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IGFBP5 Knockdown 293T Cell Line, Heterozygous

Catalog No.: RM02099

Basic Information

Catalog No.
RM02099

Category
Cell Line

Parental Cell line
293T

Genotype
Knockdown

Gene Information

Gene Symbol
IGFBP5

Species
Human

Gene ID
3488

Swiss Prot
P24593

Synonyms
IBP5

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Background

Product Information

Description
IGFBP5 Knockdown 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 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    CTGCGAGCCCTGCG**************GCAGTCGTGCGGCG
Mut   CTGCGAGCCCTGCG***Deletion***GCAGTCGTGCGGCG
Allele-1: 100bp deletion in exon1

WT    CTGCGAGCCCTGCG**************GCAGTCGTGCGGCG
Mut   CTGCGAGCCCTGCG***Deletion***GCAGTCGTGCGGCG
Allele-2: 100bp deletion in exon1
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Genome sequence analysis of PCR products from parental (WT) and IGFBP5 Knockdown (KD) 293T cells, using sanger sequencing.