Chapter 3 : Supplementary Material Figure Legends

Supplementary Table 3a: Proteins identified in MV's from CM derived from RG/C2 ($6x10^6$ cells) as outlined Figure 3.6.

The MV fraction was isolated from the CM and the proteins were separated on a 4-12% Tris-Glycine gel, the whole lane was cut into 10 bands and the proteins were reduced, alkylated and digested with Trypsin for ms/ms analysis. The raw files generated from all 10 samples were searched against a human database generated from an nr database (downloaded from www.ncbi.nlm.nih.gov) using Bioworks Browser v 3.1 (Thermo Electron). The table shows there were 47 proteins identified with at least 2 first hit peptides in all 10 samples using a single threshold filter parameter of Xcorr vs charge state (+/-1: 1.50, +/-2: 2.00, +/-3: 2.50). Peptides from EMMPRIN or any of its alternative names (CDI47, Basignin) were not identified.

Supplementary Table 3b: Proteins identified in MV's from CM derived from RG/C2 cells ($1.2x10^7$ cells) as outlined in Figure 3.7.

The MV fraction was isolated from the CM and the proteins were separated on a 4-12% Tris-Glycine gel, the region between 70-40kDa was excised as 4 bands and the proteins were reduced, alkylated and digested with Trypsin for ms/ms analysis. The raw files generated from all 4 samples were searched against a human database generated from an nr database (downloaded from www.ncbi.nlm.nih.gov) using Bioworks Browser v 3.1 (Thermo Electron). The table shows there were 194 proteins identified with at least 2 first hit peptides in the 4 samples combined using a single threshold filter parameter of Xcorr vs charge state (+/-1: 1.50, +/-2: 2.00, +/-3:

2.50). Peptides from EMMPRIN or any of its alternative names (CDI47, Basignin) were not identified.

Supplementary Table 3c: Proteins identified in MV's from CM derived from RG/C2 cells ($1.2x10^7$ cells) as outlined in Figure 3.8.

The MV fraction was isolated from the CM and the proteins were separated on a 4-12% Tris-Glycine gel, the region between 70-40kDa was excised as 6 bands and the proteins were reduced, alkylated and digested with Trypsin for ms/ms analysis. The raw files generated from all 6 samples were searched against a human database generated from an nr database (downloaded from www.ncbi.nlm.nih.gov) using Bioworks Browser v 3.1 (Thermo Electron). The table shows there were 163 proteins identified with at least 2 first hit peptides in the 6 samples combined using a single threshold filter parameter of Xcorr vs charge state (+/-1: 1.50, +/-2: 2.00, +/-3: 2.50). Peptides from EMMPRIN or any of its alternative names (CDI47, Basignin) were not identified.