

# Resource Summary Report

Generated by [RRID](#) on Jul 29, 2026

**+/mT1 [umnIs52] II; uev-2(ve670[LoxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + LoxP])/mT1 [dpy-10(e128)] III.**

RRID:WB-STRAIN:WBStrain00049409

Type: Organism

## Proper Citation

RRID:WB-STRAIN:WBStrain00049409

## Organism Information

**URL:** <http://www.wormbase.org/db/get?name=WBStrain00049409>

**Proper Citation:** RRID:WB-STRAIN:WBStrain00049409

**Description:** *Caenorhabditis elegans* with name +/mT1 [umnIs52] II; uev-2(ve670[LoxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + LoxP])/mT1 [dpy-10(e128)] III. from WB.

**Species:** *Caenorhabditis elegans*

**Synonyms:** +/mT1 [umnIs52] II; uev-2(ve670[LoxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + LoxP])/mT1 [dpy-10(e128)] III.

**Notes:** Made\_by: RG KO Group| "umnIs52 [myo-2p::mKate2 + NeoR, III: 8856215 (intergenic)] II. Homozygous sterile. Deletion of 1228 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+ heterozygotes, GFP+ non-mKate2 sterile adults (ve670 homozygotes), sterile Dpy non-GFP mKate2+ (mT1 homozygotes), and dead eggs (aneuploids). Maintain by picking wild-type GFP+ mKate2+ and check for correct segregation of progeny. Left flanking Sequence: aagatccagcttaggttcagttaacgcggc ; Right flanking sequence: tatggaatttttcagatttttctcaaaaaa. sgRNA #1: GGATACTTCCATGTATCCCA; sgRNA #2: AACGTCGAATAATAGCGCAT. Please reference Au et al., G3 9(1): 135-144 2019 in any work resulting from use of this mutation."| "umnIs52 [myo-2p::mKate2 + NeoR, III: 8856215 (intergenic)] II. Homozygous sterile. Deletion of 1228 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+ heterozygotes, GFP+ non-mKate2 sterile adults (ve670 homozygotes), sterile Dpy non-GFP mKate2+ (mT1 homozygotes), and dead eggs (aneuploids). Maintain by picking wild-

type GFP+ mKate2+ and check for correct segregation of progeny. Left flanking Sequence: aagatccagcttaggttcagttaacgcggc ; Right flanking sequence: tatggaatttttcagatttttctcaaaaa. sgRNA #4: GGATACTTCCATGTATCCCA; sgRNA #5: AACGTCGAATAATAGCGCAT. Please reference Au et al., G3 9(1): 135-144 2019 in any work resulting from use of this mutation."

**Affected Gene:** WBGene00001072(dpy-10)|WBGene00003514(myo-2)|WBGene00004496(rps-27)|WBGene00006731(uev-2)|WBGene00006789(unc-54)

**Genomic Alteration:** WBGene00001072(dpy-10), WBGene00003514(myo-2), WBGene00004496(rps-27), WBGene00006731(uev-2), WBGene00006789(unc-54)

**Catalog Number:** WB-STRAIN:WBStrain00049409

**Database:** WormBase (WB)

**Database Abbreviation:** WB

**Availability:** unknown

**Organism Name:** +/-mT1 [umnIs52] II; uev-2(ve670[LoxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + LoxP])/mT1 [dpy-10(e128)] III.

**Record Creation Time:** 20230227T013832+0000

**Record Last Update:** 20260725T172706+0000

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## Ratings and Alerts

No rating or validation information has been found for +/-mT1 [umnIs52] II; uev-2(ve670[LoxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + LoxP])/mT1 [dpy-10(e128)] III..

No alerts have been found for +/-mT1 [umnIs52] II; uev-2(ve670[LoxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + LoxP])/mT1 [dpy-10(e128)] III..

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## Data and Source Information

**Source:** [Integrated Animals](#)

**Source Database:** WormBase (WB)

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.