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Supplemental Information

Methods for Systematic Identification of Membrane Proteins for Specific Capture of Cancer-Derived Extracellular Vesicles

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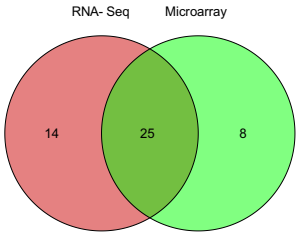

Figure S1. Number of common membrane proteins depending on the type of input RNA data. Related to Figure 1. Number of identified membrane proteins with the highest difference between tumor and normal tissues depending on the type of input transcriptome data (microarray or RNA-Seq).

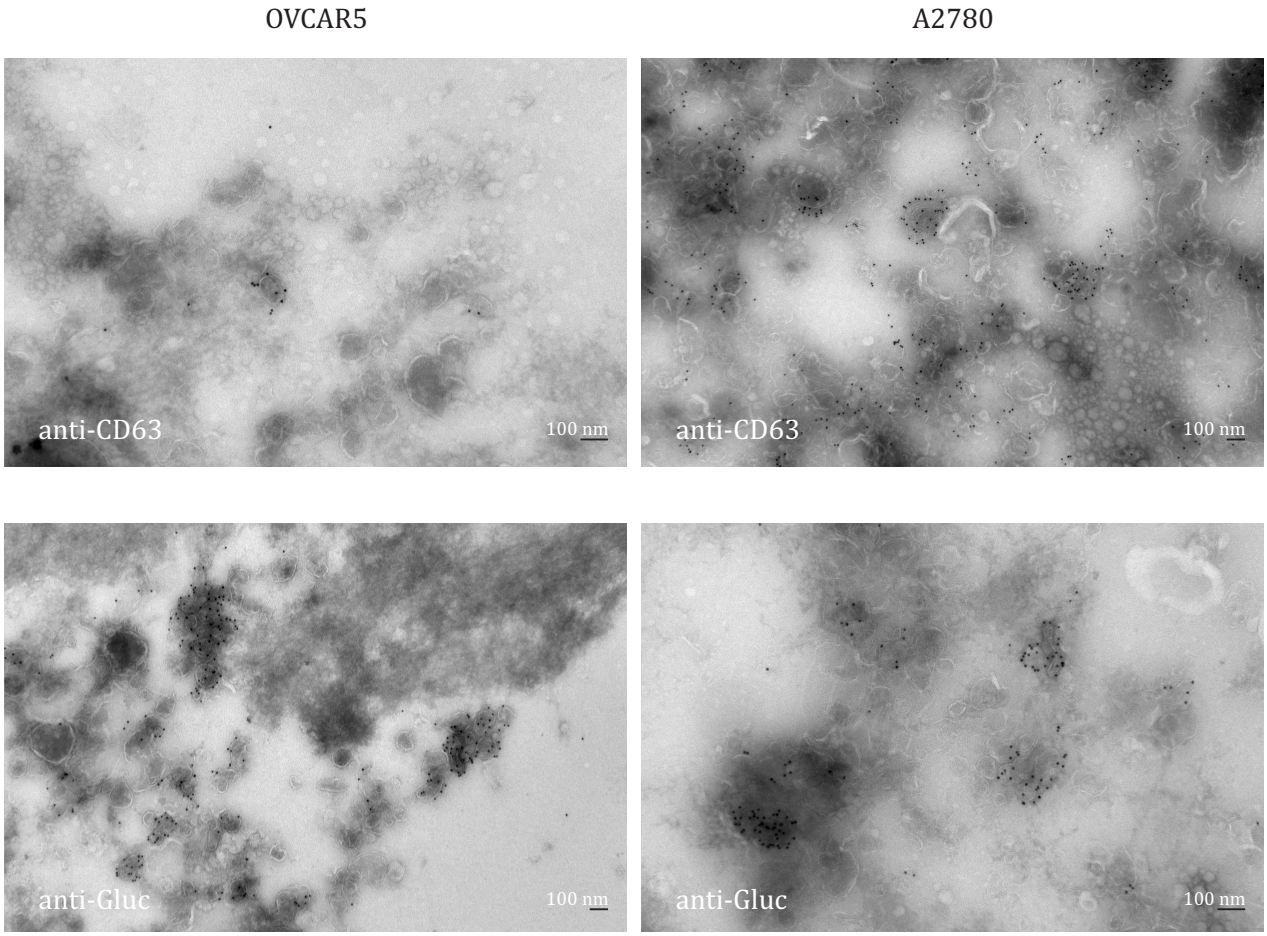

Figure S2. Transmission electron micrographs of EVs. Related to Figure 3.
Transmission electron micrographs. EVs were isolated by ultracentrifugation (100,000 × *g*, 2 hr) from OVCAR5 and A2780 cells and immunolabeled with anti-CD63 and anti-Gluc. Scale bar 100 nm.

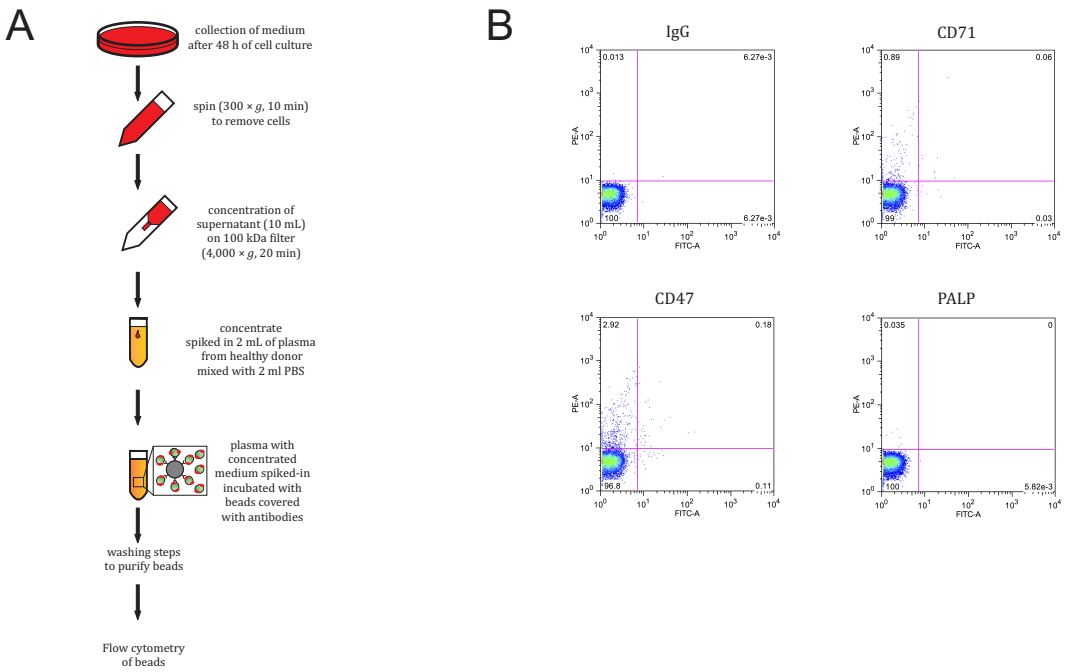

Figure S3. Analysis of cancer-derived EVs spiked-in human plasma. Related to Figure 5.
(A) Schematic of the experiment to test whether EVs extracted from conditioned medium and spiked-in human plasma can be isolated using anti-CD47, CD71 and PALP antibodies. **(B)** Flow cytometry of the beads covered with antibodies against CD71, CD47, PALP and IgG incubated with human plasma with spiked-in EVs derived from palmtdTomato-expressing Kuramochi cells (charts representative of 2 experiments, each with 3 replicates).