Table. Mass spectrometry parameters for lipidomics analysis on Waters Xevo TQS (electrospray ionization triple quadrupole mass spectrometer).

Lipid class	Adduct identified	Scan mode[a]	Cone voltage (V)	Collision energy (V)	Internal standards[b]
DGDG	$[M + NH_4]^+$	NL 341.11	40	16	DGDG(34:0); DGDG(36:0)
LPC, PC	[M + H]+	Pre 184.07	40	28	LPC(13:0); LPC(19:0)
LPE, PE	[M + H]+	NL 141.02	40	12	LPE(14:0); LPE(18:0)
LPG	$[M + NH_4]^+$	NL 189.04	25	10	LPG(14:0); LPG(18:0)
MGDG	$[M + NH_4]^+$	NL 179.06	40	14	MGDG(34:0); MGDG(36:0)
PA	$[M + NH_4]^+$	NL 115.00	40	5	PA(28:0); PA(40:0)
PG	$[M + NH_4]^+$	NL 189.00	40	8	PG(28:0); PG(40:0)
PI	$[M + NH_4]^+$	NL 277.00	40	17	PI(34:0); PI(36:0)
PS	[M + H]+	NL 185.00	40	13	PS(28:0); PS(40:0)

[a]Scan modes: NL, neutral loss; Pre, Precursor.

[b]Known amounts of the two internal standards were added to the samples. Quantification of biological analytes was performed by comparing the spectral intensity of the biological analytes to the spectral intensity/molar amount of both standards as a function of *m/z*.