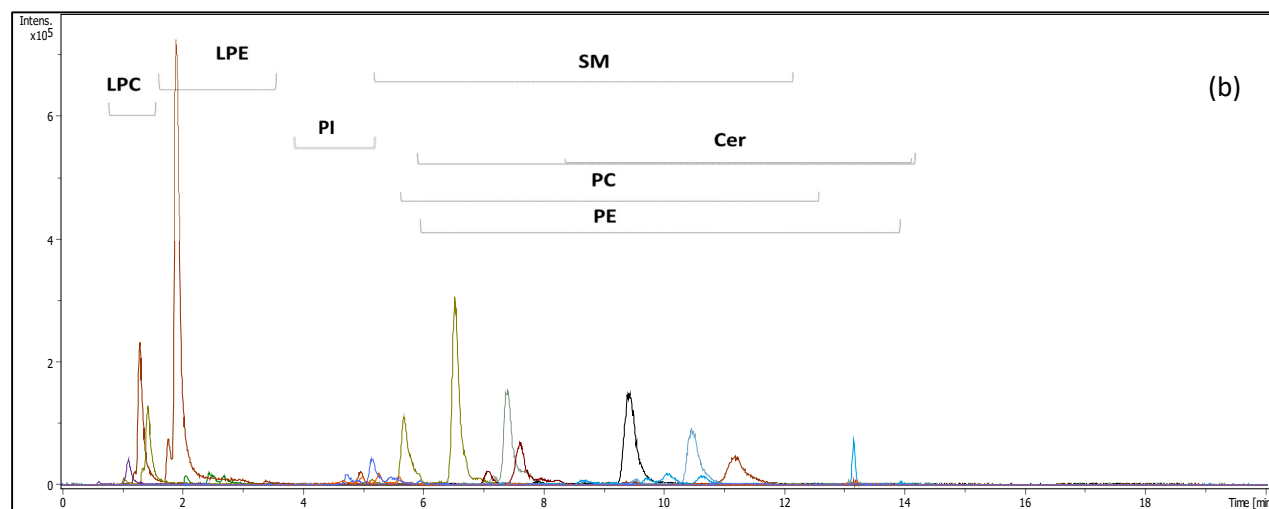
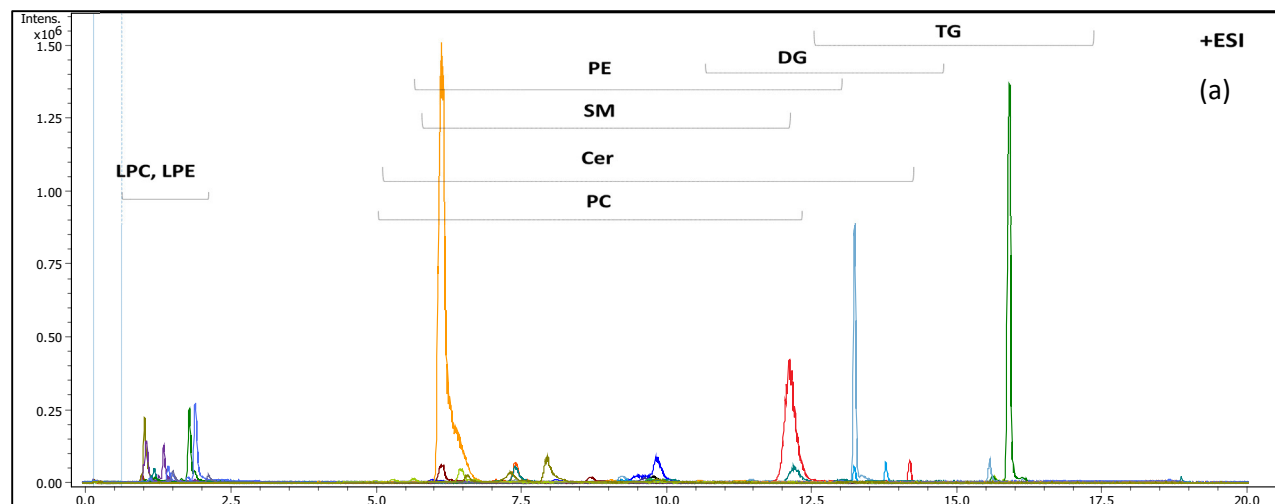


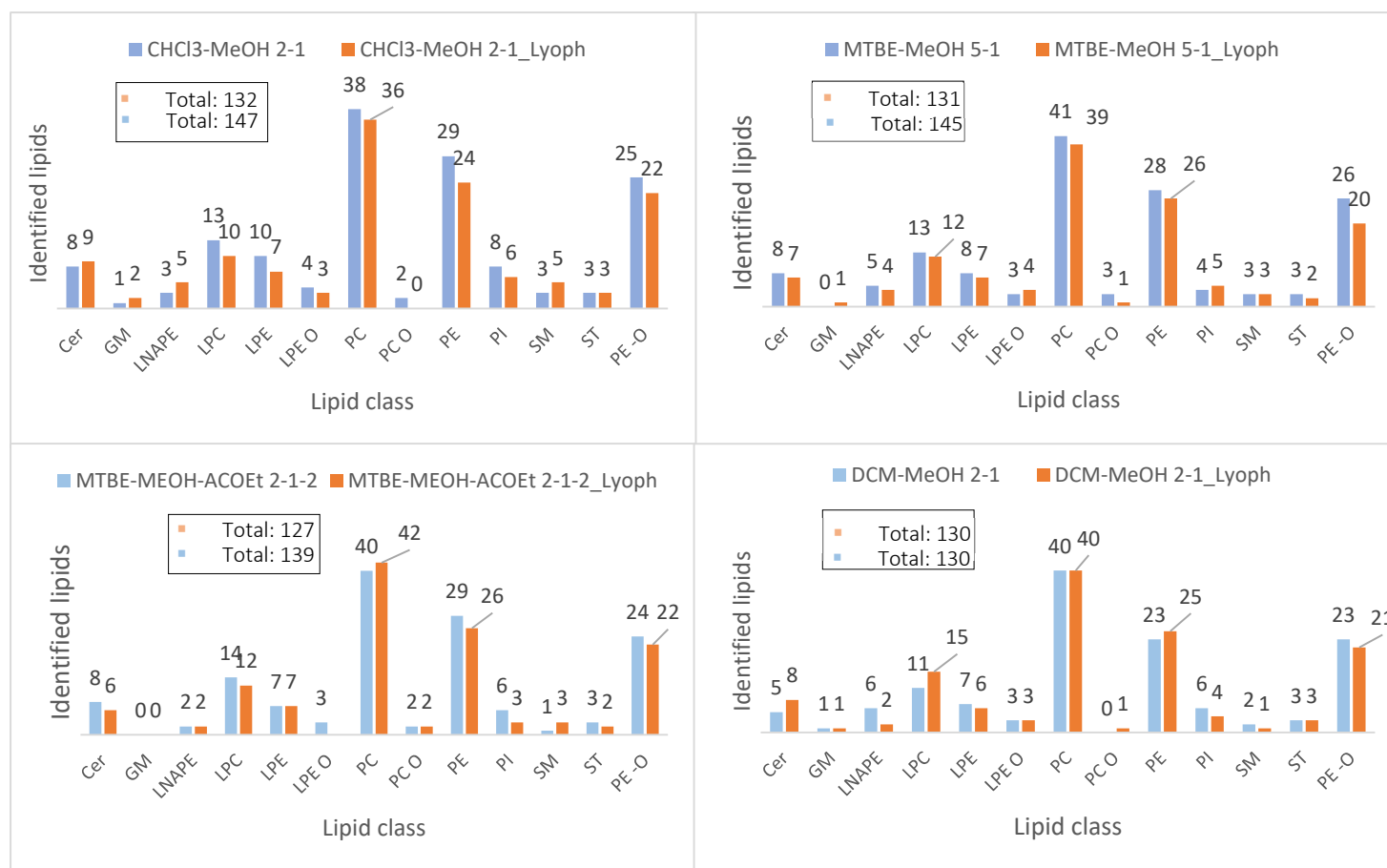
**Untargeted UHPLC-TOF/MS lipidomic analysis for the investigation of egg yolks after xylanase supplementation of the diet of laying hens**

**Table S1.** Level of supplementation and enzyme activities used in the present study.

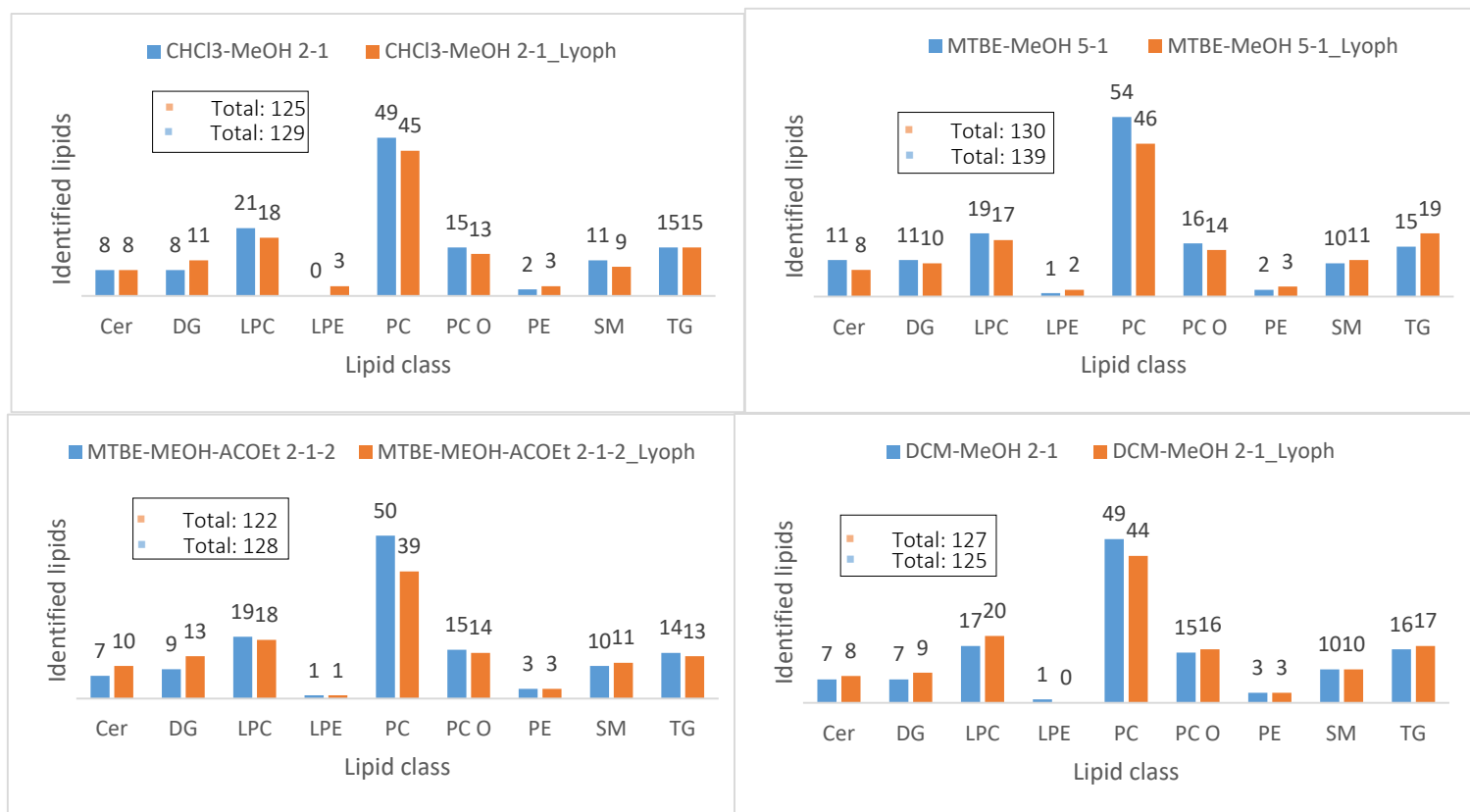
Treatment	Level of supplementation	Intended Activity	Batch Corrected Activity	Recovered Activity in Feed
T1 control	0 g/t	0 U/kg	0 U/kg	0 U/kg
T2	10 g/t	30,000 U/kg	41,058 U/kg	35,861 U/kg
T3	15 g/t	45,000 U/kg	61,587 U/kg	57,451 U/kg
T4	30 g/t	90,000 U/kg	123,174 U/kg	111,936 U/kg



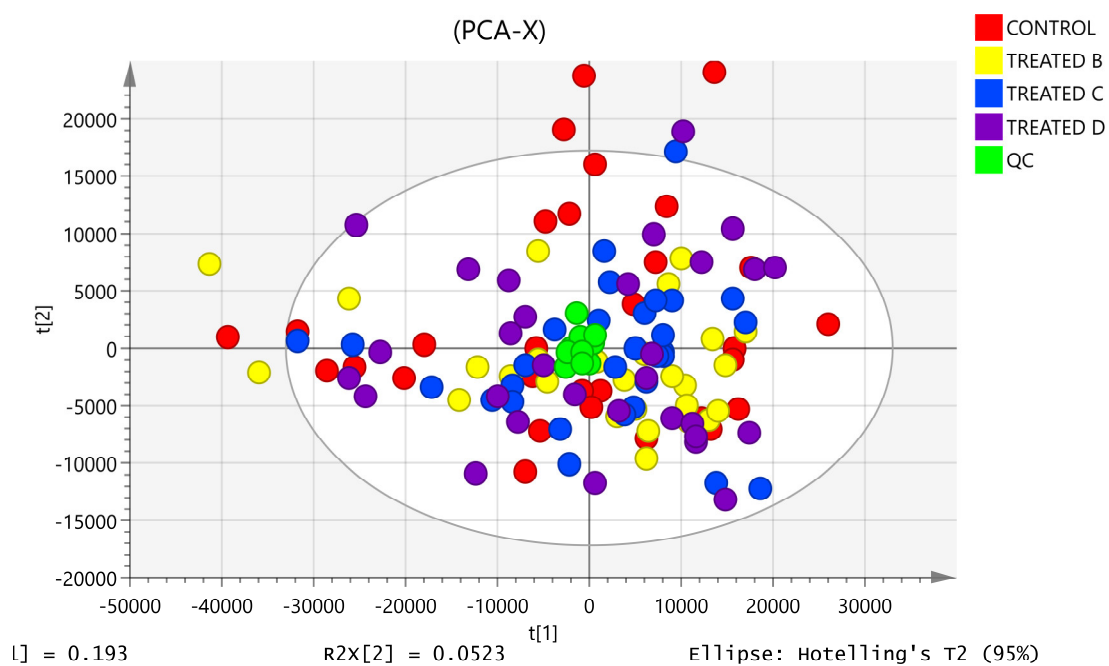
**Figure S1:** Overlaid extracted ion chromatograms of lipids present in a QC sample from different classes in (a) positive and (b) negative ESI.



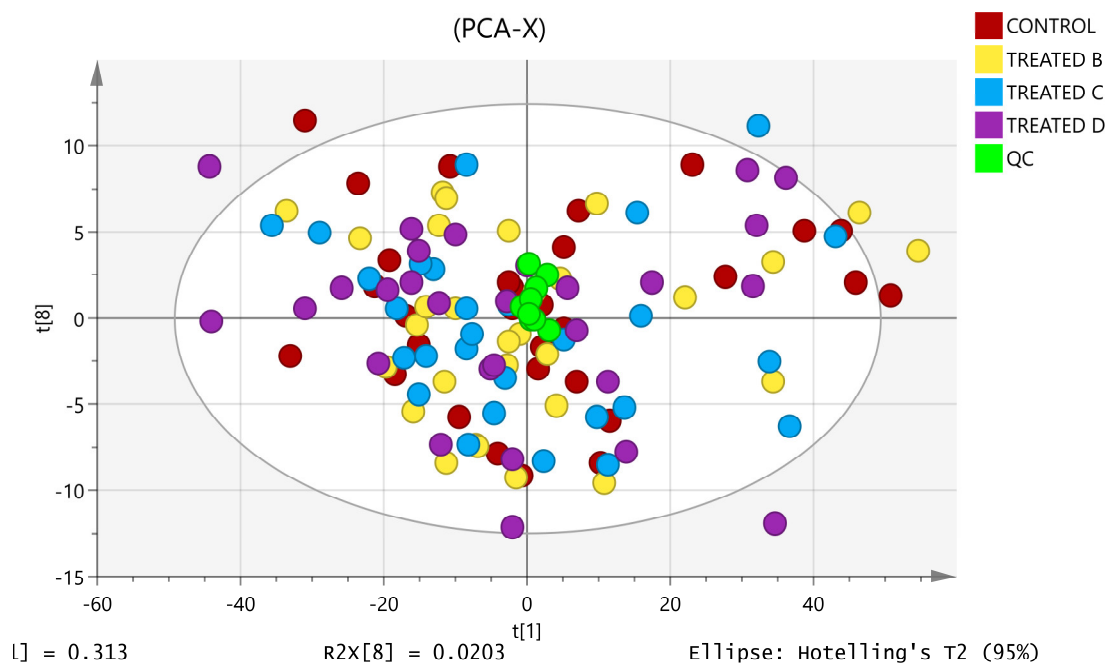
**Figure S2:** Number of identified lipids for lyophilised and non-lyophilised samples by triplicate analysis extracted with four different solvents in negative ionisation mode. Total numbers are given in the inset.



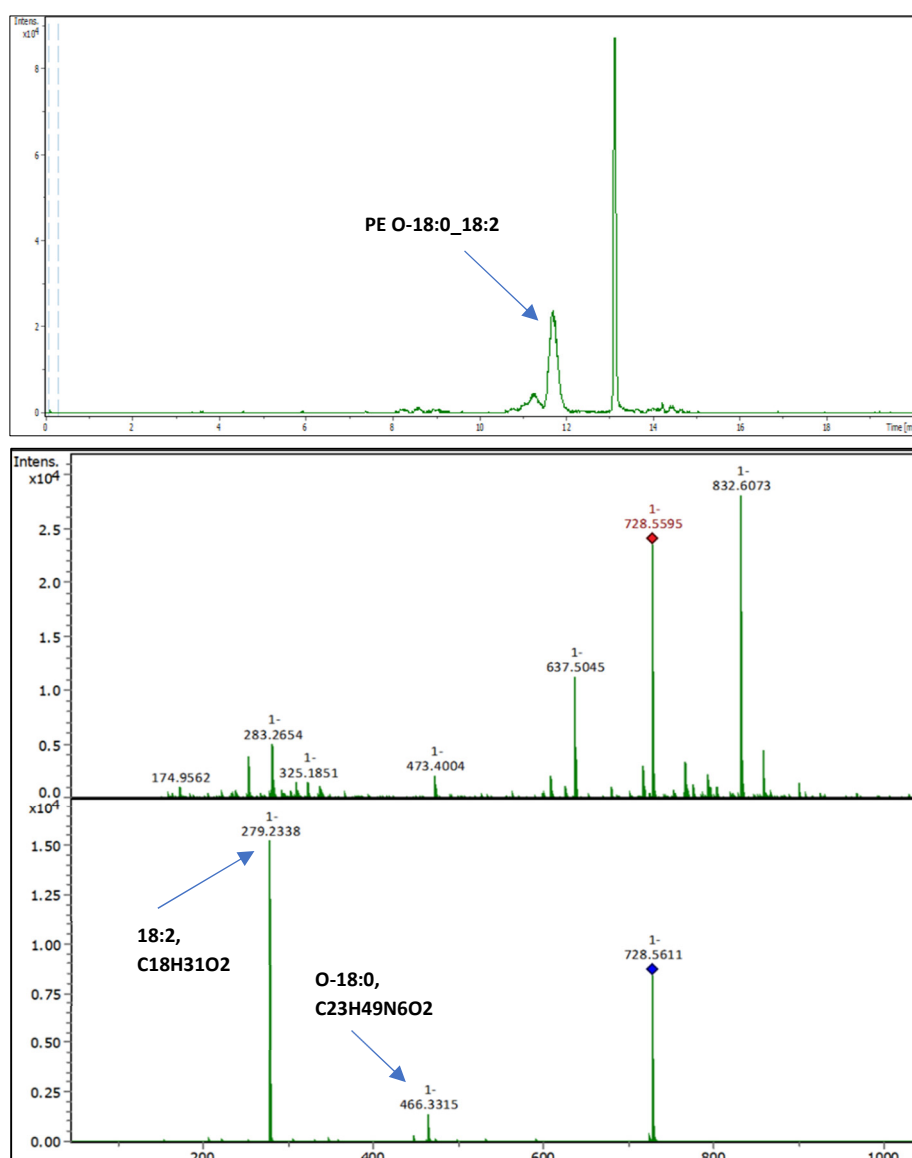
**Figure S3:** Number of identified lipids for lyophilised and non-lyophilised samples by triplicate analysis extracted with four different solvents in positive ionisation mode. Total numbers are given in the inset.



**Figure S4:** Principal component analysis (PCA) score plot of samples in negative ionisation mode showing the QC samples clustered in the centre of the plot.



**Figure S5:** Principal component analysis (PCA) score plot of samples in positive ionisation mode showing the QC samples clustered in the centre of the plot.



**Figure S6:** Chromatographic peak of phosphatidylethanolamine (PE O-18:0 18:2) together with MS and MS/MS spectrum. Precursor and MS fragments facilitated peak annotation.