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CTPS2 Knockout NIH/3T3 Cell Line, Homozygous

Catalog No.: RM02175

Basic Information

Catalog No.
RM02175

Category
Cell Line

Parental Cell line
NIH/3T3

Genotype
Knockout

Gene Information

Gene Symbol
CTPS2

Species
Mouse

Gene ID
55936

Synonyms
A830031M15Rik; AI326475; Ctpsh

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Background

Product Information

Description
CTPS2 Knockout NIH/3T3 Cell Line is engineered from NIH/3T3 cell line with Gene-Editing Technology.
Allele-1:62bp deletion in exon1
Allele-2:62bp 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 line and 1 vial knockout cell line

Shipping Conditions
Dry ice

Amount
1~5x10^6 cells/vial

Storage
Store at -20℃

Protocol
Upon arrival, it should be maintained in DMEM medium with 10%(v/v) fetal bovine serum and 100U penicillin-streptomycin, at 37℃ with 5% CO_2 condition.
1. Thaw the vial in 37℃ water bath ,and shake it to melt as soon as possible.
2. Transfer the cell suspension to a 15mL conical tube with pre-warmed 5mL complete medium and centrifuge 1000rpm for approximately 5 minutes at room temperature.
3. Remove and discard the supernatant.
4. Resuspend the cell pellet with 1mL pre-warmed complete medium and seed in 10cm dish.
5. Add 8-10mL of complete medium.
6. Incubate the culture at 37℃ incubator with 5% CO_2.
7. A subcultivation ratio of 1:2-1:4 is recommended.

Sequencing data

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WT    GATTATCGCCAGCA**************ATTAACATCGATGC
Mut   GATTATCGCCAGCA***Deletion***ATTAACATCGATGC
Allele-1：62bp deletion in exon1

WT    GATTATCGCCAGCA**************ATTAACATCGATGC
Mut   GATTATCGCCAGCA***Deletion***ATTAACATCGATGC
Allele-2：62bp deletion in exon1
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Genome sequence analysis of PCR products from parental (WT) and CTPS2 knockout (KO) NIH/3T3 cells, using sanger sequencing.

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