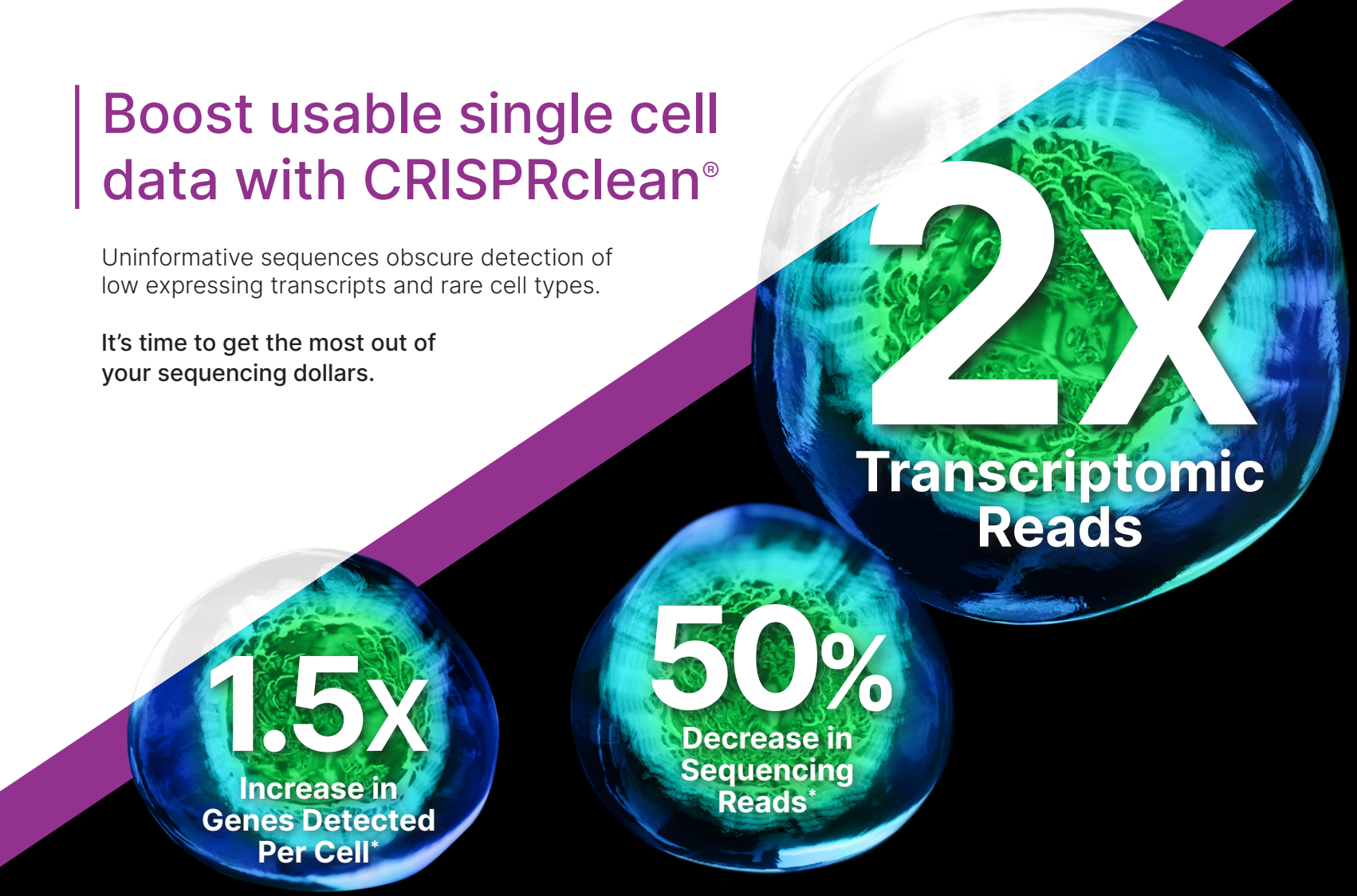
JUMPCODE GENOMICS

Boost usable single cell data with CRISPRclean®

Uninformative sequences obscure detection of low expressing transcripts and rare cell types.

It's time to get the most out of your sequencing dollars.



Remove uninformative molecules from single cell libraries—doubling your transcriptomic reads

- Gain a deeper view of expression profiles of individual cells
- Deplete sequences not used for secondary analysis including: Unaligned reads, ribosomal, mitochondrial, non-variable genes
- Gain greater differentiation in cell types without perturbing cell type calls

Get Started Now

*Data from PBMC's, some variance expected with different cell types