FAST, ACCURATE, SCALABLE GENOMIC DATA ANALYSIS

SUPERIOR ACCURACY

Compatible with all versions of BWA and GATK, the Bina platform offers superior indel and SNP detection. Our open platform accelerates all of the best-in-class pipelines.

ULTRA HIGH SPEED & THROUGHPUT

The Bina Platform takes 4 hours to process a human genome from raw fastq to annotated vcf. Monthly, Bina can process 100 whole human genomes, 1000 whole exomes or 1000 RNA-Seq samples.

LOWEST OPERATIONAL COST

Available on a subscription basis, the cost of analyzing targeted panels, whole human genomes, whole exomes, or RNA-Seq samples is lower than most in-house bioinformatics efforts. Plus, there's no annual maintenance and support fees.

Bina Genomic Analysis Platform

The Bina Genomic Analysis Platform features a fully integrated solution that provides on-premises compute with cloud-based management.

Speed, Throughput, and Scalability

The Bina Box is the expandable computer appliance that provides high-speed, high-throughput data analysis of your NGS raw reads. Capable of processing a 40X whole human genome to vcf file in about 4 hours, a 300X whole exome in about 45 min, or up to 4 RNA-Seq samples (each ~67M reads) in about 2.5 hours, the Bina Box is both fast and cost effective. Bina offers high accuracy, using BWA/GATK pipeline for detecting SNVs and indels or Tophat2 Cufflinks for RNA-Seq. Each Bina Box consists of 4 compute nodes and you can stack additional Bina Boxes to increase throughput and speed.

Streamlined Operation and Management

- The Bina Portal is the graphical user interface of the Bina Genomic Analysis Platform. Using the Bina Portal, users can assign users, setup, monitor, and review analysis results using any web browser. The Bina Portal may also be installed behind your firewall for complete privacy and security. Users can be trained within an hour to generate vcf files from whole genome, exome, RNA-Seq, and coming soon, targeted panel samples.

Available By Subscription or On Demand

We understand that capital investments can be expensive and time consuming. Additionally your high performance computer investment may be outdated in as little as a year. That's why Bina offers a subscription package that protects you from software/hardware obselescence. With a Bina subscription you get automatic software *and* hardware upgrades. Also available is Bina-On-Demand™ for pay-as-you-go pricing.

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Features and Benefits

- Security and privacy of an on-premises solution
- Linearly scalable performance with additional Bina Boxes
- Graphical user interface for ease of use and rapid workflow execution
- $0 capital investment needed
- Automatic updates to software *and* hardware
- Subscription-based model to allow operating expense budgeting
- Optional Bina-On-Demand™ for pay-as-you-go pricing
- Lowest bioinformatics cost per sample
- Available Copy Number Variation (CNV) and Structural Variation (SV) analysis on Whole Genome analysis
- Complete solution for all your whole genome, whole exome, RNA-Seq, and soon, targeted panel needs
- Bina platform accelerates genomics pipelines with improved accuracy and usability

Bina Sequencing Analysis Applications

Application	Content Size	Processing time	Output Format
Whole Human Genome (~37X)	120Gb/1.2B reads	~4 hrs*	BAM, VCF
Whole Exome (~300X)	17Gb/228M reads	~45 min*	BAM, VCF
RNA-Seq (4 samples)	5Gb/67M reads	~2.5 hrs**	BAM, TXT (counts)
Cancer - Tumor/Normal	coming soon...		

** Using the Bina Aligner and GATK; ** Using Tophat2/Cufflinks*

Scalability Without Sacrificing Accuracy or Reproducibility

# of Nodes	Alignments		SNPs	SNP het/hom	SNPs in dbSNPs 135	Indels	Indel het/hom	Indels in dbSNP 135
	Unique	Multiple						
1	84.88%	5.61%	33,369	1.595	97.06%	1,874	1.299	94.6%
4	84.88%	5.61%	33,360	1.597	97.06%	1,872	1.297	94.6%
8	84.88%	5.61%	33,367	1.598	97.09%	1,874	1.299	94.6%

A 17Gb NA12878 exome sample prepared using Agilent V2 was analyzed using accelerated BWA/GATK. Additional nodes can speed up the processing of NGS data without sacrificing accuracy and reproducibility

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