

1 Article

2 **Purity determines the effect of Extracellular Vesicles**
3 **derived from Mesenchymal Stromal Cells**
4 **(Supplementary data)**

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17 **1. Materials and methods**

18 MSC bright-field imaging and phenotyping by flow cytometry

19 Bright-field images were taken with optical microscope Nikon Eclipse TS100 (Nikon, Tokyo,
20 Japan) after 48 h before phenotyping by standard flow cytometry to determine MSC surface profile.
21 Briefly, cells growth in different conditions (proliferative media, media with EV-depleted FBS and
22 media without FBS) for 48 hours were resuspended and marked at concentration of $1 \cdot 10^5$ cells/500
23 μ L. For phenotypic analysis, cells were single labelled with fluorescein isothiocyanate (FITC) or
24 phycoerythrin (PE) conjugated monoclonal antibodies: CD105-PE, CD90-FITC, CD73-PE, CD34-PE,
25 HLA-DR-FITC (eBioscience, Thermo Fisher Scientific) and CD45-FITC (Life Technologies, Thermo
26 Fisher Scientific). After labelling, cells were incubated for 10 minutes at 4 °C in darkness. Then, cells
27 were washed with FC buffer (PBS with 20% human AB serum at pH 7.2) to remove antibodies not
28 labelled to the cells. Finally, Guava® easyCyte™ System flow cytometer (Millipore, Burlington, MA,
29 USA) was used to measure simultaneous forward (FSC) and side scatter (SSC), and to analyse the
30 multiparametric fluorescent phenotypic marker signals. Ten thousand events were acquired for each
31 analysis. Sample histogram elaboration was performed with Guava InCyte software to assess
32 fluorescent distribution.

33 Western blot

34 EV samples and MSCs were lysed in ice-cold RIPA lysis buffer containing protease inhibitor
35 (Roche Diagnostics) at the concentration recommended by the manufacturer. Non-lysate samples
36 were prepared with non-reducing loading buffer (without β -mercaptoethanol) to detect tetraspanins
37 presence. Cell lysate (cell lysate and cell lysate_{w/o}) and EV lysate samples were prepared with
38 reducing loading buffer (with β -mercaptoethanol) to detect cytochrome C and bovine serum
39 albumin. All samples were loaded with the same amount of protein (10 μ g) in a 10 or 12%
40 SDS-PAGE gels. Proteins were transferred onto nitrocellulose membrane by humid transference,
41 blocked with 10% dry skimmed milk in TBS containing 10% Tween-20 and incubated overnight at
42 4 °C with the following primary antibodies: anti-human CD9 monoclonal antibody (clone Ts9
43 diluted 1:2,000), anti-human CD63 monoclonal antibody (clone TS63, diluted 1:2,000),

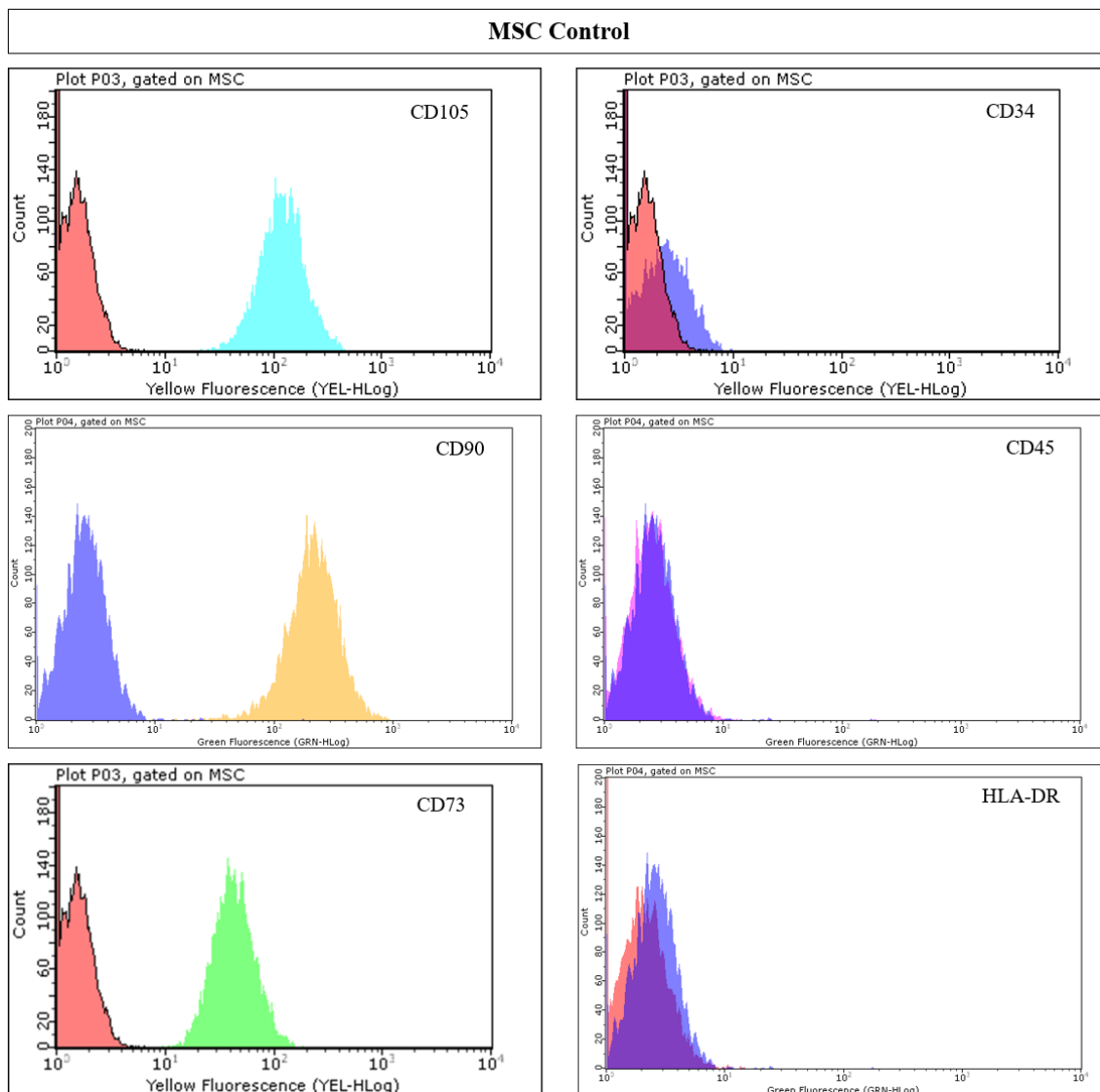
44 anti-cytochrome C monoclonal antibody (clone 37BA11, diluted 1:2,000, Abcam) and anti-Bovine
 45 Serum Albumin monoclonal antibody (clone 2A3E6, diluted 1:1,000, Santa Cruz, Dallas, TX, USA).
 46 Then, membranes were incubated for 1 h with HRP-coupled secondary antibody diluted 1:2,000. For
 47 membrane exposure, membranes were incubated with Clarity Western ECL Substrate and
 48 chemiluminescence were detected with C-DiGit® Blot scanner. Images were processed with Image
 49 Studio Digits Software version 4.0.

50 In order to confirm the correct transferring of the proteins, before blocking, membranes were
 51 then incubated with 0.2% (w/v) Ponceau S in 3% (v/v) acetic acid solution for 5 min. Then,
 52 membranes were washed with deionized water. After taking images, membranes were finally washed
 53 with TBS for 5 min.

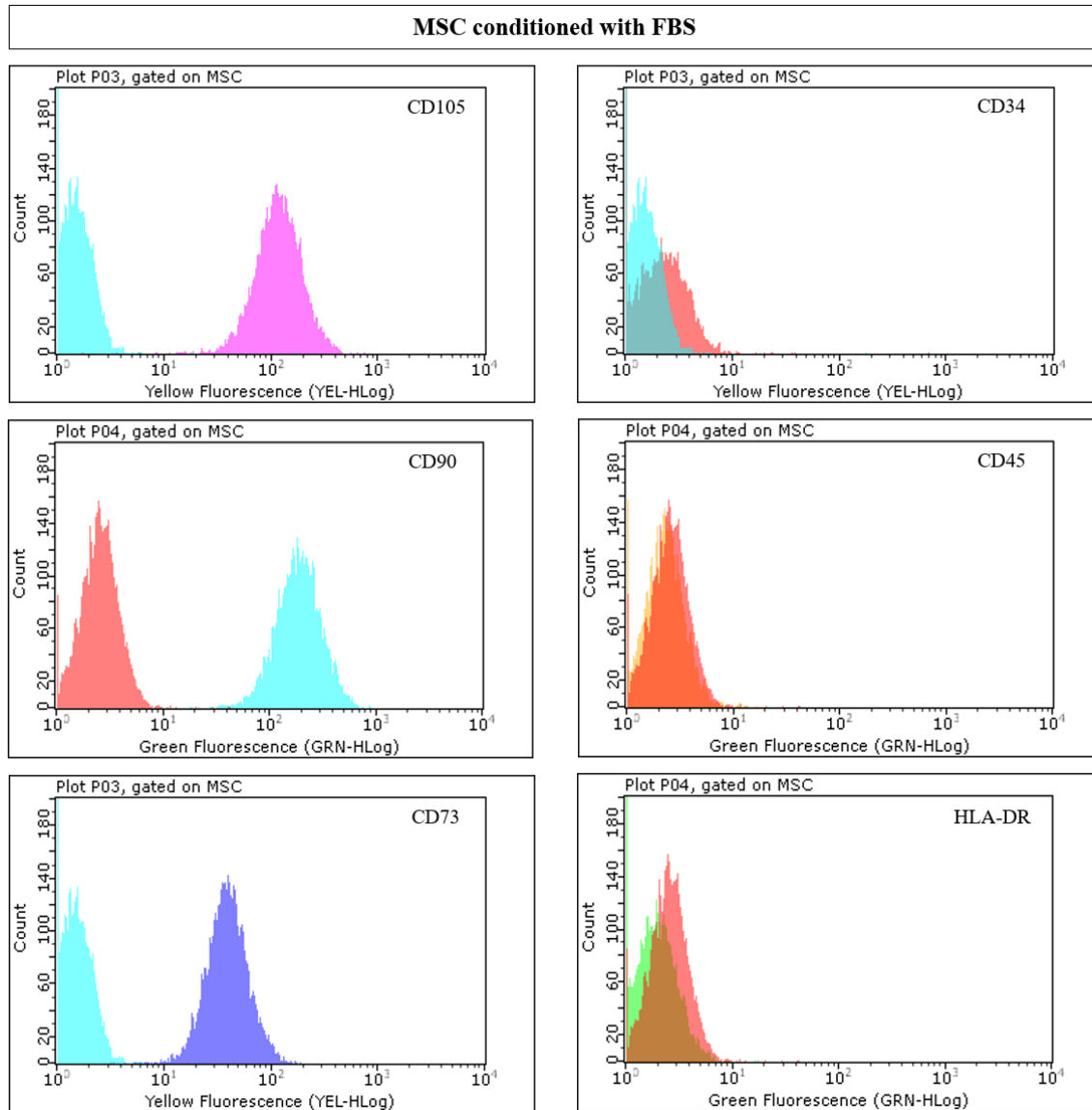
54 **2. Results**

55 MSC characterization after conditioned media collection

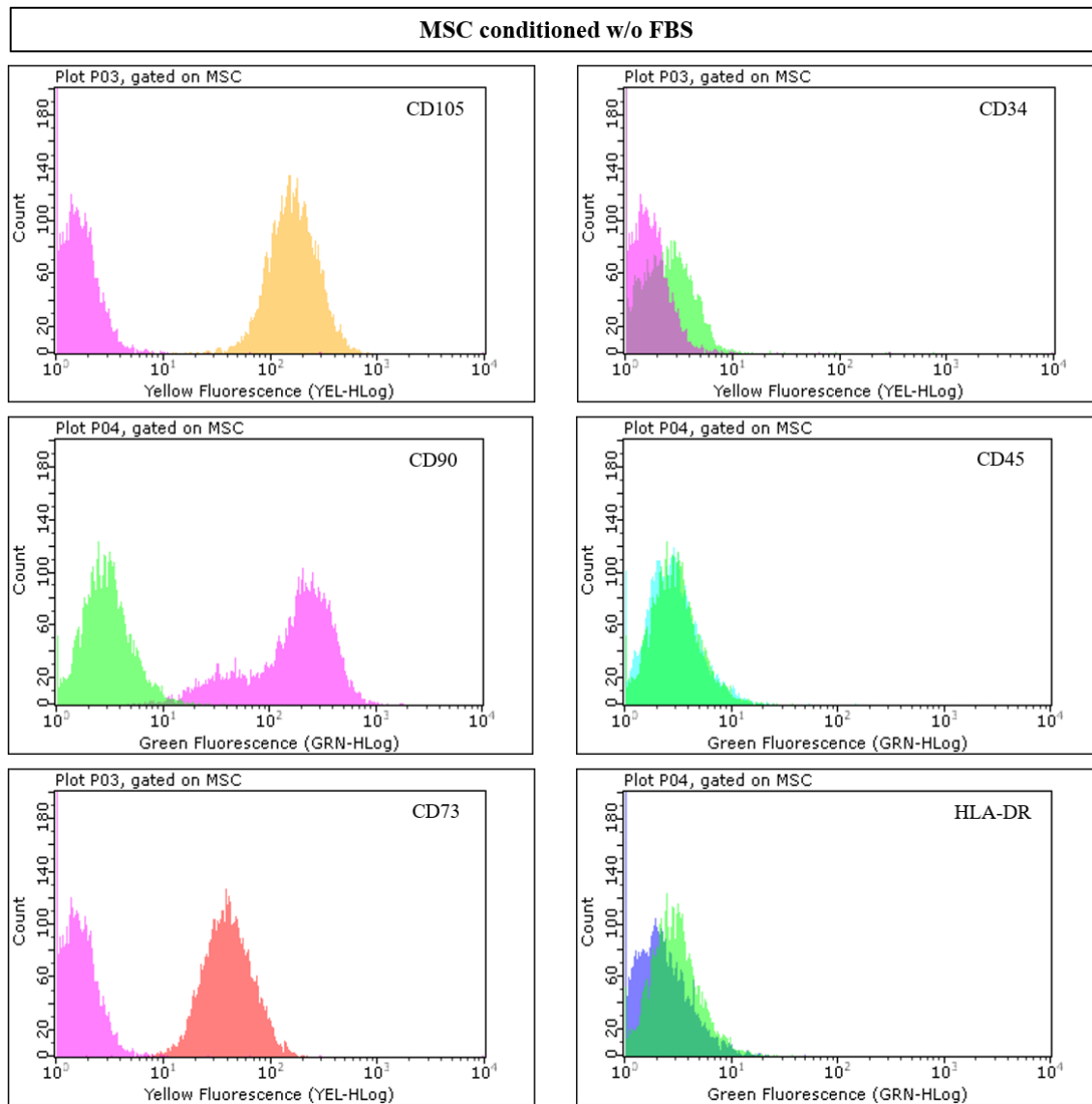
56 Figure S1, S2, S3 and S4 show representative bright-field images of MSCs in culture after
 57 collecting conditioned media under all conditions and cell surface profile plots obtained by flow
 58 cytometry. Cells did not express CD34, CD45, and HLA-DR, while being positive for CD105, CD90,
 59 and CD73, showing a typical profile of MSCs [46]. Moreover, similar % of viability for all the groups
 60 was confirmed (94.8% for control, 95.3% for MSC conditioned without FBS and 95.8% for MSCs with
 61 FBS).



63 Figure S1: MSC profile by cytometry after conditioning for 48 hours in proliferative media with 20% FBS. A
 64 typical profile of MSCs is shown after labelling cells with conjugated monoclonal antibodies: CD105-PE,
 65 CD90-FITC, CD73-PE, CD34-PE, CD45-FITC and HLA-DR-FITC.



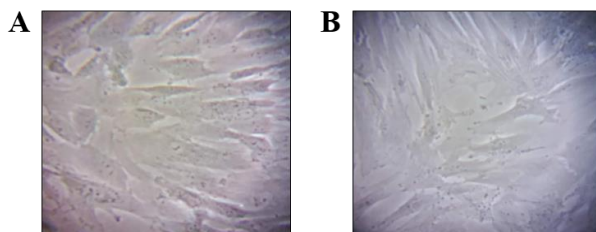
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 67 Figure S2: MSC profile by cytometry after conditioning for 48 hours in medium with 20% EV-depleted FBS. A
 68 typical profile of MSCs is shown after labelling cells with conjugated monoclonal antibodies: CD105-PE,
 69 CD90-FITC, CD73-PE, CD34-PE, CD45-FITC and HLA-DR-FITC.



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71 Figure S3: MSC profile by cytometry after conditioning for 48 hours in medium without FBS. A typical profile of
 72 MSCs is shown after labelling cells with conjugated monoclonal antibodies: CD105-PE, CD90-FITC, CD73-PE,
 73 CD34-PE, CD45-FITC and HLA-DR-FITC.

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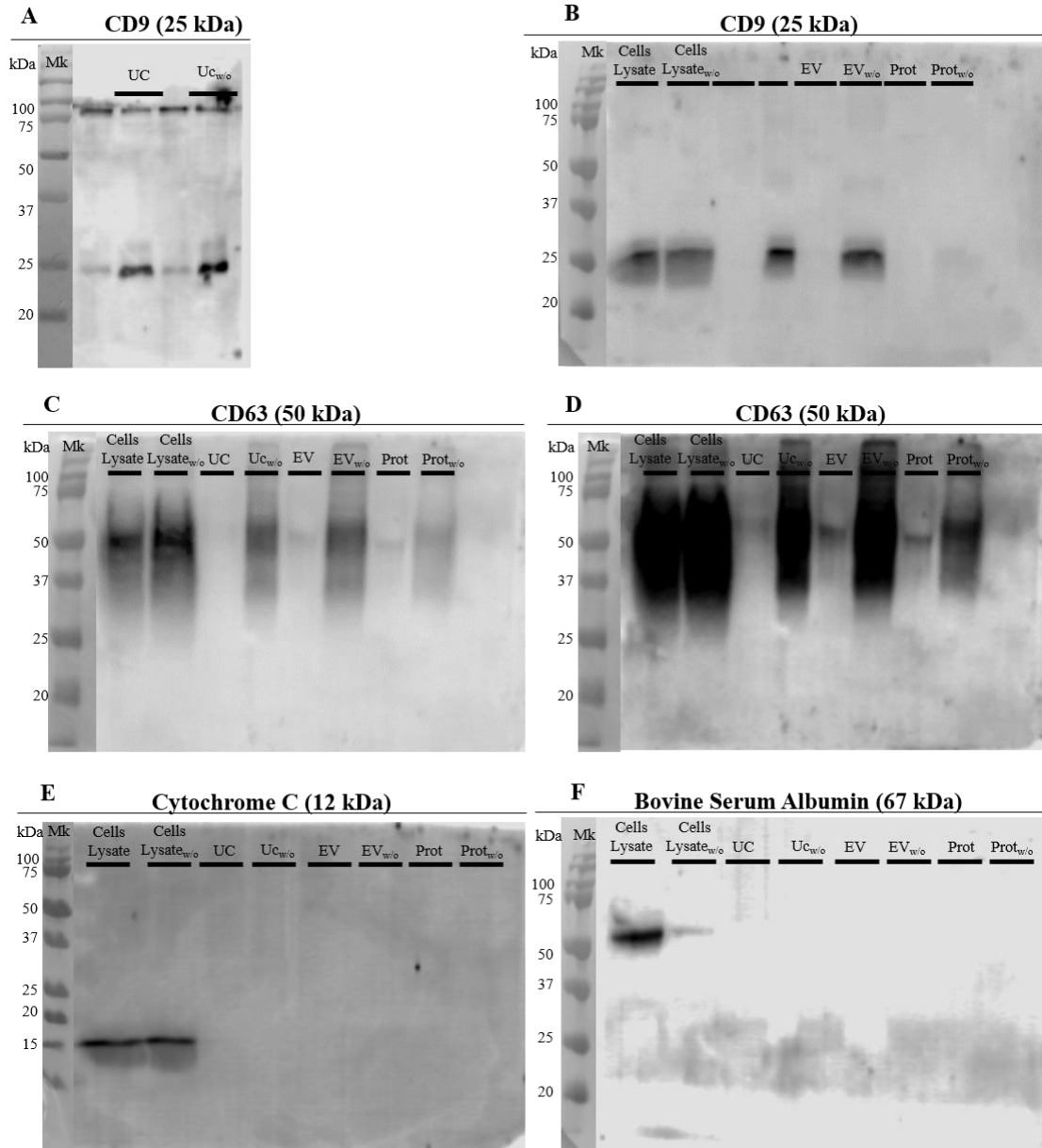


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76 Figure S4: Representative bright-field images of MSCs in culture under all conditions. Bright-field image of
 77 MSC cultured in medium with 20% EV-depleted FBS (A) or medium without FBS (B) for 48 h at 200x.

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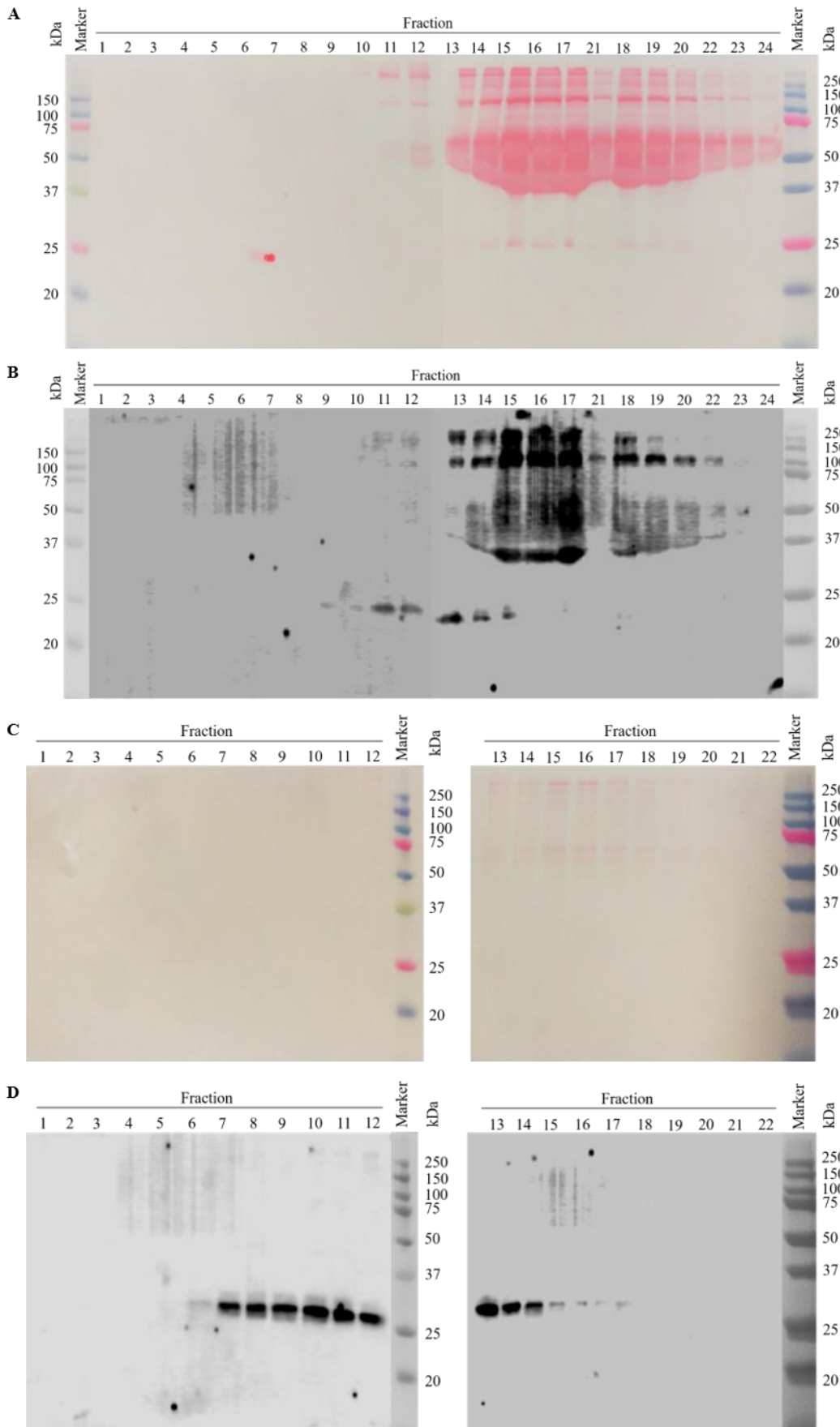


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Figure S5: EV markers on UC, UC_{w/o}, EV, EV_{w/o}, Prot and Prot_{w/o} samples and cell lysates. (A) Presence of CD9 on UC and UC_{w/o} samples. (B) Presence of CD9 in EV, EV_{w/o}, Prot and Prot_{w/o}. (C, D) Presence of CD63 in all samples at two different exposition times. (E) Absence of cytochrome C (a mitochondria marker) in all samples, except for cell lysate and cell lysate_{w/o}. (F) Absence of bovine serum albumin (as marker of FBS contaminant) in all samples, except for cell lysate from cells growth in medium with FBS.

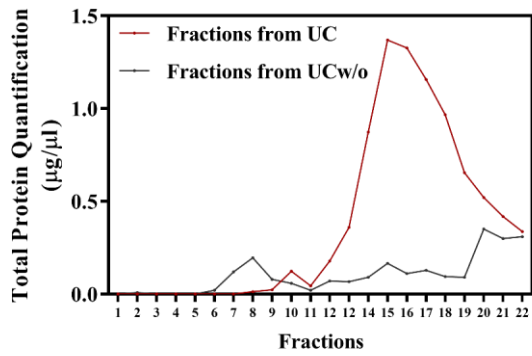


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Figure S6: Presence of proteins and EV marker in SEC fractions collected from UC and UC_{w/o} samples. Presence of proteins in nitrocellulose membranes after staining with Ponceau S in fractions eluted from UC samples (A)

91 and from UC_{w/o} samples (C). Presence of tetraspanin CD9 (24 kDa) in diferent fractions eluted from UC samples
 92 (B) and UC_{w/o} samples (D).



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94 Figure S7: Total protein quantification of SEC fractions collected from UC and UC_{w/o} samples. Protein
 95 quantification measuring absorbances at $\lambda = 280$ nm of the SEC fractions collected from UC and UC_{w/o} samples.

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