



## GENOMICS CORE iSCAN POLICIES

Please thoroughly review these policies prior to submitting samples. If you have any questions regarding this policy or any other aspect of the iScan service process, please contact us at [genomics@vai.org](mailto:genomics@vai.org).

### SAMPLE SUBMISSION

- Prior to submitting an initial project, VAI researchers will be required to meet with Genomics Core staff to discuss array goals and details of starting material.
- Projects are received on a first-come, first-served basis, and will not be entered into the project queue until samples and a completed submission form are in the possession of the Genomics Core. Once samples are entered into the queue, the Core will provide a tentative project timeline. We strive to honor this timeline; however, there are issues beyond our control that may delay the run. In the event of a delay greater than a week, the Core will email the customer to inform them of an updated run date.
- After samples are received, Core personnel will initiate an iLab request for your project. Please review and authorize the project if all looks correct.

### CUSTOMER RESPONSIBILITIES

- Dropped-off samples must be prepared to VAI specifications, unless previous permission has been granted by the Core Manager. A summary of submission requirements can be found on page 2 of this policy.

### CORE DELIVERABLES

- **QC array:** idat files, sample sheet and a report noting concordance between tumor/normal pairs, as well as likelihood of contamination to the 10% level. This report is provided in conjunction with VAI's Bioinformatics and Biostatistics Core.
- **EPIC methylation array:** idat files and sample sheet only.
- **Custom arrays:** idat files and sample sheet only.
- Data are delivered within five business days of the finished run. Further analysis may be contracted separately with the Bioinformatics and Biostatistics Core.
- The Genomics Core ensures that its technical staff's abilities and proficiency are measured to provide the best results for our customers. We will provide assessments as needed for insufficient technical results.

### EXCEPTIONS

While we will make every effort to return high-quality data output, we cannot be responsible for improperly prepared samples. Therefore, we make **no guarantees** on the quantity and quality of data generated from Illumina BeadArrays if:

- Samples are not provided at correct concentration or volume.
- Samples are degraded below 2 kb fragment size or are from FFPE tissues.
- Samples for projects greater than 16 samples are provided in 1.5 mL tubes rather than plates.
- Samples have been whole-genome amplified.

If your data do not meet these criteria, or if you have other questions/concerns regarding your data, please contact us at [genomics@vai.org](mailto:genomics@vai.org).

## MINIMUM AND OPTIMAL SAMPLE REQUIREMENTS

If the following initial QC requirements are not met, you will be informed via email. You may elect to either resubmit samples of sufficient quality and quantity or proceed with the existing samples. Should you choose to proceed with samples that do not meet our requirements, the samples will be run **AS IS**, and we make no assurances on the quality of downstream data.

### QC Arrays

- Minimum of 500 ng of gDNA at a concentration of 50 ng/μL in 10 mM Tris pH 8.0.
- Samples must be provided in batches of 24 (e.g., 24, 48, 72, 96 samples at a time).
- Quantify DNA by fluorometric methods only such as Qubit or Quantus. Spectrophotometer/Nanodrop readings are not sufficient.
- FFPE samples will incur additional costs for QC and FFPE restore protocols.
- Column-based cleanups or ethanol precipitation are **strongly** recommended prior to drop off, especially for organic extractions.

### EPIC Methylation Arrays

- Minimum of 1 μg of gDNA or FFPE gDNA at a concentration of 11 ng/μL in 10 mM Tris pH 8.0.
- Samples must be provided in batches of 8 with a minimum of 16 samples per project unless you coordinate with another lab to run samples at the same time.
- Quantify DNA by fluorometric methods only such as Qubit or Quantus. Spectrophotometer/Nanodrop readings are not sufficient.
- FFPE samples will incur additional costs for QC and FFPE restore protocols.
- Column-based cleanups or ethanol precipitation are **strongly** recommended prior to drop off, especially for organic extractions.

### All Specialty Arrays

- Must be discussed specifically with the Genomics Core prior to project submission.
- DNA arrays: minimum 500 ng of gDNA at a concentration of 50 ng/μL in 10 mM Tris pH 8.0.
- RNA arrays: will not be supported at VAI, as Illumina is phasing them out as of December 2016.
- Column-based cleanup or ethanol precipitation is strongly recommended, especially for organic extractions.

## SAMPLE LABELING

Sample names will be 6–8 characters in length, and must be composed only of alphanumeric characters. Any spaces, dashes, underscores or special characters will be removed, as they are not compatible with the array software.

## DATA STORAGE

Deliverable array data will be stored in the HPC download directory accessible by your lab. Files will be removed by the Genomics Core after two weeks due to space considerations; please be prompt in downloading your data. Raw image output from each iScan run will be stored by the Genomics Core for 90 days. If you wish to have a copy of this data, you **must** contact the Core Manager at [genomics@vai.org](mailto:genomics@vai.org) within **one month of the beginning** of your project to facilitate the transfer.

## LEFTOVER SAMPLES

Any remaining samples will be stored for 90 days after project completion. Customers are welcome to collect any leftover materials during this period, after which, they will be discarded without notification. Please contact [genomics@vai.org](mailto:genomics@vai.org) to arrange pick-up.