CloneTracker™ Lentiviral Barcode Libraries

CELLECTA

Discovery is yours™

Label Millions of Cells with Unique Barcodes for Clonal and Sub-Population Analysis

- Identify cell sub-populations with advantageous phenotypes for growth or survival
- Assess changes in cell culture heterogeneity over time or changing culture conditions
- Track clonal expansion in tumors or during differentiation or metastasis
- Link CRISPR-induced genetic knockouts with changes in expression profiles

The ability to label and trace individual cells is a powerful experimental tool in many research areas including cell development, tumor evolution, stem cell differentiation, or carcinogenesis. Cellecta's expressed barcode libraries, together with next-generation sequencing (NGS) technology, enable tracking of clonal variations in large cell populations. Using Cellecta's **CloneTracker Barcode Libraries**, it is possible to genomically label each cell, in a population of a few million, with a uniquely identifiable short nucleotide sequence (i.e., a barcode). Since the barcodes genomically integrate, they are heritable so all progeny from each cell harbor the same unique sequence and clonal expansion for each founder cell can be monitored.

The initial transduction of a lentiviral barcode library (Figure 1) into cultured cells, produces a founder or starter population in which each cell has a unique and heritable barcode label. NGS can then be used to sort out sub-populations of progeny cells derived from the original progenitors at any point during an experiment. The approach provides a convenient way to identify cell variations with unique characteristics or biology, and to understand how these groups of variant cells evolve in response to drug treatment, tumor metastasis, or other conditions.

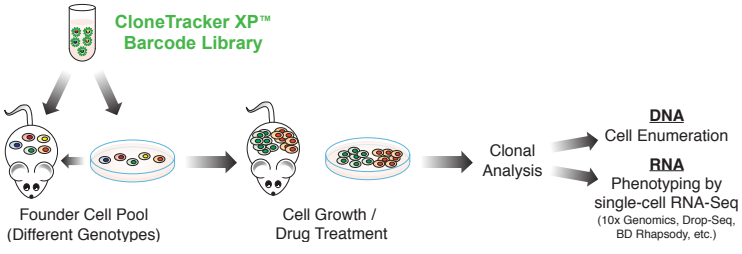

Figure 1

Cellecta's **CloneTracker XP Barcode Libraries** (Figure 2) differ from our standard CloneTracker Barcode Library in that the barcode is designed to express on an RNA transcript in the cells. As a result, it can be detected by RNA sequencing, as well as DNA sequencing. The CloneTracker XP Libraries, used in combination with single-cell RNA sequencing, allow researchers to identify which genes are actually activated or shut down in different groups of cells so that, depending on the experiment, they can identify which genes are important for drug resistance, metastasis, cell differentiation, or other processes.

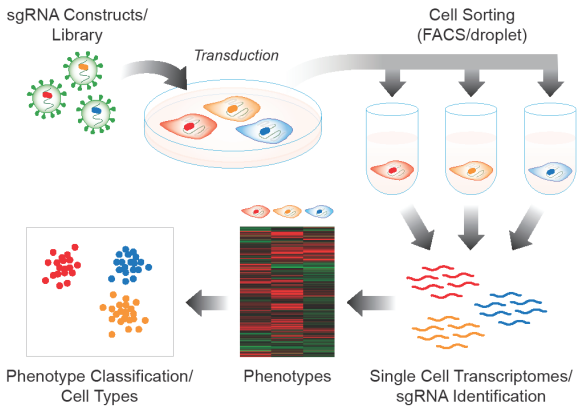

Figure 2

The CloneTracker XP™ Expressed Barcode libraries are available with barcodes expressed in the 3'- or 5'-UTR of an RNA transcript, and with fluorescent or chemiluminescent reporters.

For more information, email info@cellecta.com, or call +1-650-938-3910

Ordering Information

Catalog #	Description	Quantity
BCXP10M3RP-P	CloneTracker XP™ 10M Barcode-3' Library with RFP-Puro (plasmid)	200 ug
BCXP10M3RP-V	CloneTracker XP™ 10M Barcode-3' Library with RFP-Puro (virus)	1 x 10^8 TU
BCXP1M3RP-1S-P	CloneTracker XP™ 1M Barcode-3' Library with RFP-Puro (plasmid)	200 ug
BCXP1M3RP-1S-V	CloneTracker XP™ 1M Barcode-3' Library with RFP-Puro (virus)	1 x 10^8 TU
BCXP10M3VP-P	CloneTracker XP™ 10M Barcode-3' Library with Venus-Puro (plasmid)	200 ug
BCXP10M3VP-V	CloneTracker XP™ 10M Barcode-3' Library with Venus-Puro (virus)	1 x 10^8 TU
BCXP10M5VP-P	CloneTracker XP™ 10M Barcode-5' Library with Venus-Puro (plasmid)	200 ug
BCXP10M5VP-V	CloneTracker XP™ 10M Barcode-5' Library with Venus-Puro (virus)	1 x 10^8 TU
BCXP10M3LP-P	CloneTracker XP™ 10M Barcode-3' Library with rLuciferase-Puro (plasmid)	200 ug
BCXP10M3LP-V	CloneTracker XP™ 10M Barcode-3' Library with rLuciferase-Puro (virus)	1 x 10^8 TU