

Resource Summary Report

Generated by [dkNET](#) on Sep 1, 2026

+/mT1[umnIs52] II; vha-14(ve628[LoxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + LoxP])/ mT1 [dpy-10(e128)] III.

RRID:WB-STRAIN:WBStrain00049367

Type: Organism

Proper Citation

RRID:WB-STRAIN:WBStrain00049367

Organism Information

URL: <http://www.wormbase.org/db/get?name=WBStrain00049367>

Proper Citation: RRID:WB-STRAIN:WBStrain00049367

Description: Caenorhabditis elegans with name +/mT1[umnIs52] II; vha-14(ve628[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; vha-14(ve628[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 larval lethal. Deletion of 1453 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 dead larvae (ve628 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: atgtttttcatagaaataacaaactttt ; Right flanking sequence: caccctccgatgttcttctgttttctatg. 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 larval lethal. Deletion of 1453 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 PHENOTYPIC DESCRIPTION (ve628 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: atgtttttcatagaaataacaaactttt ; Right flanking sequence: caccctccgatgttcttctgtttctatg. 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)|WBGene00006789(unc-54)|WBGene00010130(vha-14)

Genomic Alteration: WBGene00001072(dpy-10), WBGene00003514(myo-2), WBGene00004496(rps-27), WBGene00006789(unc-54), WBGene00010130(vha-14)

Catalog Number: WB-STRAIN:WBStrain00049367

Database: WormBase (WB)

Database Abbreviation: WB

Availability: unknown

Organism Name: +/-mT1[umnIs52] II; vha-14(ve628[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: 20260829T162702+0000

Ratings and Alerts

No rating or validation information has been found for +/-mT1[umnIs52] II; vha-14(ve628[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; vha-14(ve628[LoxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + LoxP])/ mT1 [dpy-10(e128)] 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.