Statement of Work (SOW)

July 15, 2026

To: Contracting Officer

From: Project Manager (PM) Janelle Cortner, NCI/CBIIT/OCIO

Organization: HHS/NIH/NCI/CBIIT/OCIO

Project Title: DRAGEN-GATK Licenses and Support at FRCE and Biowulf

1.0. INTRODUCTION/OVERVIEW

1.1 BACKGROUND

The U.S. Department of Health and Human Services, National Institutes of Health (NIH), National Cancer Institute (NCI), Center for Biomedical Informatics and Information Technology (CBIIT), Office of the Chief Information Officer (OCIO) requires license and support for the continued use of the Illumina Dragen processors.

This acquisition will support the Whole Genome and Whole Exome Data Processing Workflow at the NCI. Raw data from Illumina whole genome and whole exome sequencing instruments requires two multi-step processing phases before the data is ready for analysis.

- In the first processing phase, the raw FASTQ files are QC'd and aligned to a reference genome to generate BAM files. Many groups, including the CCR SF, use Illumina's proprietary Dynamic Read Analysis for Genomics (DRAGEN) processor for the QC and alignment step.
- Following alignment, variant discovery tools are then used to analyze the BAM files to identify insertions, deletions (INDELs) single nucleotide polymorphisms (SNPs), and multi-nucleotypic polymorphisms (MNPs), which are then compiled into Variant Call Files (VCFs). While several tools are available for variant calling, the Broad's open-source Genomic Analysis Tool Kit (GATK) software has emerged as a widely accepted standard for variant discovery and is used by several groups at NCI, including CCBR and SF.

After the alignment and variant calling, BAM and VCF files are then returned to Investigators for more detailed analysis related to the specific genotypes of the organisms under study. To co-analyze sequencing data generated by different sources it is important that the same reference genome be used for alignment and that the same variant calling procedures are used. For this reason, studies on aggregated whole genome or whole exome data frequently require reprocessing of FASTQs to assure that the data are harmonized before more detailed analysis can occur. This can be difficult to arrange if the data to be aggregated were produced and processed by multiple different facilities. However, the proprietary DRAGEN alignment software has recently been combined with the GATK tools in a DRAGEN-GATK package and is available for deployment at cloud or on-premises computational resources via open source or commercial options. This will add to the existing capabilities of the Data Management

and Analysis Program (DMAP) at the OCIO. This resource will be a valuable addition to the NCI Genomics Toolkit hosted on the NCI Integrated Data Analysis Portal (NIDAP), as well as to any resource hosting tools for genomic data processing.

The contract history includes:

- 140D0425P0171 – Illumina, Inc. 9/29/25 – 9/28/26
- 75N91023P00870 - Illumina, Inc. 9/15/24 – 9/14/25
- 75N91023P00870 - Illumina, Inc. 9/15/23 – 9/14/24

1.2 OBJECTIVES

The purpose of this contract/task order is to provide the NCI with Illumina Dragen licenses, and processing capacity to support the Data Management and Analysis program for computational biology, sequencing computations, and bio-analysis.

DRAGEN GATK processors are an Illumina product. While the GATK software is available open source, Illumina offers the only FPGA hardware configuration, which accelerates data processing and reprocessing by up to 30X and NCI purchased those processors in a prior year. There is no commercially available equivalent using alternative software. We now seek to obtain annual licenses scoped to our projected level of usage.

2.0 CONTRACTOR WORK SCOPE/ REQUIREMENTS

Independently, and not as an agent of the Government, the Contractor shall furnish all necessary services, qualified personnel, materials, equipment, and facilities (except as otherwise specified herein) to perform the work set forth below. The Contractor shall remain solely responsible for control and supervision of employees and any Subcontractors while performing under this contract.

DRAGEN-GATK Deployment: Given that much of NCI IRP's genomic data are stored on-premises in both Frederick and Shady Grove, we plan to deploy one DRAGEN at Biowulf and one at FRCE. The commercial option for DRAGEN also includes GATK and runs as an FPGA which can be deployed on a node at either Biowulf or FRCE, with jobs managed via SLURM, and increases throughput by as much as 30X. Users will access DRAGEN either via NIDAP or directly on the batch clusters via command line. By deploying DRAGEN-GATK at both Biowulf and FRCE and making it available via NIDAP, the resource will be widely available to all NCI users.

The NCI requires:

- 2 annual software licenses for LVL 2 DRAGEN Server processors at 250,000GB throughput, one for Frederick and one for Biowulf, to support data analysis workloads in the bio-computing space.

- 2 annual Dragen Server Advance Exchange Support Plans for NCI processors installations with Remote Technical Support 8x5, one for Frederick and one for Biowulf, to support data analysis workloads in the bio-computing space.

Performance period: 9/29/2026 to 9/28/2027

2.2 DELIVERABLES

The contractor shall provide the following deliverables:

Item No.	Deliverable Description	Deliverable Due Date	Deliver To
1	**NIH/NCI/FRCE Location** - Illumina DRAGEN Server v4 1 year support. Includes Advance Exchange for Dragen Server; Remote Technical Support 8x5. Qty - 1	Throughout contract	Douglas O'Neal 8560 Progress Drive Frederick, MD 21701
2	**NIH/NCI/FRCE Location -** DRAGEN Server Lvl 2 1 year License. Throughput of 250,000 Gb on DRAGEN Server. Qty - 1	Immediately upon award	Douglas O'Neal 8560 Progress Drive Frederick, MD 21701
3	**NIH/NCI/BIOWULF Location -** Illumina DRAGEN Server v4 1 year support. Includes Advance Exchange for Dragen Server; Remote Technical Support 8x5. Qty - 1	Throughout contract	c/o Janelle Cortner 6555 Rock Spring Dr, Bethesda, MD 20817
4	**NIH/NCI/BIOWULF Location -** DRAGEN Server Lvl 2 1 year License. Throughput of 250,000 Gb on DRAGEN Server. Qty -	Immediately upon award	c/o Janelle Cortner 6555 Rock Spring Dr, Bethesda, MD 20817