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CD320 Knockout 293T Cell Lysate, Homozygous

Catalog No.: RM50010

Basic Information

Catalog No.
RM50010

Category
Cell Lysate

Parental Cell line
293T

Genotype
Knockout

Background

This gene encodes the transcobalamin receptor that is expressed at the cell surface. It mediates the cellular uptake of transcobalamin bound cobalamin (vitamin B12), and is involved in B-cell proliferation and immunoglobulin secretion. Mutations in this gene are associated with methylmalonic aciduria. Alternatively spliced transcript variants encoding different isoforms have been found for this gene.

Gene Information

Gene Symbol
CD320

Species
Human

Gene ID
51293

Swiss Prot
Q9NPF0

Synonyms
8D6; 8D6A; TCBLR; TCN2R; TCII-R; sCD320; CD320

Product Information

Description
CD320 Knockout cell line is engineered from 293T cell line with Gene-Editing Technology.
Allele-1:64bp deletion in exon1
Allele-2:64bp 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.

Contact

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Sequencing data

```
WT    GGCGGTTGGATGG**********ACTAGGCCTGGAG
Mut   GGCGGTTGGATGG***Deletion***ACTAGGCCTGGAG
Allele-1:   64bp deletion in exon1

WT    GGCGGTTGGATGG**********ACTAGGCCTGGAG
Mut   GGCGGTTGGATGG***Deletion***ACTAGGCCTGGAG
Allele-2:   64bp deletion in exon1
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Genome sequence analysis of PCR products from parental (WT) and CD320 knockout (KO) 293T cells, using sanger sequencing.