# **Submitting samples for WGS-Bulk**

## Requesting site-matched frozen tissue H&Es (to scRNA seq)

1. Set up a spreadsheet in Excel with the following: Spectrum ID, Site (all sites), MRN, Date of Collection, Sectioning Details (1 H&E, 4um)
2. Submit an iLab request form with the **Pathology Core Facility**
   1. Request Services – Request for Histology Service (Histology)
   2. **Project Title:** MSK Spectrum Ovary
   3. **Industry sponsored study:** No
   4. **When available, please upload an excel file with specimen information:** upload excel spreadsheet here
   5. **Additional Histology work requested:** H&E Staining
   6. **Comments and Special Instructions:** Will need unstained sections cut once H&E slides have been reviewed by our pathologist
   7. **Contact for pick up:** your email address
3. Save completed form and update cost center/fund, submit request to core
4. Email Cora and Biobank ([zzPDL\_PTH\_PPBC\_Biobank@mskcc.org](mailto:zzPDL_PTH_PPBC_Biobank@mskcc.org)) to notify them that a submission has been made

## Once request has been fulfilled…

1. Pick up H&Es from biobank
2. Review H&Es with pathologist to identify which site will yield highest tumour content for each patient
3. Create a new excel spreadsheet with the following: Spectrum ID, Site, Bank number, Aliq-Categ value, Sectioning Details (# of unstained slides needed)
4. Edit original iLab request with new excel spreadsheet and email Cora and Biobank to notify them that an update has been made to the submission

*Note: Occasionally they may request for you to bring back the H&Es of the requested slides for unstained sections*

1. Pick up unstained slides from biobank when ready – ensure to bring a box with dry ice to transport the frozen slides
2. Store unstained slides at -80c until ready for NFR staining and microdissection

## NFR staining, Microdissections & Extraction

1. Thaw unstained slides to room temperature
2. Stain with NFR staining (protocol at bench)
3. Once slides have fully dried, microdissect tumour based on H&E and NFR staining and put microdissected tumour tissue into a 1.5ml epi tube
4. Add ATL buffer and prot K and incubate at 56C for 2 days or until tissue has fully dissolved
5. Proceed with blood and tissue extraction protocol
6. Qubit samples and note DNA yield
7. Label (format below) and store extracted DNA in the 4C (under the extraction bench, “Spectrum DNA Extractions” box) until ready to submit for sequencing

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## WGS Submission to IGO

1. Submit an iLab request to IGO (Request Services 🡪 NGS platforms 🡪 Human or Mouse – Whole Genome Sequencing NGS platforms)
   1. **Phone number:**
   2. **All contact emails:** [limj@mskcc.org](mailto:limj@mskcc.org);[grewald@mskcc.org](mailto:grewald@mskcc.org);[mcphera1@mskcc.org](mailto:mcphera1@mskcc.org); [havasove@mskcc.org](mailto:havasove@mskcc.org)
   3. **Is this project a continuation of a previous project with IGO?** Yes
   4. **What is the project number of the previous project?** 09443
   5. **Number of Normals:**
   6. **Number of Tumours**:
   7. **Sample Types:** DNA prepped by Investigator
   8. **Submission format**: 2D Barcoded Tubes
   9. **Are any of these samples from a PDX?** No
2. Save updated form, update cost center/fund and submit request to core
3. Submit an IGO Sample Intake form
   1. **Material:** DNA
   2. **Application:** HumanWholeGenome
   3. **Species:** Human
   4. **Patient ID Type:** MSK Patients
   5. **Container:** Micronic Barcoded Tubes
   6. **# samples:**
   7. **iLabs Service ID:**
4. Generate table
   1. Micronic Tube Barcode
   2. **Sample ID:** SampleIDSite\_T (eg. 022LA\_T)
   3. **Species:** Human
   4. **Preservation:** Frozen
   5. **Sample Origin:** Tissue
   6. **Specimen Type:** Resection/Biopsy
   7. **Volume:** 50ul
   8. **Reads Requested/Coverage:** 80X
   9. **Tumour Type:** HGSOC
   10. **Sample Class:** Primary/Metastasis
   11. **MRN**
   12. **Sex**
5. Submit form
6. Send IGO Sample Receiving ([zzPDL\_SKI\_IGO\_SampleReceiving@mskcc.org](mailto:zzPDL_SKI_IGO_SampleReceiving@mskcc.org)) an email requesting barcoded tubes and barcode spreadsheet
7. Pick up barcoded tubes from IGO and transfer extracted DNA into respective barcoded tubes
8. Aliquot 50ul of DNA per sample into the provided plate
9. Bring samples to IGO for submission