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MYL9 Knockout 293T Cell Lysate, Homozygous

Catalog No.: RM02037

Basic Information

Catalog No.
RM02037

Category
Cell Lysate

Parental Cell line
293T

Genotype
Knockout

Background

Myosin, a structural component of muscle, consists of two heavy chains and four light chains. The protein encoded by this gene is a myosin light chain that may regulate muscle contraction by modulating the ATPase activity of myosin heads. The encoded protein binds calcium and is activated by myosin light chain kinase. Two transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Jul 2008]

Gene Information

Gene Symbol
MYL9

Species
Human

Gene ID
10398

Swiss Prot
P24844

Synonyms
LC20; MLC-2C; MLC2; MRLC1; MYRL2

Product Information

Description
MYL9 Knockout 293T Cell Line is engineered from 293T cell line with Gene-Editing technology.
Allele-1:100bp deletion in exon1
Allele-2:100bp 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
Store at -20℃

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.

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Sequencing data

WT GGCCACATCCAATG**********CGACATGCTGGCCT
Mut GGCCACATCCAATG***Deletion***CGACATGCTGGCCT
Allele-1: 100bp deletion in exon1

WT GGCCACATCCAATG**********CGACATGCTGGCCT
Mut GGCCACATCCAATG***Deletion***CGACATGCTGGCCT
Allele-2: 100bp deletion in exon1

Genome sequence analysis of PCR products from parental (WT) and MYL9 knockout (KO) 293T cells, using sanger sequencing.

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