NGS Services Terms and Conditions

Thank you for considering Intact Genomics. Please review the Terms and Conditions prior to submitting your samples.

Customer Responsibilities**:**

- The organism name and sequence of a phylogenetically analogous reference genome must be supplied, if available.
- Samples to be sequenced must be prepared per Intact Genomics' specifications. Sample submission guidelines can be found here.

Sample Submission:

Projects will be entered into the Intact Genomics Illumina® run queue only when **samples** and **completed submission form** are in the possession of Intact Genomics. Then, Intact Genomics will provide a tentative run date. We continuously strive to honor this run date. However, instances beyond our control could delay your run. Also, a flow cell will not be run until all lanes are filled. Intact Genomics will email customers in case of delay more than one week and will update their expected run date. Samples may be placed on any run that meets or exceeds the requested parameters to expedite sequencing.

Deliverables (per lane/chip):

- MiSeq (minimum)**:** 12 Mb reads passing filter, 70% bases Q30 (99.9% accuracy) or greater
- *Amplicon libraries (minimum)*: 20,000 reads per submitted sample.
- A FASTQC and Run Summary Report will be delivered for each library to provide overviews of run quality. **Reads will not be trimmed.**
- Data will be delivered in FASTQ format within 5 business days of run completion. If further data analysis is necessary, please contact sales@intactgenomics.com to get a separate quote. Libraries that do not meet these specifications will be re-run as soon as possible that has a run that will meet or exceed the requested parameters.

Exceptions**:**

Intact Genomics continuously strives to create successful sequencing runs with very high quality data output. However, we will not be responsible for improperly prepared samples. Therefore, no guarantees can be made on the quantity/quality of data generated from Illumina sequencing if:

1. Libraries are prepared by the user
2. Samples are submitted that do not meet our minimum submission requirements.
3. Species are sequenced for which no reference genomes are available.
4. Non-Illumina barcode/index methods are used.

Intact Genomics will inform customers via email if the preceding requirements are not met. At that point, the customer may either proceed with the existing samples or resubmit samples with required quality. We cannot guarantee good quality data if the samples do not meet our minimum sample requirements.

If you have other questions or concerns regarding your data, please contact us at sales@intactgenomics.com so that we can work out quickly to address your concerns.