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METTL3 Knockdown U2OS cell line, Heterozygous

Catalog No.: RM50187

Basic Information

Catalog No.
RM50187

Category
Cell Lysate

Parental Cell line
U2OS

Genotype
Knockdown

Gene Information

Gene Symbol
METTL3

Species
Human

Gene ID
56339

Swiss Prot
Q86U44

Synonyms
M6A; IME4; Spo8; MT-A70; hMETTL3; METTL3

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Background

This gene encodes the 70 kDa subunit of MT-A which is part of N6-adenosine-methyltransferase. This enzyme is involved in the posttranscriptional methylation of internal adenosine residues in eukaryotic mRNAs, forming N6-methyladenosine.

Product Information

Description
METTL3 Knockdown cell line is engineered from U2OS cell line with Gene-Editing Technology.
Allele-1:139bp deletion in exon2
Allele-2:138bp deletion in exon2
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
Stored in liquid nitrogen for a long time less than -130℃. Minimizing freeze-thaw cycles.

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    CATTGTCTCCAACC**********CATTGCCCACTGAT
Mut   CATTGTCTCCAACC***Deletion***CATTGCCCACTGAT
Allele-1:    139bp deletion in exon2

WT    ATTGTCTCCAACCT**********CATTGCCCACTGAT
Mut   ATTGTCTCCAACCT***Deletion***CATTGCCCACTGAT
Allele-2:    138bp deletion in exon2
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Genome sequence analysis of PCR products from parental (WT) and METTL3 knockdown (KD) U2OS cells, using sanger sequencing.