

Resource Summary Report

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dpy-5(e61) I; fjDf1 fjDf2 fjDf3 fjDf4 X.

RRID:WB-STRAIN:WBStrain00055739

Type: Organism

Proper Citation

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Organism Information

URL: <http://www.wormbase.org/db/get?name=WBStrain00055739>

Proper Citation: RRID:WB-STRAIN:WBStrain00055739

Description: *Caenorhabditis elegans* with name dpy-5(e61) I; fjDf1 fjDf2 fjDf3 fjDf4 X. from WB.

Species: *Caenorhabditis elegans*

Synonyms: dpy-5(e61) I; fjDf1 fjDf2 fjDf3 fjDf4 X.

Notes: This strain carries a dpy-5 mutation to facilitate genome modification in CeRep55 quadruple deletion background: fjDf1 (also known as fj115); fjDf2 (aka fj85); fjDf3 (aka fj123); fjDf4 (aka fj120) X. This strain lacks four major clusters of CeRep55 repeats on the X chromosome. The condensation of unpaired X chromosomes in male testes is insufficient. CeRep55 is a class of minisatellite sequences consisting of a 27-nt tandem repeat that is present on all chromosomes. Some CeRep55 clusters express long non-coding RNAs and small RNAs. Each of the four deletion sites was designed to acquire a sequence tag (TGTACAGGAAACAGCTATGACC; similar to M13 reverse) instead of the CeRep55 tandem repeats. The deletions of CeRep55 clusters can be checked by PCR with the following primers: fjDf1 in Y73B3A, CAACCTGACTCTCGCCAAGAC and GGAGAAGTAGGCGTGTCTAGTTA; fjDf2 in Y75D11A, CAAGTGCCAACTAGACTGCTC and TTCAAACGCTACGCGATACCAG; fjDf3 in Y81B9A, AAATGCCCTATCTCACAGTGG and GACTGCTAGAATCTGACTCGTC; fjDf4 in Y49A10A, CAACCTGACTCTCGCCAAGAC and GGAGAAGTAGGCGTGTCTAGTTA. The PCR check can also be performed with the M13 reverse primer and the right-side primer. Reference: Tabara H, et al. (2023) A small RNA system ensures accurate homologous pairing and unpaired silencing of meiotic chromosomes. EMBO J, e105002. This strain carries a dpy-5 mutation to facilitate genome modification in CeRep55 quadruple deletion background: fjDf1 (also known as fj115); fjDf2 (aka fj85); fjDf3 (aka fj123); fjDf4 (aka fj120) X. This strain lacks four major clusters of CeRep55 repeats on the X chromosome. The condensation of unpaired X chromosomes in male testes is insufficient. CeRep55 is a

class of minisatellite sequences consisting of a 27-nt tandem repeat that is present on all chromosomes. Some CeRep55 clusters express long non-coding RNAs and small RNAs. Each of the four deletion sites was designed to acquire a sequence tag (TGTACAGGAAACAGCTATGACC; similar to M13 reverse) instead of the CeRep55 tandem repeats. The deletions of CeRep55 clusters can be checked by PCR with the following primers: fjDf1 in Y73B3A, CAACCTGACTCTCGCCAAGAC and GGAGAAGTAGGCGTGTCTAGTTA; fjDf2 in Y75D11A, CAAGTGCCAACTAGACTGCTC and TTCAAAACGCTACGCGATACCAG; fjDf3 in Y81B9A, AAATGCCCTATCTCACAGTGG and GACTGCTAGAATCTGACTCGTC; fjDf4 in Y49A10A, CTCTTCCATTTCCAGTACAACCAG and GTTTCTATGGCTAGAGTCGTATGGTTAC. The PCR check can also be performed with the M13 reverse primer and the right-side primer. Reference: Tabara H, et al. (2023) A small RNA system ensures accurate homologous pairing and unpaired silencing of meiotic chromosomes. EMBO J, e105002."

Affected Gene: WBGene00001067(dpy-5)

Genomic Alteration: WBGene00001067(dpy-5)

Catalog Number: WB-STRAIN:WBStrain00055739

Database: WormBase (WB)

Database Abbreviation: WB

Availability: unknown

Organism Name: dpy-5(e61) I; fjDf1 fjDf2 fjDf3 fjDf4 X.

Record Creation Time: 20240716T202613+0000

Record Last Update: 20260725T172829+0000

Ratings and Alerts

No rating or validation information has been found for dpy-5(e61) I; fjDf1 fjDf2 fjDf3 fjDf4 X..

No alerts have been found for dpy-5(e61) I; fjDf1 fjDf2 fjDf3 fjDf4 X..

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.