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An improved, cost-effective and efficient protocol for perturb-seq

Stanford scientists have developed a new protocol for perturb-seq that is significantly cheaper and more efficient than existing approaches.

Perturb-seq is a high-throughput technique that combines CRISPR-based gene perturbation with single-cell RNA sequencing to study the effects of certain genes on cellular physiology. It allows researchers to dissect complex genetic interactions and cellular responses at single-cell resolution to investigate gene functions and regulatory networks. However, existing methods for perturb-seq are expensive (often in excess of $1.5MM) and have limited efficiency.

Stanford researchers therefore developed a new method that uses an innovative circularized capture approach to directly read out the sgRNA, ensuring stable capture efficiency across different cell types and enabling multiplexed delivery of distinct sgRNAs. This improves the efficiency of guide RNA detection by ~7-fold over existing approaches while reducing costs by over 20-fold.

Stage of Development
Prototype: successfully implemented protocol in the lab

Applications

- Cellular perturbation screens for basic science and drug developmento

Advantages

- ~20x less expensive than existing methods
- Enables the delivery of multiple guides in tandem
- gRNA detection is ~7x more efficient than in existing methods

- Efficient across cell types
- Can be used at high or low multiplicity of infection
- Can be used to detect gRNAs or other RNAs of interest

Patents

- Published Application: WO2025240731

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