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HMW DNA extraction for amphipods V.1

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Protocol adapted from Qiagen's [genomic DNA handbook](#) protocol for the HMW extraction of live or flash-frozen amphipods.

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HMW, Nanopore, Amphipods, DNA Extraction

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To preserve large DNA sizes, never use Vortex and only use Wide-Bore tips.

Reagent :

☒ Genomic-tip[20/G Qiagen Catalog #ID: 10223](#) Step 9☒ Buffer[G2 Qiagen Catalog #1014636](#) Step 1

[Buffer QBT Contributed by users](#) Step 10

[Buffer QF Contributed by users](#) Step 13

[Buffer QC Contributed by users](#) Step 12

[RNase](#)

[Qiagen Catalog #19101](#) Step 1

[Proteinase K \(2](#)

[ml\) Qiagen Catalog #19131](#) Step 7

[2-propanol Sigma Aldrich](#) Step 14

[Ethanol 70% \[Note: freshly prepared\] Contributed by users](#) Step 15

[Tris-EDTA \(TE\) buffer pH 8.0 1X Contributed by users](#) Step 18

Consumables :

[2 mL Eppendorf Contributed by users](#) In 2 steps

[1.5 mL Eppendorf tubes Contributed by users](#) Step 15

[15 mL Falcon tubes Contributed by users](#) Step 9

[ART Wide-Bore tips 1000 µl Contributed by users Catalog #2079GPK](#)

[ART Wide-Bore tips 200µl Contributed by users Catalog #2069GPK](#)

Equipment:

Dounce Homogenizer, 2mL
Tissue Grinder

Kimble 885300-0002 [Link](#)

2 mL with Pestles A and B



ThermoMixer
Benchtop Incubator

Eppendorf 5382000023 [↗](#)

Any heat block will suffice



Centrifuge 4K15
Sigma

Centrifuge BLE1700081

Tissue homogenization 10m

- 1 Prepare the **lysis buffer** by adding 3 μ L of **RNase A** (100 mg/mL) to 1.5 ml of **Buffer G2** per sample.

[↗ RNase](#)

[A Qiagen Catalog #19101](#)

[↗ Buffer](#)

[G2 Qiagen Catalog #1014636](#)

- 2 place live or flash-frozen amphipod in 2ml douncer and add 1 ml of **lysis buffer**

- 3 gently up and down **10 times** with the piston

- 4 transfer the **lysate** to a 2 ml tube

[↗ 2 mL Eppendorf Contributed by users](#)

- 5 rinse the douncer with 0.5 ml lysis buffer and transfer to the 2 ml tube

Lysis 2h 30m

- 6 Incubate for 30 minutes at 37°C. 30m
⚡ 37 °C ⌚ 00:30:00

- 7 Add 75 µL of **Proteinase K** (20 mg/mL) and incubate with inversion at 50°C for 2 hours. 2h
[⌘ Proteinase K \(2 ml\) Qiagen Catalog #19131](#)
⌚ 02:00:00 ⚡ 50 °C

- 8 Gently transfer in a new 2 ml tube the supernatant with a 1000 µl **wide-bore tip**, avoiding touching the pelleted debris by gravity.
[⌘ 2 mL Eppendorf Contributed by users](#)

DNA binding and washing 1h

- 9 Place a **genomic-tip 20G** column on a 15 ml tube
[⌘ 15 mL Falcon tubes Contributed by users](#)
[⌘ Genomic-tip 20/G Qiagen Catalog #ID: 10223](#)
- 10 **Equilibrate the column** with 1 mL Buffer QBT. Wait for the Genomic-tip to drain by gravity.
[⌘ Buffer QBT Contributed by users](#)
- 11 Carefully **apply the lysate to the Genomic-tip** with a 1000 µl wide-bore tip. Wait for the Genomic-tip to drain by gravity.
- 12 **Wash** the QIAGEN Genomic-tip with 3 x 1 mL Buffer QC.
[⌘ Buffer QC Contributed by users](#)

13 Elute the DNA into a new 15 mL tube with 2 x 1 mL of Buffer QF prewarm to 50°C

☒ Buffer QF Contributed by users

DNA recovery 1h 50m

14 Add 1.4 mL of room-temperature isopropanol to the éluate, mix by inversion about 10 times, and centrifuge for 30 min at 5,500g at 4°C to pellet DNA. set centrifuge deceleration speed to level3

☒ 2-propanol Sigma Aldrich

⌚ 5500 x g, 4°C, 00:30:00 , Acc 9 / Dec 3

15 Gently remove the supernatant using a P1000
Gently resuspend the pellet with 1 ml of cold 70% ethanol using a 1000µl wide-bore tip.
Transfer to a new 1.5 ml tube.

☒ Ethanol 70% [Note: freshly prepared] Contributed by users

☒ 1.5 mL Eppendorf tubes Contributed by users

16 Centrifuge for 10 min at 5,000g at 4°C to pellet DNA. set centrifuge deceleration speed to level3

⌚ 5000 x g, 4°C, 00:10:00 , Acc 9 / Dec 3

17 Remove as much supernatant as possible, avoiding touching the pellet.
Air dry the pellet 10 min at RT.

⌚ 00:10:00 ⚡ Room temperature

18 Resuspend the pellet with 50 µL of TE 1x prewarm to 50°C

☒ Tris-EDTA (TE) buffer pH 8.0 1X Contributed by users

19 Incubate for 1hour at 50°C, then overnight at RT.

⌚ 01:00:00 ⚡ 50 °C

⌚ Overnight ⚡ Room temperature

Sample QC

20 Quantify your sample with a Qubit HS.

Analyse 1 μL in a UV spectrophotometer (e.g. Nanodrop).

Visualise 1 μL of sample to estimate the molecular weight. (Tapestation)

Results

21 QC results of extraction of 4 individuals

Weight mg	[c] ng/ μL	Nanodrop A260/A280	Nanodrop A260/A230	Tapestation kb
63	39.4	1.82	1.86	57
40	30.9	1.88	2.20	57
65	82.1	1.78	1.82	50
43	197	1.86	2.33	26

22 Tapestation profiles

