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FIS1 Knockout HeLa Cell Line, Homozygous

Catalog No.: RM02131

Basic Information

Catalog No.
RM02131

Category
Cell Line

Parental Cell line
HeLa

Genotype
Knockout

Gene Information

Gene Symbol
FIS1

Species
Human

Gene ID
51024

Swiss Prot
Q9Y3D6

Synonyms
CGI-135; TTC11

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Background

The balance between fission and fusion regulates the morphology of mitochondria. TTC11 is a component of a mitochondrial complex that promotes mitochondrial fission (James et al., 2003 [PubMed 12783892]).[supplied by OMIM, Mar 2008]

Product Information

Description
FIS1 Knockout HeLa Cell Line is engineered from HeLa cell line with Gene-Editing Technology.
Allele-1:31bp deletion and 12bp deletion in exon2
Allele-2:58bp 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

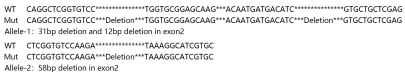
Shipping Conditions
Dry ice

Amount
1~5x10^6 cells/vial

Storage
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



Genome sequence analysis of PCR products from parental (WT) and FIS1 knockout (KO) HeLa cells, using sanger sequencing.