

Gene Section

Short Communication

EHF (ets homologous factor)

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Identity

Other names: ESE3, ESE3B, ESEJ

HGNC (Hugo): EHF

Location: 11p13

Note

This gene encodes a protein that belongs to the ETS family of transcription factor.

This gene belongs to the ETS subfamily defined as Epithelial Specific ETS (ESE) characterized by prevalent expression in epithelial cells.

The encoded protein acts as a transcriptional repressor and/or activator.

It is expressed in normal epithelium and may be involved in epithelial differentiation. Reduced expression of this gene is associated with tumorigenesis.

DNA/RNA

Note

Tumor suppressor gene.

Description

DNA Size: 39,72 kb, 9 exons.

Transcription

See below figure B.

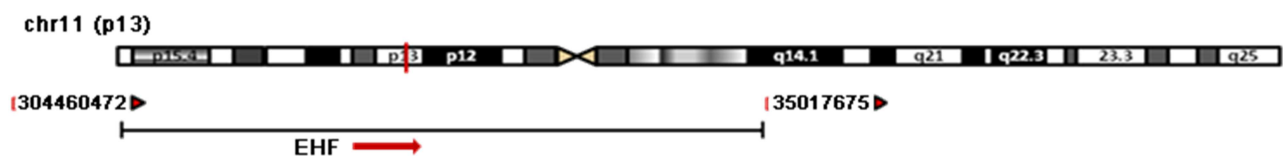


Fig. A



Fig. B

identification	type	bp	Transcripts messenger RNA	kDa	AA	Pubmed
ESE3A	splicing	2853		32,3	277	Kas, 2000.
ESE3B	splicing	3617		34,9	300	Kas,2000; Cangemi, 2008.

Schematic diagram of the EHF gene comprising 9 exons (in red). The sizes in base pairs (bp) of exons (below) are shown. B. Transcripts.

Sequence	Length	Mass (Da)
Isoform 1 (ESE-3A) FASTA	277	32345
10 20 30 40 50 60		
MILEGGGVMN LNPGNLLHQ PPAWTD SYST CNVSSGFFGS QWHEIHPQYW TKYQVWBWLQ		
70 80 90 100 110 120		
HLLDTNQLDA NCIPFQEFDI NGEHLC SMSL QEFTRAAGTA GQLLYSNLQH LKWNGQCSSD		
130 140 150 160 170 180		
LFQSTHMVW KTEQTEPSIM NTWKDENLY DTNYGSTVAE SPD MKKEQDP PAKCHTKKHN		
190 200 210 220 230 240		
PRGTHLWEFI RDILLNPKDN PGLIKWEDRS EGVFRFLKSE AVAQLWGKKK NNSSMTYEKL		
250 260 270		
SRAMRYYYKR EILERVDRRR LVYKFGKNAR GWRENE		

Sequence	Length	Mass (Da)
Isoform 2 (ESE-3B) FASTA	300	34892
10 20 30 40 50 60		
MILEGGGVMN LNPGNLLHQ PPAWTD SYST CNVSSGFFGS QWHEIHPQYW TKYQVWBWLQ		
70 80 90 100 110 120		
HLLDTNQLDA NCIPFQEFDI NGEHLC SMSL QEFTRAAGTA QQLLYSNLQH LKWNGQCSSD		
130 140 150 160 170 180		
LFQSTHMVW KTEQTEPSIM NTWKDENLY DTNYGSTVDL LDGKTF CRVQ ISMTT TSHLP		
190 200 210 220 230 240		
VAESPMKKE QDPPAKCHTK KHNPRGTHLW EFIRDILLMP DMKPLIKWE DRSEGVFRFL		
250 260 270 280 290 300		
KSEAVAQLWG KKKNNSSMTY EKLSRAMRY YKREILERVDRRLVYKFGKNARGWRENE		

Protein

Description

As reported by Kas et al., (J Biol Chem. 2000) sequence analysis revealed an open reading frame of 277 amino acids and a predicted molecular mass of 32,3 kDa for ESE-3a and an open reading frame encoding a 300-amino acid protein with a predicted molecular mass of 34,9 kDa for ESE-3b.

In addition, several potential phosphorylation sites are present in ESE-3b including two potential protein kinase C phosphorylation sites, three casein kinase II phosphorylation sites, and one potential JNK/p38/ ERK kinase phosphorylation sites ((S/T)P) in the central region of ESE-3, just behind the alternatively spliced exon.

Expression

Normal epithelium.

Localisation

Nuclear.

Function

Transcription factor that binds to DNA sequences containing the ETS factor consensus nucleotide core sequence GGAA. May act as a repressor for a specific subset of ETS/AP-1-responsive genes and as a

modulator of the nuclear response to RAS and mitogen-activated protein kinase (MAPK) signaling cascades.

Involved in negative regulation of the expression of EZH2 through ETS binding sequences on the EZH2 promoter in normal prostate epithelial cells, prostate cancer cells and prostate tumors.

Involved in positive regulation of NKX3.1 in normal prostate epithelial cells through ETS binding site in the gene promoter.

Involved in the regulation of the expression of caspase-3 through ETS binding sequences on the caspase-3 promoter in prostate cancer cells.

Involved in regulation of TNFRSF10B/DR5 expression through ETS binding sequences on the TNFRSF10B/DR5 promoter.

May play a role in regulating epithelial cell differentiation and contribute to development and tumorigenesis by acting as a tumor suppressor gene.

Mutations

Note

Unknown.

Germinal

Unknown.

Somatic

Unknown.



Schematic representation of the two ESE3 protein isoforms. The pointed domain (PNT) and the Ets binding site (Ets DNA binding) domain are shown. PNT: (Pointed domain); EBS: (Ets binding site).

Implicated in

Human malignancies

Note

Albino et al. (Cancer Research, 2012) showed that ESE3, an endogenously expressed ETS transcription factor, controls prostate epithelial cell differentiation and stem-like potential. Stable ESE3 knockdown in prostate epithelial cells induced epithelial-to-mesenchymal transition (EMT), stem-like features, tumour-initiating and metastatic properties. Conversely, re-expression of ESE3 in prostate cancer cells reduced stem-like and tumorigenic potential. Mechanistically, ESE3/EHF maintains in a repressive state key EMT and Cancer stem cells (CSC) genes, including TWIST1, ZEB2, BMI1 and POU5F1, by directly binding to novel ETS binding sites identified in their promoters. Analysis of human tissue microarrays showed that reduced ESE3 expression was an early event and frequently independent of other ETS gene alterations. Analyses of multiple microarray datasets linked loss of ESE3/EHF expression to a distinct group of prostate tumors. ESE3^{low} tumors displayed distinctive molecular and biological characteristics, including increased expression of EMT and CSC genes and close similarity to ESE3 knockdown prostate epithelial cells. Low ESE3 expression was associated with increased biochemical recurrence and reduced overall survival after prostatectomy.

Prostate cancer

Note

The ESE3 expression is reduced in prostate tumors.

Disease

Prostate cancer (possibly implicated in other solid tumors of epithelial origin).

Oncogenesis

Cangemi et al. (Oncogene 2008) and Albino et al. (Cancer Research, 2012) propose a tumor suppressor role in prostate cancer for ESE3. Albino et al. (Cancer Research, 2012) propose the possibility to identify molecularly defined tumour subgroups based on the exclusive loss of ESE3 expression level.

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