

Resource Summary Report

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Y53G8AR.6(ve661[LoxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + LoxP])/qC1 [dpy-19(e1259) glp-1(q339) qIs26]III.

RRID:WB-STRAIN:WBStrain00049400

Type: Organism

Proper Citation

RRID:WB-STRAIN:WBStrain00049400

Organism Information

URL: <http://www.wormbase.org/db/get?name=WBStrain00049400>

Proper Citation: RRID:WB-STRAIN:WBStrain00049400

Description: Caenorhabditis elegans with name Y53G8AR.6(ve661[LoxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + LoxP])/qC1 [dpy-19(e1259) glp-1(q339) qIs26]III. from WB.

Species: Caenorhabditis elegans

Synonyms: Y53G8AR.6(ve661[LoxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + LoxP])/qC1 [dpy-19(e1259) glp-1(q339) qIs26]III.

Notes: Made_by: RG KO Group|"qIs26 [lag-2::GFP + rol-6(su1006)] III.Homozygotes are unhealthy. Deletion of 1671 bp with Calarco/Colaiacovo selection cassette conferring myo-2 GFP and G418 resistance inserted at break in parental strain N2. Heterozygotes are Rol GFP+(pharynx and distal tip cell), and segregate Rol GFP+(pharynx and distal tip cell), non-Rol GFP+(pharynx) unhealthy animals (ve661 homozygotes). qC1[qIs26] is homozygous lethal(unknown stage). Maintain by picking Rol GFP+(pharynx and distal tip cell). Left flanking Sequence: aaaaatccgctagaaaccgtctaaaaaacct ; Right flanking sequence: AGGCTTCACGTGCTGAAAGATTCGGAATTA. sgRNA #1: atcaatagcgtaggctttac; sgRNA #2: ACTAACATCAAATGACGCGA. Please reference Au et al., G3 9(1): 135-144 2019 in any work resulting from use of this mutation."|"qIs26 [lag-2::GFP + rol-6(su1006)].Homozygotes are unhealthy. Deletion of 1671 bp with Calarco/Colaiacovo selection cassette conferring myo-2 GFP and G418 resistance inserted at break in parental strain N2. Heterozygotes are Rol GFP+(pharynx and distal tip cell), and segregate Rol GFP+(pharynx and distal tip cell), non-Rol GFP+(pharynx) unhealthy animals (ve661 homozygotes). qC1[qIs26] is homozygous lethal(unknown stage). Maintain by picking Rol GFP+(pharynx and distal tip cell). Left flanking Sequence:

aaaaatccgctagaaaccgtctaaaaacct ; Right flanking sequence:
AGGCTTCACGTGCTGAAAGATTCGGAATTA. sgRNA #1: atcaatagcgtaggctttac; sgRNA
#2: ACTAACATCAAATGACGCGA. Please reference Au et al., G3 9(1): 135-144 2019 in
any work resulting from use of this mutation."

Affected Gene: WBGene00001078(dpy-19)|WBGene00001609(glp-1)|WBGene00003514(myo-2)|WBGene00004496(rps-27)|WBGene00006789(unc-54)

Genomic Alteration: WBGene00001078(dpy-19), WBGene00001609(glp-1),
WBGene00003514(myo-2), WBGene00004496(rps-27), WBGene00006789(unc-54)

Catalog Number: WB-STRAIN:WBStrain00049400

Database: WormBase (WB)

Database Abbreviation: WB

Availability: unknown

Organism Name: Y53G8AR.6(ve661[LoxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + LoxP])/qC1 [dpy-19(e1259) glp-1(q339) qIs26]III.

Record Creation Time: 20230227T013832+0000

Record Last Update: 20260829T162702+0000

Ratings and Alerts

No rating or validation information has been found for Y53G8AR.6(ve661[LoxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + LoxP])/qC1 [dpy-19(e1259) glp-1(q339) qIs26]III..

No alerts have been found for Y53G8AR.6(ve661[LoxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + LoxP])/qC1 [dpy-19(e1259) glp-1(q339) qIs26]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.