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Gene Section

Short Communication

SNW1 (SNW domain containing 1)

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Abstract

SNW1 is a spliceosomal component and transcriptional co-regulator that provides a modulatory coupling of transcription initiation and splicing. SNW1 appears to be an essential cancer cell survival factor by co-transcriptionally regulating mRNA splicing of proteins involved in cell cycle checkpoints. As a co-regulator, SNW1 is shown to attune the activity of a number of transcription factors, including nuclear hormone receptors as well as CBF1, Smad2/3, and MyoD by modulating a transition step between the repressing and activating transcription complex assembly. SNW1 is also involved in the cell cycle progression through the involvement in cell cycle checkpoint-dependent changes in gene expressions during cellular proliferation and viral infections.

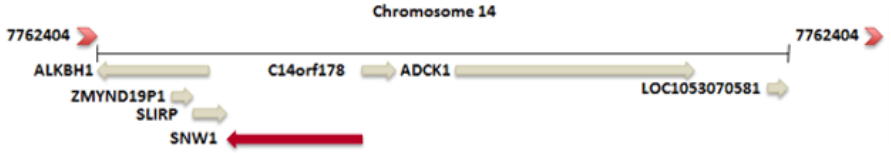
Keywords
SNW1; cancer; transcription regulation

Identity

Other names
Homolog Of Drosophila BX42 (Bx42), Nuclear Receptor Coactivator NCoA-62 (NCOA-62), Prp45, PRPF45, SKI Interacting Protein (SKIP), SKIIP

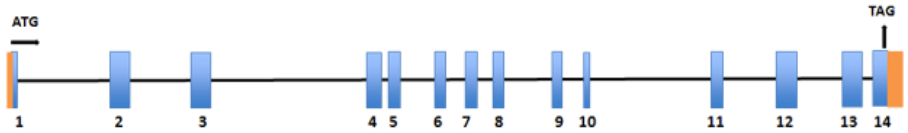
HGNC (Hugo)
SNW1

Location
14q24.3. Genomic coordinates: 14: 77717599-77761220



Human SNW1 located on chromosome 14q24.3 is on the reverse strand. (https://www.ncbi.nlm.nih.gov/gene/22938, 2017)

DNA/RNA



Exons are shown in boxes; introns are indicated by lines. The encoding exons are in blue. The start codon ATG and stop codon TAG are shown.

Description

The human SNW1 gene contains 14 exons.

Transcription

As a result of alternative splicing, SNW1 has two transcript variants (https://www.ncbi.nlm.nih.gov/gene/22938, 2017). The transcript 1, the long isoform, has 2207 nt mRNA which encodes a 571 amino acid (aa)-long protein (protein ID: NP_001305773.1). The transcript 2, which has 2146 nucleotides, differs in the 3' UTR and displays multiple coding region differences compared to transcript 1. One of the coding region differences results in a frame shift, giving rise to the isoform 2, which has 536 amino-acids with a distinct carboxyl-terminus (protein ID: NP_036377.1).

Pseudogene

There is one reported pseudogene located on chromosome 1 (https://www.ncbi.nlm.nih.gov/gene/22938, 2017).

Protein

Note

SNW domain containing protein 1 is also known as nuclear protein SkiP, nuclear receptor coactivator NcoA-62 or Ski interacting protein (SKIP).

Description

The genes encoding SNW proteins are present throughout eukaryotic phylla, including lower eukaryotes, plants, fungi and animals. There is only one gene per genome, which encodes for a 60-80 kDa protein that predominantly localizes to the nucleus (Folk at al., 2004). SNW1 is suggested to contain protein interaction domains as well as a carboxyl-terminally located dimerization domain (Folk at al., 2004).

Expression

SNW1 is expressed in the brain, endocrine tissues, bone marrow and immune system, muscle, lung, liver, gall bladder, pancreas, gastrointestinal tract, kidney, urinary bladder, male and female specific tissues, adipose and soft tissues and skin, in which the expression levels are high except kidney (http://www.proteinatlas.org/ENSG00000100603-SNW1/tissue, 2017).

Localisation

SNW1 localizes in the nucleus (Dahl et al., 1998).

Function

SNW1 acts as a co-regulator for transcriptions regulated by vitamin D and RARA / RARB / RARG (retinoic acid receptors) as well as steroid hormone receptors including NR3C1 (glucocorticoid receptor), ESR1 / ESR2 (estrogen receptors), and AR (androgen receptor) (Folk at al., 2004). SNW1 also plays critical roles in the function of v-Ski avian retroviral oncogene, bone morphogenetic protein (BMP) during vertebrate embryogenesis (Wu et al, 2011), telomere function (Lackner et al, 2011) and Notch signaling-mediated transcription (Vasquez-Del Carpio, 2013). SNW1 is reported to counteract transcriptional repression induced by RB1 (retinoblastoma protein) as well (Prathapam et al. 2002). In addition to being a transcriptional co-regulator, SNW1 is an integral component of spliceosome by interacting with the U5 small nuclear ribonucleoprotein (snRNP) subcomplex of the activated spliceosome as a part of the PRPF19/nineteen complex (NTC) (Neubauer et al, 1998; Makarova et al, 2004). SNW1 inactivation is reported to cause a rapid loss of sister chromatid cohesion (Van Der Lelij et al, 2014) mitotic spindle and cytokinesis defects (Kittler et al, 2004; Kittler et al, 2005). It is also suggested that the involvement of SNW1 in the p21-gene specific splicing is critical for cancer cell survival under stress (Chen et al, 2011).

Homology

Homologs of SNW1 are found in chimpanzee, Rhesus monkey, dog, cow, mouse, rat, chicken, zebrafish, fruit fly, mosquito, C.elegans, S.pombe, M.oryzae, N.crassa, A.thaliana, rice, and frog (https://www.ncbi.nlm.nih.gov/gene/22938, 2017).

Mutations

There are no gene mutations described for SNW1.

Implicated in

Bladder cancer

SNW1 displays a higher expression in bladder tumor tissue than surrounding normal adjacent tissues. Higher expression of SNW1 appears to be correlated with poor prognosis of bladder cancer. It is also reported that high-grade urothelial carcinoma samples express higher levels of SNW1 compared with low-grade urothelial carcinoma samples (Wang et al., 2014).

Breast cancer

Immunohistochemical and western blot analyses of breast carcinoma samples showed that the SNW1 expression is augmented in breast cancer tissues compared with adjacent noncancerous tissues. SNW1 overexpression appears to have a positive correlation with the histological grade of cancerous tissues. Moreover, it is suggested that there is an inverse relationship between the SNW1 expression and pathologic prognostic parameters including estrogen (ER) and progesterone receptors status. In ER positive cell models derived from breast carcinoma, there is a lower expression of SNW1 when it is compared with the expression levels of SNW1 in ER negative cell models (Liu et al., 2014).

Hepatocellular carcinoma

Expression analyses of SNW1 with samples of hepatocellular carcinoma patients and normal liver samples revealed that SNW1 is overexpressed in cancerous cells when compared with noncancerous liver samples. There is a positive correlation between high SNW1 expression and aggressiveness of hepatocellular carcinoma (Liu et al., 2013).

Malignant pleural mesothelioma

As in other cancer types, SNW1 is overexpressed in malignant pleural mesotheliomas (MPM) patients, which is correlated with poor prognosis. Overexpression of SNW1 also correlates with a reduced survival rate in MPM patient cohort (Turkcu et al., 2016).

References

Chen Y, Zhang L, Jones KA. SKIP counteracts p53-mediated apoptosis via selective regulation of p21Cip1 mRNA splicing. Genes Dev. 2011 Apr 1;25(7):701-16

Dahl R, Wani B, Hayman MJ. The Ski oncoprotein interacts with Skip, the human homolog of Drosophila Bx42. Oncogene. 1998 Mar 26;16(12):1579-86

Folk P, Půta F, Skruzný M. Transcriptional coregulator SNW/SKIP: the concealed tie of dissimilar pathways. Cell Mol Life Sci. 2004 Mar;61(6):629-40

Kittler R, Pelletier L, Ma C, Poser I, Fischer S, Hyman AA, Buchholz F. RNA interference rescue by bacterial artificial chromosome transgenesis in mammalian tissue culture cells. Proc Natl Acad Sci U S A. 2005 Feb 15;102(7):2396-401

Lackner DH, Durocher D, Karlseder J. A siRNA-based screen for genes involved in chromosome end protection. PLoS One. 2011;6(6):e21407

Liu G, Huang X, Cui X, Zhang J, Wei L, Ni R, Lu C. High SKIP expression is correlated with poor prognosis and cell proliferation of hepatocellular carcinoma. Med Oncol. 2013;30(3):537

Liu X, Ni Q, Xu J, Sheng C, Wang Q, Chen J, Yang S, Wang H. Expression and prognostic role of SKIP in human breast carcinoma. J Mol Histol. 2014 Apr;45(2):169-80

Makarova OV, Makarov EM, Urlaub H, Will CL, Gentzel M, Wilm M, Lührmann R. A subset of human 35S U5 proteins, including Prp19, function prior to catalytic step 1 of splicing. EMBO J. 2004 Jun 16;23(12):2381-91

Neubauer G, King A, Rappsilber J, Calvio C, Watson M, Ajuh P, Sleeman J, Lamond A, Mann M. Mass spectrometry and EST-database searching allows characterization of the multi-protein spliceosome complex. Nat Genet. 1998 Sep;20(1):46-50

Prathapam T, Kühne C, Banks L. Skip interacts with the retinoblastoma tumor suppressor and inhibits its transcriptional repression activity. Nucleic Acids Res. 2002 Dec 1;30(23):5261-8

Türkcü G, Alaballk U, Keles AN, Ibiloglu I, Küçüköner M, Sen HS, Büyükbayram H. Comparison of SKIP expression in malignant pleural mesotheliomas with Ki-67 proliferation index and prognostic parameters. Pol J Pathol. 2016 Jun;67(2):108-13

Vasquez-Del Carpio R, Kaplan FM, Weaver KL, VanWye JD, Alves-Guerra MC, Robbins DJ, Capobianco AJ. Assembly of a Notch transcriptional activation complex requires multimerization. Mol Cell Biol. 2011 Apr;31(7):1396-408

Wang L, Zhang M, Wu Y, Cheng C, Huang Y, Shi Z, Huang H. SKIP expression is correlated with clinical prognosis in patients with bladder cancer. Int J Clin Exp Pathol. 2014;7(4):1695-701

Wu MY, Ramel MC, Howell M, Hill CS. SNW1 is a critical regulator of spatial BMP activity, neural plate border formation, and neural crest specification in vertebrate embryos. PLoS Biol. 2011 Feb 15;9(2):e1000593

van der Lelij P, Stocsits RR, Ladurner R, Petzold G, Kreidl E, Koch B, Schmitz J, Neumann B, Ellenberg J, Peters JM. SNW1 enables sister chromatid cohesion by mediating the splicing of sororin and APC2 pre-mRNAs. EMBO J. 2014 Nov 18;33(22):2643-58

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