

Discover

- Whole genome and transcriptome
- Solutions for cell-free and ultra-low samples



Target

- Epigenomics, exome and actionable variants
- Disease and custom targeted panels



Verify

- Digital PCR and custom assays
- Digital insights for data and pathway analysis

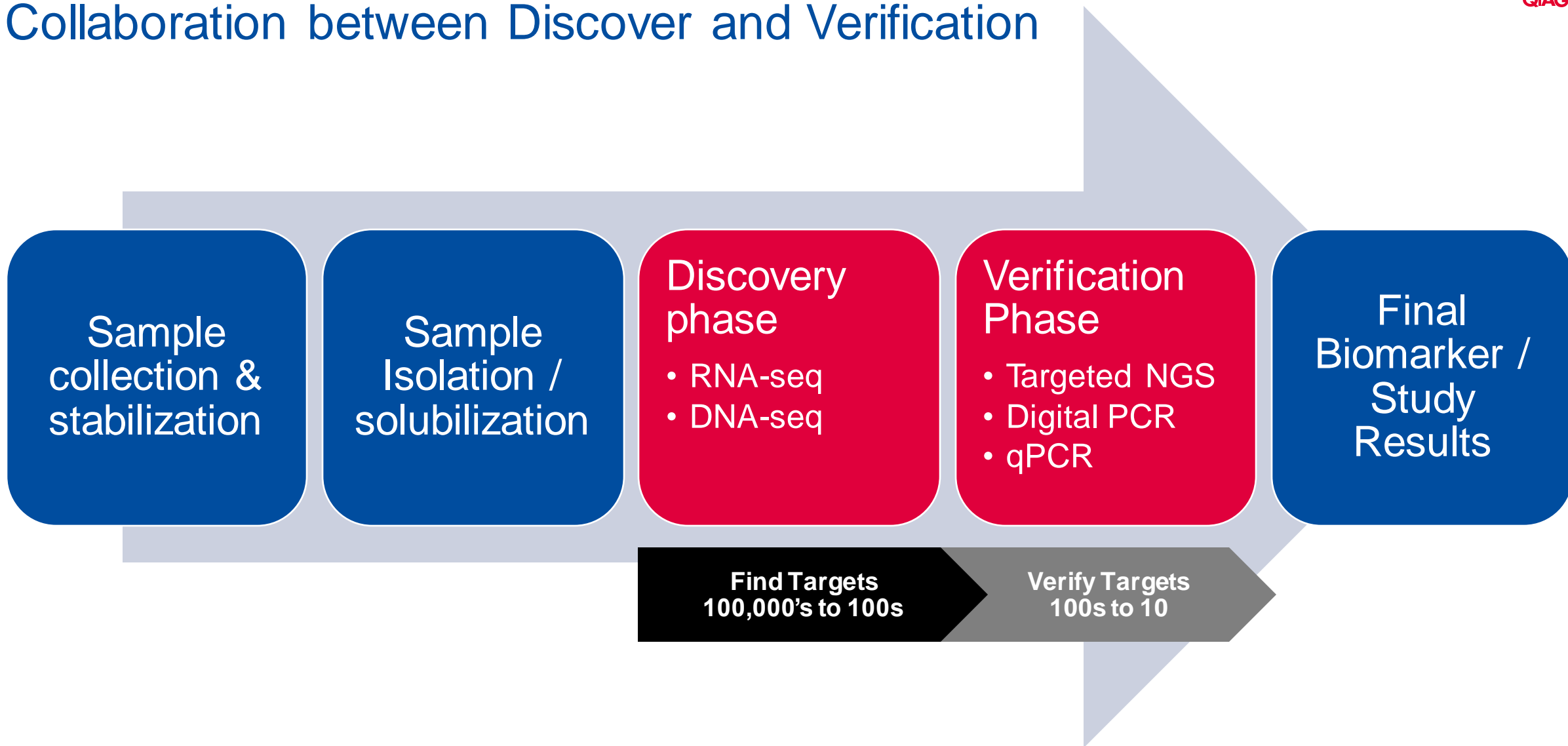


Simplify your NGS Workflows with QIAseq Lightspeed Collaboration

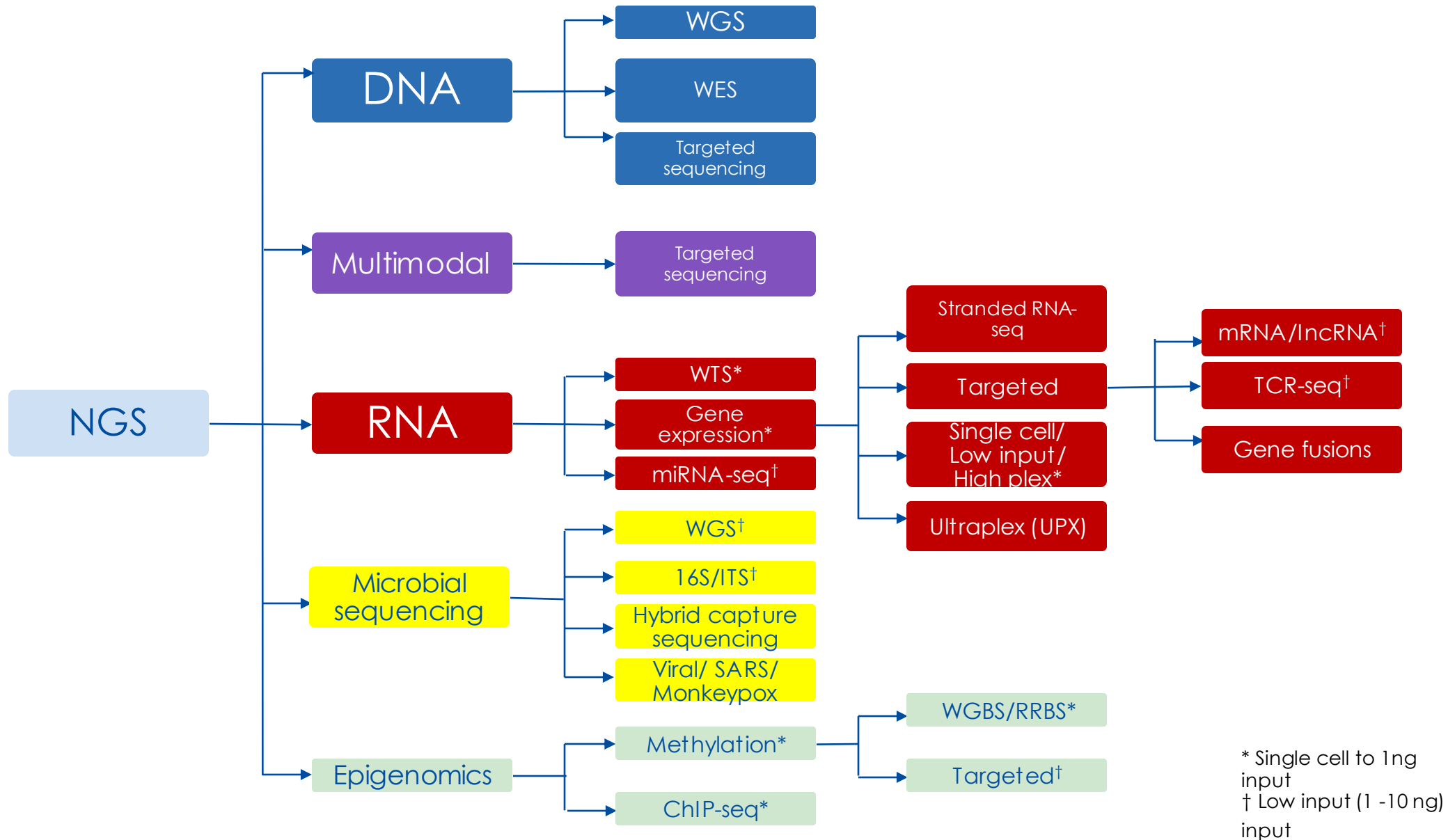
Samuel Rulli – Director Global Product Management NGS applications

October 2023

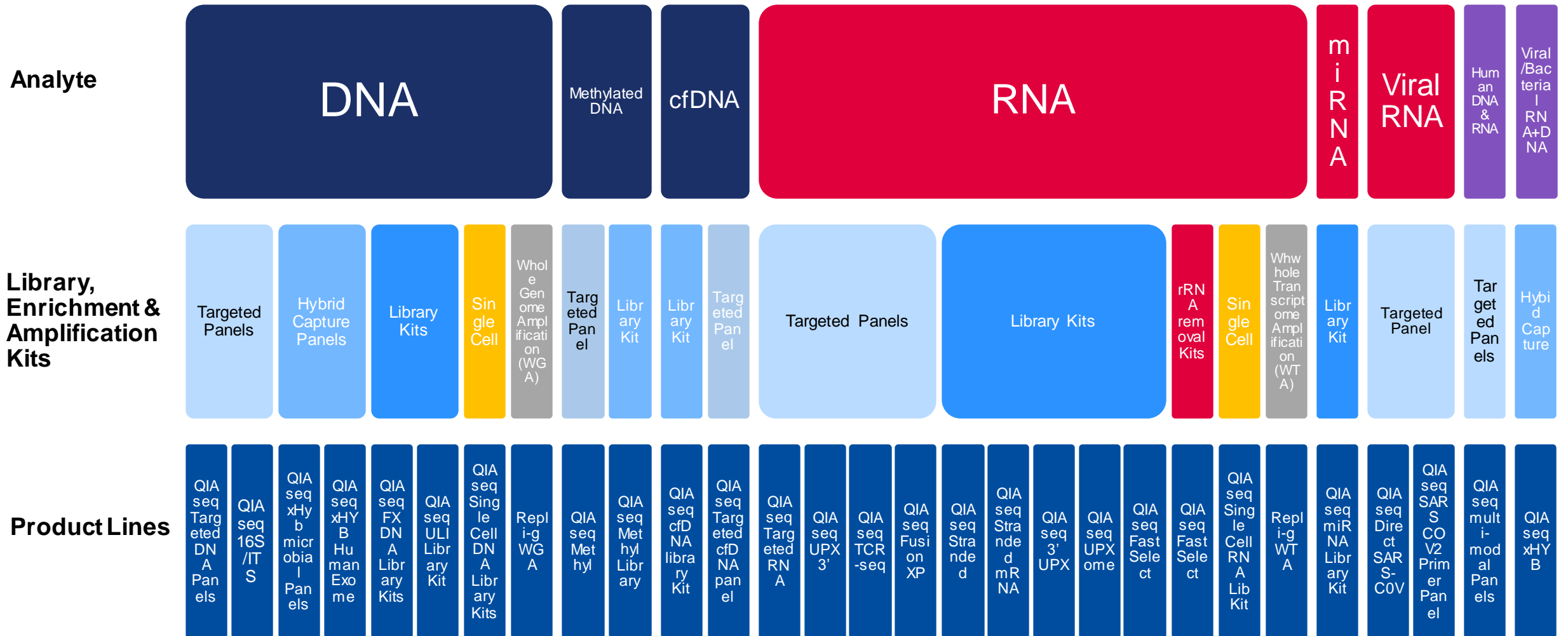
Typical Research Workflow- Collaboration between Discover and Verification



Introduction to the QIAseq portfolio



QIAseq portfolio by Analyte





How can we speed up and simplify RNA-seq workflows?

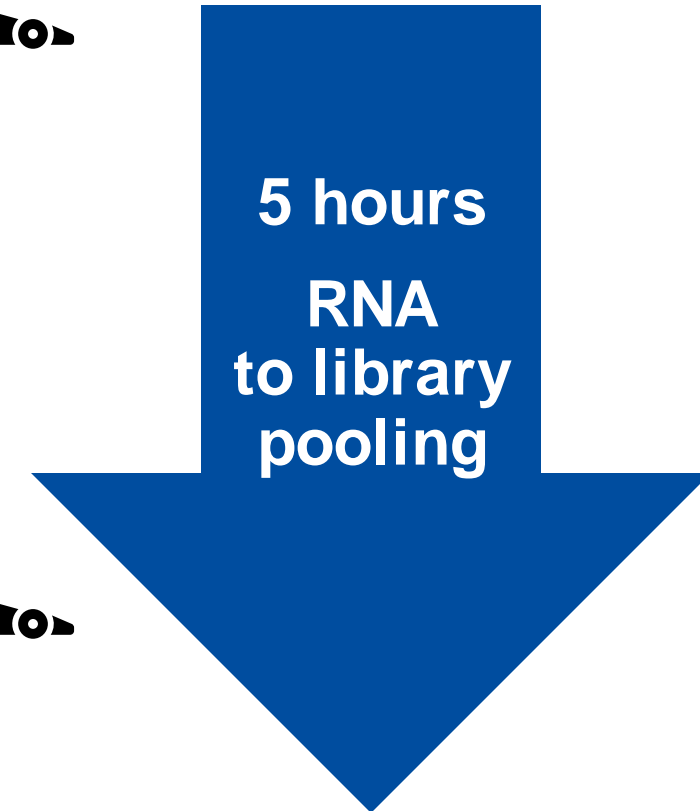


Speed up and Simplify your RNA-seq Workflows

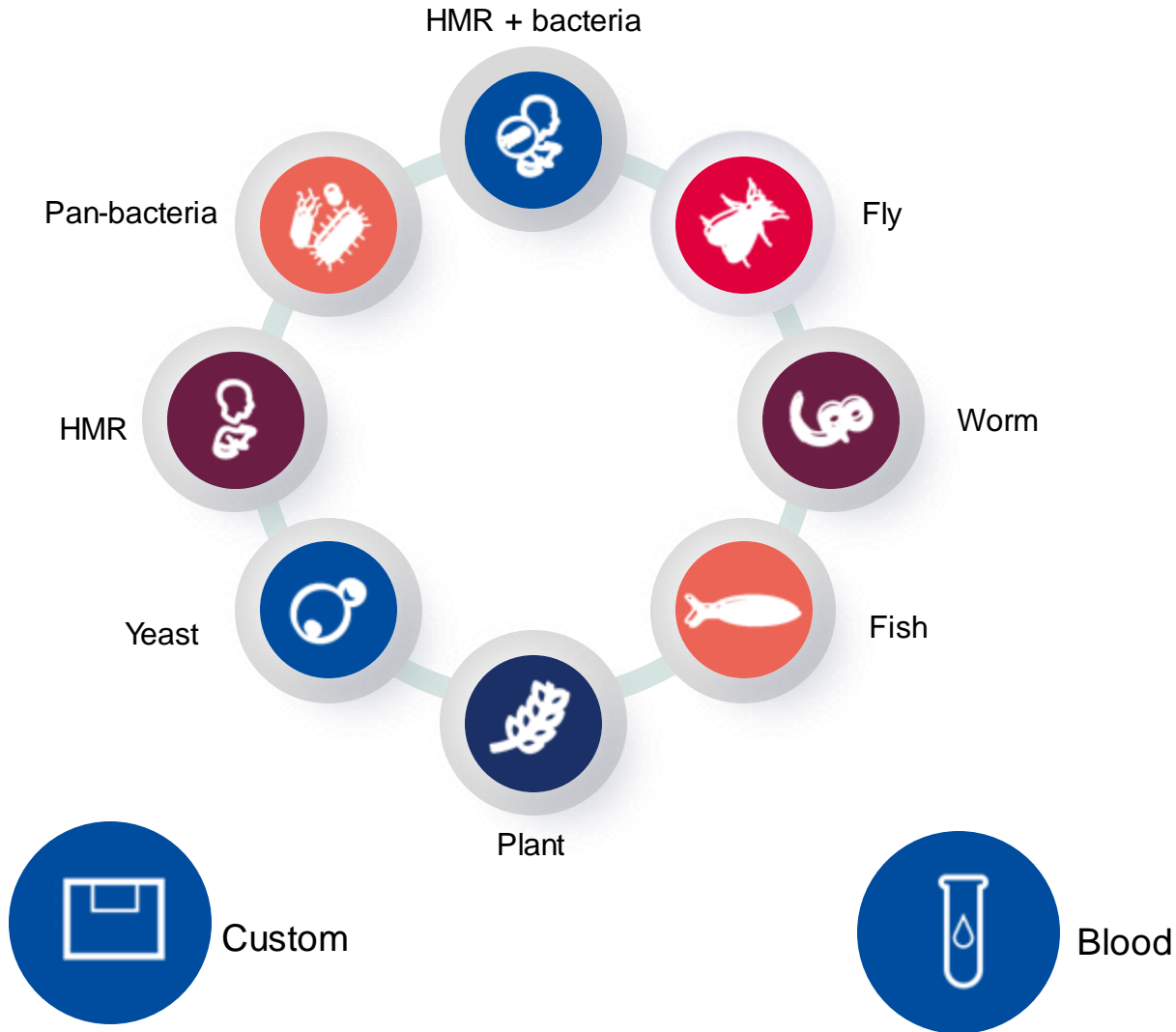
QIAseq FastSelect RNA library kit and QIAseq Normalizer



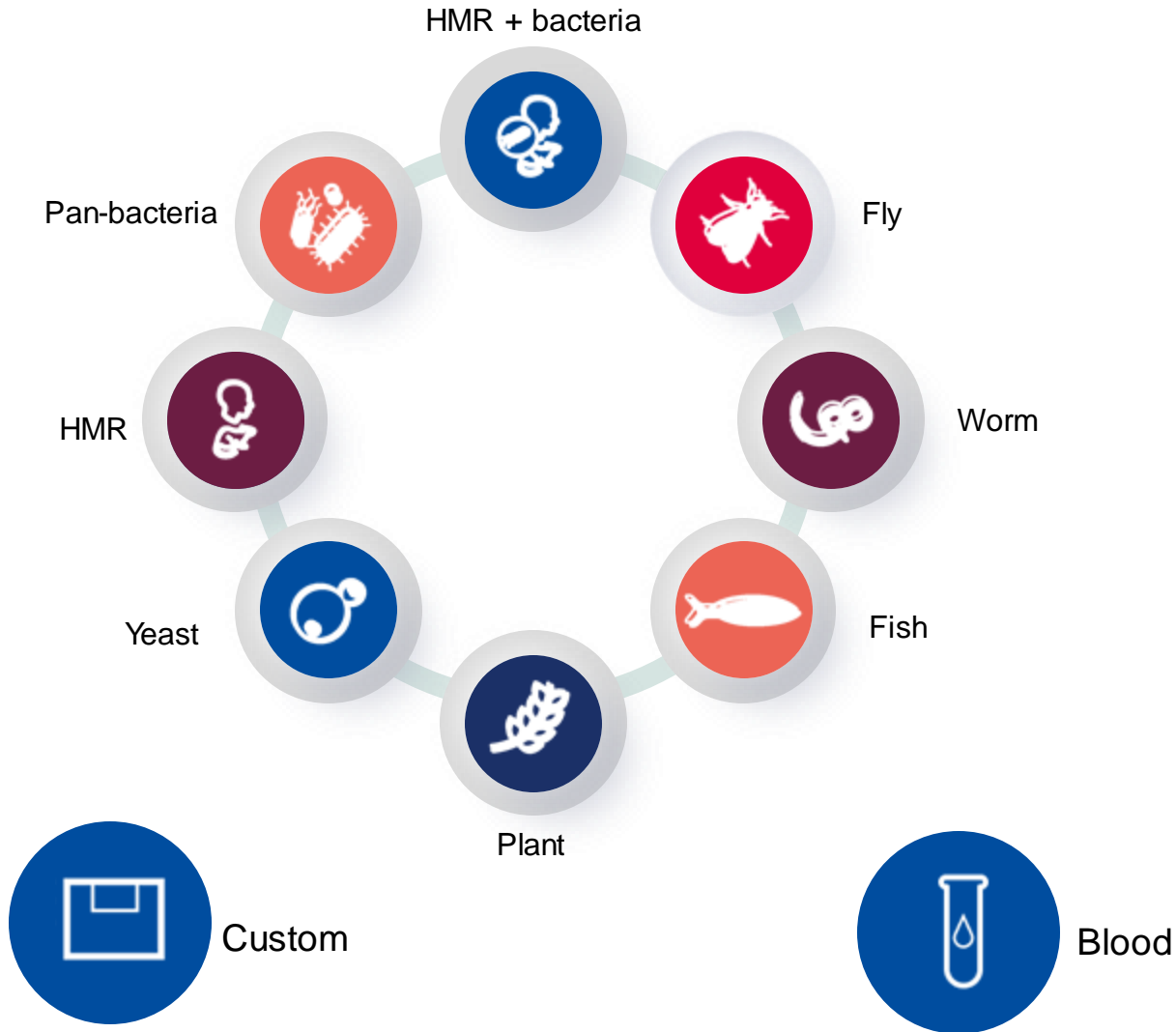
Step	QIAseq FastSelect RNA Library Kit Workflow Time
rRNA Removal + RNA fragmentation	16 minutes 
cDNA synthesis	90 minutes
QIAseq bead cleanup	45 minutes
Universal amplification and index assignment:	1000 ng input: 17 cycles – 36 minutes 100ng input: 20 cycles – 42 minutes 10 ng input: 24 cycles – 50 minutes 1 ng input: 27 cycles – 60 minutes
QIAseq bead cleanup	45 minutes
Library Normalization with QIAseq Normalizer	30 minutes – 45 minutes 
Sequence Ready libraries @ 4nM concentration	



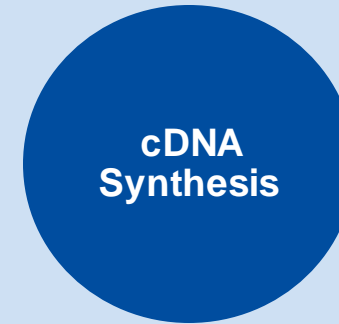
QIAseq FastSelect supports model organisms and more



QIAseq FastSelect supports model organisms and more



Heat samples then cool sample



QIAseq FastSelect removed rRNA from FFPE samples



Experimental Setup

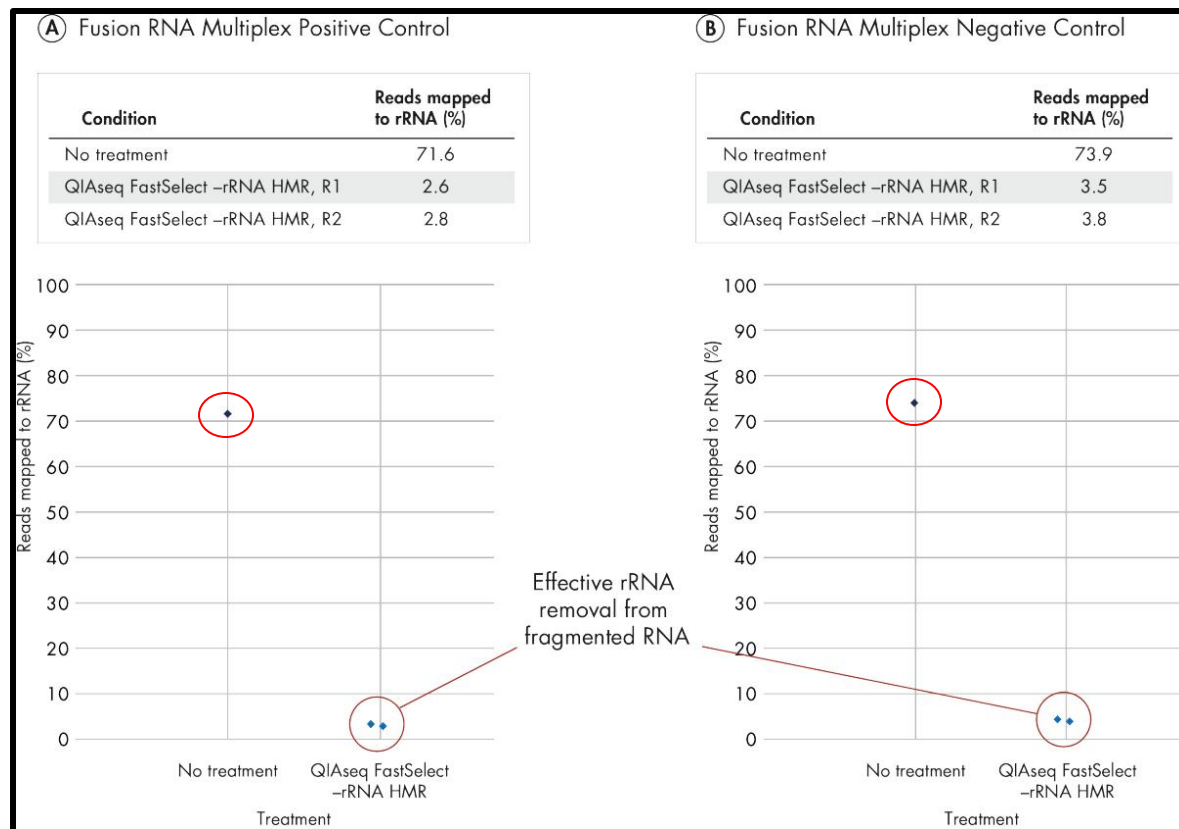
Sample: Horizon FFPE RNA reference standards

A FFPE Horizon 5-Fusion Multiplex Positive

B FFPE Horizon 5-Fusion Multiplex Negative Control

Amount of RNA used for library construction is dependent on the RNA library kit

Results: 95% of ribosomal RNA is removed



FastSelect has been used for what?





- Oxford nanopore sequencing



Protocol

Application of Oxford Nanopore Technology to Plant Virus Detection

Lia W. Liefting *, David W. Waite  and Jeremy R. Thompson * 

Plant Health and Environment Laboratory, Ministry for Primary Industries, P.O. Box 2095, Auckland 1140, New Zealand; David.Waite@mpi.govt.nz

* Correspondence: Lia.Liefting@mpi.govt.nz (L.W.L.); Jeremy.Thompson@mpi.govt.nz (J.R.T.)

Abstract: The adoption of Oxford Nanopore Technologies (ONT) sequencing as a tool in plant virology has been relatively slow despite its promise in more recent years to yield large quantities of long nucleotide sequences in real time without the need for prior amplification. The portability of the MinION and Flongle platforms combined with lowering costs and continued improvements in read accuracy make ONT an attractive method for both low- and high-scale virus diagnostics. Here, we provide a detailed step-by-step protocol using the ONT Flongle platform that we have developed for the routine application on a range of symptomatic post-entry quarantine and domestic surveillance plant samples. The aim of this methods paper is to highlight ONT's feasibility as a valuable component to the diagnostician's toolkit and to hopefully stimulate other laboratories towards the eventual goal of integrating high-throughput sequencing technologies as validated plant virus diagnostic methods in their own right.

FastSelect has been used for what?





- Oxford nanopore sequencing
- Illumina sequencing with KAPA NEB, Illumina, Takara, Thermo-Fisher library Kits
- Removal of hemolytic miRNAs
- Removal of unwanted RNAs for hybrid capture workflows
- High quality RNA to FFPE RNA
- Single cell to bulk sequencing




Speed up and Simplify your RNA-seq Workflows

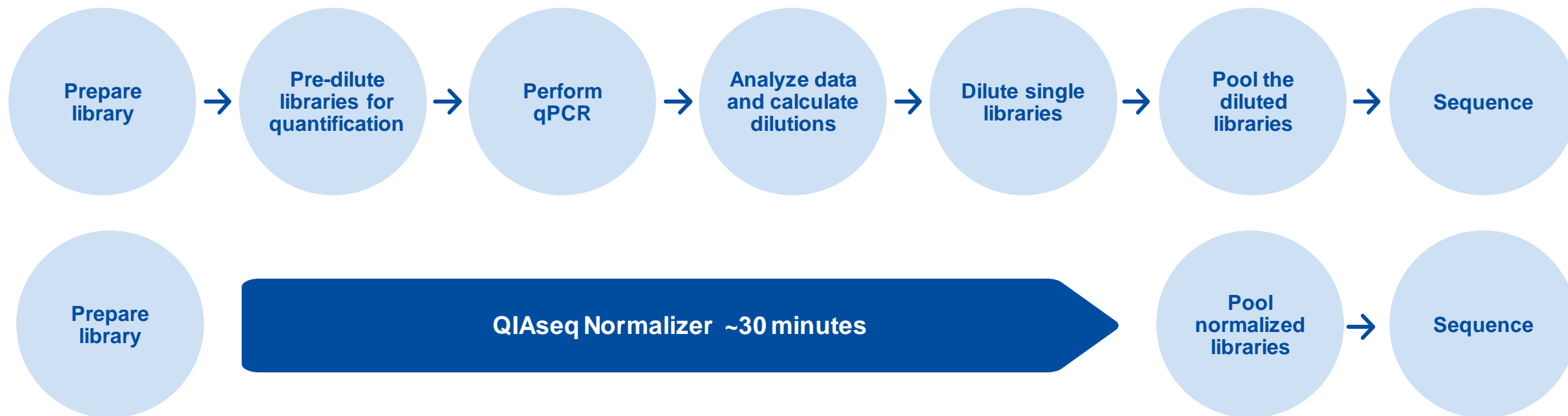
QIAseq FastSelect RNA library kit and QIAseq Normalizer

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QIAseq bead cleanup	45 minutes
Library Normalization with QIAseq Normalizer	30 minutes – 45 minutes 
Sequence Ready libraries @ 4nM concentration	

**5 hours
RNA
to library
pooling**

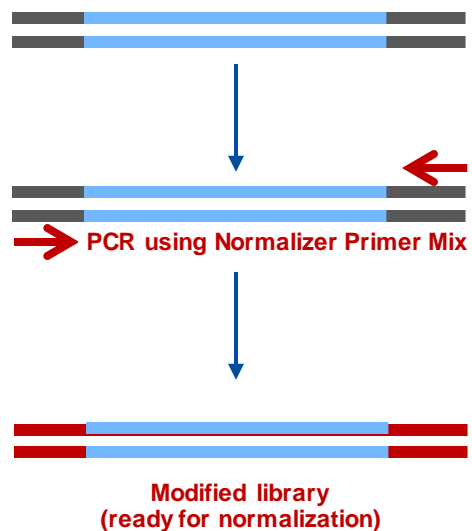


QIAseq Normalizer Kits: A streamlined method to create ready-to-sequence normalized dsDNA libraries



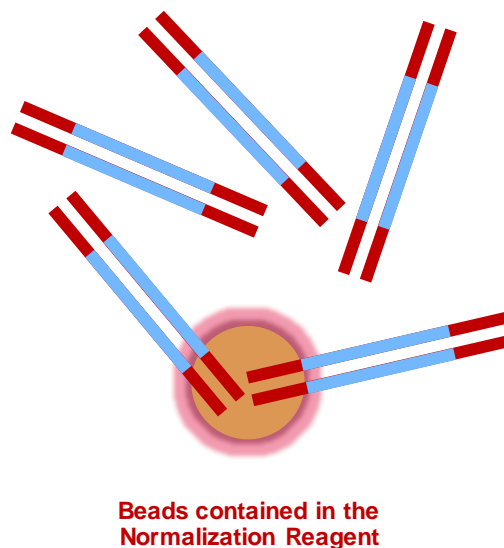
QIAseq Normalizer: Bind, wash, elute

Modify the libraries to be normalized



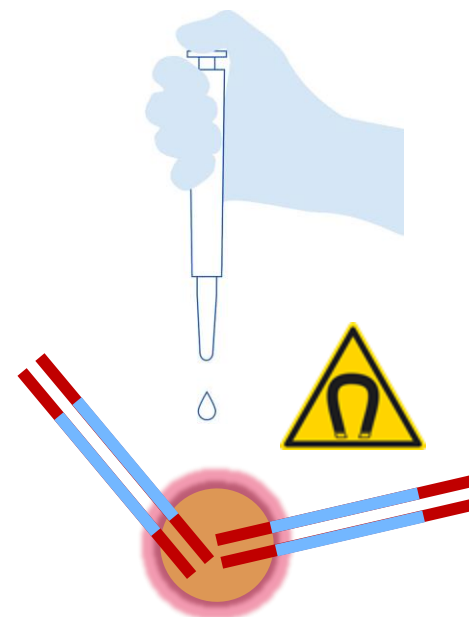
Modification is always required for normalization:

Bind modified libraries to beads

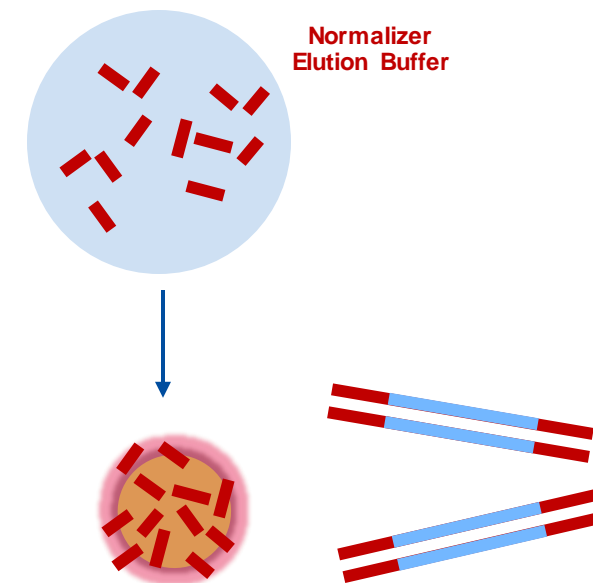


Limited bead capacity

Wash away unbound library molecules



Elute the normalized libraries (~4 nmoI/l)

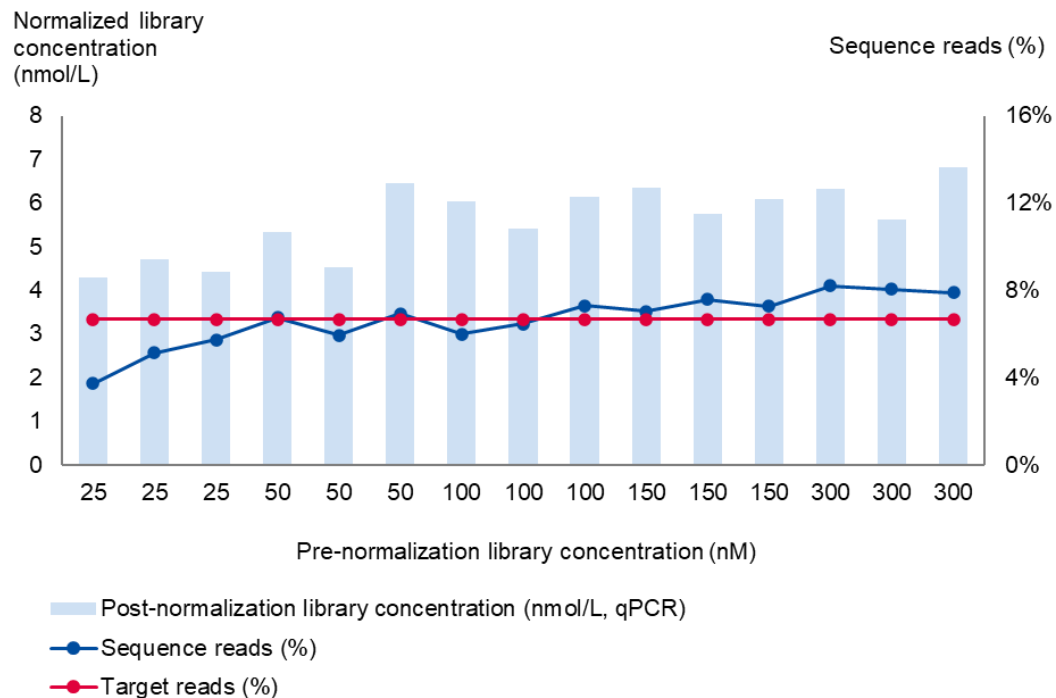


Eluted libraries are dsDNA

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



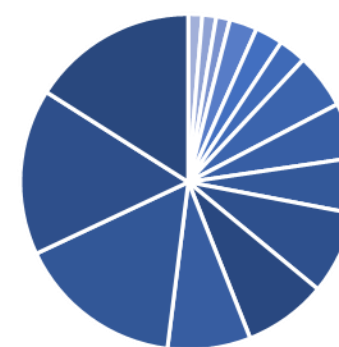
Normalization of QIAseq FX DNA libraries



Library representation

Before normalization

After normalization



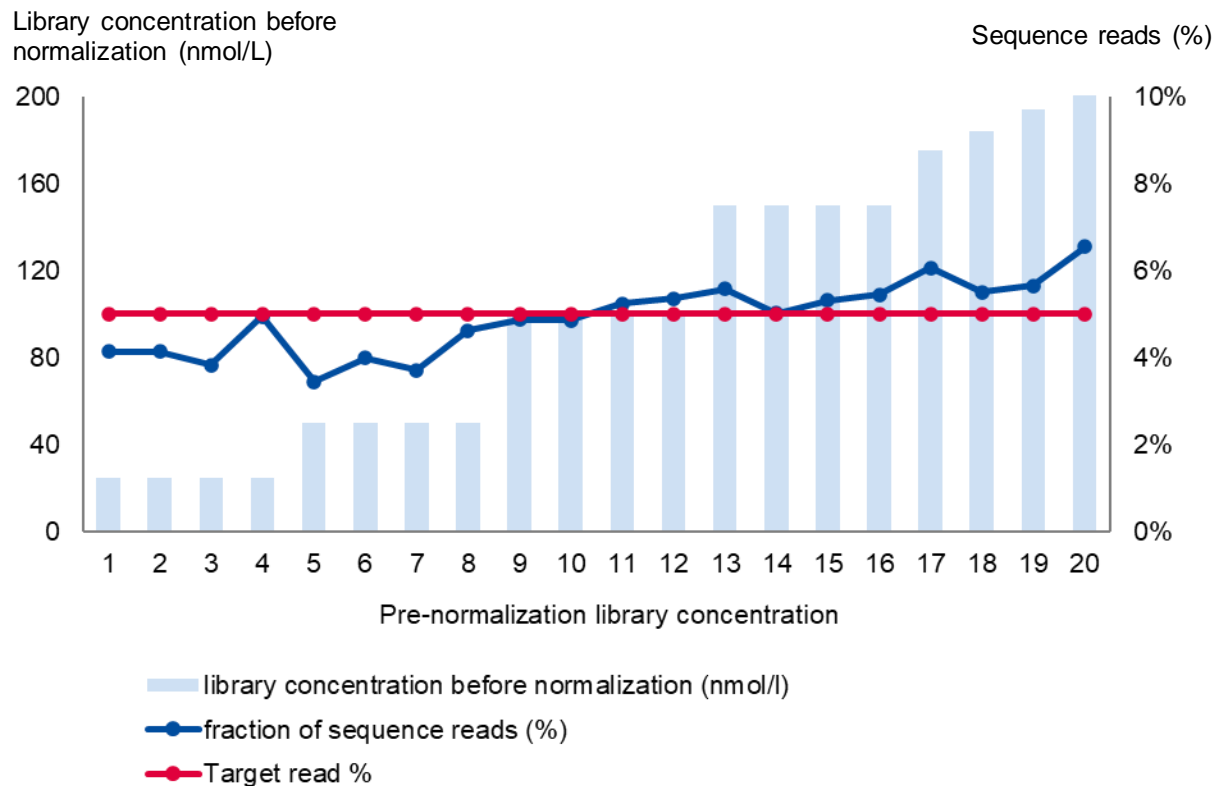
	Before normalization (qPCR)	After normalization (sequencing)
CV%	80.7 %	18 %
GINI*	0.416	0.096

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

QIAseq Library Normalizer for cfDNA libraries



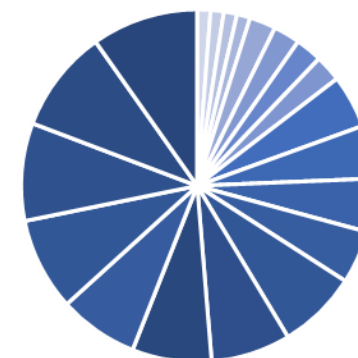
QIAseq Ultralow Input with cfDNA as input



Library representation

Before normalization

After normalization



	Before normalization (qPCR)	After normalization (qPCR)	After normalization (sequencing)
CV%	62 %	18.1 %	13.6 %
GINI	0.33	0.09	0.07

Effective normalization of cfDNA libraries with concentrations between 20 and 200 nmol/L

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

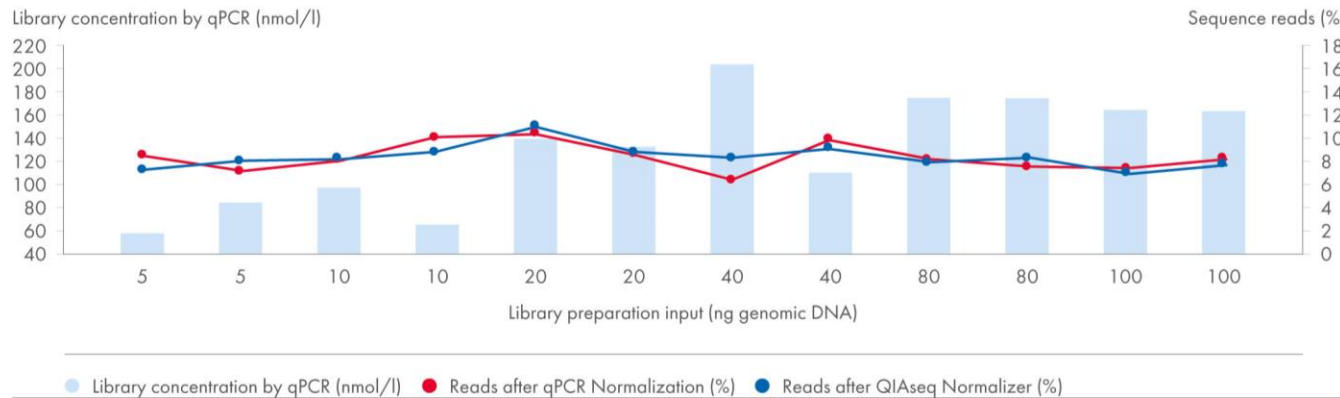
QIAseq Universal Normalizer for targeted DNA libraries



Universal workflow:



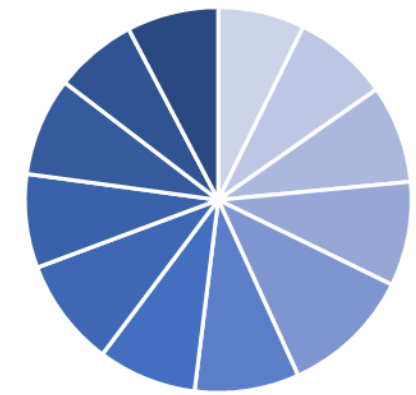
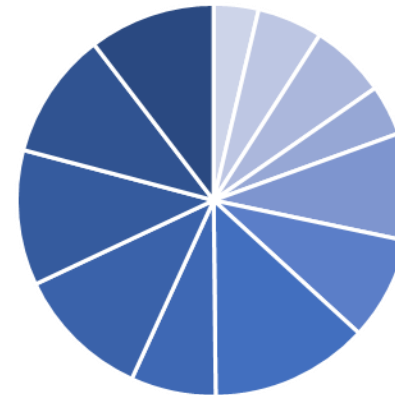
Normalization of targeted DNA panels
(library input range: 5–100 ng)



Library representation

Before normalization

QIAseq Normalizer



The QIAseq Normalizer matches the performance of the “qPCR+dilute” gold standard with minimized hands-on time

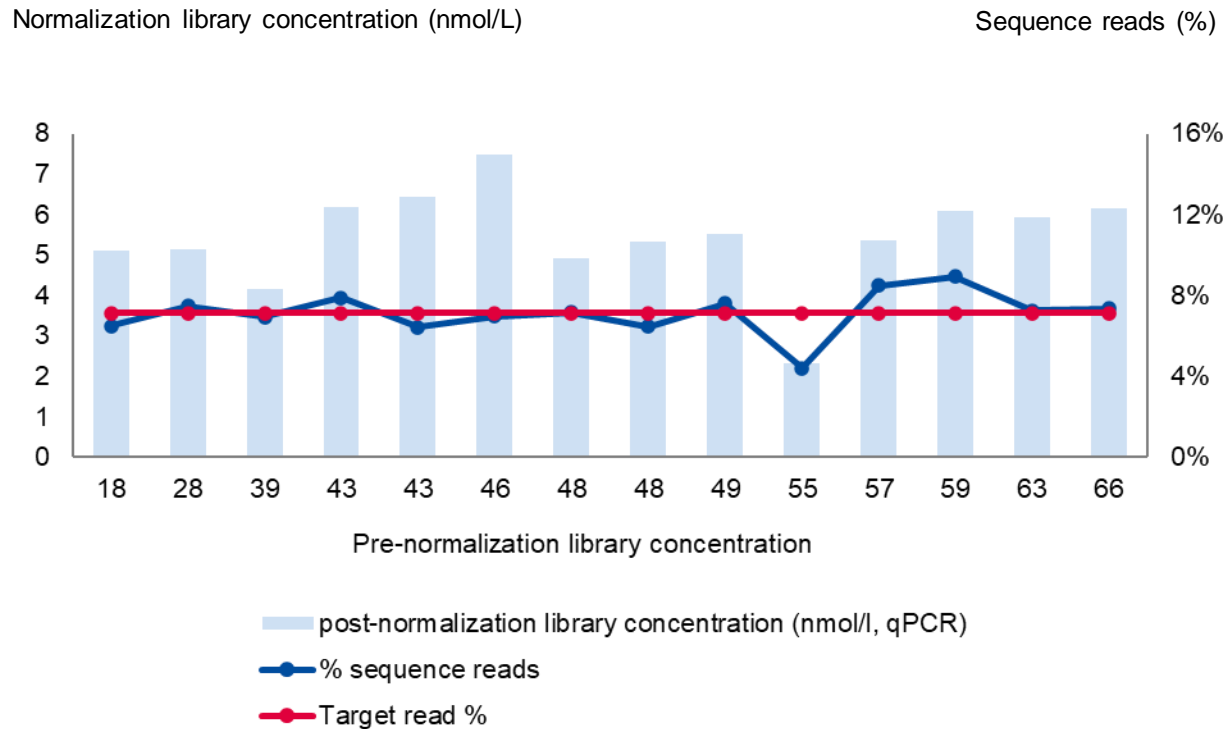
	Before normalization (qPCR of native library)	Sequence reads (qPCR/dilute/pool)	Sequence reads (QIAseq Normalizer)
CV%	36.4 %	14.8 %	12.4 %
GINI	0.2	0.08	0.06

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

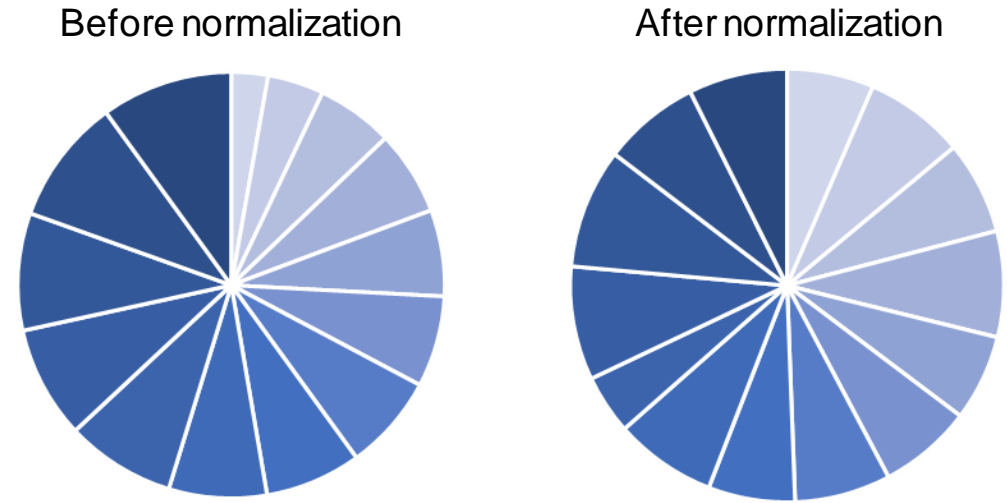
QIAseq Library Normalizer for QIAseq Stranded RNA Libraries



Normalization of QIAseq Stranded RNA Libraries



Library representation





	Before normalization (qPCR)	After normalization (sequencing)
CV%	27.5%	15.0%
GINI	0.15	0.076

Integrated workflow: Library modification happens during library preparation/amplification

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

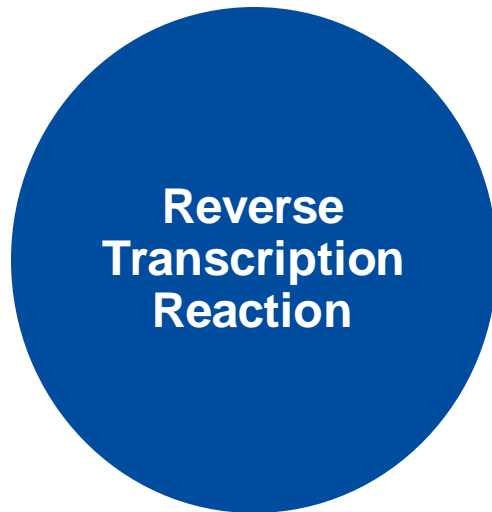
Speed up and Simplify your RNA-seq Workflows

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Sequence Ready libraries @ 4nM concentration	



Simplify your library preparation with 1 kit for most applications



Oligo-dt

3' RNAseq

Random hexamer

Full Transcriptome

Oligo-dt
+
Random hexamer

**3' RNAseq +
Full Transcriptome**

The ultimate in RNA library prep versatility

QIAsSeq FastSelect RNA Library Kit

- Stranded-seq
- 3'-seq
- rRNA removal
- RNAseq Analysis Portal access
- Low-input RNA
- Sample barcoding

Simplify your library preparation with 1 kit for most applications



**cDNA
Sample Barcoding**

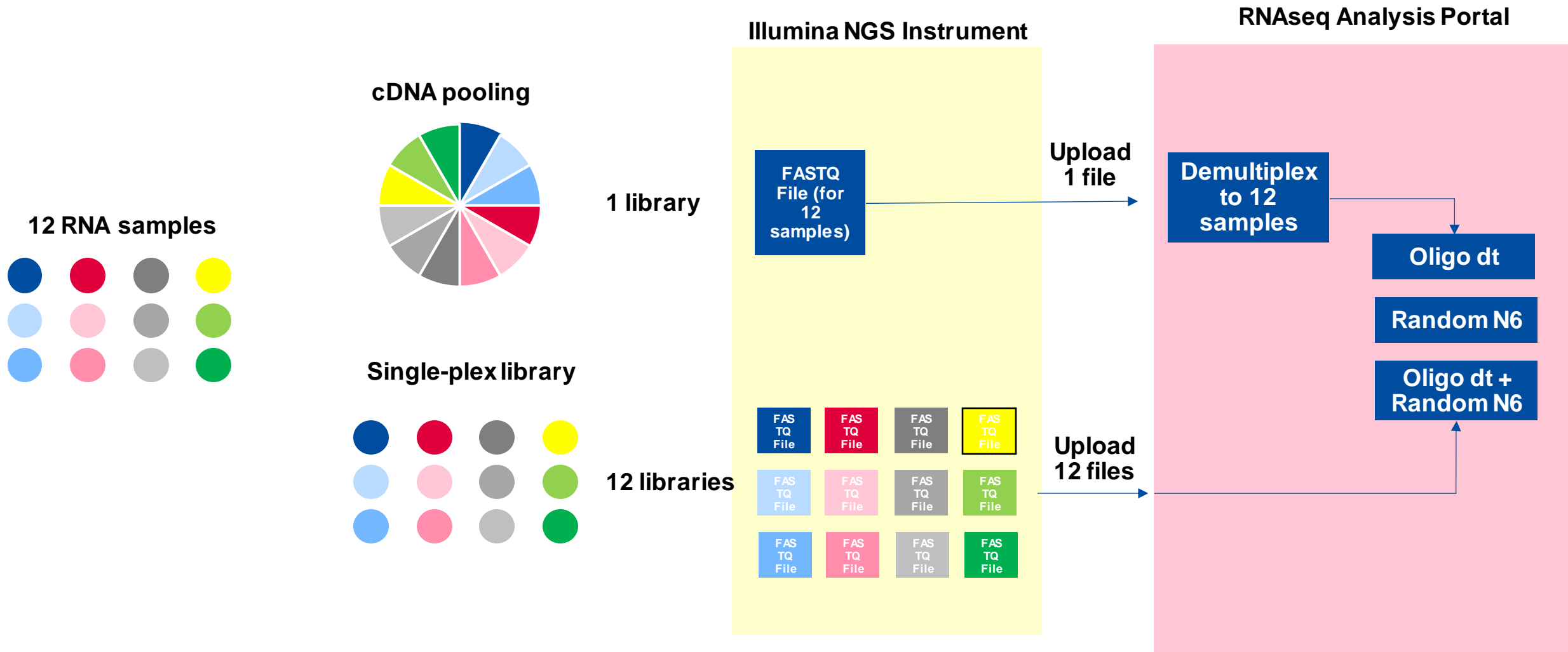
The ultimate in RNA library prep versatility

QIAGEN FastSelect RNA Library Kit

Stranded-seq
3'-seq
rRNA removal
RNAseq Analysis Portal access
Low-input RNA
Sample barcoding

The image shows a red Swiss Army knife with a red handle. The handle has the text "QIAGEN FastSelect RNA Library Kit" in white. The knife is open, showing several tools. The tools are labeled: "Stranded-seq", "3'-seq", "rRNA removal", "RNAseq Analysis Portal access", "Low-input RNA", and "Sample barcoding". The "Sample barcoding" tool is highlighted in yellow.

QIAseq FastSelect libraries can also be pooled after cDNA



Collaborate between Discover to Verification with BIOX



QIAGEN CLC Genomics Workbench for NGS analysis



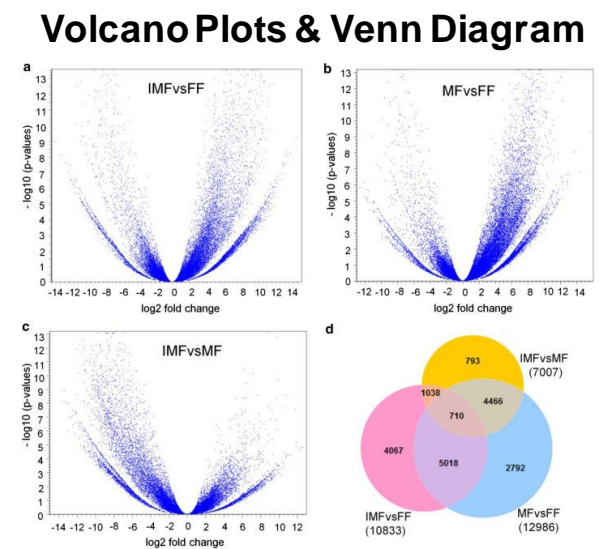
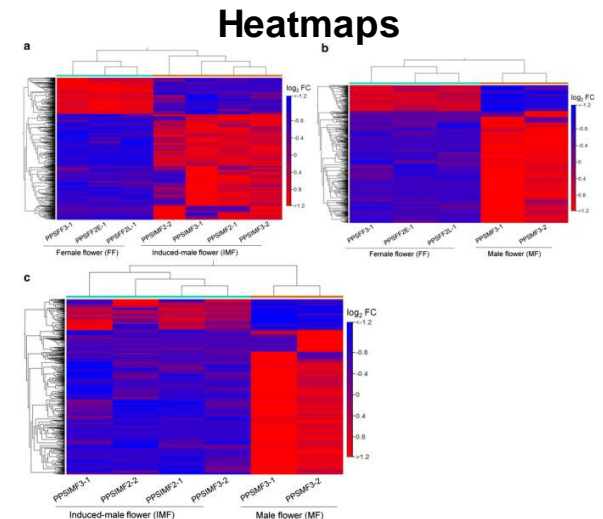
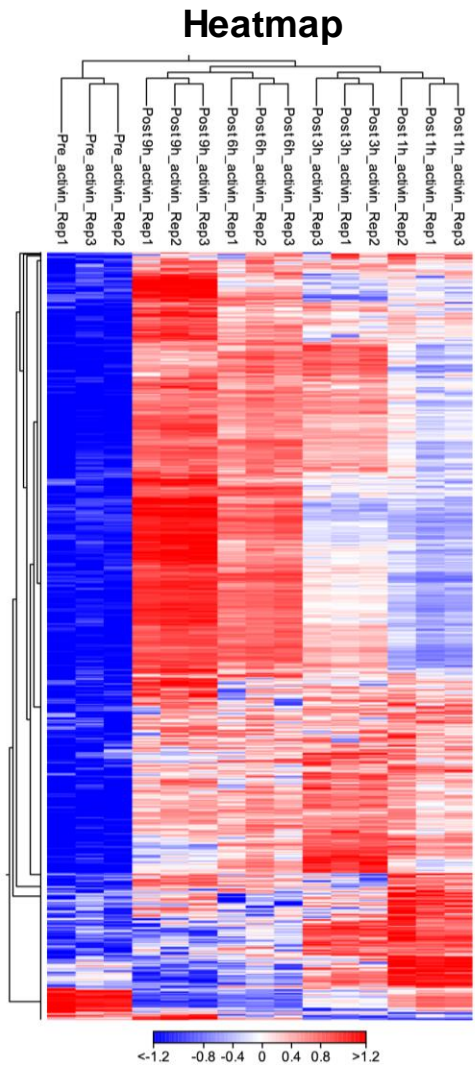
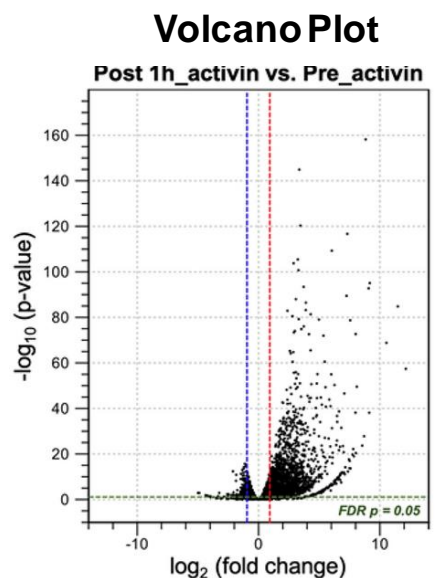
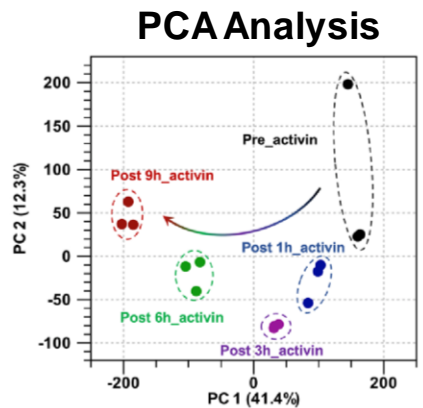
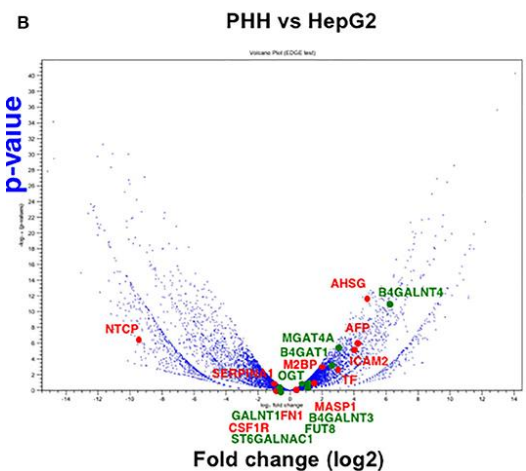
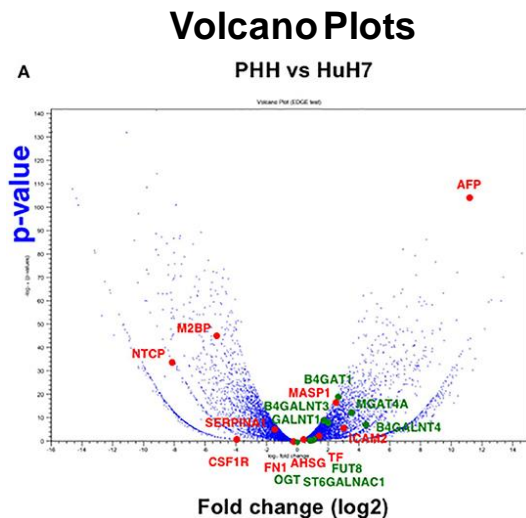
CLC Genomics server:

- Scale to any number of samples and any type of genomes
- Integrate any command line and parametrize for easy button for novice GUI users
- Control access via LDAP/Active directory using any scheduler out there (or ours)

CLC Cloud module:

- Instant scaling to any degree if you have Amazon account
- Eliminate need for costly hardware
- Eliminate need for hardware maintenance
- Pipe reads straight from base space to Amazon without pulling it down
- No idle costs

QIAGEN CLC Genomics Workbench for NGS analysis



Angata K, et al. Glycogene Expression Profiling of Hepatic Cells by RNA-Seq Analysis for Glyco-Biomarker Identification. *Front Oncol.* (2020). PMC7402167.

Satou-Kobayashi Y, et al. Temporal transcriptomic profiling reveals dynamic changes in gene expression of *Xenopus* animal cap upon activin treatment. *Sci Rep.* (2021). PMC8282838.

Adal AM, et al. Comparative RNA-Seq analysis reveals genes associated with masculinization in female *Cannabis sativa*. *Planta.* (2021). PMC7779414.

QIAGEN Ingenuity Pathway Analysis for NGS interpretation



IPA

File Edit View Window Help

Genes and Chemicals Diseases and Functions

Create New...

Public or own dataset

Advanced Search

Provide Feedback | Support Tim Hou Close IPA

QIAGEN Land Explorer

QIAGEN

microRNA Target Filter

49 microRNA have targeting information available. Filtered to 38 microRNAs targeting 235 mRNAs.

Add/Replace mRNA dataset Expression Pairing

Details Summary

Add To My Pathway Add To My List Create Dataset Display As Network

Rows: 1 - 332 (1/1)

Use **T** to filter a column. Edit columns using **+**.

microRNA dataset: RAvsHealthy.miRNA				mRNA dataset: RAvsHealthy.mRNA			
ID	Symbol	Expr Log Ratio	Relationship	ID	Symbol	Expr Log Ratio	Pathway
hsa-let-7d-5p	let-7a-5p (and other miRNAs)	↑5.892	TargetScan Mouse, TargetSc	ENSG00000174684.7	B4GAT1	↓-0.319	Melatonin Degradat...all 6
hsa-let-7d-5p	let-7a-5p (and other miRNAs)	↑5.892	TargetScan Mouse, TargetSc	ENSG00000117560.8	FASLG	↓-0.315	Airway Pathology i...all 47
hsa-let-7d-5p	let-7a-5p (and other miRNAs)	↑5.892	TargetScan Mouse, TargetSc	ENSG00000127452.9	FBXL12	↓-0.327	
hsa-let-7d-5p	let-7a-5p (and other miRNAs)	↑5.892	TarBase	ENSG00000178950.17	GAK	↓-0.364	Clathrin-mediated E...all 1
hsa-let-7d-5p	let-7a-5p (and other miRNAs)	↑5.892	TargetScan Mouse, TargetSc	ENSG00000169635.10	HIC2	↓-0.305	
hsa-let-7d-5p	let-7a-5p (and other miRNAs)	↑5.892	TargetScan Mouse	ENSG00000126003.7	PLAGL2	↓-0.243	
hsa-let-7d-5p	let-7a-5p (and other miRNAs)	↑5.892	TarBase	ENSG00000106628.10	POLD2	↓-0.563	NER (Nucleotide Exc...all 1
hsa-let-7d-5p	let-7a-5p (and other miRNAs)	↑5.892	TargetScan Mouse, TargetSc	ENSG00000101445.10	PPP1R16B	↓-0.450	3-phosphoinositide ...all 6
hsa-let-7d-5p	let-7a-5p (and other miRNAs)	↑5.892	TargetScan Mouse, TargetSc	ENSG00000119906.13	SLF2	↓-0.202	
hsa-let-7d-5p	let-7a-5p (and other miRNAs)	↑5.892	TargetScan Mouse, TarBase, Experimentally Observed, Mc	ENSG00000092531.10	SNAP23	↓-0.488	SNARE Signaling Pa...all 1
hsa-let-7d-5p	let-7a-5p (and other miRNAs)	↑5.892	TarBase	ENSG00000008282.8	SYPL1	↓-0.271	
hsa-let-7d-5p	let-7a-5p (and other miRNAs)	↑5.892	TargetScan Mouse, TargetSc	ENSG00000152818.18	UTRN	↓-0.206	Agri Interactions at...all 2
hsa-let-7d-5p	let-7a-5p (and other miRNAs)	↑5.892	TargetScan Mouse, TargetSc	ENSG00000047056.16	WDR37	↓-0.243	
hsa-let-7d-5p	let-7a-5p (and other miRNAs)	↑5.892	TargetScan Human	ENSG00000156853.13	ZNF689	↓-0.243	
hsa-miR-99b-5p	miR-100-5p (and other miRN)	↑7.378	TargetScan Mouse, Ingenuity	ENSG00000198793.13	MTOR	↓-0.264	
hsa-miR-99b-5p	miR-100-5p (and other miRN)	↑7.378	TargetScan Human	ENSG00000128789.21	PSMG2	↓-0.378	
hsa-miR-99b-5p	miR-100-5p (and other miRN)	↑7.378	TargetScan Human	ENSG00000127616.18	SMARCA4	↓-0.325	
hsa-miR-99b-5p	miR-100-5p (and other miRN)	↑7.378	TargetScan Mouse	ENSG00000167987.11	VPS37C	↓-0.287	
hsa-miR-101-2-5p	miR-101b-5p (and other miRN)	↑7.659	TargetScan Mouse	ENSG00000165138.18	ANKS6	↓-0.234	
hsa-miR-10b-5p	miR-10a-5p (and other miRN)	↑8.377	TargetScan Human	ENSG000001176390.12	CRLF3	↓-0.289	
hsa-miR-10b-5p	miR-10a-5p (and other miRN)	↑8.377	TargetScan Human	ENSG00000071626.16	DAZAP1	↓-0.269	
hsa-miR-10b-5p	miR-10a-5p (and other miRN)	↑8.377	TargetScan Mouse	ENSG00000093183.14	SEC22C	↓-0.295	
hsa-miR-4508	miR-12197-3p (and other miR)	↑7.651	TargetScan Human	ENSG00000028310.18	BRD9	↓-0.318	
hsa-miR-4508	miR-12197-3p (and other miR)	↑7.651	TargetScan Human	ENSG00000129757.13	CDKN1C	↓-0.415	
hsa-miR-4508	miR-12197-3p (and other miR)	↑7.651	TargetScan Mouse	ENSG00000156136.10	DCK	↓-0.445	
hsa-miR-4508	miR-12197-3p (and other miR)	↑7.651	TargetScan Mouse	ENSG00000179348.12	GATA2	↓-0.267	
hsa-miR-4508	miR-12197-3p (and other miR)	↑7.651	TargetScan Human	ENSG00000110324.10	IL10RA	↓-0.425	
hsa-miR-4508	miR-12197-3p (and other miR)	↑7.651	TargetScan Mouse, TargetSc	ENSG00000099326.9	MZF1	↓-0.252	
hsa-miR-4508	miR-12197-3p (and other miR)	↑7.651	TargetScan Human	ENSG00000214106.9	PAKIP1-AS2	↓-0.311	
hsa-miR-4508	miR-12197-3p (and other miR)	↑7.651	TargetScan Mouse, TargetSc	ENSG00000079313.15	REXO1	↓-0.247	
hsa-miR-4508	miR-12197-3p (and other miR)	↑7.651	TargetScan Mouse	ENSG000001131378.14	RFTN1	↓-0.674	
hsa-miR-4508	miR-12197-3p (and other miR)	↑7.651	TargetScan Mouse, TargetSc	ENSG00000100241.21	SBF1	↓-0.325	
hsa-miR-4508	miR-12197-3p (and other miR)	↑7.651	TargetScan Human	ENSG00000160190.14	SLC37A1	↓-0.171	

Selected/Total rows: 0/332

View Filter Summary

My Pathways

Overlay: RAvsHealthy.miRNA, Expr Log Ratio

Prediction Legend

- miR where in frame
- Increased measurement
- Decreased measurement
- miR confidence
- Predicted activation
- Predicted inhibition
- Glow indicates activity when opposite of measurement
- Predicted Relationships
 - Leads to activation
 - Leads to inhibition
 - Findings inconsistent with state of downstream molecule
 - Effect not predicted

miR-219a-5p (and other miRNAs w/seed CCUGGCA)

miR-219a-5p (and other miRNAs w/seed GAUUGUC)

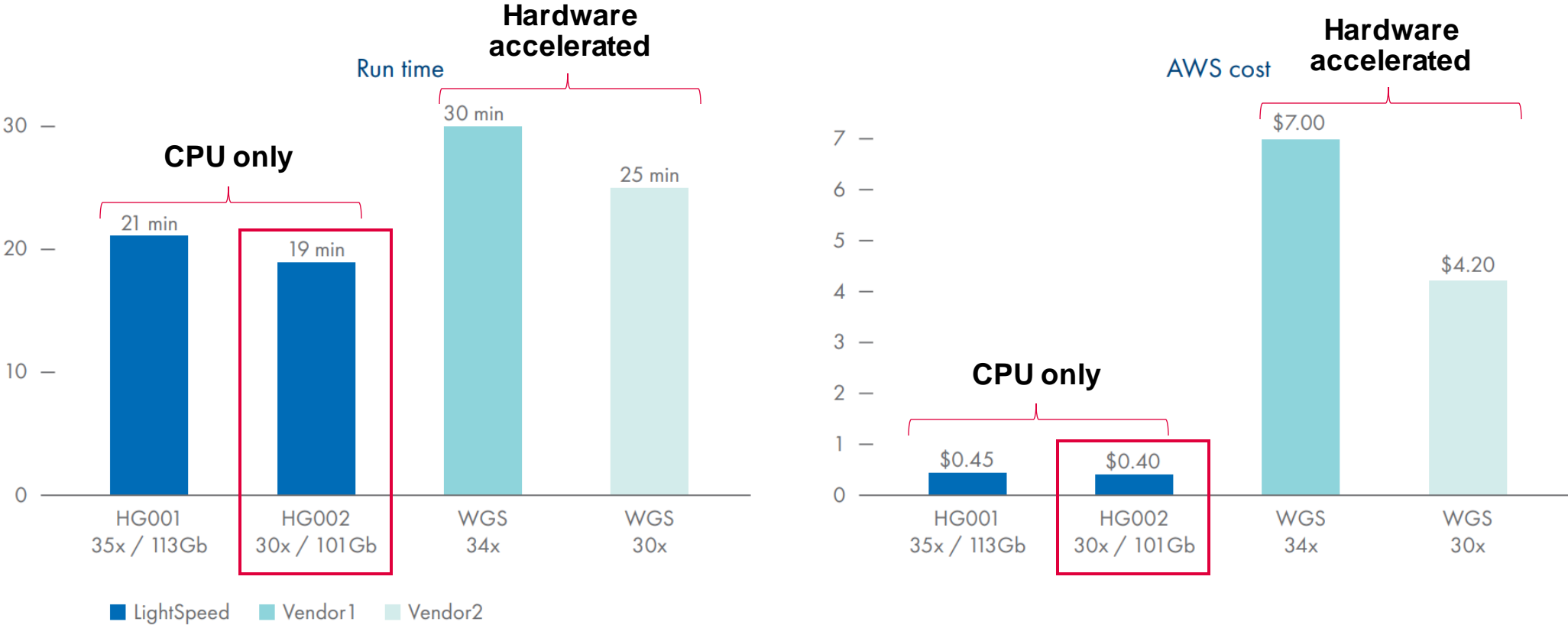
CXCL11 FASLG IL12B

Save Cancel

Breaking speed and cost barriers with LightSpeed



LightSpeed is the fastest and cheapest-to-run hereditary FASTQ-to-VCF WGS pipeline available



Less than 20 minutes and 40 cents for 30x WGS on AWS

Beyond exomes: Ultrafast FASTQ to interpretation



CLC Genomics Workbench 23.0.4 - <New Workspace> - Evaluation 534 days remaining

File Edit View Connections Utilities Download Toolbox Help

Show Bookmark New Save Import Export Graphics Print Launch Undo Redo Delete

Workspace Plugins References Download Workflows Support

Genome Browser View X

Navigation overview: Chromosome 1

13,178,880 13,178,900 13,178,920 13,178,940 13,178,960 13,178,980 13,179,000 13,179,020

Unresolved track

Homo_sapiens_ensembl_v106
1_hg38_no_alt_analysis_set_Genes

Homo_sapiens_ensembl_v106
1_hg38_no_alt_analysis_set_RNA

Homo_sapiens_ensembl_v106
1_hg38_no_alt_analysis_set_CDS

Amino Acid Track-SRR13386239 (Variants, OA) (Amino Acids)
Amino acids

Germline Variants-SRR13386239 (Variants, OA) (Repeats, AAC, EXON)(filtered)

Germline Variants-SRR13386239... X

Rows: 1,143 / 212,451 Table view: Genome

Filter to Selection... Match any Match all

Zygosity contains Homozygous + -

type (Homo_sapiens_ensembl_v106.1_hg38_no_alt_analysis_RNA) contains mRNA + -

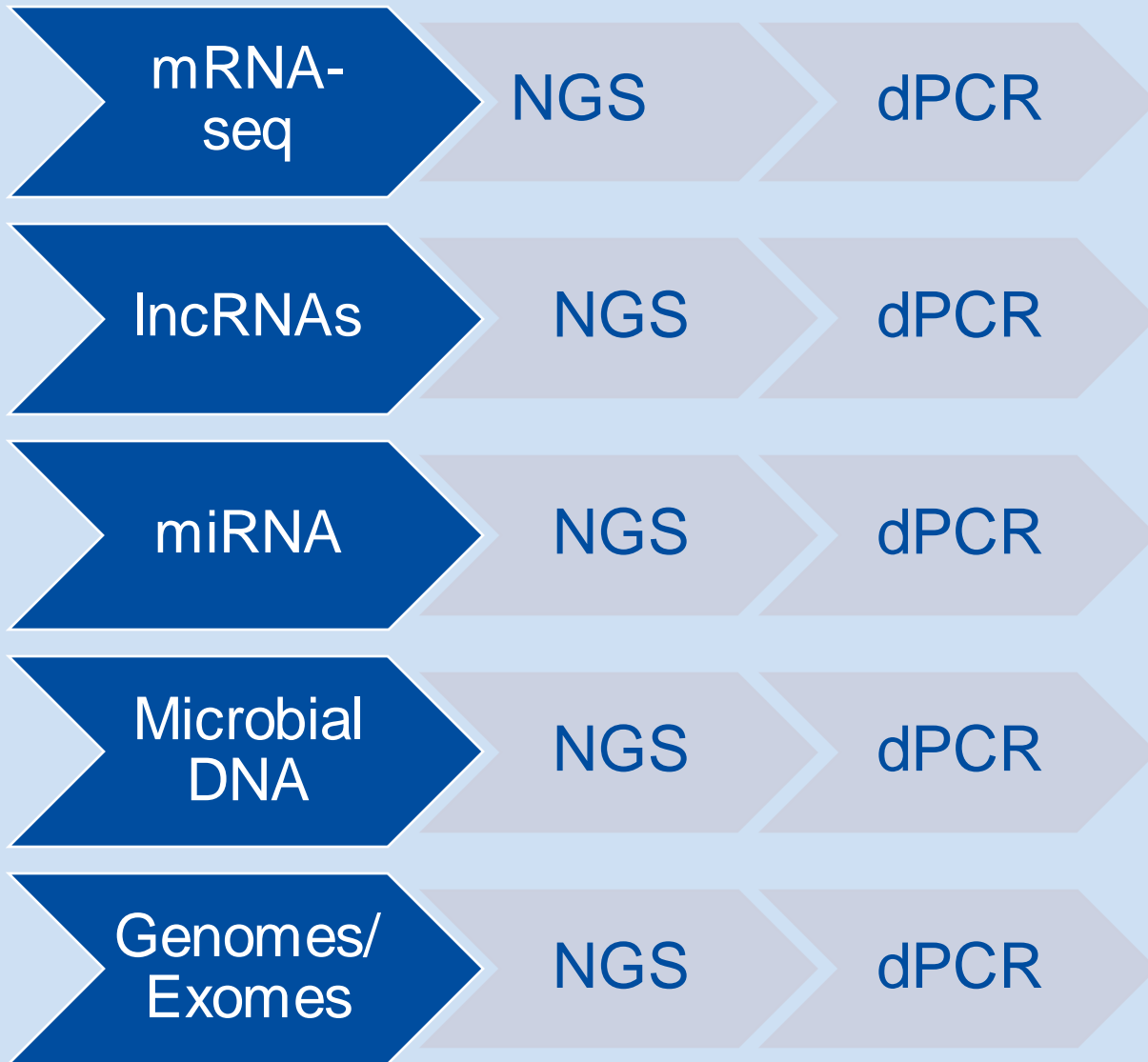
Non-synonymous contains YES + -

Coverage > 30 + - Filter

Chromosome	Region	Type	Reference	Allele	Reference ...	Length	Zygosity	Count	Coverage	Frequency	QUAL	Genotype	Homo_sapiens_e...	Homo_sapiens_ensem...	constitutive...	ensembl_en...	ensembl_ph...	rank (Homo...	version (Ho...	type (Homo...	source (
1	69610	SNV	C	T	No		1 Homozygous	32	32	100.00	99	T/T	OR4F5-201	OR4F5	1	-1,0	-1,0	1,2,3	1,2	mRNA	havana
1	12794279	SNV	C	T	No		1 Homozygous	88	88	100.00	99	T/T	PRAMEF1-201	PRAMEF1	0	-1,2	-1,2	1,2,3,4	2,1,7	mRNA	ensembl
1	12827720	SNV	T	G	No		1 Homozygous	145	145	100.00	99	G/G	PRAMEF11-201	PRAMEF11	1	-1,2	2,-1	4,3,2,1	1	mRNA	ensembl
1	12882298	SNV	T	C	No		1 Homozygous	188	188	100.00	99	C/C	PRAMEF4-201	PRAMEF4	1	-1,2	2,-1	4,3,2,1	2,1,6	mRNA	ensembl
1	12920302	SNV	C	G	No		1 Homozygous	77	77	100.00	99	G/G	PRAMEF7-202, PR...	PRAMEF7	0,1	-1,2	-1,0,2	1,2,3,4	1,4,3,6	mRNA	ensembl
1	13178951	SNV	G	A	No		1 Homozygous	104	104	100.00	99	A/A	PRAMEF9-201	PRAMEF9	1	-1,2	-1,2	1,2,3,4	2,1,3	mRNA	ensembl
1	13225359	SNV	A	G	No		1 Homozygous	89	89	100.00	99	G/G	PRAMEF18-202	PRAMEF18	1	-1,2	2,0	3,2,1	2,1	mRNA	ensembl
1	13265667	SNV	A	C	No		1 Homozygous	96	96	100.00	99	C/C	PRAMEF23-201	PRAMEF23	1	-1,2	1,2	1,2,3,4	2,1	mRNA	ensembl

Create Track from Selection

Idle...




Collaborate across technologies for discovery to verification

Join QIAGEN to Speed up and Simplify



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RNA-seq Analysis portal is the bridge between NGS and digital PCR

Analysis Portal Samples Help

All Projects > Demo project v4.0

Demo project v4.0

Collection of demo data for exploring RNA-seq Analysis Portal views and reports

109 samples Created: 09-03-2023

6 experiments

- QIAseq Stranded RNA - Cell line mixtures with FastSelect** 12 samples Done
- QIAseq Stranded RNA - Tissue types with FastSelect 6 samples Done
- QIAseq miRNA - Tissue types 6 samples Done
- QIAseq Stranded RNA - FastSelect vs no rRNA depletion 6 samples Done
- QIAseq 3' UPX - T-cell gene changes after gene knockout 48 samples Done
- QIAseq UPXome RNA Library Kit - Cell line mixtures with FastSelect 31 samples Done

Create experiment Send copy of project

QIAseq Stranded RNA - Cell line mixtures with FastSelect

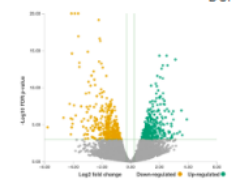
Stranded transcriptome libraries prepared from mixtures of two cell lines, UHRR (Universal Human Reference RNA) and HBRR (Human Brain Reference RNA), using QIAseq Stranded Total RNA Lib Kit. QIAseq FastSelect for depletion of rRNA. Three replicates for each sample mixture.

12 samples: QIAseq Stranded mRNA Select/Total RNA Lib Kit , Homo sapiens (GRCh38.103)

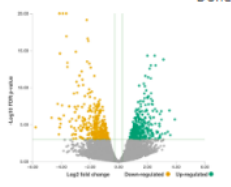
Experiment design: Test differential expression due to Mixture. Compare Against control group (UHRR)

5 analyses, organized by type

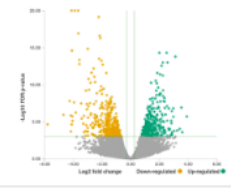
Differential expression: 3UHRR_1HBRR vs. UHRR
Analysis of Mixture: 3UHRR_1HBRR vs. UHRR



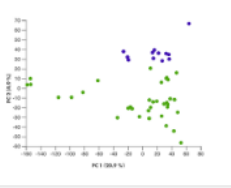
Differential expression: 1_UHRR_3_HBRR vs. UHRR
Analysis of Mixture: 1_UHRR_3_HBRR vs. UHRR




Differential expression: HBRR vs. UHRR
Analysis of Mixture: HBRR vs. UHRR



Experiment summary and QC
Experiment summary, sample review and quality control



Comparison: 3UHRR_1HBRR vs. UHRR, 1_UHRR_3_HBRR vs. UHRR, HBRR vs. UHRR
Venn diagram of differentially expressed features across the differential expression analyses:



- 1_UHRR_3_HBRR vs. UHRR
- 3UHRR_1HBRR vs. UHRR
- HBRR vs. UHRR

Delete experiment Delete analyses

Compare analyses

Secondary analysis is powered by QIAGEN CLC Genomics Workbench. Visit our website to download a free trial and unleash the power of user-friendly bioinformatics.

Powered by QIAGEN CLC Genomics Workbench and QIAGEN Ingenuity Pathway Analysis

RNA-seq Analysis Portal 4.0 Samuel Rulli

Yes vs. No

Features: 863 of 36813

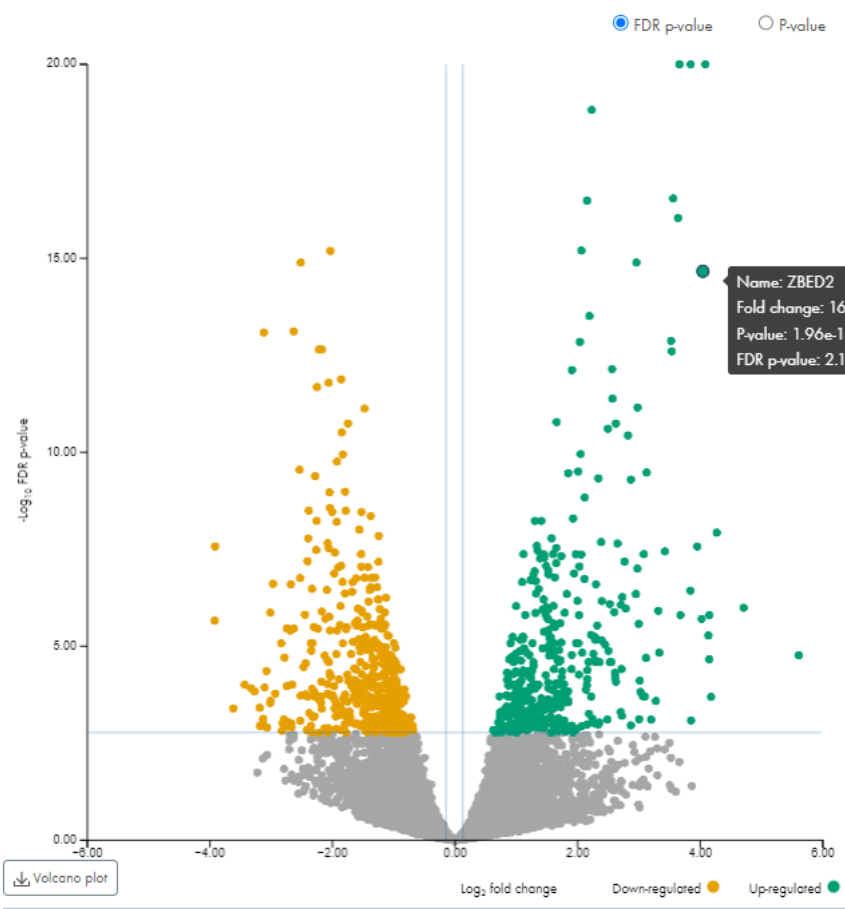
Sort by: Name (Asc) [Full feature list](#)

Name	Fold change	FDR p-value	P-value	Biotype
AAK1	-1.69	7.83e-4	3.95e-5	protein_coding
ABCE1	2.31	7.26e-4	3.56e-5	protein_coding
ABHD17A	-2.26	6.27e-4	2.97e-5	protein_coding
ABLIM1	-4.93	1.46e-4	4.94e-6	protein_coding
AC004882.3	-2.48	8.11e-4	4.12e-5	lncRNA
AC005944.1	-2.55	2.17e-5	4.80e-7	lncRNA
AC008875.3	-2.08	1.03e-3	5.56e-5	lncRNA
AC010247.2	-4.99	6.78e-4	3.30e-5	lncRNA
AC018653.3	-8.75	7.42e-4	3.66e-5	lncRNA
AC022706.1	-4.17	2.97e-8	1.58e-10	lncRNA

Biological insights Canonical pathways

Pathway	-log10 of p-value	z-score
Pathogen Induced Cytokine Storm Signaling Pathway	6.955	2.082
Multiple Sclerosis Signaling Pathway	6.762	-
Differential Regulation of Cytokine Production in Intes...	5.622	2.828
NOD1/2 Signaling Pathway	5.405	1.043
Granulocyte Adhesion and Diapedesis	5.405	-
Role of Hypercytokinemia/hyperchemokineemia in the...	4.943	1.069
Erythropoietin Signaling Pathway	4.821	-2.236
Cell Cycle Control of Chromosomal Replication	4.799	3.317
HMGB1 Signaling	4.680	2.000
TNFR2 Signaling	4.434	1.000

[View details](#)



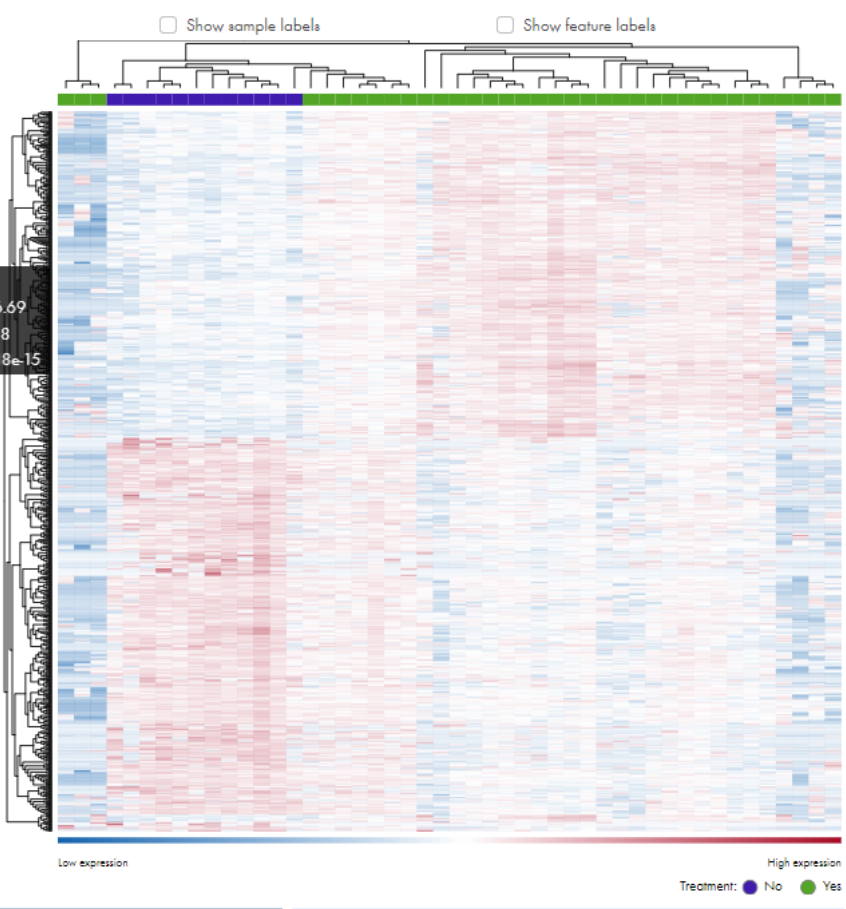
Volcano plot

Filters

FDR p-value ≤ Fold change < Fold change >

Biological insights filter: None selected

Filter not saved



What's next?
Design follow-up experiments in GeneGlobe.

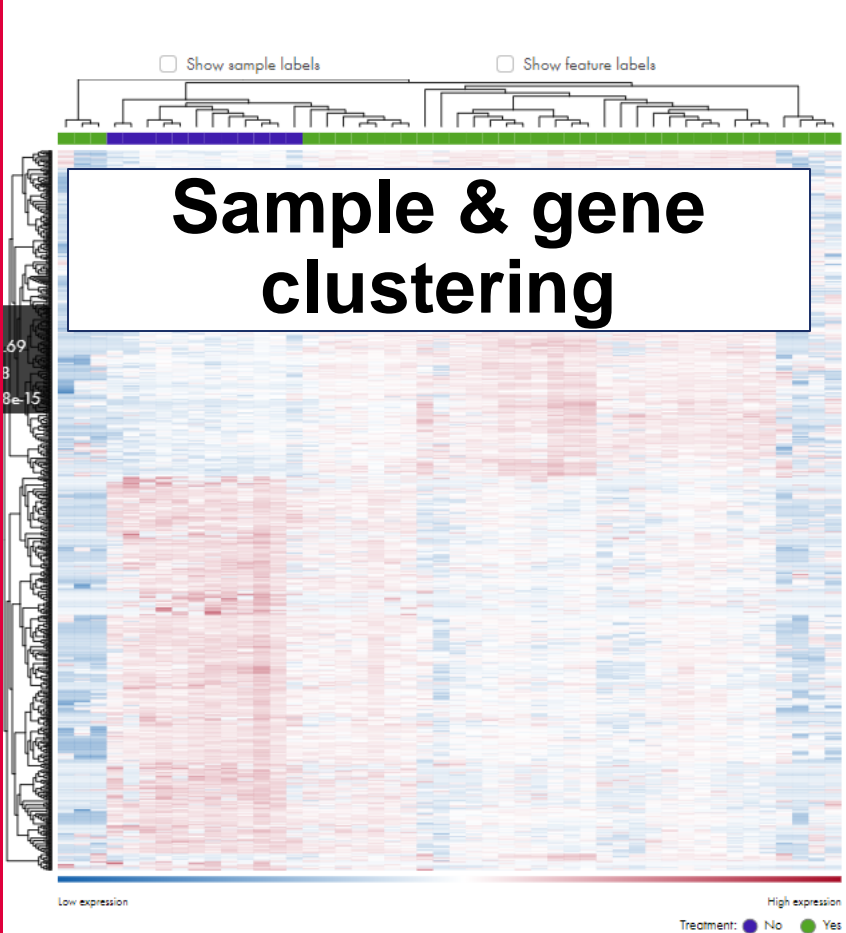
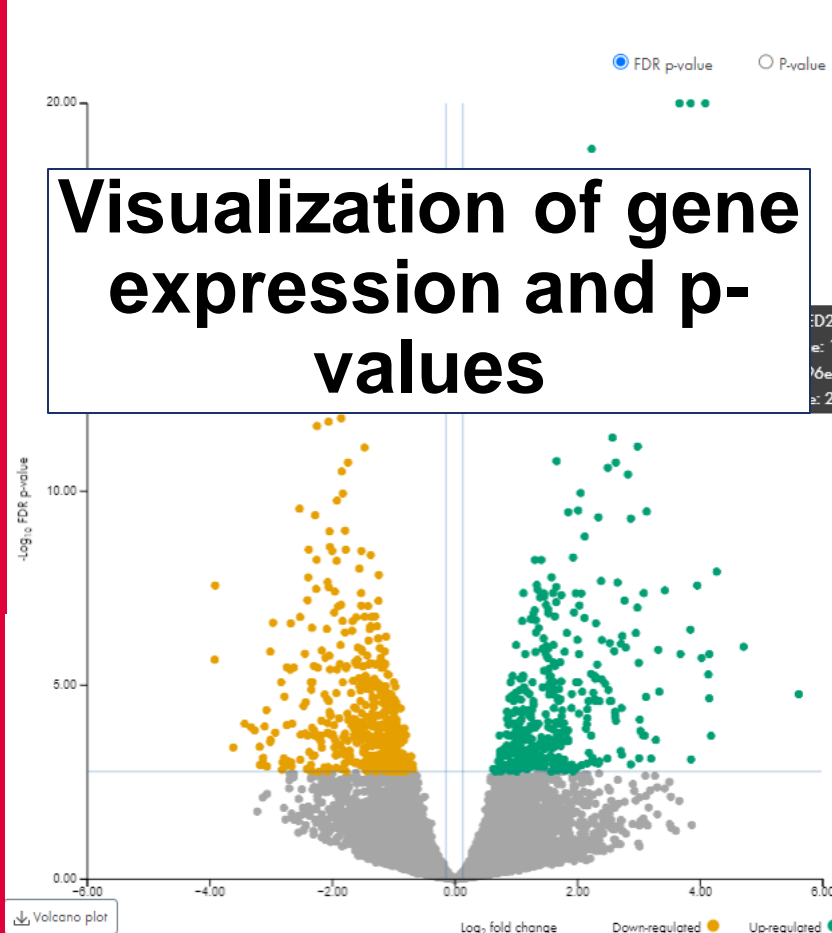
Yes vs. No

Features: 863 of 36813

Sort by: Name (Asc) [Full feature list](#)

Name	Fold change	FDR p-value	P-value	Biotype
AAK1	-1.69	7.83e-4	3.95e-5	protein_coding
ABCE1				ding
ABHD				ding
ABLIM				ding
AC004				RNA
AC005				RNA
AC008				RNA
AC010247.2	-4.99	6.78e-4	3.30e-5	lncRNA
AC018653.3	-8.75	7.42e-4	3.66e-5	lncRNA
AC022706.1	-4.17	2.97e-8	1.58e-10	lncRNA

Biological insights: Canonical pathways



Ingenuity Pathway Analysis

Pathway	-log10 of p-value	z-score
Role of Hypercytokinemia/hyperchemokine...	4.943	1.069
Erythropoietin Signaling Pathway	4.821	-2.236
Cell Cycle Control of Chromosomal Replication	4.799	3.317
HMGB1 Signaling	4.680	2.000
TNFR2 Signaling	4.434	1.000

[View details](#)

Volcano plot

Filters: FDR p-value ≤ Fold change < Fold change > [Reset](#) Filter not saved [Save](#)

Biological insights filter: None selected [Advanced filters](#)

What's next? Design follow-up experiments in GeneGlobe. [Start now](#)

Use QIAGEN IPA results to pick better biomarkers


QIAGEN IPA Biological insights

Learn about the values

Canonical Pathways	Upstream Regulators	Upstream regulators (miRNA)	Diseases and functions		
Pathway	Prediction	z-score	Overlapping genes	p-value	-log10 of pvalue
CREB Signaling in Neurons	Activated	4.765	68	3.23e-14	13.491
Glutamate Receptor Signaling	Activated	2.714	20	8.28e-13	12.082
Breast Cancer Regulation by Stathmin1	Activated	2.945	62	1.05e-11	10.979
FXR/RXR Activation	-	-	23	1.30e-9	8.886
Phagosome Formation	Activated	2.794	62	4.67e-9	8.331
G-Protein Coupled Receptor Signaling	Activated	3.302	62	8.97e-9	8.047
Maturity Onset Diabetes of Young (MODY) Si...	-	-	17	1.15e-8	7.939
Kinetochores Metaphase Signaling Pathway	Inhibited	-2.828	20	1.94e-8	7.712
Neurovascular Coupling Signaling Pathway	Activated	2.414	29	4.02e-8	7.396
Acute Phase Response Signaling	-	-0.632	25	1.36e-7	6.866

Tables display the top results (max 10) from QIAGEN IPA (Ingenuity Pathway Analysis).

Interested in exploring more?
Try QIAGEN IPA, the gold standard for pathway and systems biology analysis to dig deeper. [Find out](#) how IPA automatically uses a Knowledge Base of over 7.8 million literature findings to compare your results to a pre-computed library of over 90,000 curated gene expression datasets.



Close

Yes vs. No

Features: 30 of 36813

Sort by: Name (Asc)

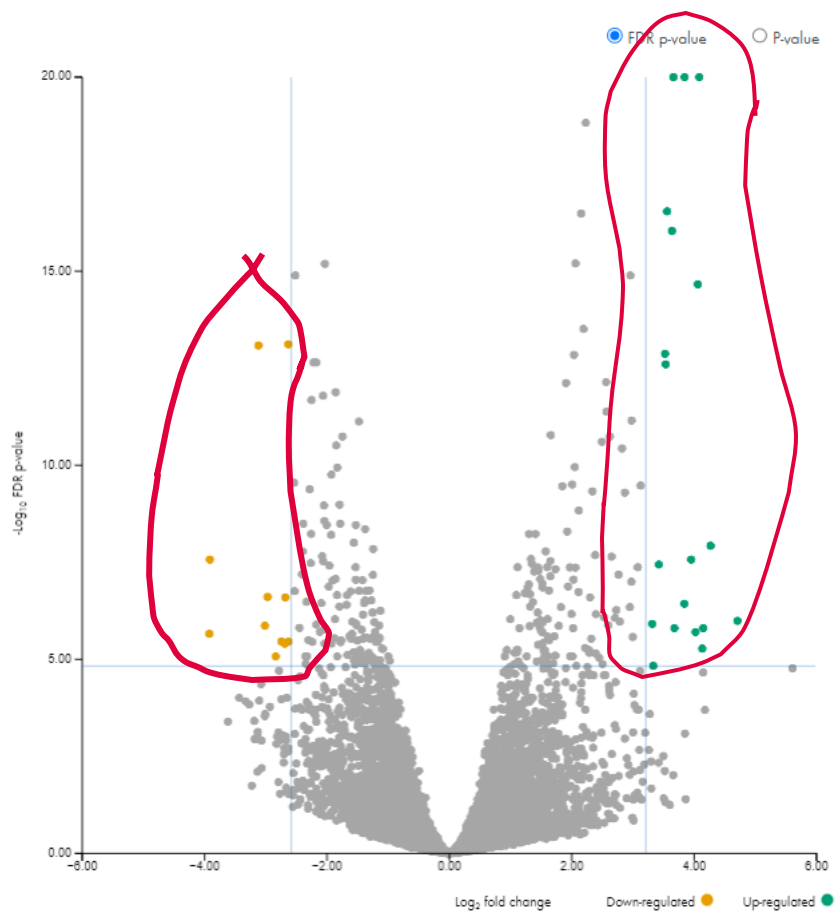
Full feature list

Name	Fold change	FDR p-value	P-value	Biotype
AC135048.1	-6.70	3.46e-6	4.97e-8	lncRNA
ADRB2	-15.07	2.68e-8	1.38e-10	protein_coding
CCDC112	-6.46	3.94e-6	5.97e-8	protein_coding
CCDC65	-7.15	8.37e-6	1.45e-7	protein_coding
CCL1	10.72	3.61e-8	2.00e-10	protein_coding
CCL3	16.96	4.80e-23	3.60e-27	protein_coding
CCL3L3	17.74	1.57e-6	1.92e-8	protein_coding
CCL4L2	11.50	1.34e-13	1.61e-16	protein_coding
CD83	16.25	1.99e-6	2.53e-8	protein_coding
EGR1	19.27	1.19e-8	5.33e-11	protein_coding

Biological insights Canonical pathways

Pathway	-log10 of p-value	z-score
Pathogen Induced Cytokine Storm Signaling Pathway	6.955	2.082
Multiple Sclerosis Signaling Pathway	6.762	-
Differential Regulation of Cytokine Production in Intes...	5.622	2.828
NOD1/2 Signaling Pathway	5.405	1.043
Granulocyte Adhesion and Diapedesis	5.405	-
Role of Hypercytokinemia/hyperchemokinememia in the...	4.943	1.069
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Cell Cycle Control of Chromosomal Replication	4.799	3.317
HMGB1 Signaling	4.680	2.000
TNFR2 Signaling	4.434	1.000

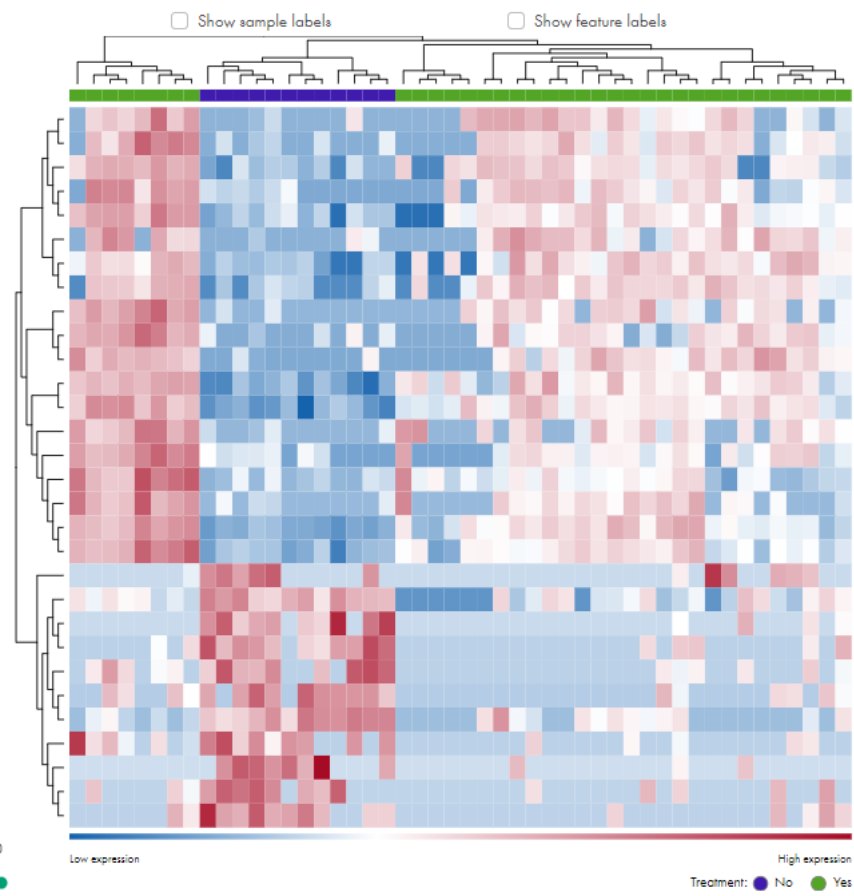
[View details](#)



Filters

FDR p-value ≤ Fold change < Fold change >

Biological insights filter: None selected



What's next?

Design follow-up experiments in GeneGlobe.

Return to GeneGlobe to find assays for dPCR or qPCR verifications

GeneGlobe Products Customize Analyze Knowledge Welcome Samuel Cart

QIAsseq Stranded RNA - Cell line mixtures with FastSelect_1

Experiment QIAsseq Stranded RNA - Cell line mixtures with FastSelect - HBRR vs. UHRR

Click the tabs below to access target-specific assays for conducting follow-up studies based on your results. Or, click the Pathways tab to explore the biological pathways most relevant to your results in GeneGlobe.

Gene Targets miRNA Upstream Regulators Pathways

Gene Targets

Select the gene targets to include in your product search. You can narrow down the target list by selecting a different Regulation Type (All, Up-regulated, or Down-regulated) and adjusting the Fold Change and p-Value Threshold values.

Regulation Type Fold Threshold p-Value Threshold

SELECTED TARGETS: 1 [Download Targets](#)

Target ↑	Fold Change	p-Value
<input type="checkbox"/> AC078815.1	628.3104360316	0.00003289
<input checked="" type="checkbox"/> ACTL6B	745.4819937953	2.265e-15
<input type="checkbox"/> ADGRA1	2560.2193544626	1.504e-7
<input type="checkbox"/> AFP	-864.5222316719	3.396e-25
<input type="checkbox"/> AGR2	-596.5738630314	0.0001152
<input type="checkbox"/> AHSG	-1204.2495674827	0
<input type="checkbox"/> AKAIN1	775.3830750548	0.000008787
<input type="checkbox"/> ALB	-1269.4801675036	0
<input type="checkbox"/> ALPK2	-1480.9327465654	0.00001045
<input type="checkbox"/> AMBR	4762.7540840348	2.114e-7

Products

Choose the type of follow-up studies you'd like to perform to see the relevant assays for your selected targets.

1. FOLLOW-UP EXPERIMENT CATEGORY
[Validation experiments](#) [Functional analysis](#) [Other follow-up analyses](#)

2. TYPE
[qPCR/dPCR validation](#) [Panel refinement/development](#) [Genetic analysis](#)

3. PRODUCT TYPE
[Custom panels & assays](#) [SYBR® Green assays](#) [Probe assays](#)

GeneGlobe ID: SBH0347459 | Cat. No.: | QuantiNova LNA PCR Assays for Real-Time PCR
HS_ACTL6B_1591265 Quantinova LNA PCR Assay
Assay targets ENST00000461605
Assay spans exon

[Product Specification](#) [CONFIGURE](#)

GeneGlobe ID: SBH0347456 | Cat. No.: | QuantiNova LNA PCR Assays for Real-Time PCR
HS_ACTL6B_1591262 Quantinova LNA PCR Assay
Assay targets 4 transcripts

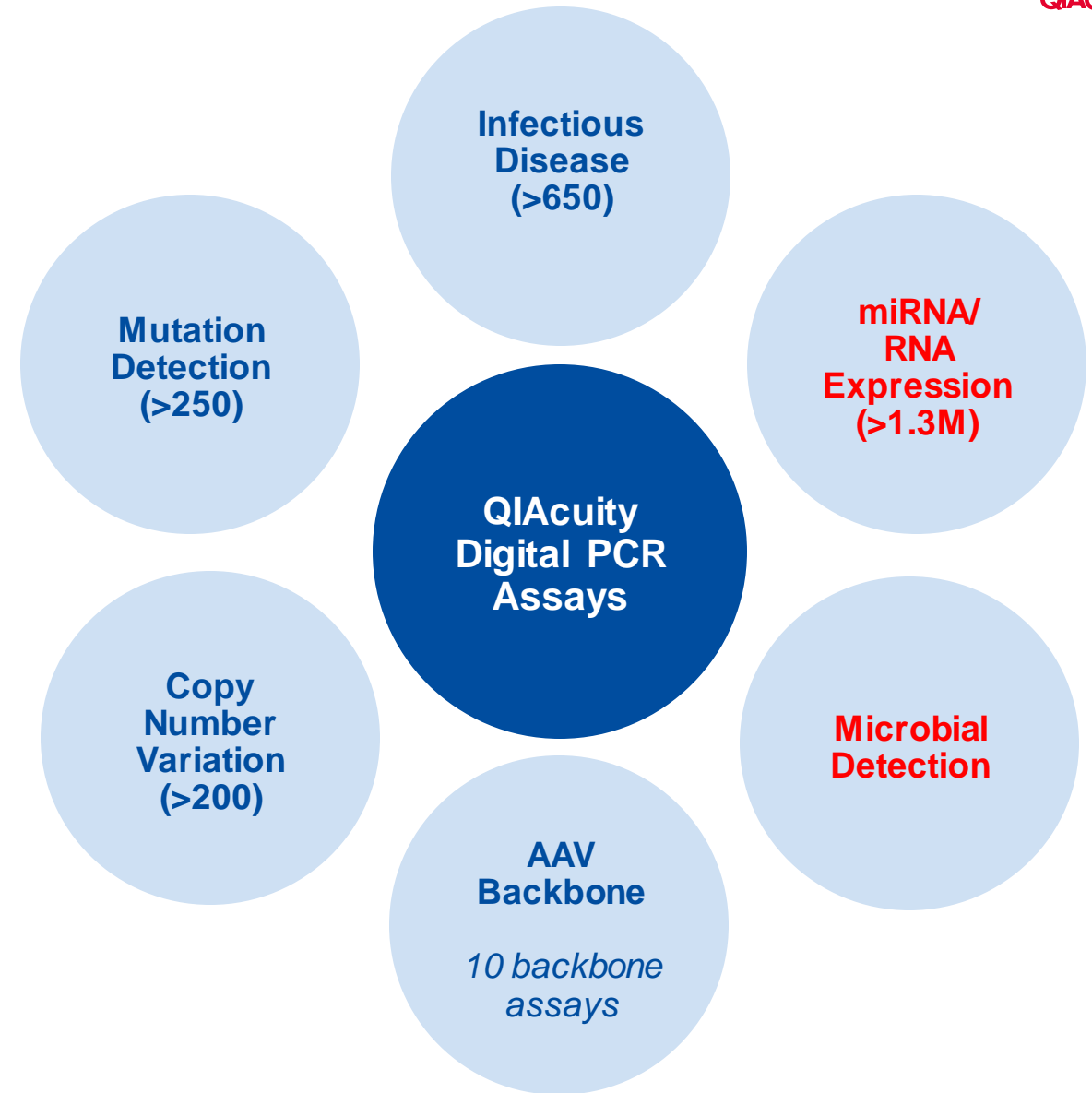
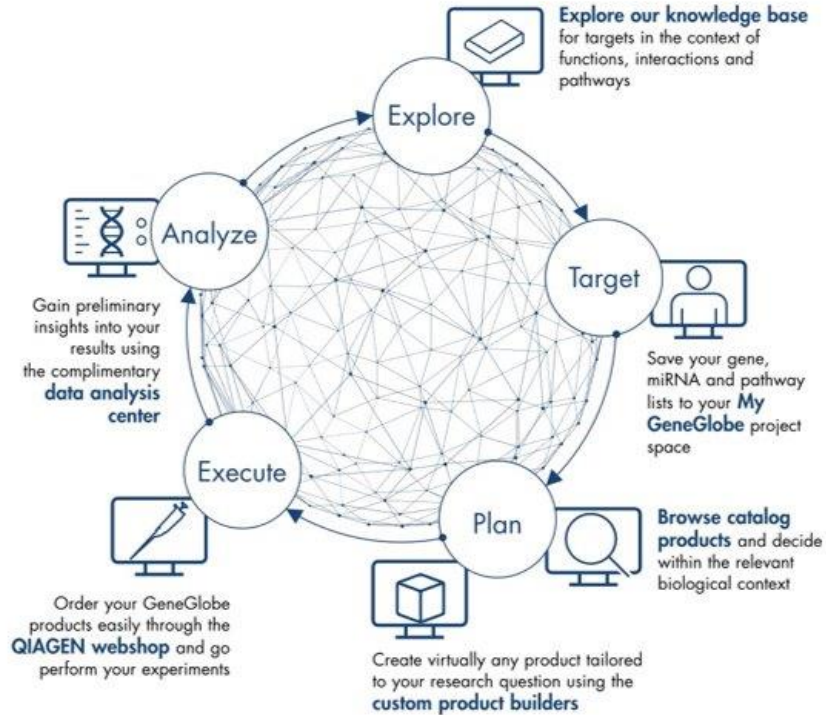
Gene Targets

Verification Assays

QIacuity Consumables—Assay Content



GeneGlobe Design & Analysis Hub





All projects > My research project > This is the title I gave to the experiment > Taxonomic profiling

What goes in must come out

482 findings

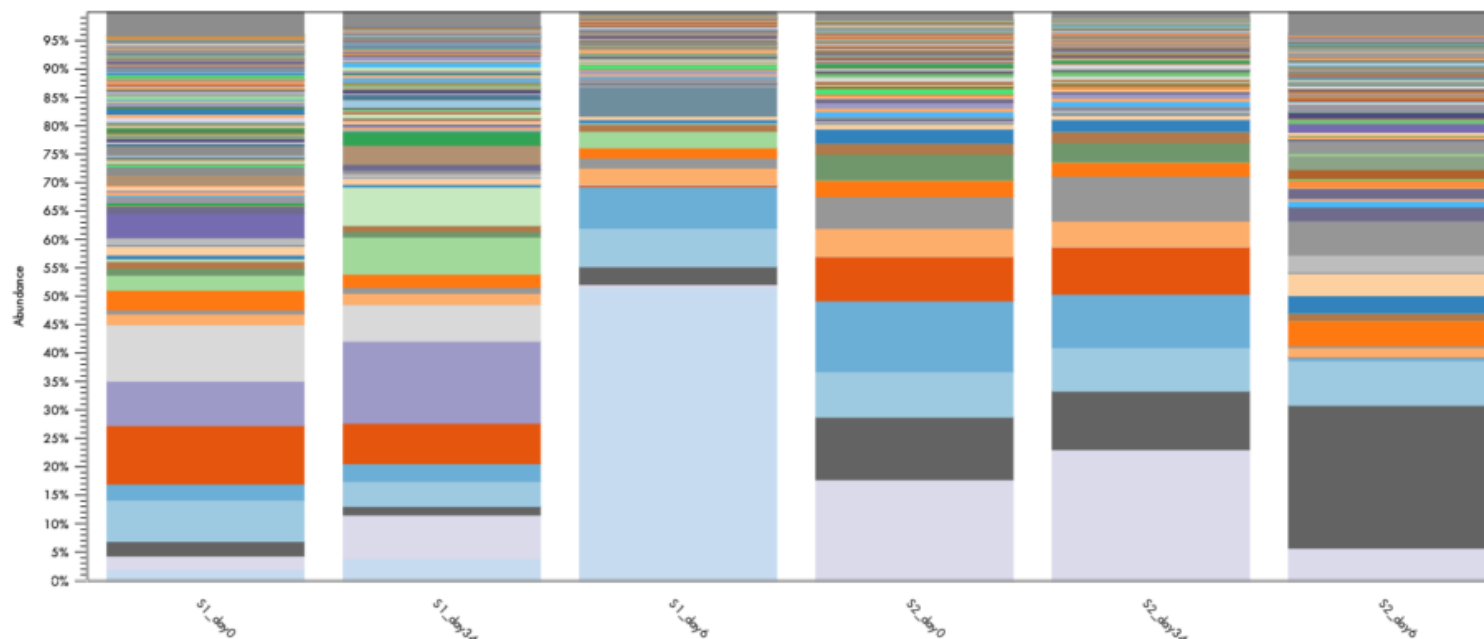
Sort by: Name (Asc)

Full feature list

Name	Assembly ID	Combined Abundance	Min
Alistipes putredinis	MGYG000001302.1	475786	866
Phocaeicola coprocola	MGYG000001306	250911	0
Barnesiella intestinihominis	MGYG000000144	337477	0
Bacteroidales (Unknown)	MGYG000000003	543104	6602
Alistipes shahii	MGYG000001378	65690	0
Bacteria (Unknown)	MGYG000000044	220285	2543
Bacteroides ovatus	MGYG000004797	478320	5222
Parabacteroides merdae	MGYG000001346	181257	422
Phocaeicola sartorii	MGYG000003681	601278	2315
Bacteroides uniformis	MGYG000000196	732217	8336
Bacteroides (Unknown)	MGYG000003844	233718	1405
Bacteroides stercoris	MGYG000004006	814512	540
Bacteroides thetaiotaomicron	MGYG000001361	29570	0
Lachnospiraceae (Unknown)	MGYG000002670	103909	8798
Ruminiclostridium_E sp900539195	MGYG000001415	29099	0
Alistipes sp000434235	MGYG000000254	22791	0
Bacteroidaceae (Unknown)	MGYG000000076	114248	1152
Sutterella wadsworthensis	MGYG000000203	133930	0
Clostridia (Unknown)	MGYG000001345	64240	3047
Agathobacter sp900546625	MGYG000001372	69259	3914
Alistipes communis	MGYG000004003	41761	0
Odoribacter splanchnicus	MGYG000003694	18677	0

Add filter

Taxonomic abundance: aggregated at Gene name/Name



Show legend

Sort samples by Name

Aggregation

Feature level Name/species

Sample level Name

Saved views and filters

Name Standard view

Save



Confidently detect
ultra-rare cell-free DNA
variants with QIAseq
Targeted cfDNA Ultra
Panels

