

TRIM21 Knockout 293T Cell Lysate, Homozygous

Catalog No.: RM02484

Basic Information

Catalog No.

RM02484

Category

Cell Lysate

Parental Cell line

293T

Genotype

Knockout

Background

This gene encodes a member of the tripartite motif (TRIM) family. The TRIM motif includes three zinc-binding domains, a RING, a B-box type 1 and a B-box type 2, and a coiled-coil region. The encoded protein is part of the RoSSA ribonucleoprotein, which includes a single polypeptide and one of four small RNA molecules. The RoSSA particle localizes to both the cytoplasm and the nucleus. RoSSA interacts with autoantigens in patients with Sjogren syndrome and systemic lupus erythematosus. Alternatively spliced transcript variants for this gene have been described but the full-length nature of only one has been determined. [provided by RefSeq, Jul 2008]

Gene Information

Gene Symbol

TRIM21

Species

Human

Gene ID

6737

Swiss Prot

P19474

Synonyms

RNF81; RO52; Ro/SSA; SSA; SSA1

Contact

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Product Information

Description

TRIM21 Knockout 293T Cell Line is engineered from 293T cell line with Gene-Editing technology.

Allele-1:176bp deletion in exon1

Allele-2:172bp 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

Amount

4°C

50μL, 2μg/μL.

Storage

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

Protocol

To be used as WB control. Lysate is supplied in $1\times$ 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

WT AGAATCTCCGGCCC*************CATGGTCCCTCTTG
Mut AGAATCTCCGGCCC***Deletion***CATGGTCCCTCTTG
Allele-1: 176bp deletion in exon1

WT ATCTCCGGCCCAAT***********************CCATGGTCCCTCTT
Mut ATCTCCGGCCCAAT***Deletion****CCATGGTCCCTCTT

Allele-2: 172bp deletion in exon1

Genome sequence analysis of PCR products from parental (WT) and TRIM21 knockout (KO) 293T cells, using sanger sequencing.