MagExo™ Enables Reproducible Isolation of Plasma Extracellular Vesicles: A Multi-Omics-Compatible Platform for Early Cancer Biomarker Discovery and Validation

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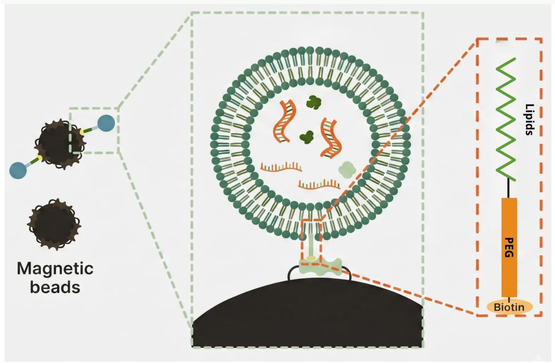
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Introduction

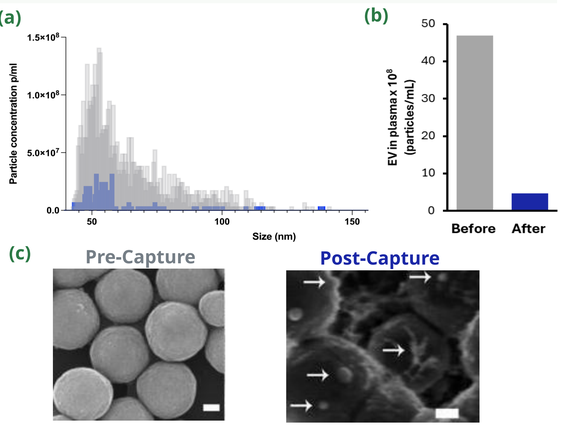
Liquid biopsy has emerged as one of the most promising sample types for early cancer detection, offering a minimally invasive window into tumor biology before disease becomes clinically apparent. Among circulating analytes, plasma-derived extracellular vesicles (EVs) are particularly attractive because they are actively secreted by viable cells and carry proteins, nucleic acids, and lipids protected within a lipid bilayer, providing molecular information complementary to cell-free DNA (cfDNA) and soluble proteins. However, EV biomarker development remains limited by inconsistent isolation, plasma protein contamination, and variable recovery, which can compromise reproducibility in biomarker validation studies.

Here, we evaluate MagExo™, a magnetic bead-based EV isolation platform, for recovery, purity, multi-omics compatibility, and reproducibility.

Mechanism

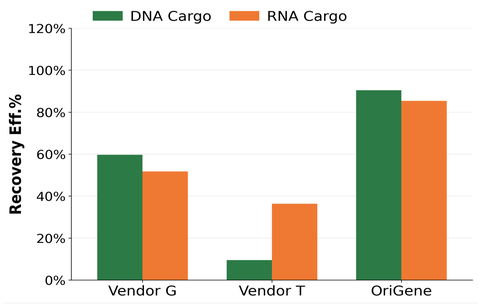


High Capture Efficiency



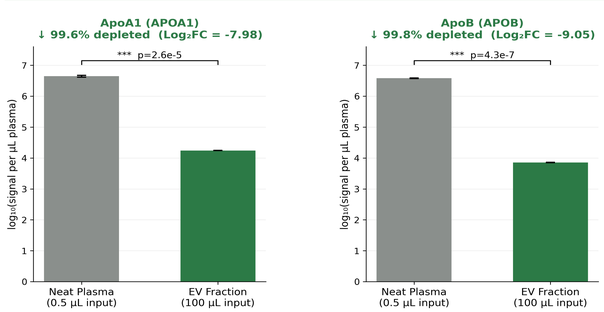
Nanoparticle analysis by NanoFCM before (grey) and after (blue) magnetic bead capture shows marked depletion of EV populations across broad size range (a) and further confirmed reduction in EV counts post-capture (b). Electron microscopy images reveal EVs (arrowheads) bound to the surface of magnetic beads, validating direct vesicle capture(c).

High Recovery of EV Nucleic Acid Cargo



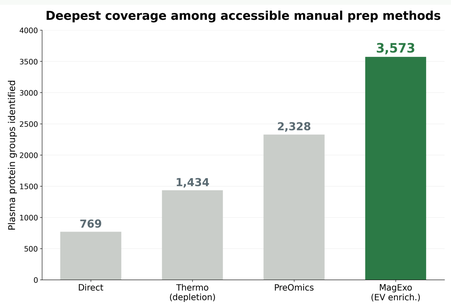
MagExo™ recovers >80% of EV-associated DNA and RNA from plasma, exceeding two benchmark isolation reagents (Vendor G, Vendor T). Recovery efficiency was calculated as (EV-spiked plasma − unspiked plasma) / total yield from pure EVs × 100%, quantified by Qubit DNA/RNA HS assay.

High Purity and Minimal Contamination



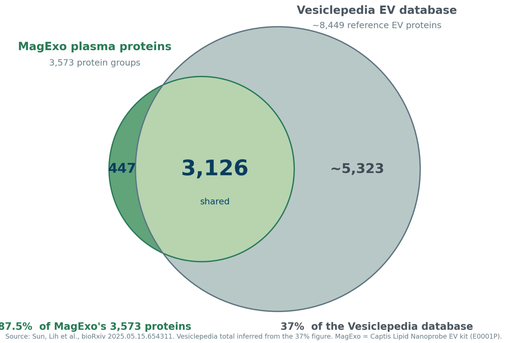
MagExo EV isolation achieves near-complete, statistically significant removal of both HDL-associated (ApoA1) and LDL/VLDL-associated (ApoB) apolipoproteins per unit of starting plasma, confirming effective lipoprotein contaminant depletion during EV enrichment.
Peptide-level LC-MS/MS quantification (DIA-NN output) for ApoA1 and ApoB was summed per protein and normalized to plasma input volume (Neat Plasma: 0.5 µL; EV Fraction: 100 µL).

Deep plasma coverage



LC-MS analysis of MagExo™-isolated EVs from as little as 100 µL plasma identifies >3,500 protein groups — substantially deeper coverage than direct blood/plasma processing methods (329–2,328 protein groups) — demonstrating exceptional EV proteome depth.

MagExo Genuinely Enriches EVs



MagExo captured all 100 of Vesiclepedia's top EV marker proteins and 3,126 catalogued EV proteins overall — 37% of the entire reference database. The workflow identifies not just more proteins but the right ones.

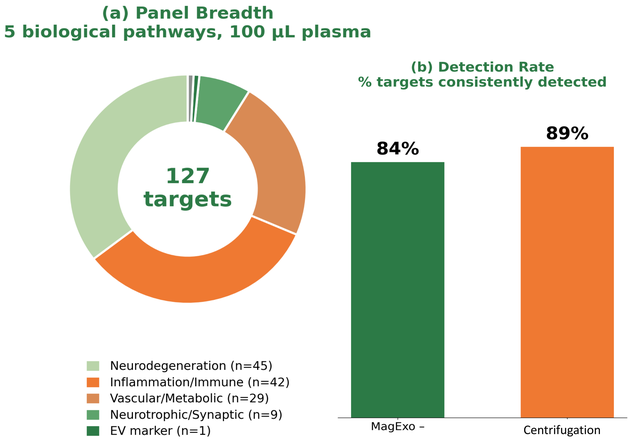
Broad Cancer Biomarker Detection Across Cell-Line-Derived EVs

EVs from 12 cancer cell lines were spiked into healthy plasma, isolated with MagExo™, and profiled by Simple Western across cancer-relevant protein classes — adhesion molecules, oncogenic receptors, and immune-modulatory factors — revealing both conserved EV markers and cell-line-specific biomarker signatures.

MagExo™: Infrastructure for Biomarker Discovery and Validation

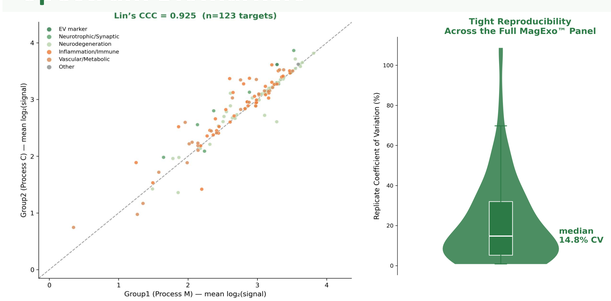
- High recovery (>90% EV capture, >80% nucleic acid yield), high purity (>99.5% contaminant depletion), and strong reproducibility (86.7% detectability, median CV <15% across 12 independent specimens) address the core barriers to plasma-based biomarker validation
- Multi-omics compatibility (LC-MS, NuLISA, Olink, NGS) from just 100 µL plasma enables flexible, scalable biomarker discovery workflows.
- We welcome collaboration with investigators interested in applying MagExo™ to specimen reference sets and biomarker validation studies.
- For more data and technical details, contact: *gma@origene.com*

Compatibility with High-sensitivity Assay Platforms



NuLISA 127-plex profiling of MagExo™-processed plasma EVs. (a) Category breakdown of the 127-target panel. (b) Detection rate by processing variant, where a target was scored "consistently detected" if found in ≥4 of 6 replicates. Detection by MagExo workflow was high and comparable to centrifugation, showing consistent MagExo™ performance across diverse protein classes.

Reproducible Quantification across Broad-Spectrum Biomarkers



Lin's Concordance Correlation Coefficient (CCC) computed on $\log_2$-transformed paired means; 0.925 CCC value proves the MagExo processing yield highly concordant protein abundance measurements comparing to centrifugation. Low median CV reflects consistency of MagExo™ performance across independent specimens. MagExo delivers tight, reproducible quantification across the full biomarker panel..

References

Sun Z, Lih TM, Hoàng T, et al. Deep Blood Proteomics Identifies over 12,000 Proteins Providing Valuable Information about the State of the Human Body. bioRxiv [Preprint]. 2025 May 20:2025.05.15.654311. doi: 10.1101/2025.05.15.654311.