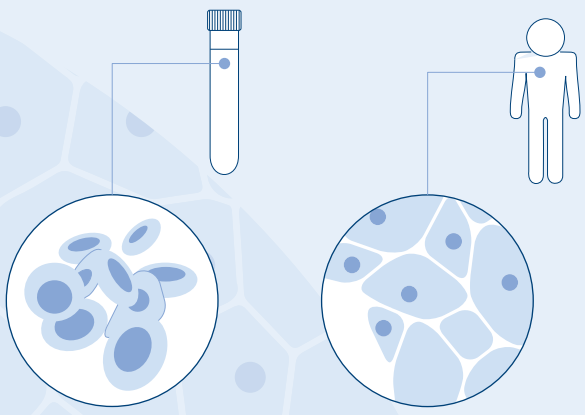
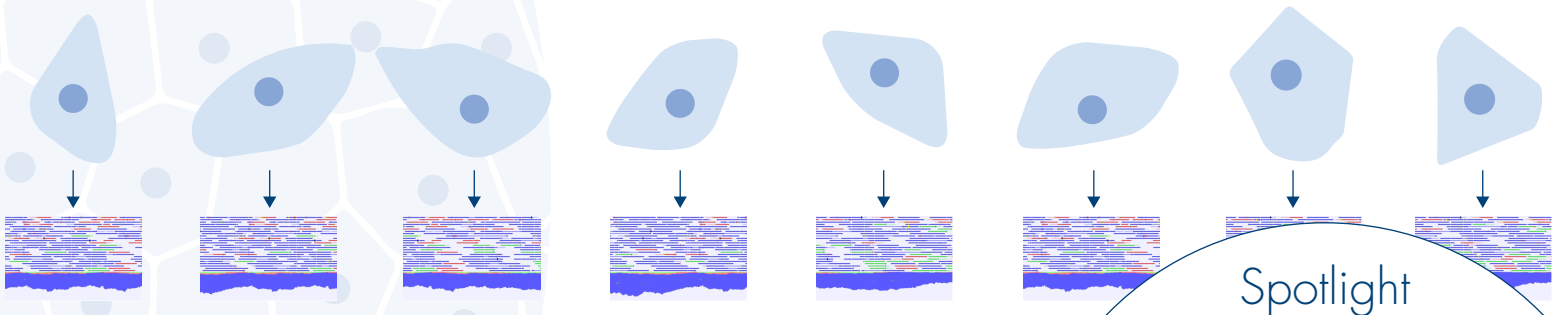
Achieve improved variant detection in single cell sequencing



"For clinical samples with a limited number of cells, such as fine-needle aspirates or circulating tumour cells, the most interesting genetic variants are shared among the cells, … it is most efficient to perform 'census-based variant detection' from multiplexed sequencing of independently amplified single-cell DNA libraries, each sequenced to modest depths (~1x)."[1]

Accurate variant detection in rare cells – feasible and affordable

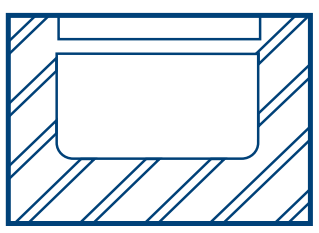
Prepare single cell libraries from multiple single cells



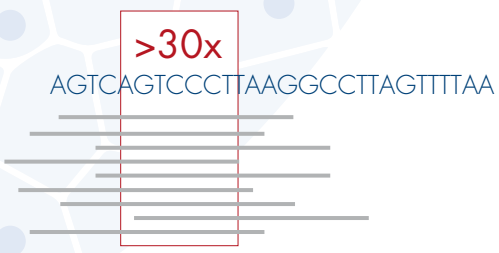
Uniform genome coverage during whole genome amplification is required

Spotlight

With REPLI-g® Single Cell Kits, you can achieve highly uniform and comprehensive coverage with superior accuracy



No need for you to sequence at high depth as required in bulk sample variant detection



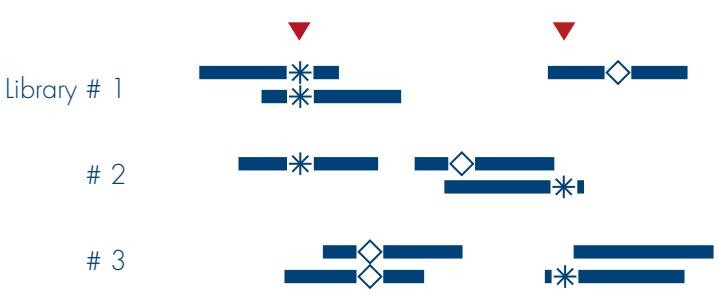
Pool single cell libraries

Sequence at modest depth (~1x per cell)

Why is single cell variant detection in cancer important?

- Facilitates your identification of tumor subpopulation and founder mutations
- Enables you to analyze circulating cells for non-invasive monitoring and early detection
- Simplifies your understanding of tumor phylogenetic trees and cell lineages

Census-based variant detection: increase variant detection power and reduce false positives from library preparation[1]



✳ Accept (variant allele detected in ≥2 libraries)
◇ Reject (variant allele detected in 1 library only)

[1] Zhang, C.-Z. et al. (2015) Calibrating genomic and allelic coverage bias in single-cell sequencing, Nat. Comm. **6**, 6822.

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Sample to Insight