Gene Section

Short Communication

SNW1 (SNW domain containing 1)
Cagla Ece Olgun and Mesut Muyan

Middle East Technical University, Department of Biological Sciences, Cankaya 06800, Ankara, Turkey; colgun@metu.edu.tr; mmuyan@metu.edu.tr

Published in Atlas Database: August 2017
Online updated version: http://AtlasGeneticsOncology.org/Genes/SNW1ID42348ch14q24.html
Printable original version: http://documents.revuees.inist.fr/bitstream/handle/2042/68909/08-2017-SNW1ID42348ch14q24.pdf
DOI: 10.4267/2042/68909

This work is licensed under a Creative Commons Attribution-Noncommercial-No Derivative Works 2.0 France Licence. © 2018 Atlas of Genetics and Cytogenetics in Oncology and Haematology

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

DNA/RNA

Human SNW1 located on chromosome 14q24.3 is on the reverse strand.
SNW1 (SNW domain containing 1)

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**

**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**

**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 (Türkcü et al., 2016).

References

Makarova OV, Makarov EM, Urlaub H, Will CL, Gentzel M, Wilm M, Lühmann 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
Prathapam T, Köhne 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

This article should be referenced as such: