DLX5 (distal-less homeobox 5)
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Identity
Other names: SHFM1D
HGNC (Hugo): DLX5
Location: 7q21.3
Local order: -DLX6-DLX5-ACN9-

DNA/RNA
Description
The DLX5 gene is composed of 3 exons spanning a genomic region of 4442 bp.

Transcription
The DLX5 coding sequence consists of 870 bp from the start of the first codon to the stop codon (Simeone et al., 1994).

Pseudogene
None known.

Protein
Description
The DLX5 protein consists of 289 amino acids with a calculated molecular weight of 31.5 kDa.
The protein contains two motifs, one dubbed homeobox protein distal-less-like N terminal and a second known as a homeodomain.

Localisation
Nucleus.

Function
Transcription factor important in the control of bone formation in embryonic development (Hassan et al., 2004).

Homology
None reported to date.

Local order of DLX5 and flanking genes DLX6 and ACN9 is shown, with centromere at left and telomere (qter) at right. Arrows indicate transcriptional orientation of individual genes. DLX6 gene range: 96635290 - 96640352; DLX5 gene range: 96649702 - 96654143; ACN9 gene range: 96745905 - 96811075 (Hillier et al., 2003).

Mutations

Germinal

A novel DLX5 mutation (c.A533C: p.Q178P) was identified in a family with autosomal recessive split hand and foot malformation (Shamseldin et al., 2012).

Somatic

A DLX5 mutation (c.C119G: p.S40C) was observed in an ovarian carcinoma (Cancer Genome Atlas Research Network, 2011). Overexpression of DLX5 has been reported in several types of human malignancy including lung cancer (Kato et al., 2008; Xu and Testa, 2009), T-cell lymphoma (Tan et al., 2008), and ovarian cancer (Tan et al., 2010), etc.

Implicated in

Lung cancer

Note

The DLX5 gene was reported to be overexpressed in the great majority of human non-small cell lung cancers examined by Kato et al., 2008. Furthermore, immunohistochemical studies revealed that positive immunostaining for DLX5 correlated with tumor size and poorer prognosis.

Lymphoma

Note

DLX5 was found to be highly expressed in 3 of 7 (42%) patient-derived T-cell lymphomas compared with that observed in nonmalignant lymph node samples (Tan et al., 2008). In addition, these investigators found repeated upregulation of Dlx5 in T-cell lymphomas from transgenic mice in which the Lck promoter was used to drive expression of a constitutively active form of Akt2 in the thymus. Dlx5 was overexpressed due to a novel chromosome inversion that placed the T-cell receptor beta (Tcrb) enhancer region near the Dlx5 locus.

Breast cancer

Note

Both DLX5 and DLX6 were found to be upregulated during metastasis formation after intravenous injection of MDA-MB-231 breast cancer cells. The in vitro treatment of MDA-MB-231 cells with endothelin 1, a peptide associated with breast cancer invasive phenotype, resulted in a switch from DLX2 to DLX5 expression. Mutually exclusive expression of DLX2 and DLX5 was found in both MDA-MB-231 cells and human breast cancer specimens. This evidence suggested that DLX genes are involved in human breast cancer progression, and that expression of DLX2 and DLX5 genes might serve as prognostic markers (Morini et al., 2010).

Various cancers

Note

DLX5 mRNA is abundantly expressed in many cancer cell lines derived from malignant tissues of breast, brain, lung, skin, and ovarian cancer patients, whereas expression of DLX5 was low or undetectable in tumor cells from patients with leukemia or with colorectal, prostate, and kidney cancers (Tan et al., 2010).

References


Xu J, Testa JR. DLX5 (distal-less homeobox 5) promotes tumor cell proliferation by transcriptionally regulating MYC. J Biol Chem. 2009 Jul 31;284(31):20593-601


This article should be referenced as such: