

General Terms and Conditions

Version: Rev01 (24/07/2019)

Validity of the offer

This offer is valid from its date of issue until the 60th calendar day thereafter. Upon expiry of the period, unless IGA Technology Services receives formal acceptance from the Customer, the Offer will be considered to have expired.

Orders

The Customer must send the order to IGA Technology Services (orders@igatechnology.com) before or, at the latest at the same time, as the samples are shipped.

Samples

Samples should be sent together with the compiled **Samples Spreadsheet** (available on www.igatechnology.com), providing the quote reference. Include the printout with the shipped parcel and send a copy via e-mail. To be able to properly track and safeguard your samples please send us the Tracking Number via e-mail when available

The samples must meet the quality and quantity criteria, and the shipping conditions, as indicated inside each application-specific "Sample Requirements" document on our website. In case such specifications are not available the Customer shall enquire before sending any material. The Customer will be alerted in case of any non-compliance during the sample processing and will have to decide whether to carry out the service anyway or to replace non-compliant samples/libraries. Additional fee may be applied for extra sample manipulation, QC or library preparation. In the event the Customer decides to proceed with the processing of non-compliant samples, IGA Technology Services will not be responsible for any partial or total failure. In case the Customer decides not to proceed, only the sustained handling costs will be charged. If the sequencing of non-compliant samples results in insufficient data quality/quantity, IGA Technology Services will not take responsibility to provide extra manipulation and services and the full price will be invoiced.

In the event the supplied sample is only partially used its restitution can be requested by and no later than 30 days from delivery of the results.

Sequencing yields

The standard quality policy is set to a minimum of 95% of target sequencing coverage (expressed in millions of reads or Gbp). Samples exceeding this threshold will be considered as completed unless agreed differently before the order is placed. This applies to single-sample experiments (i.e. where each sample is barcoded separately and manipulated independently), it does not apply to pooled-samples experiment (this may include, but not limited to, ddRAD genotyping, Allegro genotyping, custom target enrichment) where a 90% threshold is considered on the aggregated value of each pool depending on the strategy adopted.

Customer-provided libraries

Customers submitting libraries direct to sequencing (i.e. already containing the due multiplexing indexes) must provide complete, exhaustive and correct information on index sequences and kit references (or adapter sequences along with custom protocol) in the specific sheet of the "Sample Spreadsheet" form. If erroneous information is provided, leading to barcode collision or, to any extent, hampering the successful sequencing of libraries due to sample mis-assignment, IGA Technology Services will be not responsible for any loss of data and the experiment will be charged regardless of the outcome. If any inconsistency in the information is found or the standard library QC/quantification is failed, IGA Technology Services has discretion to refuse to continue with the experiment and only QC fees will be applied.

Pseudonymization

Any sample of human origin, including but not limited to DNA, RNA, blood, tissue, saliva, stool, must be provided in pseudonym form. This means that all personally identifiable information **must be REMOVED** and not appear to IGA Technology Services (this may include, but it is not limited to, name, surname, date of birth, fiscal code, etc.). Means of transmission include, but are not limited to mail, Sample Spreadsheet, shipped envelopes or direct labeling of tubes. Reception of samples along with any sensitive data will hamper the ability of sequencing them. Client will be requested to provide new sample identification in pseudonymized form. IGA Technology Services will be responsible to destroy any personal information related to the samples. If pseudonymization (or destruction of information) is not possible due to direct labeling of sample containers with personal data, these will be shipped back to the sender. **Non-personal data** which might be used for the only scope of the analysis (e.g. age, weight, prognosis, sex, drug treatment, etc.) can be submitted through the Sample Spreadsheet without limitations.

Communications

All requests for information about the service must only be sent via email (orders@igatechnology.com) and will be dealt with within 2 working days from receipt. In the event problems arise during the processing, the Customer will be contacted directly to agree on possible solutions. Otherwise, the Customer will only be contacted at the end of the service. The contact person will be the one as provided in the Sample Spreadsheet form (for standard sample reception, QC results and delivery notifications).

Invoicing

For orders of net amounts less than 10,000 EUR, invoicing will take place at the end of the service. For orders of net amounts greater than 10,000 EUR, invoicing will take place in two stages:

- 50% on receipt of the samples;
- 50% at the end of the service.

Should the service not be successful due to technical problems, it will be repeated without any additional charges to the Customer. Should the service not be successful on two consecutive occasions, 50% of the amount of the order will be invoiced in any case to partially cover the costs sustained.

Delivery times

Our standard data delivery time is between 8 and 10 working weeks, based on the type of service required, the need of specific data analysis and the optimization of the use of the Illumina platform, as described below. The time will be counted from sample QC date until data is delivered. In case some samples fail the incoming QC and a replacement is requested, time will be counted once the replacements pass the incoming QC. Alternatively, customer must send a written (e-mail) communication with acceptance to proceed with sample analyses despite the quality requirements are not met. In any case, we will guarantee delivery of the data within maximum 16 weeks from the date of receipt of the samples.

For special projects in terms of sample number or for the development of dedicated protocols (e.g. thousands of samples for Target Genotyping by Sequencing or ddRAD genotyping) the time for data delivery will be agreed with the client on a project basis.

Usage optimization of the Illumina platform

A flowcell consists of more than one lane (from 2 to 8, depending on run type) and each lane can accommodate one or more samples depending on the level of multiplexing/reads number chosen by the Customer. Should the service require only the partial use of a flowcell, the samples will be processed when the remaining capacity of the flowcell is taken up by the samples of other Customers. For this reason, the delivery times given in the Offer could undergo modifications (maximum 16 weeks).

In any case, IGA Technology Services will not be responsible for delayed deliveries or services cancelled due to *force majeure* or, in any event, factors beyond its control, such as technical problems with the instrumentation, delays in the delivery of the reagents by the suppliers or samples provided in formats or quality that do not meet our application-specific requirements.

Method of delivery and data storage

At the end of the service, the data will be made available to the Customer on a server of IGA Technology Services. The Customer will receive a username and personal password to access the data, which must be downloaded from the server within 15 days from receipt of the notification of availability.

The Customer may request the delivery of the data saved onto an external hard-disk, sustaining the associated additional costs.

The data will be retained on a server of IGA Technology Services for **3 months, starting from the date of delivery**. After this period, data will be deleted without notification. If extended persistence is required, it must be notified beforehand (within 2 months from data delivery). Extra charge will be applied for extended storage. Upon expiry of the 3 months, the data will be completely deleted. Therefore, once this period has passed, any requests to upload the data on the download service server cannot be met.

Data download and integrity check

After notification, data will be available for download for a period of two weeks. After this period, in case data is no longer available in the download page, a request must be issued to reload the data on the export server. After download, customer is responsible of checking data-integrity by the provided MD5 files. If integrity check fails, please retry the download. If data integrity issues persist, please communicate promptly to IGA Technology Services, before the 3 months' storage period terminates. To perform data integrity-check on a Windows system, download the software MD5Checker (<http://getmd5checker.com/>), once installed, start the software and load (Edit → Add/Open) the provided MD5 file, the integrity checking will start automatically. Please ensure that the MD5 file resides at the same folder level as provided in the download page.



Confidentiality and Privacy Policy

All customer information is held with strict confidence. All materials and information sent to us and the data produced by us for the order are exclusive property of the customer and will be returned to the customer or discarded in confidential manner. We archive customer materials or use for marketing activities only when agreed with the customer. For customer's **privacy policy**, please retrieve the latest document available at the following link: <http://www.igatechnology.com/igatech/documents>.

Standard Bioinformatics Services and Outputs

All the standard analyses (BRONZE) and simple sequencing delivery include either raw data or adapter-masked data. Standard applications which are executed with regular adapter included via ligation and not carrying specific features are by default provided with masking of any adapter read-through (masked by Ns). Libraries such those providing UMIs, linked-reads barcodes, deduplicators or any other sequences generated by specific primer-extension may be delivered as pure raw data. Any masking or trimming of the latter may impact the performance of downstream analyses that we are not controlling. Please consult the application-specific "**Data Delivery Specification**" on our website (or inquire if not present) to learn on each application delivery format. Quality control reports will be provided for any read set (excluding sequencing indexes). Data will be always provided as base-called and demultiplexed. Raw intensities will be never provided unless previously agreed. Samples that are sequenced on multiple lanes/runs will be provided as separated files. Data integration can be requested as an extra service.

Bioinformatics Support Services

We have divided our portfolio of bioinformatics services into four different levels of support: from the most standard established workflows to the more customized data manipulation and interactive customer-analyst follow-up toward data refinement. The document also describes the standard result bundles (“IGATech BRONZE”) for some of our most consolidated pipelines. We also provide conditions of data storage, download and checking. Please read this document carefully.

- **IGATech BRONZE (Standard output)**

Customer will receive analytical results from standard validated pipelines of IGA Technology Services and do not account any further manipulation at this level. IGATech Bronze includes the computation time for one single run of the analysis without extra support, but for data download and understanding of result files. Please inquire or visit our website to know which application is supported by standard pipeline.

- **IGATech SILVER (Data conversion - custom graphics)**

Customer will obtain transformed data (conversion of formats) or visualization products not regularly produced by our internal pipelines or by software already validated in our production pipelines. Custom conversion scripts will be developed *ad-hoc* to obtain data transformation/visualization. IGA Technology Services will maintain rights on the property and use of such software for other purposes (software products are not part of deliverables, unless otherwise agreed). Terms and costs of these services will be evaluated on a case-by-case basis prior to the order. Costs will depend on the hands-on time required by the bioinformatics staff. IGATech Silver does not include development of software for data analysis, computation or statistical inference.

- **IGATech GOLD (Custom Analysis Support)¹**

Customer will receive customized support on i) experimental design, ii) development of dedicated software for data analysis or statistics, iii) testing of new software/approaches not already accounted in our standard services, iv) custom data integration from different sources. IGA Technology Services will maintain rights on the property and use of such software for other purposes (software products are not part of deliverables, unless otherwise agreed). The main objectives, terms and costs of the study must be agreed before analysis kick-off. The completion of the analyses must be feasible in a time span of **2 months** after data production or data upload (in the case of data from third parties). The active hand-on time of bioinformatics staff will not exceed **60h**. Analyses can be repeated when it is demonstrated that previous ones have generated incorrect results or partial results for reasons due to

technical issues, incomplete data sets or wrong parameters; this does not include cases when incomplete results or due to bad starting material or wrong experimental design. Repeats cannot exceed the maximum hands-on time. Time to set up extra analyses, phone calls and meetings are counted as hands-on time, while CPU time is not counted. This level includes up to **one** extra cycle of intensive analyses² requested by the customer (unlike aforementioned repeats), regardless of the reason of the request (e.g. to change parameters, reference database or software for publication purpose).

- **IGATech PLATINUM (Custom Analysis Support)¹**

Customer will receive customized support either in i) experimental design, ii) development of dedicated software for data analysis or statistics, iii) testing of new software/approaches not already accounted in our standard services, iv) custom data integration from different sources. IGA Technology Services will maintain rights on the property and use of such software for other purposes (software products are not part of deliverables, unless otherwise agreed). The main objectives, terms and costs of the study must be agreed before analysis kick-off. The completion of the analyses must be feasible in a time span of **6 months** after data production or data upload (in the case of data from third parties). The active hand-on time of bioinformatics staff will not exceed **120h**. As a major difference from the IGATech GOLD package, during this period, Customer will have the opportunity to interact with the analysts to have feedback on the proceeding of experiments and drive downstream analyses refinement. This will be carried based on step-by-step inspection of preliminary data and analysis results during the first 4 months of the reserved time; the last two months are reserved to IGA Technology Services to complete development and analyses as agreed in advance. Analyses can be repeated when it is demonstrated that previous ones have generated incorrect results or partial results for reasons due to technical issues, incomplete data sets or wrong parameters; this does not include cases when incomplete results or due to bad starting material or wrong experimental design. Repeats cannot exceed the maximum hands-on time. Time to set up extra analyses, phone calls and meetings are counted as hands-on time, while CPU time is not counted. This level includes up to two extra cycles of intensive analyses² requested by the customer (unlike aforementioned repeats), regardless of the reason of the request (e.g. to change parameters, reference database or software for publication purpose).

¹On the basis of project complexity and customer requests a dedicated quote with presumptive man/hour will be issued. If circumstance will resolve all the analyses with a lower amount of time, the remainder hours will be accounted for further custom analyses or converted to standard bioinformatics services.

²Intensive analyses: computationally intensive tasks such as short reads alignments, SNP calling, *de novo* assembly, reads clustering or any task which can require more than 10 CPU/h.