

Figure S1. Compositional differences of the fecal microbiota related to TMAO exposure following a MMTT. **(A)** Family level relative abundance by peak-TMAO group. **(B)** Differential abundance in participants with AUC-TMAO concentration below or above the median of 29.25 $\mu\text{M}/\text{h}$ ($\beta = 0.17$, $p = 0.77$). **(C)** Relationship between Shannon α -diversity and AUC-TMAO. **(D)** Weighted UniFrac β -diversity by peak-TMAO group shows non-significant differences.

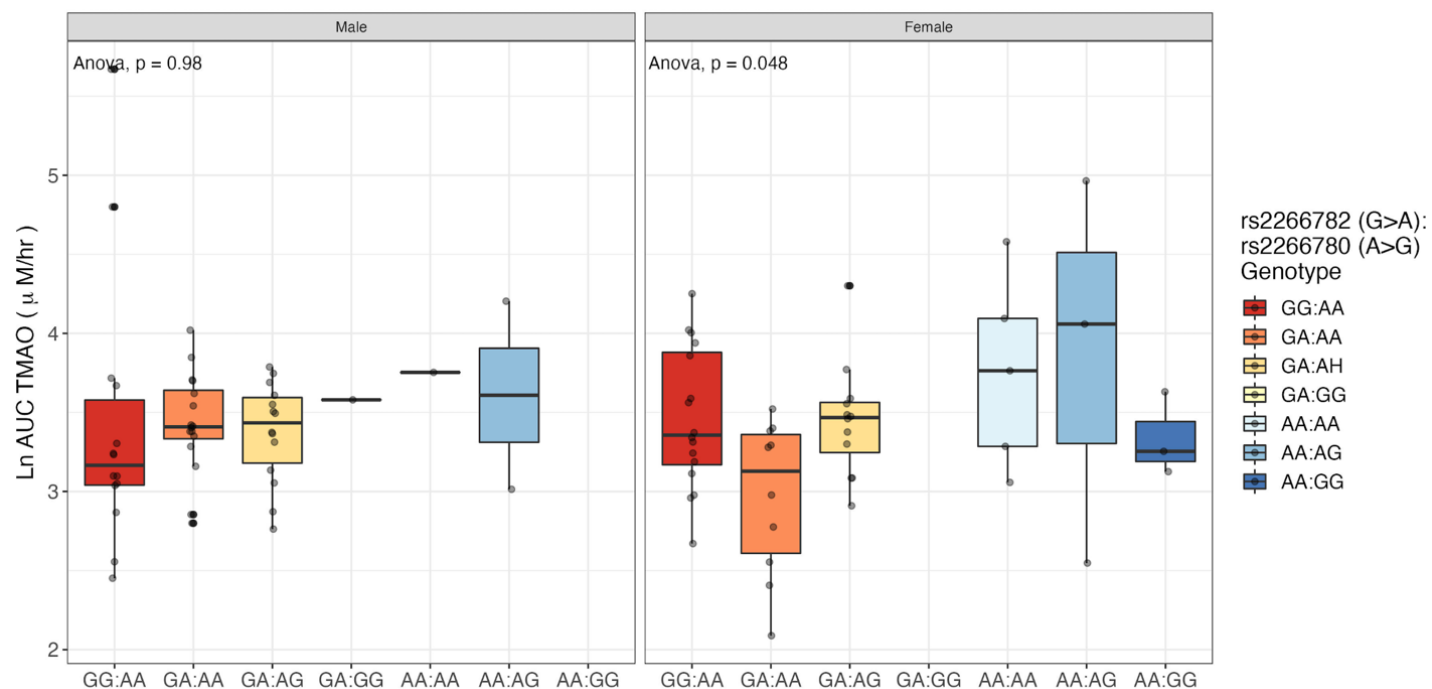


Figure S2. Relationship between *FMO3* allelotype and AUC-TMAO stratified by biological sex. Genotypes are presented by SNP rs2266782 (G>A):rs2266780 (A>G).

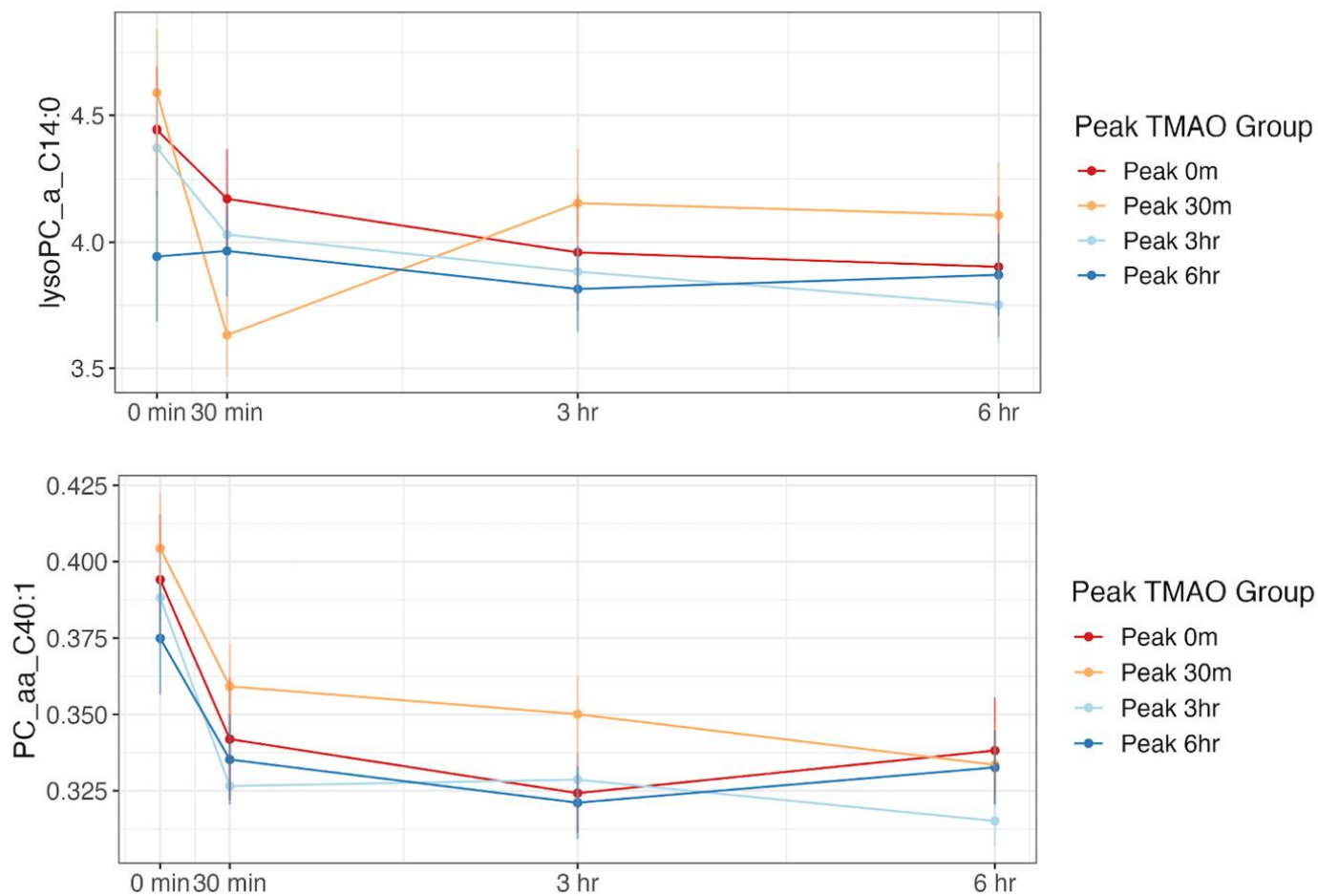


Figure S3. Postprandial responses of lysophosphatidylcholine acyl C14:0 (**top**) and phosphatidylcholine diacyl C40:1 (**bottom**) by peak-TMAO group.