PLAG1 (Pleomorphic adenoma gene 1)

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Identity
HGNC (Hugo): PLAG1
Location: 8q12
Local order: (316 cR / 86 Mb from 8pter)

DNA/RNA

Description
7313 bp, 5 exons, 4 introns.

Transcription
At least two splicing variants, including and excluding the second exon.

Protein

Description
500 amino acids with at least three functional regions: 1. Two N-terminal nuclear localisation signals, 2. Seven canonical zinc-finger domains, 3. A serine rich C-terminus.

Expression
Heart, placenta, spleen, prostate, testis, ovary, small intestine, several tumours.

Localisation
Nuclear.

Function
One of the N-terminal nuclear localisation signals (NLS1) interacts with karyopherin a2, which escorts proteins into the nucleus. Three of the seven Zn-finger domains are responsible for interaction with DNA and PLAG1 specifically activates transcription from its consensus binding site. Potential PLAG1 binding sites have been found in the promoter of IGF2.

Homology
Mouse and rat Plag1.

Mutations

Somatic
Involved in chromosome rearrangements in epithelial and mesenchymal tumours. These are typically complex structural abnormalities, resulting in an exchange of regulatory elements and abnormal expression of PLAG1.

Schematic view of the gene with approximate sizes of introns (kb) and exons (bp); the coding region (violet) translates into a 500 amino acid product with three functional subunits.
**Implicated in**

**Pleomorphic adenoma of the salivary gland**

**Disease**
Benign epithelial tumour.

**Prognosis**
Recovery after surgical removal.

**Cytogenetics**
The most common breakpoints are 3p21, 8q12, and 12q15.

**Hybrid/Mutated gene**
The following translocations have been reported to result in hybrid genes involving PLAG1:
- t(3;8)(p21;q12): CTNNB1/CTNNB1/PLAG1
- t(5;8)(p13;q12): LIFR/PLAG1

Also, rearrangements between PLAG1 and TCEA1 have been detected in cases with normal karyotypes.

**Abnormal protein**
Fusions occur in the 5′ regulatory regions, leading to promoter swapping and activation of PLAG1 expression while preserving coding sequences.

**Carcinoma ex pleomorphic adenoma**

**Disease**
Malignant epithelial tumour arising from pleomorphic adenoma.

**Prognosis**
30% five-year survival.

**Cytogenetics**
Complex karyotype including t(3;8)(p23;q12).

**Hybrid/Mutated gene**
Intragenic PLAG1 rearrangements demonstrated by fluorescence in situ hybridisation.

**Lipoblastoma**

**Disease**
Benign fat-forming tumour of childhood.

**Prognosis**
Recovery after surgical removal.

**Cytogenetics**
Structural abnormalities involving 8q11-13.

**Hybrid/Mutated gene**
The following rearrangements have been reported to result in hybrid genes involving PLAG1:
- del(8)(q12q24), r(8); HAS2/PLAG1
- t(7;8)(p22;q13); COL1A2/HAS2

**Abnormal protein**
Fusions occur in the 5′ regulatory regions, leading to promoter swapping and activation of PLAG1 expression while preserving coding sequences.

**References**


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