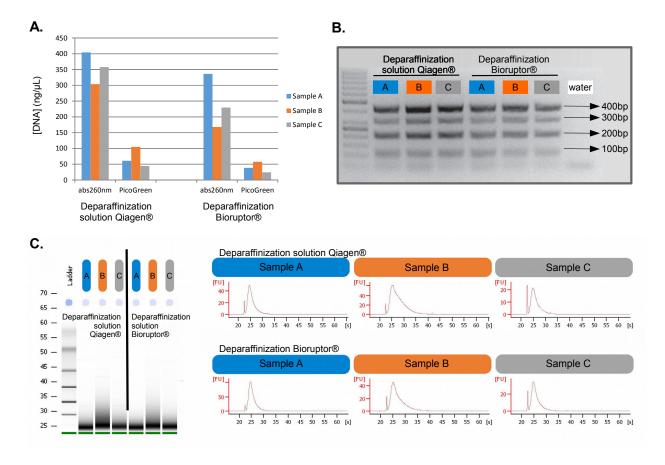
# **BIORUPTOR® DEPARAFFINIZATION**

# PREPARATION OF FFPE SAMPLES FOR NEXT-GENERATION SEQUENCING USING THE BIORUPTOR® PICO AND QIAGEN® ALLPREP FFPE DNA/RNA KIT

Deparaffinization of FFPE samples is typically performed using a non-polar solvent, such as xylene, or a mineral oil-based method which can be time consuming and messy. Claire Josse and colleagues from the Human Genetic Laboratory at the GIGA - University of Liège have developed a new protocol combining the Bioruptor® Pico with the AllPrep FFPE DNA/RNA kit from Qiagen® to efficiently prepare FFPE samples for Next-Generation Sequencing. The Bioruptor® Pico removes the paraffin and rehydrates the tissue in just one solvent-free step followed by a mild crosslink reversal to preserve DNA and RNA integrity. The nucleic acids are then extracted with the AllPrep FFPE DNA/RNA kit and sheared using the Bioruptor® Pico to the desired length for sequencing library preparation.



**Figure**: Comparison of genomic DNA and total RNA yield and quality obtained when deparaffinization is performed with the Bioruptor or the deparaffinization solution from Qiagen®. Three samples are deparaffinized by both bethods, extracted with AllPrep Qiagen® columns, and quantified **A.** by absorbance @260nm or by the the intercalating agent PicoGreen. **B.** DNA integrity is stated by amplification of fragments of 100, 200, 300 and 400 bp in a multiplex PCR of the GAPDH gene. **C.** RNA profiles are performed on a Agilent 2100 Bioanalyzer.

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#### 1. Material required

- 20 tissues sections of 4  $\mu$ M thick mounted on glass slides are used for extraction
- Sterile needle
- Bioruptor® Pico (Cat. No. B01060001) with 1.5 ml tube holder
- 1.5 ml Bioruptor® Pico Microtubes with Caps (Cat. No. C30010016)
- Allprep FFPE DNA/RNA kit, Qiagen® (Cat. No. 80234)

## 2. Procedure

<u>Day 1</u>

- Use 2 g of cells / purification. If starting from cell pellets, thaw quickly in a water bath at 37 °C.
- Optional : In order to maximize tumoral content, a pathologist should examine one tumour haematoxylineosin stained section to determine the tumour area. To isolate nucleic acids, the annotated stained section is superposed with 19 unstained sections; the tumor area is manually macro-dissected and scraped with a sterile needle.
- Scrape tissue from 10 tissue slices and harvest in 1.5 ml Bioruptor<sup>®</sup> Pico Microtubes containing 250 µL PKD buffer (Qiagen<sup>®</sup>). This operation is performed in duplicate for each sample, 10 tissues sections/tube.
- Place the 2 tubes inside the Bioruptor<sup>®</sup> and sonicate for 6 cycles (sonication cycle: 30 sec ON, 30 sec OFF). It is important to not have more than 10 tissues sections/tube in order to obtain optimal emulsification of the paraffin.
- Briefly spin down tubes and transfer the samples into new 1.5ml tubes (Qiagen®).
- Add 50 µL proteinase K (Qiagen®) and mix by vortexing.
- Incubate at 56°C for 15 min.
- Incubate on ice for 10 min. Complete cooling is important for efficient precipitation.
- Centrifuge for 15 min at 20.000 x g.
- Carefully transfer the supernatant, without disturbing the pellet, to a new RNAse free 1.5 ml tube for RNA purification. Keep the pellet for DNA purification.
- Proceed with the Qiagen<sup>®</sup> protocol for RNA and DNA purification.
- Elution step is performed with 2 x 20 µl RNAse free water for RNA purification, and with 2 x 20 µl ATE buffer (Qiagen®) for DNA purification.
- The DNA and RNA can then be analyzed by traditional methods or can be sheared with the Bioruptor<sup>®</sup> Pico for downstream NGS library preparation. Please refer to the DNA Shearing Guide for additional information. https://www.diagenode.com/en/dna-shearing-guide.

## 3. Selected publications

- 1. Boukerroucha M, Josse C, Segers K, El-Guendi S, Frères P, Jerusalem G, Bours V. **BRCA1 germline mutation and** glioblastoma development: report of cases. *BMC Cancer 2015*, *15*:181.
- Boukerroucha M, Josse C, El-Guendi S, Boujemla B, Frères P, Marée R, Wenric S, Segers K, Collignon J, Jerusalem G, Bours V: Evaluation of BRCA1-related molecular features and microRNAs as prognostic factors for triple negative breast cancers. BMC Cancer 2015, 15:755.

