

HsaEX0033220

Exon Skipping
hg19hg38

Gene

ENSG0000004487 | KDM1A

Description

lysine (K)-specific demethylase 1A [Source: HGNC Symbol;Acc:29079]

Coordinates

chr1:23356962-23377013+

Length

60 bp

Sequences

Splice sites

3' ss Seq 13.9

5' ss Seq 10.07

Exon sequences

Seq C1 exon

Seq A exon

Seq C2 exon

Protein impact

Alternative protein isoforms (Ref)

Show PDB structure

Features

Disorder rate: C1=0.988 A=1.000 C2=0.015

Domain overlap (PROSITE):

Domain overlap (PFAM):

Info

C1: NO

A: NO

C2: PF0443312=SWIRM=PU(47.3=95.6)

Degree: 12

Betweenness: 35.205

Associated events

Conservation

Mouse: chr4:136119353-136119364 (ALTERNATIVE) MmuEX0025261

Chicken: chr23:1676492-1676551 (ALTERNATIVE) GgaEX0000824

Primers PCR

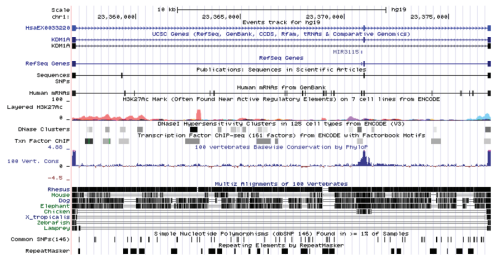
Suggestions for RT-PCR validation

F: AGCCCACTGAGAGAGAAA

R: GGTCTGTGTGTGTCACGAT

Band lengths: 148-208

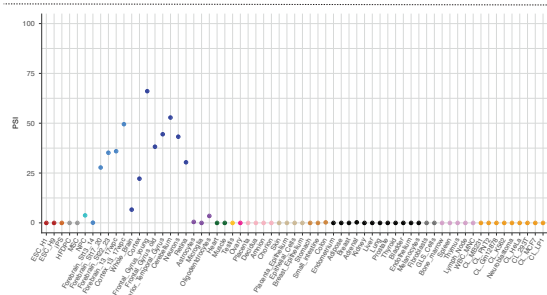
GENOMIC CONTEXT



INCLUSION LEVELS

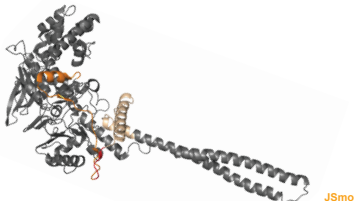
[Show All] [Show None] [Select All] [Select None] Read coverage stringency

ESC IPS Precursors NPC EmbrBrain Neural Glia Muscle Testis Ovary Placental Epithelial
Digestive tract Tissues Cells Immune hematopoiesis CLines



SPECIAL DATASETS

- GTEx
 - Autistic and control brains
 - Pancreatic cell types
- Other AS DBs:
 - FasterDB (includes CLIP-seq data)
 - AS-ALPS (AS-induced ALteration of Protein Structure, links to PiNs)
 - APPRIS (Selection of principal isoform)
 - DEU primates (only for human)



Legend
Chain
A
C1
C2

General information

- Event ID
- Gene name and gene symbol
- Genomic coordinates
- Exon length

Sequence information

- Sequence of the alternative exon
- Sequences of the two constitutive flanking exons
- Sequences and strength of the splice sites

Protein impact

- Effect on the open reading frame
- Location in the domain architecture
- Location in disordered regions
- Metrics in protein-protein interaction networks

Evolutionary conservation

- Orthologous events between species
- Distinction between conserved alternative events, conserved constitutive events, and non-conserved events

RT-PCR validation instructions

- Suggested primer sequences
- Expected band lengths for inclusion and skipping PCR products

Genomic context

- UCSC browser track
- Link to personalized view in UCSC browser website

Inclusion levels

- Tissue-specific PSI plot
- Interactive sample selection
- User-selected read coverage stringency
- Samples grouped and colored according to their biological origin
- Multiple replicates for each data point

Links to other AS databases

Special datasets

(similar to the Gene view)

Protein structure (for AltEX)

- Alternative exon and flanking exons are highlighted
- Interactive view (JSmol)

Supplemental Figure S21 – Example of an AS event view entry in VastDB

Adapted screenshot of the Event view from VastDB (<http://vastdb.crg.eu>) for a human AltEx event (based on HsaEX0033219 and HsaEX0033220). Event view includes, from top to bottom, general information, sequence information, protein impact of the alternative sequence, evolutionary conservation (currently with mouse and chicken), suggested primers for RT-PCR validation, genomic context (linking to UCSC Genome Browser), interactive plot of PSI across 63 human cell and tissue types from averaging 118 samples, plots of PSIs for other datasets of special interest, links to other AS databases, and mapping to protein structures (when available). General information, sequence data, domain mappings, conservation, PCR primers and genomic context correspond to HsaEX0033220. Associated events, inclusion levels and protein structure correspond to HsaEX0033219.