



Which INVIEW™ TRANSCRIPTOME product fits best?

EXPLORE

Ideal for high-throughput screening projects with well-known reference sequences

- Explore genes expressed at a given time and under specific conditions
- Compare expression levels of transcripts from different samples

ADVANCE

Gold standard solution for detection and quantification of differential gene expression

- Achieve a higher mapping accuracy even for large eukaryotic genomes
- Monitor rarely expressed transcripts

DISCOVER

Perfectly suited for discovery of rare and novel transcripts or for identification of splicing variants

- Strand-specific analysis enables most comprehensive insight into RNA expression levels, sequence and structure
- Unlimited application for all samples, even without prior knowledge of reference sequences

How can we meet your needs?

Our goal is to apply cutting-edge technologies and all of our know-how to create flexible and scalable solutions.

Fully automated LIMS-controlled workflows allow processing of a few or a large amount of samples with reduced bias and consistent high-quality results in short turnaround times.

Collaborative interactions ensure the innovative standard of our analyses.

Benefit from our experience in collaborative publicly funded projects. For more information about ongoing projects, feel free to contact us.



GATC Biotech provides a number of standardised and ISO 17025 accredited next generation sequencing (NGS) solutions.

Visit www.gatc-biotech.com and discover our entire product portfolio, covering services like Sanger, exome, whole genome sequencing as well as microbiome and epigenetic studies. Also discover NGSELECT™, our modular NGS service for maximum flexibility.



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GATC Sequencing Solutions

Designed to fit a multitude of transcriptome projects



Why choose **INVIEW™** TRANSCRIPTOME for your sequencing project?

- Three packages to address your individual needs
- Guaranteed express delivery times on demand
- Adaptable sequencing output in multiples of 30 million reads or read pairs
- Results summarised in a comprehensive GATC Data Analysis Report
- Standardised and streamlined workflows
- ISO 17025 accredited sequencing available upon request

Service offerings and quality highlights

INVIEW TRANSCRIPTOME

Specifications			
Product	EXPLORE	ADVANCE	DISCOVER
Library type	Random-primed cDNA		Strand-specific cDNA
Starting material	Applicable for total RNA and rRNA depleted total RNA from various sources, starting from one sample		
Sequencing technology	Illumina		
Read mode	50 bp single read	50 bp paired-end read	125 bp paired-end read
Number of reads guaranteed	Multiples of 30M single reads	Multiples of 30M read pairs	
Delivery time	Starting from 15 days	Starting from 17 days	Express 17 days; Premium 21 days
Deliverables	<ul style="list-style-type: none"> • Alignment • Tables providing information on gene expression including FPKM value (.tsv), combined gene expression, top genes expressed, pairwise differential gene expression including foldchange and p-value • SNP and InDels including annotated variants and effects 		

Best suited for			
Transcript identification	✓	✓ ✓	✓ ✓ (✓)
Differential expression	✓	✓ ✓	✓ ✓ (✓)
Novel transcripts			✓
Strand-specificity information			✓
Splice variants			✓
Rare transcripts	Flexible increase of data output (+30M)		
Mapping accuracy	Sufficient	Good	Optimal
High-quality reference	Mandatory	Beneficial	Additional

