

BNIP3 Knockout 293T Cell Lysate, Homozygous

Catalog No.: RM02480

Basic Information

Catalog No.

RM02480

Category

Cell Lysate

Parental Cell line

293T

Genotype

Knockout

Gene Information

Gene Symbol

BNIP3

Species

Human

Gene ID

664

Swiss Prot

Q12983

Synonyms

NIP3

Contact

☎ | 400-999-6126

✉ | cn.market@abclonal.com.cn

🌐 | www.abclonal.com.cn

Background

This gene encodes a mitochondrial protein that contains a BH3 domain and acts as a pro-apoptotic factor. The encoded protein interacts with anti-apoptotic proteins, including the E1B 19 kDa protein and Bcl2. This gene is silenced in tumors by DNA methylation. [provided by RefSeq, Dec 2014]

Product Information

Description

BNIP3 Knockout 293T Cell Line is engineered from 293T cell line with Gene-Editing technology.

Allele-1:134bp deletion in exon1

Allele-2:134bp 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°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 TGAGTTCCTCCGGC*****GCCATGTCGCAGAA
Mut TGAGTTCCTCCGGC***Deletion***GCCATGTCGCAGAA
Allele-1: 134bp deletion in exon1
WT TGAGTTCCTCCGGC*****GCCATGTCGCAGAA
Mut TGAGTTCCTCCGGC***Deletion***GCCATGTCGCAGAA
Allele-2: 134bp deletion in exon1

Genome sequence analysis of PCR products from parental (WT) and BNIP3 knockout (KO) 293T cells, using sanger sequencing.