



mission bio

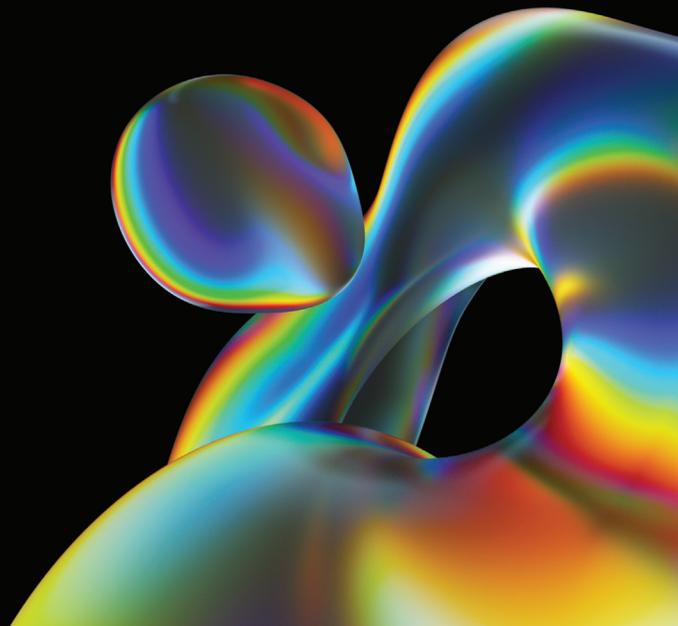
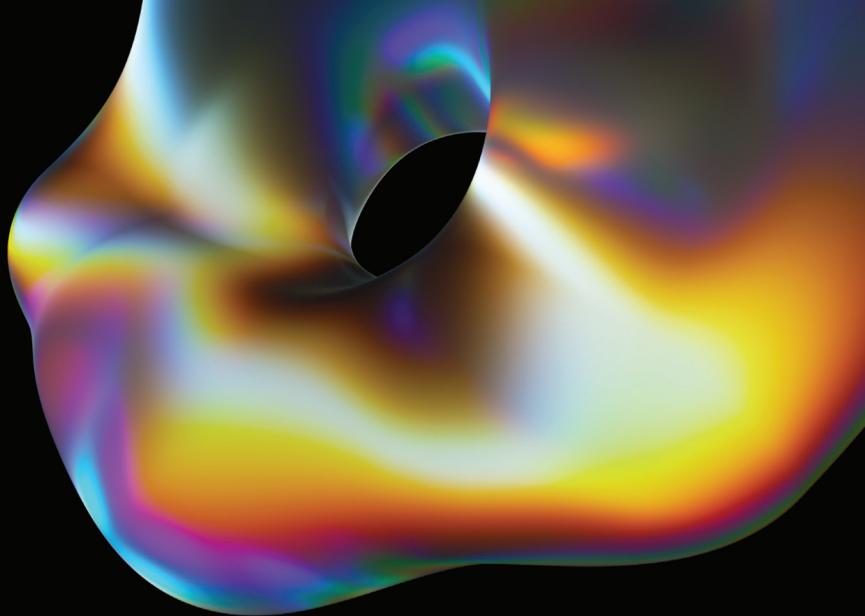
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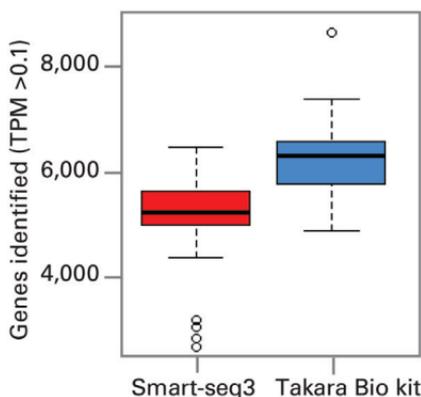
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Deeper insights into single-cell biology with Takara Bio's SMART-Seq® technology:

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- High library yields for easy adaptation to high-throughput sequencers



Number identified	Takara Bio kit	10x Chromium
Total SNPs	31,058	5,459
SNPs in ClinVar	862	184

Takara Bio plate-based (left) and automated (right) methods enable the discovery of more genes and SNPs compared to popular scRNA-seq methods.

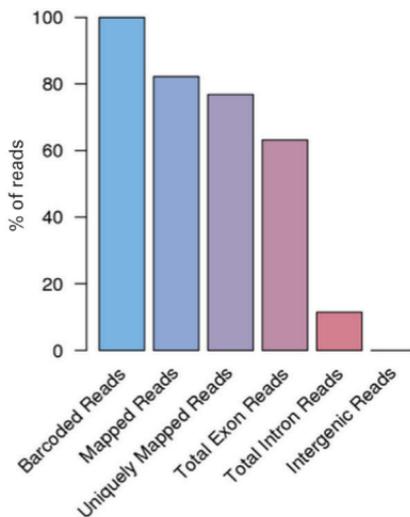


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Easy-to-use data analysis software and tools for biomarker investigation

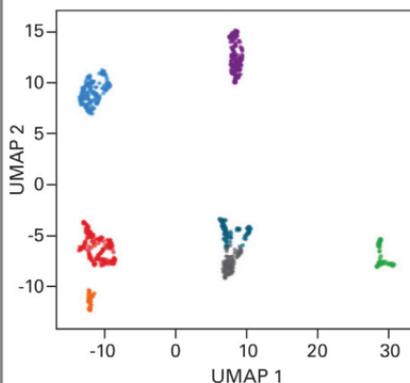
Cogent™ NGS Analysis Pipeline (CogentAP)

Generates HTML reports with mapped gene data for further analysis with CogentDS.



Cogent NGS Discovery Software (CogentDS)

Enables user-friendly analysis of sequencing data generated with Takara Bio platforms. Data can be visualized using UMAP or t-SNE.



Publication-ready figures

Takara Bio USA, Inc.

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Global DNA Methylation

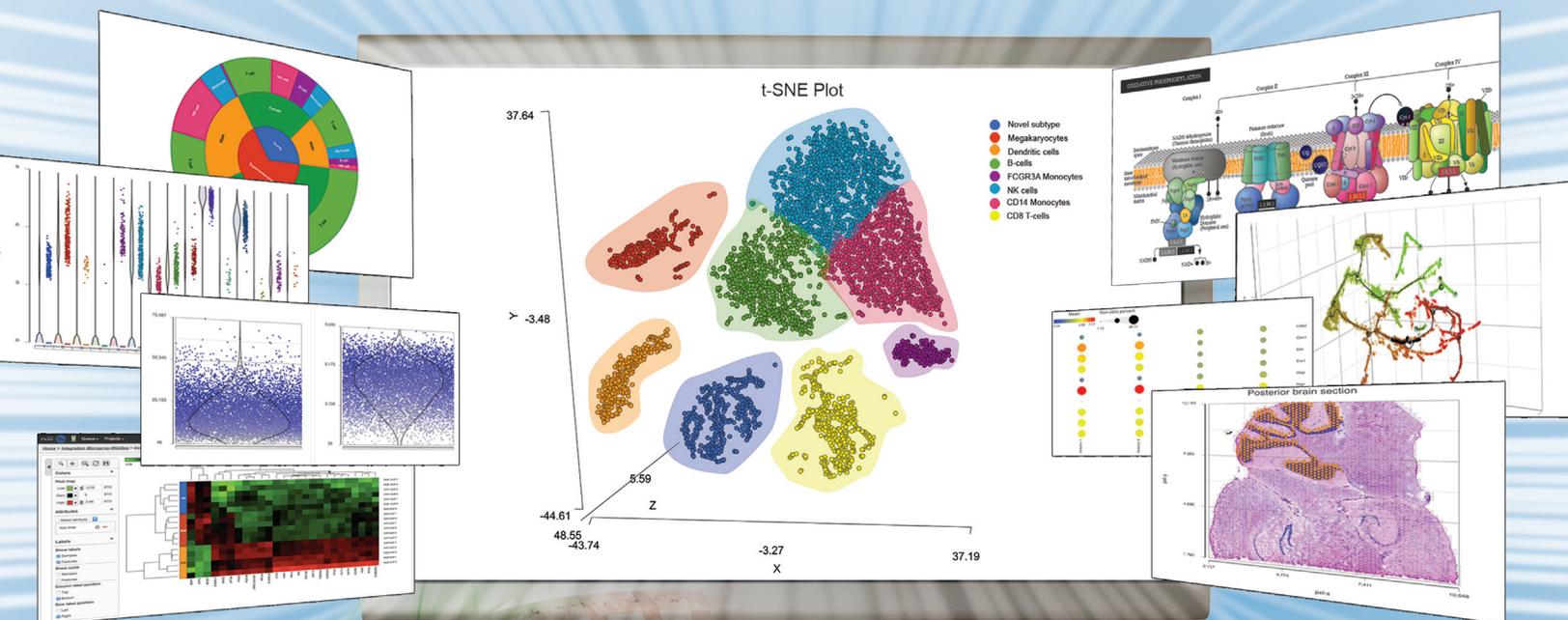
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Better Sensitivity
By optimized reaction buffer

Lower False Positive Rate
By strong recognition ability to dUTP

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By colorimetric visualization technique

Quality Assurance

QC Items	Specifications	Results
Concentration	8-10 KU/ml	<input checked="" type="checkbox"/> Pass <input type="checkbox"/> Fail
Purity	>95%	<input checked="" type="checkbox"/> Pass <input type="checkbox"/> Fail
RNase contamination	No degradation under 16 U for 2 µg total RNA at 25°C for 30 min	<input checked="" type="checkbox"/> Pass <input type="checkbox"/> Fail
DNase contamination	No degradation under 16 U for 2 µg gDNA at 37°C for 60 min	<input checked="" type="checkbox"/> Pass <input type="checkbox"/> Fail
Inactive	Complete inactive at 85°C for 5 min	<input checked="" type="checkbox"/> Pass <input type="checkbox"/> Fail

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Single Cell UMIs with novoSort

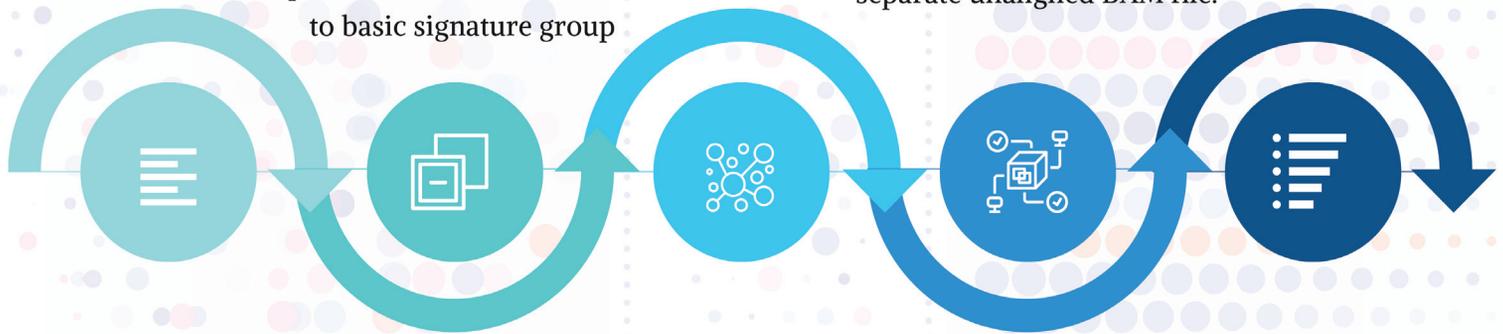
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novoSort sorts your reads and detects duplicates. Provides option to add UMIs and MBCs to basic signature group

Consensus Reads

Consensus reads can be generated from reads in duplicate groups and output to a separate unaligned BAM file.



Alignment

Align your scRNA sequences using an alignment tool of your choice.

UMI Correction & Clustering

novoSort corrects UMIs using valid UMI lists and clustering with user control of maximum edit distance.

Sorted BAM Files

Results ready for the next process.



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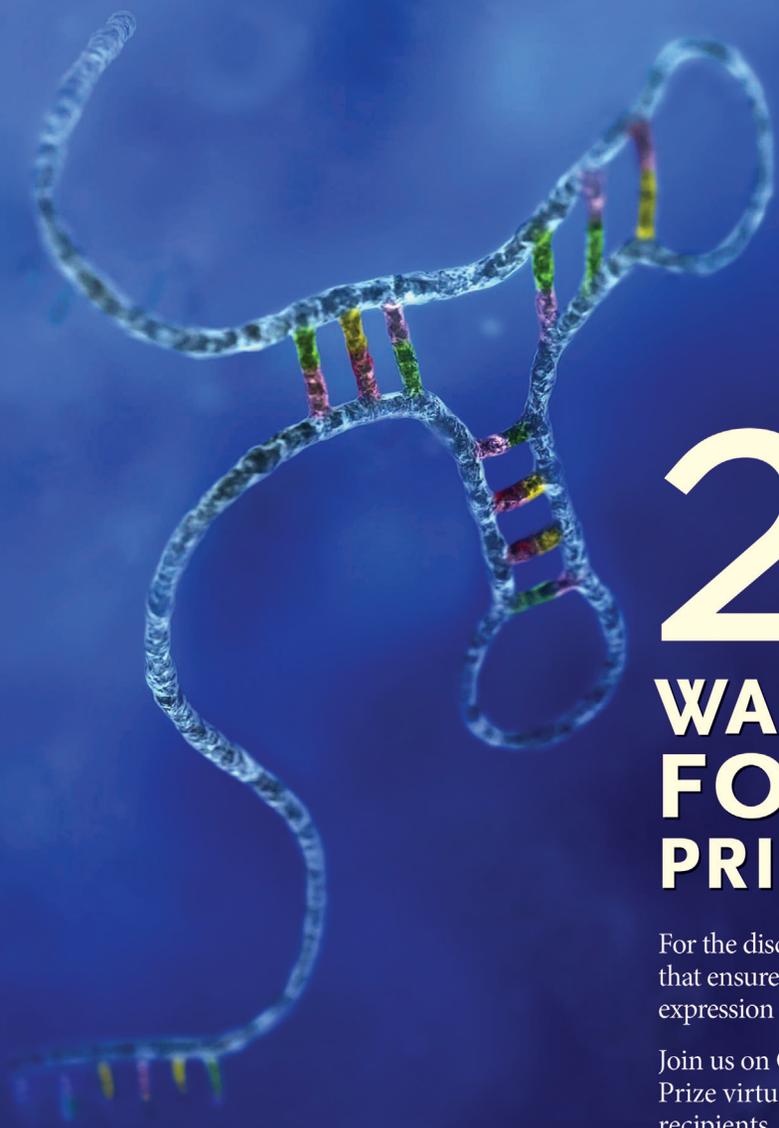
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Nominations are accepted from academic institutions, centers of research, government, or other biomedical institutions from around the world.

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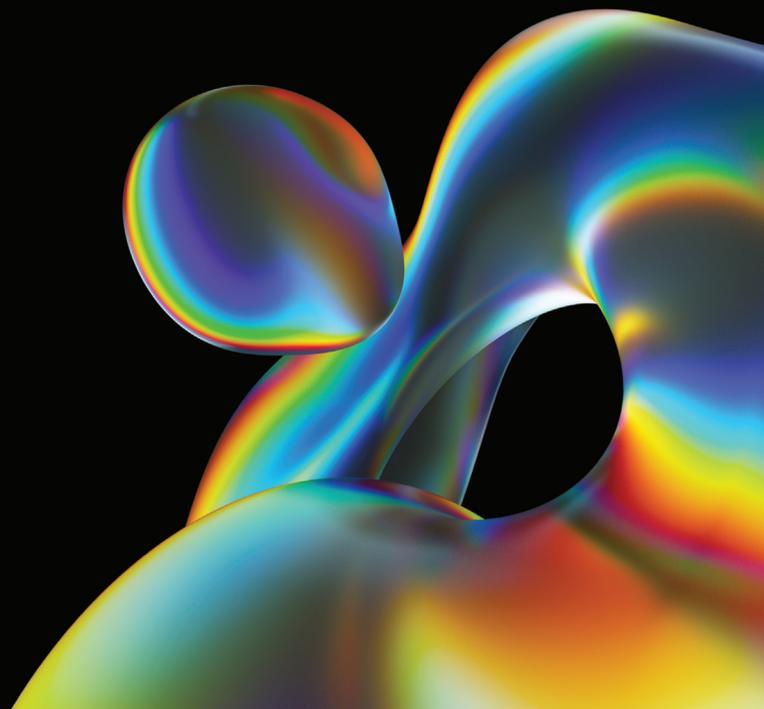
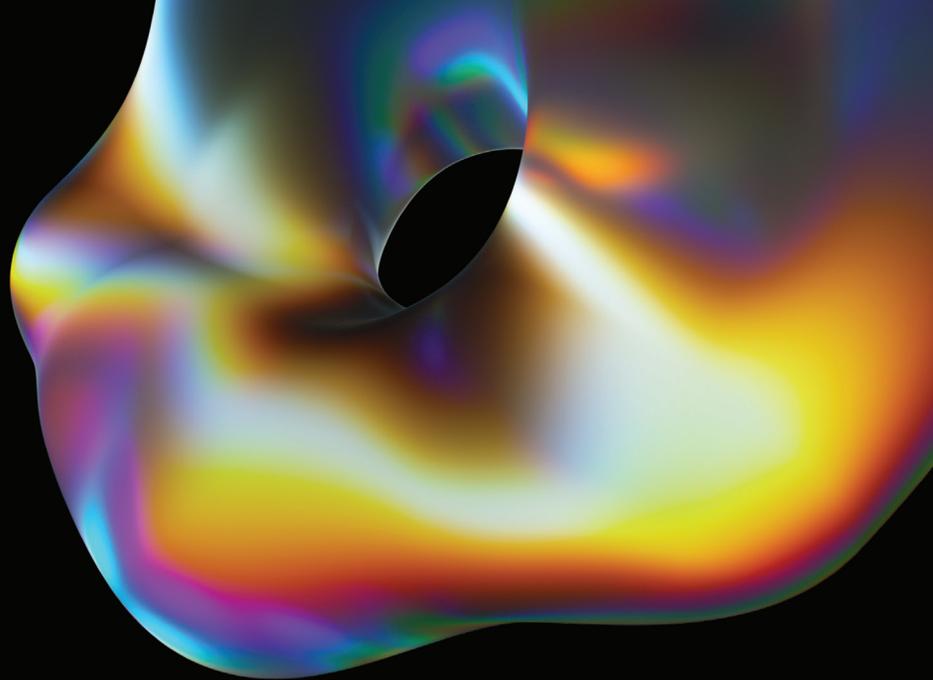
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