

Resource Summary Report

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[eif-3.C\(ve784\[LoxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + LoxP\]\)/hT2 \[umnIs73\] I; +/-hT2 \[bli-4\(e937\) let-?\(h661\)\] III.](#)

RRID:WB-STRAIN:WBStrain00055433

Type: Organism

Proper Citation

RRID:WB-STRAIN:WBStrain00055433

Organism Information

URL: <http://www.wormbase.org/db/get?name=WBStrain00055433>

Proper Citation: RRID:WB-STRAIN:WBStrain00055433

Description: Caenorhabditis elegans with name eif-3.C(ve784[LoxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + LoxP])/hT2 [umnIs73] I; +/-hT2 [bli-4(e937) let-?(h661)] III. from WB.

Species: Caenorhabditis elegans

Synonyms: eif-3.C(ve784[LoxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + LoxP])/hT2 [umnIs73] I; +/-hT2 [bli-4(e937) let-?(h661)] III.

Notes: Homozygous early larval lethal. Deletion of 2440 bp with Calarco/Colaiacovo selection cassette conferring myo-2 GFP and G418 resistance inserted at break in parental strain N2. Heterozygotes are wild-type GFP+ mKate2+, and segregate wild-type GFP+ mKate2+, GFP+ non-mKate2 dead larvae (ve784 homozygotes), non-GFP mKate2+ arrested animals (arrest stage unknown)(hT2 homozygotes) and dead eggs (aneuploids). Pick wild-type GFP+ mKate2+ and check for correct segregation of progeny to maintain. [NOTE: Apparently the lethal mutation is closely linked but not within the balanced region of hT2. It can occasionally recombine away so that the strain will segregate Bli-4 hT2 homozygotes. (Mark Edgley)] Left flanking Sequence: CTTCTGCTGAGCATACGACGACGCATTTTCG ; Right flanking sequence: ttaaataataattattatttaatacacaat. sgRNA #1: AATTGCAACTAGCCATGTG; sgRNA #2: atctccgcgcaaatgccac. Please reference Au et al., G3 9(1): 135-144 2019 in any work resulting from use of this mutation.]"Homozygous early larval lethal. Deletion of 2440 bp with Calarco/Colaiacovo selection cassette conferring myo-2 GFP and G418 resistance inserted at break in parental strain N2. Heterozygotes are wild-type GFP+ mKate2+, and segregate wild-type GFP+ mKate2+, GFP+ non-mKate2 dead larvae (ve785

homozygotes), non-GFP mKate2+ arrested animals (arrest stage unknown)(hT2 homozygotes) and dead eggs (aneuploids). Pick wild-type GFP+ mKate2+ and check for correct segregation of progeny to maintain. [NOTE: Apparently the lethal mutation is closely linked but not within the balanced region of hT2. It can occasionally recombine away so that the strain will segregate Bli-4 hT2 homozygotes. (Mark Edgley)] Left flanking Sequence: CTTCTGCTGAGCATACGACGACGCATTTTCG ; Right flanking sequence: ttaaataataatttattttaatcacaat. sgRNA #1: AATTCGCAACTAGCCATGTG; sgRNA #2: atctccgcgcaaagcccac. Please reference Au et al., G3 9(1): 135-144 2019 in any work resulting from use of this mutation."|"Made_by: RG KO Group"

Affected Gene: WBGene00000254(bli-4)|WBGene00003514(myo-2)|WBGene00004496(rps-27)|WBGene00006789(unc-54)

Genomic Alteration: WBGene00000254(bli-4), WBGene00003514(myo-2), WBGene00004496(rps-27), WBGene00006789(unc-54)

Catalog Number: WB-STRAIN:WBStrain00055433

Database: WormBase (WB)

Database Abbreviation: WB

Availability: unknown

Organism Name: eif-3.C(ve784[LoxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + LoxP])/hT2 [umnIs73] I; +/-hT2 [bli-4(e937) let-?(h661)] III..

Record Creation Time: 20240716T202610+0000

Record Last Update: 20260815T163845+0000

Ratings and Alerts

No rating or validation information has been found for eif-3.C(ve784[LoxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + LoxP])/hT2 [umnIs73] I; +/-hT2 [bli-4(e937) let-?(h661)] III..

No alerts have been found for eif-3.C(ve784[LoxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + LoxP])/hT2 [umnIs73] I; +/-hT2 [bli-4(e937) let-?(h661)] III..

Data and Source Information

Source: [Integrated Animals](#)

Source Database: WormBase (WB)

Usage and Citation Metrics

We have not found any literature mentions for this resource.