

MYSM1 Knockout HeLa Cell Lysate, Homozygous

Catalog No.: RM50044

Basic Information

Catalog No.

RM50044

Category

Cell Lysate

Parental Cell line

HeLa

Genotype

Knockout

Gene Information

Gene Symbol

MYSM1

Species

Human

Gene ID

114803

Swiss Prot

Q5VVJ2

Synonyms

2ADUB; BMFS4; 2A-DUB; MYSM1

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Background

Enables histone binding activity; peptidase activity; and transcription coactivator activity. Involved in several processes, including chromatin remodeling; monoubiquitinated histone H2A deubiquitination; and positive regulation of transcription by RNA polymerase II. Located in nucleolus and nucleoplasm. Part of protein-containing complex. Implicated in diabetic retinopathy.

Product Information

Description

MYSM1 Knockout cell line is engineered from HeLa cell line with Gene-Editing Technology.

Allele-1:exon1 was deleted

Allele-2:exon1 was deleted

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°C

Amount

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× 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 TCGGGA GGAC*****TCCGGCAAGGGAAA
Mut TCGGGA**TCTT**GGAC***Deletion***TCCGGCAAGGGAAA
Allele-1: exon1 was deleted

WT TCTCGGGAGGACGG*****GCGGGCCCTGGGAA
Mut TCTCGGGAGGACGG***Deletion***GCGGGCCCTGGGAA
Allele-2: exon1 was deleted

Genome sequence analysis of PCR products from parental (WT) and MYSM1 knockout (KO) HeLa cells, using sanger sequencing.