

NDUFAF3 Knockout HeLa Cell Lysate, Homozygous

Catalog No.: RM50002

Basic Information

Catalog No.

RM50002

Category

Cell Lysate

Parental Cell line

HeLa

Genotype

Knockout

Background

This gene encodes a mitochondrial complex I assembly protein that interacts with complex I subunits. Mutations in this gene cause mitochondrial complex I deficiency, a fatal neonatal disorder of the oxidative phosphorylation system. Alternatively spliced transcript variants encoding different isoforms have been identified.

Gene Information

Gene Symbol

NDUFAF3

Species

Human

Gene ID

25915

Swiss Prot

Q9BU61

Synonyms

2P1; E3-3; C3orf60; MC1DN18

Contact

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Product Information

Description

NDUFAF3 Knockout cell line is engineered from HeLa cell line with Gene-Editing Technology. Allele-1:113bp deletion in exon2

Allele-2:113bp deletion in exon2

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 GCTCTCGCCGGCGG***********CTCGGCCCCTGCGC
Mut GCTCTCGCCGGCGG***Deletion***CTCGGCCCTGCGC
Allele-1: 113bp deletion in exon2

WT GCTCTCGCCGGCGG***********CTCGGCCCCTGCGC
Mut GCTCTCGCCGGCGG***Deletion***CTCGGCCCCTGCGC
Allele-2: 113bp deletion in exon2

Genome sequence analysis of PCR products from parental (WT) and NDUFAF3 knockout (KO) HeLa cells, using sanger sequencing.