# Decrease experiment costs and increase assay sensitivity using BD Rhapsody™ Enhanced Cell Capture Beads

The BD Rhapsody™ Enhanced Cartridge Reagent Kit is designed and validated to work together with the complete portfolio of BD single-cell instruments, multiomic assays and bioinformatics tools, helping to unravel the complexity of biological systems.

**Compatible with:**

- BD Rhapsody™ Single-Cell Analysis System
- BD® Single-Cell Multiplexing Kits
- BD® AbSeq Assays
- BD Rhapsody™ Targeted mRNA or Whole Transcriptome Amplification Kits
- BD Rhapsody™ TCR/BCR Multiomic Assay
- BD Rhapsody™ Analysis Pipelines and SeqGeq™ Software

**Offset cell labels to enable decreased PhiX**

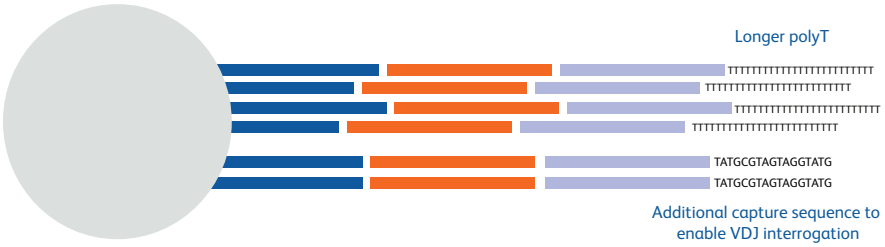


**Figure 1.** Design changes to enhanced beads enable higher sensitivity and lower experiment cost.

The BD Rhapsody™ Enhanced Cell Capture Beads (enhanced beads or EB) were developed to decrease experiment costs and increase assay sensitivity. Compared to the original BD Rhapsody™ Cell Capture Beads (V1), the enhanced beads have a minimal PhiX requirement, increased sensitivity for whole-transcriptome profiling at similar read depth, broader sequencer compatibility and new 5' capture capabilities to enable immune repertoire profiling. The enhanced beads have been thoroughly tested and validated to generate greater or equal performance compared to the current cell capture beads (V1) on all existing BD Rhapsody™ Assays, including WTA, Targeted, AbSeq and sample multiplexing, as well as all assay combinations. For information on assays running in conjunction with the VDJ assay, contact **scomix@bdscomix.bd.com.**

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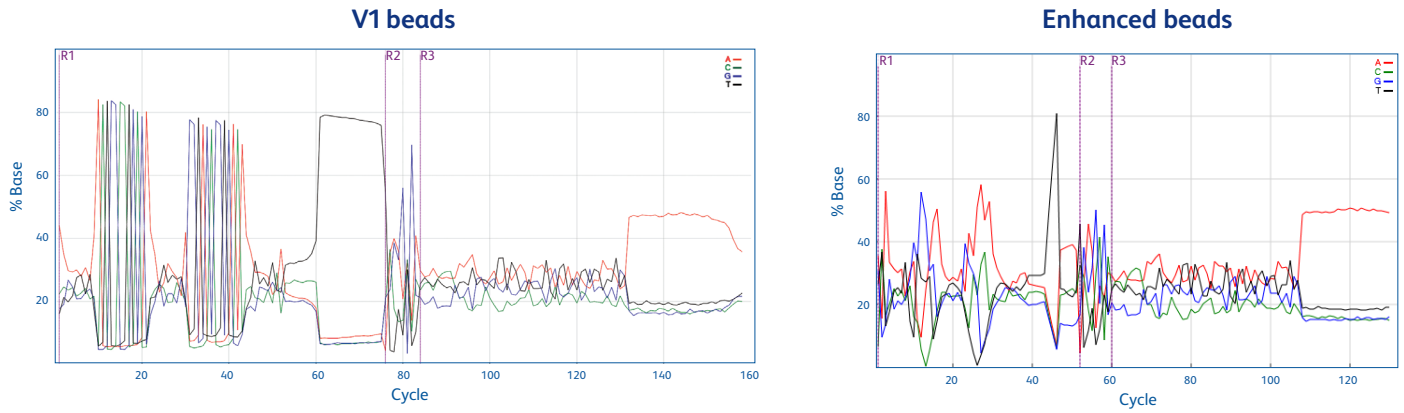



**Figure 2.** Offset cell labels increase sequence diversity at linker sequences, decreasing the amount of PhiX required.

# Using enhanced beads allows for decreased sequencing cost and increased sensitivity for whole-transcriptome profiling

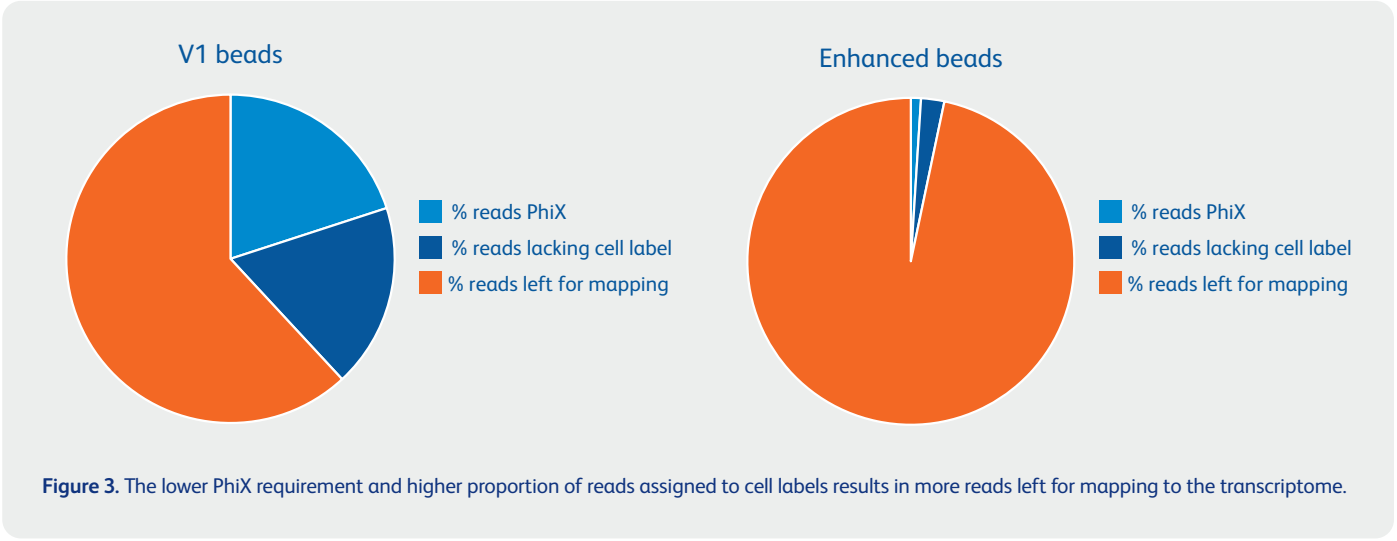



**Figure 3.** The lower PhiX requirement and higher proportion of reads assigned to cell labels results in more reads left for mapping to the transcriptome.

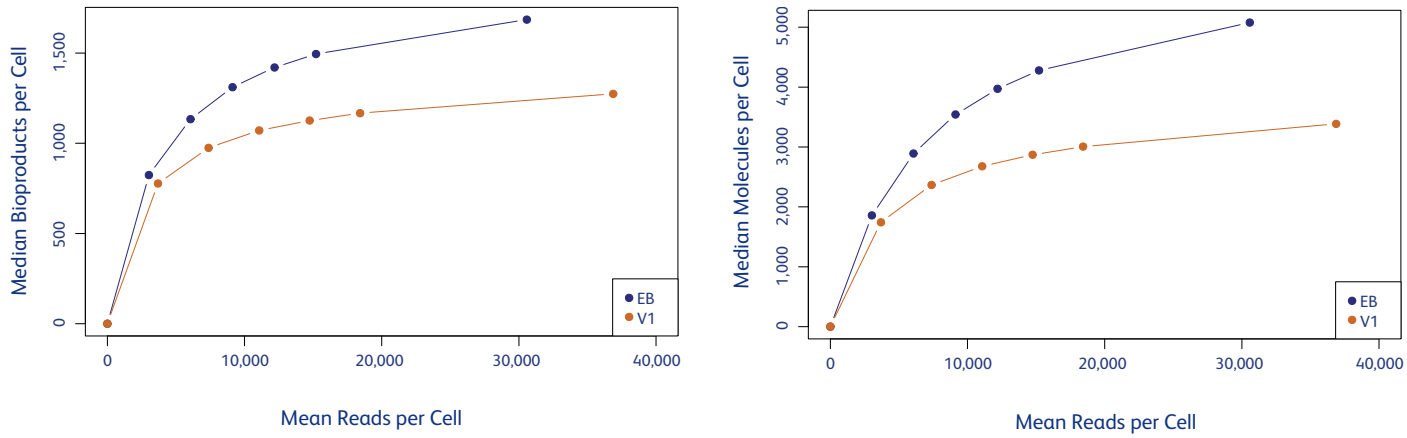
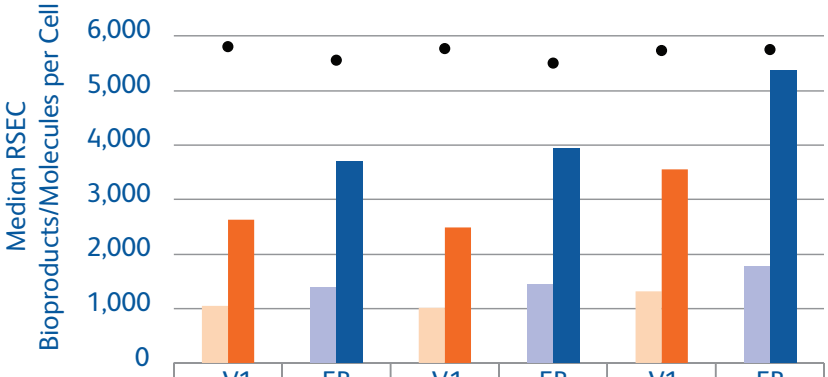



**Figure 4.** Enhanced beads show more bioproducts and molecules detected per cell compared to the original cell capture beads (V1).

# Enhanced beads produced higher bioproducts and molecules per cell than V1 beads at similar sequencing saturation

**WTA assay sensitivity at different cellular inputs for V1 and EB**




| | | | | | | |
|---|---|---|---|---|---|---|
| Approximate Cells Captured | 100 | | 2,000 | | 20,000 | |
| Median Bioproducts per Cell | 1,055 | 1,392 | 1,027 | 1,444 | 1,318 | 1,784 |
| Median Molecules per Cell | 2,632 | 3,704 | 2,486 | 3,942 | 3,563 | 5,358 |

**Figure 5.** WTA assay sensitivity at different cellular inputs for V1 and EB. Sequencing saturation >93.

**Correlation between mean molecules per cell of V1 beads (x-axis) compared to EBs (y-axis) for 20,000 cell input**

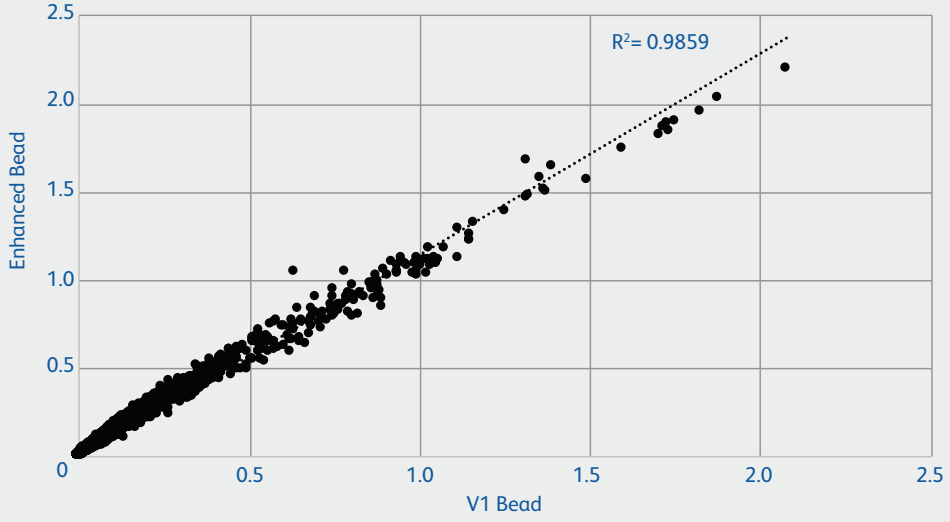
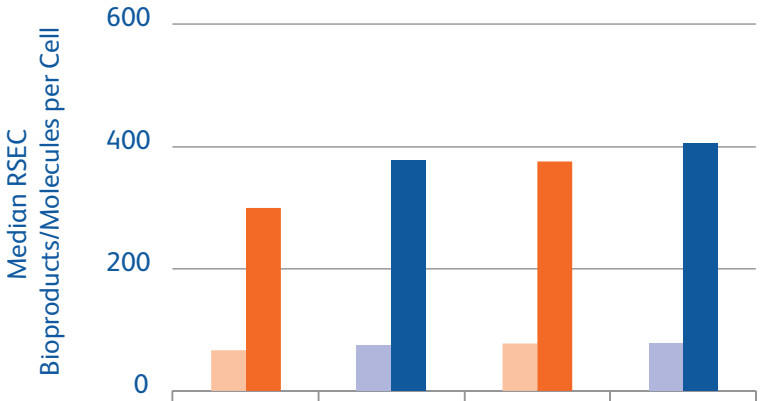



**Figure 6.** High concordance between WTA data ($Log_{10}$(mean molecules per cell + 1) is plotted) from V1 (x-axis) and enhanced beads (y-axis) shows that changes in bead architecture do not bias molecule representation.

# Enhanced beads produced comparable data to V1 beads for targeted mRNA and AbSeq profiling

**Targeted assay sensitivity across targeted mRNA + combination assays at different cell input levels**




| | | | | |
|---|---|---|---|---|
| Approximate Cells Captured | 2,000 | | 10,000 | |
| Median Bioproducts per Cell | 67 | 74 | 78 | 78 |
| Median Molecules per Cell | 300 | 377 | 375 | 405 |

**Figure 7.** Comparable sensitivity for targeted mRNA assay when run in combination with AbSeq across multiple cell inputs. Sequencing saturation >90.

**High concordance between targeted mRNA run with AbSeq from V1 and enhanced beads shows that changes in bead architecture do not bias molecule representation**

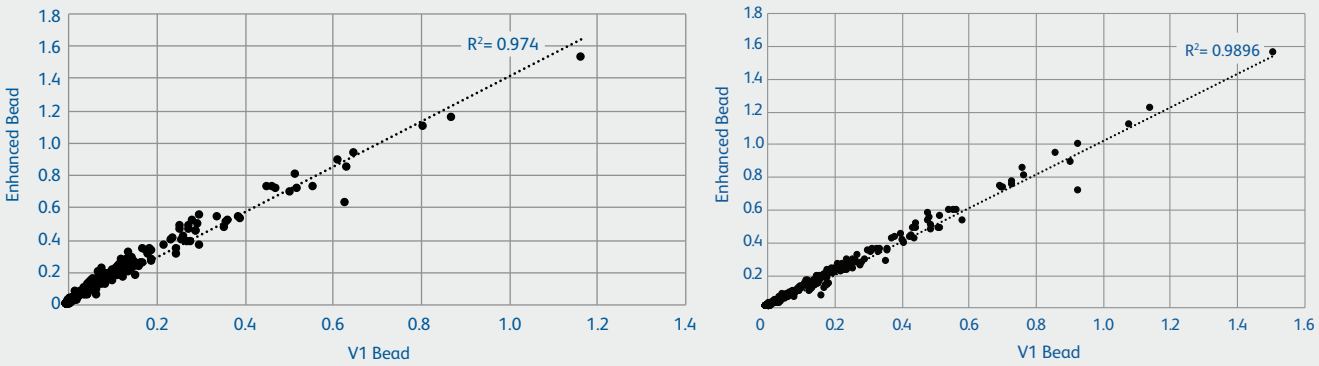



**Figure 8.** Left: Correlation between mean molecules per cell ($Log_{10}$(mean molecules per cell +1) is plotted) in V1 beads (x-axis) compared to EBs (y-axis) for 2,000 cell input is shown. Right: Correlation between mean molecules per cell ($Log_{10}$(mean molecules per cell +1) is plotted) in V1 beads (x-axis) compared to EBs (y-axis) for 10,000 cell input is shown.

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