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TET1 Knockdown 293T Cell Lysate, Heterozygous

Catalog No.: RM02038

Basic Information

Catalog No.
RM02038

Category
Cell Lysate

Parental Cell line
293T

Genotype
Knockdown

Background

DNA methylation is an epigenetic mechanism that is important for controlling gene expression. The protein encoded by this gene is a demethylase that belongs to the TET (ten-eleven translocation) family. Members of the TET protein family play a role in the DNA methylation process and gene activation. [provided by RefSeq, Sep 2015]

Gene Information

Gene Symbol
TET1

Species
Human

Gene ID
80312

Swiss Prot
Q8NFU7

Synonyms
CXXC6; LCX; bA119F7.1

Product Information

Description
TET1 Knockdown 293T Cell Line is engineered from 293T cell line with Gene-Editing technology.
Allele-1:155bp deletion in exon1
Allele-2:168bp deletion in exon1
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.

Contact

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Sequencing data

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WT    TAAACCACCCGTGC**************GTCGTAGCCAAATC
Mut   TAAACCACCCGTGC***Deletion***GTCGTAGCCAAATC
Allele-1：155bp deletion in exon1

WT    AACCTAAACCACCC**************AAATCCAAAAAGGT
Mut   AACCTAAACCACCC***Deletion***AAATCCAAAAAGGT
Allele-2：168bp deletion in exon1
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Genome sequence analysis of PCR products from parental (WT) and TET1 knockdown (KD) 293T cells, using sanger sequencing.