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Xpress-seq service terms and conditions

In addition to Xpress Genomics' (XG's) general terms and conditions, the service and deliverables for plate-based full-length scRNA-seq using Xpress-seq is closer defined in these terms.

What is in included in Xpress-seq service package?

- Lysis plate and sealing foil
- Library preparation (cDNA generation & amplification; tagmentation and library prep)
- Library QC (TapeStation)
- Sequencing (see more on sequencing depth below)
- Data processing (Barcode error correction, alignment to genome and user-provided transgenes, gene assignment, count tables and statistics)
- Data delivery on XG's FTP service

What are the deliverables and specifications of the service?

1. Sequencing depth is an approximate estimate based on XG's own internal scRNA-seq libraries and previous customer experiences. We do not guarantee that all cells reach a certain depth, as the effective depth depends on the quality of the cells isolated by the customer. Tables (a) and (b) define which number of plates per sequencing run are pooled at most by XG. Variations in depth between plates may exist within reasonable quantification and pooling accuracy.

Read lengths offered (PE100 and PE150) refer to the raw read and in case of UMI-containing reads, the first read in the pair only contains 86 or 136 bp of cDNA, respectively.

(a) Gene Expression Depth:

SEQUENCING SYSTEM	MAXIMUM NUMBER OF PLATES PER RUN	INTERNAL VALIDATED OUTPUT	TYPICAL OUTPUT
G99	1	120M reads 312,000 reads/cell	80M reads 208,000 reads/cell
G400	12	2000M reads 430,000 reads/cell	1500M reads 325,000 reads/cell
T7	36	5800M reads 420,000 reads/cell	4500M reads 325,000 reads/cell

(b) Isoform & Allele Depth:

SEQUENCING SYSTEM	MAXIMUM NUMBER OF PLATES PER RUN	INTERNAL VALIDATED OUTPUT	TYPICAL OUTPUT
G400	4	2000M reads 1,300,000 reads/cell	1500M reads 975,000 reads/cell
T7	12	5800M reads 1,250,000 reads/cell	4500M reads 975,000 reads/cell

Internal validated output is generated using Xpress-seq v2 libraries from human cell line samples with a sort efficiency of >95% of wells.

2. Xpress-seq v2 libraries contain both internal reads spanning the full transcript length as well as 5′ reads containing UMI counts. While we always strive for a balanced ratio or adjust experimental settings to customer's demands, Xpress Genomics does not guarantee a particular % UMI vs internal read ratio. Note that while Xpress-seq v2 libraries outputs reads containing UMIs as well as reads spanning the entire transcript length, not all sequenced reads will have a UMI or span the full transcript.

3. While Xpress Genomics ensures high-quality automated processing of submitted plates, we cannot guarantee a particular % of wells of a plate being successful (QC passing), as factors such as cell health and sorting efficiency are influenced and determined by the customer's experimental setup and procedure.

Add-on services at additional cost:

1. In case XG determines that the library QC of Xpress-seq libraries generated for a customer project are below expectation (and potentially indicating compromised quality or well success rate), we will contact you before proceeding with sequencing. At this stage, customer can choose to proceed with:
    a. Sequencing as planned according to above table and quote costs
    b. QC sequencing on the smallest flow cell we offer (G99, PE150 read length, 80-120M reads). For QC sequencing, the currently valid service sequencing price applies. As of 30 June 2025, list price for G99 PE150 flow cell is 9,000 SEK)
    c. Abort the service for QC failed plates without sequencing. Plates that do not proceed after library QC are charged at 4,000 SEK / plate.
2. In case the customer is not satisfied with the ratio of UMI and internal reads, XG can attempt re-tagmentation under different experimental conditions to fine-tune the read ratio. Re-tagmentation is invoiced at 4,000 SEK / plate and needs to be combined with a re-sequencing service and re-processing of data (see below).
3. In case the customer would like to get additional sequencing coverage on existing Xpress-seq libraries, the currently valid service sequencing price list and flow cell options apply. Re-sequencing is only possible if XG has leftover library, please contact us to discuss.
4. In case the customer asks XG to re-run the Xpress-seq data processing pipeline (eg. after re-sequencing), a data processing charge applies. Data processing is invoiced at 1,000 SEK / commenced 1000M reads.

Acknowledgement
We kindly ask to acknowledge Xpress-seq data in your publication as follows:
Xpress-seq full-length scRNA-seq was generated by Xpress Genomics AB, Stockholm, Sweden.

Your method section may describe Xpress-seq as follows:
Full-length single-cell RNA-seq library preparation using the Xpress-seq (v2) method was performed at Xpress Genomics (Stockholm, Sweden). In brief, single cells were FACS-sorted into provided 384-well plates containing lysis buffer, spun down and stored at -80 °C. Upon submitting plates to Xpress Genomics, robotic automated library preparation was performed. Sequencing was performed on the DNBSEQ G99RS/G400RS/T7RS platforms (MGI Tech) using App-D sequencing primers.