

Gene Section

Short Communication

SGOL1 (shugoshin-like 1 (*S. pombe*))

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Identity

Other names: NY-BR-85, SGO, Sgo1

HGNC (Hugo): SGOL1

Location: 3p24.3

Local order: Telomeric to ZNF385D (zinc finger protein 385D); centromeric to KAT2B (lysine acetyltransferase 2B).

Note

The Sgo1 gene was identified in fission yeast as a factor protecting centromeric Rec8 from degradation during meiosis I, and human Sgo1 homolog, SGOL1, was identified as a homologue of yeast Sgo1 on databases (Kitajima et al., 2004).

DNA/RNA

Description

The SGOL1 gene is composed of 9 exons and spans 25698 bases.

Transcription

Transcript variant A2 (NM_001012410) has the longest coding sequence and encodes a protein comprised of 561 aa. Transcript variant A1 (NM_001012409) lacks exon 9 and encodes a protein comprised of 527 aa. Typically, "SGOL1" corresponds to type A1 or A2. Transcript variant B2 (NM_001012412) lacks a large proportion of exon 6 and encodes a protein comprised of 309 aa.

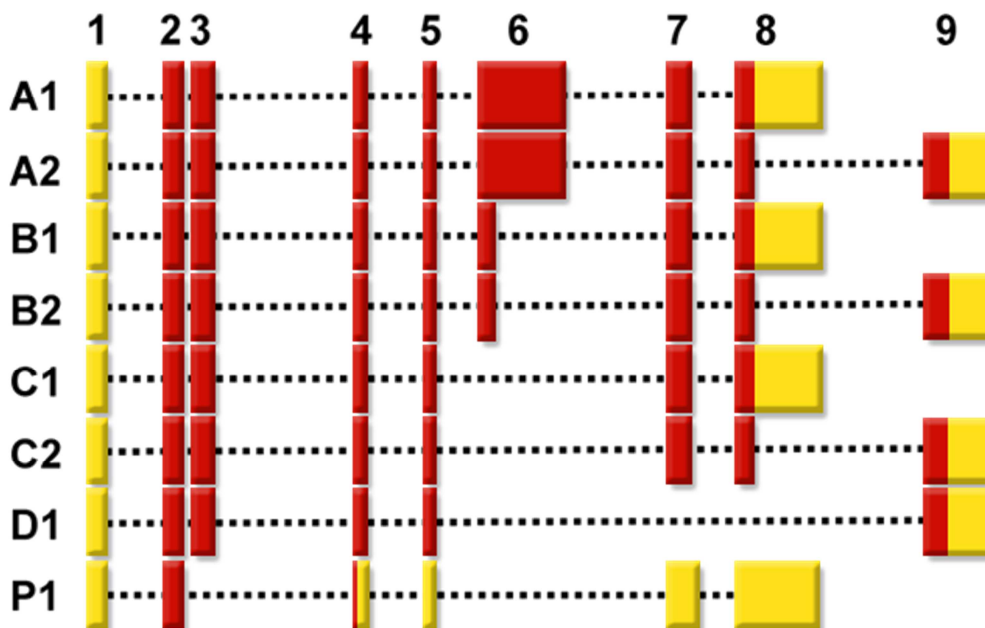


Figure 1. Scheme of SGOL1 transcript variants. Exon numbers are shown at the top. Red and yellow boxes indicate exons of CDS and UTR, respectively.

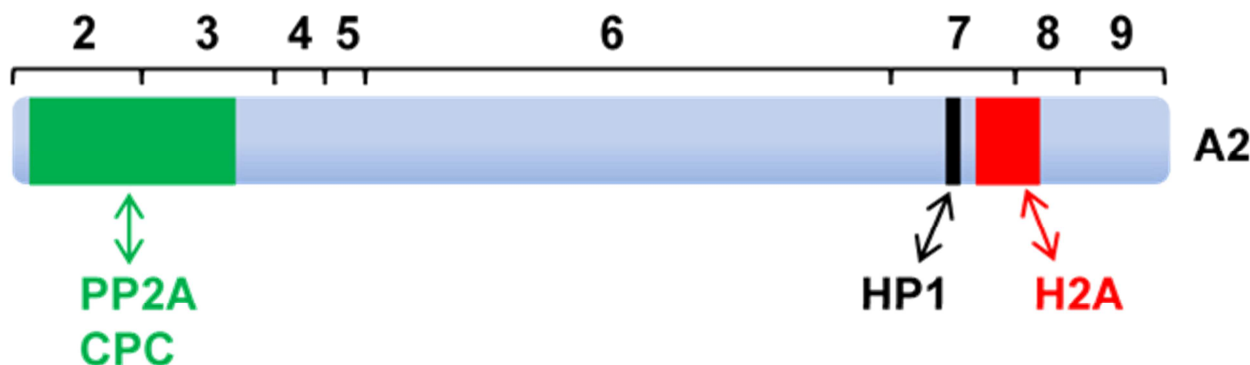


Figure 2. Green, black and red boxes represent an N-terminal conserved coiled-coil region, a P-V-I motif and a C-terminal conserved basic region, respectively. Indicated numbers mean the exon numbers shown at Fig.1. SGOL1-interacting proteins are shown at the bottom.

Transcript B1 (NM_001012411) lacks exon 9 in addition to a large proportion of exon 6 and encodes a protein comprised of 275 aa.

Transcript C2 (NM_138484) skips exon 6 and encodes a protein comprised of 292 aa.

Transcript C1 (NM_001012413) lacks exon 9 in addition to exon 6 and encodes a protein comprised of 258 aa. Transcript D1 (NM_001199257) lacks exon 7 and exon 8 in addition to a large proportion of exon 6 and encodes a protein comprised of 215 aa. Transcript P1 (AB567656) lacks exon 3, resulting in leading to a stop codon within exon 4, and encodes a protein comprised of 59 aa.

Furthermore, several transcript variants that have an alternate 5' UTR exon are also stored in databases (NM_001199251, NM_001199253, NM_001199255, NM_001199252, NM_001199254 and NM_001199256).

Pseudogene

There are two pseudogenes on chromosome 1 (PGOHUM00000244068) and chromosome 7 (PGOHUM00000232695).

Protein

Description

SGOL1 protein (type A2) is a 64.2 kDa protein and has an N-terminal coiled-coil region, a P-V-I motif and a C-terminal conserved basic region.

The N-terminal coiled-coil regions are required for the interaction with PP2A (Yamagishi et al., 2008) and the chromosomal passenger complex (CPC) (Tsukahara et al., 2010) at centromere.

The P-V-I motif and the C-terminal basic region of SGOL1 are required for the interaction with HP1 (heterochromatin protein 1) and phosphorylated histone H2A at centromere, respectively (Yamagishi et al., 2008; Kawashima et al., 2010).

Expression

Serum antibodies against NY-BR-85, which encodes

SGOL1, are detected in breast cancer patients, and the expression of NY-BR-85 mRNA was detected in several tissues, including thymus and testis (Scanlan et al., 2001).

Expression of SGOL1 was also detected in the extraction of HeLa

cells (Salic et al., 2004; Kitajima et al., 2005) and various human leukemia cell lines (Yang et al., 2013), while the expression of SGOL1 was downregulated in the colorectal cancers (Iwaizumi et al., 2009).

Localisation

Nucleus. During prophase and metaphase, SGOL1 localizes to the inner centromere (Salic et al., 2004; Kitajima et al., 2005).

Function

SGOL1 is a crucial factor to protect centromeric cohesin during mitosis and to maintain genomic stability in human cells. SGOL1-knockdown caused severe mitotic arrest and precocious separation of centromeric cohesin in HeLa cells (Salic et al., 2004; Kitajima et al., 2006) and HCT116 cells, resulting in chromosomal instability (Iwaizumi et al., 2009; Kahyo et al., 2011).

In addition, SGOL1 was needed for the kinetochore localization of PLK1 and CENP-F in HeLa cells (Salic et al., 2004; Pouwels et al., 2007).

Several short isoforms of SGOL1 showed aberrant cell phenotypes including unstable chromatid cohesion (Suzuki et al., 2006; Kahyo et al., 2011).

These results suggest that the short isoforms of SGOL1 function as a negative factor to native SGOL1, and that abundant expression of the SGOL1 short isoforms can be responsible for chromosomal instability.

Homology

The coiled-coil and basic regions of shugoshin or shugoshin-like proteins are highly conserved between different species (Kitajima et al., 2004). SGOL2, a paralogue of SGOL1, was required for the PP2A-

mediated protection of cohesin and the MCAK-mediated chromosome congression in HeLa cells (Tanno et al., 2010).

Mutations

Somatic

Losses of heterozygosity at several polymorphic markers in SGOL1 locus (c.416+39_42delGAAA, c.504A>T and c.1461C>T) were detected in 31.2 % of human colorectal cancers (Iwaizumi et al., 2009).

Implicated in

Breast cancer

Note

NY-BR-85 is a serologically defined breast cancer antigen (Scanlan et al., 2001). NY-BR-86 was overexpressed in 90% of breast cancers.

Colorectal cancer

Note

The expression of SGOL1 was significantly downregulated in the colorectal cancer tissue in comparison with the paired normal mucosa, and the tumors in the SGOL1-downregulated group tended to be located on the left side of the large bowel, especially in the rectum, rather than in the other regions of the large bowel (Iwaizumi et al., 2009). The mRNA of the shortest isoform SGOL1-P1, the overexpression of which caused unstable chromatid cohesion in HCT116 cells, was detected specifically in colorectal cancer tissues (Kahyo et al., 2011).

Oncogenesis

While Sgo1 homozygous mutant mice (Sgo1^{-/-}) showed embryonic lethality, Sgo1 heterozygous mice (Sgo1^{+/-}) showed an increase in formation of colonic aberrant crypt foci and accelerated development of colon tumors after exposure to azoxymethane, a colon carcinogen (Yamada et al., 2012).

Hematological malignancies

Note

SGOL1 was aberrantly expressed in various human leukemia cell lines and freshly isolated leukemia cells. SGOL1-knockdown suppressed the cell proliferation in several leukemia cell lines (Yang et al., 2013).

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