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BAZ1B Knockout 293T Cell Line, Homozygous

Catalog No.: RM02450

Basic Information

Catalog No.
RM02450

Category
Cell Line

Parental Cell line
293T

Genotype
Knockout

Background

This gene encodes a member of the bromodomain protein family. The bromodomain is a structural motif characteristic of proteins involved in chromatin-dependent regulation of transcription. This gene is deleted in Williams-Beuren syndrome, a developmental disorder caused by deletion of multiple genes at 7q11.23. [provided by RefSeq, Jul 2008]

Gene Information

Gene Symbol
BAZ1B

Species
Human

Gene ID
9031

Swiss Prot
Q9UIG0

Synonyms
WBSCR10; WBSCR9; WSTF

Product Information

Description
BAZ1B Knockout 293T Cell line is engineered from 293T cell line with Gene-Editing Technology.
Allele-1:73bp deletion in exon1
Allele-2:73bp 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.

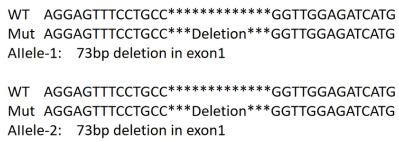
Contact

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Sequencing data



Genome sequence analysis of PCR products from parental (WT) and BAZ1B knockout (KO) 293T cells, using sanger sequencing.

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