

Resource Summary Report

Generated by [dkNET](#) on Aug 23, 2026

+/*nT1* [*umnl*s49] IV; F58H1.6(ve540[LoxP + myo-2p::*GFP*::*unc-54* 3' UTR + *rps-27p*::*neoR*::*unc-54* 3' UTR + LoxP)]/*nT1* V.

RRID:WB-STRAIN:WBStrain00047447

Type: Organism

Proper Citation

RRID:WB-STRAIN:WBStrain00047447

Organism Information

URL: <http://www.wormbase.org/db/get?name=WBStrain00047447>

Proper Citation: RRID:WB-STRAIN:WBStrain00047447

Description: *Caenorhabditis elegans* with name +/*nT1* [*umnl*s49] IV; F58H1.6(ve540[LoxP + myo-2p::*GFP*::*unc-54* 3' UTR + *rps-27p*::*neoR*::*unc-54* 3' UTR + LoxP)]/*nT1* V. from WB.

Species: *Caenorhabditis elegans*

Synonyms: +/*nT1* [*umnl*s49] IV; F58H1.6(ve540[LoxP + myo-2p::*GFP*::*unc-54* 3' UTR + *rps-27p*::*neoR*::*unc-54* 3' UTR + LoxP)]/*nT1* V.

Notes: Made_by: RG KO Group|"*umnl*s49 [*myo-2p*::*mKate2* + NeoR, V: 1005689 (intergenic)] IV. Homozygous Ste with a few escapers. Deletion of 1527 bp with Calarco/Colaiacovo selection cassette conferring myo-2 GFP and G418 resistance inserted at break in parental strain PD1074. Heterozygotes are wild-type GFP+ *mKate2*+, and segregate wild-type GFP+ *mKate2*+, Sterile GFP+ non-*mKate2* (ve540 homozygotes, some escapers will lay broods), Vul non-GFP *mKate2*+, (*nT1* homozygotes) and dead eggs. Maintain by picking wild-type GFP+ *mKate2*+. Left flanking Sequence: aagtccgagataaataatctacatcctcat ; Right flanking sequence: TATCCAAGAAACACAGATTGGGATTGCAAA. Please reference Au et al., G3 9(1): 135-144 2019 in any work resulting from use of this mutation."|"*umnl*s49 [*myo-2p*::*mKate2* + NeoR, V: 1005689 (intergenic)] IV. Homozygous Ste with a few escapers. Deletion of 1527 bp with Calarco/Colaiacovo selection cassette conferring myo-2 GFP and G418 resistance inserted at break. Heterozygotes are wild-type GFP+ *mKate2*+, and segregate wild-type GFP+ *mKate2*+, Sterile GFP+ non-*mKate2* (ve540 homozygotes, some escapers will lay broods), Vul non-GFP *mKate2*+, (*nT1* homozygotes) and dead eggs. Maintain by picking wild-type GFP+ *mKate2*+. Left flanking Sequence:

aagtccgagataaataatctacatcctcat ; Right flanking sequence:
TATCCAAGAAACACAGATTGGGATTGCAAA. Please reference Au et al., G3 9(1): 135-144 2019 in any work resulting from use of this mutation."

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

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

Catalog Number: WB-STRAIN:WBStrain00047447

Database: WormBase (WB)

Database Abbreviation: WB

Availability: unknown

Organism Name: +/-nT1 [umnl49] IV; F58H1.6(ve540[LoxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + LoxP])/nT1 V.

Record Creation Time: 20230227T013818+0000

Record Last Update: 20260815T163622+0000

Ratings and Alerts

No rating or validation information has been found for +/-nT1 [umnl49] IV; F58H1.6(ve540[LoxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + LoxP])/nT1 V..

No alerts have been found for +/-nT1 [umnl49] IV; F58H1.6(ve540[LoxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + LoxP])/nT1 V..

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.