

Oct 07, 2019

Version 2

The 'Three Peaks' faecal DNA extraction method for long-read sequencing V.2

DOI

<https://dx.doi.org/10.17504/protocols.io.7rshm6e>

Josh Quick¹

¹Sam Nicholls [University of Birmingham], Nicholas Loman [University of Birmingham]

Long Read Club

Tech. support email: n.j.loman@bham.ac.uk



Josh Quick

University of Birmingham

Create & collaborate more with a free account

Edit and publish protocols, collaborate in communities, share insights through comments, and track progress with run records.

Create free account

OPEN  ACCESS



DOI: <https://dx.doi.org/10.17504/protocols.io.7rshm6e>

External link: <https://www.slideshare.net/scalene/the-three-peak-challenge-for-longread-ultradeep-stool-metagenomics-on-the-promethion>

Protocol Citation: Josh Quick 2019. The 'Three Peaks' faecal DNA extraction method for long-read sequencing. **protocols.io**
<https://dx.doi.org/10.17504/protocols.io.7rshm6e>

Manuscript citation:

<https://doi.org/10.1093/gigascience/giz043>

License: This is an open access protocol distributed under the terms of the **Creative Commons Attribution License**, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

Protocol status: Working

We use this protocol and it's working

Created: September 27, 2019

Last Modified: October 07, 2019

Protocol Integer ID: 28178

Keywords: Microbiome research, metagenomics, long-read sequencing, nanopore sequencing, genomics, DNA extraction, sample preparation, faecal dna extraction method, dna extraction, dna, extraction

Materials

MATERIALS

 MetaPolyzyme **Merck MilliporeSigma (Sigma-Aldrich) Catalog #MAC4L-5MG**

STEP MATERIALS

 500 µL PBS pH 7.5

 DNA/RNA Shield **Zymo Research Catalog #R1100-50**

 MetaPolyzyme **Merck MilliporeSigma (Sigma-Aldrich) Catalog #MAC4L-5MG**

Resuspend the contents of the bottle in  500 µL PBS pH 7.5 and aliquot for optimal activity.

This protocol is adapted and uses reagents from the Quick-DNA HMW MagBead Kit (Zymo, D4081).

Protocol materials

 MetaPolyzyme **Merck MilliporeSigma (Sigma-Aldrich) Catalog #MAC4L-5MG**

 DNA/RNA Shield **Zymo Research Catalog #R1100-50**

 OMNigene•GUT **DNA Genotek Catalog #OMR-200**



- 1 Add  100 mg fresh stool or  50 μL OMNIgene GUT to  200 μL DNA/RNA Shield, vortex briefly and place on a tube rotator for  00:10:00 at  20 rpm .

 OMNIgene•GUT **DNA Genotek Catalog #OMR-200**

 DNA/RNA Shield **Zymo Research Catalog #R1100-50**

- 2 Centrifuge at  5000 x g for  00:05:00 and retain up to  200 μL supernatant depending on size of pellet.
- 3 Add  100 μL PBS and resuspend material by pipetting up and down, centrifuge at  5000 x g  00:05:00 and retain up to  100 μL supernatant depending on size of pellet.
- 4 Add  1 mL PBS and resuspend material by pipetting up and down, centrifuge at  5000 x g for  00:05:00 and discard supernatant.



- 5 Add  100 μL PBS and  5 μL MetaPolzyme, mix by pipetting and incubate at  35 $^{\circ}\text{C}$ for  02:00:00 . Gently mix by pipetting up and down to ensure solution is homogeneous before proceeding.

 MetaPolzyme **Merck MilliporeSigma (Sigma-Aldrich) Catalog #MAC4L-5MG**

- 6 Add  100 μL DNA/RNA Shield,  10 μL [M] 10 % (w/v) SDS and  10 μL [M] 20 mg/mL Proteinase K and mix by pipetting. Incubate at  55 $^{\circ}\text{C}$ for  00:30:00 with  300 rpm mixing. Gently mix by pipetting up and down to ensure solution is homogeneous before proceeding.

- 7 Centrifuge at  5000 x g for  00:05:00 and retain up to  200 μL supernatant depending on size of pellet.

- 8 Resuspend pellet in  750 μL Lysis Solution and transfer to a ZR BashingBead Lysis Tube. Bead-beat on a FastPrep instrument for 1 cycle of  00:00:40 at  6 m/s



Equipment

FastPrep-24 5G

NAME

Bead-beater

TYPE

MP Biomedicals

BRAND

116005500

SKU

<https://uk.mpbio.com/fastprep-24-5g-instrument>

LINK



- 9 Centrifuge tube at  10000 x g for  00:01:00 and retain  400 μ L supernatant.
- 10 Pool the supernatants retained at each of the steps in a 2 ml Eppendorf tube and measure the volume using a P1000 pipette.
- 11 Add 2 volumes of Genomic Lysis Buffer and  50 μ L MagBinding beads and place on a tube rotator for  00:10:00 at  20 rpm .
- 12 Put tube on a magnetic rack and incubate for  00:02:00 or until clear. Discard supernatant taking care not to disturb bead pellet.



- 13 Remove from the magnetic rack and using a P1000 pipette add  100 µL DNA elution buffer. Mix by pipetting up and down x10.
- 14 Add  500 µL Quick-DNA MagBinding Buffer and place on a tube rotator for  00:10:00 at  20 rpm .
- 15 Put tube on a magnetic rack and incubate for  00:02:00 or until clear. Discard supernatant taking care not to disturb bead pellet.
- 16 Remove from the magnetic rack and using a P1000 pipette add  900 µL DNA Pre-Wash Buffer. Mix by pipetting up and down x10 and transfer to a new  1.5 mL Eppendorf tube.
- 17 Put tube on a magnetic rack and incubate for  00:02:00 or until clear. Discard supernatant taking care not to disturb bead pellet.
- 18 Remove from the magnetic rack and using a P1000 pipette add  900 µL g-DNA Wash Buffer. Mix by pipetting up and down x10 and transfer to a new  1.5 mL Eppendorf tube.
- 19 Put tube on a magnetic rack and incubate for  00:02:00 or until clear. Discard supernatant taking care not to disturb bead pellet.
- 20  [go to step #18](#) and repeat wash with g-DNA Wash Buffer for a second time.
- 21 Using a P1000 wide-bore pipette tip to reduce turbulence add  900 µL DNA elution buffer to the front of the tube and immediately remove it again. Try to do this in a fast, smooth motion disturbing the beads as little as possible.
- 22 Remove the residual buffer from the bottom of the tube and discard.
- 23 With a P1000 pipette add  50 µL DNA elution buffer to the tube and mix by pipetting up and down x10.
- 24 Place on a tube rotator for  00:05:00 at  20 rpm .



- 25 Put tube on a magnetic rack and incubate for  00:02:00 or until clear. Transfer DNA to a new  1.5 mL Eppendorf tube. Store DNA at  5 °C for up to a month or use immediately.