



Ultra-fast ✓

6 min for WGS analysis

Highly-integrated ✓

ZLIMS offers One-step automatic analysis,
ZMART application market

User-friendly ✓

Flexible deployment with
concise content

Cost-effective ✓

Each saves dozens of hardware
investment costs

MGI-ZBOLT™

Bioinformatics Analysis **Accelerator**



MegaBOLT Bioinformatics Analysis Accelerator Series (hereinafter called MegaBOLT) is an MGI-developed MPS-dedicated acceleration system for bioinformatics analysis. MegaBOLT supports analysis of Whole Genome Sequencing (WGS), Whole Exome Sequencing (WES) and Panel Sequencing on Germline or Somatic data, which can be 100 times faster than classical algorithms.

ZMART, the bioinformatics application market integrated with MegaBOLT, supports more than 100 add-on applications to provide extended functionality. MegaBOLT is ultra-fast, highly-integrated, user-friendly and cost-effective, which can greatly reduce computing costs, save time and be free from worry, and help your business develop efficiently.



The basic version (MegaBOLT) comes in the form of a workstation server that excels in both computing power and ease of use / deployment.

The professional version (ZBOLT Pro) is a rack server that provides even higher performance.



MegaBOLT workstation server

- ✓ With 30 TB hard disk storage and a display
- ✓ Flexible deployment, plug and play
- ✓ Integrated with ZMART application market
- ✓ Integrated with ZLIMS Lite lab info management system
- ✓ Includes 100Tbp WGS/WES basic analysis package license
- ✓ Annual full-load analysis capacity up to 12,000 WGS (30 ×)/set



Laboratories



Hospitals



ZBOLT rack server

(ZBOLT is a component of the ZTRON Appliance product)

- ✓ 2U computing-only rack server without storage
- ✓ Suitable for computationally intensive customers
- ✓ Server room/rack required
- ✓ Includes 300Tbp WGS/WES basic analysis package license
- ✓ Annual full-load analysis capacity up to 36,000 WGS (30 ×)/set



Research institutes

ZBOLT Pro rack server with ultra-high performance

- ✓ 2U computing-only rack server without storage
- ✓ Suitable for computationally intensive customers
- ✓ Server room/rack required
- ✓ Includes 1200Tbp WGS/WES basic analysis package license
- ✓ Annual full-load analysis capacity up to 80,000 WGS (30 ×)/set



Enterprises



MegaBOLT accelerates algorithms such as SOAPnuke, Minimap2, BWA, GATK HaplotypeCaller + MuTect2 through multi-stream and highly parallelized computing architecture, which contributes to a massive speedup in data analysis.

Analysis time comparison	Classical Algorithm	MegaBOLT	ZBOLT	ZBOLT Pro
Germline WGS 30× Basic	26.26h	0.69h	0.24h	0.11h
Germline WGS 30× Full	27.20h	0.80h	0.27h	0.12h
Germline WES 100× Basic	4.27h	0.10h	0.04h	0.02h
Germline WES 100× Full	4.37h	0.13h	0.04h	0.02h
Somatic WGS 40× Tumor + 40× Normal	46.44h	3.66h	1.47h	0.42h
Somatic WES 400× Tumor + 400× Normal	7.64h	0.36h	0.14h	0.06h

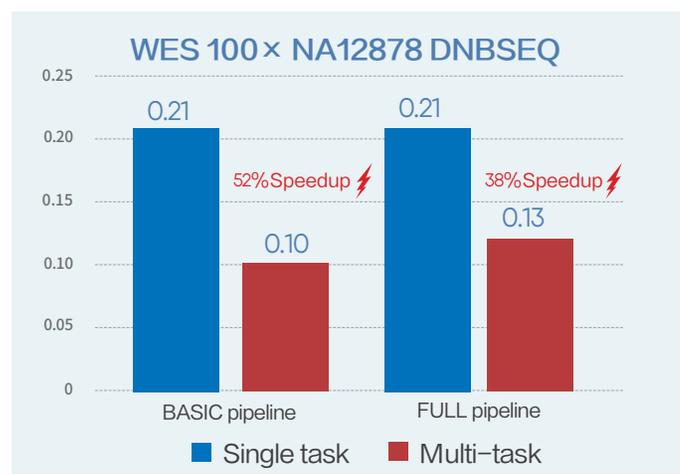
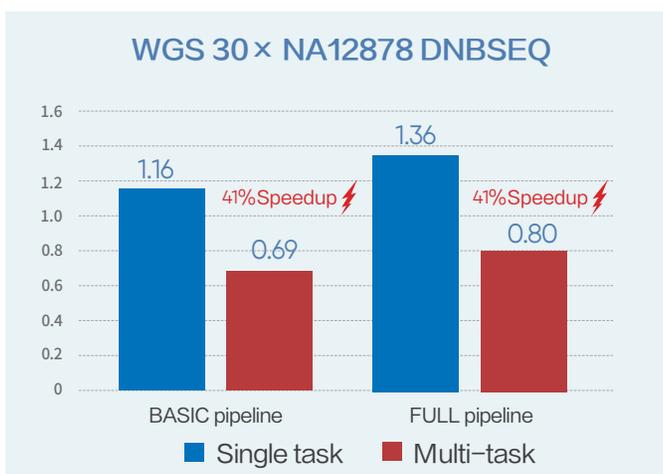
* Basic: Including the analysis steps from clean data after quality control to variant calls, taking the average time of multiple tasks.

* Full: Includes extra steps of quality control and report generating in addition to the Basic workflow.

* The time consumed is measured by taking the average of completing 6 identical tasks (MegaBOLT)/ 12 (ZBOLT) / 32 (ZBOLT Pro).

➤ Multi-task scheduling system acceleration

Integrated with the self-developed multi-task scheduling system, MegaBOLT supports simultaneous multi-task computing on one single server. The computing efficiency is further improved by 38%~52%. When only a single task needs to be analyzed, the single-task mode can be used to enhance performance by 13% to 30%.



* The time consumed is measured by taking the average of completing 6 identical tasks.

➤ Precision performance

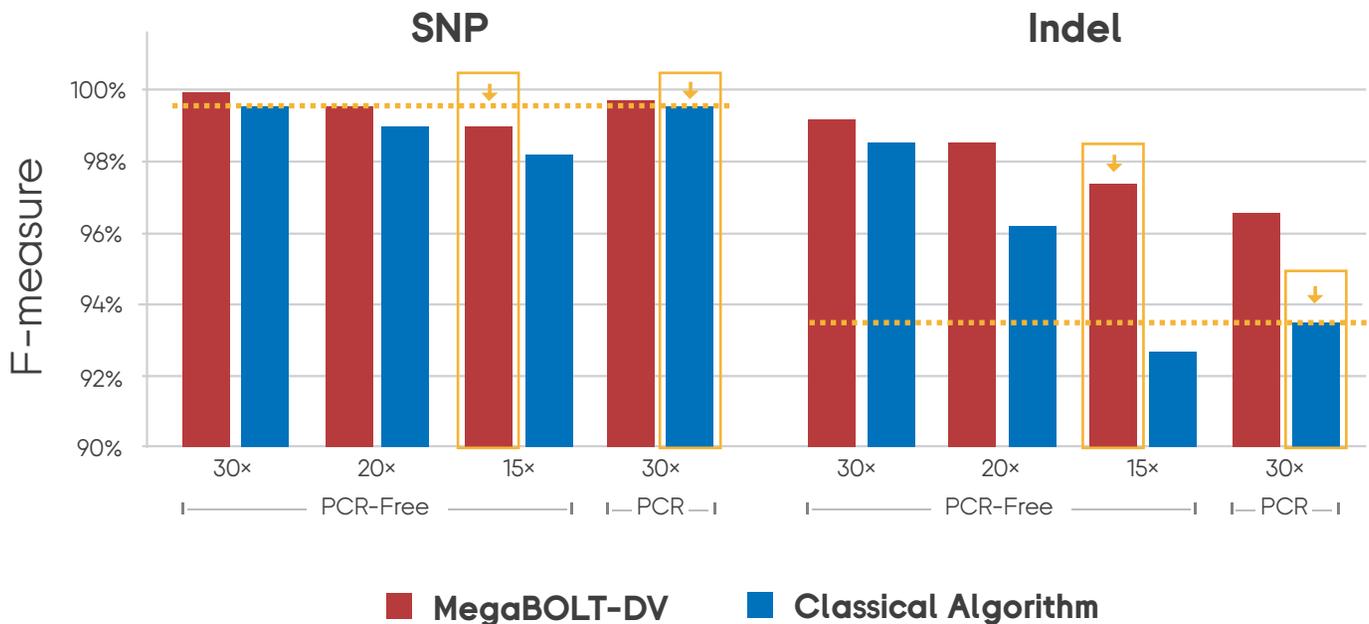
After speedup, the analysis precision remains steadfast. MegaBOLT is also configured with a deep learning variant calling module, MegaBOLT-DV, which is optimized by algorithms and specified neural network model training. When MegaBOLT-DV is used in combination with PCR-Free library preparation and MGI DNBSEQ™ sequencing technologies, the human WGS variant calling precision can reach an excellent SNP 99.9% and Indel 99%. Even more, MegaBOLT-RC, a new recalibrating module based on machine learning, can improve precision significantly without using a lot of extra computing resource.

		SNP			Indel		
		Precision	Sensitivity	F-measure	Precision	Sensitivity	F-measure
DNBSEQ PCR PE100 94Gbp	MegaBOLT	99.90%	99.39%	99.65%	95.42%	94.24%	94.83%
	MegaBOLT-RC	99.92%	99.54%	99.73%	97.90%	96.35%	97.12%
	MegaBOLT-DV	99.88%	99.71%	99.80%	97.56%	97.42%	97.49%
	Classical Algorithm	99.88%	99.65%	99.76%	95.35%	94.32%	94.83%
DNBSEQ PCR PE150 138Gbp	MegaBOLT	99.91%	99.82%	99.86%	97.34%	97.56%	97.45%
	MegaBOLT-RC	99.95%	99.82%	99.89%	99.19%	98.61%	98.90%
	MegaBOLT-DV	99.92%	99.89%	99.91%	98.96%	98.97%	98.97%
	Classical Algorithm	99.87%	99.88%	99.87%	97.28%	97.55%	97.42%
DNBSEQ PCR-Free PE150 126Gbp	MegaBOLT	99.93%	99.80%	99.86%	99.51%	99.18%	99.35%
	MegaBOLT-RC	99.95%	99.84%	99.89%	99.62%	99.38%	99.50%
	MegaBOLT-DV	99.92%	99.90%	99.91%	99.57%	99.52%	99.55%
	Classical Algorithm	99.90%	99.86%	99.88%	99.52%	99.21%	99.37%
NBSEQ MGIEasy Exome V5 PE150 11Gbp	MegaBOLT	99.86%	97.98%	98.91%	91.68%	86.03%	88.77%
	MegaBOLT-RC	99.88%	98.25%	99.06%	97.79%	88.92%	93.15%
	MegaBOLT-DV	99.84%	98.27%	99.05%	96.08%	92.92%	94.48%
	Classical Algorithm	99.82%	97.96%	98.88%	91.60%	86.17%	88.80%

Deep learning making sequencing more cost-effective

The deep learning variant calling module, MegaBOLT-DV, helps to greatly reduce the sequencing depth and cost without affecting the analysis precision.

Compared with the GATK variant calling results of 30× PCR data, SNP of 15× PCR-Free data from MegaBOLT-DV is already close and Indel is far better.

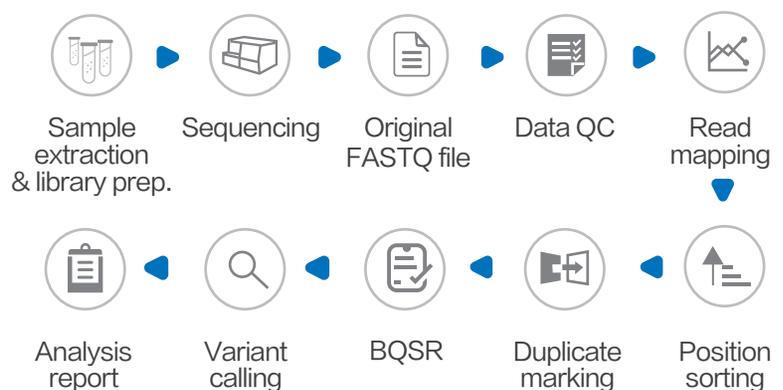


Highly-integrated

Integrated with the self-developed laboratory information management system ZLIMS, MegaBOLT realizes fully automated sequencing and analysis. It can work together with MGI DNBSEQ™ sequencers or sequencers of other platforms.

Integrated functions

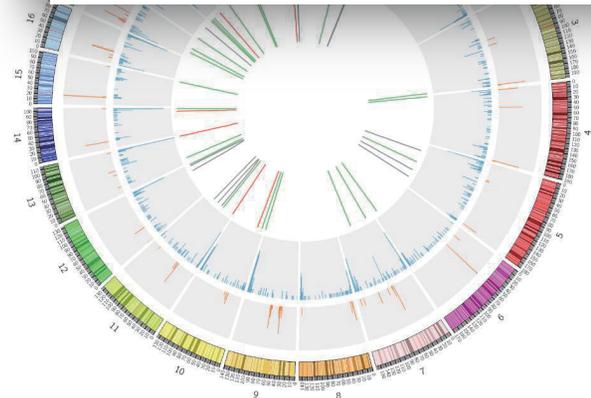
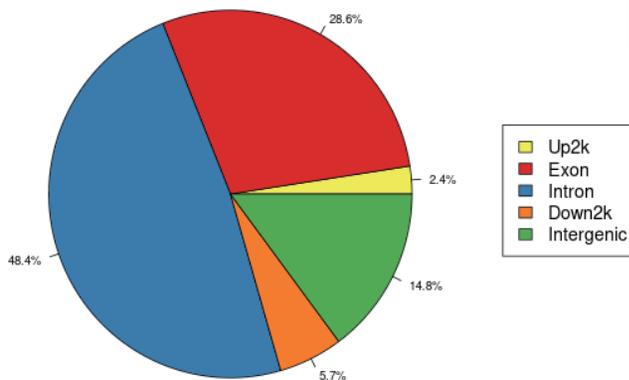
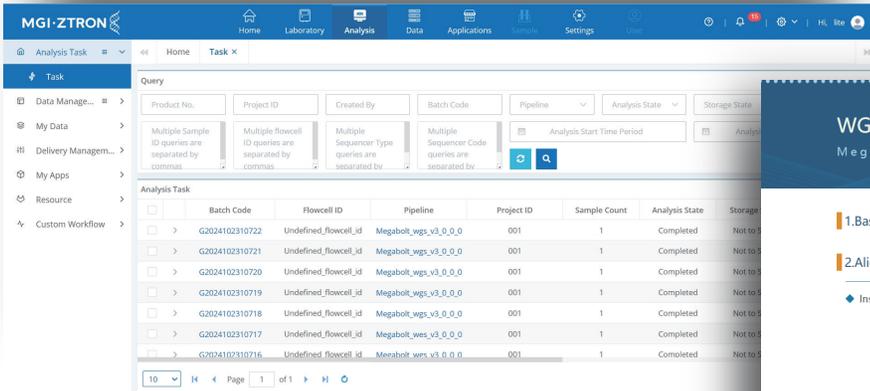
- ☑ Laboratory equipment management and real-time monitoring
- ☑ Sample experiment information recording and tracking
- ☑ Data transmission and management
- ☑ Analysis task scheduling and computing
- ☑ Management and visualization of analysis results and reports



User-friendly



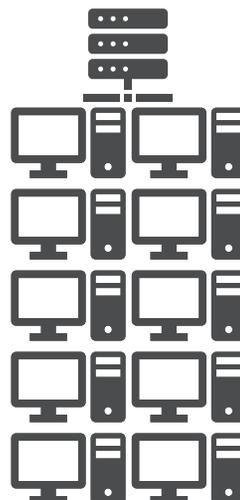
The Web design makes MegaBOLT simple and easy to use. You can just click a couple of buttons to submit a task and check the results on the website. In this case, a bioinformatic technical background is no longer necessary.



Cost-effective



With a prominent speedup in computing and rigid control over hardware prime cost, MegaBOLT/ZBOLT/ZBOLT Pro has the computing power of more than 10 computers combined and is without doubt highly cost-effective.



vs

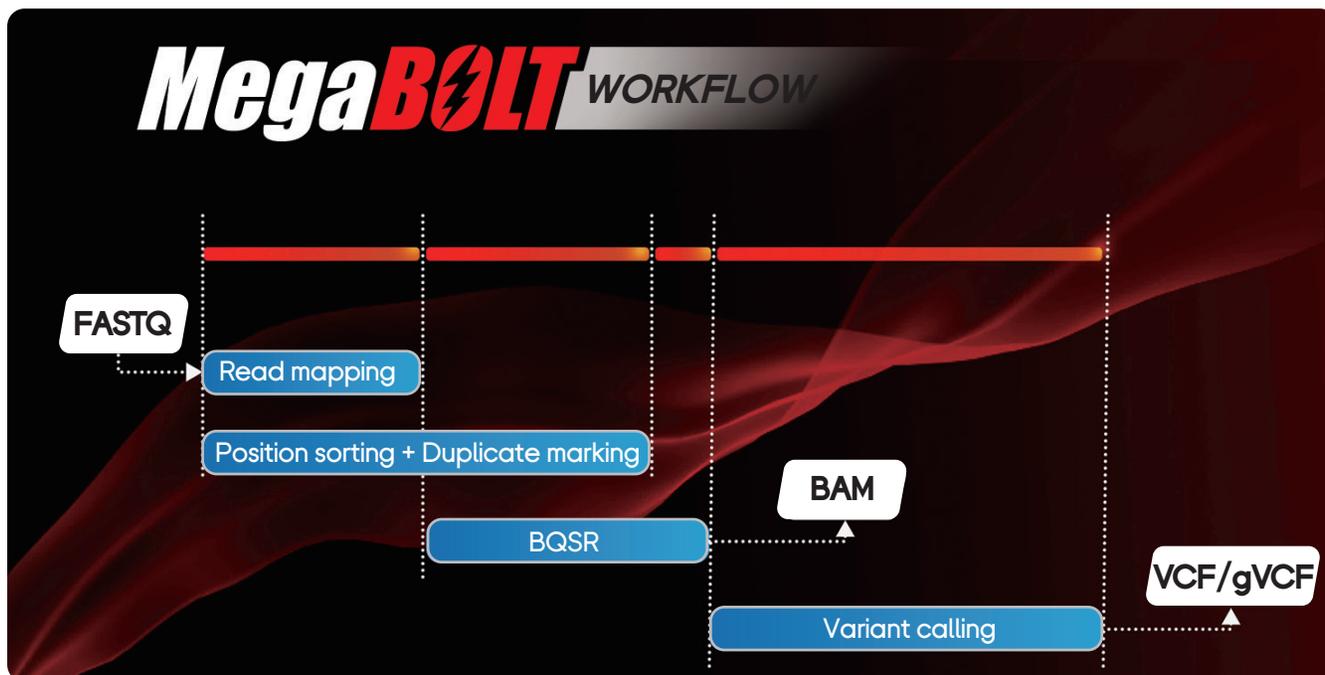


MegaBOLT™
MGI-ZBOLT™

Parallel computing accommodates high-speed sequence analysis



MegaBOLT adopts a multi-stream computing architecture and divide data into smaller granules for higher efficiency. We also further streamlined the whole process and developed a highly parallelized computing architecture, thus realizing highspeed WGS/WES analysis and computing.



Ordering information



Catalog No.	Product
900-000555-00	MegaBOLT Bioinformatics Analysis accelerator (workstation server)
900-001003-00	ZBOLT Bioinformatics Analysis Accelerator (rack server)
900-000460-00	ZBOLT Pro Bioinformatics Analysis accelerator (rack server)
970-000037-00	MegaBOLT WGS/WES basic analysis package license/100Gbp

MegaBOLT™

Bioinformatics Analysis Accelerator



- MegaBOLT workstation

MGI-ZBOLT™

Bioinformatics Analysis Accelerator



- ZBOLT rack server
- Ultra high performance ZBOLT Pro rack server

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