Press Release

February 3, 2025
Mitate Zepto Technica Inc,

Mitate Zepto Technica Unveils RASEN Accelerator Prototype with BWA-Comparable Accuracy

～Verified 99.8% Concordance Rate Through Collaborative Study with Tohoku University～

Mitate Zepto Technica (MZT, headquartered in Tokyo JAPAN; CEO: Keisuke Harashima) announced today that its genome analysis-specific accelerator prototype, “RASEN,” has achieved precision equivalent to conventional methods. In a joint study with Tohoku University, RASEN demonstrated a 99.8% concordance rate compared to the widely used BWA tool, achieving a balance of speed and accuracy never before realized.

Summary of Verification Results

- High Concordance:
  - Achieved an average concordance rate of 99.8% across all 12 samples.
  - Several samples showed a perfect 100% match.
- Consistent Precision:
  - Maintained a concordance rate above 99.6% across all samples.
  - No bias observed related to ethnicity or gender.
- Reliable Mapping Accuracy:
  - Discrepancies were minimal and consistent across samples.
  - High reliability was confirmed through detailed visual inspections.

Future Outlook

The RASEN prototype has already been validated to complete whole-genome sequencing within five minutes, as confirmed by MZT's internal speed tests. These results showcase the feasibility of realizing a final product using advanced semiconductor technology.

Building on this success, MZT will accelerate the development of its semiconductor-integrated final product. The newly developed semiconductor will significantly enhance processing speed and energy efficiency.

RASEN aims to become a vital infrastructure for next-generation genome analysis, addressing the growing need for rapid, large-scale genomic data processing in clinical and research settings. By enabling researchers and medical institutions to quickly utilize data, it will contribute to advancements in personalized medicine and early detection of genetic disorders.

MZT will strengthen collaborations with domestic and international partners to incorporate real-world feedback, driving continuous improvement and optimization of the product.

Through RASEN, MZT is committed to addressing a wide range of needs from research to clinical applications, paving the way for groundbreaking innovations in genomics, medicine, and biotechnology.

Comment from Associate Professor Jun Takayama, Tohoku University School of Medicine

"The accuracy validation using the RASEN prototype demonstrates its capability to sufficiently achieve the design objective of accuracy equivalent to or better than BWA. This milestone highlights its potential for widespread use in genome analysis."

Comment from Keisuke Harashima, CEO, MZT

"The precision verification results from Tohoku University represent a significant milestone for our technology. Confirming BWA-comparable accuracy, coupled with our speed verification, signifies that a new era of genome analysis powered by semiconductor technology is within reach.

Since our establishment, we have strived to create a world where genomic information is effortlessly accessible. We aim to deliver meaningful value in fields ranging from rapid clinical diagnostics to efficient large-scale research, with a focus on real-world applications.

As we move toward product commercialization, we will ensure that our semiconductor devices are user-friendly for medical and research institutions alike."

Details of Validation with the RASEN Prototype

Reference Genome:

Japanese reference genome sequence JG2.1.

- Sample Selection: 12 samples (2 males and 2 females each from CEU, YRI, and JPT groups of the 1000 Genomes Project).

Target Analysis Regions:

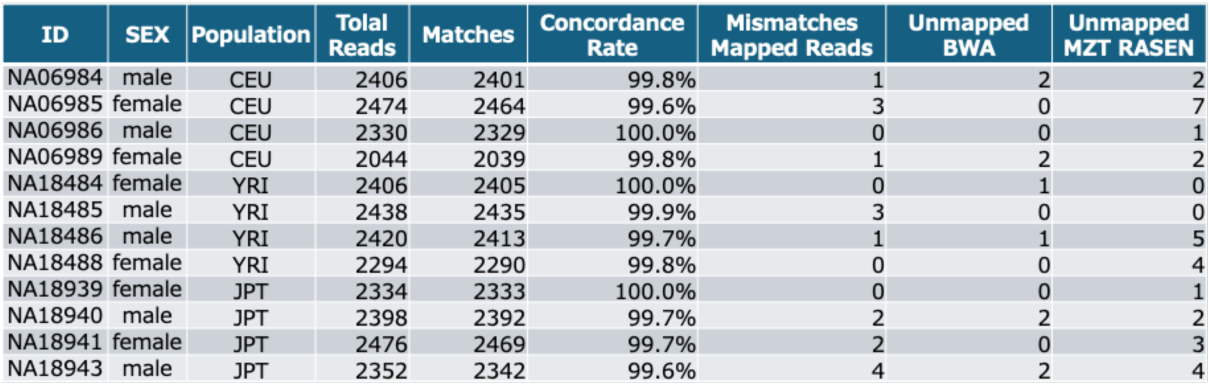
Regions containing five known polymorphisms (2kb each):

- LCT gene (rs4988234)
- FADS1 gene (rs174570)
- ALDH2 gene (rs671)
- SLC24A5 gene (rs1426652)
- TP53 gene (rs1042522)

Validation Procedure:

1. Mapping analysis of fastq data from 12 samples across five SNP regions against JG2.1 using both RASEN and BWA.
2. Comparative analysis of mapping results.
3. Visual validation using IGV to ensure reliability.

Results



ID	SEX	Population	Tolal Reads	Matches	Concordance Rate	Mismatches Mapped Reads	Unmapped BWA	Unmapped MZT RASEN
NA06984	male	CEU	2406	2401	99.8%	1	2	2
NA06985	female	CEU	2474	2464	99.6%	3	0	7
NA06986	male	CEU	2330	2329	100.0%	0	0	1
NA06989	female	CEU	2044	2039	99.8%	1	2	2
NA18484	female	YRI	2406	2405	100.0%	0	1	0
NA18485	male	YRI	2438	2435	99.9%	3	0	0
NA18486	male	YRI	2420	2413	99.7%	1	1	5
NA18488	female	YRI	2294	2290	99.8%	0	0	4
NA18939	female	JPT	2334	2333	100.0%	0	0	1
NA18940	male	JPT	2398	2392	99.7%	2	2	2
NA18941	female	JPT	2476	2469	99.7%	2	0	3
NA18943	male	JPT	2352	2342	99.6%	4	2	4

Verification Environment

The validation utilized the FPGA-based RASEN prototype, a high-speed processing platform designed for semiconductor integration. The system configuration included a Ryzen 9 7900 CPU, simulating the performance of the final product.

About Mitate Zepto Technica

Mitate Zepto Technica is a pioneering venture leveraging cutting-edge semiconductor technology to revolutionize genome analysis. By enabling the efficient utilization of genomic data, MZT aims to address global challenges in medicine, food, and energy.

For more information, visit: https://mitatezeptotechnica.com/en/

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