

# FLOT1 Knockout 293T Cell Lysate, Homozygous

Catalog No.: RM02472

## Basic Information

### Catalog No.

RM02472

### Category

Cell Lysate

### Parental Cell line

293T

### Genotype

Knockout

## Gene Information

### Gene Symbol

FLOT1

### Species

Human

### Gene ID

10211

### Swiss Prot

O75955

## Contact

 | 400-999-6126

 | [cn.market@abclonal.com.cn](mailto:cn.market@abclonal.com.cn)

 | [www.abclonal.com.cn](http://www.abclonal.com.cn)

## Background

This gene encodes an protein that localizes to the caveolae, which are small domains on the inner cell membranes. This protein plays a role in vesicle trafficking and cell morphology. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Jan 2016]

## Product Information

### Description

FLOT1 Knockout 293T Cell Line is engineered from 293T cell line with Gene-Editing technology.

Allele-1:62bp deletion in exon4

Allele-2:119bp deletion in exon4

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

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WT GCGGCCGCCTGTC\*\*\*\*\*CACCAGAGGGCCAT  
Mut GCGGCCGCCTGTC\*\*\*Deletion\*\*\*CACCAGAGGGCCAT  
Allele-1: 62bp deletion in exon4  
WT ACAGGTAAAAATCC\*\*\*\*\*CACATGACTGTGGA  
Mut ACAGGTAAAAATCC\*\*\*Deletion\*\*\*CACATGACTGTGGA  
Allele-2: 119bp deletion in exon4

Genome sequence analysis of PCR products from parental (WT) and FLOT1 knockout (KO) 293T cells, using sanger sequencing.