

XENOVEA SERVICE GUIDE

GENE EXPRESSION PROFILING (GEX)

In some cases mRNA-seq is not the best choice for the analysis of the polyadenylated transcriptome in eukaryotes – for example, when the starting material does not meet the strict quality criteria for mRNA-seq, or when less complex datasets are sufficient for answering the scientific question. Gene expression profiling (GEx) offers a solution for both cases. The resulting data provides information about the level of gene expression per locus, which can be used for differential expression analysis. Because the method does not require full length mRNA, GEx is tolerant to low RNA quality and can be safely used even for difficult samples such as FFPE. GEx data are stranded – information on the direction of transcription is preserved.

Although GEx is largely RNA quality-independent, a thorough initial quality control is performed for each submitted sample to ensure proper quality and relevant end results. In case of doubt or upon request, Xenovea also offers RNA isolation services using validated and matrix-specific workflows.

If the specifications for starting materials are fully met, we guarantee that we deliver at least 95% of the requested total raw data amount of your project (with at least 85% raw data amount for any individual sample) within the agreed timeframe.

SPECIFICATION

Starting material	Properly transported and/or preserved tissue/biosample, or ideally ≥ 20
	μ , \geq 40 ng/ μ l total RNA ¹
Library prep	QuantSeq 3' mRNA-Seq V2 Library Prep Kit with UDI (Lexogen)
Inclusions	RNA isolation (optional)
	initial RNA sample quality control
	library preparation
	final quality control
	filtering, trimming, data transfer
Sequencing chemistry	Illumina
Sequencing setup and quality	Single-end (SE) setup, 75 nt minimum read length; Q30 ≥ 85%
metrics	
Sequencing depth	standard (10M SE reads)
	deep (20M SE reads)
	custom
Bioinformatic analysis	Optional, please inquire for details
Turnaround time (raw data)	4-5 weeks from sample receipt
Turnaround time (with high-level	Upon agreement
bioinformatics)	

¹GEx can be performed using RNA of any quality; however, using RNA with high degradation rate may lead to reduced reproducibility and data reliability.

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