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FOXA1 Knockdown 293T Cell Lysate, Heterozygous

Catalog No.: RM02568

Basic Information

Catalog No.
RM02568

Category
Cell Lysate

Parental Cell line
293T

Genotype
Knockdown

Gene Information

Gene Symbol
FOXA1

Species
Human

Gene ID
3169

Swiss Prot
P55317

Synonyms
HNF3A; TCF3A

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Background

This gene encodes a member of the forkhead class of DNA-binding proteins. These hepatocyte nuclear factors are transcriptional activators for liver-specific transcripts such as albumin and transthyretin, and they also interact with chromatin. Similar family members in mice have roles in the regulation of metabolism and in the differentiation of the pancreas and liver. [provided by RefSeq, Jul 2008]

Product Information

Description
FOXA1 Knockdown 293T Cell Line is engineered from 293T cell line with Gene-Editing technology.
Allele-1:137bp deletion in exon2
Allele-2:WT
Mammalian cells such as human, rat and mouse cells are normally diploid with two alleles. Homozygote: both alleles were knocked out, mRNA has no signal, no expression of proteins. Heterozygote: only one allele was knocked out, the mRNA transcript levels was decreased compared to wild type, and the protein expression levels was also lower than that of the wild type.

Packaging
1 vial parental cell Lysate and 1 vial knockout cell Lysate

Shipping Conditions
4℃

Amount
50μL, 2μg/μL.

Storage
Lysate is stable for 12 months when stored at -20℃. Minimizing freeze-thaw cycles.

Protocol
To be used as WB control. Lysate is supplied in 1× SDS sample buffer (2% SDS, 60 mM Tris-HCl pH 6.8, 10% Glycerol, 0.02% Bromophenol blue, 60 mM beta-mercaptoethanol). Lysate should be boiled for 3 - 5 minutes before loading onto gel.

Sequencing data

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WT    AACATGACCCCGGC**********TGAGCCCGAGCGGC
Mut   AACATGACCCCGGC***Deletion***TGAGCCCGAGCGGC
Allele-1:    137bp deletion in exon2

WT    AACATGACCCCGGC**********TGAGCCCGAGCGGC
Mut   AACATGACCCCGGC**********TGAGCCCGAGCGGC
Allele-2:    WT
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Genome sequence analysis of PCR products from parental (WT) and FOXA1 Knockdown (KD) 293T cells, using sanger sequencing.