCACCATCAACTCCACGGGCATC  311
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2828  GGAGGACCCCAGGGCTTTCTTGGCTCAGCAGATGTTGCCACCATCAACTCCACGGGCATC  2887

Query  312   ACCCTCTCCCTGTCCTCAGAGGAGTCAGAGTCCAGCAAGGAATCAGAGGGAAGCCTGCAG  371
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2888  ACCCTCTCCCTGTCCTCAGAGGAGTCAGAGTCCAGCAAGGAATCAGAGGGAAGCCTGCAG  2947

Query  372   AGGACAGGGTCAGGATCTGGAGGACATGTGCTGTCAAGAGCATCAGCAGGAGCTGGCACA  431
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2948  AGGACAGGGTCAGGATCTGGAGGACATGTGCTGTCAAGAGCATCAGCAGGAGCTGGCACA  3007

Query  432   GGACCCGGCTCCCCCTCGGCTGCCCCTTTGGACCAGAACAAGAAAAGGAGCAGCAGCATA  491
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3008  GGACCCGGCTCCCCCTCGGCTGCCCCTTTGGACCAGAACAAGAAAAGGAGCAGCAGCATA  3067

Query  492   GCCTCCACCCTGGGGCTGAAAAAGCTCTTCTCAGCCCTGGGCCAGAGTTCCCGGCCCAAG  551
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3068  GCCTCCACCCTGGGGCTGAAAAAGCTCTTCTCAGCCCTGGGCCAGAGTTCCCGGCCCAAG  3127

Query  552   CTGGGCAAGTCCCGCAGCTACAGTGTGGAGCAGTTGCAGCCCGCCCCGCCTGGCCTGACG  611
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3128  CTGGGCAAGTCCCGCAGCTACAGTGTGGAGCAGTTGCAGCCCGCCCCGCCTGGCCTGACG  3187

Query  612   TCACAGTCCAGGGCCCCATCGTTACAATCCCTGCACCCGGTGTCACCCTCTCACCAGCGT  671
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3188  TCACAGTCCAGGGCCCCATCGTTACAATCCCTGCACCCGGTGTCACCCTCTCACCAGCGT  3247

Query  672   CGGAAAGCTGCCTCTTTTCAGAACCTCCATTCTCTGCTGAGCAGCAAGGGGGACCGGTCC  731
             ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  3248  CGGAAAGCTGCCTCTTTTCAGAACCTCCATTCTCTGCTGAGCAGCAAGGGGAACCGGTCC  3307

Query  732   AGCCTCTACCTGGTAGCAGGGCCAGGGGACCACAGTGCAGCTGGCA-GCCGGCCAAGACT  790
             |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct  3308  AGCCTCTACCTGGTAGCAGGGCCAGGGGACCACAGTGCAGCTGGCAGGCCGGCCAAGACT  3367

Query  791   TCACCACGGCGTGCCCTCAGTGTGGAGGACGTGGGTGCTCCCAGCCTGTCTCGCACCGTG  850
             |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  3368  TCACCACGGCGTGCCCTCAGTGTGGAGGACGTGGGTGCTCCCAGCCTGGCTCGCACCGTG  3427

Query  851   GGCCGCCTGGTGGAGGTGTTCCCAGACAGCACCAGCCAGCTGCAGCTGCAGCGCTCTCCA  910
             ||||||||||||||||||||||||||| |||||||||||||||||||||||||||| |||
Sbjct  3428  GGCCGCCTGGTGGAGGTGTTCCCAGACGGCACCAGCCAGCTGCAGCTGCAGCGCTCCCCA  3487
```

```
Query  911    -AGGGCACTTTCGGCTTCTGCGT-GCCTCTGGGAAT-GGCGCCCAGACTCAGGGACGCAC  967
                ||||||||||||||||||||| |||||||||||| |||||||||||||||| | || |
Sbjct  3488   GGGGGCACTTTCGGCTTCTGCGTGGCCTCTGGGAATGGGCGCCCAGACTCAGGTATGCCC  3547

Query  968    TCTC  971
              ||||
Sbjct  3548   TCTC  3551
```

WDR70- ANKLE2

```
TTGGGGTTCTGCGGCGTGCGGCCAGCCATGGAGCGCTCTGGGCCCAGCGAAGTGACAGGCTCAGACGCATCGGGACCGGACCCGCAGCTTGCGGTCACCATG
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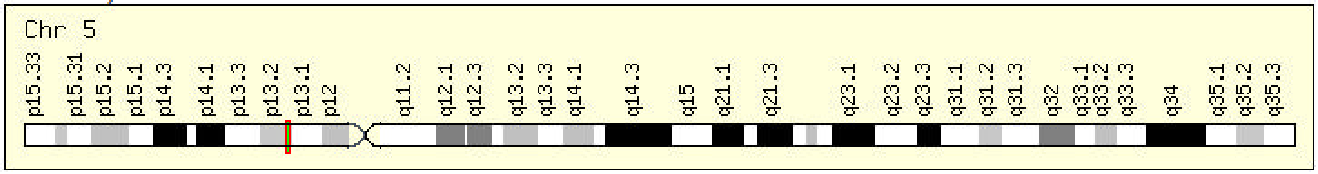
5’ partner: WDR70



Junction point
exon=3 150..233
/gene="WDR70"
/gene_synonym="FLJ10233"

BLAST vs mRNA

```
>ref|NM_018034.2| Homo sapiens WD repeat domain 70 (WDR70), mRNA
Length=2247
Score =  334 bits (370),  Expect = 4e-95
Identities = 193/198 (97%), Gaps = 0/198 (0%)

Strand=Plus/Plus

Query  5      GGTTCTGCGGCGTGCGGCCAGCCATGGAGCGCTCTGGGCCCAGCGAAGTGACAGGCTCAG  64
              ||||||| || |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  36     GGTTCTGGGGTGTGCGGCCAGCCATGGAGCGCTCTGGGCCCAGCGAAGTGACAGGCTCAG  95

Query  65     ACGCATCGGGACCGGACCCGCAGCTTGCGGTCACCATGGGCTTCACGGGGTTCGGTAAAA  124
              |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  96     ACGCGTCGGGACCGGACCCGCAGCTTGCGGTCACCATGGGCTTCACGGGGTTCGGTAAAA  155

Query  125    AAGCTCGCACATTTGACTTGGAAGCAATGTTTGAACAAACTCGAAGAACAGCTGTGGAAA  184
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct  156    AAGCTCGCACATTTGACTTGGAAGCAATGTTTGAACAAACTCGAAGGACAGCTGTGGAAA  215

Query  185    GAAGTTGCAAAACACTGG  202
              ||||| ||||||||||||
Sbjct  216    GAAGTCGCAAAACACTGG  233
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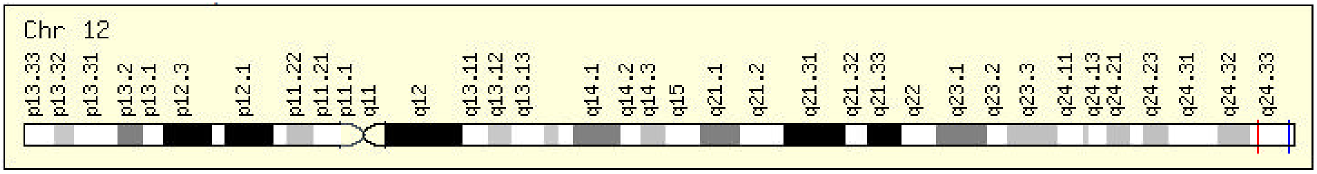
🡅

3’ partner: ANKLE2



Junction point
exon=2 249..707
/gene="ANKLE2"

```
/gene_synonym="FLJ22280; FLJ36132; KIAA0692; LEMD7"
```

BLAST vs mRNA

```
>ref|NM_015114.1| Homo sapiens ankyrin repeat and LEM domain containing 2 (ANKLE2), mRNA
Length=4491
GENE ID: 23141 ANKLE2 | ankyrin repeat and LEM domain containing 2 [Homo sapiens]
Score = 1517 bits (1682),  Expect = 0.0
Identities = 986/1049 (93%), Gaps = 45/1049 (4%)

Strand=Plus/Plus

                ↓
Query  202   GGTGAAATGACAATGGATGCTCTGTTGGCTCGATTGAAACTTCTGAATCCAGATGACCTT  261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  248   GGTGAAATGACAATGGATGCTCTGTTGGCTCGATTGAAACTTCTGAATCCAGATGACCTT  307

Query  262   AGAGAAGAAATCGTCAAAGCCGGATTGAAATGTGGACCCATTACATCAACTACAAGGTTC  321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  308   AGAGAAGAAATCGTCAAAGCCGGATTGAAATGTGGACCCATTACATCAACTACAAGGTTC  367

Query  322   ATTTTTGAGAAAAAATTGGCTCAGGCTTTACTGGAGCAAGGAGGAAGGCTGTCTTCTTTC  381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  368   ATTTTTGAGAAAAAATTGGCTCAGGCTTTACTGGAGCAAGGAGGAAGGCTGTCTTCTTTC  427

Query  382   TACCACCATGAGGCAGGTGTCACAGCTCTCAGCCAGGACCCACAAAGGATTTTGAAGCCA  441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  428   TACCACCATGAGGCAGGTGTCACAGCTCTCAGCCAGGACCCACAAAGGATTTTGAAGCCA  487

Query  442   GCTGAAGGGAACCCAACTGATCAGGCTGGTTTTTCTGAAGACAGAGATTTTGGTTACAGT  501
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  488   GCTGAAGGGAACCCAACTGATCAGGCTGGTTTTTCTGAAGACAGAGATTTTGGTTACAGT  547

Query  502   GTGGGCCTGAATCCTCCAGAGGAGGAAGCTGTGACATCCAAGACCTGCTCGGTGCCTCCT  561
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  548   GTGGGCCTGAATCCTCCAGAGGAGGAAGCTGTGACATCCAAGACCTGCTCGGTGCCCCCT  607

Query  562   AGTGACACCGACACCTACAGAGCTGGAGCGACTGCGTCTAAGGAGCCGCCCCTGTACTAT  621
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  608   AGTGACACCGACACCTACAGAGCTGGAGCGACTGCGTCTAAGGAGCCGCCCCTGTACTAT  667

Query  622   GGGGTGTGTCCAGTGTATGAGGACGTCCCAGCGAGAAATGAAAGGATCTATGTTTATGAA  681
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  668   GGGGTGTGTCCAGTGTATGAGGACGTCCCAGCGAGAAATGAAAGGATCTATGTTTATGAA  727

Query  682   AATAAAAAGGAAGCATTGCAAGCTGTCAAGATGATCAAAGGGTCCCGATTTAAAGCTTTT  741
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  728   AATAAAAAGGAAGCATTGCAAGCTGTCAAGATGATCAAAGGGTCCCGATTTAAAGCTTTT  787

Query  742   TCTACCAGAGAAGACGCTGAGAAATTTGCTAGAGGAATTTGTGATTATTTCCCTTCTCCA  801
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  788   TCTACCAGAGAAGACGCTGAGAAATTTGCTAGAGGAATTTGTGATTATTTCCCTTCTCCA  847

Query  802   AGCAAAACGTCCTTACCACTGTCTCCTGTGAAAACAGCTCCACTCTTTAGCAATGACAGG  861
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  848   AGCAAAACGTCCTTACCACTGTCTCCTGTGAAAACAGCTCCACTCTTTAGCAATGACAGG  907

Query  862   TTGAAAGATGGTTTGTGCTTGTCGG-ATCAG-AACAGTCAACAAAGAGCGAGCGAACAGT  919
             ||||||||||||||||||||||||| ||||| ||||||||||||||||||||||||||||
Sbjct  908   TTGAAAGATGGTTTGTGCTTGTCGGAATCAGAAACAGTCAACAAAGAGCGAGCGAACAGT  967
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TAF11- FAM62B

```
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CAGCTGGAAAACGGGACGACCCTGGGACAGTCTCCACTGGGGCAGATCCAGCTGACCATCCGGCACAGCTCGCAGAGAACAAGCTTATCGTGGTCGTGCATG
CTGCAGAAACCTCATTGCTTCTCTGAGACGCTCTGACCCTATGTCGCATGTATTTATTACGGACAGAGCGGTCAGGAGAGAAACCCCCGGTCAAGAAAATTA
TCAATGTTGATCAGCTGATCAGTTCGTACAAAATGCAAGAACCTGACGTGCTGAGACTGCGCTCGTCAGACAGGTCCTGGCAGATTGTGTCTGCACCTGAAA
CTTGCCA
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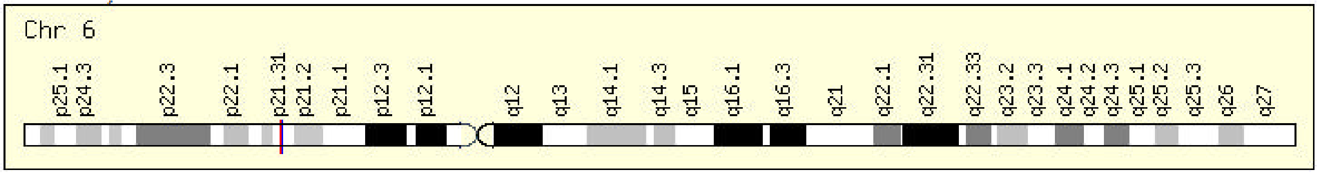
5' partner: TAF11



```
Junction point
exon=1 1..256
/gene="TAF11"
/gene_synonym="MGC:15243; PRO2134; TAF2I; TAFII28"

BLAST vs mRNA

>ref|NM_005643.2| Homo sapiens TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated
factor, 28kDa (TAF11), mRNA
Length=1599
GENE ID: 6882 TAF11 | TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 28kDa
[Homo sapiens]
Score =  405 bits (448),  Expect = 2e-116
Identities = 224/224 (100%), Gaps = 0/224 (0%)

Strand=Plus/Plus

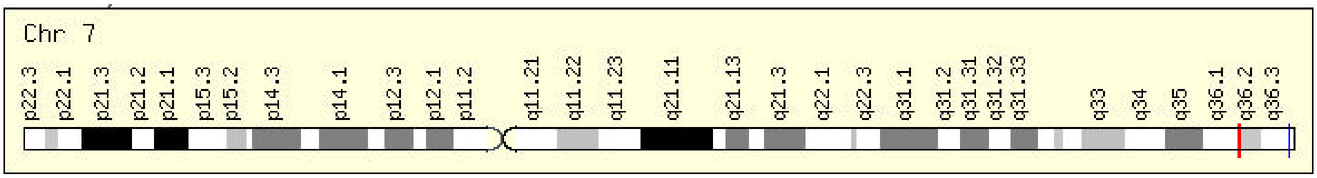
Query  4    GCTTCTGCCTCAGGCATCTCCGCGATCTCCTCTCCCCTCCAATCCTATCCGTGATGGACG  63
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  33   GCTTCTGCCTCAGGCATCTCCGCGATCTCCTCTCCCCTCCAATCCTATCCGTGATGGACG  92

Query  64   ATGCCCACGAGTCGCCCTCCGACAAAGGTGGAGAGACAGGGGAGTCGGATGAGACGGCCG  123
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  93   ATGCCCACGAGTCGCCCTCCGACAAAGGTGGAGAGACAGGGGAGTCGGATGAGACGGCCG  152

Query  124  CTGTGCCCGGGGACCCGGGGGCTACCGACACCGATGGAATCCCAGAGGAAACTGACGGAG  183
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  153  CTGTGCCCGGGGACCCGGGGGCTACCGACACCGATGGAATCCCAGAGGAAACTGACGGAG  212

Query  184  ACGCAGATGTGGACTTGAAAGAAGCTGCAGCGGAGGAAGGCGAG  227
            ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  213  ACGCAGATGTGGACTTGAAAGAAGCTGCAGCGGAGGAAGGCGAG  256
                                                      ↑
```

3' partner: FAM62B



```
Junction point
exon=15 1705..1791
/gene="FAM62B"
/gene_synonym="CHR2SYT; ESYT2; KIAA1228"

BLAST vs mRNA

>ref|NM_020728.2| Homo sapiens family with sequence similarity 62 (C2 domain containing) member B
(FAM62B), mRNA
Length=5957
GENE ID: 57488 FAM62B | family with sequence similarity 62 (C2 domain containing) member B [Homo
sapiens]
Score = 1321 bits (1464),  Expect = 0.0
Identities = 802/828 (96%), Gaps = 18/828 (2%)

Strand=Plus/Plus



                       ↓
Query  217   AGGAAGGCGAGATTCGATACAAAACCAATGAACCTGTGTGGGAGGAAAACTTCACTTTCT  276
             ||||  || |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1694  AGGAGAGCAAGATTCGATACAAAACCAATGAACCTGTGTGGGAGGAAAACTTCACTTTCT  1753
```

```
Query  277   TCATTCACAATCCCAAGCGCCAGGACCTTGAAGTTGAGGTCAGAGACGAGCAGCACCAGT  336
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1754  TCATTCACAATCCCAAGCGCCAGGACCTTGAAGTTGAGGTCAGAGACGAGCAGCACCAGT  1813

Query  337   GTTCCCTGGGGAACCTGAAGGTCCCCCTCAGCCAGCTGCTCACCAGTGAGGACATGACTG  396
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1814  GTTCCCTGGGGAACCTGAAGGTCCCCCTCAGCCAGCTGCTCACCAGTGAGGACATGACTG  1873

Query  397   TGAGCCAGCGCTTCCAGCTCAGTAACTCGGGTCCAAACAGCACCATCAAGATGAAGATTG  456
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1874  TGAGCCAGCGCTTCCAGCTCAGTAACTCGGGTCCAAACAGCACCATCAAGATGAAGATTG  1933

Query  457   CCCTGCGGGTGCTCCATCTCGAAAAGCGAGAAAGGCCTCCAGACCACCAACACTCAGCTC  516
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1934  CCCTGCGGGTGCTCCATCTCGAAAAGCGAGAAAGGCCTCCAGACCACCAACACTCAGCTC  1993

Query  517   AAGTCAAACGTCCCTCTGTGTCCAAAGAGGGGAGGAAAACATCCATCAAATCTCATATGT  576
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1994  AAGTCAAACGTCCCTCTGTGTCCAAAGAGGGGAGGAAAACATCCATCAAATCTCATATGT  2053

Query  577   CTGGGTCTCCAGGCCCTGGTGGCAGCAACACAGCTCCATCCACACCAGTCATTGGGGGCA  636
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2054  CTGGGTCTCCAGGCCCTGGTGGCAGCAACACAGCTCCATCCACACCAGTCATTGGGGGCA  2113

Query  637   GTGATAAGCCTGGTATGGAAGAAAAGGCCCAGCCCCCTGAGGCCGGCCCTCAAGGGCTGC  696
             |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  2114  GTGATAAGCCTGGTATGGAAGAAAAGGCCCAGCCCCCTGAGGCCGGCCCTCAGGGGCTGC  2173

Query  697   ACGACCT-GGCAGAAGCTCCTCCAGCCTCCTGGCCTCCCCAGGCCACATCTCAGTCAAGG  755
             ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2174  ACGACCTGGGCAGAAGCTCCTCCAGCCTCCTGGCCTCCCCAGGCCACATCTCAGTCAAGG  2233

Query  756   AGCCGACCCCCAGCATCGCCTCGGACATCTCGCTGCCCATCGCCACCCAGGAGCTGCGGC  815
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2234  AGCCGACCCCCAGCATCGCCTCGGACATCTCGCTGCCCATCGCCACCCAGGAGCTGCGGC  2293
```

NOL11- C7orf42

```
TCAAATTATAACAAGTCCAGCTGTGTGCAACTTTCAAACTGGAGAGTATGTTGTTGTACACGGTTAATAAGGTTTTAAGAATATGGAATAATGAAGATGTAA
CCTGGATAAAGTATTTAAAGCTACATTGTCAGCAGAAGTATATAGGATACTTTCAGTGCAAGGGACAGAACCCTTGGTGCTCTTCAAGGAAGGTGCTGTTCG
GGTTTAGAGGCCTTGCTTGCAGACCCCCAGCAGAAAATTGAAACTGTTATCTCTGATGAAGAAGTGATTAAACAGCCACCGCACTGTGTTCCTGACACGTAC
GCAACGCCACGTTCTGGTACAAGATCTTCACAACTGCCAGGGATGCCAACACAAAATACGCCCAAGATTACAATCCTTTCTGGTGTTATAAGGGGGCCATTG
AAAAGTTTATCATGCTTTAAATCCCAAGCTTACAGTGATTGTTCCAGATGATGACCGTTCATTAATAAATTTGCATATCAAGCACACCAGTTACTTCCTAAA
GTGATGGTGTTAACAATGTTTTGAAAAGATGTAATCTTGGGCTGACGTAGCAAAAAGAGTCAGAGCAATCAAGAAAAAATCCCGAGAAGGTGGATTTGG
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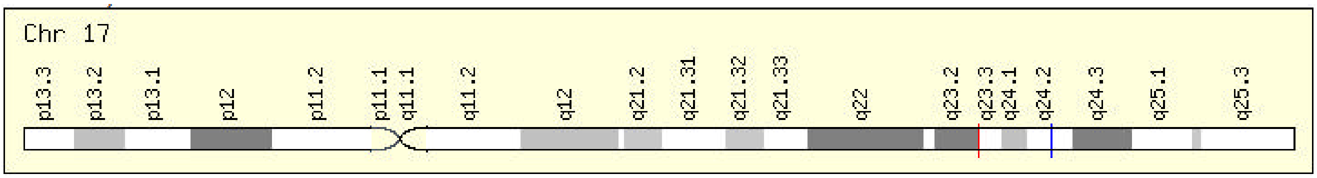
5’ partner: NOL11



```
Junction point
exon=4 316..464
/gene="NOL11"
/gene_synonym="DKFZp586L0724"

BLAST vs mRNA

>ref|NM_015462.3| Homo sapiens nucleolar protein 11 (NOL11), mRNA
Length=2454
GENE ID: 25926 NOL11 | nucleolar protein 11 [Homo sapiens]
Score =  484 bits (536),  Expect = 2e-140
Identities = 275/278 (98%), Gaps = 1/278 (0%)

Strand=Plus/Plus

Query  5    CTTGGGGAGCTGGTCAGTGAAACAAGGTCAAATTATAACATGTCCAGCTGTGTGCAACTT  64
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  162  CTTGGGGAGCTGGTCAGTGAAACAAGGTCAAATTATAACATGTCCAGCTGTGTGCAACTT  221

Query  65   TCAAACTGGAGAGTATGTTGTTGTACACGATAATAAGGTTTTAAGAATATGGAATAATGA  124
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  222  TCAAACTGGAGAGTATGTTGTTGTACACGATAATAAGGTTTTAAGAATATGGAATAATGA  281

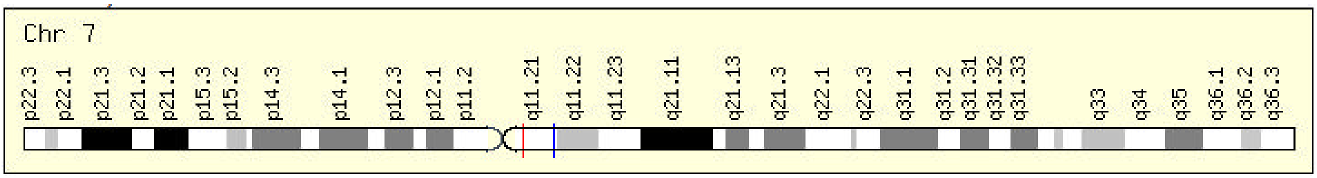
Query  125  AGATGTAAACCTGGATAAAGTATTTAAAGCTACATTGTCAGCAGAAGTATATAGGATACT  184
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  282  AGATGTAAACCTGGATAAAGTATTTAAAGCTACATTGTCAGCAGAAGTATATAGGATACT  341

Query  185  TTCAGTGCAAGGGACAGAACCCTTGGTGCTCTTCAAGGAAGGTGCTGTTCGTGGTTTAGA  244
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  342  TTCAGTGCAAGGGACAGAACCCTTGGTGCTCTTCAAGGAAGGTGCTGTTCGTGGTTTAGA  401
```

```
Query  245  GGCCTTGCTTGCAGACCCCCAGCAGAAAATTGAAACTGTTATCTCTGATGAAGAAGTGAT  304
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  402  GGCCTTGCTTGCAGACCCCCAGCAGAAAATTGAAACTGTTATCTCTGATGAAGAAGTGAT  461

Query  305  TAAA  308
            ||||
Sbjct  462  TAAA  465
              ↑
```

3’ partner: C7orf42



Junction point
exon=5 861..1044
/gene="C7orf42"
/gene_synonym="FLJ10099; FLJ13090"

BLAST vs mRNA

```
>ref|NM_017994.4| Homo sapiens chromosome 7 open reading frame 42 (C7orf42), mRNA
Length=4238
GENE ID: 55069 C7orf42| chromosome 7 open reading frame 42 [Homo sapiens]
Score =  475 bits (526),  Expect = 2e-137
Identities = 309/338 (91%), Gaps = 1/338 (0%)

Strand=Plus/Plus
```

```
              ↓
Query  308   ACAGCCACCGCACTGTGTTCCTGACACGTACAGCAACGCCACGCTCTGGTACAAGATCTT  367
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  861   ACAGCCACCGCACTGTGTTCCTGACACGTACAGCAACGCCACGCTCTGGTACAAGATCTT  920

Query  368   CACAACTGCCAGAGATGCCAACACAAAATACGCCCAAGATTACAATCCTTTCTGGTGTTA  427
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  921   CACAACTGCCAGAGATGCCAACACAAAATACGCCCAAGATTACAATCCTTTCTGGTGTTA  980

Query  428   TAAGGGGGCCATTGGAAAAGTCTATCATGCTTTAAATCCCAAGCTTACAGTGATTGTTCC  487
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  981   TAAGGGGGCCATTGGAAAAGTCTATCATGCTTTAAATCCCAAGCTTACAGTGATTGTTCC  1040

Query  488   AGATGATGACCGTTCATTAATAAATTTGCATCTCATGCACACCAGTTACTTCCTCTTTGT  547
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1041  AGATGATGACCGTTCATTAATAAATTTGCATCTCATGCACACCAGTTACTTCCTCTTTGT  1100

Query  548   GATGGTGATAACAATGTTTTGCTATGCTGTTATCAAGGGCAGACCTAGCAAATTGCGTCA  607
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1101  GATGGTGATAACAATGTTTTGCTATGCTGTTATCAAGGGCAGACCTAGCAAATTGCGTCA  1160

Query  608   GAGCAATCCTGAATTTTGTCCCGAGAAGGTGGCTTTGGCTGAAGCCTAATTCCACAGCTC  667
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1161  GAGCAATCCTGAATTTTGTCCCGAGAAGGTGGCTTTGGCTGAAGCCTAATTCCACAGCTC  1220

Query  668   CTTGTTTTTAGAGAGAGACTGAGAGAACCATAATCCTTGCCTGCTGAACCCAGCCTGGGC  727
             ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1221  CTTGTTTTTTGAGAGAGACTGAGAGAACCATAATCCTTGCCTGCTGAACCCAGCCTGGGC  1280

Query  728   CTGGATGCTCTGTGAATACATTATCTTGCGATGTTGGGTTATTCCAGCCAAAGACATTTC  787
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1281  CTGGATGCTCTGTGAATACATTATCTTGCGATGTTGGGTTATTCCAGCCAAAGACATTTC  1340

Query  788   AAGTGCCTGTAACTGATTTGTACATATTTAT-AAAATCTATTCAGA  832
             ||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  1341  AAGTGCCTGTAACTGATTTGTACATATTTATAAAAATCTATTCAGA  1386
```

NSUN5B- CPSF3

```
TTGGGCCGCCAGGGCTCTATCAAGGGGCTGGTGTACTCCAGCAACTTCCAGAACGTGAAGCAGCTGTACGCGCTGGTGTGCGAAACGCAGCGCTACTCCGCC
TGCTGGATGCCGTGATCTCCAGCGCCGGCCTCCTCAGTGCGAAGAAGCTGCAGCCGCACCTGGCCAAGGGTGCAGTACAGAAGGTTTTTAAAAAATTAGAAA
GCACGTTTACAGCAAGAGGTTGGAGATCATGCTCCAGGACATATTTGGAGAAGACTGTGTAAGTGTAAAGGATGACTCTATTTTTAGCGTCACAGTGGACGG
AAAACTGCCAACCTTAACTTGGAGACACGGACTGTAGAATGTGAAGAGGGAAGTGAAGACGATGAATCCCTCCGAGAAATGGTGGAGCTGGCTGCACAGAGA
TGTACGAGGCCCTGACGCCAGTTCACTGAGACTGTGCCTGTATATGAACTTTGAAAAAATACTTGACTTTACTTTTGTTACCTAAAATAAAATGCATTCGTT
TTTTG
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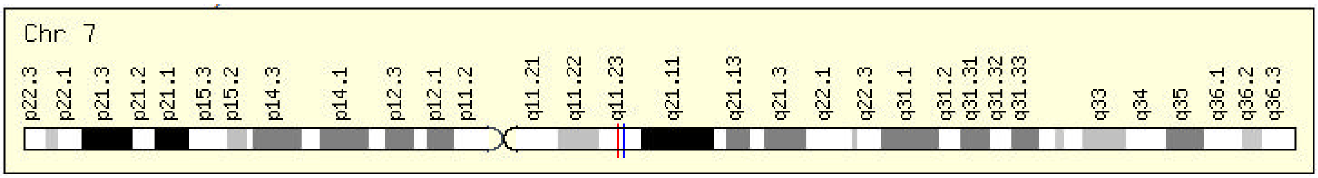
5’ partner: NSUN5B



```
Junction point
exon=2 121..241
/gene="NSUN5P1"
/gene_synonym="FLJ99347; MGC129801; NSUN5B; WBSCR20B"
```

BLAST vs mRNA

```
>ref|NR_033322.2| Homo sapiens NOP2/Sun domain family, member 5 pseudogene 1 (NSUN5P1), non-coding RNA
Length=1751
GENE ID: 155400 NSUN5P1| NOP2/Sun domain family, member 5 pseudogene 1 [Homo sapiens]
Score =  311 bits (168),  Expect = 3e-84
Identities = 168/168 (100%), Gaps = 0/168 (0%)

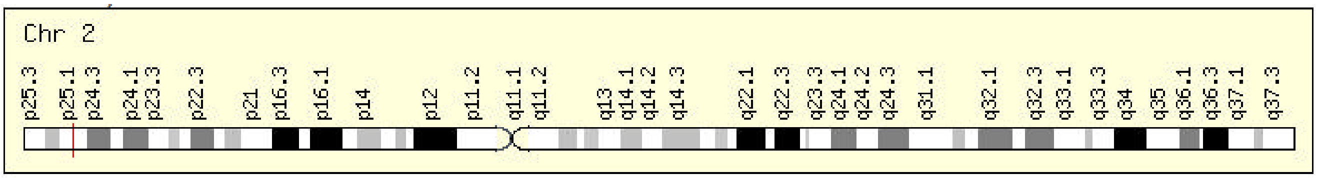
Strand=Plus/Plus

Query  5    GCCGCCAGGGCTCTATCAAGGGGCTGGTGTACTCCAGCAACTTCCAGAACGTGAAGCAGC  64
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  74   GCCGCCAGGGCTCTATCAAGGGGCTGGTGTACTCCAGCAACTTCCAGAACGTGAAGCAGC  133

Query  65   TGTACGCGCTGGTGTGCGAAACGCAGCGCTACTCCGCCGTGCTGGATGCCGTGATCTCCA  124
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  134  TGTACGCGCTGGTGTGCGAAACGCAGCGCTACTCCGCCGTGCTGGATGCCGTGATCTCCA  193

Query  125  GCGCCGGCCTCCTCAGTGCGAAGAAGCTGCAGCCGCACCTGGCCAAGG  172
            ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  194  GCGCCGGCCTCCTCAGTGCGAAGAAGCTGCAGCCGCACCTGGCCAAGG  241
                                                          ↑
```

3’ partner: CPSF3



```
Junction point
exon=16 1822..1891
/gene="CPSF3"
/gene_synonym="CPSF; CPSF-73; CPSF73; YSH1"
```

BLAST vs mRNA

```
>ref|NM_016207.2| Homo sapiens cleavage and polyadenylation specific factor 3, 73kDa (CPSF3), mRNA
Length=2286
Score =  609 bits (674),  Expect = 5e-178
Identities = 343/347 (98%), Gaps = 0/347 (0%)

Strand=Plus/Plus

                 ↓
Query  169   AAGGGTGCAGTACAGAAGGTTTTTAAAAAATTAGAAATGCACGTTTACAGCAAGAGGTTG  228
             || ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  1818  AAAGGTGCAGTACAGAAGGTTTCTAAAAAATTAGAAATGCACGTTTACAGCAAGAGGTTG  1877

Query  229   GAGATCATGCTCCAGGACATATTTGGAGAAGACTGTGTAAGTGTAAAGGATGACTCTATT  288
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1878  GAGATCATGCTCCAGGACATATTTGGAGAAGACTGTGTAAGTGTAAAGGATGACTCTATT  1937

Query  289   TTTAGCGTCACAGTGGACGGGAAAACTGCCAACCTTAACTTGGAGACACGGACTGTAGAA  348
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1938  CTTAGCGTCACAGTGGACGGGAAAACTGCCAACCTTAACTTGGAGACACGGACTGTAGAA  1997
```

```
Query  349   TGTGAAGAGGGAAGTGAAGACGATGAATCCCTCCGAGAAATGGTGGAGCTGGCTGCACAG  408
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1998  TGTGAAGAGGGAAGTGAAGACGATGAATCCCTCCGAGAAATGGTGGAGCTGGCTGCACAG  2057

Query  409   AGACTGTACGAGGCCCTGACGCCAGTTCACTGAGACTGTGCCTGTATATGAACTTTGAAA  468
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2058  AGACTGTACGAGGCCCTGACGCCAGTTCACTGAGACTGTGCCTGTATATGAACTTTGAAA  2117

Query  469   AAATACTTGACTTTACTTTTGTTACCTAAAATAAAATGCATTCGTTT  515
             ||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  2118  AAATACTTGACTCTACTTTTGTTACCTAAAATAAAATGCATTCGTTT  2164
```

MSMB- POLE4

```
AATGCCAACTTTGTACAAAAAAGTTGGAGGAGTCCTGCTTATCACAATGAATGTTCTCCTGGGCAGCGTTGTGATCTTTGCCACCTTCGTGACTTTATGCAA
GCATCATGCTATTTCATACCTAATGAGGGAGTTCCAGGAGATTCAACCAGGAAATGCATGGATCTCAAAGGAAACAAACACCCAATAAACTCGGAGTGGCAG
CTGACAACTGTGAGACATGCACTTGCTACGAAACAGAAATTTCATGTTGCACCCTATAATGCAATAGAAGCTGTGGATGAATTTGCTTTTCTGGAAGGTACT
TAGATTGATTGCCGAGCGGGGCAGTTTTGTGAGCCTTCATCTGAAGCCTTCAGTTCACCCCTCTGCACAGGCCTCAGCTTTGAAGAACGGAGTCTTTGCACT
ACACACACTCTTCCTGTTCTGCCTTCACCTATGCCGGGATAAGCAGAGATCTCATCAATTAGCTCTTCTCTGCAAGGTCTTCCACTGTTTCTGTCTGTCTTC
ATATCAAGCCTGGATGCAGCTGCTGCTGCTTAGAGCAGAGATGAAGAAAGTGTTCTGCATAAGTGGCTTCCTGAATGATGAGGACCAGAATAAAGGTTTTTG
TCAACCTC
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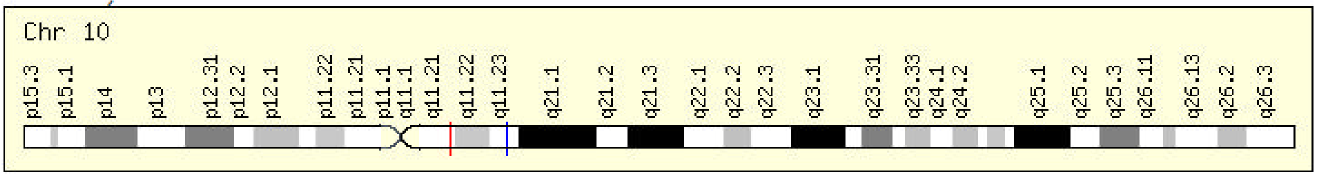
5’ partner: MSMB



Junction point
exon=3 142..247
/gene="MSMB"
/gene_synonym="HPC13; IGBF; MSP; MSPB; PN44; PRPS; PSP;
PSP-94; PSP57; PSP94"

BLAST vs mRNA

```
>ref|NM_002443.2| Homo sapiens microseminoprotein, beta- (MSMB), transcript variant PSP94, mRNA
Length=572
GENE ID: 4477 MSMB microseminoprotein, beta- [Homo sapiens]
Score =  423 bits (468),  Expect = 1e-122
Identities = 234/234 (100%), Gaps = 0/234 (0%)

Strand=Plus/Plus

Query  28   AGGAGTCCTGCTTATCACAATGAATGTTCTCCTGGGCAGCGTTGTGATCTTTGCCACCTT  87
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  14   AGGAGTCCTGCTTATCACAATGAATGTTCTCCTGGGCAGCGTTGTGATCTTTGCCACCTT  73

Query  88   CGTGACTTTATGCAATGCATCATGCTATTTCATACCTAATGAGGGAGTTCCAGGAGATTC  147
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  74   CGTGACTTTATGCAATGCATCATGCTATTTCATACCTAATGAGGGAGTTCCAGGAGATTC  133

Query  148  AACCAGGAAATGCATGGATCTCAAAGGAAACAAACACCCAATAAACTCGGAGTGGCAGAC  207
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  134  AACCAGGAAATGCATGGATCTCAAAGGAAACAAACACCCAATAAACTCGGAGTGGCAGAC  193

Query  208  TGACAACTGTGAGACATGCACTTGCTACGAAACAGAAATTTCATGTTGCACCCT  261
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  194  TGACAACTGTGAGACATGCACTTGCTACGAAACAGAAATTTCATGTTGCACCCT  247
                                                              ↑
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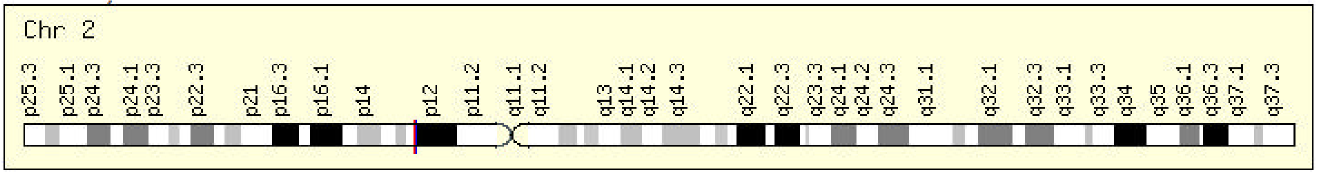
3’ partner: POLE4



Junction point
exon=3 331..372
/gene="POLE4"
/gene_synonym="p12"

BLAST vs mRNA

```
>ref|NM_019896.2| Homo sapiens polymerase (DNA-directed), epsilon 4 (p12 subunit) (POLE4), mRNA
Length=710
GENE ID: 56655 POLE4| polymerase (DNA-directed), epsilon 4 (p12 subunit) [Homo sapiens]
Score =  654 bits (724),  Expect = 0.0
Identities = 364/365 (99%), Gaps = 0/365 (0%)

Strand=Plus/Plus

               ↓
Query  262  ATAATGCAATAGAAGCTGTGGATGAATTTGCTTTTCTGGAAGGTACTTTAGATTGATTGC  321
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  331  ATAATGCAATAGAAGCTGTGGATGAATTTGCTTTTCTGGAAGGTACTTTAGATTGATTGC  390

Query  322  CGAGCGGGGCAGTTTTGTGAGCCTTCATCTGAAGCCTTCAGTTCACCCCTCTGCACAGGC  381
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  391  CGAGCGGGGCAGTTTTGTGAGCCTTCATCTGAAGCCTTCAGTTCACCCCTCTGCACAGGC  450

Query  382  CTCAGCTTTGAAGAACGGAGTCTTTGCACTTACACACACTCTTCCTGTTCTGCCTTCACC  441
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  451  CTCAGCTTTGAAGAACGGAGTCTTTGCACTTACACACACTCTTCCTGTTCTGCCTTCACC  510

Query  442  TATGCCGGGATAAGCAGAGATCTCATCAATTAGCTCTTCTCTGCAAGGTCTTCCACTGTT  501
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  511  TATGCCGGGATAAGCAGAGATCTCATCAATTAGCTCTTCTCTGCAAGGTCTTCCACTATT  570

Query  502  TCTGTCTGTCTTCCATATCAAGCCTGGATGCAGCTGCTGCTGCTTAGAGCAGAGATGAAG  561
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  571  TCTGTCTGTCTTCCATATCAAGCCTGGATGCAGCTGCTGCTGCTTAGAGCAGAGATGAAG  630

Query  562  AAAGTGTTCTGCATAAGTGGCTTCCTGAATGATGAGGACCAGAATAAAGGTTTTTGATCA  621
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  631  AAAGTGTTCTGCATAAGTGGCTTCCTGAATGATGAGGACCAGAATAAAGGTTTTTGATCA  690

Query  622  ACCTC  626
            |||||
Sbjct  691  ACCTC  695
```

AZGP1-GJC3

```
TTGGAGAATGGTGCCTGTCCTGCTGTCTCTGCTGCTGCTTCTGGGTCCTGCTGTCCCCCAGGAGAACCAAGATGGTCGTTACTCTCTGACCTATATCTACAC
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CCATGGGACTCTGGAGACAGGTGGAAGGAATGGAGGATTGGAAGCAGGACAGCCAACTTCAGAAGGCCAGGGAGGACATCTTTATGGAGACCCTGAAAGACA
CGTGGAGTATTACAACGACAGTAACGGATGTGTGGCAGGTTCCTGCGGCGGCTGCTGGCGGAGGAGAGCCGGCGCTCCACCCCCGTGGGGCGCCTCTTGCTT
CCGTGCTCCTGGGATTCCGCCTTGTGCTGCTGGCTGCCAGTGGGCCTGGAGTCTATGGTGATGAGCAGAGTGAATTCGTGTGTCACACCCAGCAGCCGGGCT
CAAGGCTGCCTGCTTCGATGCCTTCCACCCCCTCTCCCCGCTGCGTTTCTGGGTCTTCCAGGTCATCTTGGTGGCTGTACCCAGCGCCCTCTATATGGGTTT
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GATGCCCAGCTCCTTTGCATGTCGCCGAGAACCTTGCCTTGGTAGTATAACCTGCAATCTGTCCCGCTCCTCTGAGAAGACCATTTTTCCTAAAGACCATGT
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TCTAACTCGAAAGCACCGAAGACCAAGAAGCACGATAGCCTCCCAGTGGGTGATCAAGAGCCATTCAGAGCAGTTCAGGAGAGCTAGCTAGGAAAACAAGAA
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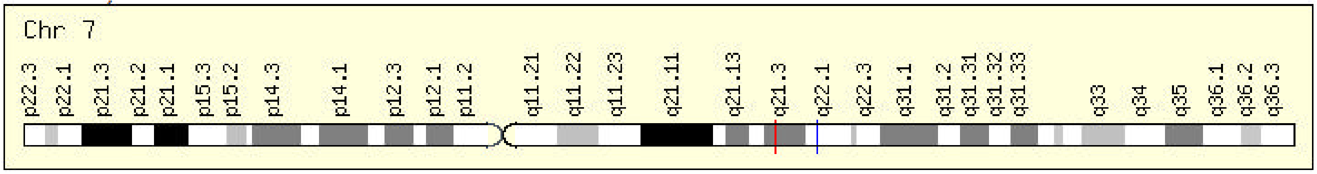
5' partner: AZGP1



Junction point
exon=2 169..429
/gene="AZGP1"
/gene_synonym="ZA2G; ZAG"

BLAST vs mRNA

```
>ref|NM_001185.3| UniGene info linked to NM_001185.3GEO profiles info linked to NM_001185.3Gene info
linked to NM_001185.3Genome view with mapviewer linked to NM_001185.3 Homo sapiens alpha-2-glycoprotein
1, zinc-binding (AZGP1), mRNA
Length=1278
GENE ID: 563 AZGP1 | alpha-2-glycoprotein 1, zinc-binding [Homo sapiens]
Score =  614 bits (332),  Expect = 2e-174
Identities = 332/332 (100%), Gaps = 0/332 (0%)

Strand=Plus/Plus
```

```
Query  5    AGAATGGTGCCTGTCCTGCTGTCTCTGCTGCTGCTTCTGGGTCCTGCTGTCCCCCAGGAG  64
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  99   AGAATGGTGCCTGTCCTGCTGTCTCTGCTGCTGCTTCTGGGTCCTGCTGTCCCCCAGGAG  158

Query  65   AACCAAGATGGTCGTTACTCTCTGACCTATATCTACACTGGGCTGTCCAAGCATGTTGAA  124
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  159  AACCAAGATGGTCGTTACTCTCTGACCTATATCTACACTGGGCTGTCCAAGCATGTTGAA  218

Query  125  GACGTCCCCGCGTTTCAGGCCCTTGGCTCACTCAATGACCTCCAGTTCTTTAGATACAAC  184
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  219  GACGTCCCCGCGTTTCAGGCCCTTGGCTCACTCAATGACCTCCAGTTCTTTAGATACAAC  278

Query  185  AGTAAAGACAGGAAGTCTCAGCCCATGGGACTCTGGAGACAGGTGGAAGGAATGGAGGAT  244
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  279  AGTAAAGACAGGAAGTCTCAGCCCATGGGACTCTGGAGACAGGTGGAAGGAATGGAGGAT  338

Query  245  TGGAAGCAGGACAGCCAACTTCAGAAGGCCAGGGAGGACATCTTTATGGAGACCCTGAAA  304
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  339  TGGAAGCAGGACAGCCAACTTCAGAAGGCCAGGGAGGACATCTTTATGGAGACCCTGAAA  398

Query  305  GACATCGTGGAGTATTACAACGACAGTAACGG  336
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Sbjct  399  GACATCGTGGAGTATTACAACGACAGTAACGG  430
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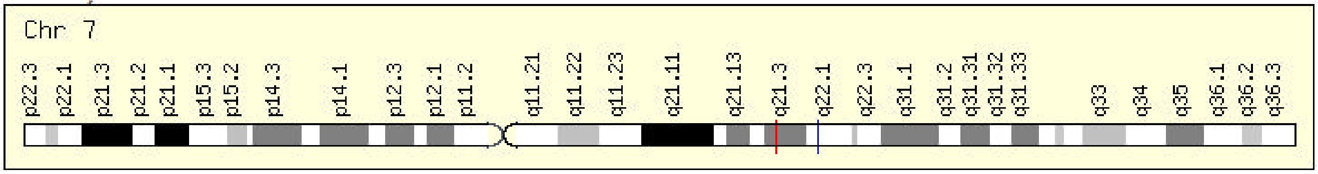
3' partner: GJC3



Junction point
exon=1 1..781
/gene="GJC3"
/gene_synonym="CX29; CX30.2; CX31.3; GJE1"

BLAST vs mRNA

>ref|NM_181538.2| UniGene info linked to NM_181538.2GEO profiles info linked to NM_181538.2Gene info linked to NM_181538.2Genome view with mapviewer linked to NM_181538.2 Homo sapiens gap junction protein, gamma 3, 30.2kDa (GJC3), mRNA
Length=1131
GENE ID: 349149 GJC3 | gap junction protein, gamma 3, 30.2kDa [Homo sapiens]
Score = 1266 bits (685), Expect = 0.0
Identities = 806/857 (95%), Gaps = 37/857 (4%)

Strand=Plus/Plus

```
             ↓
Query  337   ATGTGTGGCAGGTTCCTGCGGCGGCTGCTGGCGGAGGAGAGCCGGCGCTCCACCCCCGTG  396
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     ATGTGTGGCAGGTTCCTGCGGCGGCTGCTGGCGGAGGAGAGCCGGCGCTCCACCCCCGTG  60

Query  397   GGGCGCCTCTTGCTTCCCGTGCTCCTGGGATTCCGCCTTGTGCTGCTGGCTGCCAGTGGG  456
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GGGCGCCTCTTGCTTCCCGTGCTCCTGGGATTCCGCCTTGTGCTGCTGGCTGCCAGTGGG  120

Query  457   CCTGGAGTCTATGGTGATGAGCAGAGTGAATTCGTGTGTCACACCCAGCAGCCGGGCTGC  516
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   CCTGGAGTCTATGGTGATGAGCAGAGTGAATTCGTGTGTCACACCCAGCAGCCGGGCTGC  180

Query  517   AAGGCTGCCTGCTTCGATGCCTTCCACCCCCTCTCCCCGCTGCGTTTCTGGGTCTTCCAG  576
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   AAGGCTGCCTGCTTCGATGCCTTCCACCCCCTCTCCCCGCTGCGTTTCTGGGTCTTCCAG  240

Query  577   GTCATCTTGGTGGCTGTACCCAGCGCCCTCTATATGGGTTTCACTCTGTATCACGTGATC  636
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   GTCATCTTGGTGGCTGTACCCAGCGCCCTCTATATGGGTTTCACTCTGTATCACGTGATC  300

Query  637   TGGCACTGGGAATTATCAGGAAAGGGGAAGGAGGAGGAGATCTCTGATCCAGGGACGGGA  696
             |||||||||||||||||||||||||||||||||||||||| | |||||||||||||||||
Sbjct  301   TGGCACTGGGAATTATCAGGAAAGGGGAAGGAGGAGGAGACC-CTGATCCAGGGACGGGA  359

Query  697   GGGCAACACAGATGTCTCTAGGGGCTGGAAGCTCTCACGCTGCTCTGGGCTTATGTGGCT  756
             |||||||||||||||| | ||||||||||||| |||| ||||||||||||||||||||||
Sbjct  360   GGGCAACACAGATGTCCC-AGGGGCTGGAAGC-CTCAGGCTGCTCTGGGCTTATGTGGCT  417

Query  757   CAGCTGGGGGCTCGGCTTGTCCTGTAGGGGGCAGCCCTGGGGTTGCAGTACCACCTGTAT  816
             |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  418   CAGCTGGGGGCTCGGCTTGTCCTGGAGGGGGCAGCCCTGGGGTTGCAGTACCACCTGTAT  477
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```
Query  817   GGGTTCCAGATGCCCAGCTCCTTTGCATGTCGCCGAGAACCTTGCCTTGGTAGTATAACC  876
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  478   GGGTTCCAGATGCCCAGCTCCTTTGCATGTCGCCGAGAACCTTGCCTTGGTAGTATAACC  537

Query  877   TGCAATCTGTCCCGCTCCTCTGAGAAGACCATTTTTCCTAAAGACCATGTTTGGAGTCAG  936
             ||||||||||||||| ||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  538   TGCAATCTGTCCCGCCCCTCTGAGAAGACCATTTT-CCTAAAGACCATGTTTGGAGTCAG  596

Query  937   CGGTTTCTGTCTCTTGTTTACTTTTTTGGAGCTTGTGCTTCTGGGTTTGGGGAGATGGTG  996
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  597   CGGTTTCTGTCTCTTGTTTACTTTTTTGGAGCTTGTGCTTCTGGGTTTGGGGAGATGGTG  656
```

SLC25A16-DNA2

```
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TTTCCAAGAACAGTTCTGAGCACAGGAATGGATAACCGGTACCTGGTGTTGGCAGTCAATACTGTACAGAACAAAGAGGGAAACTGTGAAAAGCGCCTGGTC
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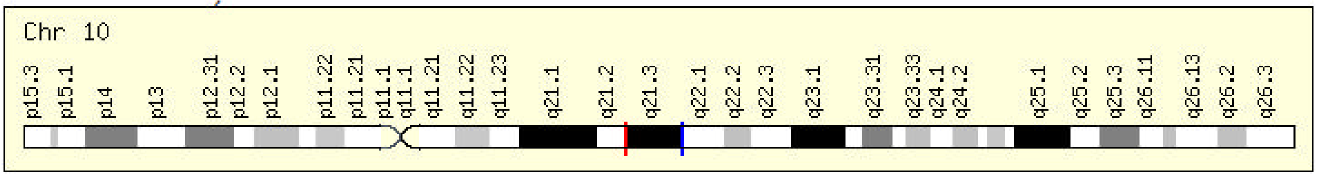
5’ partner: SLC25A16



Junction point
exon=8 922..990
/gene="SLC25A16"
/gene_synonym="D10S105E; GDA; GDC; HGT.1; hML7; MGC39851; ML7"

BLAST vs mRNA

>ref|NM_152707.3| Homo sapiens solute carrier family 25 (mitochondrial carrier; Graves disease autoantigen), member 16 (SLC25A16), nuclear gene encoding mitochondrial protein, mRNA
Length=2264
GENE ID: 8034 SLC25A16 solute carrier family 25 (mitochondrial carrier; Graves disease autoantigen), member 16 [Homo sapiens]
Score = 327 bits (177), Expect = 3e-88
Identities = 177/177 (100%), Gaps = 0/177 (0%)

Strand=Plus/Plus

```
Query  5    TACCCTTCTTGGCAGACCTTCATCAGACAATCCTAATGTCTTAGTTTTGAAAACTCATGT  64
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  814  TACCCTTCTTGGCAGACCTTCATCAGACAATCCTAATGTCTTAGTTTTGAAAACTCATGT  873

Query  65   AAACTTACTTTGTGGTGGTGTTGCTGGAGCAATAGCGCAGACAATATCCTACCCATTTGA  124
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  874  AAACTTACTTTGTGGTGGTGTTGCTGGAGCAATAGCGCAGACAATATCCTACCCATTTGA  933

Query  125  TGTGACTCGTCGGCGAATGCAATTAGGAACTGTTCTGCCGGAATTTGAAAAGTGCCT  181
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  934  TGTGACTCGTCGGCGAATGCAATTAGGAACTGTTCTGCCGGAATTTGAAAAGTGCCT  990
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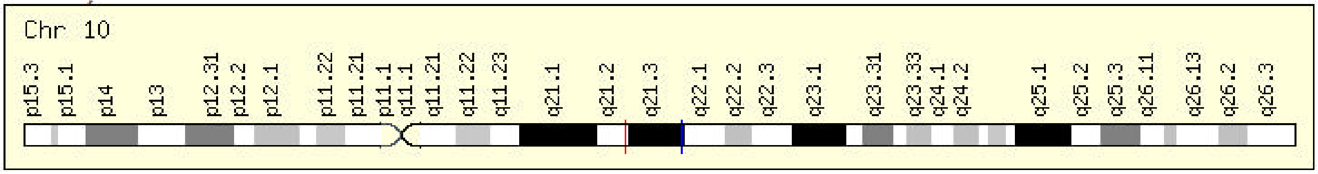
3’ partner: DNA2L



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exon=2 184..366
/gene="DNA2"
/gene_synonym="DNA2L; FLJ10063; KIAA0083; MGC133297"
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BLAST vs mRNA

```
>ref|NM_001080449.2| Gene info linked to NM_001080449.2 Homo sapiens DNA replication helicase 2 homolog
(yeast) (DNA2), mRNA
Length=4287
GENE ID: 1763 DNA2 | DNA replication helicase 2 homolog (yeast) [Homo sapiens]
Score = 1496 bits (810),  Expect = 0.0
Identities = 933/984 (95%), Gaps = 41/984 (4%)

Strand=Plus/Plus

                ↓
Query  180   CTATTTCAGAAGAAAGTGGTAGCTTCCTTTCCAAGAACAGTTCTGAGCACAGGAATGGAT  239
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  182   CTATTTCAGAAGAAAGTGGTAGCTTCCTTTCCAAGAACAGTTCTGAGCACAGGAATGGAT  241

Query  240   AACCGGTACCTGGTGTTGGCAGTCAATACTGTACAGAACAAAGAGGGAAACTGTGAAAAG  299
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  242   AACCGGTACCTGGTGTTGGCAGTCAATACTGTACAGAACAAAGAGGGAAACTGTGAAAAG  301

Query  300   CGCCTGGTCATCACTGCTTCACAGTCACTAGAAAATAAAGAACTATGCATCCTTAGGAAT  359
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  302   CGCCTGGTCATCACTGCTTCACAGTCACTAGAAAATAAAGAACTATGCATCCTTAGGAAT  361

Query  360   GACTGGTGTTCTGTTCCAGTAGAGCCAGGAGATATCATTCATTTGGAGGGAGACTGCACA  419
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  362   GACTGGTGTTCTGTTCCAGTAGAGCCAGGAGATATCATTCATTTGGAGGGAGACTGCACA  421

Query  420   TCTGACACTTGGATAATAGATAAAGATTTTGGATATTTGATTCTGTATCCAGACATGCTG  479
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  422   TCTGACACTTGGATAATAGATAAAGATTTTGGATATTTGATTCTGTATCCAGACATGCTG  481

Query  480   ATTTCTGGCACCAGCATAGCCAGTAGTATTCGATGTATGAGAAGAGCTGTCCTGAGTGAA  539
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Sbjct  482   ATTTCTGGCACCAGCATAGCCAGTAGTATTCGATGTATGAGAAGAGCTGTCCTGAGTGAA  541

Query  540   ACTTTTAGGAGCTCTGATCCAGCCACACGCCAAATGCTAATTGGTACGGTTCTCCATGAG  599
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  542   ACTTTTAGGAGCTCTGATCCAGCCACACGCCAAATGCTAATTGGTACGGTTCTCCATGAG  601

Query  600   GTGTTTCAAAAAGCAATAAATAATAGCTTTGCCCCAGAAAAGCTACAAGAACTTGCTTTT  659
             |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  602   GTGTTTCAAAAAGCCATAAATAATAGCTTTGCCCCAGAAAAGCTACAAGAACTTGCTTTT  661

Query  660   CAAACAATTCAAGAA-TAAGACATTTGAAGGAAATGTACCGCTTAAATCTAAGTCAAGAT  718
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  662   CAAACAATTCAAGAAATAAGACATTTGAAGGAAATGTACCGCTTAAATCTAAGTCAAGAT  721

Query  719   GAAATAAAACAAGAAGTAGAGGACTATCTTCCTTCGTTTTGTAAATGGGCAGGAGATTTC  778
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  722   GAAATAAAACAAGAAGTAGAGGACTATCTTCCTTCGTTTTGTAAATGGGCAGGAGATTTC  781

Query  779   ATGCATAAAAACACTTCGACTGACTTCCCTCAGATGCAGCTCTCTCTGCCAAGTGATAAT  838
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  782   ATGCATAAAAACACTTCGACTGACTTCCCTCAGATGCAGCTCTCTCTGCCAAGTGATAAT  841
```

PACRGL-LIMCH1

```
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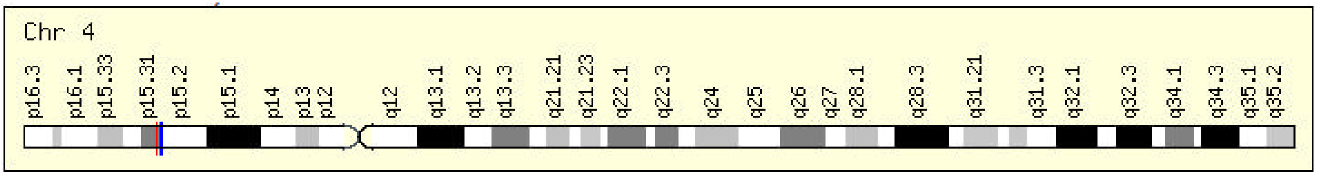
5’ partner: PACRGL



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Junction point
  exon=3 444..598
  /gene="PACRGL"
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  /gene_synonym="C4orf28; MGC29898"
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BLAST vs mRNA

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Gene info linked to NM_001130727.1Genome view with mapviewer linked to NM_001130727.1 Homo sapiens
PARK2 co-regulated-like (PACRGL), transcript variant 2, mRNA
Length=1796
GENE ID: 133015 PACRGL | PARK2 co-regulated-like [Homo sapiens]
Score =  394 bits (213),  Expect = 1e-108
Identities = 221/225 (99%), Gaps = 0/225 (0%)

Strand=Plus/Plus

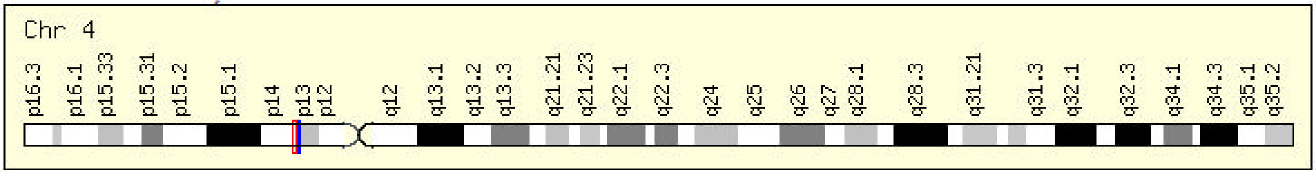
Query  156  GGAGTGAAAGGGAAGCAATGCAAAAATCAAAGGGCTCTGGAGGTACACAGTTGAAAAACA  215
            |||||||||||||||||||||| |||||| ||||||||||||||||||||||||||||||
Sbjct  375  GGAGTGAAAGGGAAGCAATGCAGAAATCAGAGGGCTCTGGAGGTACACAGTTGAAAAACA  434

Query  216  GAGCAACAGGTAACTATGATCAAAGGACATCATCAAGCACACAGTTAAAACACAGGAATG  275
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  435  GAGCAACAGGTAACTATGATCAAAGGACATCATCAAGCACACAGTTAAAACACAGGAATG  494

Query  276  CAGTTCAGGGAAGCAAATCCTCATTGTCAACCAGTTCTCCAAAGTCTGCAAGAAAACTTC  335
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  495  CAGTTCAGGGAAGCAAATCCTCATTGTCAACCAGTTCTCCAGAGTCTGCAAGAAAACTTC  554

Query  336  ATCCTAAACCAAGTGATAAACTGAACCCTAAAACAATTAATCCGG  380
            |||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  555  ATCCTAGACCAAGTGATAAACTGAACCCTAAAACAATTAATCCGG  599
                                                     ↑
```

3’ partner: LIMCH1



Junction point
exon=11 647..773
/gene="LIMCH1"
/gene_synonym="DKFZp434I0312; DKFZp686A01247;

BLAST vs mRNA

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NM_001112720.1Gene info linked to NM_001112720.1Genome view with mapviewer linked to NM_001112720.1
Homo sapiens LIM and calponin homology domains 1 (LIMCH1), transcript variant 5, mRNA
Length=5722
GENE ID: 22998 LIMCH1 | LIM and calponin homology domains 1 [Homo sapiens]
Score =  472 bits (255),  Expect = 7e-132
Identities = 258/259 (99%), Gaps = 1/259 (0%)

Strand=Plus/Plus


            ↓
Query  379  GGAGCACCAGCATGTTTGACATGCGGTGTGAGGAGGAGGCCGCGGTGCAGCCGCACAGCA  438
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  646  GGAGCACCAGCATGTTTGACATGCGGTGTGAGGAGGAGGCCGCGGTGCAGCCGCACAGCA  705

Query  439  GGGCCCGCCAGGAGCAGCTGCAGCTGATAAATAACCAGCTGAGGGAAGAGGACGACAAAT  498
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  706  GGGCCCGCCAGGAGCAGCTGCAGCTGATAAATAACCAGCTGAGGGAAGAGGACGACAAAT  765

Query  499  GGCAAGATGACCTGGCTCGTTGGAAGAGTCGTAGAAGAAGTGTTTCTCAGGACTTAATCA  558
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  766  GGCAAGATGACCTGGCTCGTTGGAAGAGTCGTAGAAGAAGTGTTTCTCAGGACTTAATCA  825

Query  559  AGAAAGAGGAAGAAAGGaaaaaaaTGGAGAAGTTACTGGCTGGAGAAAGATGGGACAAGT  618
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  826  AGAAAGAGGAAGAAAGGAAAAAAATGGAGAAGTTACTGGCTGGAGAA-GATGGGACAAGT  884

Query  619  GAACGAAGGAAAAGCATCA  637
            |||||||||||||||||||
Sbjct  885  GAACGAAGGAAAAGCATCA  903
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TXNL1-CDH2

```
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AATGAAAGTGATGAGCATGGATTTGACAACTGTTTACGAAAAGACACAACCTTCTTGGAATCTGACTGTGATGAACAGCTGCTTATTACTGTGGCATTCAATC
AACCTGTTAAGCTTTATTCCATGAAATTTCAAGGGCCAGATAATGGTCAGGGCCCTAAATATGTAAAAATTTTTATCAACCTACCCCGATCTATGGATTTTGA
AGAGGCAGAAAGAAGTGAACCAACTCAAGCTCTGGAACTGACAGAGGATGATATTAAAGAAGATGGCATTGTTCCACTTCGTTATGTTAAGTTTCAGAATGTT
AACAGTGTAACTATATTTGTTCAGTCGAATCAAGGTGAAGAGGAAACAACAAGAATTTCATATTTTACTTTTATTGGTACTCCAGTCCAGGCAACAAATATGA
ATGACTTCAAACGAAAAGTGCAACAGTATACGTTAATAATTCAAGCTACAGACATGGAAGGCAATCCCACATATGGCCTTTCAAACACAGCCACGGCCGTCAT
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CAACGACGGGTTAGTCACCGTGGTCAAACAATCGACTTTGAAACAAATAGGATGTTTGTCCTTACTGTTTGCTGCCGAAAAATCAAGTGCCATTAGCCAAGGC
AATTCAGCACCCGCCTCAGTCAACTGCAACCGTGTCTGTTACAGTTATTGACGTAAATGAAAACCCTTATTTTGCCCCCAATCCTAAGATCATTCGCCAGAAA
AAGGCTTCATGCCGTACCATGTTGAAAAATTCACTGGCTCAGACCGAATTCGATATATGCAGGCAAAATTTAGAAACCACTTAATTTATCTGGATCCTGGCCA
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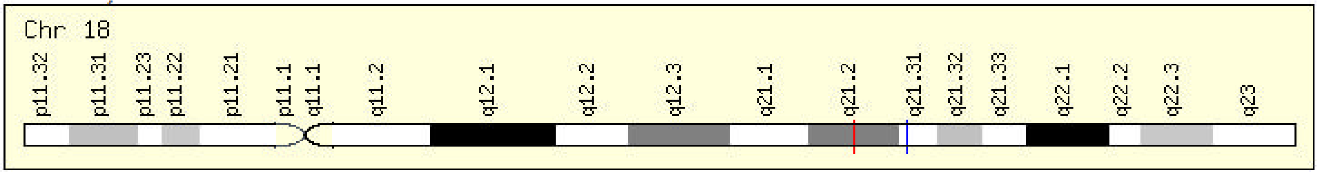
5’ partner: TXNL1



Junction point
exon=8 1090..1194
/gene="TXNL1"
/gene_synonym="TRP32; Txl; TXL-1; TXNL"

BLAST vs mRNA

>ref|NR_024546.1| Gene info linked to NR_024546.1Genome view with mapviewer linked to NR_024546.1 Homo sapiens thioredoxin-like 1 (TXNL1), transcript variant 2, non-coding RNA
Length=1434
GENE ID: 9352 TXNL1 | thioredoxin-like 1 [Homo sapiens]
Score = 957 bits (518), Expect = 0.0
Identities = 523/525 (99%), Gaps = 2/525 (0%)

Strand=Plus/Plus

```
Query  5     CTTAGAAAATGACCTCTGAGAAGCAATGAGGACACAGATATTCCAAAAGGCTATATGGAT  64
             |||||||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  672   CTTAGAAAATGACC-CTG-GAAGCAATGAGGACACAGATATTCCAAAAGGCTATATGGAT  729

Query  65    TTAATGCCTTTTATTAACAAAGCTGGTTGTGAATGTCTTAATGAAAGTGATGAGCATGGA  124
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  730   TTAATGCCTTTTATTAACAAAGCTGGTTGTGAATGTCTTAATGAAAGTGATGAGCATGGA  789

Query  125   TTTGACAACTGTTTACGAAAAGACACAACCTTCTTGGAATCTGACTGTGATGAACAGCTG  184
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  790   TTTGACAACTGTTTACGAAAAGACACAACCTTCTTGGAATCTGACTGTGATGAACAGCTG  849

Query  185   CTTATTACTGTGGCATTCAATCAACCTGTTAAGCTTTATTCCATGAAATTTCAAGGGCCA  244
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  850   CTTATTACTGTGGCATTCAATCAACCTGTTAAGCTTTATTCCATGAAATTTCAAGGGCCA  909

Query  245   GATAATGGTCAGGGCCCTAAATATGTAAAAATTTTTATCAACCTACCCCGATCTATGGAT  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  910   GATAATGGTCAGGGCCCTAAATATGTAAAAATTTTTATCAACCTACCCCGATCTATGGAT  969

Query  305   TTTGAAGAGGCAGAAAGAAGTGAACCAACTCAAGCTCTGGAACTGACAGAGGATGATATT  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  970   TTTGAAGAGGCAGAAAGAAGTGAACCAACTCAAGCTCTGGAACTGACAGAGGATGATATT  1029

Query  365   AAAGAAGATGGCATTGTTCCACTTCGTTATGTTAAGTTTCAGAATGTTAACAGTGTAACT  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1030  AAAGAAGATGGCATTGTTCCACTTCGTTATGTTAAGTTTCAGAATGTTAACAGTGTAACT  1089

Query  425   ATATTTGTTCAGTCGAATCAAGGTGAAGAGGAAACAACAAGAATTTCATATTTTACTTTT  484
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1090  ATATTTGTTCAGTCGAATCAAGGTGAAGAGGAAACAACAAGAATTTCATATTTTACTTTT  1149

Query  485   ATTGGTACTCCAGTCCAGGCAACAAATATGAATGACTTCAAACGA  529
             |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1150  ATTGGTACTCCAGTCCAGGCAACAAATATGAATGACTTCAAACGA  1194
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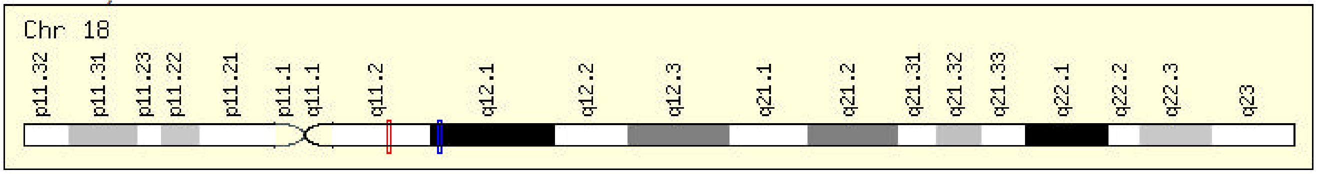
3’ partner: CDH2



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Junction point
exon=8 1480..1617
/gene="CDH2"
/gene_synonym="CD325; CDHN; CDw325; NCAD"

BLAST vs mRNA

>ref|NM_001792.3| UniGene info linked to NM_001792.3GEO profiles info linked to NM_001792.3Gene info
linked to NM_001792.3Genome view with mapviewer linked to NM_001792.3 Homo sapiens cadherin 2, type 1,
N-cadherin (neuronal) (CDH2), mRNA
Length=4380
GENE ID: 1000 CDH2 | cadherin 2, type 1, N-cadherin (neuronal) [Homo sapiens]
Score = 1000 bits (541),  Expect = 0.0
Identities = 634/673 (95%), Gaps = 29/673 (4%)

Strand=Plus/Plus


Query  529   AAAAGTGCAACAGTATACGTTAATAATTCAAGCTACAGACATGGAAGGCAATCCCACATA  588
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1479  AAAAGTGCAACAGTATACGTTAATAATTCAAGCTACAGACATGGAAGGCAATCCCACATA  1538

Query  589   TGGCCTTTCAAACACAGCCACGGCCGTCATCACAGTGACAGATGTCAATGACAATCCTCC  648
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1539  TGGCCTTTCAAACACAGCCACGGCCGTCATCACAGTGACAGATGTCAATGACAATCCTCC  1598

Query  649   AGAGTTTACTGCCATGACGTTTTATGGTGAAGTTCCTGAGAACAGGGTAGACATCATAGT  708
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1599  AGAGTTTACTGCCATGACGTTTTATGGTGAAGTTCCTGAGAACAGGGTAGACATCATAGT  1658

Query  709   AGCTAATCTAACTGTGACCGATAA-GATCAACCCCATACACCAGCCTGGAACGCAGTGTA  767
             |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  1659  AGCTAATCTAACTGTGACCGATAAGGATCAACCCCATACACCAGCCTGGAACGCAGTGTA  1718

Query  768   CAGAATCAGTGGCGGAGATCCTACTGGACGGTTCGCCATCCAGACCGACCCAAACAGCAA  827
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1719  CAGAATCAGTGGCGGAGATCCTACTGGACGGTTCGCCATCCAGACCGACCCAAACAGCAA  1778

Query  828   CGACGGGTTAGTCACCGTGGTCAAAC-AATCGACTTTGAAACAAATAGGATGTTTGTCCT  886
             |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  1779  CGACGGGTTAGTCACCGTGGTCAAACCAATCGACTTTGAAACAAATAGGATGTTTGTCCT  1838

Query  887   TACTGTTTGCTGCCGAAAAATCAAGTGCCATTAGCCAAGGGAATTCAGCACCCGCCTCAG  946
             ||||||| ||||| ||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  1839  TACTGTT-GCTGCAGAAAA-TCAAGTGCCATTAGCCAAGGGAATTCAGCACCCGCCTCAG  1896

Query  947   TCAACTGCAACCGTGTCTGTTACAGTTATTGACGTAAATGAAAACCCTTATTTTGCCCCC  1006
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1897  TCAACTGCAACCGTGTCTGTTACAGTTATTGACGTAAATGAAAACCCTTATTTTGCCCCC  1956
```

EEF1G-AHNAK

```
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CTCACCTGCCCAAGAGGACTGTAGAAGCGGCCAGGAAGAAAACCACCCCCTTTTAAGGTTGTTTTTGTGACCGTTTTTTGGAGCATTGTTCTAAAAATGGGA
ATTACATATTGCTGTGCCAAGGGCAACAAACACCTGCAGTTAAAGGAATACCTTCCGCGAGGCGGCTTTTCGGAGCATGCATGTTTATAGCTCCAGCCAGGC
AGACCGAGGGCTGCTGCATAAGCCCTGCTTGGTGCATTTCTTTACTTGCAAGGGGACAGAGTGTGGGCTTAGGTTTGGGACTAGAGGGGGCTTTGGCAACTA
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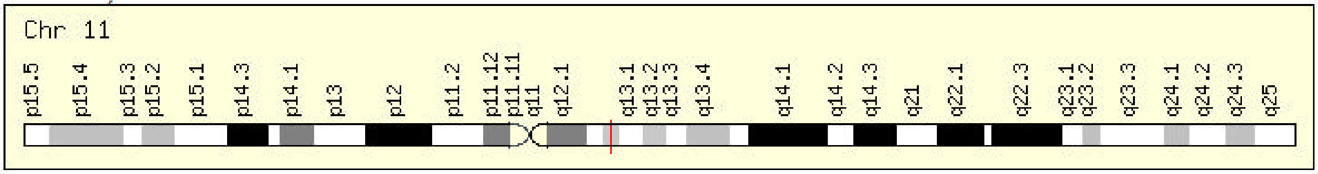
5’ partner: EEF1G



Junction point
exon=7 799..1003

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/gene="EEF1G"
/gene_synonym="EF1G; GIG35"
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BLAST vs mRNA

```
>ref|NM_001404.4| UniGene info linked to NM_001404.4GEO profiles info linked to NM_001404.4Gene info
linked to NM_001404.4Genome view with mapviewer linked to NM_001404.4 Homo sapiens eukaryotic
translation elongation factor 1 gamma (EEF1G), mRNA
Length=1552
GENE ID: 1937 EEF1G | eukaryotic translation elongation factor 1 gamma [Homo sapiens]
Score =  398 bits (215),  Expect = 1e-109
Identities = 218/219 (99%), Gaps = 1/219 (0%)

Strand=Plus/Plus

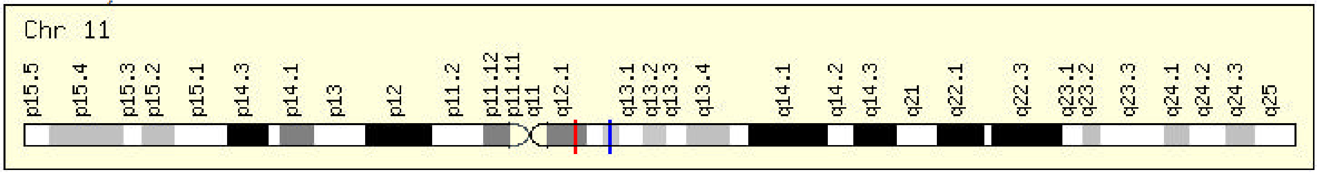
Query  5     GGCCCAGTTTGATGCTAAAAAG-TTGCAGAGACCCAACCTAAAAAGGACACACCACGGAA  63
             |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  785   GGCCCAGTTTGATGCTAAAAAGTTTGCAGAGACCCAACCTAAAAAGGACACACCACGGAA  844

Query  64    AGAGAAGGGTTCACGGGAAGAGAAGCAGAAGCCCCAGGCTGAGCGGAAGGAGGAGAAAAA  123
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  845   AGAGAAGGGTTCACGGGAAGAGAAGCAGAAGCCCCAGGCTGAGCGGAAGGAGGAGAAAAA  904

Query  124   GGCGGCTGCCCCTGCTCCTGAGGAGGAGATGGATGAATGTGAGCAGGCGCTGGCTGCTGA  183
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  905   GGCGGCTGCCCCTGCTCCTGAGGAGGAGATGGATGAATGTGAGCAGGCGCTGGCTGCTGA  964

Query  184   GCCCAAGGCCAAGGACCCCTTCGCTCACCTGCCCAAGAG  222
             |||||||||||||||||||||||||||||||||||||||
Sbjct  965   GCCCAAGGCCAAGGACCCCTTCGCTCACCTGCCCAAGAG  1003
                                                  ↑
```

3' partner: AHNAK



Junction point

```
exon=7 743..1090
/gene="AHNAK"
/gene_synonym="AHNAKRS; MGC5395"
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BLAST vs mRNA

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>ref|NM_024060.2| UniGene info linked to NM_024060.2GEO profiles info linked to NM_024060.2Gene info
linked to NM_024060.2Genome view with mapviewer linked to NM_024060.2 Homo sapiens AHNAK nucleoprotein
(AHNAK), transcript variant 2, mRNA
Length=1108
GENE ID: 79026 AHNAK | AHNAK nucleoprotein [Homo sapiens]
Score =  630 bits (341),  Expect = 9e-180
Identities = 345/347 (99%), Gaps = 0/347 (0%)



Strand=Plus/Plus

              ↓
Query  221   AGGACTGTAGAAGCGGCCAGGAAGAAAACCACCCCCTTTTAAGGTTGTTTTTGTGACCGT  280
             |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct  741   AGGACTGTAGAAGCGGCCAGGAAGAAAACCACCCCCTCTTAAGGTTGTTTTTGTGACCGT  800

Query  281   TTTTTGGAGCATTGTTCTAAAAATGGGAAATTACATATTGCTGTGCCAAGGGCAACAAAC  340
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  801   TCTTTGGAGCATTGTTCTAAAAATGGGAAATTACATATTGCTGTGCCAAGGGCAACAAAC  860

Query  341   ACCTGCAGTTAAAGGAATACCTTCCGCGAGGCGGCTTTTCGGAGCATGCATGTTTATAGC  400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  861   ACCTGCAGTTAAAGGAATACCTTCCGCGAGGCGGCTTTTCGGAGCATGCATGTTTATAGC  920

Query  401   TCCAGCCAGGCCAGACCGAGGGCTGCTGCATAAGCCCTGCTTGGTGCATTTCTTTACTTG  460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  921   TCCAGCCAGGCCAGACCGAGGGCTGCTGCATAAGCCCTGCTTGGTGCATTTCTTTACTTG  980

Query  461   CAAGGGGACAGAGTGTGGGCTTAGGTTTGGGACTAGAGGGGGCTTTGGCAACTATGGTGC  520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  981   CAAGGGGACAGAGTGTGGGCTTAGGTTTGGGACTAGAGGGGGCTTTGGCAACTATGGTGC  1040
```

```
Query  521   TCAGGTGATTATCCTTCGCTCGTTTATCCAATAAACATTTATCAAGC  567
             |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1041  TCAGGTGATTATCCTTCGCTCGTTTATCCAATAAACATTTATCAAGC  1087
```

MBD1-CCDC11

```
TGGTGCCTGGCTGCCCTAGCAAGGCAGTAGACCCAGGCCTGCCTTCTGTGAAGCAAGAGCACTGACCCAGAGGAGGACAAGGAGGAGAACAAGGATGATTCT
CCTCCAAATTGGCCCCAGAGGAAGAGGCAGGAGGGGCTGGCACACCCGTGATCACGGAGATTTTCAGCCTGGGTGGAACCCGCTTCCGAGATACAGCAGTCT
GTTGCCAAGAGATCCAAGCCTCCTAAAGGCCAAGGAGCTGAGCACCATCTAGAAAGAATCCGACGCAGCCATCAGAAGCATAATGCTATTTTGGCTTCCATT
AGTCAAGTGAGCGGGATCGCTTGAAAGCTGAGTGGGACCAGCACAATGACTGCAAGATTTTGGACAGCCTTGTGCGAGCAAGAATCAAGGATGCTGTGCAAG
GTTTATCATTAACATTGAAGAAAGACGAAATAAGTAAGGCTCACAAACCTGGGACATAAACCATGAAATATTCCTAAAACCACAATTTGAGATTGACCAGTC
AAAATCAAATTTAGCAAGGATCATGGCTGAGATATTTATATTAAATCCATAGCTATTGCTGGTTAATATTTTTAATATTTTTATTTGTGATAGCCTGTATTT
GATGAAAAACAATATATTGTTTCATATTTCATT
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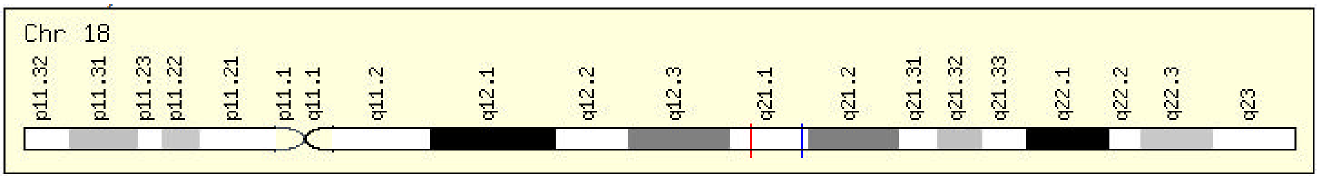
5’ partner: MBD1



Junction point
exon=16 2004..2065
/gene="MBD1"
/gene_synonym="CXXC3; PCM1; RFT"

BLAST vs mRNA

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>ref|NM_001204141.1| Gene info linked to NM_001204141.1 Homo sapiens methyl-CpG binding domain protein
1 (MBD1), transcript variant 10, mRNA
Length=2860
GENE ID: 4152 MBD1 | methyl-CpG binding domain protein 1 [Homo sapiens]
Score =  388 bits (210),  Expect = 7e-107
Identities = 215/217 (99%), Gaps = 2/217 (0%)

Strand=Plus/Plus

Query  1     TGGTGCCTGGCTGCCCTAGCAAGGCAGTAGACCCAGGCCTGCCTTCTGTGAAGCAAGAG-  59
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1849  TGGTGCCTGGCTGCCCTAGCAAGGCAGTAGACCCAGGCCTGCCTTCTGTGAAGCAAGAGC  1908

Query  60    CA-CTGACCCAGAGGAGGACAAGGAGGAGAACAAGGATGATTCTGCCTCCAAATTGGCCC  118
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1909  CACCTGACCCAGAGGAGGACAAGGAGGAGAACAAGGATGATTCTGCCTCCAAATTGGCCC  1968

Query  119   CAGAGGAAGAGGCAGGAGGGGCTGGCACACCCGTGATCACGGAGATTTTCAGCCTGGGTG  178
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1969  CAGAGGAAGAGGCAGGAGGGGCTGGCACACCCGTGATCACGGAGATTTTCAGCCTGGGTG  2028

Query  179   GAACCCGCTTCCGAGATACAGCAGTCTGGTTGCCAAG  215
             |||||||||||||||||||||||||||||||||||||
Sbjct  2029  GAACCCGCTTCCGAGATACAGCAGTCTGGTTGCCAAG  2065
                                                ↑
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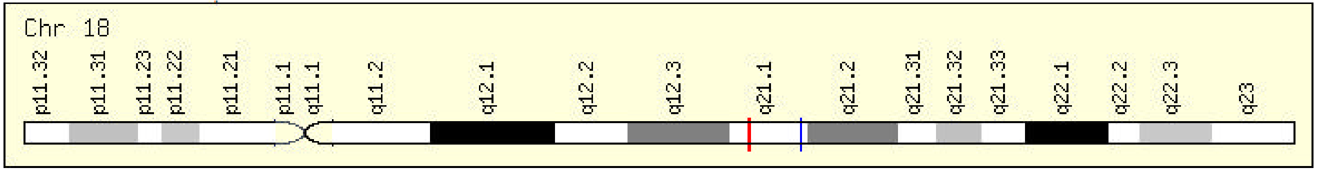
3’ partner: CCDC11



Junction point
exon=2 161..390
/gene="CCDC11"
/gene_synonym="FLJ32743"

BLAST vs mRNA

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linked to NM_145020.3Genome view with mapviewer linked to NM_145020.3 Homo sapiens coiled-coil domain
containing 11 (CCDC11), mRNA
Length=1837
GENE ID: 220136 CCDC11 | coiled-coil domain containing 11 [Homo sapiens]
Score = 429 bits (232),  Expect = 4e-119
Identities = 232/232 (100%), Gaps = 0/232 (0%)

Strand=Plus/Plus

             ↓
Query  215   GAGATCCAAGCCTCCTAAAGGCCAAGGAGCTGAGCACCATCTAGAAAGAATCCGACGCAG  274
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  160   GAGATCCAAGCCTCCTAAAGGCCAAGGAGCTGAGCACCATCTAGAAAGAATCCGACGCAG  219

Query  275   CCATCAGAAGCATAATGCTATTTTGGCTTCCATTAAGTCAAGTGAGCGGGATCGCTTGAA  334
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  220   CCATCAGAAGCATAATGCTATTTTGGCTTCCATTAAGTCAAGTGAGCGGGATCGCTTGAA  279

Query  335   AGCTGAGTGGGACCAGCACAATGACTGCAAGATTTTGGACAGCCTTGTGCGAGCAAGAAT  394
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  280   AGCTGAGTGGGACCAGCACAATGACTGCAAGATTTTGGACAGCCTTGTGCGAGCAAGAAT  339

Query  395   CAAGGATGCTGTGCAAGGGTTTATCATTAACATTGAAGAAAGACGAAATAAG  446
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  340   CAAGGATGCTGTGCAAGGGTTTATCATTAACATTGAAGAAAGACGAAATAAG  391
```

CORO7-MAGMAS

```
TTGGGGCGCTAATGGGCAGCCCTGGCTTCTCAGCCTGCAGCCTCCTGACATGAGCCCAGTGAGCCAAGCCCCCCGAGAGGCCCCTGCTCGTCGGGCCCCATC
TCAGCGCAGTACCTGGAAGAAAAGTCTGACCAGCAAAAGAAGGAGGAGCTGCTGAATGCCATGGTGGCAAAACTGGGGAACCGGGAGGACCCACTCCCCCAG
ACTCCTTTGAAGGCGTGGACGAGGACGAGTGGGCCAAGTACCTGGCCCAGATCATTGTGATGGGCGTGCAGGTGGTGGGCAGGGCCTTTGCACGGGCCTTGC
GCAGGAGTTTGCAGCCAGCCGGGCCGCAGCTGATGCCCGAGGACGCGCTGGACACCGGTCTGCAGCCGCTTCCAACCTCTCCGGCCTCAGCCTCCAGGAGGC
CAGCAGATTCTCAACGTGTCCAAGCTGAGCTCTGAGGAGGTCCAGAAGACTATGAACACTTATTTAACGTGAATGATAAATCCGTGGGTGGCTCCTTCTACC
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TGTGCACGAACGTCCTAACAGTCAATAATCGTATGCCATCCGCCTGATCCTAAGACGATAATGCCACGTTTCGGACCTGCCGTTCCATCTAAGTTCTTGCAA
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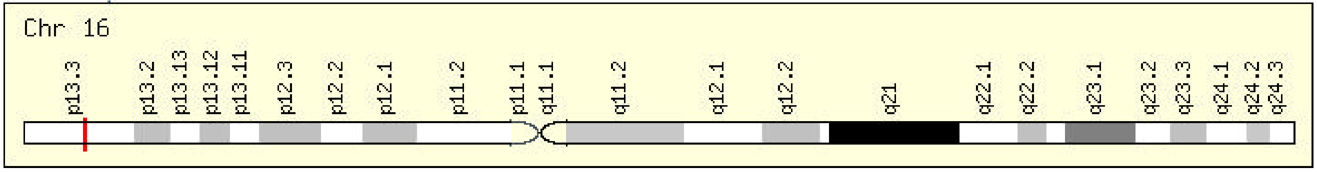
5' partner: CORO7



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Junction point
exon=27 2874..2960
/gene="CORO7"
/gene_synonym="0610011B16Rik; CRN7; FLJ22021; FLJ44188; POD1"

BLAST vs mRNA

>ref|NM_001201473.1| Gene info linked to NM_001201473.1 Homo sapiens coronin 7 (CORO7), transcript
variant 3, mRNA
Length=3599
GENE ID: 79585 CORO7 | coronin 7 [Homo sapiens]
Score =  435 bits (235),  Expect = 1e-120
Identities = 235/235 (100%), Gaps = 0/235 (0%)

Strand=Plus/Plus

Query  5     GGCGCTAATGGGCAGCCCTGGCTTCTCAGCCTGCAGCCTCCTGACATGAGCCCAGTGAGC  64
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2727  GGCGCTAATGGGCAGCCCTGGCTTCTCAGCCTGCAGCCTCCTGACATGAGCCCAGTGAGC  2786

Query  65    CAAGCCCCCCGAGAGGCCCCTGCTCGTCGGGCCCCATCCTCAGCGCAGTACCTGGAAGAA  124
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2787  CAAGCCCCCCGAGAGGCCCCTGCTCGTCGGGCCCCATCCTCAGCGCAGTACCTGGAAGAA  2846

Query  125   AAGTCTGACCAGCAAAAGAAGGAGGAGCTGCTGAATGCCATGGTGGCAAAACTGGGGAAC  184
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2847  AAGTCTGACCAGCAAAAGAAGGAGGAGCTGCTGAATGCCATGGTGGCAAAACTGGGGAAC  2906

Query  185   CGGGAGGACCCACTCCCCCAGGACTCCTTTGAAGGCGTGGACGAGGACGAGTGGG  239
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2907  CGGGAGGACCCACTCCCCCAGGACTCCTTTGAAGGCGTGGACGAGGACGAGTGGG  2961
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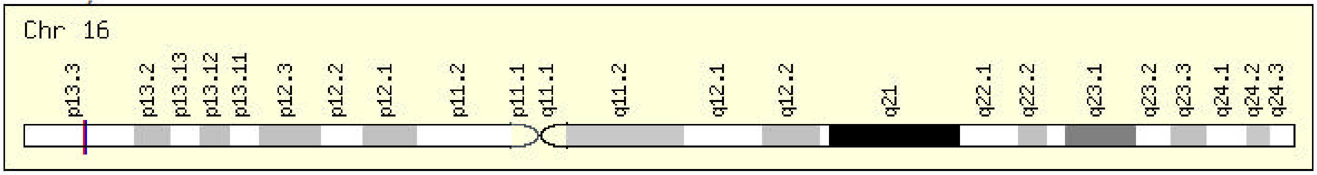
3’ partner: MAGMAS



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Junction point
exon=2 142..226
/gene="PAM16"
/gene_synonym="CGI-136; MAGMAS; TIM16; TIMM16"

BLAST vs mRNA

>ref|NM_016069.9| Gene info linked to NM_016069.9 Homo sapiens presequence translocase-associated motor
16 homolog (S. cerevisiae) (PAM16), nuclear gene encoding mitochondrial protein, mRNA
Length=600
GENE ID: 51025 PAM16 | presequence translocase-associated motor 16 homolog (S. cerevisiae) [Homo
sapiens]
Score =  721 bits (390),  Expect = 0.0
Identities = 428/444 (97%), Gaps = 12/444 (2%)

Strand=Plus/Plus

               ↓
Query  238  GGCCAAGTACCTGGCCCAGATCATTGTGATGGGCGTGCAGGTGGTGGGCAGGGCCTTTGC  297
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  141  GGCCAAGTACCTGGCCCAGATCATTGTGATGGGCGTGCAGGTGGTGGGCAGGGCCTTTGC  200

Query  298  ACGGGCCTTGCGGCAGGAGTTTGCAGCCAGCCGGGCCGCAGCTGATGCCCGAGGACGCGC  357
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  201  ACGGGCCTTGCGGCAGGAGTTTGCAGCCAGCCGGGCCGCAGCTGATGCCCGAGGACGCGC  260

Query  358  TGGACACCGGTCTGCAGCCGCTTCCAACCTCTCCGGCCTCAGCCTCCAGGAGGCACAGCA  417
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  261  TGGACACCGGTCTGCAGCCGCTTCCAACCTCTCCGGCCTCAGCCTCCAGGAGGCACAGCA  320

Query  418  GATTCTCAACGTGTCCAAGCTGAGCTCTGAGGAGGTCCAGAAGA-CTATGAACACTTATT  476
            ||||||||||||||||||||||||| |||||||||||||||||| |||||||||||||||
Sbjct  321  GATTCTCAACGTGTCCAAGCTGAGCCCTGAGGAGGTCCAGAAGAACTATGAACACTTATT  380

Query  477  TAACGTGAATGATAAATCCGTGGGTGGCTCCTTCTACCTGCAGTCAAAGGTGGTCCGCGC  536
            ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  381  TAAGGTGAATGATAAATCCGTGGGTGGCTCCTTCTACCTGCAGTCAAAGGTGGTCCGCGC  440

Query  537  AAAGGAGCGCCTGGATGAGGAACTCAAAATCCAGGCCCAGGAG-ACAGAGAAAAAGG-CA  594
            ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||| ||
Sbjct  441  AAAGGAGCGCCTGGATGAGGAACTCAAAATCCAGGCCCAGGAGGACAGAGAAAAAGGGCA  500

Query  595  GATGCCTCATACGTGACTGCTCG-CTCCCCC-GCC-ACCC-GC-GCCTCTAATTAATAGC  649
            |||||| |||||||||||||||| ||||||| ||| |||| || |||||||||| |||||
Sbjct  501  GATGCCCCATACGTGACTGCTCGGCTCCCCCGCCCACCCCGCCGCCTCTAATTTATAGC  560

Query  650  T-G-TAATAA-TT-CTTTTCTGCA  669
            | | |||||| || ||||||||||
Sbjct  561  TTGGTAATAAATTTCTTTTCTGCA  584
```

TYMP-SCO2

```
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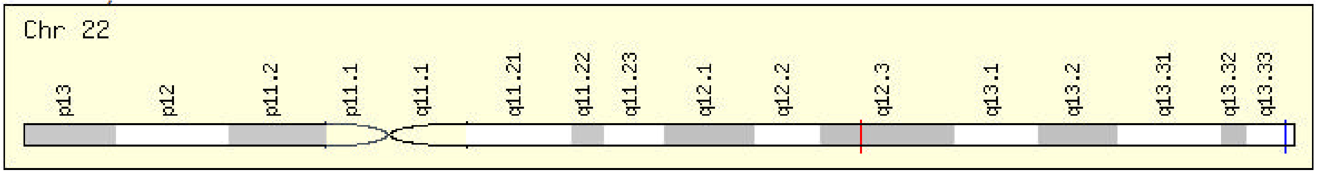
5’ partner: TYMP



Junction point
exon=8 1049..1279
/gene="TYMP"
/gene_synonym="ECGF; ECGF1; hPD-ECGF; MEDPS1; MNGIE; MTDPS1; PDECGF; TP"

BLAST vs mRNA

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>ref|NM_001113756.1|  Homo sapiens thymidine phosphorylase (TYMP), transcript variant 3, mRNA
Length=1587
GENE ID: 1890 TYMP| thymidine phosphorylase [Homo sapiens]
Score =  881 bits (477),  Expect = 0.0
Identities = 477/477 (100%), Gaps = 0/477 (0%)

Strand=Plus/Plus
Query  5     CGCTCTGGTGGTGGACGTTAAGTTCGGAGGGGCCGCCGTCTTCCCCAACCAGGAGCAGGC  64
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  804   CGCTCTGGTGGTGGACGTTAAGTTCGGAGGGGCCGCCGTCTTCCCCAACCAGGAGCAGGC  863

Query  65    CCGGGAGCTGGCAAAGACGCTGGTTGGCGTGGGAGCCAGCCTAGGGCTTCGGGTCGCGGC  124
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  864   CCGGGAGCTGGCAAAGACGCTGGTTGGCGTGGGAGCCAGCCTAGGGCTTCGGGTCGCGGC  923

Query  125   AGCGCTGACCGCCATGGACAAGCCCCTGGGTCGCTGCGTGGGCCACGCCCTGGAGGTGGA  184
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  924   AGCGCTGACCGCCATGGACAAGCCCCTGGGTCGCTGCGTGGGCCACGCCCTGGAGGTGGA  983

Query  185   GGAGGCGCTGCTCTGCATGGACGGCGCAGGCCCGCCAGACTTAAGGGACCTGGTCACCAC  244
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  984   GGAGGCGCTGCTCTGCATGGACGGCGCAGGCCCGCCAGACTTAAGGGACCTGGTCACCAC  1043

Query  245   GCTCGGGGGCGCCCTGCTCTGGCTCAGCGGACACGCGGGGACTCAGGCCCAGGGCGCTGC  304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1044  GCTCGGGGGCGCCCTGCTCTGGCTCAGCGGACACGCGGGGACTCAGGCCCAGGGCGCTGC  1103

Query  305   CCGGGTGGCCGCGGCGCTGGACGACGGCTCGGCCCTTGGCCGCTTCGAGCGGATGCTGGC  364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1104  CCGGGTGGCCGCGGCGCTGGACGACGGCTCGGCCCTTGGCCGCTTCGAGCGGATGCTGGC  1163

Query  365   GGCGCAGGGCGTGGATCCCGGTCTGGCCCGAGCCCTGTGCTCGGGAAGTCCCGCAGAACG  424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1164  GGCGCAGGGCGTGGATCCCGGTCTGGCCCGAGCCCTGTGCTCGGGAAGTCCCGCAGAACG  1223

Query  425   CCGGCAGCTGCTGCCTCGCGCCCGGGAGCAGGAGGAGCTGCTGGCGCCCGCAGATGG  481
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1224  CCGGCAGCTGCTGCCTCGCGCCCGGGAGCAGGAGGAGCTGCTGGCGCCCGCAGATGG  1280
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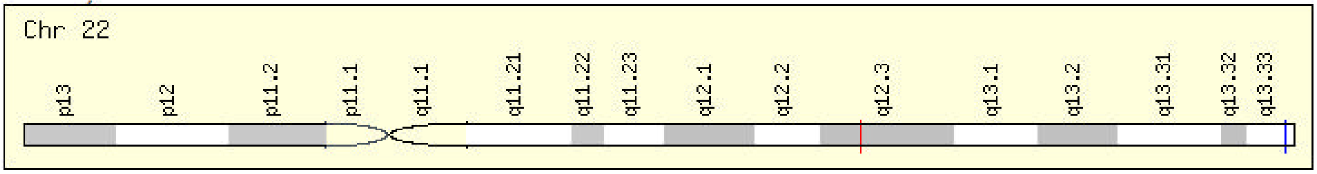
3’ partner: SCO2



Junction point
exon=2 146..1002
/gene="SCO2"
/gene_synonym="MGC125823; MGC125825; SCO1L"

BLAST vs mRNA

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>ref|NM_001169110.1|  Homo sapiens SCO cytochrome oxidase deficient homolog 2 (yeast) (SCO2), nuclear
gene encoding mitochondrial protein, transcript variant 3, mRNA
Length=1002
GENE ID: 9997 SCO2| SCO cytochrome oxidase deficient homolog 2 (yeast) [Homo sapiens]
Score =  828 bits (448),  Expect = 0.0
Identities = 560/609 (92%), Gaps = 28/609 (4%)
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```
Strand=Plus/Plus

                ↓
Query  479   TGGAGCATCAGATCCATGCTGCTGCTGACTCGGAGCCCCACAGCTTGGCACAGGCTCTCT  538
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  144   TGGAGCATCAGATCCATGCTGCTGCTGACTCGGAGCCCCACAGCTTGGCACAGGCTCTCT  203

Query  539   CAGCTCAAGCCTCCGGTCCTCCCTGGGACCCTGGGAGGCCAGGCCCTGCATCTGAGGTCC  598
             ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  204   CAGCTCAAGCCTCGGGTCCTCCCTGGGACCCTGGGAGGCCAGGCCCTGCATCTGAGGTCC  263

Query  599   TGGCTTTTGTCAAGGCAGGGCCCTGCAGAGACAGGTGGGCAGGGCCAGCCCCAGGGCCCT  658
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  264   TGGCTTTTGTCAAGGCAGGGCCCTGCAGAGACAGGTGGGCAGGGCCAGCCCCAGGGCCCT  323

Query  659   GGGCTTCGAACCCGGCTGCTGATCACAGGCCTGTTCGGGGCTGGACTCGGTGGGGCCTGG  718
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  324   GGGCTTCGAACCCGGCTGCTGATCACAGGCCTGTTCGGGGCTGGACTCGGTGGGGCCTGG  383

Query  719   CTGGCCCTGAGGGCTGAGAAGGAGAGGCTGCAGCAGCAAAAAGCGAACAGAAGCCCTGCG  778
             ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  384   CTGGCCCTGAGGGCTGAGAAGGAGAGGCTGCAGCAGCAAAA-GCGAACAGAAGCCCTGCG  442

Query  779   CCGGGCAGCTGTGGGCCAGGGGCGACTTCCACCTGCTGGATCACAGATGCCCGGGCTCGC  838
             || |||||||||||||||||| ||||||||||||||||||||||||| ||| ||||||||
Sbjct  443   CCAGGCAGCTGTGGGCCAGGG-CGACTTCCACCTGCTGGATCACAGAGGCC-GGGCTCGC  500

Query  839   TGCCAGGCTGACTTCCCGGGGCCAGTGGGTGCTGATGTACTTTGGCTTCCCTCCACTGCC  898
             ||| |||||||||||| |||||||||||||||||||||||||||||||| ||| ||||||
Sbjct  501   TGCAAGGCTGACTTCC-GGGGCCAGTGGGTGCTGATGTACTTTGGCTTCACTC-ACTGCC  558

Query  899   CCT-ACATCTGCCCAAAACAAACTGGAAAAAGCTTGGTGCAAGGTGGTGCGGGCAGCTGG  957
             | | ||||||||||| | | | ||||| || ||| |||||| |||||||||| |||||||
Sbjct  559   C-TGACATCTGCCCAGA-CGAGCTGGAGAA-GCT-GGTGCA-GGTGGTGCGG-CAGCTGG  612
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PPCS-LOC100507214

GCACGAGGCCGCTTCCCACCCCAGACTTGGCTGTCCGCTCTGCGGCCTTCGGGCCCAGCCCTTTCGGGCTTGCTGAGCCTGGAGGCCGAGGAGAATGCACTT
CGGGTTTTGCTGAGGCTCTGAGGAGCTACCAGGAGGCTGCGGCTGCAGGCACCTTCCTGGCAGTAGAGTTCACCACTTTGGCGGACTATTTGCATCTGTTGC
GGCTGCGGCCCAGGCACTCAATCCGCTAGGCCCTTCTGCGATGTTTTACCTGGCTGCGGCTGTGTCAGATTTCTATGTTCCTGTCTCTGAAATGCCTGAACA
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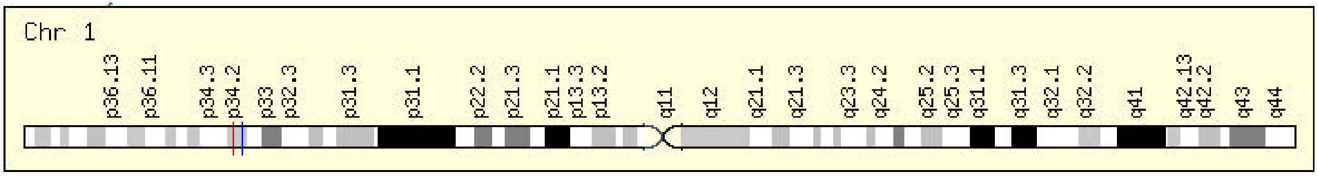
5’ partner: PPCS



Junction point
exon=2 573..676
/gene="PPCS"
/gene_synonym="FLJ11838; MGC117357; MGC138220;
RP11-163G10.1"

BLAST vs mRNA

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>ref|NM_024664.2|  Homo sapiens phosphopantothenoylcysteine synthetase (PPCS), transcript variant 1,
mRNA
Length=1489
GENE ID: 79717 PPCS| phosphopantothenoylcysteine synthetase [Homo sapiens]
Score =  612 bits (331),  Expect = 4e-174
Identities = 331/331 (100%), Gaps = 0/331 (0%)

Strand=Plus/Plus

Query  9    CCGCTTCCCACCCCAGACTTGGCTGTCCGCTCTGCGGCCTTCGGGCCCAGCCCTTTCGGG  68
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  346  CCGCTTCCCACCCCAGACTTGGCTGTCCGCTCTGCGGCCTTCGGGCCCAGCCCTTTCGGG  405

Query  69   CTTGCTGAGCCTGGAGGCCGAGGAGAATGCACTTCCGGGTTTTGCTGAGGCTCTGAGGAG  128
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  406  CTTGCTGAGCCTGGAGGCCGAGGAGAATGCACTTCCGGGTTTTGCTGAGGCTCTGAGGAG  465

Query  129  CTACCAGGAGGCTGCGGCTGCAGGCACCTTCCTGGCAGTAGAGTTCACCACTTTGGCGGA  188
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  466  CTACCAGGAGGCTGCGGCTGCAGGCACCTTCCTGGCAGTAGAGTTCACCACTTTGGCGGA  525
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Query  189  CTATTTGCATCTGTTGCAGGCTGCGGCCCAGGCACTCAATCCGCTAGGCCCTTCTGCGAT  248
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  526  CTATTTGCATCTGTTGCAGGCTGCGGCCCAGGCACTCAATCCGCTAGGCCCTTCTGCGAT  585

Query  249  GTTTTACCTGGCTGCGGCTGTGTCAGATTTCTATGTTCCTGTCTCTGAAATGCCTGAACA  308
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  586  GTTTTACCTGGCTGCGGCTGTGTCAGATTTCTATGTTCCTGTCTCTGAAATGCCTGAACA  645

Query  309  CAAGATCCAGTCATCTGGGGGCCCACTGCAG  339
            |||||||||||||||||||||||||||||||
Sbjct  646  CAAGATCCAGTCATCTGGGGGCCCACTGCAG  676
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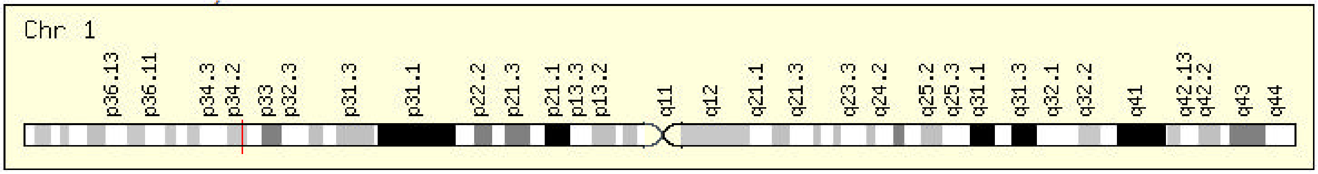
3’ partner: LOC100507214



BLAST vs mRNA

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>ref|XR_113349.1| PREDICTED: Homo sapiens hypothetical LOC100507214 (LOC100507214), partial miscRNA
Length=668
GENE ID: 100507214 LOC100507214| hypothetical LOC100507214 [Homo sapiens]
Score =  544 bits (294),  Expect = 1e-153
Identities = 296/297 (99%), Gaps = 0/297 (0%)
Strand=Plus/Plus
```

```
            ↓
Query  338  AGGGAAAAGTTCAGTTAGAAGACATACTTCACCATCTTGAAAAAGAAGAAATCAATCCCC  397
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  371  AGGGAAAAGTTCAGTTAGAAGACATACTTCACCATCTTGAAAAAGAAGAAATCAATCCCC  430

Query  398  TTGCTACTACAGAAGAACAACTCTGTTTGGTGCTTATTCCAGCCAGCACAGTGAAGACAG  457
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  431  TTGCTACTACAGAAGAACAACTCTGTTTGGTGCTTATTCCAGCCAGCACAGTGAAGACAG  490

Query  458  GCTGAGGACTGCTACCACAGATGTAGAAGAGCTTATAGTGAAGCACATGGGTGAAACAAA  517
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Sbjct  491  GCTGAGGACTGCTACCACAGATGTAGAAGAGCTTATAGTGAAGCACATGGGTGAAACAAA  550

Query  518  AGAAGTGAGAACTAATAGCATAGAATTTTAAAGACACCTGTGATTTTGTTCATTGCCCTT  577
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  551  AGAAGTGAGAACTAATAGCATAGAATTTTAAAGACACCTGTGATTTTGTTCATTGCCCTT  610

Query  578  CATTAAATTAACATATTAAAAACTAATGTTTGGCTATCACTGTATAGTTTGAAAAGC  634
            ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  611  CATTAAATTGACATATTAAAAACTAATGTTTGGCTATCACTGTATAGTTTGAAAAGC  667
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RMND5A-ANAPC1

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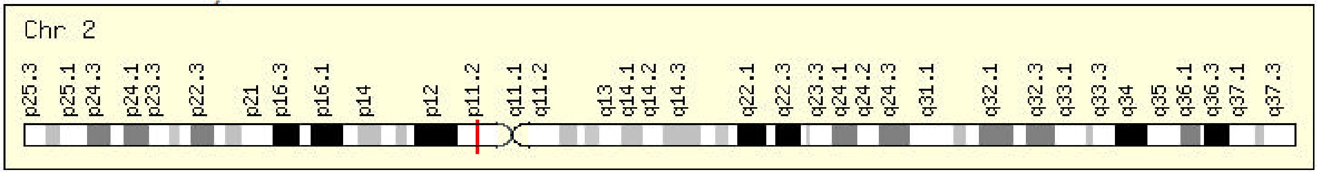
5’ partner: RMND5A



Junction point
exon=2 520..662
/gene="RMND5A"