



S I N G U L A R
G E N O M I C S

G4 BENCHTOP SEQUENCER:
ENHANCE YOUR CORE LAB'S
SEQUENCING CAPABILITY

WACD 2023

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Sr Manager Field Application Science



INTRODUCING G4

THE WORLD'S MOST POWERFUL BENCHTOP SEQUENCER

Flexibility

1–4 flow cells
4–16 lanes

Unparalleled operational efficiency

Speed

Daily Sequencing

Industry leading run times across applications

Power

up to 3.2 Billion Reads*
480 Gb

More data per day than any other benchtop sequencer

Accuracy

80–90% bases
≥ Q30

Novel 4 color, Rapid SBS chemistry



* 3.2 billion reads on Max Read Kits and 480Gb for F3 2x150

G4 SEQUENCER IS DESIGNED FOR DAILY SEQUENCING

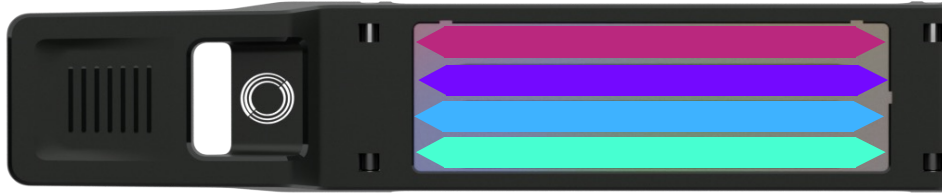
	Reagent Configuration ¹	Run Time ²
F2 Flow Cell	100 cycles	~11 hours
	200 cycles	~15 hours
	300 cycles	~19 hours
F3 Flow Cell	50 cycles	8–11 hours
	100 cycles	11–14 hours
	200 cycles	15–19 hours
	300 cycles	19–24 hours
Max Read	10x Single Cell	~30 hours
	10x Spatial FFPE	~24 hours



¹ Reagents include 50 additional cycles above what is represented to account for adapters and indices.
² Run time measured from run start through clustering, sequencing and instrument wash for non-indexed reads.

FLOW CELL AND LANE COMPARTMENTALIZATION ACCOMMODATING DIVERSE EXPERIMENTAL NEEDS

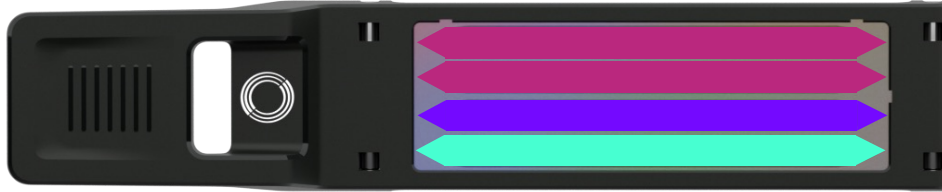
Lane Ownership



F2 Flow Cell

~50M Clusters per Lane
~200 M Clusters per Flow Cell

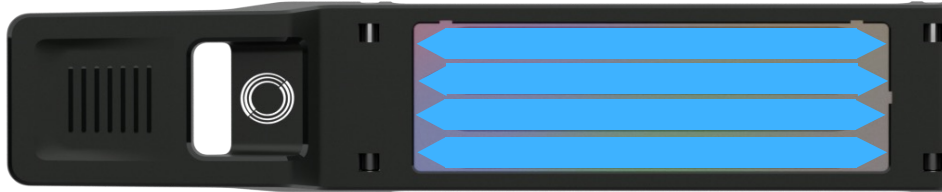
Multi-Lane Samples



F3 Flow Cell

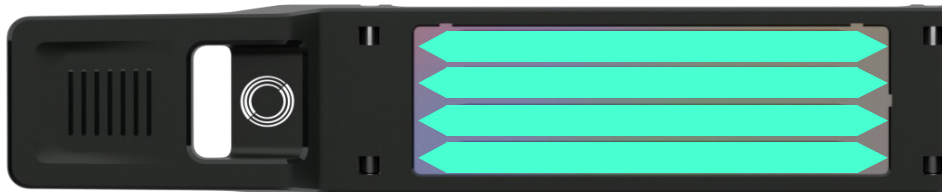
~100M Clusters per Lane
~400 M Clusters per Flow Cell

Flow Cell Ownership

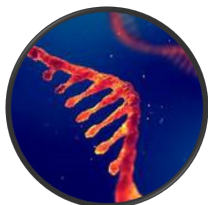


\$150–\$250 per Lane
\$600–\$1,000 per Flow Cell

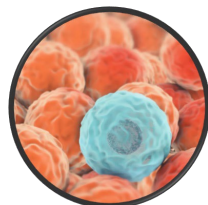
Flow Cell Ownership



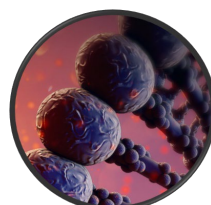
SEQUENCING APPLICATIONS



RNA



Single Cell RNA



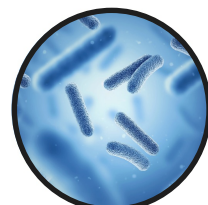
Targeted Panel



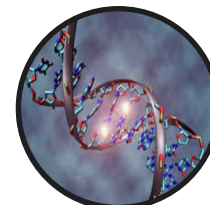
Whole Exome



Whole Genome



Metagenomics



Methyl-seq

Unmatched Versatility Serving a Broad Range of Applications

G4 has been designed to deliver fast, flexible sequencing

APPLICATION NOTE
RNA Sequencing on the G4™

The unique flow cell design and scalable capacity of the G4 sequencing lane to process 6-48 samples per run across 12-48 lanes and 4 to 15 lanes.

- The G4 Sequencing Platform allows accurate RNA sequencing data highly correlated with the industry standard sequencing process in just to 15 hours.

Introduction

RNA sequencing (RNA-seq) can now generate transcriptomic data with high resolution gene expression, detect novel transcripts, and characterize new isoforms of existing genes. This information can be used to understand the genetic mechanisms that differentiate normal and diseased cells. RNA-seq data is used to identify novel transcripts, measure changes in gene expression, and discover novel isoforms. RNA-seq data is used to identify novel transcripts, measure changes in gene expression, and discover novel isoforms.

RNA-Seq Parameters

Parameter	6	12	24	48
Sequencing	12,000	24,000	48,000	96,000
Reads/Run	1,000,000,000	2,000,000,000	4,000,000,000	8,000,000,000
Reads/Cell	100,000,000	200,000,000	400,000,000	800,000,000
Reads/Cell/Run	10,000,000,000	20,000,000,000	40,000,000,000	80,000,000,000
Reads/Cell/Run/Cell	1,000,000,000	2,000,000,000	4,000,000,000	8,000,000,000
Reads/Cell/Run/Cell/Run	100,000,000	200,000,000	400,000,000	800,000,000
Reads/Cell/Run/Cell/Run/Cell	10,000,000,000	20,000,000,000	40,000,000,000	80,000,000,000
Reads/Cell/Run/Cell/Run/Cell/Run	1,000,000,000	2,000,000,000	4,000,000,000	8,000,000,000

Table 1. RNA-Seq sequencing parameters.

APPLICATION NOTE
Single Cell RNA Sequencing on the G4™

- Rapid SBS enables cost-efficient delivery of 1-8 single cell RNA sequencing samples in 12-15 hours.
- Seamless integration of the G4 into existing library prep workflows and bioinformatics pipelines.
- G4 delivers highly accurate read data comparable to leading single-cell platforms.

Introduction

Single cell RNA sequencing (scRNA-seq) has revolutionized single cell transcriptomic analysis in embryology, developmental biology, and cancer by enabling the resolution of single cell populations and heterogeneity within a population. A major goal of single cell RNA-seq is to identify novel transcripts and isoforms. This information can be used to understand the genetic mechanisms that differentiate normal and diseased cells. RNA-seq data is used to identify novel transcripts, measure changes in gene expression, and discover novel isoforms.

scRNA-Seq Sequencing Parameters

Parameter	6	12	24	48
Sequencing	12,000	24,000	48,000	96,000
Reads/Run	1,000,000,000	2,000,000,000	4,000,000,000	8,000,000,000
Reads/Cell	100,000,000	200,000,000	400,000,000	800,000,000
Reads/Cell/Run	10,000,000,000	20,000,000,000	40,000,000,000	80,000,000,000
Reads/Cell/Run/Cell	1,000,000,000	2,000,000,000	4,000,000,000	8,000,000,000
Reads/Cell/Run/Cell/Run	100,000,000	200,000,000	400,000,000	800,000,000
Reads/Cell/Run/Cell/Run/Cell	10,000,000,000	20,000,000,000	40,000,000,000	80,000,000,000
Reads/Cell/Run/Cell/Run/Cell/Run	1,000,000,000	2,000,000,000	4,000,000,000	8,000,000,000

Table 1. scRNA-Seq sequencing parameters.

APPLICATION NOTE
Targeted Sequencing Using Agilent SureSelect and the G4™ Sequencing Platform

- Rapid, accurate, and cost-efficient analysis of key variant types for oncology, translational and clinical research with Agilent SureSelect products.
- Seamless integration of the G4 into the Agilent SureSelect Exome V6 library preparation workflow and bioinformatics pipeline.
- Highly accurate targeted sequencing data generated on the G4 Platform with a lower duplication rate and coverage bias than the Illumina HiSeq 4000.

Introduction

Agilent SureSelect Exome V6 (SSE) has become a standard for targeted sequencing (TS) in clinical and research settings. SSE has been used for a wide range of applications, including the identification of novel variants, the discovery of novel transcripts, and the characterization of novel isoforms. SSE has been used for a wide range of applications, including the identification of novel variants, the discovery of novel transcripts, and the characterization of novel isoforms.

Agilent SureSelect Exome v6 and XT HSZ Kits

The SureSelect Exome V6 and XT HSZ Kits are designed for the identification of novel variants, the discovery of novel transcripts, and the characterization of novel isoforms. SSE has been used for a wide range of applications, including the identification of novel variants, the discovery of novel transcripts, and the characterization of novel isoforms.

APPLICATION NOTE
Whole Exome Sequencing on the G4™

- Rapid sequencing by synthesis (SBS) enables cost-efficient delivery of 8-64 samples in less than 24 hours.
- The G4 delivers highly accurate read data comparable to leading platforms with SPW and INDEL, F1 scores at 99% and 99%, respectively.

Introduction

Whole exome sequencing (WES) enables the discovery and characterization of genetic variants across the entire coding region of the genome. WES has been used for a wide range of applications, including the identification of novel variants, the discovery of novel transcripts, and the characterization of novel isoforms. WES has been used for a wide range of applications, including the identification of novel variants, the discovery of novel transcripts, and the characterization of novel isoforms.

TECHNICAL NOTE 1.0
Human Genome Sequencing

Performance Characterization of the G4 Sequencing Platform for Human Whole Genome Sequencing

Introduction

The G4 Sequencing Platform is a high-accuracy, high-throughput sequencing platform designed for the identification of novel variants, the discovery of novel transcripts, and the characterization of novel isoforms. The G4 Sequencing Platform is a high-accuracy, high-throughput sequencing platform designed for the identification of novel variants, the discovery of novel transcripts, and the characterization of novel isoforms.

Application Note
Multiplex PCR Targeted Enrichment Solution on the G4™ Sequencing Platform

Abstract

This application note demonstrates the capability of the G4 Sequencing Platform for multiplex PCR targeted enrichment. The G4 Sequencing Platform is a high-accuracy, high-throughput sequencing platform designed for the identification of novel variants, the discovery of novel transcripts, and the characterization of novel isoforms.

Introduction

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Application Focus

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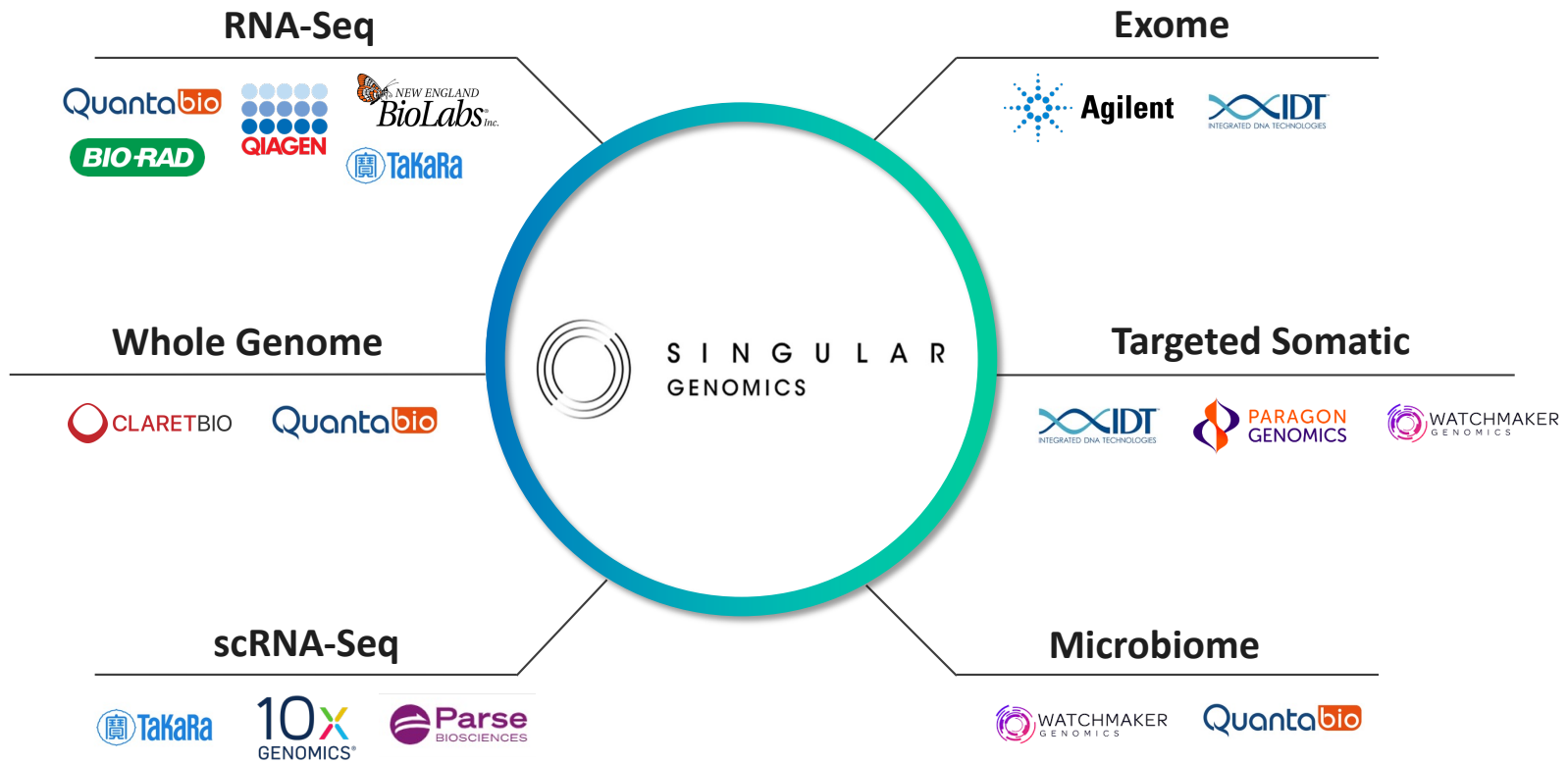
Parameter	6	12	24	48
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Reads/Cell/Run	10,000,000,000	20,000,000,000	40,000,000,000	80,000,000,000
Reads/Cell/Run/Cell	1,000,000,000	2,000,000,000	4,000,000,000	8,000,000,000
Reads/Cell/Run/Cell/Run	100,000,000	200,000,000	400,000,000	800,000,000
Reads/Cell/Run/Cell/Run/Cell	10,000,000,000	20,000,000,000	40,000,000,000	80,000,000,000
Reads/Cell/Run/Cell/Run/Cell/Run	1,000,000,000	2,000,000,000	4,000,000,000	8,000,000,000

Table 1. Multiplex PCR Targeted Enrichment Solution on the G4 Sequencing Platform parameters.



LEADING LIBRARY PREP COMPATIBILITY VALIDATED PROTOCOLS FOR EASE OF ADOPTION

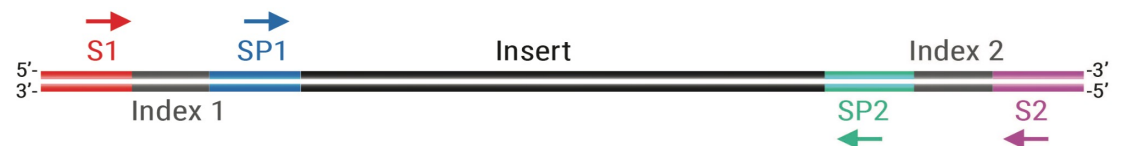
2 G4 Platform




LIBRARY PREPARATION

De novo

Through existing Library Prep partners.
Adapters for PCR and PCR-Free workflows
Indexed (96 UDI, 12 bp) and non-indexed PCR primers.



By adapting existing libraries

- Option A: Original indexing information is kept 
PCR protocol and PCR primers available (non-indexed primers).

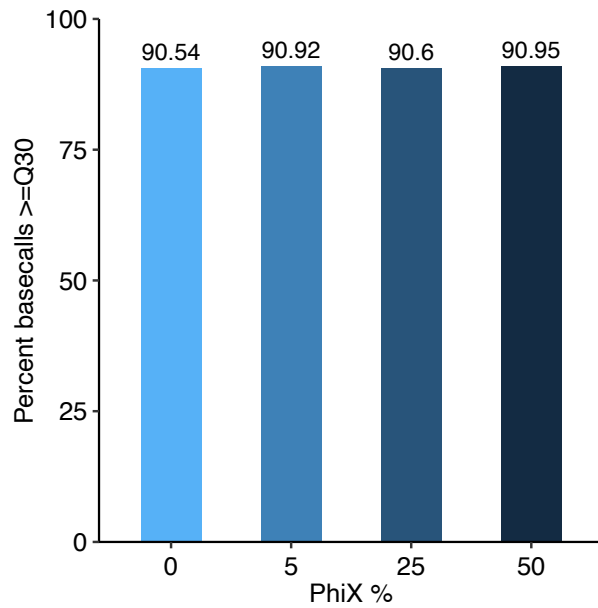
- Option B: Original indexing information can be replaced 
PCR protocol and PCR primers available (indexed and non-indexed primers).



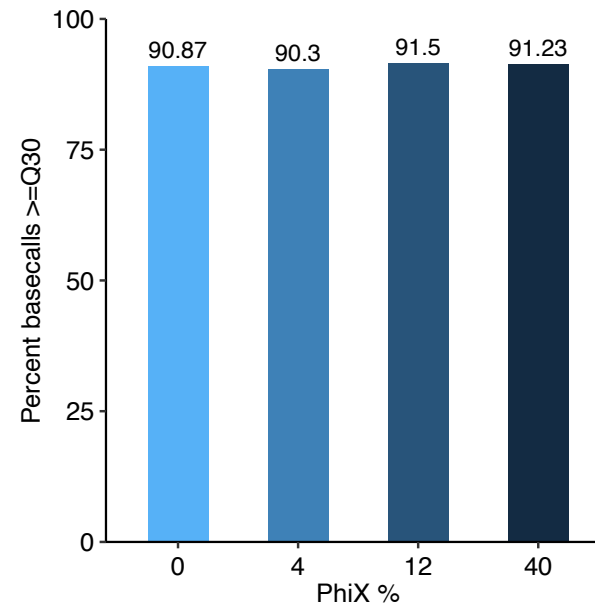
STRONG PERFORMANCE WITH LOW DIVERSITY LIBRARIES

NO NEED FOR PHIX

Percent PhiX vs quality score for EM-Seq library



Percent PhiX vs quality score for an extremely low diversity (two-amplicon) library



Optimized Workflow

Unmatched 3.2 billion reads per run on a benchtop system
Perfectly matches existing Chromium kits



Chromium

4 rxn kits



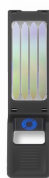
1-4



16 rxn kits



1-4



5-8



9-12



13-16





Sequence

Sample Flexibility
4-16 samples provides ultimate flexibility

Scalable, Consistent Economics

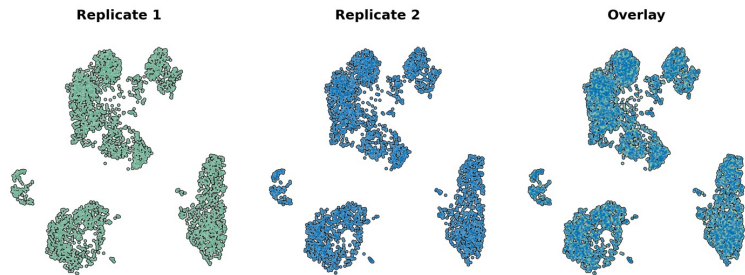
Maximizing throughput and decreasing cost for single cell sequencing
Savings up to \$600 per sample, or over \$6,000 per run

		4 Samples	16 Samples
G4	Flow Cell	M3 (800M reads)	4x M3 (3,200M reads)
	Price / Sample	\$200 	\$200 
NextSeq 2000	Flow Cell ¹	P3 100 cycle (1,200M reads)	3x P3 100 cycle (3 runs, 3,600M reads)
	Price / Sample ²	\$832	\$624

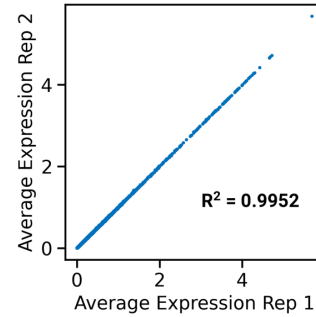
¹ Assumes 10,000 cells and 20,000 reads
² Reflects publicly available list prices

MAX READS METHOD HIGHLY ACCURATE FOR SINGLE CELL SEQ CONCORDANT WITH INDUSTRY STANDARD SEQUENCING

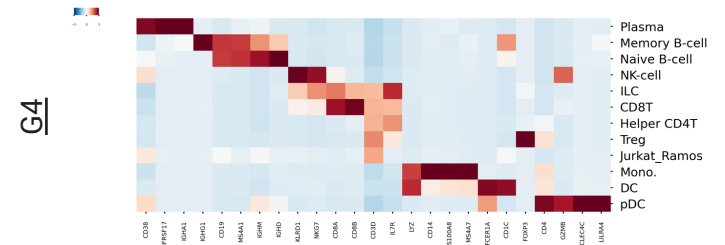
Technical Replicate Performance



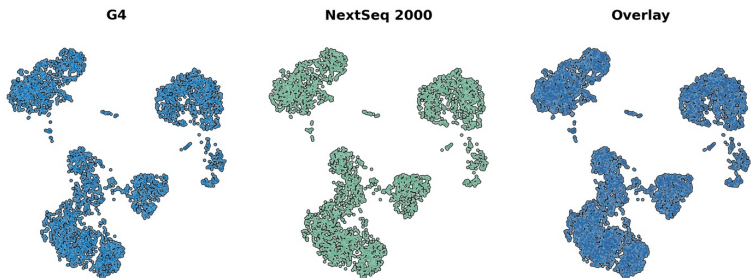
Correlation Across Replicates



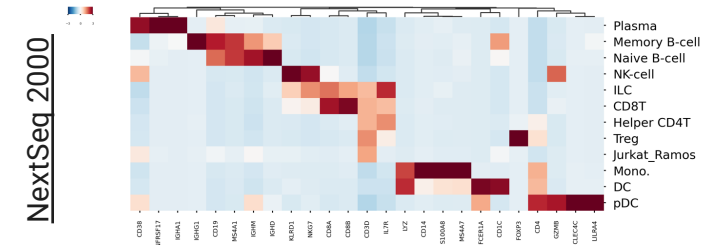
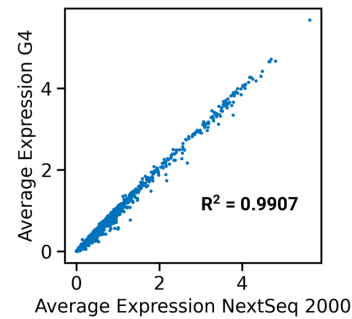
Immune Cell Marker Expression



Comparison to NextSeq 2000



Correlation Across Platforms



ON-MARKET FEEDBACK

CUSTOMER QUOTES

2 G4 Platform

“The flexibility and speed of the G4 has enabled our Spatial Technologies Unit to use a single instrument for new single cell and spatial transcriptomic assay pilots as well as production, decrease turnaround times, and meet demanding deadlines for our clients.”



“We have been very excited by the enthusiasm of the researchers we support for the G4 with **many labs already submitting projects** to be run on the sequencer. These include samples for RNA-Seq (both standard and high-throughput), CUT&RUN, as well as custom protocols where the laboratories are preparing their own libraries.”

“... I’m blown away by the fact that we’re able to get such **high-quality sequencing results back in less than a day!** We’re looking forward to continuing to collaborate with Singular Genomics in 2023 and being able to share some of the exciting sequencing projects we’re working on!”



“The flexibility and consumable costs were undeniably compelling to purchase the G4. Substantially better than an Illumina instrument with excellent flexibility in flow cell loading tolerances. **Output is much higher than reported in company spec sheets.**”

SUMMARY

Industry Leading Speed and Flexibility

The G4 combines rapid SBS with flexible throughput to reduce turnaround times for sequencing labs.

Plug and Play

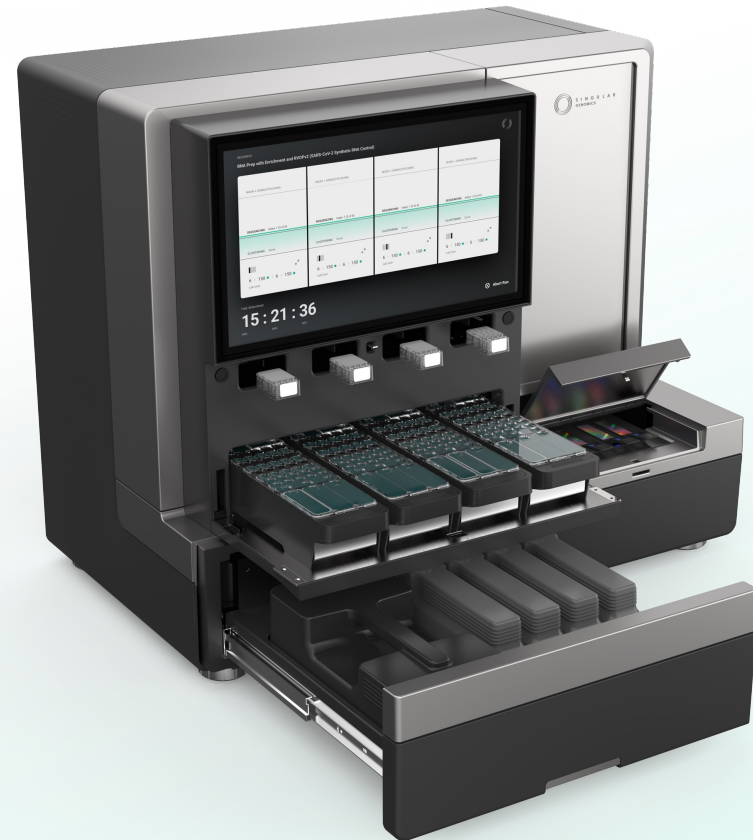
The G4 fits into the existing lab ecosystem and enables superior flexibility.

Highly Accurate

The G4 shows high concordance with the leading NGS platform across applications.

Max Reads

Maximizing throughput and decreasing cost for single-cell sequencing.





THANK YOU

