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Gene Section
Review

MIR106B (microRNA 106b)

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Identity

Other names: MIRN106B

HGNC (Hugo): MIR106B

Location: 7q22.1

Local order: miR-106b resides in the 13th intron of MCM7 (minichromosome maintenance complex component 7) gene. Genes flanking MCM7 are:
- ZNF3 (7q22.1): zinc finger protein 3
- COPS6 (7q22.1): COP9 signalosome subunit 6
- MCM7 (7q21.3-7q22.1): minichromosome maintenance complex component 7
-- **MIR106B (7q22.1): microRNA 106b**
-- MIR93 (7q22.1): microRNA 93
-- MIR25 (7q22.1): microRNA 25
- AP4M1 (7q22.1): adaptor-related protein complex4, mu 1 subunit
- TAF6 (7q22.1): TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor.

DNA/RNA

Description

miR-106b is a member of microRNA cluster, miR-106b-25. All members of the cluster (miR-25, miR-93, miR-106b) reside in the 13th intron of MCM7 gene.

Transcription

Pre-miRNA
Length: 82 bp.
Sequence:
5'
CCUGCCGGGGCUAAAGUGCUGACAGUGCAGA
UAGUGGUCCUCUCCGUGCUACCGCACUGUGG
GUACUUGCUGCUCCAGCAGG 3'
Mature miRNA
Length: 21 bp
Sequence:
12- 5' UAAAGUGCUGACAGUGCAGAU 3'- 32 (between 12th and 32nd nucleotides of the precursor miRNA).

Pseudogene

No pseudogene was reported.

Protein

Note
miRNAs are not translated into aminoacids.

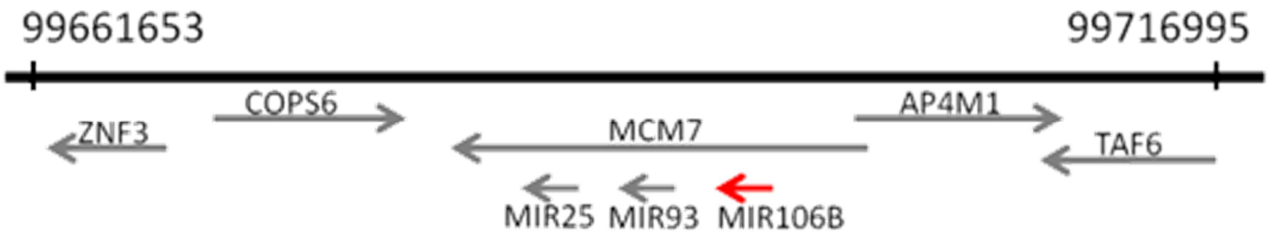

Figure 1. Genes flanking MCM7 gene on 7q22.1. → stands for positive strand, ← stands for negative strand.

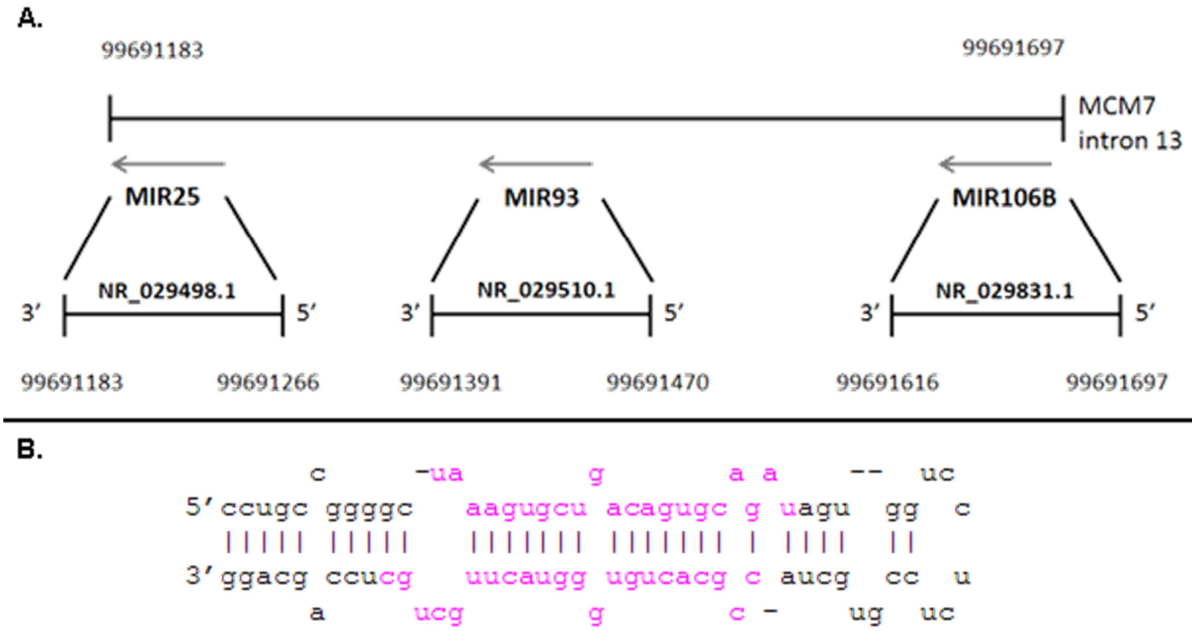

Figure 2. A. Genomic localization of miR-106b-25 members on chromosomal band 7q22.1. B. Stem loop structure of miR-106b.

Mutations

Note

No mutations have been reported so far. However, a single nucleotide polymorphism (SNP), rs999885, was reported in the promoter region of miR-106b host gene (MCM7). A to G base change of rs999885 was suggested to have a protective role for chronic Hepatitis B virus (HBV) infection in AG/GG genotypes; however the same polymorphism was also linked to higher risk of hepatocellular carcinoma (HCC) in HBV carriers (Liu et al., 2012). Furthermore, expression level of miR-106b-25 cluster was found to be significantly higher in AG/GG individuals than in AA carriers in non-tumor liver tissues (Liu et al., 2012).

Implicated in

Various cancers

Note

Deregulated expression of miR-106b has been implicated in various tumor types. In connection, miR-106b is thought to play an important role in cell cycle progression by targeting CDKN1A (p21) and E2F1 which in turns increase the proliferation rate of cells.

Gastric cancer

Note

In a microarray study of 20 gastric primary tumors, miR-106b was shown to be upregulated together with miR-25 and miR-93 (other members of miR-106b-25 cluster) (Petrocca et al., 2008). Moreover,
in a study conducted with 60 gastric cancer patients and 60 matched controls, plasma expression level of 15 selected microRNAs were measured by quantitative RT-PCR and 3 plasma microRNAs miR-106b, miR-20a, and miR-221 were found to be significantly increased.
Hence, these microRNAs were suggested as potential bio-markers for early detection of gastric cancer (Cai et al., 2013).

Esophageal adenocarcinoma

Note

5 esophageal cultured cells, 68 esophageal tissues (24 Barrett's esophagus, 22 esophageal adenocarcinoma and 22 normal epithelia) were analyzed by microarray to have a profile of differentially expressed miRNAs and miR-106b-25 cluster was shown to be upregulated in esophageal carcinoma (Kan et al., 2009).

Prostate cancer

Note

In a microarray study conducted with 60 prostate tumors and 16 non-tumor prostate tissues, tumor samples were found to have higher levels of miR-106b-25 cluster compared to non-tumor tissues (Ambs et al., 2008).
Tumorigenic effects of miR-106b in prostate cancer was suggested to be exerted by targeting PTEN (phosphate and tensin homolog) - a tumor suppressor gene.
PTEN inhibits the PI3K-Akt pathway which is a signal transduction pathway taking role in cell survival, proliferation, motility and angiogenesis (Poliseno et al., 2010).

Hepatocellular carcinoma

Note

56 pairs of hepatocellular carcinoma (HCC) samples and corresponding non-tumor liver samples were

analyzed and significant up-regulation of miR-106b was observed in tumor samples. Moreover in this study, decrease in the proliferation of two hepatoma-derived cell lines was shown after inhibiting miR-106b by an anti-miR-106b oligo. BCL2L11 (Bim) was identified as target of miR-106b and correlation between BCL2L11 (Bim) (pro-apoptotic gene) and miR-106b was shown in hepatocellular carcinoma. Bim expression was higher in tumors that have down regulated expression of miR-106b (Li et al., 2009). The same upregulated pattern of miR-106b was shown in the study of Shen et al. (2013), in which HCC cell lines and tissues were analyzed by quantitative RT-PCR in terms of miR-106b expression. It was depicted that miR-106b upregulation affected G_1/S transition by upregulating cyclin D1 and downregulating adenomatous polyposis coli (APC) - an important tumor suppressor gene. APC was shown as a direct target of miR-106b in this study.

Hepatocellular carcinoma (HCC) and hepatitis B virus (HBV) infection

Note

A genetic variant (SNP A>G) in the promoter region of miR-106b-25 cluster suggested to provide a protective effect against HBV chronic infection. However, the polymorphism was also predicted to cause increased risk for HCC by increasing expression of miR-106b-25 cluster (Liu et al., 2012).

Breast cancer

Note

In a study conducted with 204 lymph node negative breast cancers, high expression of miR-106b was shown to be correlated with high proliferation and estrogen receptor positivity (Jonsdottir et al., 2012). The role of miR-106b-25 cluster in breast cancer was depicted with study of Smith and his colleagues. The relation between miR-106b-25, TGFβ and homeobox protein SIX1 (Six1) was studied. It was shown that miR-106b-25 cluster can target Smad-7 - a TGFβ inhibitor - and activate TGFβ pathway as a downstream effect of SIX1 overexpression. Hence, miR-106b-25 cluster overcomes TGFβ mediated growth suppression and also promote TGFβ pathway signaling in favor of tumorigenesis (Smith et al., 2012).

Loss of membranous E-cadherin is known as one of the hallmarks for epithelial-to-mesenchymal transition (EMT). miR-106b-25 cluster overexpressing breast cancer cells had decreased membrane bound E-cadherin, which was in agreement with EMT (Smith et al., 2012).

Laryngeal carcinoma

Note

Inhibition of miR-106b by antisense oligonucleotides showed a decrease in proliferation of two laryngeal carcinoma cell lines and this inhibition resulted in G_0/G_1 arrest (Cai et al., 2011). Retinoblastoma protein (Rb), which is a tumor suppressor and has a role in G_1/S transition, was shown as a direct target of miR-106b in laryngeal carcinoma.

Glioma

Note

miR-106b levels were assessed in 71 glioma samples and overexpression was observed in the majority of samples by in situ hybridization (ISH) and real-time PCR. Moreover, expression of miR-106b was found to be positively correlated with the tumor grade. After the transfection of antisense oligonucleotides for miR-106b in three human glioma cell lines, a decrease in the proliferation of these cells was observed. RBL2 (retinoblastoma like-2) was also shown to be target of miR-106b and miR-106b promoted cell cycle progression by negatively regulating RBL2 (Zhang et al., 2013).

Alzheimer's disease (AD)

Note

miR-106b levels were shown to be reduced in sporadic AD patients. Important role of TGFβ pathway has been implicated in AD pathogenesis (Tesseur et al., 2006; Caraci et al., 2011) and direct regulation of TGFβ receptor 2 (TGFBR2) by miR-106b was revealed. Hence, potential role of miR-106b in AD pathogenesis via affecting TGFβ pathway was suggested (Wang et al., 2010).

Induced pluripotent stem cells (iPSC)

Note

In iPSC, miR-106b-25 cluster is induced in early reprogramming phases and inhibition of this cluster reduces the reprogramming efficiency. miR-93 and miR-106b target TGFBR2 and CDKN1A (p21) which have already been linked to iPSC induction (Li et al., 2011).

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