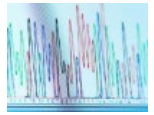
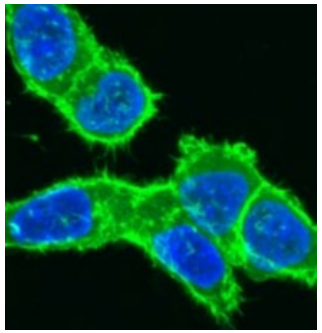
Drive biomarker discovery with new research tools for core labs

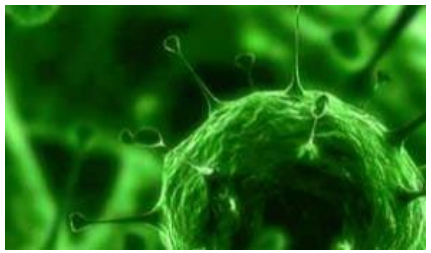
Andrew Farmer, D. Phil., CSO/Head of R&D

that's GOOD science!®

Takara Bio: core capabilities







that's GOOD science!®

NGS

- SMARTer® and SMART-Seq® RNA-seq library preparation kits
- PicoPLEX® and ThruPLEX® DNA-seq library preparation kits

PCR, qPCR, RT-PCR

- TaKaRa Ex Premier™, LA Taq™, PrimeSTAR® GXL, SeqAmp™,Titanium® polymerases, & PrimeScript™ RT
- EcoDry™ lyophilized enzymes and kits

Cloning

- In-Fusion® Snap Assembly Cloning

Nucleic acid purification

Gene delivery

- Lenti-X™, Adeno-X™, Retro-X™, and AAVpro® systems | Xfect™ transfection reagent
- RetroNectin® reagent

Functional genomics

- Tet systems and iDimerize™ systems
- Guide-it™ CRISPR/Cas9 genome editing products
- Living Colors® fluorescent proteins

Protein expression & purification

- TALON® and His60 Ni protein purification

TaKaRa

Custom, bulk, and OEM capabilities

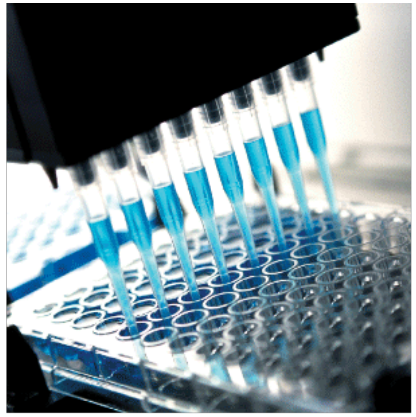
Products & Services

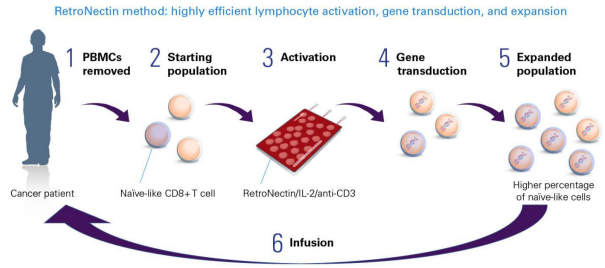
A broad portfolio of products is available for custom/bulk needs and OEM supply, such as:

- Polymerases & other core molecular biology enzymes
- Molecular biology kits
- TaqStart® antibodies
- Registered GPRs (general purpose reagents)
- Select GMP-grade products

Recognized for

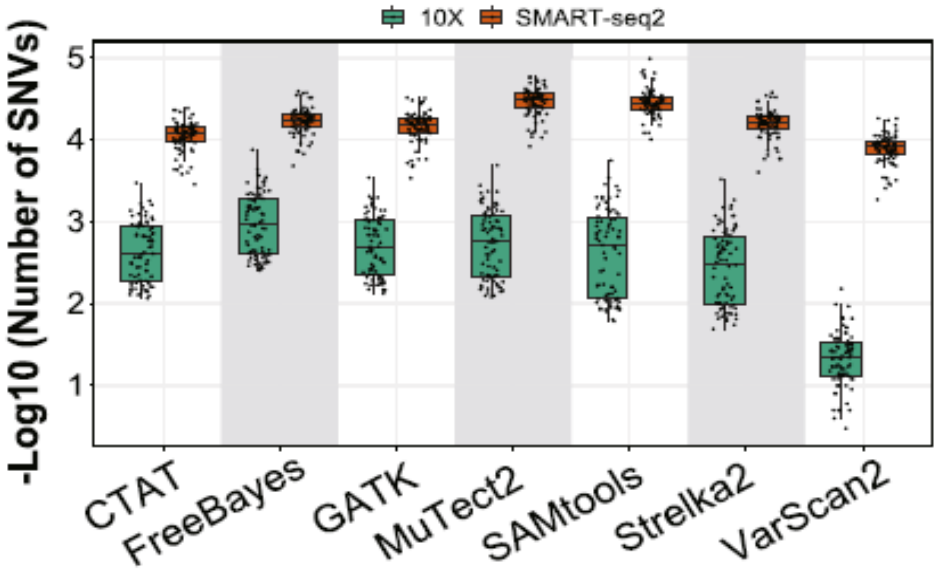
- Expert manufacturing, including GMP facilities
- Reliable quality, ISO 13485:2016 certification
- Prompt delivery
- Flexible packaging options
- Competitive pricing
- Long-standing customer relationships





RetroNectin reagent:
A gold standard for engineered T-cell therapy

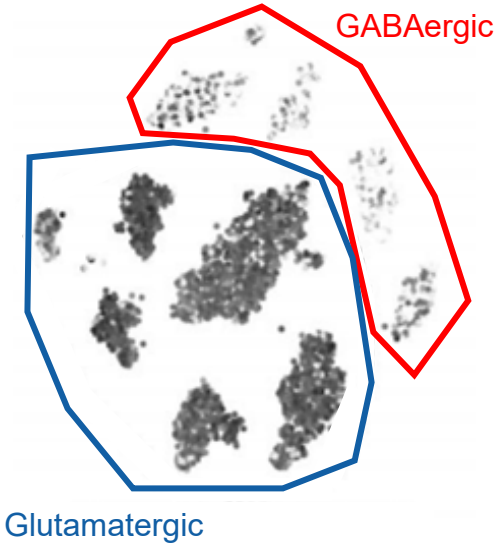
The power of sensitivity and full gene body coverage



Log-transformed counts of SNVs detected using different sequencing platforms.

Figure adapted from ”Systematic comparative analysis of single-nucleotide variant detection methods from single-cell RNA sequencing data.” (Liu F. et al. 2019, *Genome Biol*) under a CC BY 4.0 license.

Nondifferential gene: *Unc5c*



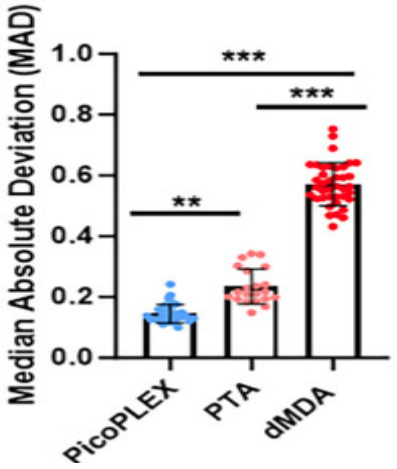
Differential isoform: *Unc5c-208*

The Allen Institute for Brain Science published a preprint paper that was later published in Nature using Takara Bio's SMART-Seq chemistry for full-length analysis.

Figure adapted from ‘Isoform cell type specificity in the mouse primary motor cortex.” (Booeshaghi AS. et al. 2020 *bioRxiv*) under a CC BY 4.0 license.

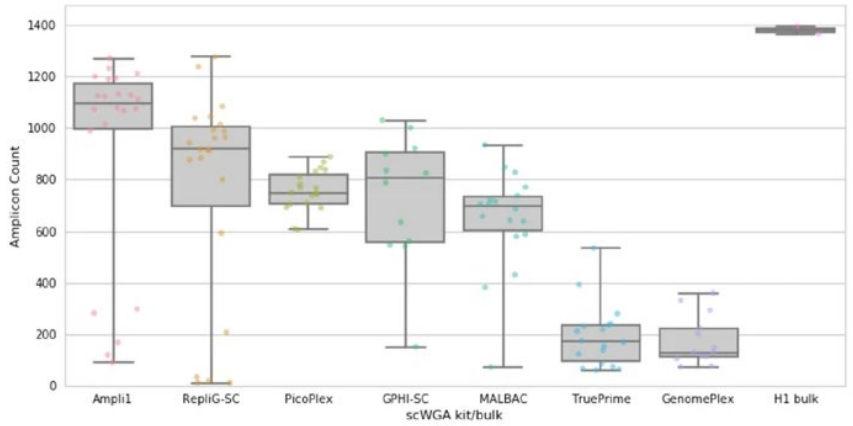
Sensitive, uniform & reproducible whole-genome sequencing

Most even



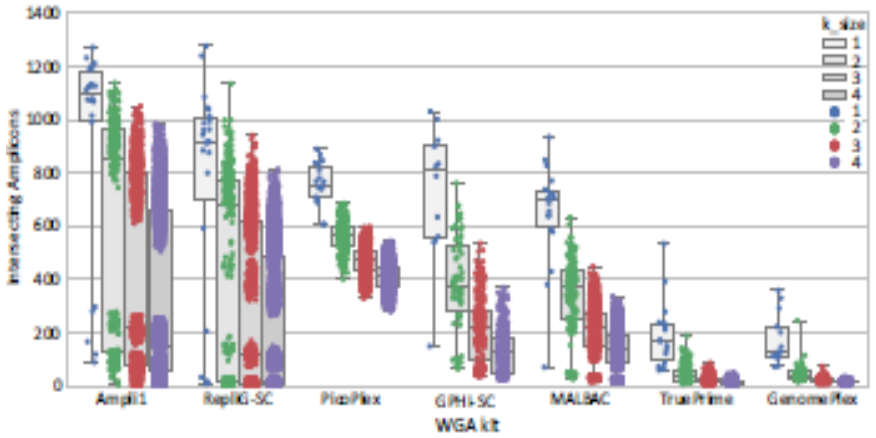
PTA provided the broadest amplification, but PicoPLEX provided the most even amplification (2023)

Most reliable



scWGA genome coverage analysis: PicoPLEX was the most reliable kit, with the tightest interquartile region (IQR) of all kits, and no failed cells.

Most reproducible



scWGA reproducibility analysis: PicoPLEX demonstrated high reproducibility for all cells

2021: Comparison of seven single cell whole genome amplification commercial kits using targeted sequencing | Scientific Reports (nature.com)

Figure adapted from "Single-cell somatic copy number variants in brain using different amplification methods and reference genomes." (Ester Kalef-Ezra. et al. 2023, *bioRxiv*) under CC BY 4.0 license.

Figures adapted from "Comparison of seven single cell whole genome amplification commercial kits using targeted sequencing." (Biezuner T. et al. 2021, *Sci. Rep.*) under a CC BY 4.0 license.

Advances in scale of single-cell RNA sequencing over the years

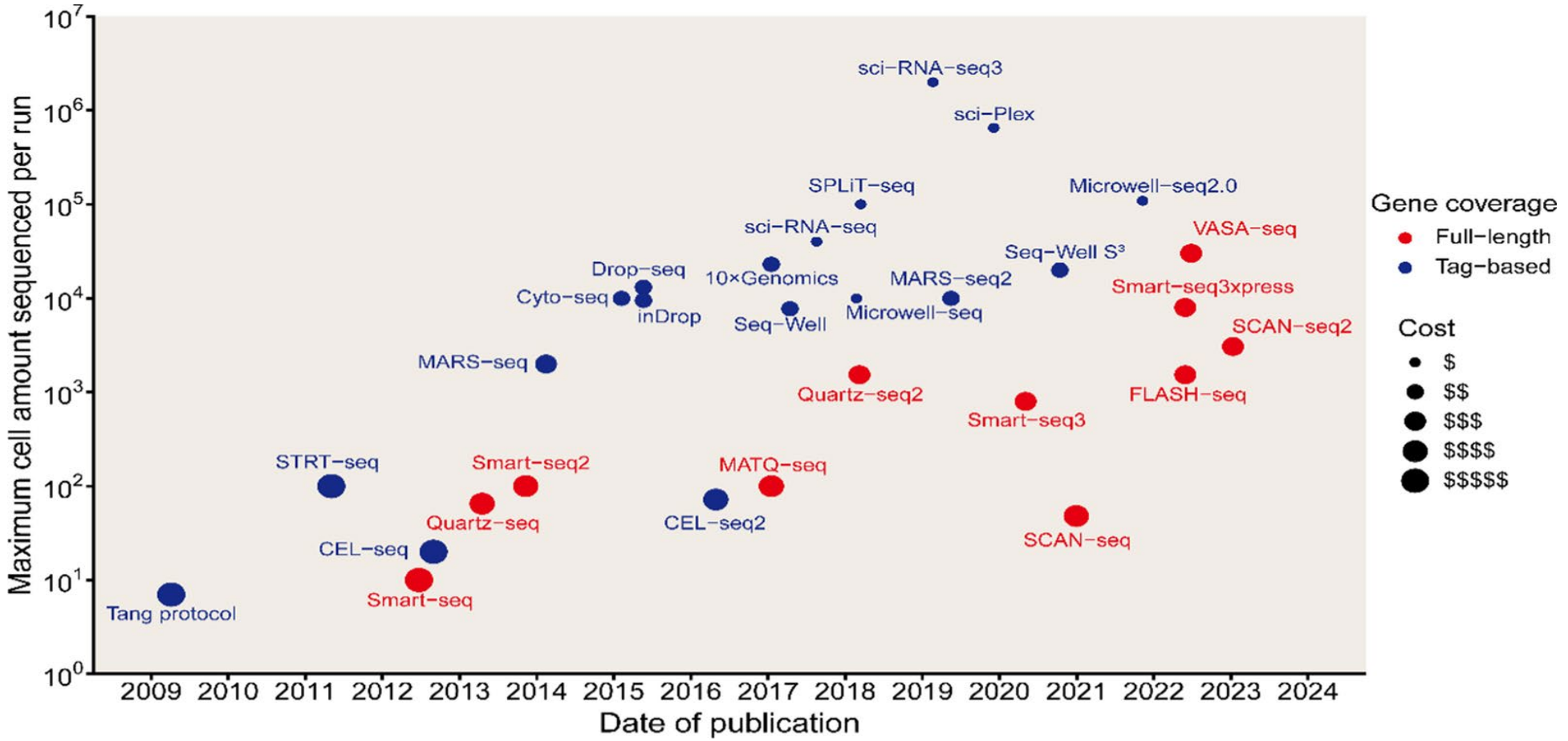


Figure adapted from "Advances in single-cell RNA sequencing and its applications in cancer research." (Huang et al. 2023, *J Hematology & Oncology*) under a CC BY 4.0 license.

Takara Bio's Shasta™ Total RNA-Seq: overview

Two-day workflow:

- Random-primed Total RNA-Seq
- Full-length gene body coverage

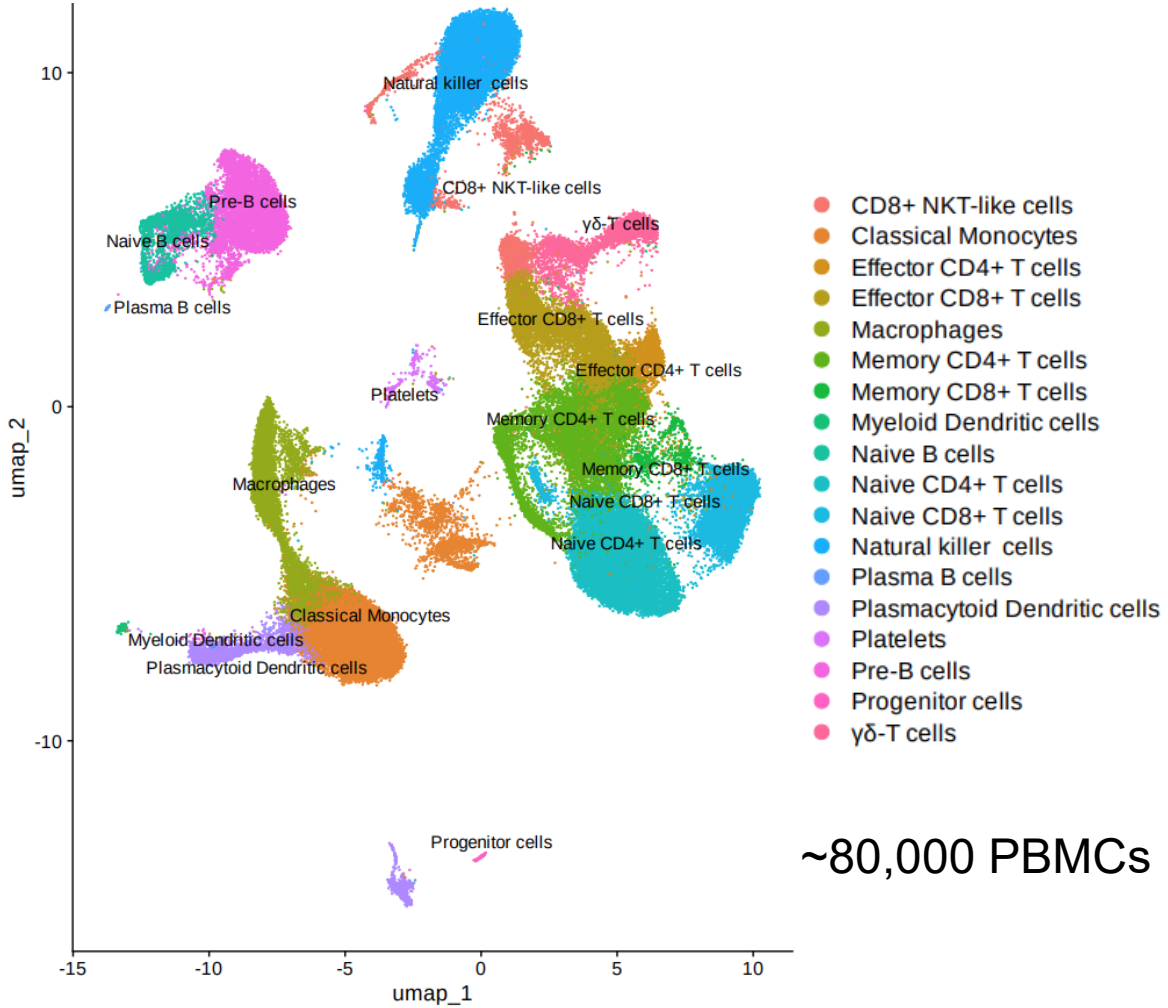
Two rounds of barcoding:

- Reduces cell loss, workflow time, and reagent costs

High throughput:

- ~100,000 cells with low doublet rate
- Up to 96 samples per experiment

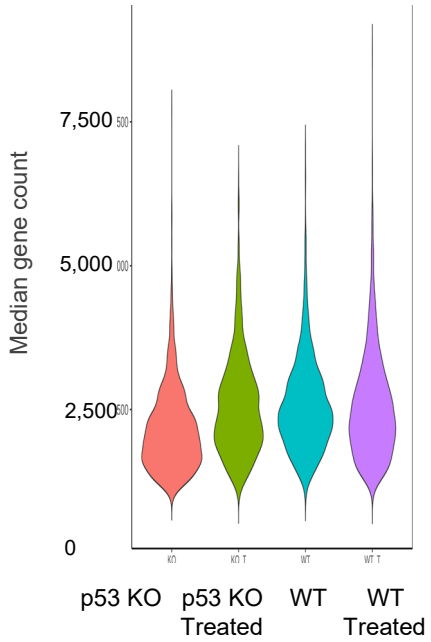
Powered by Cogent™ NGS pipeline



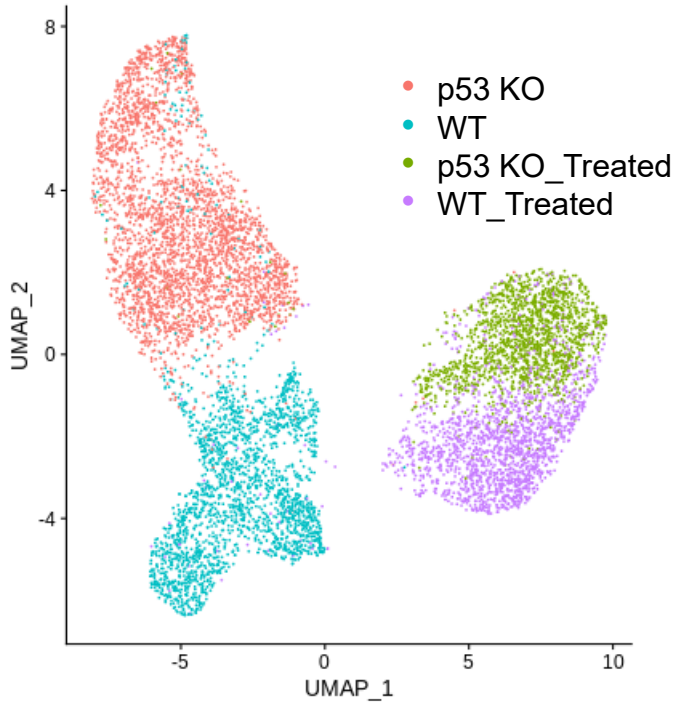
~80,000 PBMCs

Differentially expressed lncRNAs

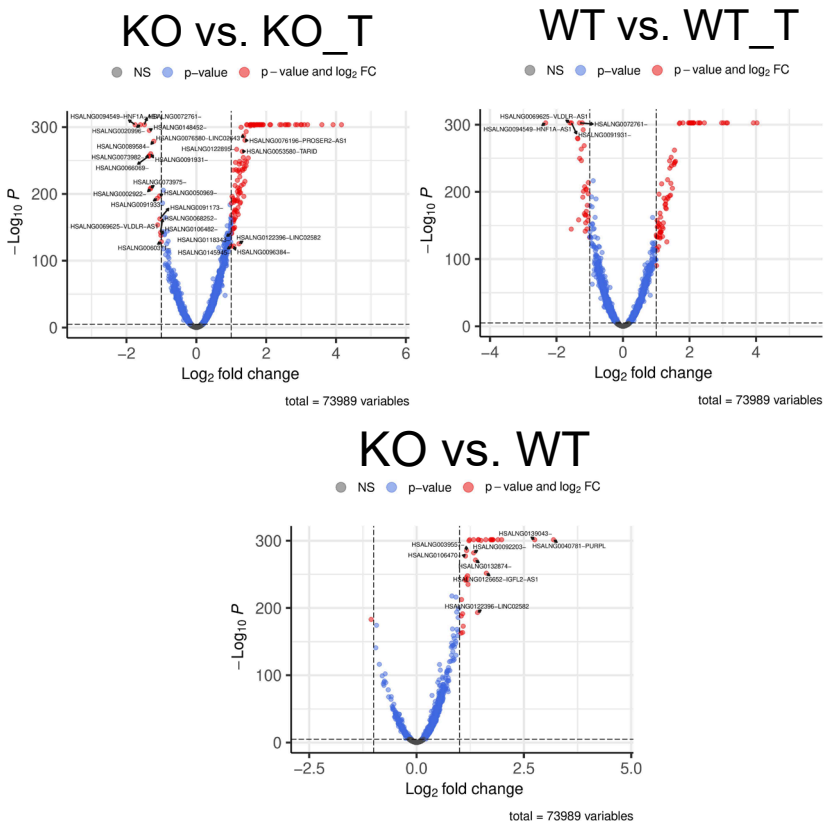
Sensitivity
lncRNA detection



UMAP



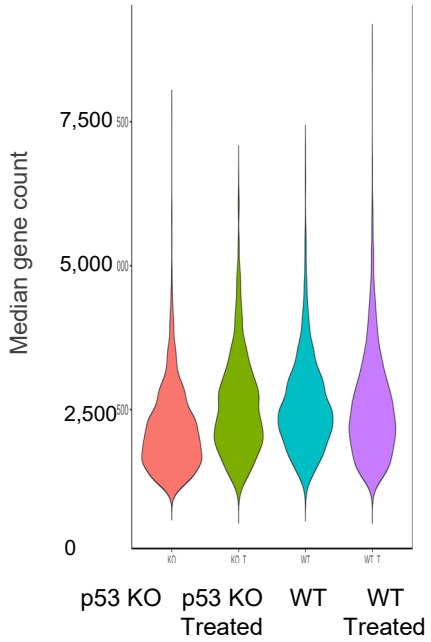
Identify differentially expressed lncRNAs



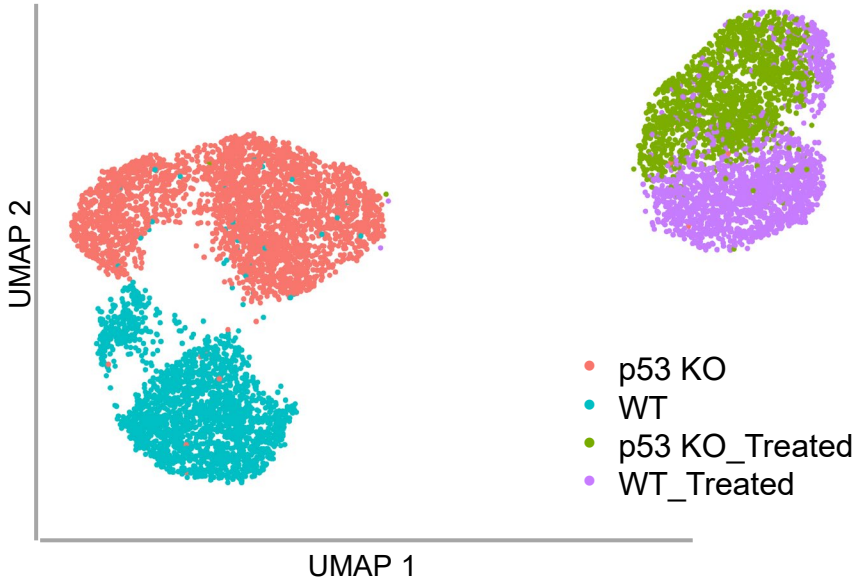
lncRNA: Analyzed using Cogent AP with RNAcentral reference containing only ncRNAs

Differentially expressed lncRNAs

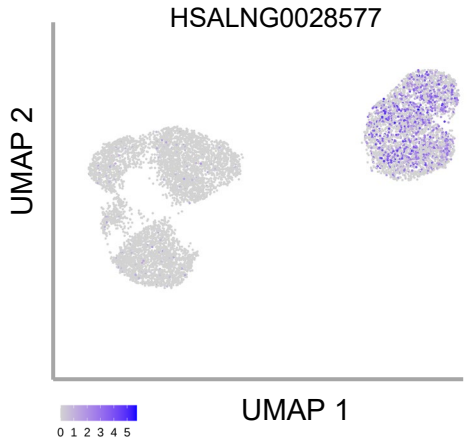
Sensitivity
lncRNA detection

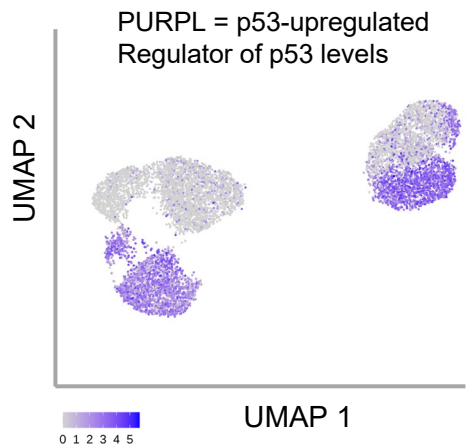


UMAP



Example of differentially expressed genes



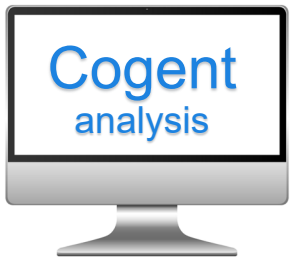


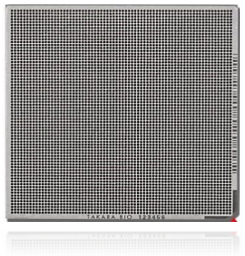
lncRNA: Done using current Cogent AP with LncBook v2 reference containing only ncRNAs

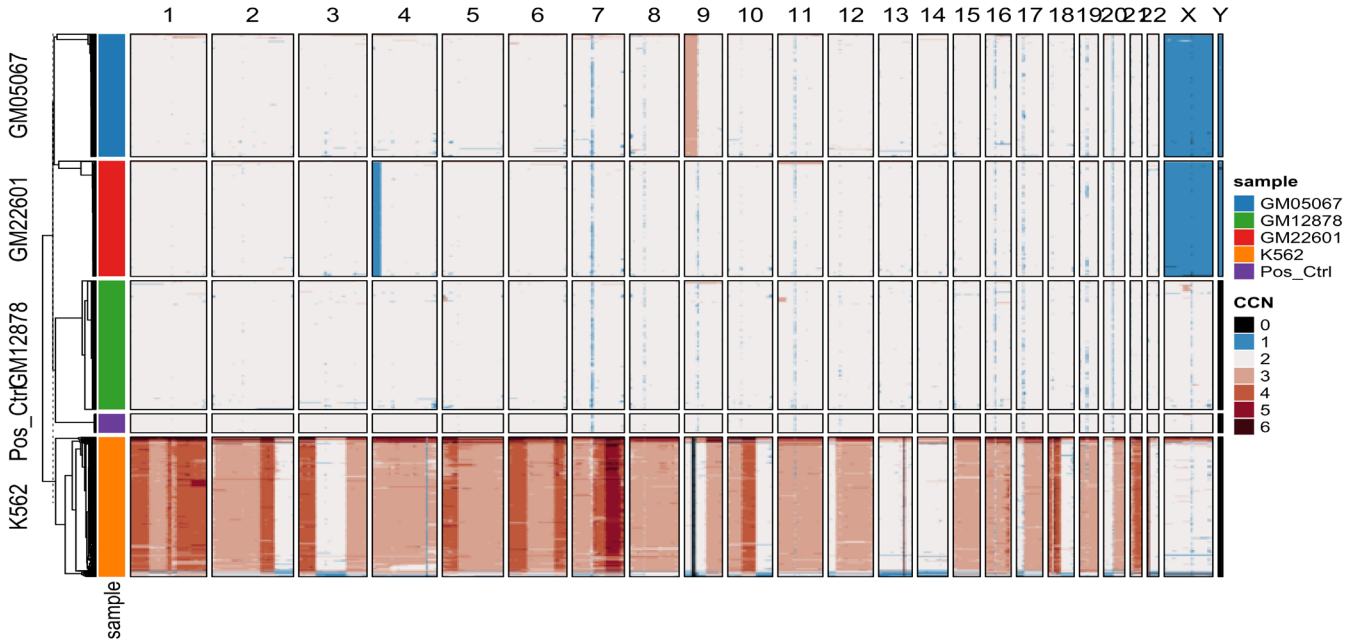
Automated, high-throughput solution for single-cell WGA

Shasta
Whole Genome Amplification

- ✓ Process single-cell WGA library for >1,000 cells per run
- ✓ Generate libraries in one day
- ✓ Avail of the renowned uniformity and reproducibility of PicoPLEX WGA
- ✓ Acquire an end-to-end solution including Cogent bioinformatics tools







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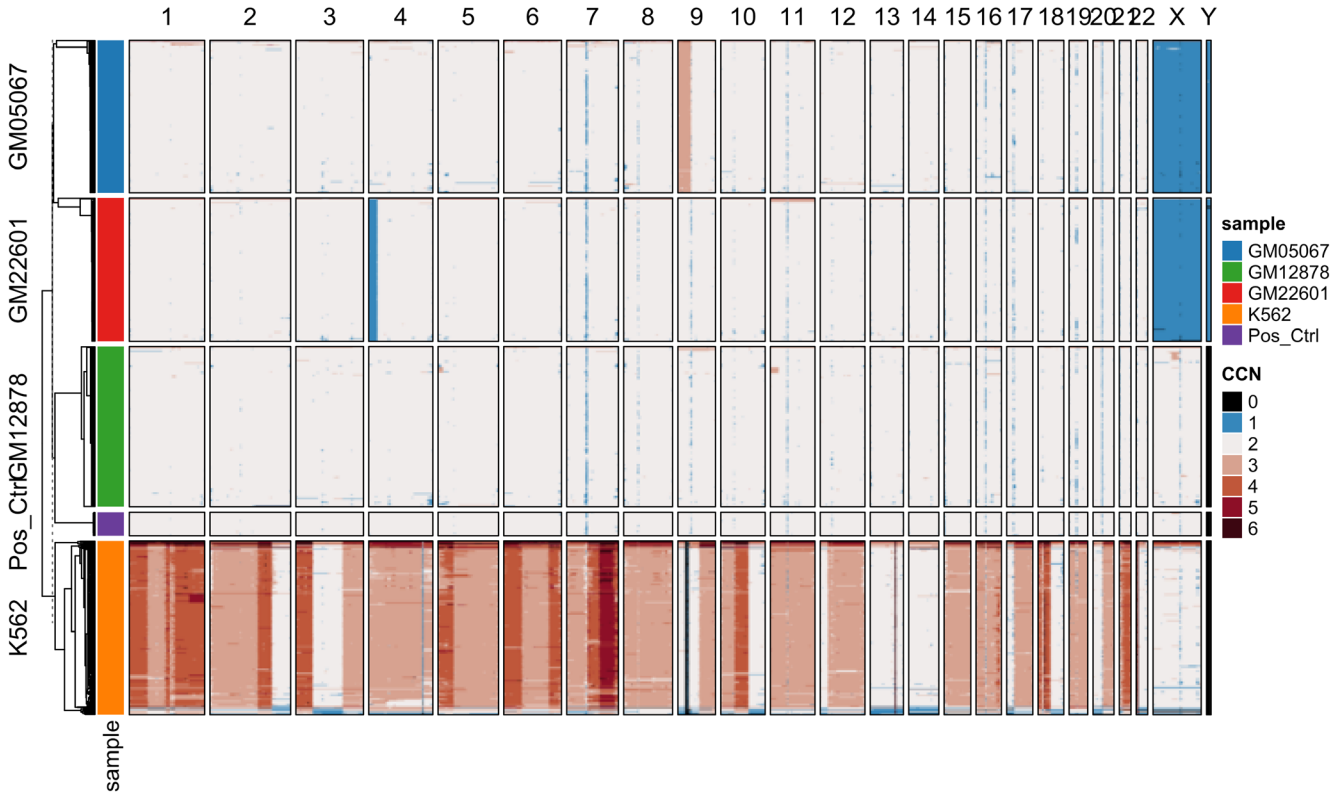
Single-cell CNV-driven clustering with pseudo-bulk SNV analysis

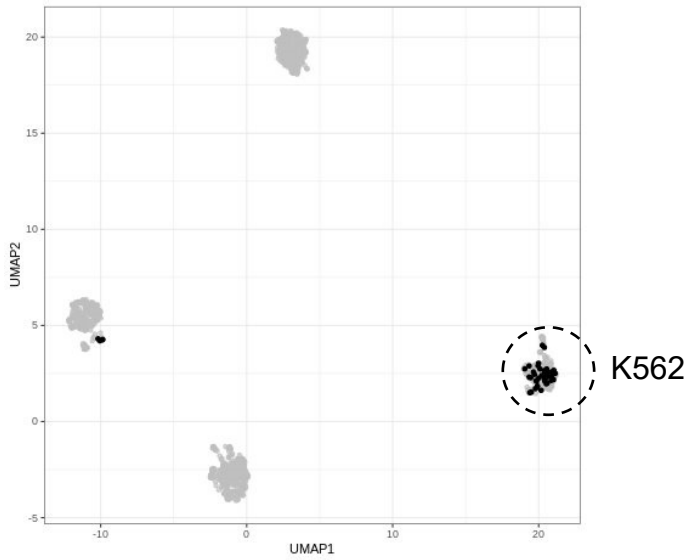
Copy number profile heatmap of 1,124 single cells from four cell lines

Segmental CNVs detectable: >50 Mb insertions/deletions at 250,000 read pairs/cell for ≥90% of the single cells

CNV heatmap and phylogenetic tree



Pseudo-bulk SNV analysis for cell clusters

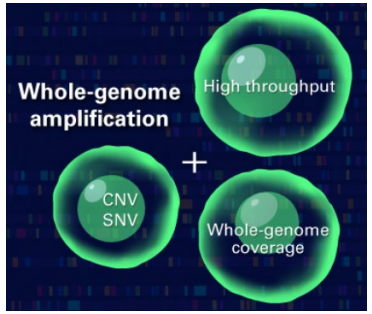


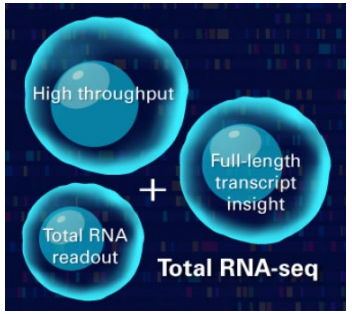
Chr 7: 55034534: A:C
A variant within the *EGFR* gene

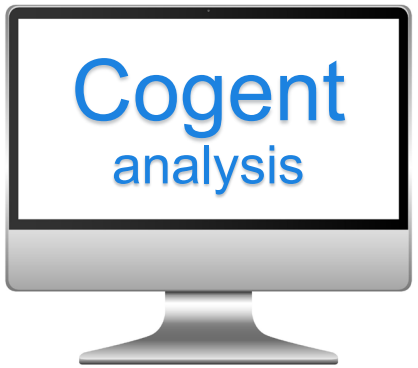
Summary

More cells. More biomarkers. More discoveries. More breakthroughs!

- Retain coverage and sensitivity at scale without compromise
- Integrate automation, chemistries, and bioinformatics solutions
- Deliver the biomarkers other technologies miss







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