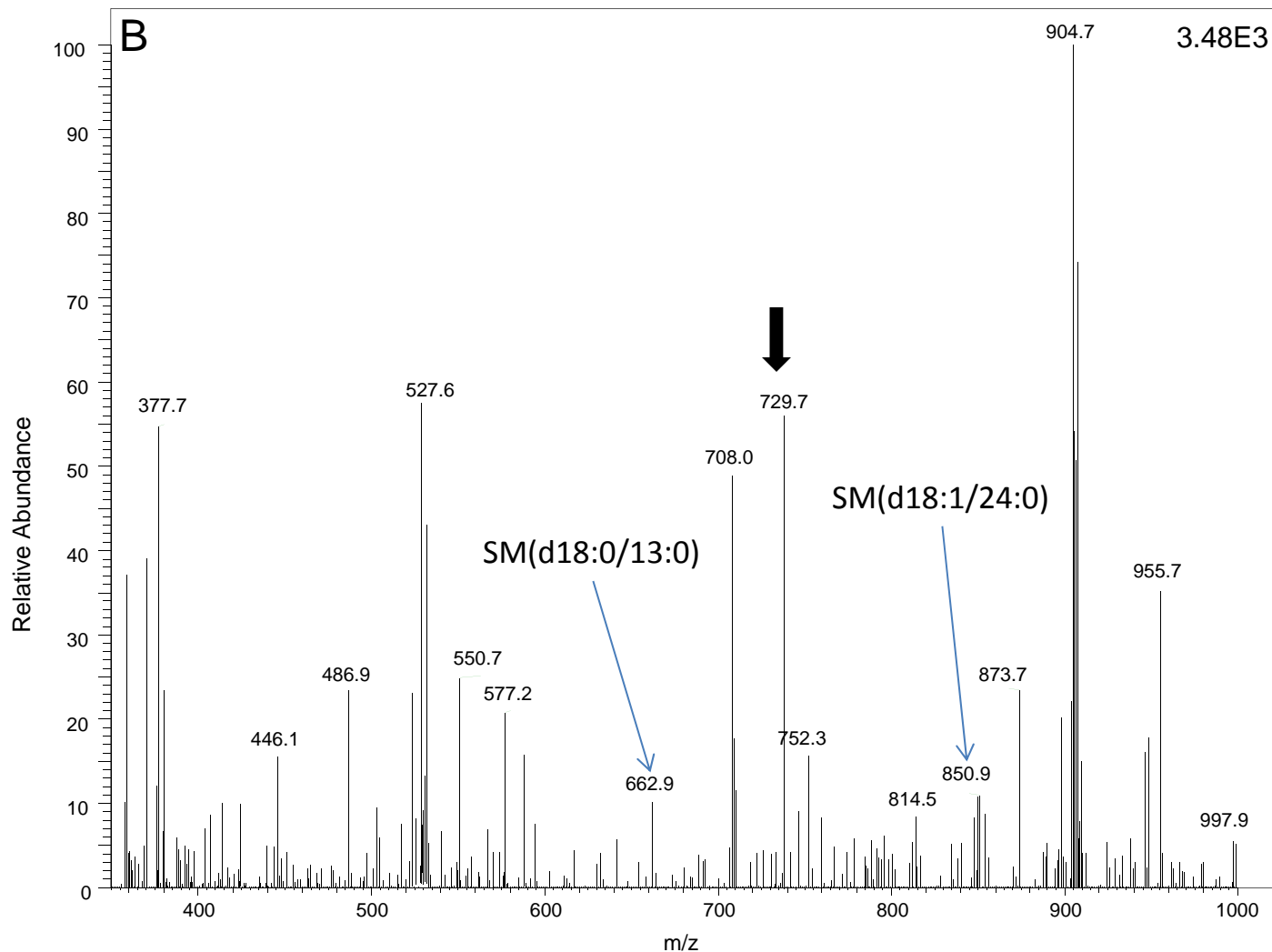
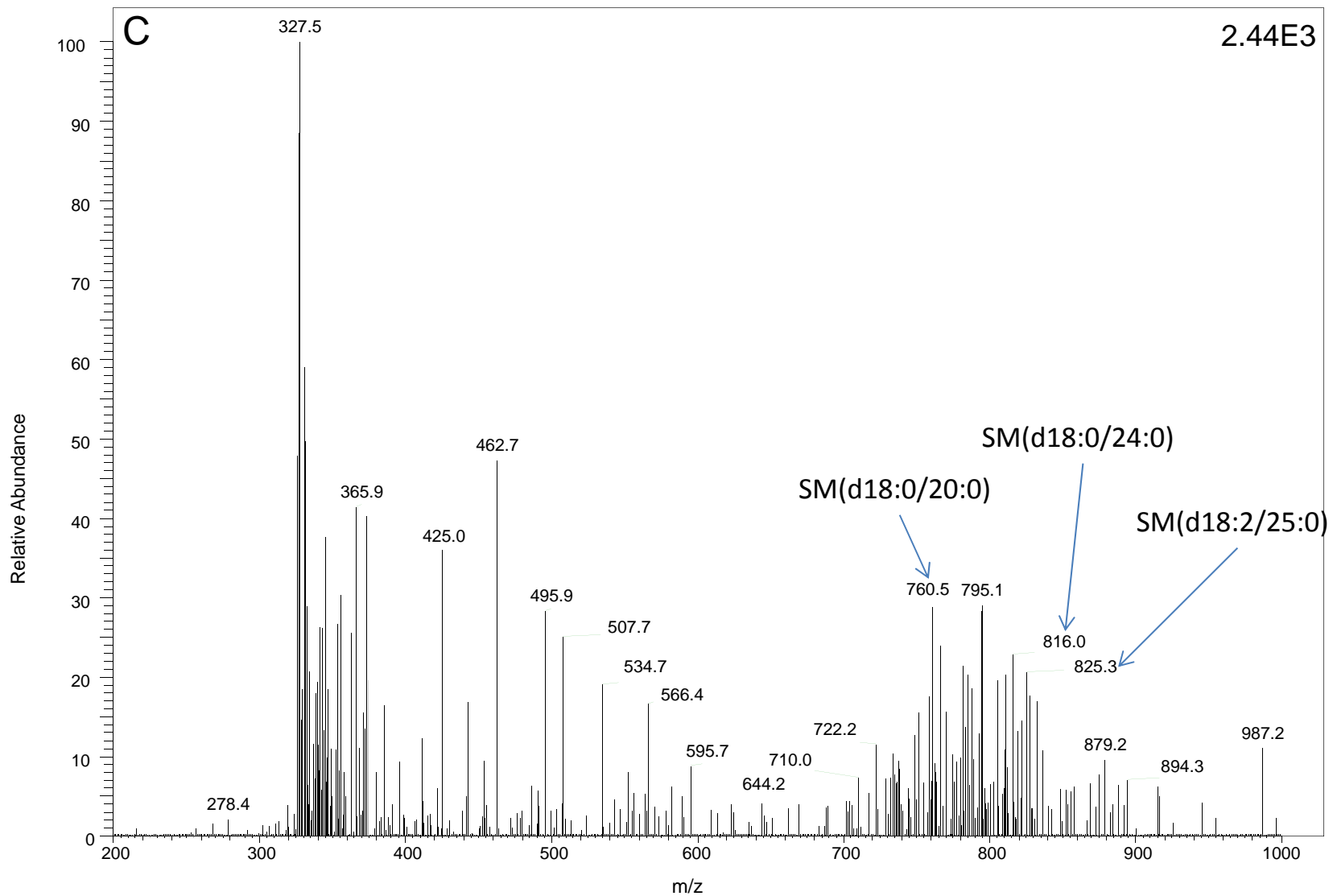


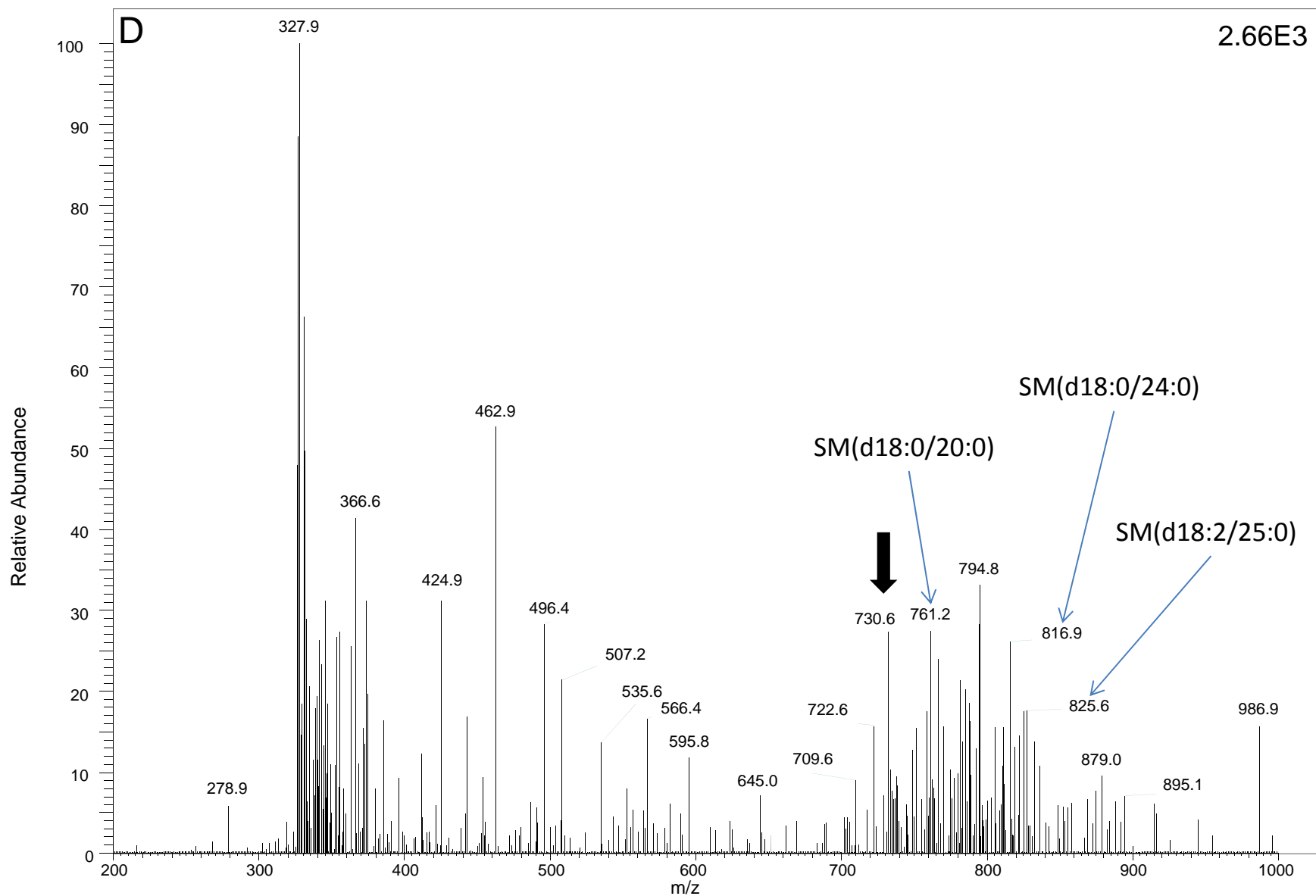
Supplementary Figure 1 Representative electrospray ionization tandem mass spectrometric analysis of sphingomyelins extracted from control human aqueous humor (AQH) in positive-ion mode. **(A)** Neutral loss scan (NLS) of m/z 213.2 corresponding to sphingomyelin class. Thin arrows depict identified species as indicated.



Supplementary Figure 1 Representative electrospray ionization tandem mass spectrometric analysis of sphingomyelins extracted from control human aqueous humor (AQH) in positive-ion mode. **(B)** NIS as in (A) with internal standard addition (arrow head; m/z ratio of 729.1) enabling ratiometric quantification of all identified lipids in sphingomyelin class. Thin arrows depict identified species as indicated.



Supplementary Figure 1 Representative electrospray ionization tandem mass spectrometric analysis of sphingomyelins extracted from control human aqueous humor (AQH) in positive-ion mode. **(C)** Precursor ion scan (PIS) of m/z 184 corresponding to choline moiety within the sphingomyelins. Thin arrows depict identified species as indicated.



Supplementary Figure 1 Representative electrospray ionization tandem mass spectrometric analysis of sphingomyelins extracted from control human aqueous humor (AQH) in positive-ion mode. (D) Precursor ion scan (PIS) of m/z 184 as in (C) with internal standard addition (arrow head; m/z ratio of 729.1) enabling ratiometric quantification of all identified lipids in sphingomyelin class using PIS. Thin arrows depict identified species as indicated.