

# CPAC sample processing recommendations

- **Sample types and requirements (setup/installation phase)**

- **Cells**

- **Frozen cell pellets (dry ice), washed 1x with PBS, collected by scraping**
  - Sample processing using the Preomics Kit (1-100 ug material),
    - **Minimal input requirement: 300 000 cells**
    - **one shot samples: 10 000 cells**
    - **pellet of 1x 6-well**

- **Native Tissue**

- **Transfer frozen (dry ice)**
  - Sample processing: tissue homogenization (mixer, douncer), sonication in vial tweeter
  - Sample processing using the Preomics Kit (1-100 ug material),
    - **input requirement: 2 mm biopsy punch (lengths ca. 0.5-1 cm); biopsy slice (10-20  $\mu\text{m}$  thickness of a tissue block, 1cmx1-2 cm)**
    - **for statistical data evaluation three punches/slices (biological replicates) are required**

- **Formalin-fixed Tissue (FFPE)**

- **Transfer RT**
  - Sample processing: de-waxing using a series of Xylene/Heptane and Ethanol; tissue homogenization (mixer, douncer), sonication in vial tweeter
  - Sample processing using the Preomics Kit (1-100 ug material), protocol for FFPE tissue
    - **input requirement: 1 mm biopsy punch (lengths ca. 0.5-1 cm) or biopsy slice (10-20  $\mu\text{m}$  thickness of a tissue block, 1cm x 1.5 cm); ~weight input material 0.5-1 mg**

- **for statistical data evaluation three punches/slices (biological replicates) are required**

- **Quality Control Standards**

- Bovine Fetuin/A1AG as spike-in reference for sample processing at the protein level
- iRT spike tides as reference for MS performance and Spectronaut evaluation
- QuiC software as tool to monitor MS performance (Biognosys, Spectronaut pipeline)