Paste the bedGraph formatted data below, including the initial configuration line, into a new plain text document with the extension “.wig” to create a bedgraph disguised as a wig. Such a file will upload and correctly display as a genomic profile in GBrowse2. The “.wig” extension and stating that “track type=wiggle\_0” in the configuration line are crucial.

track type=wiggle\_0 name=name description=test

2L 100 1000 1000

2L 7531 7607 100

2L 7620 7621 100

2L 7621 7695 200

2L 7695 7697 100

2L 7710 7786 100

2L 8318 8394 100

2L 8789 8799 100

2L 8799 8865 200

2L 8865 8875 100

2L 8899 8975 100

2L 9129 9205 100

2L 9236 9256 100

2L 9256 9312 200

2L 9312 9332 100

2L 9400 9476 100

2L 9868 9904 100

2L 9904 9905 200

2L 9905 9906 400

2L 9906 9929 500

2L 9929 9933 600

2L 9933 9944 700

2L 9944 9960 600

2L 9960 9980 700

2L 9980 9981 500

2L 9981 9982 400

2L 9982 9983 300

2L 9983 10004 400

2R 100 1000 1000

2R 7531 7607 100

2R 7620 7621 100

2R 7621 7695 200

2R 7695 7697 100

2R 7710 7786 100

2R 8318 8394 100

2R 8789 8799 100

2R 8799 8865 200

2R 8865 8875 100

2R 8899 8975 100

2R 9129 9205 100

2R 9236 9256 100

2R 9256 9312 200

2R 9312 9332 100

2R 9400 9476 100

2R 9868 9904 100

2R 9904 9905 200

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3R 9256 9312 200

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3R 9400 9476 100

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X 100 1000 1000

X 7531 7607 100

X 7620 7621 100

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X 9929 9933 600

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X 9944 9960 600

X 9960 9980 700

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X 9981 9982 400

X 9982 9983 300

X 9983 10004 400