BaseSpace® Onsite Sequence Hub

A local version of the BaseSpace Sequence Hub enabling storage, analysis, and sharing of data from the MiniSeq®, MiSeq®, MiSeqDx® (in RUO mode), NextSeq® 500, NextSeq 550, HiSeq® 2500, HiSeq 3000, and HiSeq 4000 Systems over a private network.

Highlights

- **Seamless Data Management Workflow**
  Seamless NGS workflow solutions include sample, library, and run preparation and a wide range of informatics analysis apps
- **Secure, Local Environment**
  Fault-tolerant informatics appliance operates without internet connection and protects data with access controls and encryption
- **Affordable NGS Management**
  Easy installation, maintenance, and scalability minimize bioinformatics and IT assistance

Introduction

Next-generation sequencing (NGS) has revolutionized biological research. Historically, storing, processing, organizing, and analyzing data have required assistance from bioinformatics professionals to run command-line software and IT departments to set up and maintain dedicated infrastructure. The BaseSpace Onsite Sequence Hub eliminates these challenges by providing affordable, secure access to a growing ecosystem of easy-to-use applications for managing sequencing workflows.

The BaseSpace Onsite Sequence Hub is a local version of BaseSpace Sequence Hub that offers a secure data storage and computing solution that does not require an internet connection. Researchers using BaseSpace Onsite Hub can take advantage of most of the core features and benefits in the BaseSpace Sequence Hub*, whereas all data remains on site and accessible only over a private network. Available as an option for the MiniSeq, MiSeq, MiSeqDx (in RUO mode), NextSeq 500, NextSeq 550, HiSeq 2500, HiSeq 3000, and HiSeq 4000 Systems, BaseSpace Onsite Hub is an appliance that ships with the sequencing instrument, allowing biologists to set up and analyze NGS experiments in hours (Figure 1).

Seamless Data Management Workflow

BaseSpace Onsite Sequence Hub software guides researchers from experimental design through actionable analysis. Run preparation, data processing, and collaboration tools are integrated into a single environment with the MiniSeq, MiSeq, MiSeqDx (in RUO mode), NextSeq 500, NextSeq 550, HiSeq 2500, HiSeq 3000, and HiSeq 4000 System workflows (Figure 2), and can be accessed from any web browser (Figure 3).

Easy Sample and Run Management

Researchers using the MiniSeq, NextSeq 500, and NextSeq 550 Systems can access the BaseSpace Onsite Hub “Prep” tab to plan sequencing runs in 4 easy steps, tracking thousands of samples and experiments (Figure 4A).

Figure 1: BaseSpace Onsite Appliance—BaseSpace Onsite Sequence Hub provides an affordable, secure, easy-to-use solution for storing, analyzing, and sharing NGS data generated using a MiniSeq, MiSeq, MiSeqDx (in RUO mode), NextSeq 500, NextSeq 550, HiSeq 2500, HiSeq 3000, or HiSeq 4000 System over a private network.

The intuitive interface prompts users to enter or import sample information, place samples onto library preparation plates, and pool libraries for sequencing. Automated quality control is performed at each step of the process. Index compatibility is confirmed before the sequencing run begins. The NextSeq Control Software retrieves run information directly from the BaseSpace Onsite Hub Prep tab.

Researchers using the MiSeq, MiSeqDx (in RUO mode), HiSeq 2500, HiSeq 3000, and HiSeq 4000 Systems can plan sequencing runs in a few easy steps using the Illumina Experiment Manager and sample sheet wizard (Figure 4B). The wizard includes options for application selection, workflow parameters selection, and sample selection to generate a sample sheet (.csv) file. The sample sheet is then uploaded to the MiSeq or HiSeq System where the MiSeq Control Software or HiSeq Control Software coordinates the sample information with the sequencing run and BaseSpace Onsite Hub analysis.

* Learn more about BaseSpace Apps at www.illumina.com/informatics/sequencing-microarray-data-analysis/basespace-core-apps.ilmn.

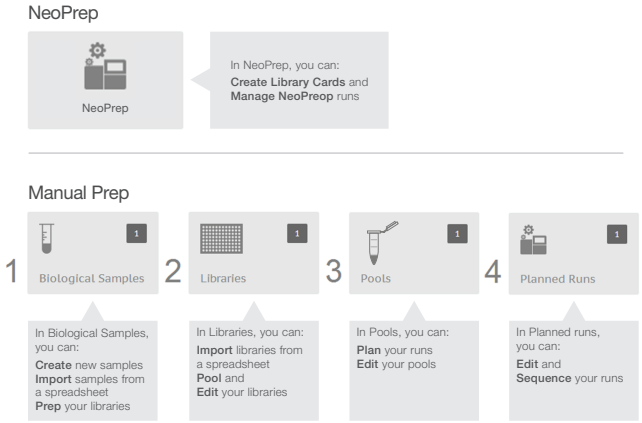
Seamless Integration

BaseSpace Onsite Hub integrates seamlessly with the MiniSeq, MiSeq, MiSeqDx (in RUO mode), NextSeq 500, NextSeq 550, HiSeq 2500, HiSeq 3000, and HiSeq 4000 Systems. To start a run, simply load the flow cell and reagent cartridge into the instrument. The on-instrument software, MiSeq Control Software, NextSeq Control Software, or HiSeq Control Software, retrieves the run information and performs a series of checks before starting the sequencing run automatically (Figure 5). As the run progresses, base calls and quality metrics are transferred instantly to BaseSpace Onsite Hub where the data are available for review in the "Runs" tab (Figure 6).

Figure 2: Seamless Data Management Workflow Using BaseSpace Onsite Hub—BaseSpace Onsite Hub software guides researchers using the MiniSeq, MiSeq, MiSeqDx (in RUO mode), NextSeq 500, NextSeq 550, HiSeq 2500, HiSeq 3000, or HiSeq 4000 Systems from experimental design through variant identification.

Figure 3: Log In to BaseSpace Onsite Hub From Any Instrument or Computer—Secure login features enable researchers to access data in BaseSpace Onsite Hub from any web browser. Login screen shown is for the HiSeq 2500 Control Software; screen to access the MiniSeq, MiSeq and NextSeq Control Software is similar.

A. Use the Prep tab in the MiniSeq, NextSeq 500 and NextSeq 550 Systems using NeoPrep or Manual Prep



B. Use the Illumina Experiment Manager for the MiSeq, MiSeqDx (in RUO mode), HiSeq 2500, HiSeq 3000 and HiSeq 4000 Systems

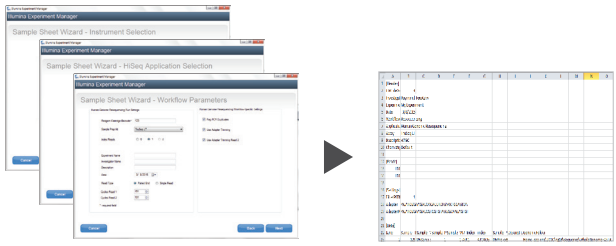


Figure 4: Easy Sample Management—BaseSpace Onsite Hub software enables sequencing and tracking of thousands of samples and experiments.

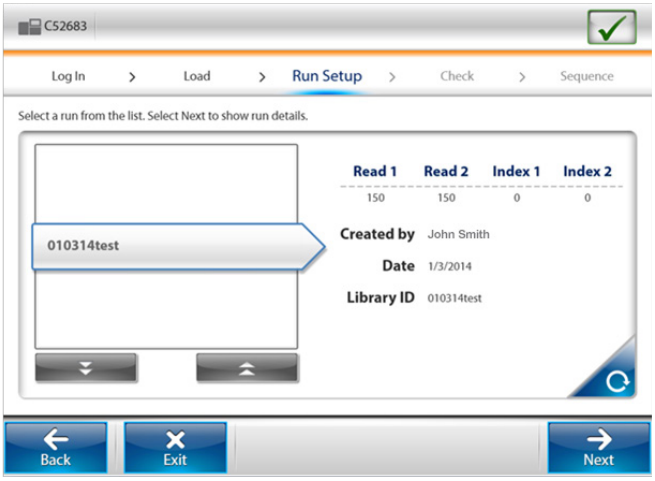


Figure 5: Run SetUp Using BaseSpace Onsite Hub—The MiniSeq, NextSeq 500, and NextSeq 550 Control Software retrieves run information from BaseSpace Onsite Hub for seamless sample tracking throughout sequencing and analysis.

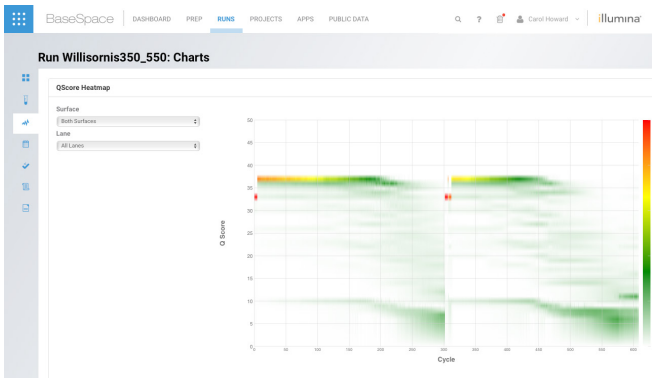


Figure 6: BaseSpace Onsite Hub Enables Real-Time Data Review in the Runs Tab—Base calls and quality metrics from a sequencing run transfer instantly to BaseSpace Onsite Hub for review in real time. Provided plot illustrates the Runs feature and does not correspond to actual MiniSeq, MiSeq, MiSeqDx (in RUO mode), NextSeq 500, NextSeq 550, HiSeq 2500, HiSeq 3000, or HiSeq 4000 System data.

Figure 7: BaseSpace Apps Empower NGS Analysis—BaseSpace Onsite Hub includes access to a wide range of apps for analyzing NGS data.

Push-Button Data Processing

Empowered by a suite of tailor-made data processing and analysis applications, BaseSpace Onsite Hub converts data to answers with the push of a button. Easy-to-use BaseSpace Apps support some of the most popular biological applications (Figure 7) enabled by Illumina NGS technology:

- RNA sequencing (RNA-Seq) using industry-standard TopHat[1] and Cufflinks[2] methods
- Exome/enrichment sequencing with BWA/GATK or Isaac™ Genome Alignment Software,[3,4] a fast and accurate alignment and variant calling method developed by Illumina
- Whole-genome sequencing (WGS) using BWA/GATK or Isaac Genome Alignment Software
- Tumor-normal sequencing with Illumina Strelka[5]-based combined calling
- VariantStudio variant analysis, including annotation, filtering, classification, and reporting†
- 16S metagenomics using taxonomic classification of ribosomal RNA (rRNA)-targeted amplicon reads
- Targeted genomic panels including TruSeq® Custom Amplicon, TruSeq Amplicon Cancer, and the TruSight® Myeloid, TruSight Tumor, and TruSight Cancer Sequencing Panels
- WGS long-read assembly
- WGS phasing analysis
- DNA Methylation
- Visualization with the Integrative Genome Viewer (IGV)
- FASTQ Utilities
- FASTQ Quality Assessment
- Third-party apps for *de novo* assembly

BaseSpace Apps transform the BaseSpace Onsite Hub into a convenient NGS data analysis solution. With push-button data analysis, researchers spend significantly less time processing data and more time focusing on the next discovery.

Local Collaboration

Collaboration is simple with BaseSpace Onsite Hub (Figure 8). Users can share runs and projects instantly with colleagues. Data sharing with BaseSpace Onsite Hub is an efficient way to exchange ideas and NGS data with colleagues who prefer to use their own analysis methods to view or compare results.

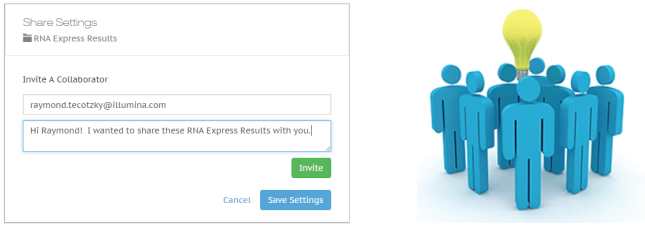


Figure 8: Easy Sharing of NGS Data and Analysis Results—With BaseSpace Onsite Hub, researchers can share run information and raw or processed NGS data to get help, troubleshoot, or exchange ideas.

† Learn more about VariantStudio software at www.illumina.com/variantstudio.

Secure, Local Environment

The BaseSpace Onsite Hub is designed with extreme attention to data security and integrity. Server-grade components reduce failures though redundant components avoid downtime in the event of failure. Common repairs can be performed on site by laboratory personnel with or without assistance from Illumina. Security and permissions designated by the system owner restrict user interface access. If necessary, data can be encrypted. All information is stored in BaseSpace Onsite Hub, and can be archived on any network-attached storage (NAS) device available from Illumina or other manufacturers supporting the Common Internet File System (CIFS) standard.

Affordable to Install, Maintain, and Scale

With BaseSpace Onsite Hub, NGS labs no longer require multiple third-party tools or daily assistance from IT administrators. The single environment significantly reduces the cost associated with developing and maintaining infrastructure. Server capacity can be scaled easily by connecting 2 or more systems. Illumina engineers install BaseSpace Onsite Hub within hours, without additional installation expense. Researchers can contact Illumina Technical Support with any questions, from library preparation to analysis.

Learn More

To learn more about BaseSpace Onsite Hub, visit www.illumina.com/basespaceonsite.

Ordering Information

Product	Catalog No.
BaseSpace Onsite Hub LT System	20001331
BaseSpace Onsite Hub HT System	20001332
BaseSpace Onsite Hub HT Storage 2X	20001333
BaseSpace Onsite Hub HT Storage 3X+Rack	20001334
BaseSpace Onsite Hub HT Storage 4X+Rack	20001335

BaseSpace Onsite Hub Specifications[a]

Specification		BaseSpace® Onsite Hub HT System	BaseSpace® Onsite Hub LT System
CPU	Model	E5-2690	E5-2630 v2
	# of CPU	2	2
	Cores	16	12
	Speed (GHz)	2.9	2.6
Memory, Speed		128 GB, 1600 MHz	128 GB, 1600 MHz
Encryption		Yes	Yes
Raid Controller		LSI 9280-16i4e	LSI 9361-8i
Hard Disk Storage		2 x 2 TB (RAID 1)=4 TB OS	2 x 2 TB (RAID 1)=4 TB OS
		6 x 4 TB=24 TB Data	4 x 2 TB=8 TB Data
		5 x 4 TB=**20 TB Usable** NGS Data Storage in RAID 5 Configuration	3 x 2 TB=**6 TB Usable** NGS Data Storage in RAID 5 Configuration
Enterprise Grade Disks		Yes	Yes
Disk Cache		2 TB SSD	4 TB non-SSD
BMC, USB3, Dual Power Supply		Yes	Yes
MiniSeq Instruments Supported		No[b]	Yes
MiSeqDx (research mode) Instruments Supported		Yes	Yes
NextSeq 500, 550 Instruments Supported		Yes	Not Recommended
HiSeq 2500, 3000, 4000 Instruments Supported		Yes	Not Recommended

a. Specifications upgraded regularly. Contact your local Illumina account manager for the most current configuration.
b. In development for future release.

References

1. Kim D, Pertea G, Trapnell C, et al. TopHat2: accurate alignment of transcriptomes in the presence of insertions, deletions, and gene fusions. *Genome Biol*. 2013;14(4): R36.
2. Trapnell C, Hendrickson DG, Sauvageau M, et al. Differential analysis of gene regulation at transcript resolution with RNA-Seq. *Nat Biotechnol*. 2013;31(1): 46-53.
3. Fast, accurate, and easy alignment and variant calling with Isaac Genome Alignment Software and Isaac Variant Caller. www.illumina.com/documents/products/whitepapers/whitepaperiasscworkflow.pdf. Accessed 20 March 2015.
4. Raczy C, Petrovski R, Saunders CT, et al. Isaac: ultrafast whole-genome secondary analysis on Illumina sequencing platforms. *Bioinformatics*. 2013;29(16): 2041-2043.
5. Saunders C, Wong W, Swamy S, et al. Strelka: accurate somatic small-variant calling from sequenced tumor-normal sample pairs. *Bioinformatics*. 2012;28:1811-1817.

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