

Figure S1, related to Figure 3

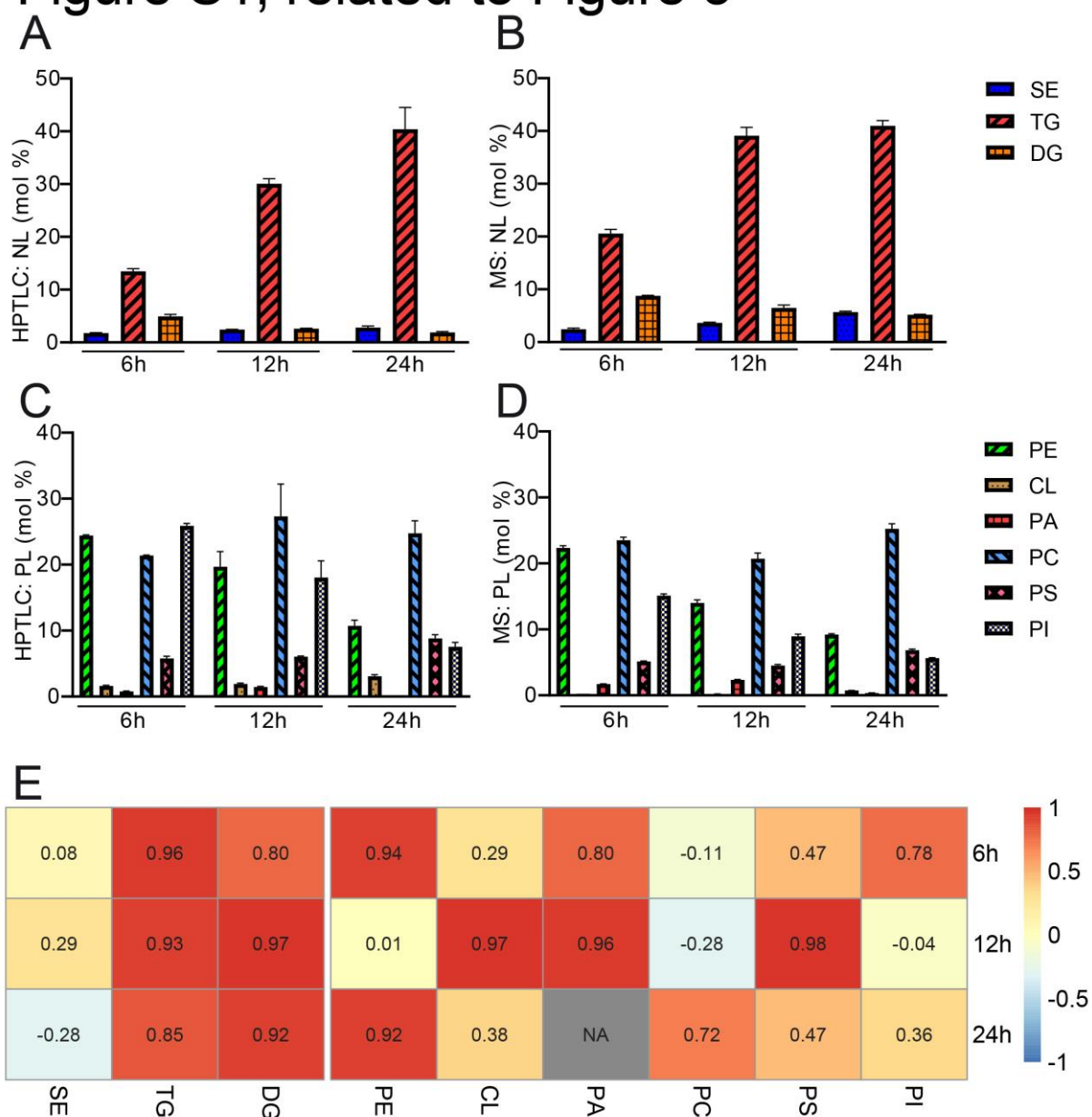


Figure S1: Relative quantification of HPTLC-lipidomics and MS-assisted shotgun lipidomics.

(A, B) HPTLC-derived neutral lipidomic quantification (A) and analysis of the same samples by MS-based shotgun lipidomics (B) deliver a comparable overall picture of neutral lipid content in yeast. (C, D) HPTLC-derived phospholipidomic quantification (C) and analysis of the same samples by shotgun lipidomics (D) deliver a comparable overall picture of the major phospholipid classes in yeast. (E) Pearson correlation analysis comparing HPTLC with MS results. Related to Figure 3.

Figure S2, related to Figure 3

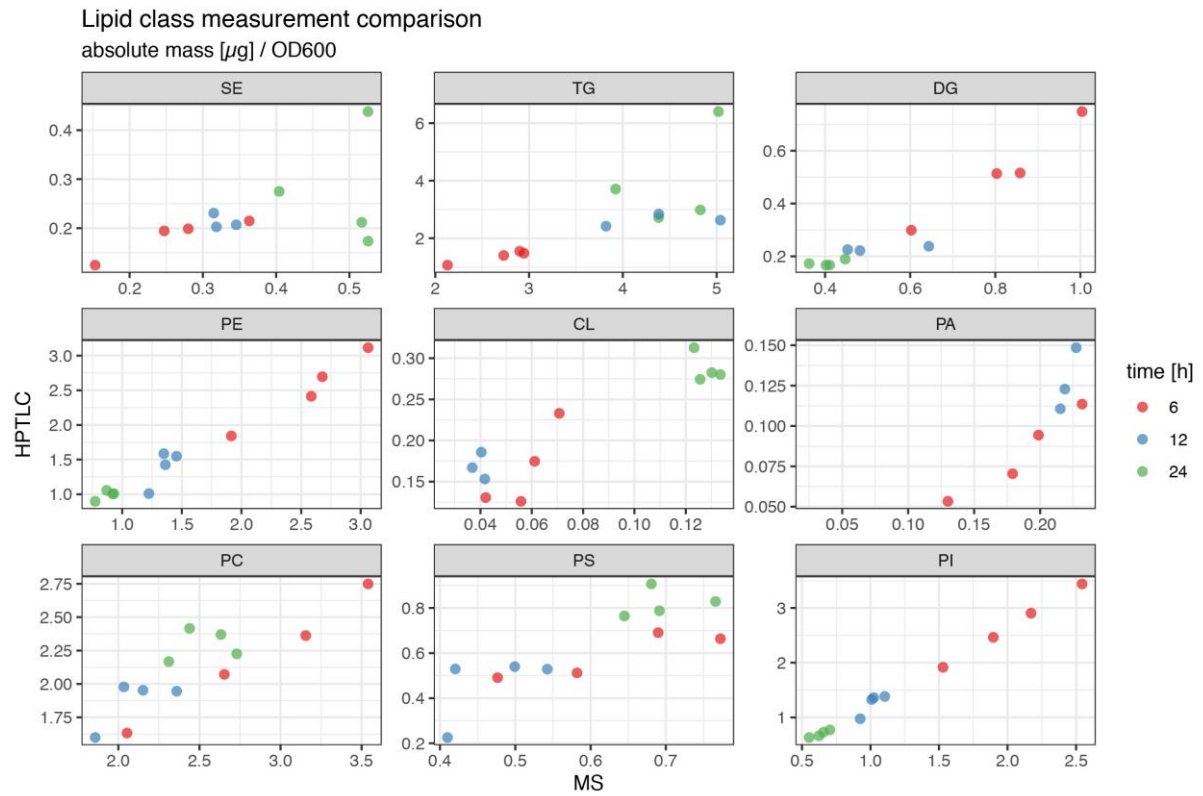


Figure S2: Comparison of lipid class measurements.

Individual data pairs are shown in a scatter plot to support the Pearson correlation analysis.
Related to Figure 3.

Figure S3, related to Figure 4

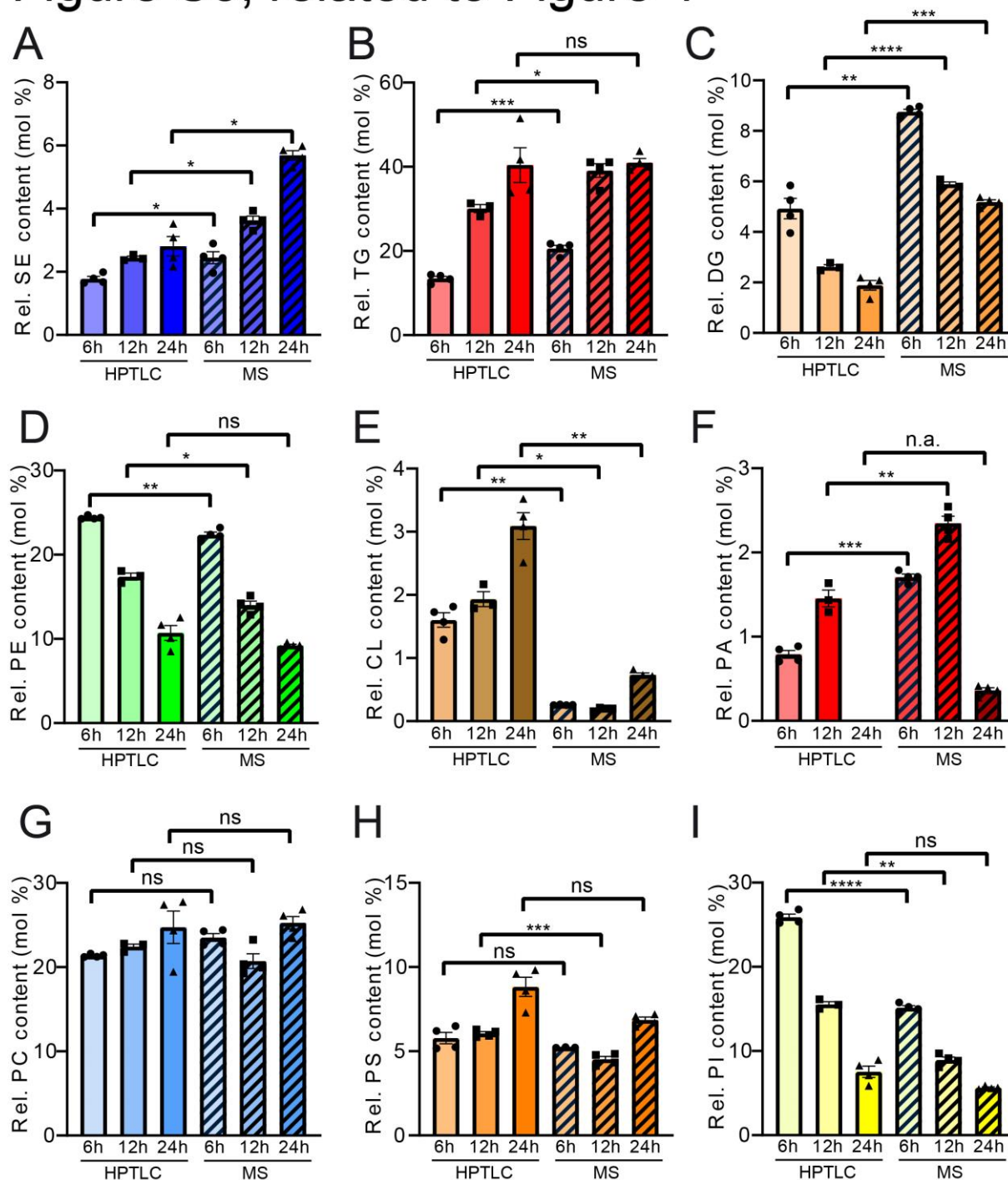


Figure S3: Paired statistical analysis of individual lipid classes (relative) for HPTLC-lipidomics vs. MS-assisted shotgun lipidomics reveals differences between both methods. Neutral lipids are compared in panels (A-C) and phospholipid comparisons are given in panels (D-I). Statistical analysis was performed using paired tests: TG, DG, SE, CL and PA were analysed using mixed effects analysis with Sidaks's multiple comparisons test; PE, PC, PS, and PI were analysed using RM ANOVA with Sidak's multiple comparisons test. Related to Figure 4.