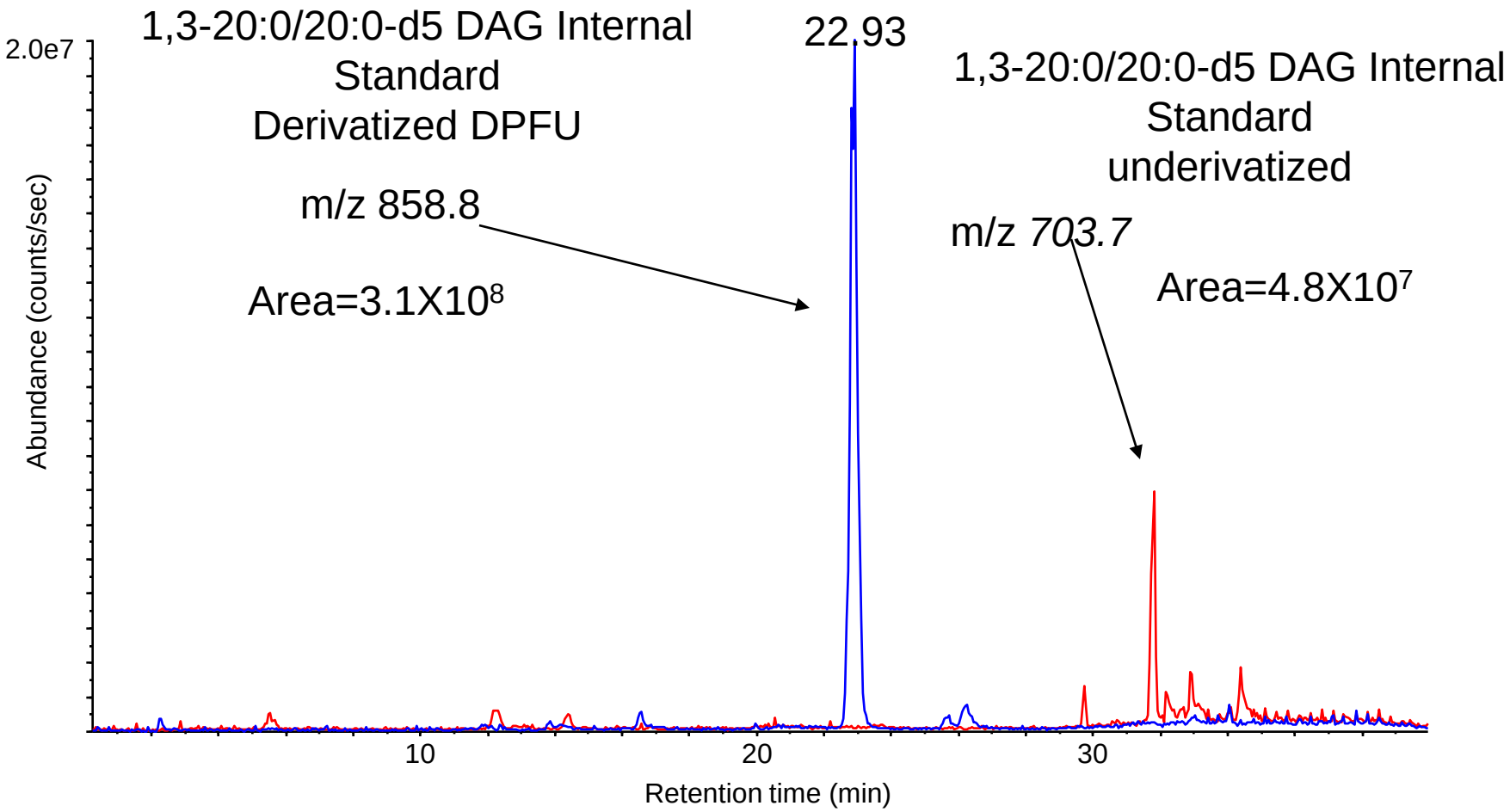
Legends (Supplemental Figures)

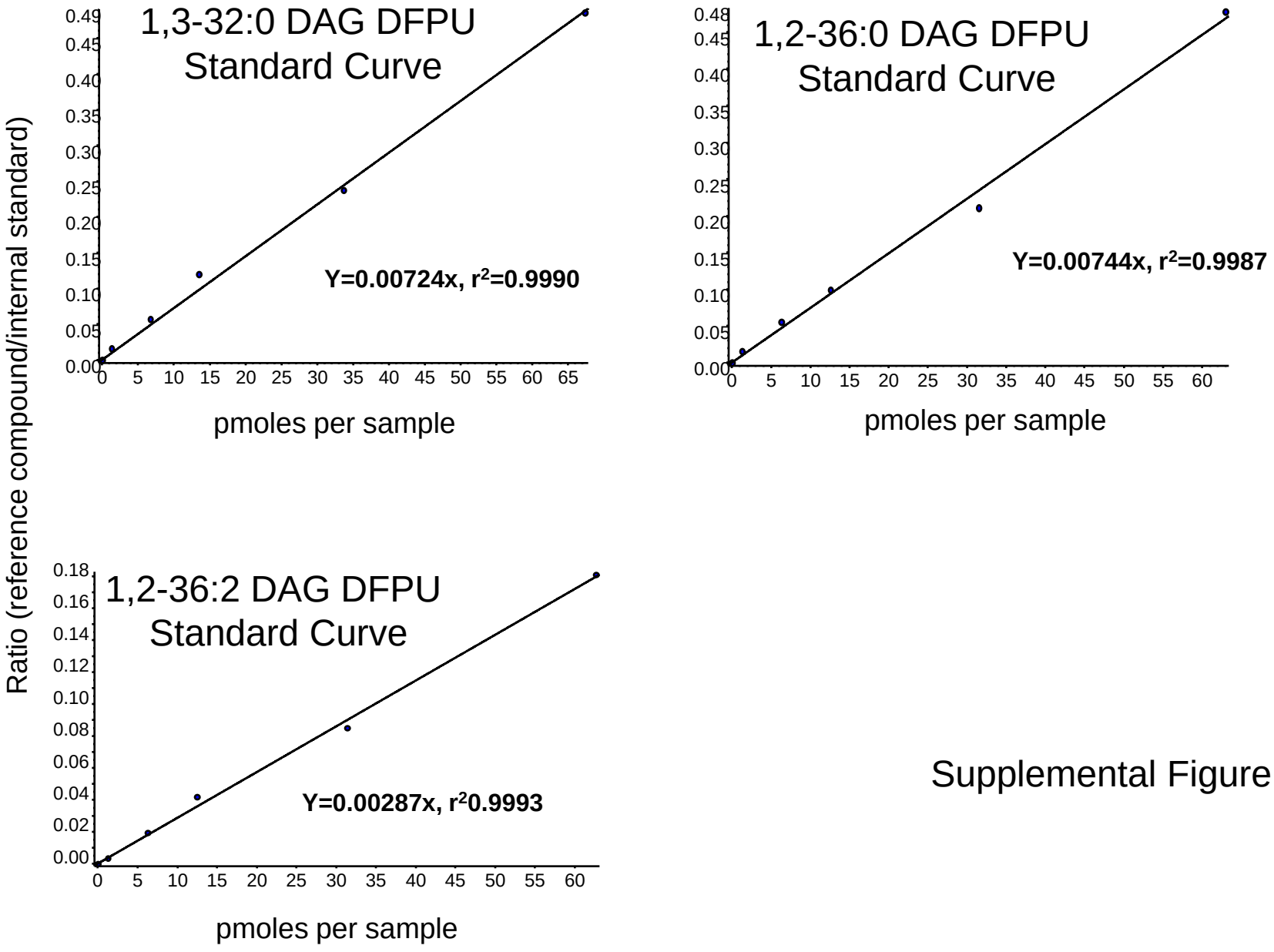
Supplemental Figure 1. Normal phase LC/MS analysis of the neutral lipids extracted from bone marrow cells differentiated in culture to macrophages, then derivatized with difluorophenyl isocyanate to the urethane derivative of the free hydroxyl moiety (Sample in Figure 2). Blue trace-extraction of derivatized internal standard ion $[M+NH_4]^+$signal m/z 858.8 and Red-extraction of underivatized internal standard ion $[M+NH_4]^+$m/z 703.7 to reveal the extent of derivatization in this biological extract.

Supplemental Figure 2. Standard curves to convert ion abundance (area) from three different reference standards of 1,3-and 1,2-DAG DPFU $[M+NH_4]^+$ ions ratioed to the abundance of the internal standard 1,3-20:0/20:0-DAG DPFU $[M+NH_4]^+$ ions to the pmoles of 1,3 and 1,2-DAG molecular species. The slope of the 1,3-32:0 DAG DFPU was used for all 1,3-DAG molecular species while the average of the two 1,2-DAG DPFU slopes were used for the 1,2-DAG molecular species.

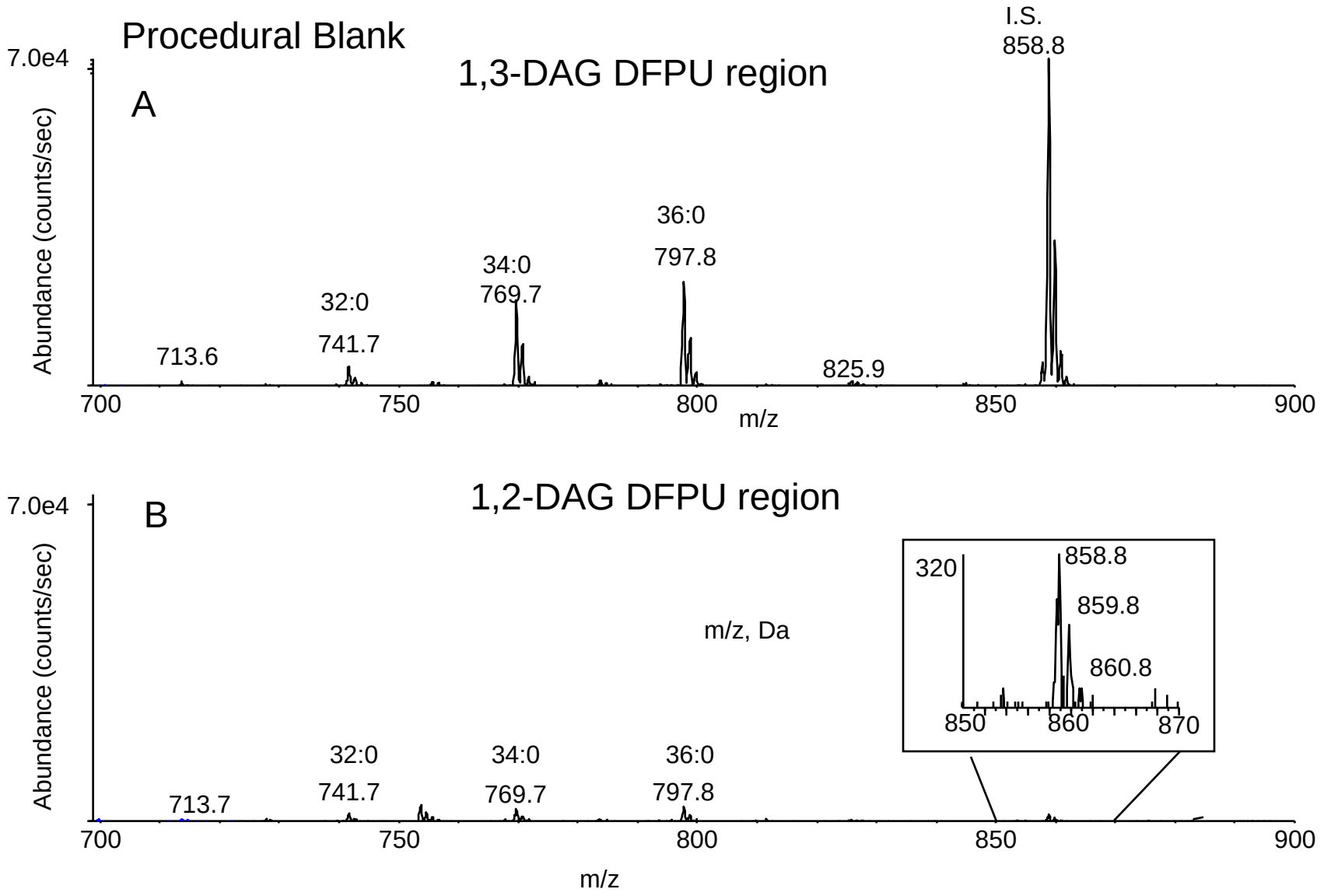
Supplemental Figure 3. Summation of all ion abundances **f**rom the (A) 1,3- and -(B)1,2-DAG DPFU elution region for a representative procedural blank sample (internal standard added) used to correct the abundances of DAG species which contaminated solvents and glassware used during extraction and purification. The region for the 1,2-20:0/20:0-DAG DPFU $[M+NH_4]^+$ in the 1,2-DAG DPFU elution region is expanded to observe the abundance of this isomer that arose from acyl group migration during extraction, derivatization, and chromatographic separation.



Supplemental Figure 1



Supplemental Figure 2



Supplemental Figure 3