How QIAGEN Works with Genomics Cores

Creative Partnerships that Drive Growth

Shu Liang, Genomics Field Application Specialist, QIAGEN

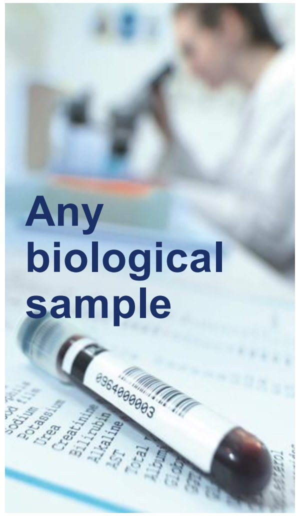
Legal disclaimer

QIAGEN products shown here are intended for molecular biology applications. These products are not intended for the diagnosis, prevention or treatment of a disease.

For up-to-date licensing information and product-specific disclaimers, see the respective QIAGEN kit instructions for use or user operator manual. QIAGEN instructions for use and user manuals are available at www.qiagen.com or can be requested from QIAGEN Technical Services (or your local distributor).

Sample to Insight

Samples



Any biological sample

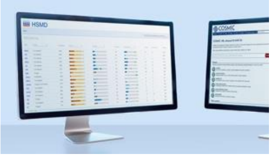
Sample preparation

Sample technologies

Detection

PCR

QIAcuity dPCR

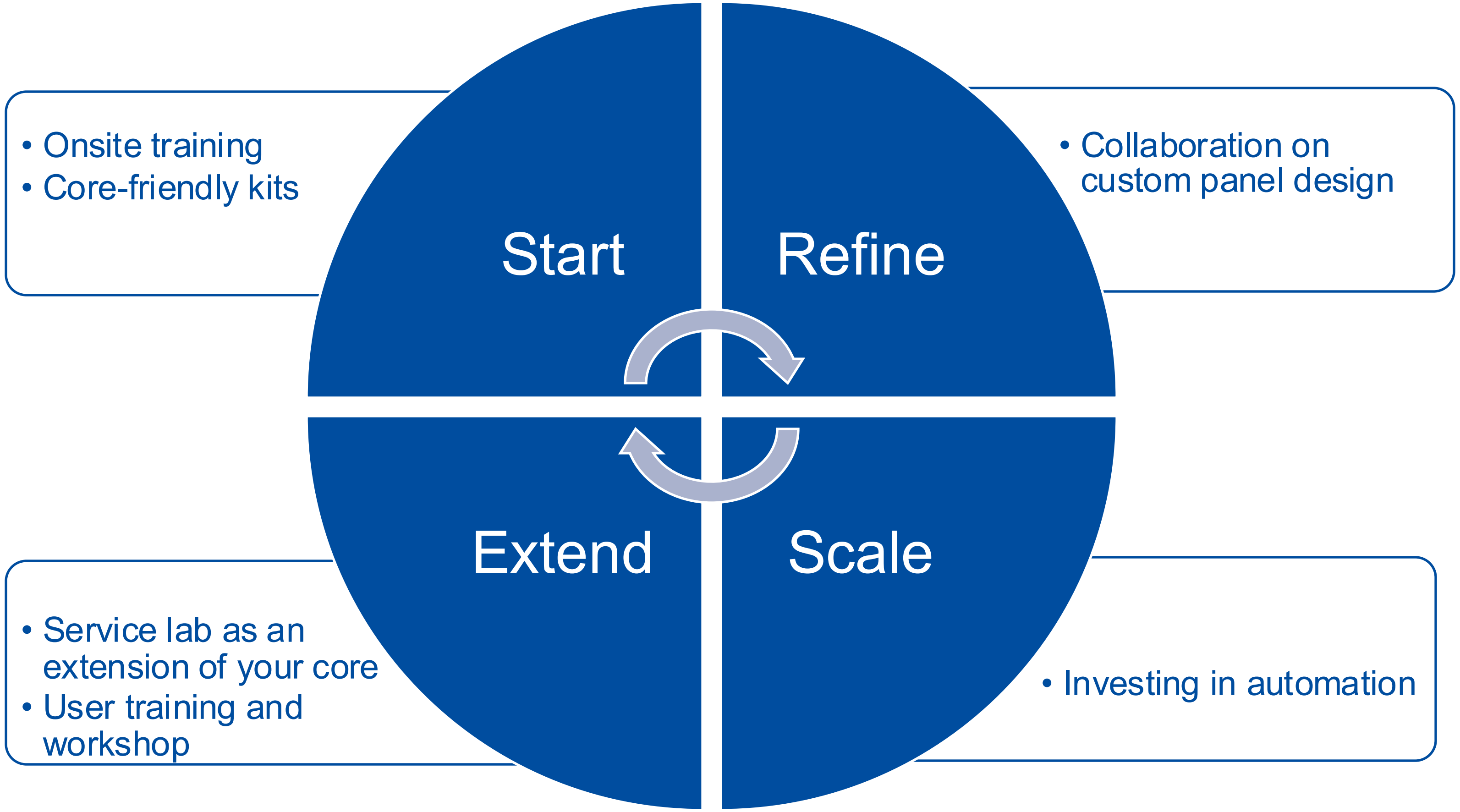


Genomics / NGS
QIAseq
QIAGEN Digital Insights

Diagnostic Solutions
QuantiFERON
QIAstat-Dx

Insights

Partnering with Genomics Cores at Every Stage of Growth



- Onsite training
- Core-friendly kits

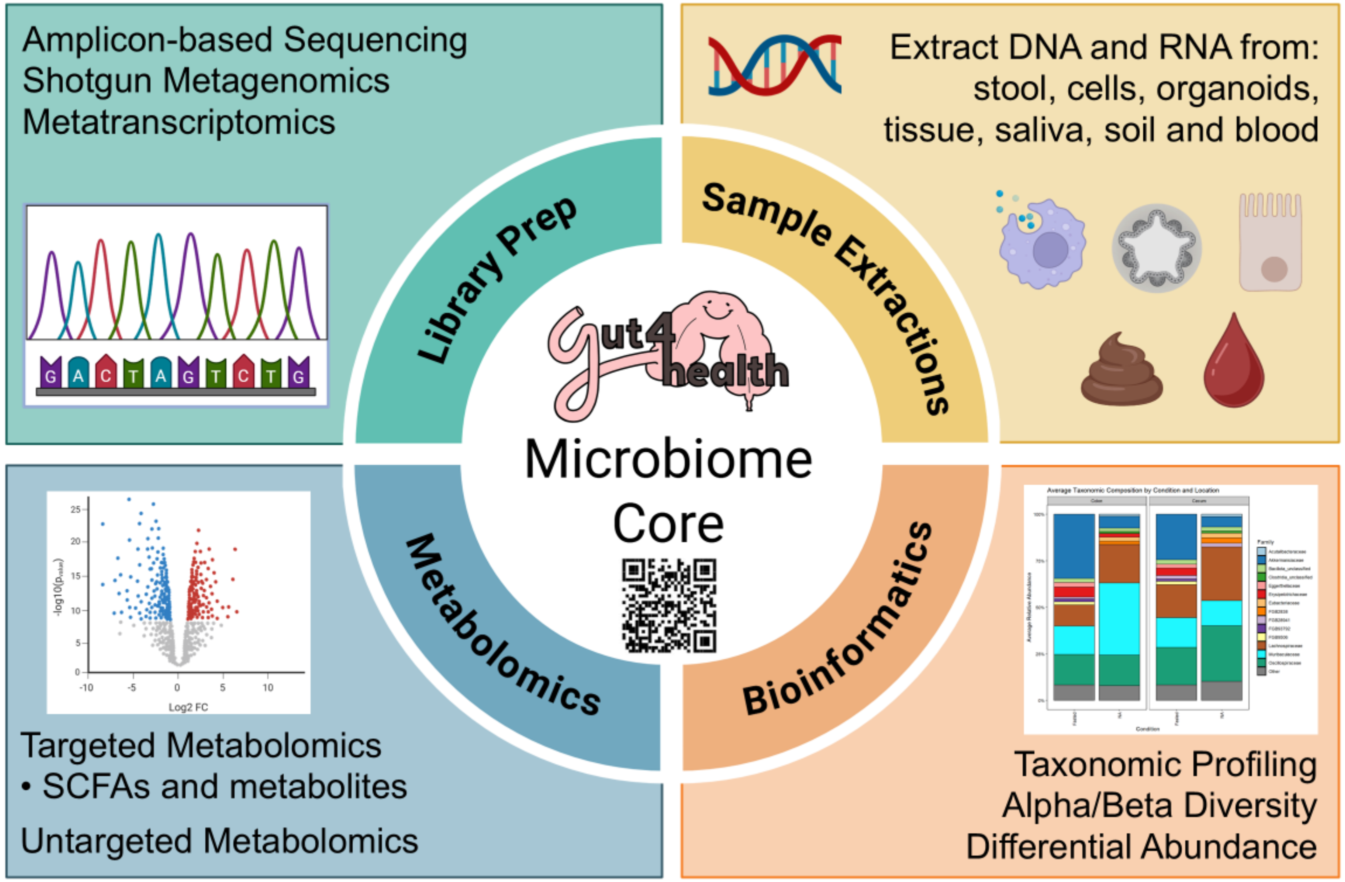
- Collaboration on custom panel design

- Service lab as an extension of your core
- User training and workshop

- Investing in automation

Start: Bringing new NGS service into the Core

- Gut4Health @BC Children's Hospital Research Institute
- A microbiome core looking to provide NGS service beyond 16S taxonomic analysis
- Metagenomics:
- QIAseq FX DNA Library Kit + Normalizer
- Metatranscriptomics:
- QIAseq FastSelect RNA Lib Epidemiology Kit (with built-in rRNA removal)
- On-site training to onboard the protocols
- Virtual support on workflow optimization (best practice, template document building, sequencing multiplexing strategies etc..)
- QIAGEN Digital Insight for data analysis


Amplicon-based Sequencing
Shotgun Metagenomics
Metatranscriptomics

Extract DNA and RNA from:
stool, cells, organoids,
tissue, saliva, soil and blood

Targeted Metabolomics
- SCFAs and metabolites

Untargeted Metabolomics

Taxonomic Profiling
Alpha/Beta Diversity
Differential Abundance

For more information find us at: https://www.bcchr.ca/Gut4Health

BC Children's Hospital Research Institute

QIAseq FX DNA Library Kit
From Purified DNA to Sequencer-ready Libraries in One Day

Purified gDNA 20 pg – 1 µg

↓

Single-tube FX reaction (50–60 min)

↓

Adapter ligation (45 min)

↓

QIAGEN HiFi library amplification
(45 min; optional)

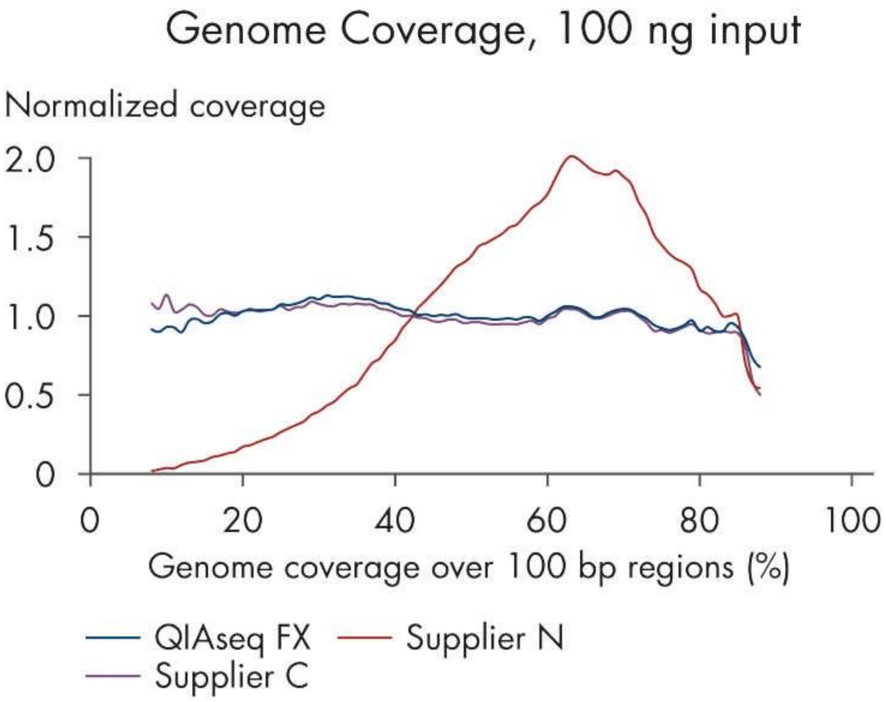
↓

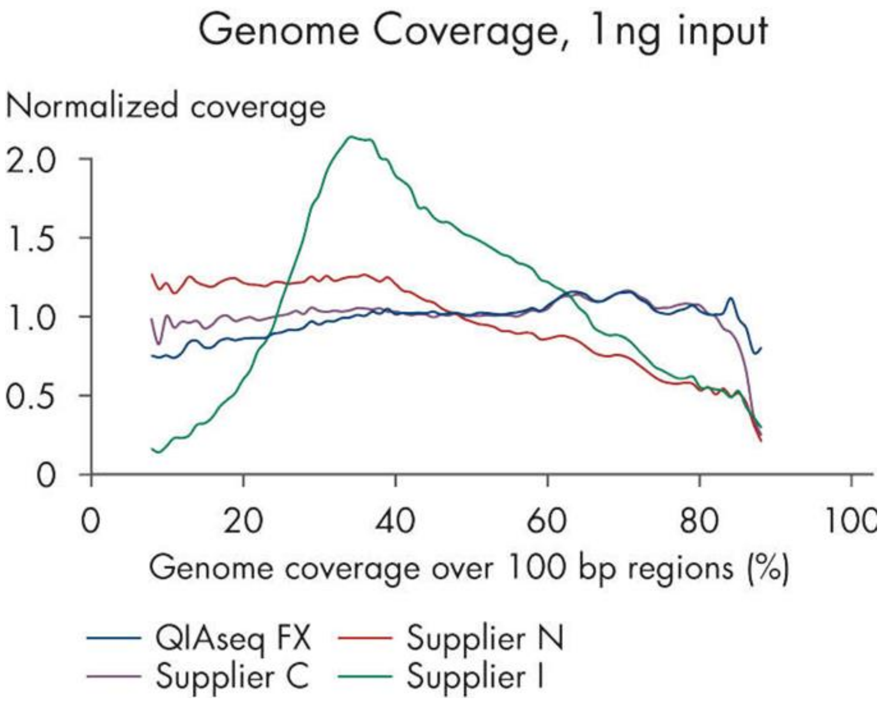
Hybrid capture (optional)

1-day workflow

Automation friendly

Covaris-quality fragmentation from an all-enzymatic workflow


Genome Coverage, 100 ng input


Genome Coverage, 1ng input

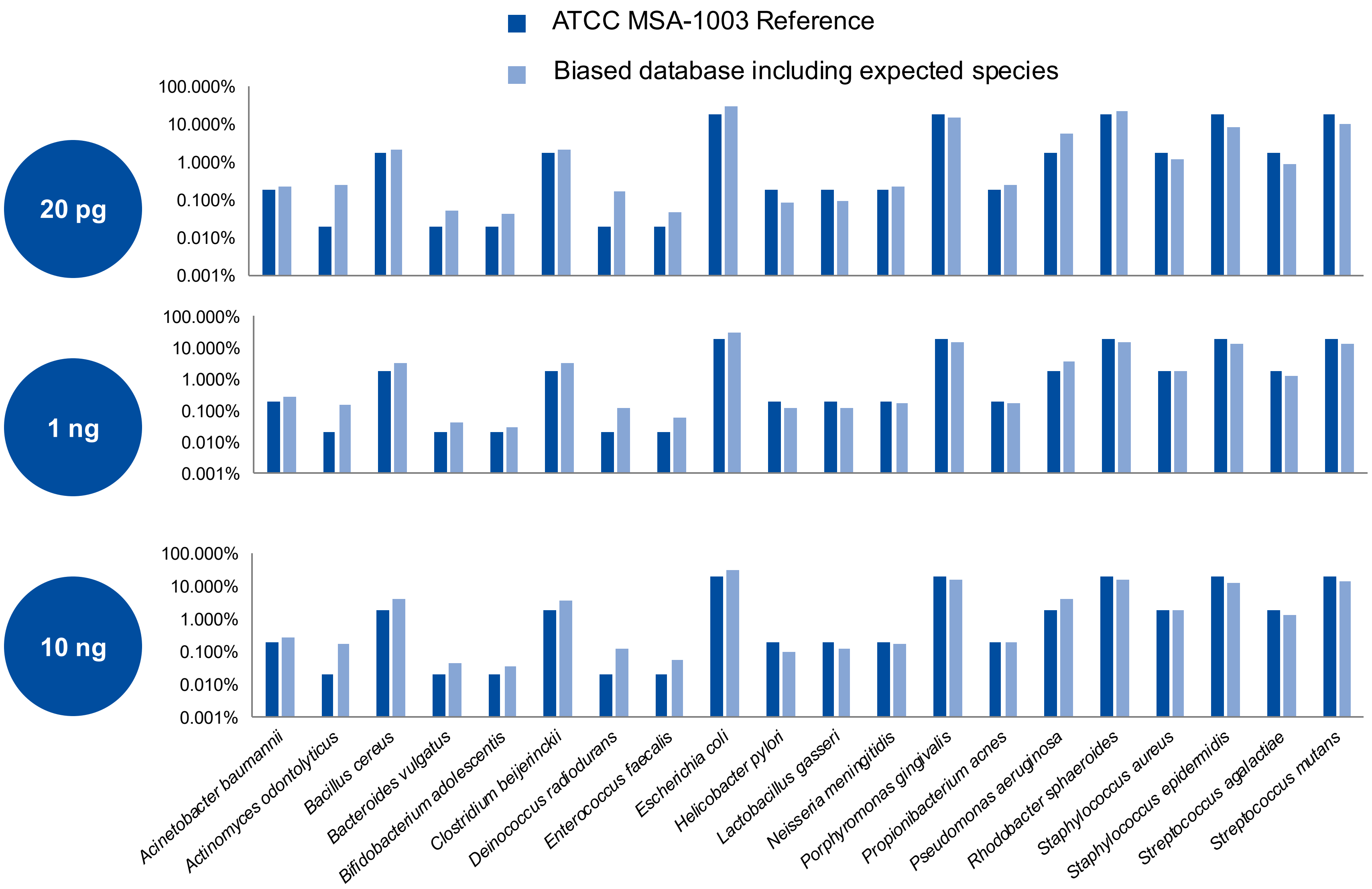
Other supplier methods:

Supplier C: mechanical shearing combined with a standard library prep; **Supplier N:** fragmentase; **Supplier I:** tagmentation

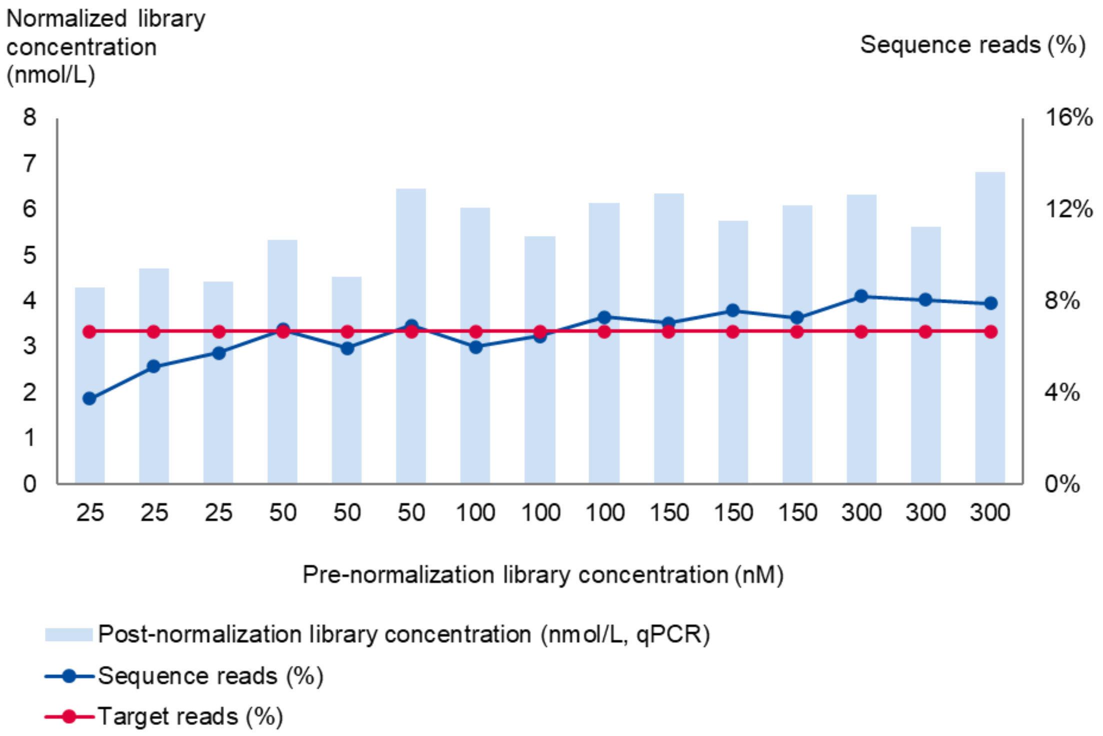
Data obtained through experiments conducted by QIAGEN R&D, Hilden, Germany.

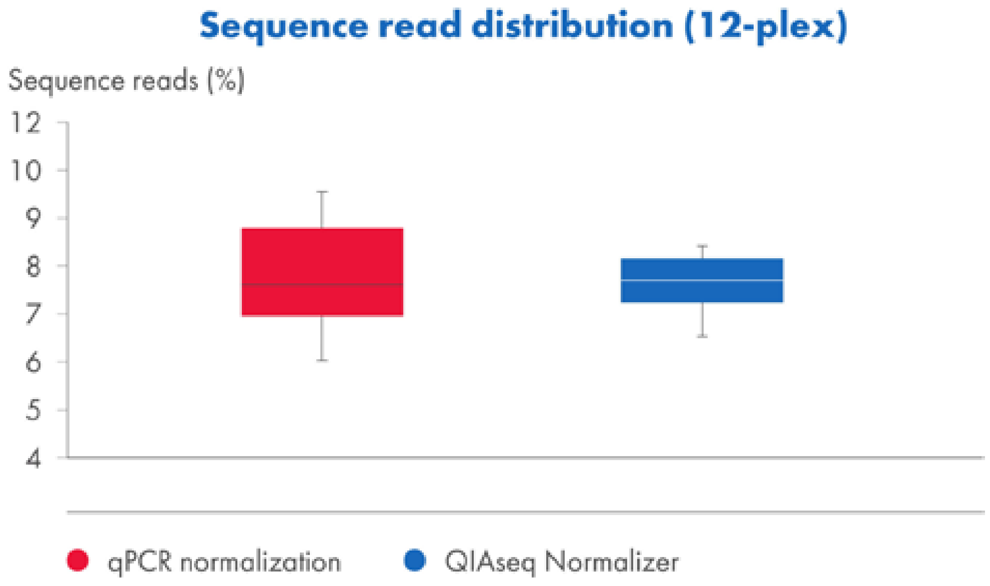
Consistent performance from any input

- Identification of 20 microbial species from ATCC MSA-1003 (0.02–18%)
- Library preparation from 20 pg, 1 ng and 10 ng results in abundance levels highly similar to ATCC MSA-1003 Reference levels
- Reliable microbial detection for mix abundances as low as 0.02%



QIAseq Library Normalizer effectively normalizes QIAseq FX DNA libraries from a broad range of library concentrations

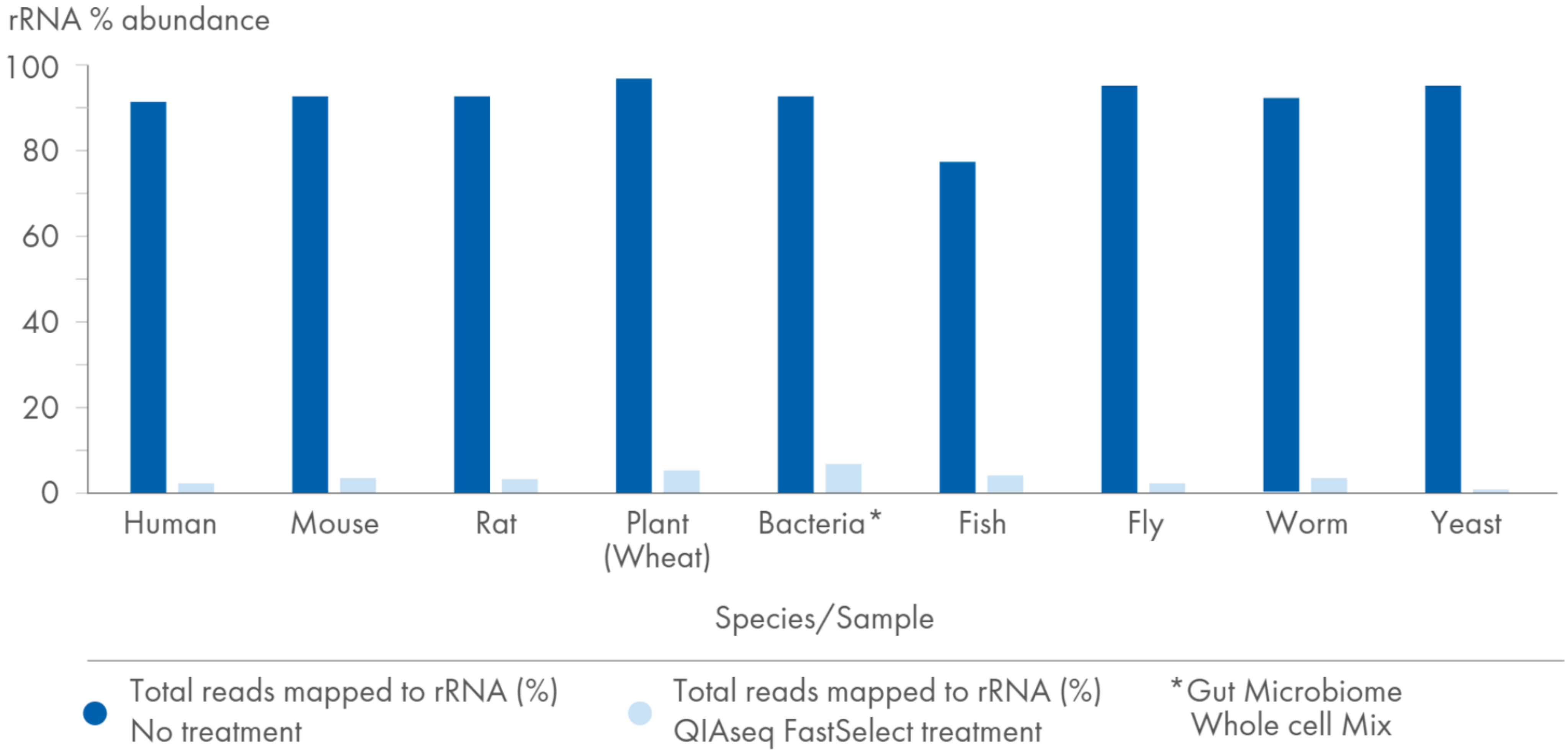




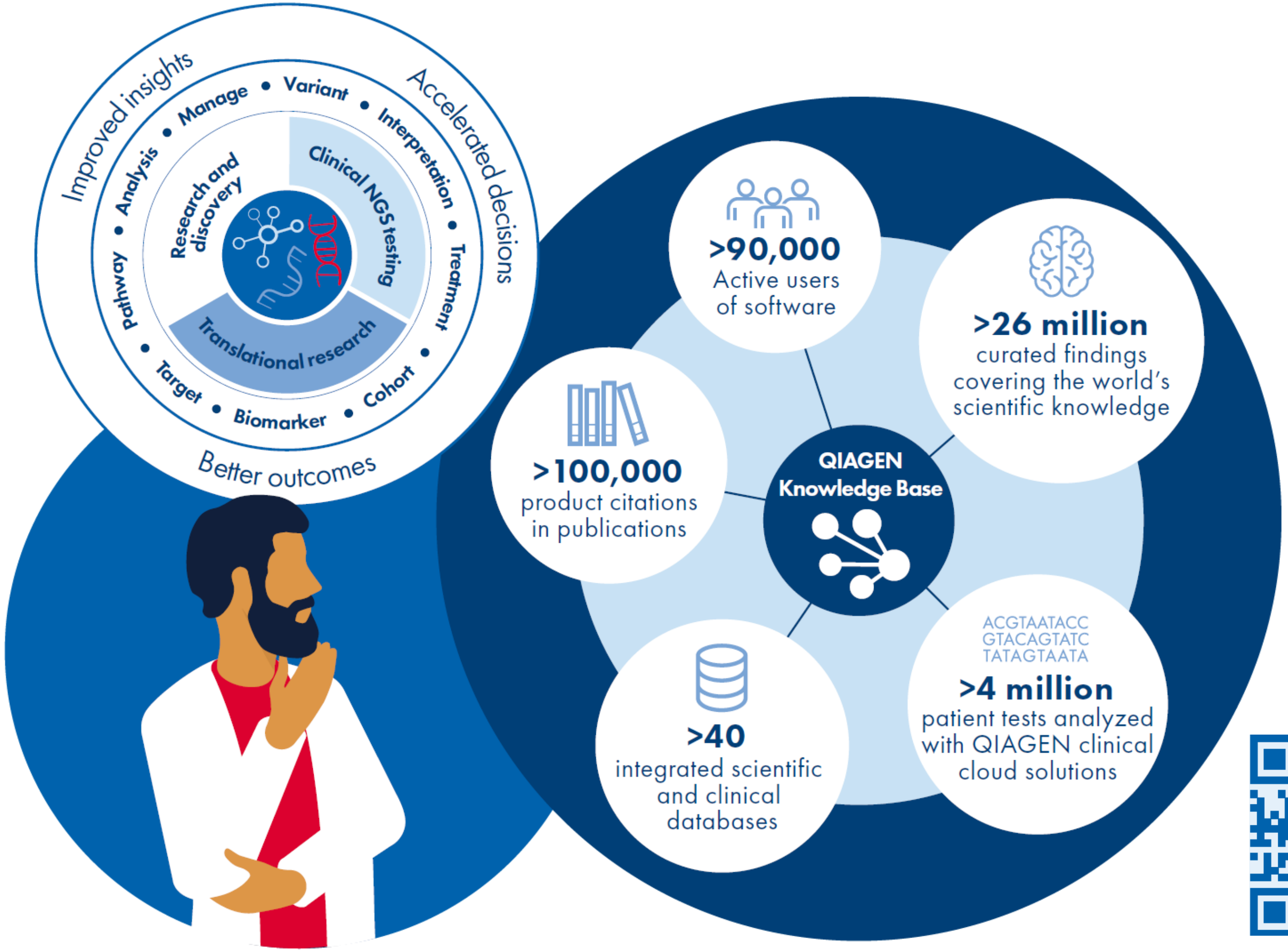
	Before normalization (qPCR)	After normalization (sequencing)
CV%	80.7%	18%
GINI*	0.416	0.096

*GINI coefficient (0.0 –1.0); 0: All libraries are equally represented; 1: One library has all sequencing reads

QIAseq FastSelect effectively removes rRNA from sequencing libraries



Complete your workflow with QIAGEN Digital Insight



QIAGEN Knowledge Base

>90,000
Active users
of software

>26 million
curated findings
covering the world's
scientific knowledge

>100,000
product citations
in publications

>40
integrated scientific
and clinical
databases

>4 million
patient tests analyzed
with QIAGEN clinical
cloud solutions

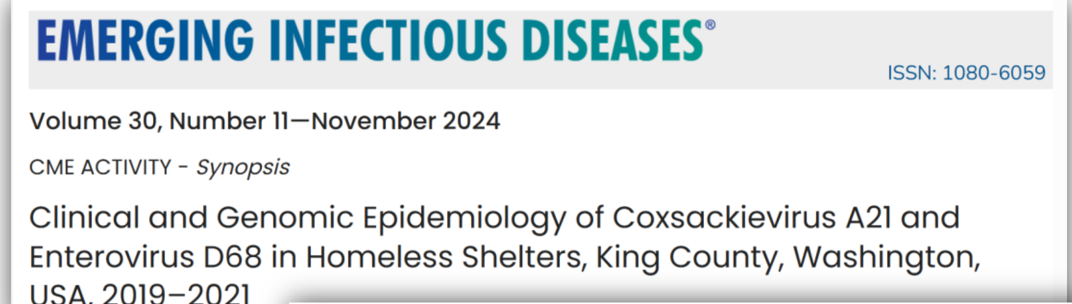
Secondary analysis

- **QIAGEN CLC Genomics**: Scale your DNA and RNA sequence data analyses with our comprehensive set of bioinformatics tools that give you flexible access from a laptop, your local server or the cloud

Interpretation and visualization

- **QIAGEN Ingenuity® Pathway Analysis (IPA®)**: Accelerate your research with our advanced pathway analysis tool that lets you analyze your data, compare results and contextualize your findings

Refine: Designing Custom Products with QIAGEN



EMERGING INFECTIOUS DISEASES®

ISSN: 1080-6059

Volume 30, Number 11—November 2024

CME ACTIVITY - *Synopsis*

Clinical and Genomic Epidemiology of Coxsackievirus A21 and Enterovirus D68 in Homeless Shelters, King County, Washington, USA, 2019–2021

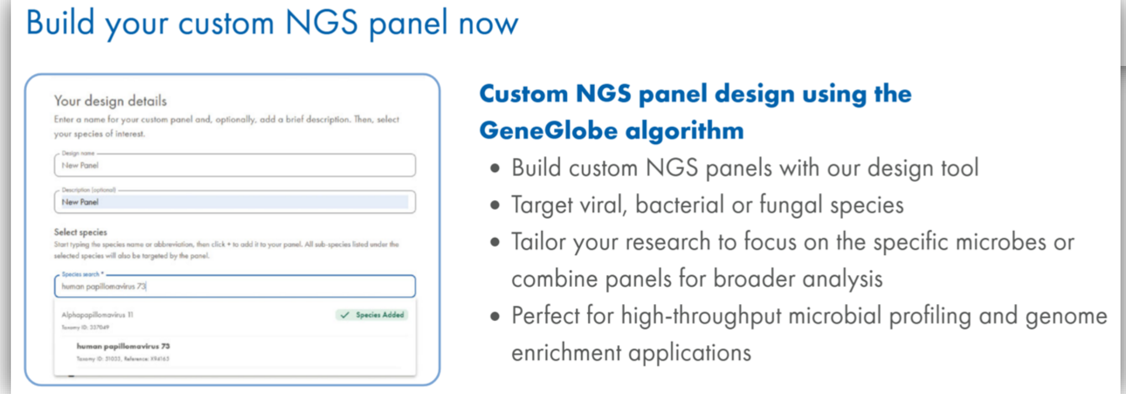
JOURNAL ARTICLE

Epidemiology of Human Metapneumovirus Infection in a Community Setting, Seattle, Washington, USA

Annalyse Elias-Warren ✉, Julia C Bennett, Chidozie D Iwu, Lea M Starita, Jeremy Stone, Ben Capodanno, Robin Prentice, Peter D Han, Zack Acker, Sally B Grindstaff ... Show more

Author Notes

The Journal of Infectious Diseases, Volume 232, Issue Supplement_1, 15 July 2025, Pages S78–S92, https://doi.org/10.1093/infdis/jiaf142



Build your custom NGS panel now

Your design details

Enter a name for your custom panel and, optionally, add a brief description. Then, select your species of interest.

Design name: New Panel

Description (optional): New Panel

Select species

Start typing the species name or abbreviation, then click + to add it to your panel. All sub-species listed under the selected species will also be targeted by the panel.

Species search *: human papillomavirus 73

Alphapapillomavirus 11
Taxomy ID: 337049

human papillomavirus 73
Taxomy ID: 51033, Reference: X94165

Custom NGS panel design using the GeneGlobe algorithm

- Build custom NGS panels with our design tool
- Target viral, bacterial or fungal species
- Tailor your research to focus on the specific microbes or combine panels for broader analysis
- Perfect for high-throughput microbial profiling and genome enrichment applications

- Pavitra Roychoudhury @ UW Virology
- Using the off-the-shelf QIAseq xHYB Respiratory Panel, they has published a few papers

- Improve Efficiency – lower cost, faster turnaround in sequencing and analysis
- Boost Accuracy – reliable target detection
- Attract Users – niche expertise draws new projects

QIAseq xHyb Microbial Custom Panels | New Design | GeneGlobe

QIAseq xHYB Viral and Bacterial Panels

Respiratory

Includes probes for whole genome enrichment, detection and characterization of 89 separate viral targets, including SARS-CoV-2, influenza, rhinovirus, enterovirus and more

Viral STI (sexually transmitted infections)

Sequencing and detection of common STI viruses: HBV, HIV-1 and 19 types of high-risk HPV

HIV-1 panel is available now

AMR (antimicrobial resistance)

Sequencing and detection of the presence of 2786 antimicrobial resistance genes (6200+ AMR markers) in bacteria

Consists of targets pulled from the QIAGEN CLC QMI-AR database

Mycobacterium tuberculosis

Allows for the comprehensive culture-free whole genome sequencing of tuberculosis from samples such as sputum or cerebrospinal fluid, streamlining the process and facilitating rapid detection and characterization of MTB strains

Adventitious Agent

For the detection of viruses that can be problematic contaminants in bioreactors for biotherapeutics manufacturing including 132 separate viral targets, such as human adenovirus, norovirus, rotavirus, influenza, SARS-CoV-2, HPV, Epstein-Barr, HIV, hepatitis A/B viruses and more

MPXV Panel

Contains all reagents necessary for the hybrid capture enrichment of the whole genome of MPXV

Enriches for the whole genome of all MPXV clades, including ITRs

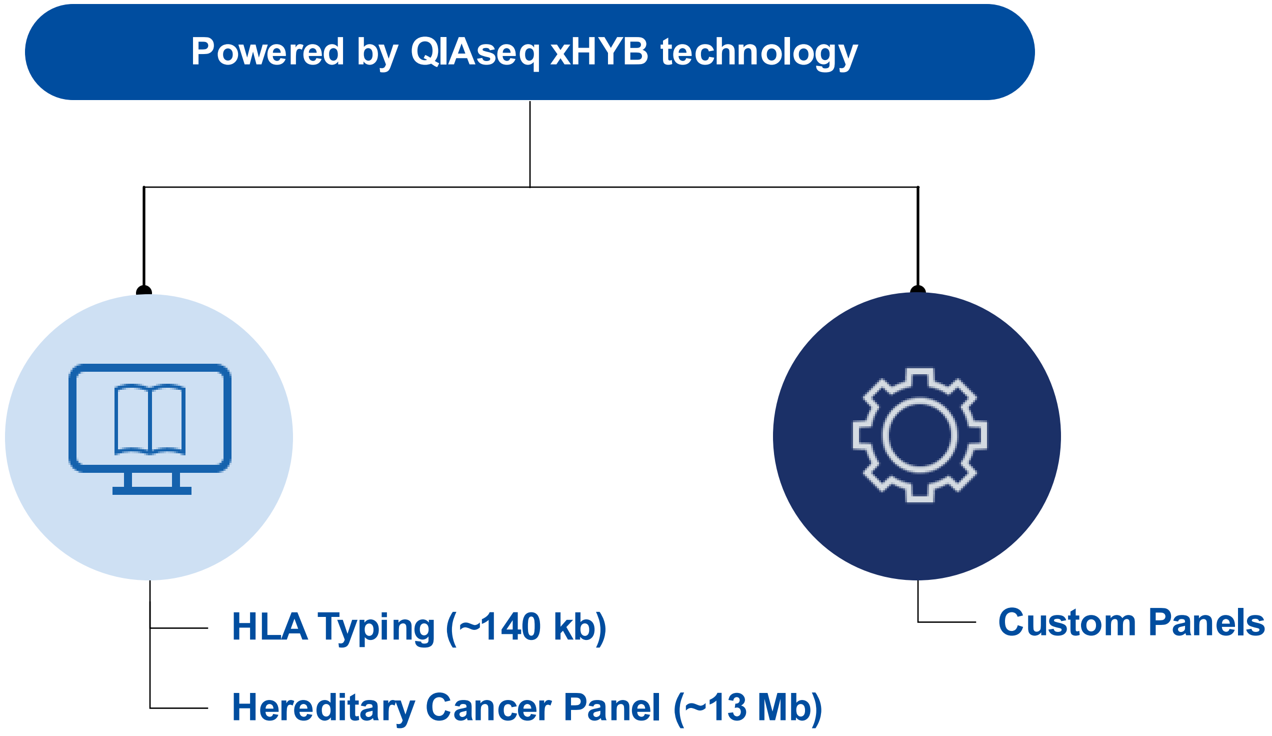
HepC

Enriches the whole genome of all hepatitis C virus genotypes, allowing deep characterization of the full viral diversity.

Custom

Create a custom panel designed against any microbial or or viral targets of your choice

QIAseq xHYB Long Read Panels provide insights into complex genomic regions



Powered by QIAseq xHYB technology

- **HLA Typing (~140 kb)**
- **Hereditary Cancer Panel (~13 Mb)**

Custom Panels

Repeat expansion disorder analysis

Precisely characterize repeat expansions in neurological and genetic disorders

Phasing of genetic variants

Determine haplotype structures of genomic variants for critical insights into inheritance patterns and allele-specific expression

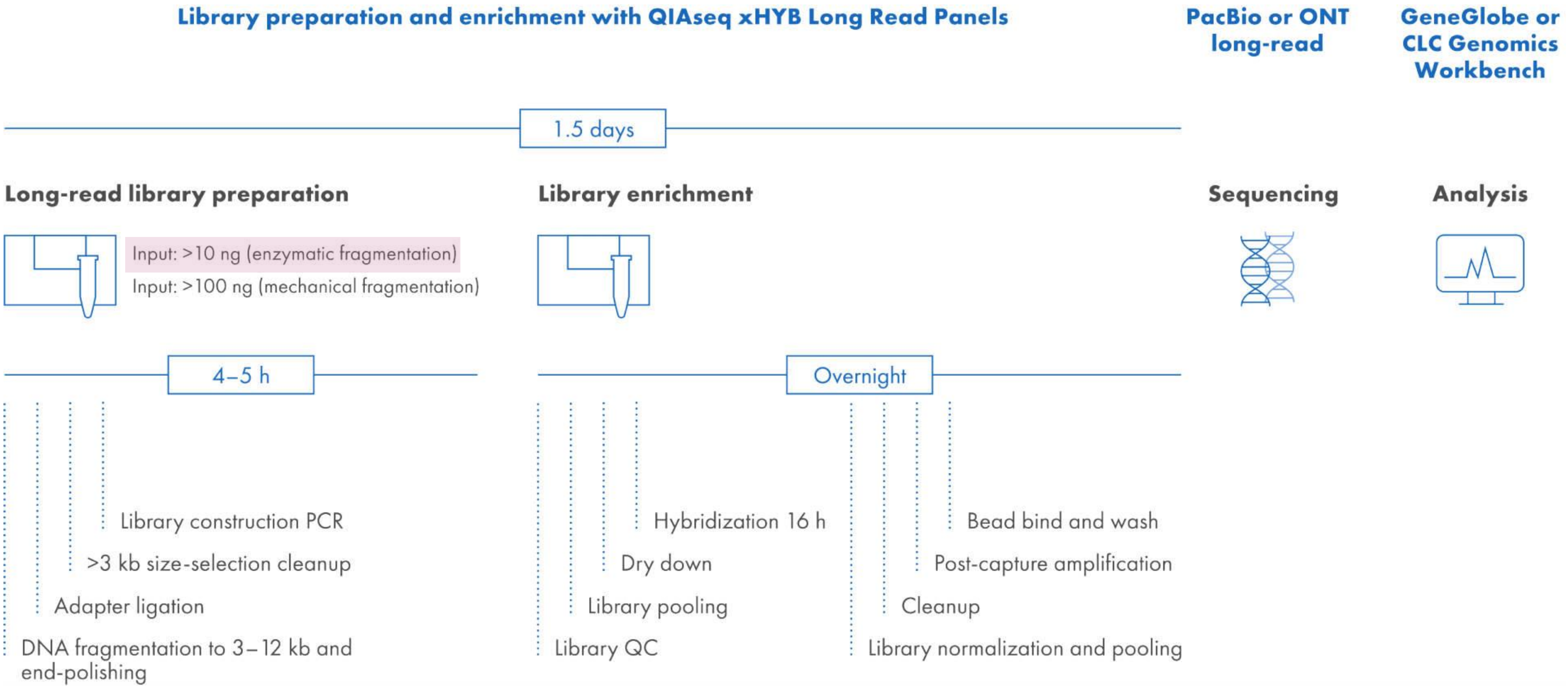
HLA typing

Resolve polymorphic HLA regions for accurate genotyping in immunogenomics and transplantation

Structural variant detection

Accurately detect large-scale genomic alterations for cancer, genetic disease and evolutionary research

QIAseq xHyb Long Read panels



Library preparation and enrichment with QIAseq xHYB Long Read Panels

PacBio or ONT long-read

GeneGlobe or CLC Genomics Workbench

1.5 days

Long-read library preparation

Input: >10 ng (enzymatic fragmentation)

Input: >100 ng (mechanical fragmentation)

4–5 h

Library construction PCR

>3 kb size-selection cleanup

Adapter ligation

DNA fragmentation to 3–12 kb and end-polishing

Library enrichment

Overnight

Hybridization 16 h

Dry down

Library pooling

Library QC

Bead bind and wash

Post-capture amplification

Cleanup

Library normalization and pooling

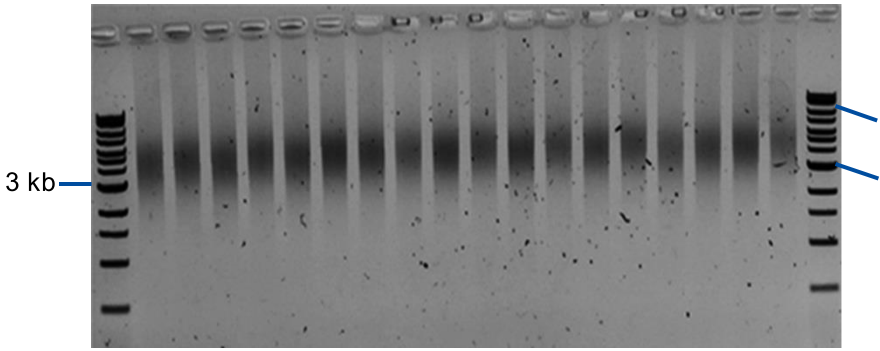
Sequencing

Analysis

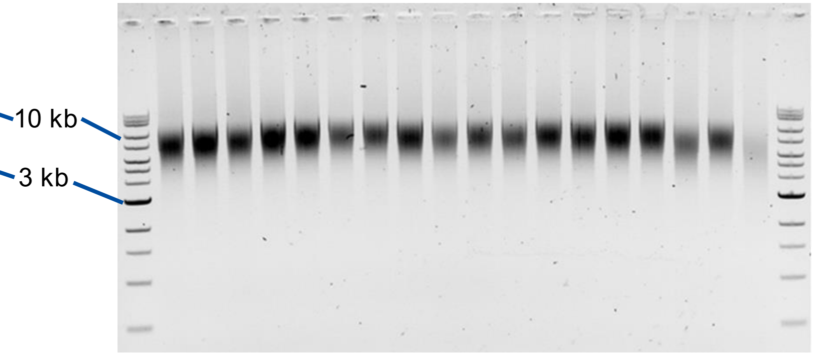
Robust flexible library construction workflow

- Robust, consistent library construction using enzymatic fragmentation or mechanical fragmentation
- Our bead-based size-selection chemistry is user-friendly, with no ethanol wash, and effectively removes DNA <3 kb
- Consistent, clean, post-capture amplification of longer DNA fragments gives excellent results with large and small capture panels

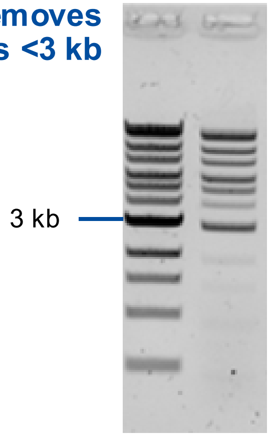
Enzymatic fragmentation long-read library construction



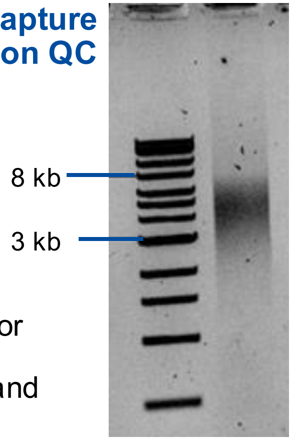
gTUBE fragmentation long-read library construction



Size selection removes fragments <3 kb

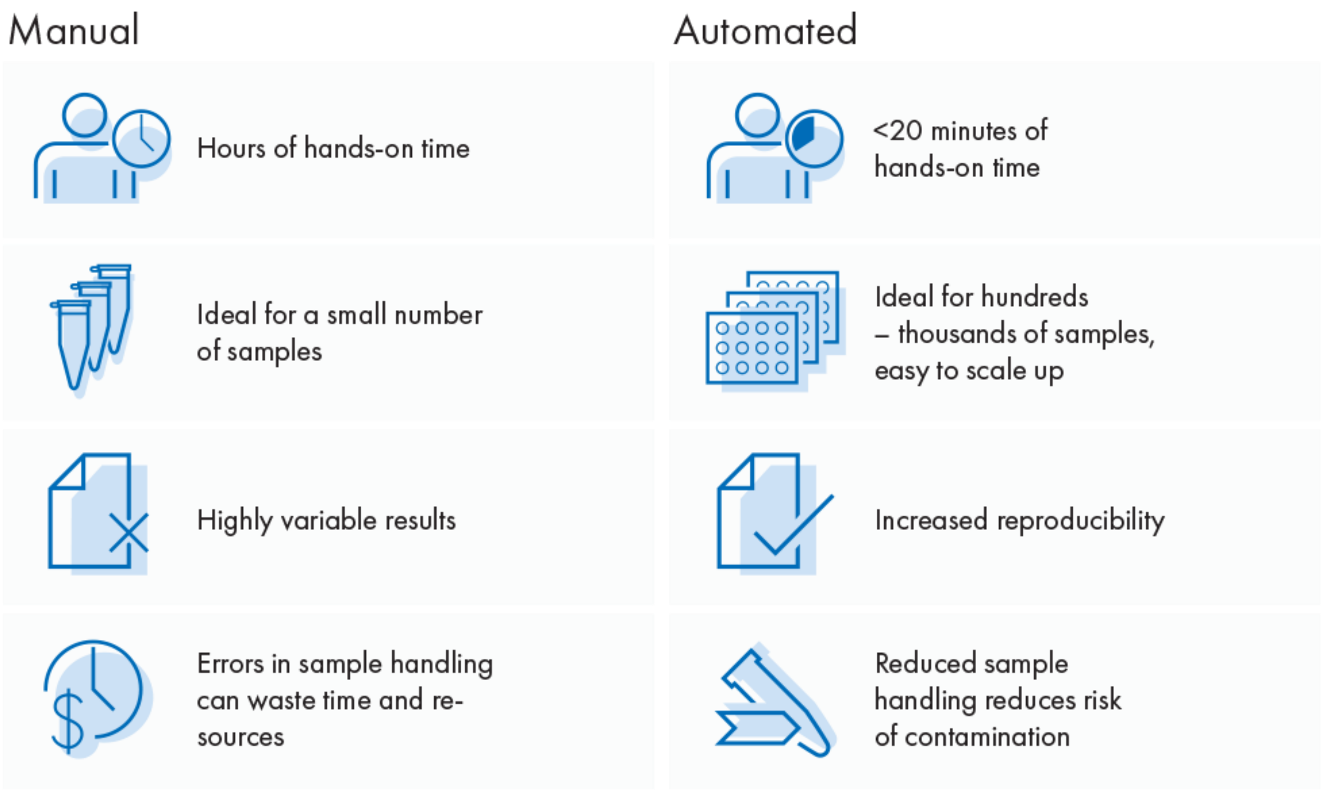


Post-capture amplification QC



Libraries can be prepared for sequencing on the PacBio platform after QC for yield and size distribution.

Scale: Growing with Automation

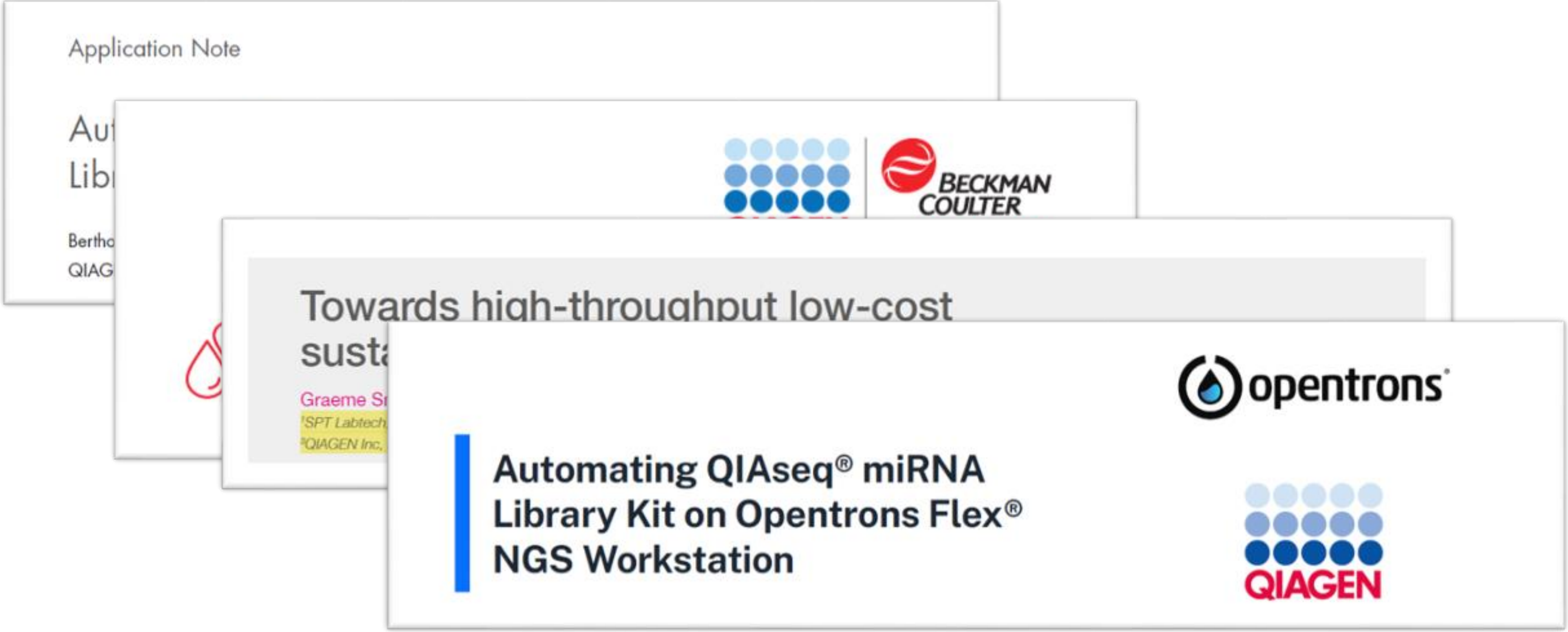


Manual	Automated
Hours of hands-on time	<20 minutes of hands-on time
Ideal for a small number of samples	Ideal for hundreds – thousands of samples, easy to scale up
Highly variable results	Increased reproducibility
Errors in sample handling can waste time and re-sources	Reduced sample handling reduces risk of contamination

Why Freeing Up Staff Matters

- Reduces time spent on repetitive manual tasks
- Allows staff to focus on consulting and innovation
- Improves job satisfaction and retention
- Increases the scientific impact of the core

QIAGEN invests in workflow automation



Application Note

Au

Lib

Bertho

QIAG

BECKMAN COULTER

Towards high-throughput low-cost

susta

Graeme S

¹SPT Labtech

²QIAGEN Inc,

opentrons

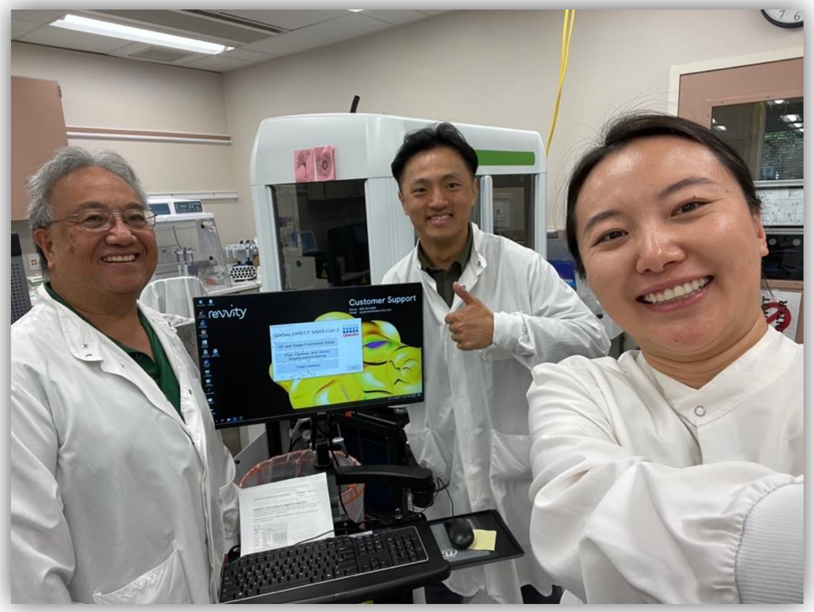
Automating QIAseq® miRNA Library Kit on Opentrons Flex® NGS Workstation

QIAGEN

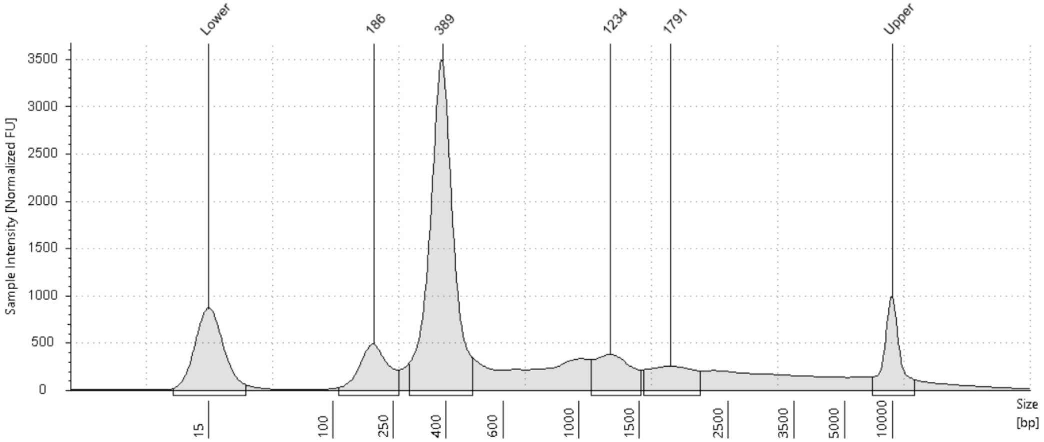
[NGS library prep automation | NGS automation - QIAGEN]

Wastewater SARS-CoV-2 sequencing @ WA Department of Health

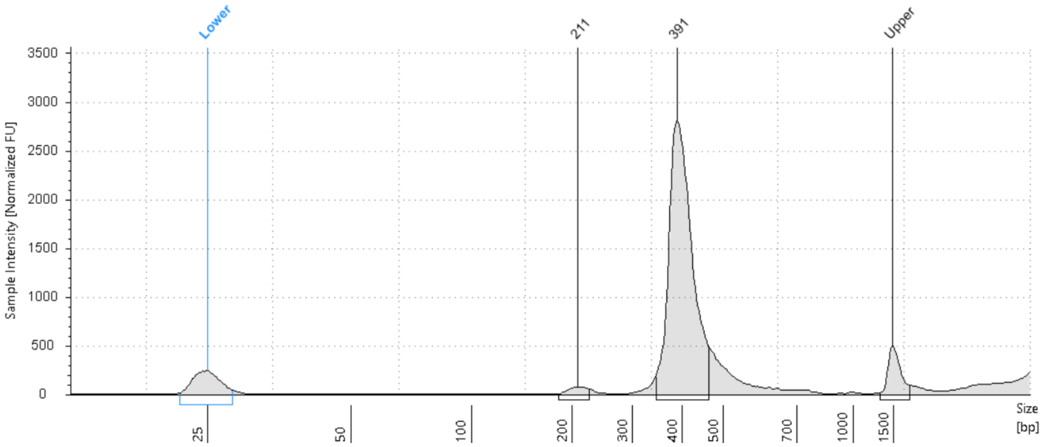
- Limited staff resources and a long (changing) list of projects
- Automation would provide consistency in not only data quality, but also the availability of an assay.
- QIAGNE has invested in script development with Revvity.
- FAS to support onsite script installation.



Manual pipetting

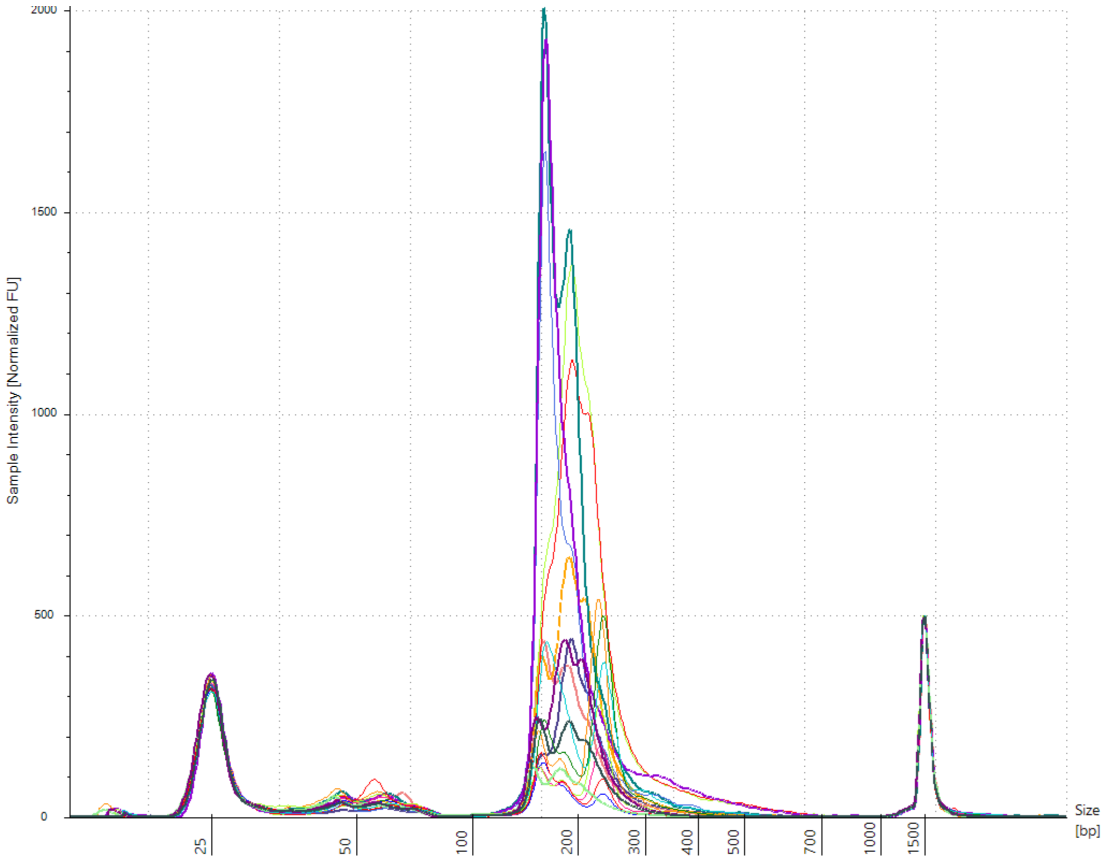


Automation

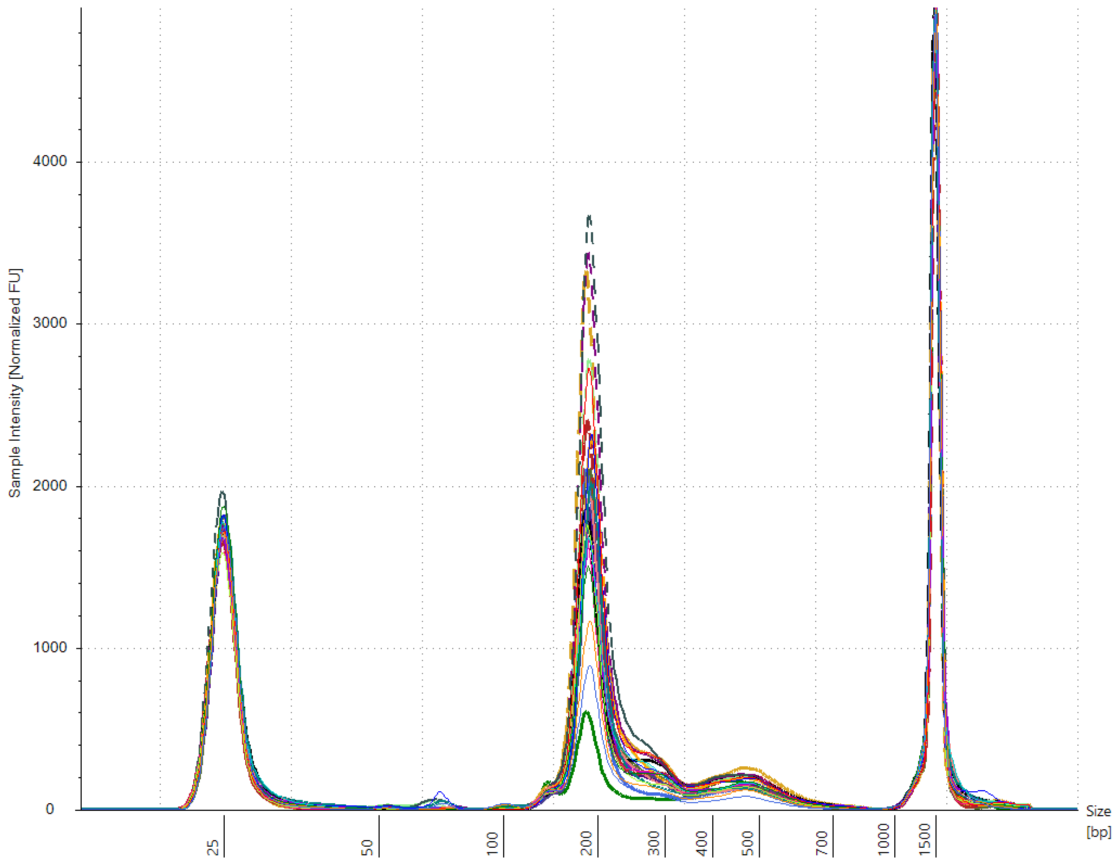


miRNA sequencing @Harvard Medical School BPF Genomics Core

QIAseq miRNA libraries generated manually



QIAseq miRNA libraries generated on Firefly



Biopolymers Facility

Extend: Comprehensive multi-omics services portfolio with Genomic Services

	Transcriptomics	Genomics	Microbiomics
	Nucleic acid isolation service		
NGS	**miRNA** • miRNA-seq **mRNA** • 3′mRNA-seq • mRNA-seq **Immune repertoire profiling** **Whole transcriptome** • Whole transcriptome-seq **Targeted RNA** • Targeted 3′mRNA • Targeted RNA-seq panels • Fusion gene detection	**Whole genome sequencing** • Human whole genome-seq • Animal, plant whole genome-seq **Targeted DNA** • Multimodal cancer genomics profiling • Targeted DNA sequencing	**Microbial profiling** • Microbiome analysis 16S/ITS • Metagenomic sequencing **Viral genotyping** • SARS-CoV-2 whole genome sequencing
PCR	**miRNA** • miRNA-qPCR **mRNA** • mRNA-qPCR **lncRNA** • lncRNA qPCR	**Digital PCR services** • Custom assay designs • CNV, mutation assays **Whole genome amplification**	

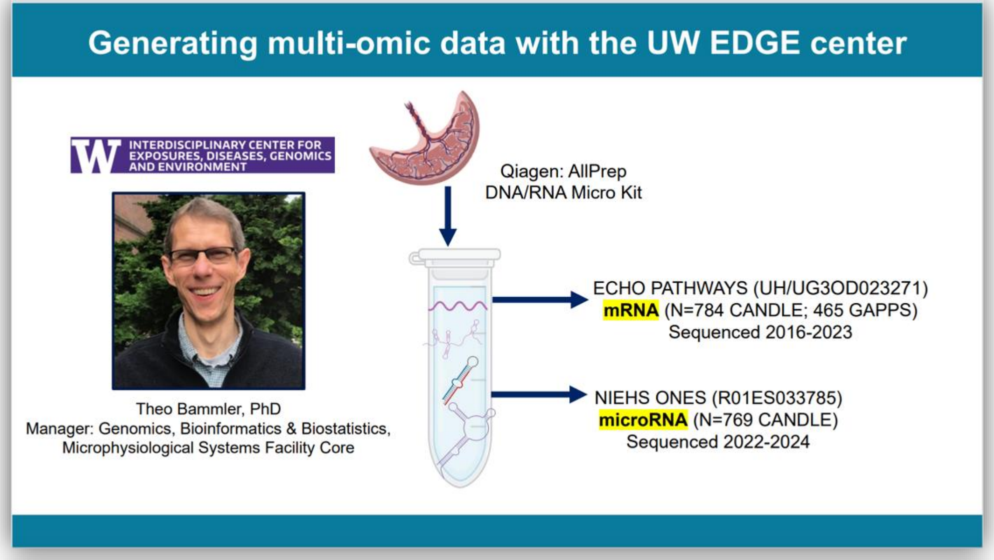
miRNA Analysis @University of Washington

- Theo is a core manager @ UW Center for Exposures, Diseases, Genomics, and Environment (EDGE)
- Alison is an EHS Core Investigator EDGE

NIH NIEHS
UW EDGE CENTER
P30ES007033

NIH NIEHS
ONES R01
R01ES033785 (AGP)

- Transcriptomic analysis on placenta sample (mRNA + miRNA)



Generating multi-omic data with the UW EDGE center

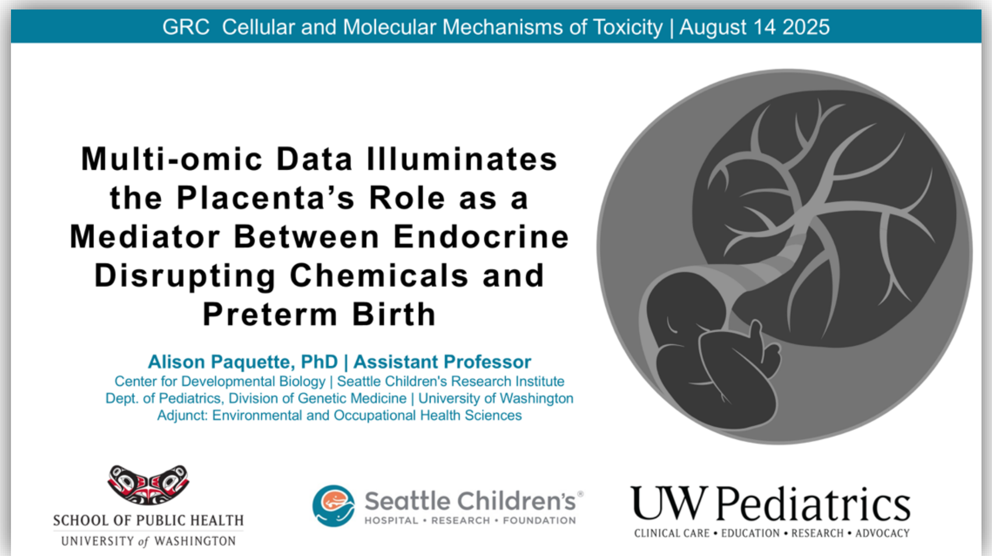
INTERDISCIPLINARY CENTER FOR EXPOSURES, DISEASES, GENOMICS AND ENVIRONMENT

Theo Bammler, PhD
Manager: Genomics, Bioinformatics & Biostatistics, Microphysiological Systems Facility Core

Qiagen: AllPrep DNA/RNA Micro Kit

ECHO PATHWAYS (UH/UG3OD023271)
mRNA (N=784 CANDLE; 465 GAPPS)
Sequenced 2016-2023

NIEHS ONES (R01ES033785)
microRNA (N=769 CANDLE)
Sequenced 2022-2024



GRC Cellular and Molecular Mechanisms of Toxicity | August 14 2025

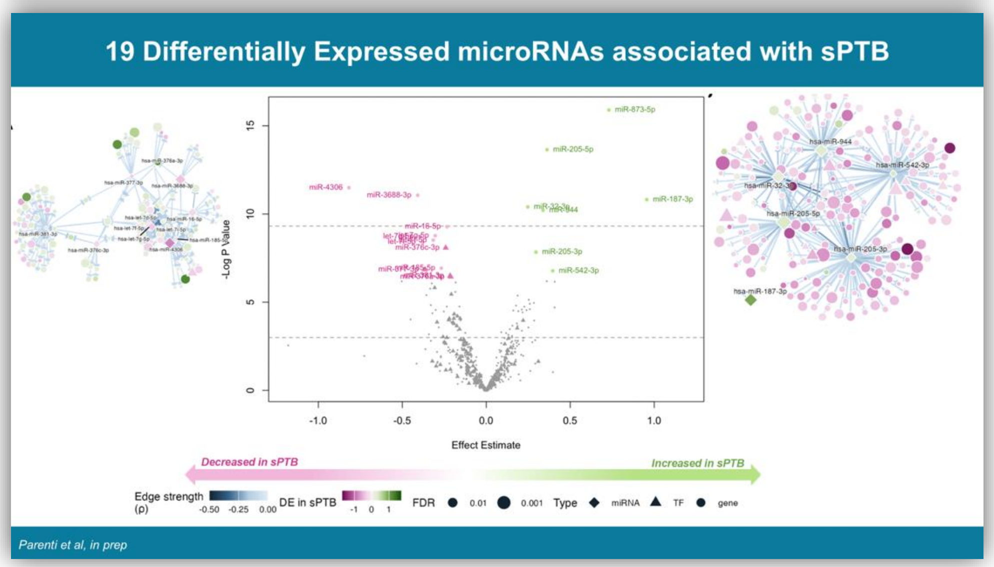
Multi-omic Data Illuminates the Placenta's Role as a Mediator Between Endocrine Disrupting Chemicals and Preterm Birth

Alison Paquette, PhD | Assistant Professor
Center for Developmental Biology | Seattle Children's Research Institute
Dept. of Pediatrics, Division of Genetic Medicine | University of Washington
Adjunct: Environmental and Occupational Health Sciences

SCHOOL OF PUBLIC HEALTH
UNIVERSITY of WASHINGTON

Seattle Children's®
HOSPITAL • RESEARCH • FOUNDATION

UW Pediatrics
CLINICAL CARE • EDUCATION • RESEARCH • ADVOCACY

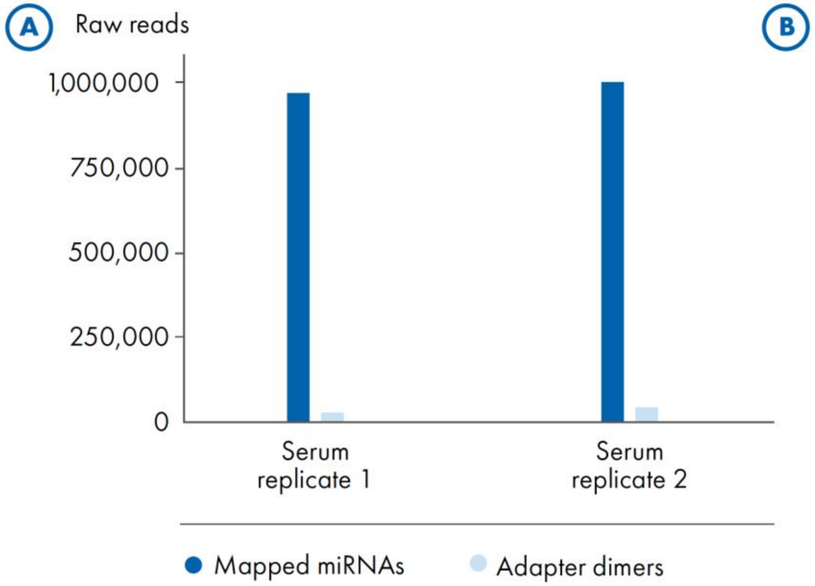


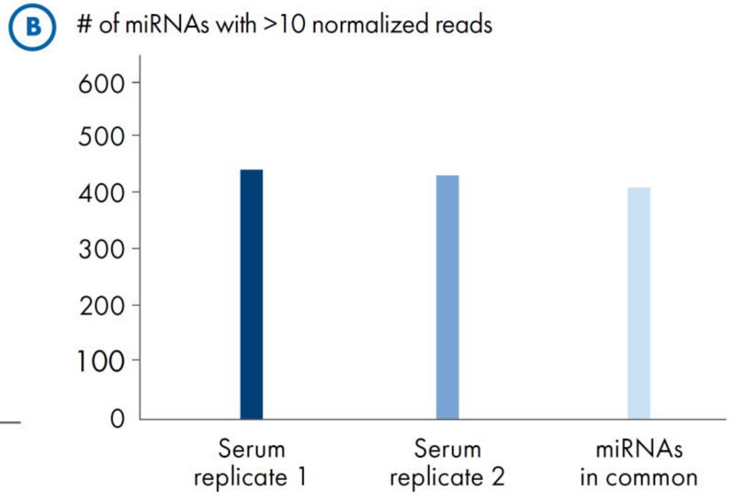
19 Differentially Expressed microRNAs associated with sPTB

Parenti et al, in prep

[Genomics, Bioinformatics & Biostatistics, Microphysiological Systems Facility Core | Interdisciplinary Center for Exposures, Diseases, Genomics and Environment]

QIAseq miRNA Library Kits are trusted for biomarker research





(A) Read distribution in serum samples. This figure shows mapped reads compared to adapter dimers in serum samples. The QIAseq miRNA Library Kit still shows superior mapping of miRNAs, even with limited samples.

(B) Robust detection of miRNA. The QIAseq miRNA Library Kit has been designed to enhance yields from biofluids such as serum. This figure shows robust detection of miRNA from serum samples.

Ultimate accuracy
Unique molecular indices (UMIs) increase accurate quantification of individual miRNA molecules

Low-input requirements
Works with just 1 ng RNA extracted from serum, plasma, cerebrospinal fluid, saliva, urine and more

High-throughput capability
Includes 768 unique dual indices (UDIs) for miRNA-seq on Illumina® NovaSeq® platforms without the risk of index hopping

Expanding list of citations
With >700 publications* and >7000 citations*, QIAseq miRNA Library Kits are trusted by a growing list of researchers

Cost-effective workflow
Fast, gel-free miRNA library prep workflow increases sample throughput, enables automation and decreases sample costs

Comprehensive data analysis
Includes access to the RNA-seq Analysis Portal for straightforward miRNA-seq alignment, differential expression and pathway information

QIAseqmiRNA Interactive Product Profile

Extend: Promotion & Training to Expand Core Users

- Rebecca is the manager of @Genomics & Spatial Biology CoLab-Seattle Children's Research Institute
- Users' requests for NGS library preparation training were rejected due to limited human resources.

- Evaluation promotion + onsite training with FAS
- Access to timely and specific support for core users
- Shorten idle time for the sequencers in CoLab

- Increase awareness of the CoLab
- Build a community of genomic researchers.

Genomics & Spatial Biology CoLab Seattle Children's Research Institute

Seattle Children's

QIAGEN

Seattle Children's Genomics and Spatial Biology CoLab & QIAseq NGS Library Prep

Available Now!

Get In-lab, hands-on training with YOUR QIAseq NGS Library generation. Run on the NextSeq in the Seattle Children's GSB Core now.

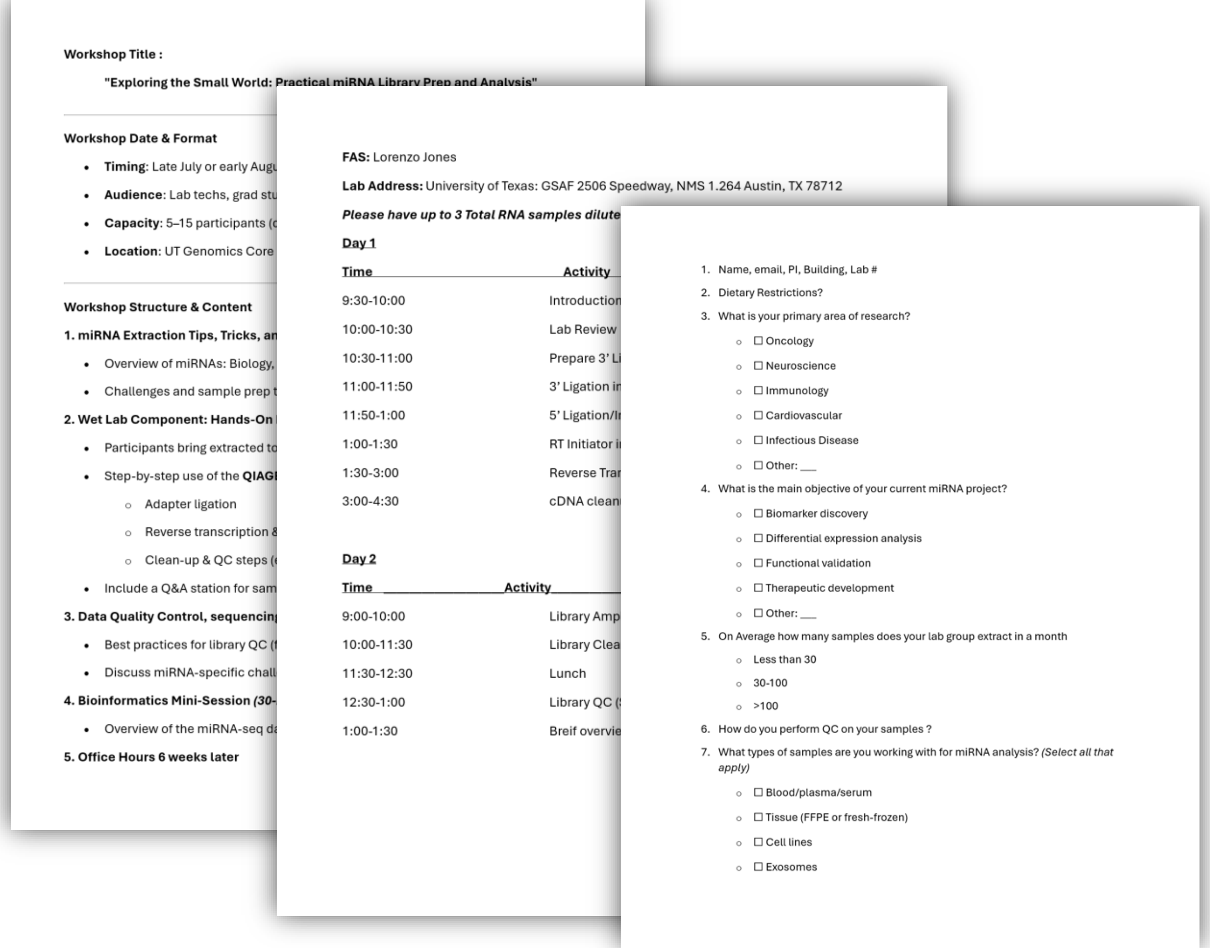
The scientific training you want, library prep kit materials and sequencer availability is yours now. Why wait?

rebecca.martin@seattlechildrens.org

elizabeth.conzevoy@qiagen.com

Extend: User Workshop

- University of Texas Genomic Sequencing and Analysis Facility



Workshop Title :

"Exploring the Small World: Practical miRNA Library Prep and Analysis"

Workshop Date & Format

- **Timing**: Late July or early Augu
- **Audience**: Lab techs, grad stu
- **Capacity**: 5–15 participants (c
- **Location**: UT Genomics Core

Workshop Structure & Content

1. miRNA Extraction Tips, Tricks, an

- Overview of miRNAs: Biology,
- Challenges and sample prep t

2. Wet Lab Component: Hands-On

- Participants bring extracted to
- Step-by-step use of the **QIAGI**
    - Adapter ligation
    - Reverse transcription &
    - Clean-up & QC steps (
- Include a Q&A station for sam

3. Data Quality Control, sequencin

- Best practices for library QC (
- Discuss miRNA-specific chall

4. Bioinformatics Mini-Session *(30-*

- Overview of the miRNA-seq da

5. Office Hours 6 weeks later

FAS: Lorenzo Jones

Lab Address: University of Texas: GSAF 2506 Speedway, NMS 1.264 Austin, TX 78712

Please have up to 3 Total RNA samples dilute

Day 1

Time	Activity
9:30-10:00	Introduction
10:00-10:30	Lab Review
10:30-11:00	Prepare 3' Li
11:00-11:50	3' Ligation in
11:50-1:00	5' Ligation/Ir
1:00-1:30	RT Initiator i
1:30-3:00	Reverse Trar
3:00-4:30	cDNA clean

Day 2

Time	Activity
9:00-10:00	Library Amp
10:00-11:30	Library Clea
11:30-12:30	Lunch
12:30-1:00	Library QC (
1:00-1:30	Breif overvie

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1. Name, email, PI, Building, Lab #
2. Dietary Restrictions?
3. What is your primary area of research?
    - ☐ Oncology
    - ☐ Neuroscience
    - ☐ Immunology
    - ☐ Cardiovascular
    - ☐ Infectious Disease
    - ☐ Other: __
4. What is the main objective of your current miRNA project?
    - ☐ Biomarker discovery
    - ☐ Differential expression analysis
    - ☐ Functional validation
    - ☐ Therapeutic development
    - ☐ Other: __
5. On Average how many samples does your lab group extract in a month
    - Less than 30
    - 30-100
    - >100
6. How do you perform QC on your samples ?
7. What types of samples are you working with for miRNA analysis? *(Select all that apply)*
    - ☐ Blood/plasma/serum
    - ☐ Tissue (FFPE or fresh-frozen)
    - ☐ Cell lines
    - ☐ Exosomes

You're invited to

***Space is limited - only the first 6 applicants will be accepted

Exploring the Small World: Practical miRNA Library Prep and Analysis Workshop

Topic(s):	• Overview of miRNAs: Biology, function, and relevance in disease • Successful Extraction • Applications of miRNA-seq in research • Wet Lab Component: Hands-On Library • Step-by-step use of the QIAGEN miRNA Library Prep Kit • Data Quality Control & Sequencing Planning
Speaker(s):	Lorenzo Jones, M.S. QIAGEN, Senior Field Application Specialist, Genomics All participants will receive a virtual invite to miRNA Extraction Tips and Tricks on 8/29; presented by: Anna Babushkina, Ph.D, QIAGEN, Senior Field Application Specialist,
When:	Tuesday September 16th - Wednesday September 17th
Where:	TBD (MBB or NMS), location and virtual zoom invitation to follow
Registration:	Scan QR code above or register here: https://forms.office.com/e/FCTAKPNj8U
Get in touch:	Please reach out to Lucy Eiler (lucy.eiler@qiagen.com) with any questions or extraction kit support.

Sample to Insight

QIAGEN can support you

01

Start

Core helps cores launch new NGS services with reliable, ready-to-run workflows.

02

Refine

We partners with cores to design custom panels and targeted solutions to strengthen core expertise.

03

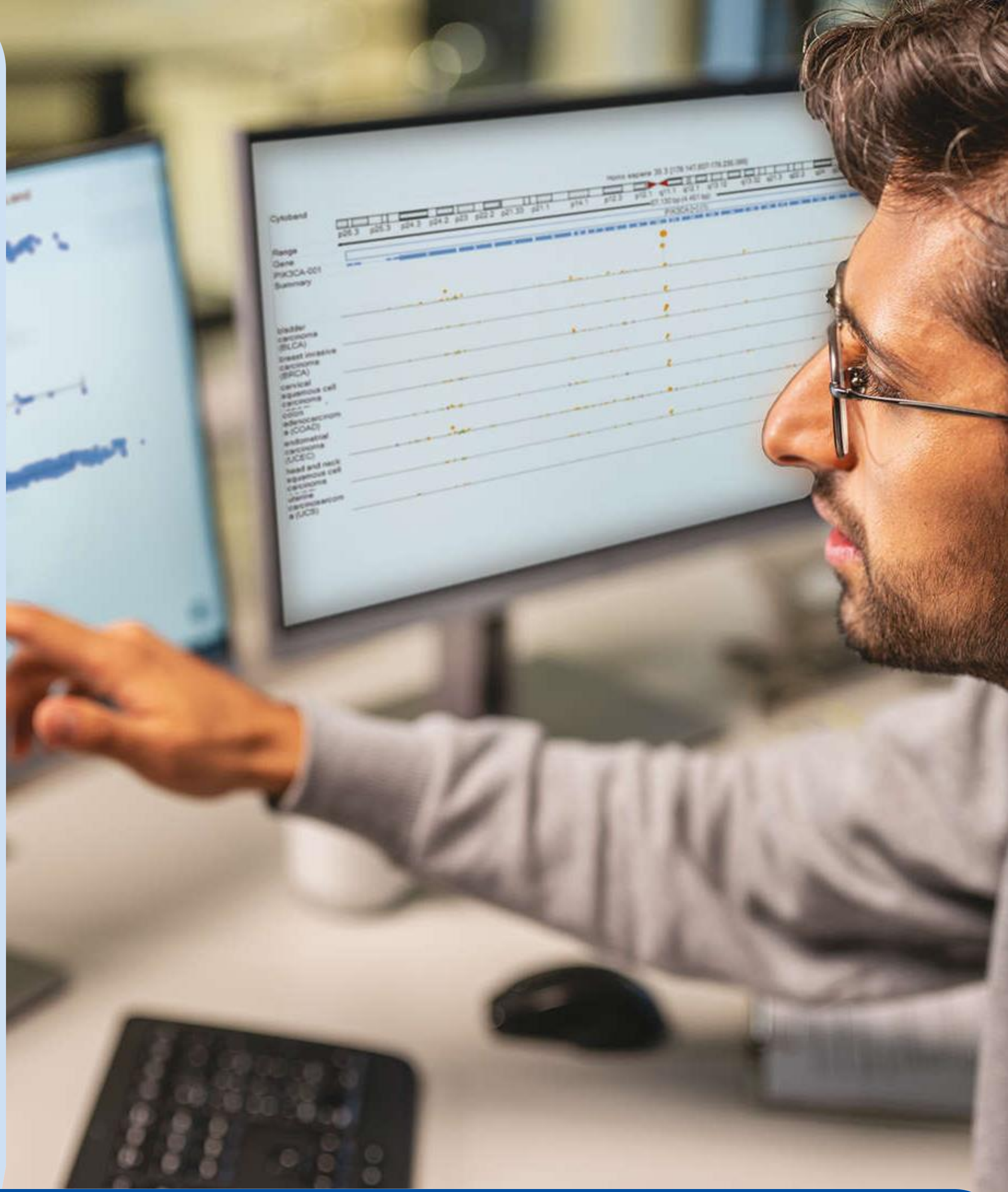
Scale

We supports growth through automation effort that frees up staff and increases efficiency

04

Extend

We empower cores to expand their reach through advanced services and community engagement.



Thank you for your attention. Questions?

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