FocuSCOPE® Single Cell Multiomics mRNA x Clonal Hematopoiesis Kit

Clonal Hematopoiesis of Indeterminate Potential (CHIP) is a condition related to aging, characterized by the accumulation of mutations in hematopoietic stem cells during middle age. The mutations are not cancerous but associated with an increased risk of developing blood cancer or cardiovascular disease.

FocuSCOPE® Single Cell Multiomics mRNA x Clonal Hematopoiesis Kit, can precisely detect mutations implicated in the development of CHIP, in addition to capturing the entire transcriptome, bringing us one step closer to understanding this aging-related disease and developing treatments.

Highlights

Comprehensive information linking genetic variation to gene expression

- Simultaneous detection of mutations seen in CHIP and whole transcriptome at a single cell level

High mutation coverage:

- The most frequently mutated genes seen in CHIP are covered

Easy workflow:

- No instrument is necessary. Straightforward process to analyze thousands of cells in parallel to identify genetic and cellular heterogeneity in your samples

Principle

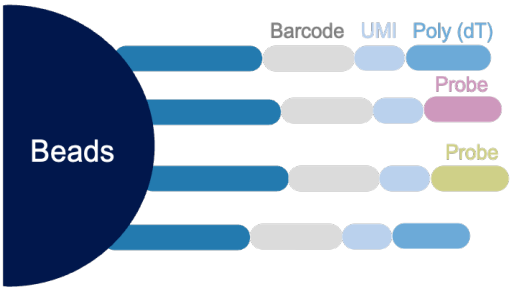

Figure 1: Specially designed Barcoding Beads allow capturing simultaneously both whole transcriptome and CHIP specific mutations.

FocuSCOPE® Single Cell Multiomics mRNA x Clonal Hematopoiesis Kit uses specially designed Barcoding Beads that contain two types of oligonucleotides (Figure 1).

The first type of oligonucleotides contain Illumina sequencing primer sequence, a unique cell barcode for identifying the cell origin of the RNA, a unique molecular index (UMI) for cDNA quantification, poly (dT) sequence for capturing mRNA, and the second type of oligonucleotides contain probes designed specifically to capture genes that harbor druggable mutations (left).

Following reverse transcription and enrichment of targeted regions, two separate libraries are obtained and combined for sequencing (Figure 2).

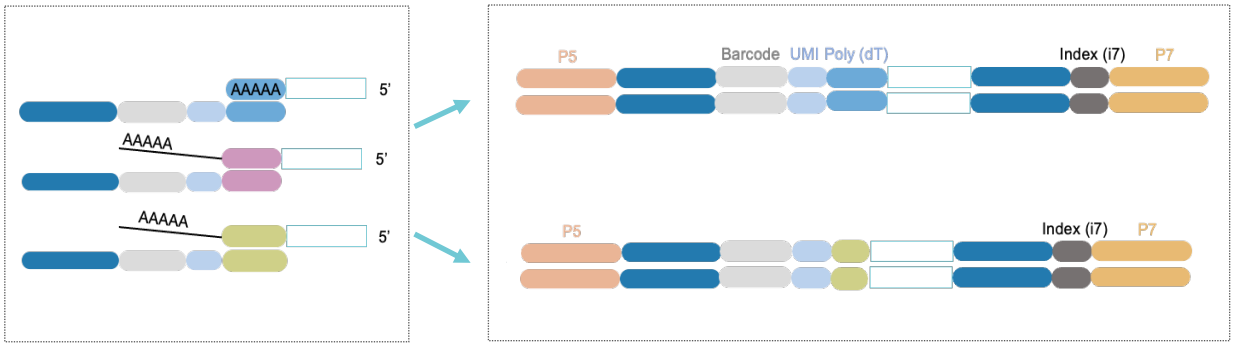

Figure 2. Barcoding Beads capture both whole mRNA and CHIP mutation sites. Following reverse transcription and target gene enrichment, two seprate libraries are obtained that can be combined for sequencing.

High Detection Rate Compared to Poly-T Capturing Only

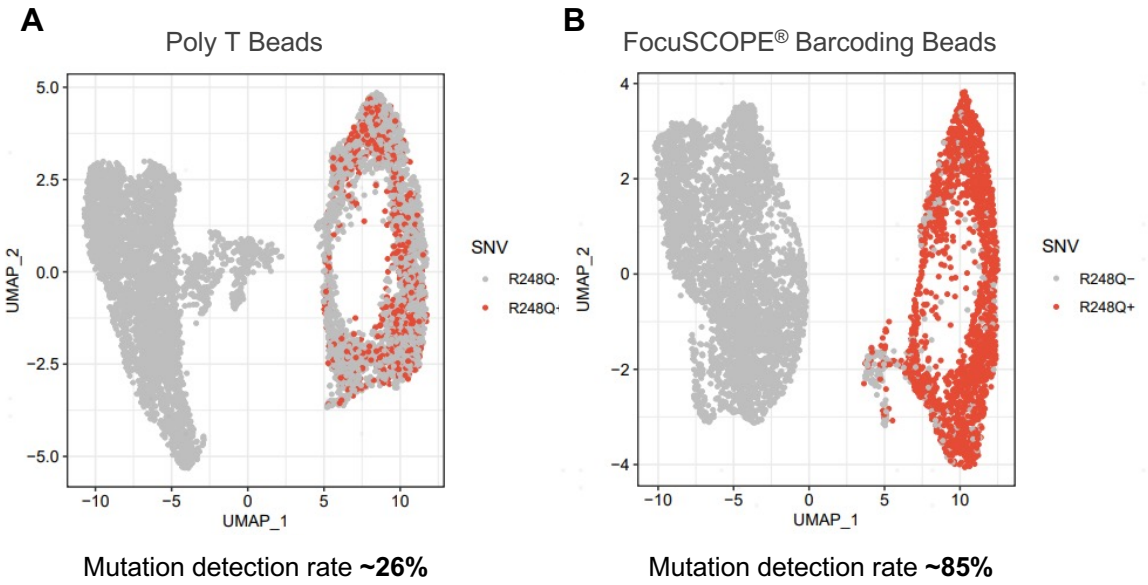

Figure 3. CCRF and K562 were mixed in equal proportions. Libraries were prepared in the same way by either specially designed FocuSCOPE® barcoding beads (B) or Poly T beads (A). CCRF cell line contains TP53 mutation (R248Q), whereas K562 doesn't contain this mutation. Using FocuSCOPE® Beads dramatically increased the detection of the mutation.

Gene	Target site
DNMT3A	R882H
TET2	I1873T/*/N , R1261H/C , R1359C/H/S/G , H1380Y/P/Qfs*68/R
TP53	R175H,G245S, R248Q, R248W, R249S,R273H, R273S, and R282W
ASXL1	p.G643WfsX12
JAK2	V617F

Table: Clonal hematopoiesis panel genes and targeted sites are shown.

Product	Cell
	2 RXNs / 16 RXNs
FocuSCOPE® Single Cell Multiomics mRNA x Clonal Hematopoiesis Kit cell	4341011/4341012
FocuSCOPE® Single Cell Multiomics mRNA x Clonal Hematopoiesis Kit cell for Matrix	4341021/4341022

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