

Vesicode® Surface 550

Highly multiplexed surface protein profiling of individual human extracellular vesicles

Powered by svPBA™ (single vesicle Proximity Barcoding Assay)

Vesicode® Surface 550 is a PBA reagent kit for highly multiplexed profiling of surface proteins on individual human extracellular vesicles (EVs). By preserving protein co-localization, it enables analysis of EV composition, combinatorial surface signatures and biological heterogeneity.

550 proteins

Highly multiplexed surface protein panel

100,000 – 1 million EVs

Profiled per sample

<5 µL plasma

Low sample input

UMI-based molecular counting

Unique molecular identifiers support quantitative counting of detected molecules

What can you study with Surface 550?

- Compare EV surface-protein profiles across samples, conditions or cohorts
- Identify protein co-localization and combinatorial surface signatures
- Characterize molecularly distinct EV subpopulations
- Investigate EV heterogeneity beyond population-averaged measurements
- Explore candidate molecular patterns for biomarker research

Available kit configurations

Kit size	Catalog number
8 reactions	KEV0001M8
16 reactions	KEV0001M16
24 reactions	KEV0001M24
48 reactions	KEV0001M48
96 reactions	KEV0001M96

Explore the complete Surface 550 panel

Download the complete target list from our product page.

Broad biological coverage

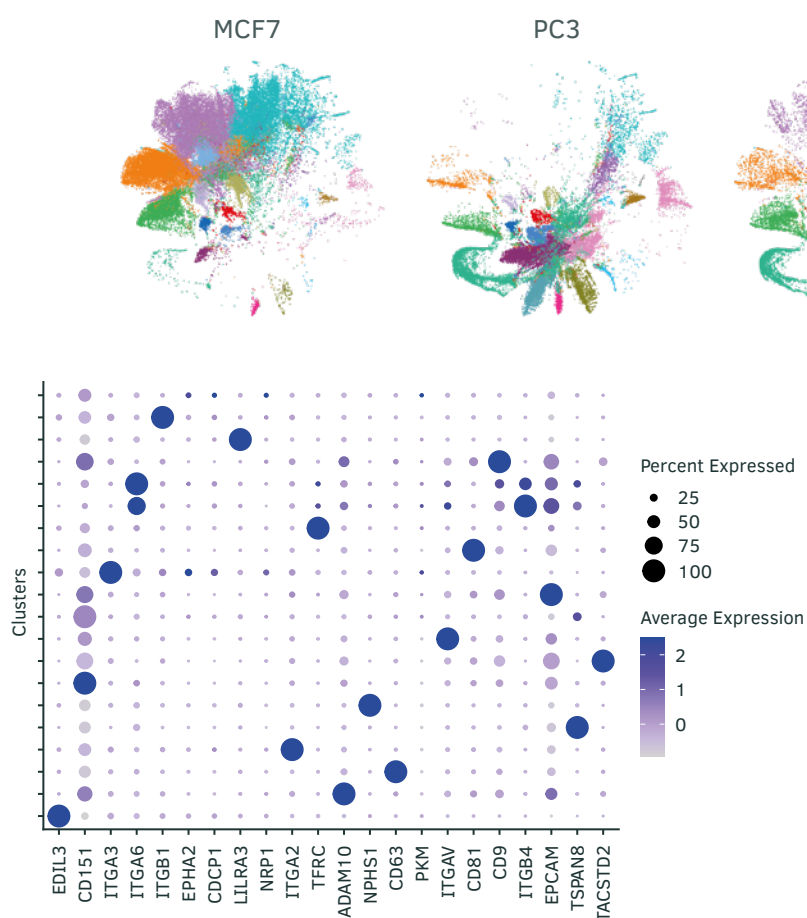
550 surface-protein targets spanning immune biology, cell adhesion, disease, cancer and therapeutic targets.

Vesicode workflow

Day 0	Sample and EV capture plate preparation	Prepare samples and the EV capture plate.
Day 1	PBA workflow	EV capture, probe binding, PBA template attachment and proximity barcoding via DNA extension. Approximately 6 hours hands-on time.
Day 2	Library construction	Sample indexing, library amplification, pooling and purification. Approximately 4 hours hands-on time.
Day 3	Sequencing	Sequence prepared libraries by next-generation sequencing (NGS).

Distinct EV subpopulations and surface-protein signatures

Surface 550 resolves molecularly distinct EV subpopulations and their surface-protein signatures across four human cancer cell lines. The t-SNE plots reveal heterogeneous populations within each cell line, while the dot plot highlights proteins enriched in individual clusters.



Interpreting the data

- Colored points represent molecularly distinct EV subpopulations within each cell line.
- Individual EV clusters display characteristic surface-protein signatures.
- These signatures can be compared across EV subpopulations and samples.
- Dot size indicates the proportion of EVs positive for each protein, color indicates relative expression.