Supplementary

Lipidomic analysis reveals sphingomyelin and phosphatidylcholine species associated with renal impairment and all-cause mortality in type 1 diabetes

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<u>Supplementary file including</u>:

- Supplementary methods
- Supplementary Figure s1
- Supplementary report

Lipidomic analyses, PROFIL:

The serum samples were prepared according to the previously published Folch procedure[1] with minor modifications. Briefly, 10 µL of 0.9% NaCl, 92 µL of $CHCl_3$:MeOH (2:1, v/v) and 28 µL of a 10 µg mL^{-1} working standard solution of chosen lipid standards (for quality control and data normalization purposes) were added to 10 µL of each serum sample. The standard solution contained nine different lipid standards representing different lipid classes. The following compounds were purchased from Avanti Polar Lipids, Inc. (Alabaster, Alabama, USA): 1,2-diheptadecanoyl-*sn*-glycero-3-phosphoethanolamine (PE(17:0/17:0)), N-heptadecanoyl-D-*erythro*-sphingosylphosphorylcholine (SM(d18:1/17:0)), N-heptadecanoyl-D-*erythro*-sphingosine (Cer(d18:1/17:0)), 1,2-diheptadecanoyl-*sn*-glycero-3-phosphocholine (PC(17:0/17:0)), 1-heptadecanoyl-2-hydroxy-*sn*-glycero-3-phosphocholine (LPC(17:0)) and 1-palmitoyl-d31-2-oleoyl-*sn*-glycero-3-phosphocholine (PC(16:0/d31/18:1)). Additionally, 1,2-Dimyristoyl-*sn*-glycero-3-phospho(choline-d_{13}) (PC(14:0/d13)) was purchased from Sigma-Aldrich Denmark A/S (Copenhagen, Denmark) and Tripalmitin-1,1,1-13C3 (TG(16:0/16:0/16:0)-13C3) and Trioctanoin-1,1,1-13C3 (TG(8:0/8:0/8:0)-13C3) from Larodan (Solna, Sweden) for the same purpose. After the addition of the working standard solution of the chosen lipid standards, the samples were vortex mixed and allowed to stand on ice for 30 min. The samples were then centrifuged (9400 × *g*, 3 min, 4 °C), 60 µL from the lower layer of each sample was transferred to a glass vial with an insert and 60 µL of $CHCl_3$:MeOH (2:1, v/v) was added to each sample. The samples were then stored at -80 °C until analysis.

Calibration curves (at concentration levels of 100, 500, 1000, 1500, 2000 and 2500 ng mL^{-1}) for quantification of lipids were prepared using 1-hexadecyl-2-(9Z-octadecenoyl)-sn-glycero-3-phosphocholine (PC(16:0e/18:1(9Z))), 1-(1Z-octadecenyl)-2-(9Z-octadecenoyl)-sn-glycero-3-phosphocholine (PC(18:0p/18:1(9Z))), 1-octadecanoyl-sn-glycero-3-phosphocholine (LPC(18:0)), 1-(1Z-octadecenyl)-2-docosahexaenoyl-*sn*-glycero-3-phosphocholine (PC(18:0p/22:6)), 1-stearoyl-2-arachidonoyl-*sn*-glycero-3-phosphoinositol (PI(18:0/20:4)) and 1-stearoyl-2-linoleoyl-*sn*-glycerol (DG(18:0/18:2)) from Avanti Polar Lipids, Inc., 1-Palmitoyl-2-Hydroxy-sn-Glycero-3-Phosphatidylcholine (LPC(16:0)) from Larodan, and 1,2,3-Triheptadecanoylglycerol (TG(17:0/17:0/17:0)) and 3β-Hydroxy-5-cholestene 3-linoleate (ChoE(18:2)), 3β-Hydroxy-5-cholestene 3-oleate (ChoE(18:1(9Z))), 5-Cholesten-3β-yl octadecenoate (ChoE(18:0)) and 5-Cholestene 3-palmitate (ChoE(16:0)) from Sigma-Aldrich.

The samples were prepared and analysed using previously published methods.[1-3] and quality control was performed throughout the data set by including blanks, pure standard samples, extracted standard samples and control plasma samples. Relative standard deviations (%RSDs) for retention times and peak areas for lipid standards representing each lipid class in the serum samples and in the control plasma samples were calculated. The %RSDs for the retention times were on below 3.8% for both the serum samples and for the control plasma samples. The %RSDs for the normalized (to PC(16:0/d30/18:1)) peak areas were within accepted analytical limits below 15.4% and 16.8% for the serum samples and for the control plasma samples, respectively. This shows that the method is reliable and repeatable throughout the sample set.

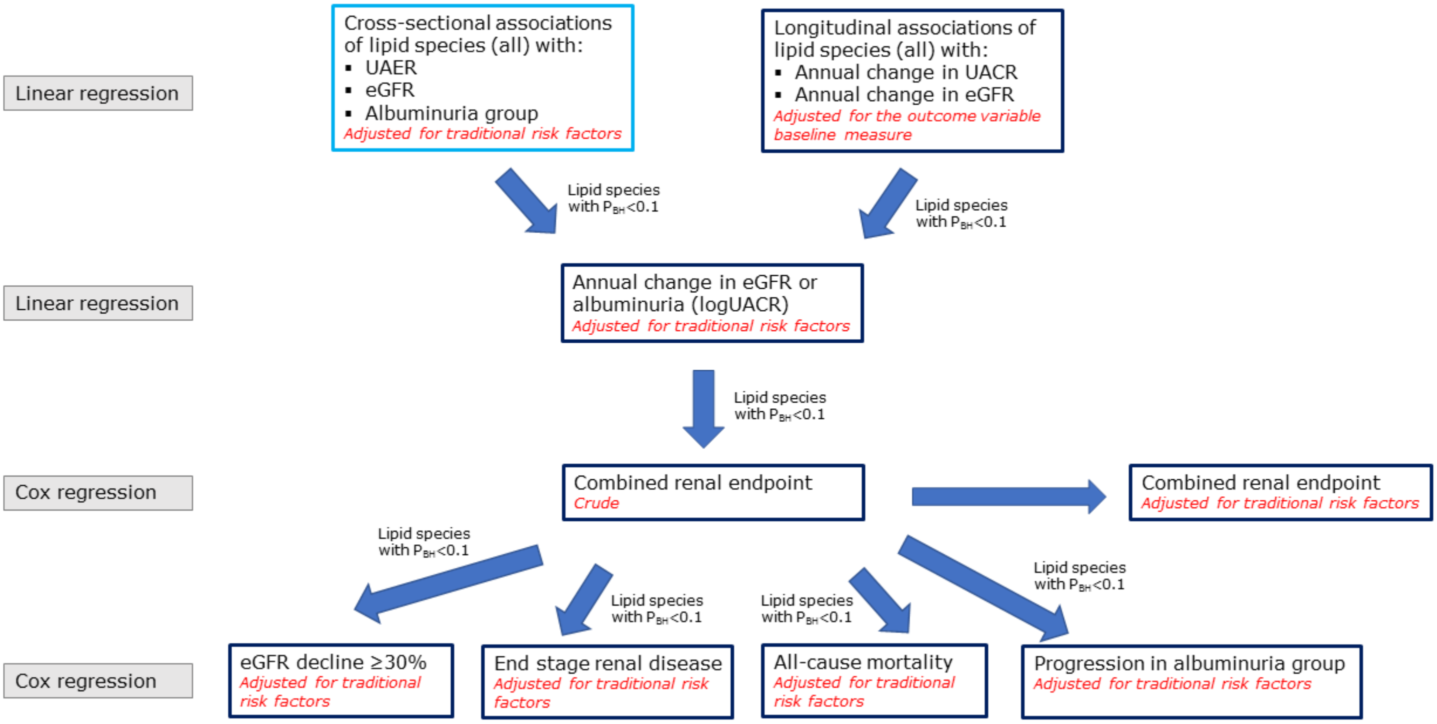
References:

1. Folch, J., M. Lees, and G.H.S. Stanley, *A Simple Method for the Isolation and Purification of Total Lipides from Animal Tissues.* Journal of Biological Chemistry, 1957. **226**(1): p. 497-509.

2. O'Gorman, A., et al., *Identification of a plasma signature of psychotic disorder in children and adolescents from the Avon Longitudinal Study of Parents and Children (ALSPAC) cohort.* Translational Psychiatry, 2017. **7**: p. e1240.

3. Luukkonen, P.K., et al., *Impaired hepatic lipid synthesis from polyunsaturated fatty acids in TM6SF2 E167K variant carriers with NAFLD.* Journal of Hepatology. **67**(1): p. 128-136.

Supplementary Figure S1 Statistical analyses - flow chart



Flow chart illustrating how lipid species were tested for associations with kidney-related clinical variables and outcomes in a narrowing-down approach. P_{BH} corrected for multiple testing using the Benjamini-Hochberg method. UAER urinary albumin excretion rate, UACR urinary albumin to creatinine ratio, eGFR estimated glomerular filtration rate. Traditional risk factors included age, sex, HbA_{1c}, systolic blood pressure, smoking, body mass index, statin treatment, p-triglycerides, total p-cholesterol and, further, eGFR or UAER, where appropriate.

0033_PROFIL_2017: Statistical Analysis of the Lipidome in Relation to Renal Complications

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Abstract

This document is Supplementary Material to the paper *Lower Serum Sphingomyelin and Phosphatidylcholine Levels Are Associated with Higher Risk of Progression to Diabetic Kidney Disease and All-Cause Mortality in Type 1 Diabetes* by Nete Tofte, Tommi Suvitaival, Linda Ahonen, Signe A. Winther, Simone Theilade, Tarun S. Ahluwalia, Marie Frimodt-M{o}ller and Peter Rossing.

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1 Step 1: Lipidome-Wide Screening

1.1 Step 1A: Cross-Sectional Analysis of All Lipids

1.1.1 Albuminuria Groups

1.1.1.1 Crude Model

1.1.1.1.1 Table of Model Coefficients

```
##
##
## Table: Coefficients for  GroupT1D Micro
## Results of the crude model for albuminuria group variable.
## Shown in the table are name of the lipid (Name),
## model coefficient (Coefficient),
## its lower and upper confidence intervals (CI.L, CL.R),
## average value of the variable (AveExpr),
## p-value of the coefficient (P.Value) and
## the p-value after correction for multiple testing (adj.P.Val).
## The rows of the table are shown in an increasing order by the respective p-value.
##
## Name                  Coefficient      CI.L       CI.R   AveExpr    P.Value   adj.P.Val
## -------------------  ------------  --------  ---------  --------  ---------  ----------
## LPC(18:2)                -0.21600   -0.3290   -0.10300      24.0   0.000193      0.0205
## SM(d18:1/24:0)           -0.11100   -0.1900   -0.03330      23.6   0.005250      0.2690
## SM(d40:1)                -0.10100   -0.1750   -0.02680      24.0   0.007620      0.2690
## SM(d41:1)                -0.11300   -0.2000   -0.02590      22.7   0.011100      0.2930
## PC(O-36:3)               -0.12200   -0.2220   -0.02250      20.4   0.016400      0.3240
## PC(O-34:3)               -0.11100   -0.2040   -0.01680      21.9   0.020900      0.3240
## PC(O-36:2)               -0.10600   -0.1960   -0.01570      20.5   0.021400      0.3240
## LPC(18:0)                -0.07150   -0.1390   -0.00353      24.0   0.039200      0.5200
## PC(O-34:2)               -0.11200   -0.2280    0.00426      21.5   0.059000      0.6880
## PC(16:0e/18:1(9Z))       -0.07300   -0.1520    0.00622      21.8   0.070900      0.6880
## LPC(18:1)                -0.07860   -0.1650    0.00734      23.7   0.073000      0.6880
## PC(34:2)                  0.12400   -0.0139    0.26300      26.0   0.077900      0.6880
## LPC(16:0)                -0.03320   -0.0714    0.00498      25.3   0.088200      0.7190
## PC(O-38:5)               -0.06050   -0.1330    0.01200      22.7   0.102000      0.7530
## PC(37:2)                 -0.09810   -0.2170    0.02110      19.3   0.107000      0.7530
## SM(d38:1)                -0.05430   -0.1240    0.01540      23.1   0.127000      0.7740
## PC(O-38:4)               -0.07400   -0.1700    0.02170      21.7   0.129000      0.7740
## TG(18:1/18:1/18:1)       -0.09750   -0.2250    0.02980      24.8   0.133000      0.7740
## SM(d39:1)                -0.07570   -0.1770    0.02570      21.1   0.143000      0.7740
## TG(48:3)                  0.17700   -0.0646    0.41800      20.6   0.151000      0.7740
## PC(O-38:6)               -0.05660   -0.1350    0.02200      20.4   0.158000      0.7740
## TG(54:4)                 -0.08030   -0.1950    0.03450      21.4   0.170000      0.7740
## PC(O-36:4)               -0.05940   -0.1450    0.02580      22.9   0.171000      0.7740
## TG(45:0)                 -0.04070   -0.0996    0.01820      23.1   0.175000      0.7740
## PC(36:2)                 -0.03870   -0.0971    0.01970      26.1   0.194000      0.8230
## TG(54:5)                 -0.08890   -0.2300    0.05180      20.6   0.215000      0.8500
## TG(18:1/18:2/18:2)       -0.09800   -0.2630    0.06700      23.6   0.244000      0.8500
## TG(18:2/18:1/16:0)       -0.05250   -0.1430    0.03760      25.3   0.253000      0.8500
## SM(d38:2)                -0.04320   -0.1180    0.03160      21.3   0.257000      0.8500
## PC(O-36:5)               -0.04430   -0.1250    0.03620      22.3   0.280000      0.8500
## TG(18:2/18:1/18:1)       -0.07270   -0.2070    0.06130      24.4   0.287000      0.8500
## TG(18:0/18:1/20:4)        0.10400   -0.0883    0.29600      21.3   0.289000      0.8500
## TG(50:2)                  0.06080   -0.0517    0.17300      21.2   0.289000      0.8500
## TG(47:1)                 -0.07790   -0.2230    0.06750      19.6   0.293000      0.8500
## TG(54:6)                  0.10000   -0.0874    0.28700      19.5   0.295000      0.8500
## TG(18:1/12:0/18:1)        0.09550   -0.0836    0.27500      22.5   0.296000      0.8500
## TG(46:1)                  0.09600   -0.0845    0.27600      21.3   0.297000      0.8500
## SM(d36:1)                -0.03080   -0.0921    0.03040      23.4   0.323000      0.8760
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## TG(14:0/18:1/18:1)        0.06810   -0.0683    0.20500      24.4   0.327000      0.8760
## TG(18:1/18:1/16:0)       -0.04900   -0.1510    0.05280      25.6   0.345000      0.8760
## PC(38:6)                 -0.03460   -0.1080    0.03900      25.3   0.357000      0.8760
## TG(46:2)                  0.08830   -0.1060    0.28200      20.1   0.372000      0.8760
## TG(18:2/18:2/18:2)        0.08330   -0.1000    0.26600      22.1   0.373000      0.8760
## LPC(20:4)                -0.04990   -0.1610    0.06120      21.4   0.379000      0.8760
## PC(38:5)                 -0.02340   -0.0755    0.02880      24.5   0.379000      0.8760
## TG(54:3)                 -0.04420   -0.1440    0.05510      21.7   0.383000      0.8760
## SM(d41:2)                -0.03550   -0.1170    0.04630      22.5   0.394000      0.8760
## SM(d32:1)                 0.03230   -0.0432    0.10800      22.3   0.401000      0.8760
## PC(36:4)                 -0.01950   -0.0653    0.02640      26.0   0.405000      0.8760
## PC(35:2)                 -0.03880   -0.1350    0.05710      21.8   0.427000      0.9050
## PC(34:1)                  0.02720   -0.0412    0.09560      25.9   0.436000      0.9050
## PC(40:7)                 -0.04130   -0.1490    0.06640      21.4   0.451000      0.9200
## SM(d33:1)                -0.02810   -0.1060    0.04970      21.3   0.479000      0.9340
## PC(34:3)                 -0.05330   -0.2030    0.09630      22.5   0.484000      0.9340
## TG(18:2/22:5/16:0)        0.08070   -0.1490    0.31000      22.1   0.490000      0.9340
## PC(38:2)                 -0.02810   -0.1090    0.05250      21.3   0.493000      0.9340
## TG(14:0/16:0/18:1)        0.06120   -0.1210    0.24300      22.8   0.509000      0.9350
## SM(d40:2)                -0.02120   -0.0868    0.04440      23.7   0.527000      0.9350
## TG(56:6)                  0.03590   -0.0785    0.15000      19.9   0.538000      0.9350
## TG(16:0/18:2/18:3)       -0.07270   -0.3060    0.16000      22.0   0.541000      0.9350
## PC(35:1)                 -0.02740   -0.1170    0.06240      21.8   0.549000      0.9350
## PC(36:5)                  0.04910   -0.1200    0.21800      24.3   0.569000      0.9350
## TG(56:4)                 -0.05560   -0.2470    0.13600      20.0   0.569000      0.9350
## TG(52:3)                 -0.02200   -0.1010    0.05680      22.3   0.584000      0.9350
## TG(16:0/18:2/18:2)       -0.04320   -0.2010    0.11500      24.5   0.591000      0.9350
## PC(40:6)                 -0.02820   -0.1390    0.08290      23.9   0.619000      0.9350
## TG(50:1)                  0.04450   -0.1320    0.22100      24.3   0.621000      0.9350
## SM(d34:1)                 0.00817   -0.0258    0.04210      24.9   0.637000      0.9350
## PC(32:1)                  0.03550   -0.1130    0.18400      23.3   0.638000      0.9350
## TG(53:4)                 -0.04010   -0.2210    0.14100      19.7   0.663000      0.9350
## TG(50:3)                  0.03260   -0.1140    0.17900      23.5   0.664000      0.9350
## PC(32:2)                 -0.02900   -0.1630    0.10500      20.8   0.671000      0.9350
## TG(56:7)                  0.02750   -0.1020    0.15700      19.6   0.677000      0.9350
## PC(36:3)                 -0.01720   -0.0983    0.06400      25.6   0.678000      0.9350
## SM(42:2)                 -0.01200   -0.0710    0.04690      25.2   0.688000      0.9350
## PC(40:5)                 -0.01920   -0.1180    0.07950      22.0   0.703000      0.9350
## PC(32:0)                 -0.01000   -0.0619    0.04180      22.5   0.704000      0.9350
## TG(58:9)                  0.05100   -0.2160    0.31800      19.9   0.708000      0.9350
## PC(33:1)                 -0.01950   -0.1240    0.08520      20.9   0.715000      0.9350
## TG(46:0)                  0.03130   -0.1410    0.20300      20.4   0.721000      0.9350
## TG(52:4)                 -0.02130   -0.1390    0.09660      21.7   0.723000      0.9350
## TG(49:3)                 -0.00361   -0.0239    0.01670      20.7   0.727000      0.9350
## PC(38:3)                 -0.01550   -0.1040    0.07310      24.0   0.732000      0.9350
## TG(53:3)                 -0.02780   -0.1940    0.13800      20.7   0.742000      0.9360
## TG(54:2)                 -0.02610   -0.1910    0.13900      23.4   0.757000      0.9370
## SM(d16:1/18:1)           -0.01070   -0.0798    0.05830      22.8   0.760000      0.9370
## TG(49:2)                  0.01520   -0.1080    0.13900      20.4   0.809000      0.9710
## TG(18:1/18:1/22:6)        0.02830   -0.2420    0.29900      20.7   0.837000      0.9710
## SM(d18:2/24:1)            0.00707   -0.0609    0.07510      24.0   0.838000      0.9710
## TG(16:0/18:2/22:6)        0.02900   -0.2700    0.32800      21.0   0.849000      0.9710
## TG(56:5)                 -0.01350   -0.1590    0.13200      20.3   0.856000      0.9710
## TG(51:2)                  0.01390   -0.1460    0.17400      21.6   0.865000      0.9710
```

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## TG(14:0/18:2/18:2)        0.01550   -0.1960    0.22700       21.2   0.885000       0.9710
## TG(56:3)                  0.01110   -0.1550    0.17700       19.9   0.896000       0.9710
## TG(49:1)                  0.00811   -0.1300    0.14600       20.9   0.908000       0.9710
## SM(d36:2)                -0.00347   -0.0695    0.06250       21.4   0.918000       0.9710
## TG(52:5)                 -0.00992   -0.2010    0.18100       19.8   0.919000       0.9710
## TG(50:0)                 -0.00995   -0.2160    0.19600       20.8   0.924000       0.9710
## TG(53:2)                 -0.00738   -0.1850    0.17000       20.7   0.935000       0.9710
## LPC(16:1)                -0.00448   -0.1140    0.10500       20.0   0.936000       0.9710
## TG(51:1)                 -0.00610   -0.1800    0.16800       20.3   0.945000       0.9710
## TG(16:0/18:0/18:1)       -0.00714   -0.2310    0.21700       23.1   0.950000       0.9710
## TG(51:3)                 -0.00517   -0.1690    0.15900       20.7   0.951000       0.9710
## TG(16:0/22:5/18:1)        0.00424   -0.1360    0.14500       22.7   0.953000       0.9710
## PC(38:4)                 -0.00123   -0.0575    0.05500       25.2   0.966000       0.9720
## TG(52:2)                 -0.00133   -0.0757    0.07310       22.6   0.972000       0.9720
##
##
## Table: Coefficients for  GroupT1D Macro
## Results of the crude model for albuminuria group variable.
## Shown in the table are name of the lipid (Name),
## model coefficient (Coefficient),
## its lower and upper confidence intervals (CI.L, CL.R),
## average value of the variable (AveExpr),
## p-value of the coefficient (P.Value) and
## the p-value after correction for multiple testing (adj.P.Val).
## The rows of the table are shown in an increasing order by the respective p-value.
##
## Name                  Coefficient       CI.L       CI.R   AveExpr    P.Value   adj.P.Val
## -------------------  ------------  ---------  ---------  --------  ---------  ----------
## PC(O-34:3)                -0.26200   -0.35200   -0.17300      21.9   0.00e+00    1.50e-06
## SM(d18:1/24:0)            -0.18100   -0.25600   -0.10600      23.6   2.50e-06    1.33e-04
## SM(d40:1)                 -0.16100   -0.23100   -0.08980      24.0   9.70e-06    3.44e-04
## PC(O-36:3)                -0.21200   -0.30700   -0.11600      20.4   1.47e-05    3.89e-04
## SM(d41:1)                 -0.17200   -0.25500   -0.08820      22.7   5.85e-05    1.24e-03
## PC(O-36:2)                -0.17500   -0.26100   -0.08890      20.5   7.44e-05    1.31e-03
## PC(16:0e/18:1(9Z)         -0.13200   -0.20800   -0.05650      21.8   6.47e-04    9.80e-03
## PC(34:2)                   0.22000    0.08720    0.35200      26.0   1.18e-03    1.44e-02
## PC(O-38:6)                -0.12400   -0.19900   -0.04910      20.4   1.22e-03    1.44e-02
## TG(45:0)                  -0.08900   -0.14500   -0.03270      23.1   2.00e-03    2.12e-02
## TG(56:3)                   0.23600    0.07690    0.39500      19.9   3.69e-03    3.55e-02
## PC(32:2)                  -0.18800   -0.31600   -0.05960      20.8   4.13e-03    3.65e-02
## PC(O-34:2)                -0.15700   -0.26800   -0.04580      21.5   5.73e-03    4.67e-02
## TG(18:0/18:1/20:4)         0.24400    0.06010    0.42800      21.3   9.39e-03    6.78e-02
## SM(d39:1)                 -0.12800   -0.22500   -0.03100      21.1   9.77e-03    6.78e-02
## PC(37:2)                  -0.14900   -0.26300   -0.03460      19.3   1.07e-02    6.78e-02
## LPC(18:2)                 -0.14000   -0.24800   -0.03170      24.0   1.14e-02    6.78e-02
## SM(d38:1)                 -0.08610   -0.15300   -0.01940      23.1   1.15e-02    6.78e-02
## TG(56:4)                   0.23100    0.04720    0.41400      20.0   1.38e-02    7.25e-02
## PC(32:0)                  -0.06220   -0.11200   -0.01260      22.5   1.41e-02    7.25e-02
## PC(38:6)                  -0.08800   -0.15800   -0.01760      25.3   1.44e-02    7.25e-02
## PC(O-36:5)                -0.09540   -0.17200   -0.01840      22.3   1.52e-02    7.31e-02
## TG(53:3)                   0.18700    0.02810    0.34500      20.7   2.11e-02    9.73e-02
## SM(d40:2)                 -0.07230   -0.13500   -0.00956      23.7   2.40e-02    1.06e-01
## TG(53:2)                   0.18600    0.01640    0.35600      20.7   3.17e-02    1.34e-01
## PC(36:5)                  -0.17300   -0.33500   -0.01100      24.3   3.64e-02    1.48e-01
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```
## PC(38:4)               0.05710   0.00328   0.11100    25.2  3.76e-02   1.48e-01
## TG(54:3)               0.09910   0.00411   0.19400    21.7  4.09e-02   1.51e-01
## PC(35:2)              -0.09520  -0.18700  -0.00341    21.8  4.21e-02   1.51e-01
## SM(d41:2)             -0.08100  -0.15900  -0.00268    22.5  4.27e-02   1.51e-01
## TG(51:2)               0.15700   0.00374   0.31000    21.6  4.47e-02   1.53e-01
## PC(40:6)              -0.10200  -0.20800   0.00467    23.9  6.09e-02   1.96e-01
## TG(52:2)               0.06750  -0.00366   0.13900    22.6  6.30e-02   1.96e-01
## TG(52:4)               0.10700  -0.00582   0.22000    21.7  6.30e-02   1.96e-01
## PC(38:2)              -0.07250  -0.15000   0.00461    21.3  6.53e-02   1.97e-01
## TG(16:0/18:2/18:3)     0.20900  -0.01450   0.43200    22.0  6.68e-02   1.97e-01
## TG(52:5)               0.16800  -0.01430   0.35100    19.8  7.08e-02   2.03e-01
## TG(56:6)               0.10000  -0.00936   0.21000    19.9  7.30e-02   2.04e-01
## TG(53:4)               0.15600  -0.01700   0.32900    19.7  7.71e-02   2.10e-01
## PC(33:1)              -0.08850  -0.18900   0.01160    20.9  8.30e-02   2.15e-01
## PC(40:7)              -0.09110  -0.19400   0.01200    21.4  8.31e-02   2.15e-01
## PC(O-38:4)            -0.07950  -0.17100   0.01210    21.7  8.87e-02   2.21e-01
## SM(d38:2)             -0.06150  -0.13300   0.01000    21.3  9.17e-02   2.21e-01
## TG(16:0/22:5/18:1)     0.11500  -0.01910   0.25000    22.7  9.24e-02   2.21e-01
## TG(56:5)               0.11900  -0.02020   0.25900    20.3  9.36e-02   2.21e-01
## TG(51:3)               0.13200  -0.02500   0.28900    20.7  9.93e-02   2.29e-01
## TG(54:2)               0.12800  -0.02990   0.28600    23.4  1.12e-01   2.52e-01
## TG(54:6)               0.14300  -0.03630   0.32200    19.5  1.18e-01   2.57e-01
## TG(16:0/18:2/18:2)     0.12000  -0.03100   0.27100    24.5  1.19e-01   2.57e-01
## TG(14:0/18:1/18:1)     0.10200  -0.02800   0.23300    24.4  1.24e-01   2.57e-01
## TG(50:2)               0.08450  -0.02320   0.19200    21.2  1.24e-01   2.57e-01
## TG(18:2/18:2/18:2)     0.13100  -0.04420   0.30600    22.1  1.43e-01   2.91e-01
## TG(18:1/18:1/18:1)     0.09030  -0.03150   0.21200    24.8  1.46e-01   2.92e-01
## TG(52:3)               0.05480  -0.02060   0.13000    22.3  1.54e-01   2.98e-01
## TG(50:3)               0.10200  -0.03860   0.24300    23.5  1.55e-01   2.98e-01
## PC(34:3)              -0.10100  -0.24400   0.04270    22.5  1.69e-01   3.19e-01
## TG(18:2/18:1/18:1)     0.08940  -0.03890   0.21800    24.4  1.72e-01   3.19e-01
## TG(54:4)               0.07300  -0.03680   0.18300    21.4  1.92e-01   3.49e-01
## PC(O-38:5)            -0.04560  -0.11500   0.02380    22.7  1.97e-01   3.49e-01
## PC(36:3)              -0.05100  -0.12900   0.02670    25.6  1.98e-01   3.49e-01
## SM(42:2)              -0.03490  -0.09130   0.02140    25.2  2.24e-01   3.78e-01
## PC(38:5)              -0.03090  -0.08080   0.01900    24.5  2.24e-01   3.78e-01
## PC(40:5)              -0.05820  -0.15300   0.03610    22.0  2.26e-01   3.78e-01
## TG(54:5)               0.08220  -0.05230   0.21700    20.6  2.31e-01   3.78e-01
## LPC(20:4)              0.06480  -0.04150   0.17100    21.4  2.32e-01   3.78e-01
## PC(O-36:4)            -0.04880  -0.13000   0.03270    22.9  2.40e-01   3.83e-01
## SM(d34:1)              0.01940  -0.01310   0.05190    24.9  2.42e-01   3.83e-01
## PC(32:1)              -0.08240  -0.22400   0.05950    23.3  2.55e-01   3.94e-01
## LPC(16:0)             -0.02100  -0.05760   0.01550    25.3  2.59e-01   3.94e-01
## TG(50:1)               0.09700  -0.07200   0.26600    24.3  2.60e-01   3.94e-01
## TG(14:0/18:2/18:2)     0.11400  -0.08760   0.31600    21.2  2.67e-01   3.98e-01
## TG(56:7)               0.06900  -0.05510   0.19300    19.6  2.75e-01   4.05e-01
## PC(35:1)              -0.04720  -0.13300   0.03860    21.8  2.81e-01   4.05e-01
## TG(18:1/18:2/18:2)     0.08630  -0.07140   0.24400    23.6  2.83e-01   4.05e-01
## SM(d33:1)             -0.03980  -0.11400   0.03460    21.3  2.94e-01   4.16e-01
## TG(51:1)               0.08310  -0.08300   0.24900    20.3  3.26e-01   4.55e-01
## LPC(18:0)             -0.03110  -0.09610   0.03380    24.0  3.47e-01   4.77e-01
## TG(48:3)               0.10900  -0.12200   0.34000    20.6  3.53e-01   4.77e-01
## TG(16:0/18:0/18:1)     0.10100  -0.11300   0.31500    23.1  3.56e-01   4.77e-01
## PC(36:4)               0.01880  -0.02500   0.06270    26.0  4.00e-01   5.30e-01
```

```
## TG(18:1/18:1/16:0)        0.04080   -0.05660    0.13800      25.6   4.11e-01    5.33e-01
## SM(d16:1/18:1)           -0.02750   -0.09350    0.03860      22.8   4.14e-01    5.33e-01
## SM(d36:1)                -0.02420   -0.08280    0.03440      23.4   4.17e-01    5.33e-01
## LPC(18:1)                -0.03350   -0.11600    0.04870      23.7   4.24e-01    5.35e-01
## TG(18:1/12:0/18:1)        0.06740   -0.10400    0.23900      22.5   4.40e-01    5.49e-01
## TG(49:3)                 -0.00742   -0.02680    0.01200      20.7   4.52e-01    5.58e-01
## SM(d36:2)                 0.02310   -0.04000    0.08620      21.4   4.73e-01    5.76e-01
## TG(49:2)                  0.04040   -0.07760    0.15800      20.4   5.02e-01    6.05e-01
## PC(36:2)                 -0.01740   -0.07330    0.03850      26.1   5.41e-01    6.41e-01
## TG(49:1)                  0.04000   -0.09170    0.17200      20.9   5.51e-01    6.41e-01
## TG(14:0/16:0/18:1)        0.05240   -0.12200    0.22700      22.8   5.55e-01    6.41e-01
## TG(47:1)                 -0.04140   -0.18000    0.09770      19.6   5.59e-01    6.41e-01
## TG(18:2/22:5/16:0)        0.06480   -0.15500    0.28400      22.1   5.62e-01    6.41e-01
## SM(d32:1)                 0.01700   -0.05520    0.08920      22.3   6.44e-01    7.24e-01
## TG(18:1/18:1/22:6)        0.06000   -0.19900    0.31900      20.7   6.49e-01    7.24e-01
## SM(d18:2/24:1)           -0.01470   -0.07970    0.05040      24.0   6.58e-01    7.27e-01
## TG(46:2)                  0.03090   -0.15500    0.21700      20.1   7.44e-01    8.05e-01
## TG(16:0/18:2/22:6)       -0.04760   -0.33400    0.23900      21.0   7.44e-01    8.05e-01
## TG(46:0)                 -0.02080   -0.18500    0.14400      20.4   8.04e-01    8.47e-01
## TG(18:2/18:1/16:0)        0.01080   -0.07540    0.09690      25.3   8.06e-01    8.47e-01
## PC(34:1)                  0.00815   -0.05730    0.07360      25.9   8.07e-01    8.47e-01
## TG(58:9)                  0.02810   -0.22700    0.28300      19.9   8.29e-01    8.61e-01
## LPC(16:1)                -0.00809   -0.11200    0.09630      20.0   8.79e-01    9.05e-01
## TG(50:0)                  0.01180   -0.18500    0.20900      20.8   9.06e-01    9.24e-01
## TG(46:1)                  0.00909   -0.16400    0.18200      21.3   9.18e-01    9.26e-01
## PC(38:3)                  0.00258   -0.08210    0.08730      24.0   9.52e-01    9.52e-01
##
##
## Table: Coefficients for  GroupHealthy Control
## Results of the crude model for albuminuria group variable.
## Shown in the table are name of the lipid (Name),
## model coefficient (Coefficient),
## its lower and upper confidence intervals (CI.L, CL.R),
## average value of the variable (AveExpr),
## p-value of the coefficient (P.Value) and
## the p-value after correction for multiple testing (adj.P.Val).
## The rows of the table are shown in an increasing order by the respective p-value.
##
## Name                  Coefficient       CI.L       CI.R   AveExpr    P.Value   adj.P.Val
## -------------------  ------------  ---------  ---------  --------  ---------  ----------
## PC(38:3)                 4.11e-01    0.26900    0.55200      24.0   0.00e+00    1.80e-06
## LPC(18:1)               -3.29e-01   -0.46600   -0.19200      23.7   2.90e-06    1.52e-04
## LPC(18:2)               -3.88e-01   -0.56900   -0.20800      24.0   2.67e-05    9.42e-04
## PC(O-36:2)              -2.53e-01   -0.39700   -0.10900      20.5   5.79e-04    1.50e-02
## TG(14:0/18:2/18:2)       5.79e-01    0.24300    0.91500      21.2   7.68e-04    1.50e-02
## PC(O-36:3)              -2.70e-01   -0.42900   -0.11100      20.4   8.76e-04    1.50e-02
## TG(50:3)                 3.94e-01    0.16000    0.62800      23.5   9.93e-04    1.50e-02
## PC(16:0e/18:1(9Z)       -2.03e-01   -0.32900   -0.07650      21.8   1.68e-03    2.23e-02
## PC(O-38:5)              -1.80e-01   -0.29500   -0.06400      22.7   2.36e-03    2.78e-02
## TG(16:0/18:2/18:2)       3.74e-01    0.12300    0.62600      24.5   3.60e-03    3.48e-02
## PC(36:2)                -1.39e-01   -0.23200   -0.04540      26.1   3.61e-03    3.48e-02
## TG(51:3)                 3.76e-01    0.11500    0.63700      20.7   4.83e-03    4.27e-02
## TG(16:0/18:2/18:3)       5.11e-01    0.13900    0.88200      22.0   7.13e-03    5.82e-02
## TG(52:5)                 4.11e-01    0.10700    0.71500      19.8   8.21e-03    5.98e-02
```

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## PC(32:2)            2.83e-01   0.06980   0.49600    20.8  9.35e-03  5.98e-02
## TG(18:1/12:0/18:1)  3.78e-01   0.09280   0.66300    22.5  9.47e-03  5.98e-02
## TG(48:3)            5.09e-01   0.12400   0.89300    20.6  9.60e-03  5.98e-02
## TG(14:0/18:1/18:1)  2.80e-01   0.06250   0.49700    24.4  1.17e-02  6.88e-02
## TG(52:4)            2.35e-01   0.04680   0.42200    21.7  1.44e-02  7.65e-02
## TG(51:2)            3.18e-01   0.06350   0.57300    21.6  1.44e-02  7.65e-02
## TG(53:4)            3.51e-01   0.06280   0.63900    19.7  1.71e-02  8.39e-02
## TG(18:2/18:2/18:2)  3.54e-01   0.06250   0.64600    22.1  1.74e-02  8.39e-02
## TG(45:0)           -1.10e-01  -0.20400  -0.01630    23.1  2.15e-02  9.91e-02
## TG(50:2)            2.05e-01   0.02540   0.38400    21.2  2.53e-02  1.03e-01
## TG(16:0/18:2/22:6)  5.43e-01   0.06650   1.02000    21.0  2.56e-02  1.03e-01
## PC(O-38:6)         -1.42e-01  -0.26700  -0.01710    20.4  2.59e-02  1.03e-01
## PC(40:6)            2.01e-01   0.02390   0.37800    23.9  2.62e-02  1.03e-01
## TG(49:2)            2.21e-01   0.02470   0.41800    20.4  2.74e-02  1.04e-01
## TG(18:2/18:1/16:0)  1.59e-01   0.01580   0.30300    25.3  2.97e-02  1.08e-01
## TG(14:0/16:0/18:1)  3.17e-01   0.02680   0.60700    22.8  3.23e-02  1.14e-01
## TG(18:2/22:5/16:0)  3.89e-01   0.02330   0.75400    22.1  3.71e-02  1.27e-01
## TG(52:3)            1.31e-01   0.00522   0.25700    22.3  4.12e-02  1.37e-01
## TG(54:6)            2.92e-01  -0.00639   0.59100    19.5  5.51e-02  1.77e-01
## PC(36:3)            1.23e-01  -0.00588   0.25300    25.6  6.13e-02  1.91e-01
## SM(d41:1)           1.31e-01  -0.00755   0.27000    22.7  6.38e-02  1.92e-01
## PC(38:5)           -7.79e-02  -0.16100   0.00524    24.5  6.62e-02  1.92e-01
## TG(53:3)            2.47e-01  -0.01770   0.51100    20.7  6.74e-02  1.92e-01
## PC(32:0)           -7.62e-02  -0.15900   0.00640    22.5  7.05e-02  1.92e-01
## SM(d39:1)           1.49e-01  -0.01270   0.31000    21.1  7.08e-02  1.92e-01
## SM(d16:1/18:1)     -9.50e-02  -0.20500   0.01500    22.8  9.03e-02  2.39e-01
## TG(53:2)            2.41e-01  -0.04250   0.52400    20.7  9.57e-02  2.47e-01
## TG(49:3)           -2.70e-02  -0.05930   0.00527    20.7  1.01e-01  2.49e-01
## PC(O-34:3)         -1.25e-01  -0.27400   0.02450    21.9  1.01e-01  2.49e-01
## TG(52:2)            9.71e-02  -0.02140   0.21600    22.6  1.08e-01  2.60e-01
## PC(38:4)            7.16e-02  -0.01810   0.16100    25.2  1.17e-01  2.76e-01
## TG(46:2)            2.43e-01  -0.06670   0.55200    20.1  1.24e-01  2.85e-01
## TG(50:1)            2.20e-01  -0.06200   0.50100    24.3  1.26e-01  2.85e-01
## TG(51:1)            2.12e-01  -0.06430   0.48900    20.3  1.32e-01  2.92e-01
## TG(56:7)            1.49e-01  -0.05710   0.35600    19.6  1.56e-01  3.37e-01
## TG(46:1)            1.98e-01  -0.08910   0.48600    21.3  1.76e-01  3.67e-01
## TG(49:1)            1.51e-01  -0.06860   0.37000    20.9  1.78e-01  3.67e-01
## LPC(20:4)          -1.21e-01  -0.29800   0.05650    21.4  1.82e-01  3.67e-01
## PC(O-36:4)         -9.20e-02  -0.22800   0.04370    22.9  1.84e-01  3.67e-01
## PC(40:7)           -1.07e-01  -0.27900   0.06450    21.4  2.21e-01  4.33e-01
## PC(34:2)            1.36e-01  -0.08430   0.35700    26.0  2.26e-01  4.35e-01
## PC(36:4)            4.29e-02  -0.03020   0.11600    26.0  2.49e-01  4.72e-01
## TG(56:5)            1.33e-01  -0.09940   0.36500    20.3  2.62e-01  4.81e-01
## TG(16:0/22:5/18:1)  1.28e-01  -0.09640   0.35200    22.7  2.63e-01  4.81e-01
## TG(54:3)           -8.85e-02  -0.24700   0.06980    21.7  2.73e-01  4.85e-01
## TG(18:1/18:2/18:2)  1.46e-01  -0.11600   0.40900    23.6  2.75e-01  4.85e-01
## SM(d38:1)           6.00e-02  -0.05110   0.17100    23.1  2.89e-01  4.96e-01
## PC(O-34:2)         -9.99e-02  -0.28500   0.08530    21.5  2.90e-01  4.96e-01
## TG(18:1/18:1/16:0)  8.64e-02  -0.07580   0.24900    25.6  2.96e-01  4.96e-01
## SM(42:2)           -4.96e-02  -0.14400   0.04430    25.2  3.00e-01  4.96e-01
## SM(d40:1)           6.08e-02  -0.05710   0.17900    24.0  3.12e-01  5.08e-01
## TG(56:3)           -1.31e-01  -0.39500   0.13400    19.9  3.33e-01  5.35e-01
## PC(38:6)            5.72e-02  -0.06000   0.17400    25.3  3.38e-01  5.35e-01
## PC(O-38:4)         -7.19e-02  -0.22400   0.08070    21.7  3.55e-01  5.48e-01
```

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## PC(40:5)                 7.38e-02   -0.08340    0.23100       22.0   3.57e-01   5.48e-01
## SM(d34:1)               -2.47e-02   -0.07890    0.02940       24.9   3.70e-01   5.50e-01
## PC(35:1)                -6.40e-02   -0.20700    0.07900       21.8   3.80e-01   5.50e-01
## SM(d18:1/24:0)           5.57e-02   -0.06890    0.18000       23.6   3.81e-01   5.50e-01
## SM(d41:2)                5.80e-02   -0.07250    0.18800       22.5   3.83e-01   5.50e-01
## SM(d18:2/24:1)          -4.81e-02   -0.15600    0.06030       24.0   3.84e-01   5.50e-01
## TG(56:4)                -1.33e-01   -0.43900    0.17200       20.0   3.91e-01   5.51e-01
## TG(18:0/18:1/20:4)      -1.32e-01   -0.43800    0.17400       21.3   3.98e-01   5.51e-01
## PC(37:2)                -8.13e-02   -0.27100    0.10900       19.3   4.01e-01   5.51e-01
## PC(O-36:5)              -5.39e-02   -0.18200    0.07420       22.3   4.09e-01   5.56e-01
## PC(32:1)                 9.43e-02   -0.14200    0.33100       23.3   4.34e-01   5.78e-01
## TG(18:1/18:1/18:1)      -8.05e-02   -0.28300    0.12200       24.8   4.36e-01   5.78e-01
## TG(16:0/18:0/18:1)       1.33e-01   -0.22300    0.49000       23.1   4.63e-01   6.00e-01
## PC(35:2)                -5.70e-02   -0.21000    0.09590       21.8   4.65e-01   6.00e-01
## TG(58:9)                 1.46e-01   -0.27900    0.57100       19.9   5.00e-01   6.39e-01
## SM(d36:2)                3.29e-02   -0.07230    0.13800       21.4   5.39e-01   6.80e-01
## LPC(18:0)                2.98e-02   -0.07840    0.13800       24.0   5.89e-01   7.34e-01
## TG(47:1)                 6.07e-02   -0.17100    0.29200       19.6   6.07e-01   7.48e-01
## SM(d33:1)               -3.19e-02   -0.15600    0.09210       21.3   6.14e-01   7.48e-01
## TG(54:4)                -3.87e-02   -0.22200    0.14400       21.4   6.78e-01   8.16e-01
## TG(18:1/18:1/22:6)       8.04e-02   -0.35100    0.51200       20.7   7.14e-01   8.44e-01
## PC(36:5)                -4.99e-02   -0.32000    0.22000       24.3   7.16e-01   8.44e-01
## LPC(16:1)                2.63e-02   -0.14800    0.20000       20.0   7.67e-01   8.74e-01
## PC(38:2)                 1.94e-02   -0.10900    0.14800       21.3   7.67e-01   8.74e-01
## TG(18:2/18:1/18:1)       3.20e-02   -0.18200    0.24600       24.4   7.68e-01   8.74e-01
## PC(34:1)                -1.58e-02   -0.12500    0.09320       25.9   7.76e-01   8.74e-01
## SM(d40:2)                1.46e-02   -0.08990    0.11900       23.7   7.83e-01   8.74e-01
## SM(d32:1)               -1.61e-02   -0.13600    0.10400       22.3   7.92e-01   8.75e-01
## TG(50:0)                 4.06e-02   -0.28700    0.36800       20.8   8.08e-01   8.75e-01
## SM(d36:1)                1.20e-02   -0.08560    0.11000       23.4   8.09e-01   8.75e-01
## PC(33:1)                 1.89e-02   -0.14800    0.18600       20.9   8.24e-01   8.83e-01
## TG(54:5)                 1.91e-02   -0.20500    0.24300       20.6   8.67e-01   9.11e-01
## TG(54:2)                -2.24e-02   -0.28600    0.24100       23.4   8.68e-01   9.11e-01
## TG(46:0)                 1.61e-02   -0.25800    0.29000       20.4   9.08e-01   9.44e-01
## TG(56:6)                -8.82e-03   -0.19100    0.17300       19.9   9.24e-01   9.51e-01
## SM(d38:2)                4.36e-03   -0.11500    0.12300       21.3   9.43e-01   9.61e-01
## PC(34:3)                -6.02e-03   -0.24500    0.23200       22.5   9.60e-01   9.70e-01
## LPC(16:0)                8.15e-05   -0.06080    0.06100       25.3   9.98e-01   9.98e-01
```

1.1.1.1.2 Heatmaps of Model Coefficients

```
## Loading required package: stringr
```

```
##   Label Relation p.adj
## 1     #  p.adj <  0.01
## 2     x  p.adj <  0.05
## 3     *  p.adj <  0.10
```

```
##   Label Relation p.adj
## 1     #  p.adj <  0.01
## 2     x  p.adj <  0.05
## 3     *  p.adj <  0.10
```

```
##   Label Relation p.adj
## 1     #  p.adj <  0.01
## 2     x  p.adj <  0.05
## 3     *  p.adj <  0.10
```

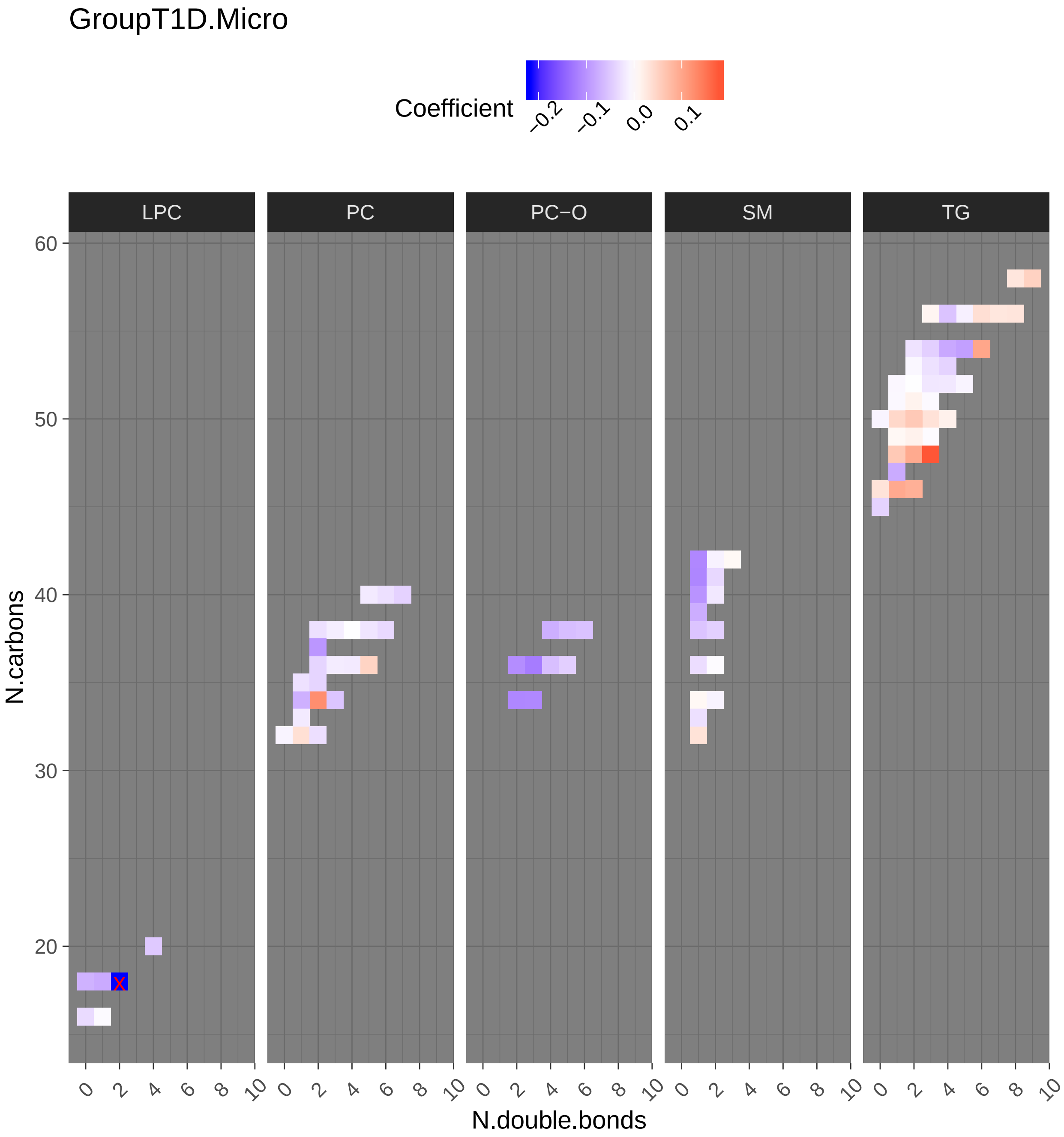


Figure 1: Heatmap of the lipid-specific model coefficents from the crude model for albuminuria groups. The name of the group is shown in the title of the figure in the top-left corner. Lipids are organized into panels (columns) by their class (from LPC to TG). One colored rectangle corresponds to one lipid species, where the coordinates in the x-axis and y-axis, respectively, show the number of double bonds (N.double.bonds) and the number of carbon atoms (N.carbons) in the fatty acid chains of the lipid. The number of double bonds corresponds to the number of unsaturated bonds in the fatty acid chains, and the number of carbon atoms corresponds to the length of the fatty acid chains and, thus, the size of the lipid. The magnitude of the lipid-specifc model coefficient is shown as the color of the rectangle (blue: negative; red: positive). Coefficient with statistical significance are annotated with symbols #, x and *, respectively, corresponding to $p < 0.01$, $p < 0.05$ and $p < 0.1$.

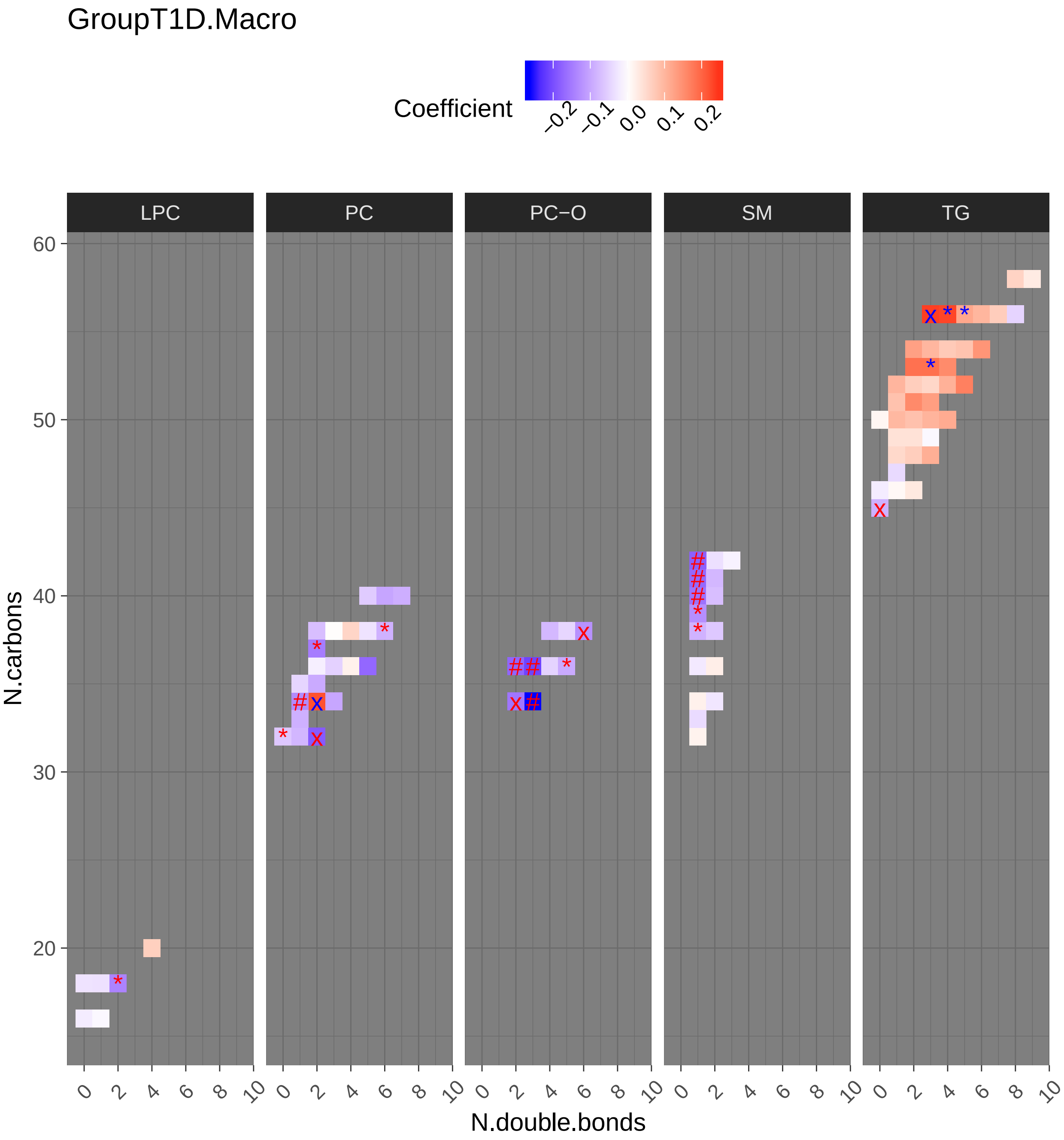


Figure 2: Heatmap of the lipid-specific model coefficents from the crude model for albuminuria groups. The name of the group is shown in the title of the figure in the top-left corner. Lipids are organized into panels (columns) by their class (from LPC to TG). One colored rectangle corresponds to one lipid species, where the coordinates in the x-axis and y-axis, respectively, show the number of double bonds (N.double.bonds) and the number of carbon atoms (N.carbons) in the fatty acid chains of the lipid. The number of double bonds corresponds to the number of unsaturated bonds in the fatty acid chains, and the number of carbon atoms corresponds to the length of the fatty acid chains and, thus, the size of the lipid. The magnitude of the lipid-specifc model coefficient is shown as the color of the rectangle (blue: negative; red: positive). Coefficient with statistical significance are annotated with symbols #, x and *, respectively, corresponding to $p < 0.01$, $p < 0.05$ and $p < 0.1$.

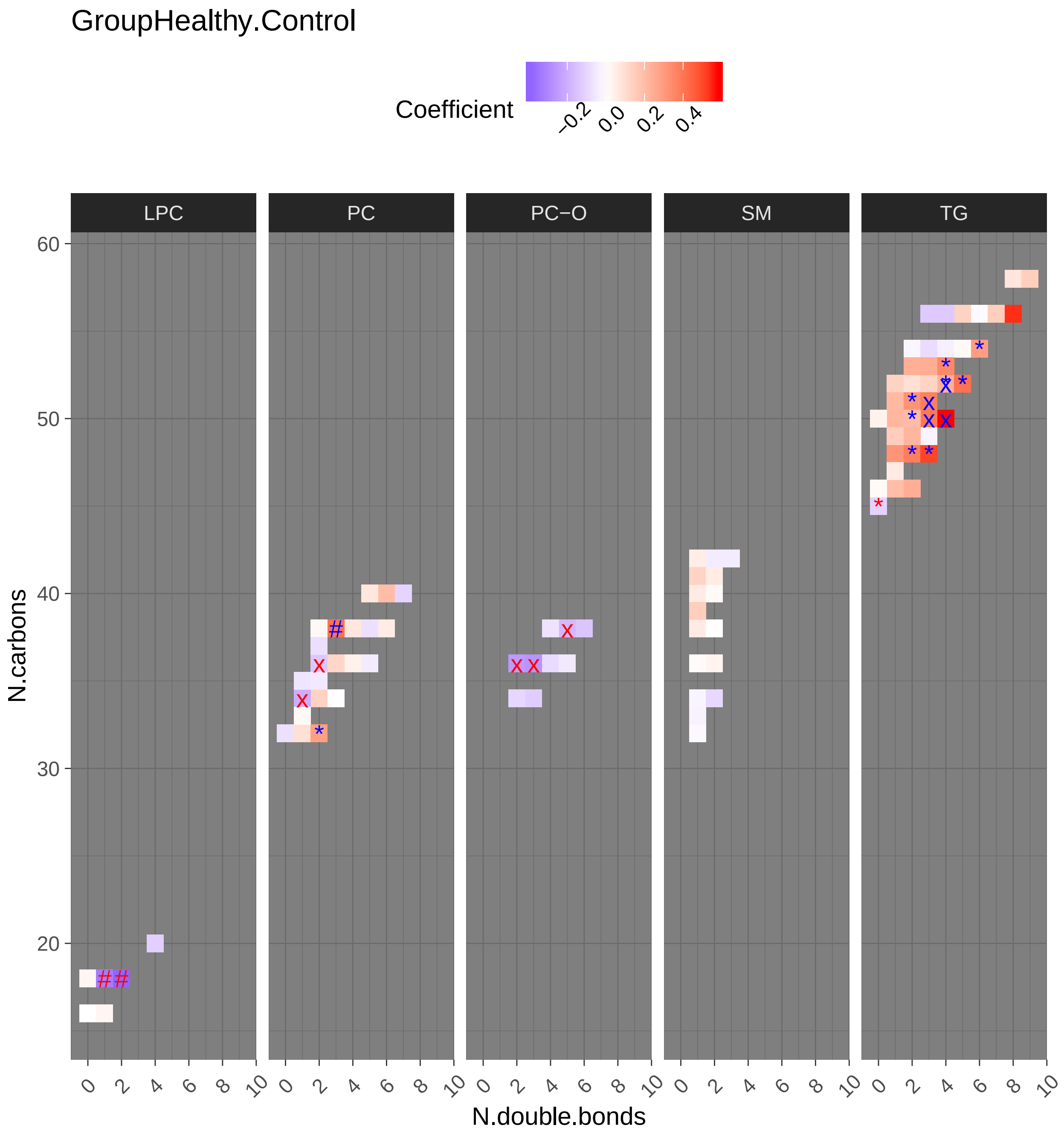


Figure 3: Heatmap of the lipid-specific model coefficents from the crude model for albuminuria groups. The name of the group is shown in the title of the figure in the top-left corner. Lipids are organized into panels (columns) by their class (from LPC to TG). One colored rectangle corresponds to one lipid species, where the coordinates in the x-axis and y-axis, respectively, show the number of double bonds (N.double.bonds) and the number of carbon atoms (N.carbons) in the fatty acid chains of the lipid. The number of double bonds corresponds to the number of unsaturated bonds in the fatty acid chains, and the number of carbon atoms corresponds to the length of the fatty acid chains and, thus, the size of the lipid. The magnitude of the lipid-specifc model coefficient is shown as the color of the rectangle (blue: negative; red: positive). Coefficient with statistical significance are annotated with symbols #, x and *, respectively, corresponding to $p < 0.01$, $p < 0.05$ and $p < 0.1$.

1.1.1.2 Adjusted Model

1.1.1.2.1 Table

```
##
##
## Table: Coefficients for GroupT1D Micro
## Results of the adjusted model for albuminuria group variable.
## Shown in the table are name of the lipid (Name),
## model coefficient (Coefficient),
## its lower and upper confidence intervals (CI.L, CL.R),
## average value of the variable (AveExpr),
## p-value of the coefficient (P.Value) and
## the p-value after correction for multiple testing (adj.P.Val).
## The rows of the table are shown in an increasing order by the respective p-value.
##
## Name                  Coefficient      CI.L        CI.R   AveExpr    P.Value   adj.P.Val
## -------------------  ------------  --------  ----------  --------  ---------  ----------
## LPC(18:2)               -0.193000   -0.3040   -8.25e-02      24.0   0.000648      0.0686
## TG(18:1/18:1/18:1)      -0.159000   -0.2580   -5.94e-02      24.8   0.001780      0.0946
## SM(d18:1/24:0)          -0.089100   -0.1520   -2.60e-02      23.6   0.005680      0.1690
## TG(54:3)                -0.093900   -0.1630   -2.44e-02      21.7   0.008130      0.1690
## SM(d40:1)               -0.076500   -0.1340   -1.89e-02      24.0   0.009270      0.1690
## SM(d36:2)               -0.073900   -0.1310   -1.69e-02      21.4   0.011200      0.1690
## TG(54:2)                -0.125000   -0.2230   -2.61e-02      23.4   0.013300      0.1690
## LPC(20:4)               -0.138000   -0.2480   -2.81e-02      21.4   0.013900      0.1690
## TG(56:5)                -0.135000   -0.2430   -2.65e-02      20.3   0.014800      0.1690
## TG(54:4)                -0.114000   -0.2060   -2.13e-02      21.4   0.016000      0.1690
## SM(d36:1)               -0.059100   -0.1090   -9.06e-03      23.4   0.020700      0.1880
## SM(d41:1)               -0.085200   -0.1580   -1.28e-02      22.7   0.021200      0.1880
## TG(56:4)                -0.162000   -0.3030   -2.07e-02      20.0   0.024700      0.1900
## TG(16:0/22:5/18:1)      -0.123000   -0.2310   -1.43e-02      22.7   0.026600      0.1900
## TG(18:2/18:1/18:1)      -0.118000   -0.2230   -1.36e-02      24.4   0.026900      0.1900
## TG(18:1/18:2/18:2)      -0.142000   -0.2740   -1.01e-02      23.6   0.034900      0.2310
## LPC(18:1)               -0.086100   -0.1710   -1.58e-03      23.7   0.045900      0.2860
## TG(54:5)                -0.118000   -0.2370   -4.78e-05      20.6   0.049900      0.2940
## PC(O-38:6)              -0.072700   -0.1470    1.29e-03      20.4   0.054100      0.3020
## SM(d38:1)               -0.055500   -0.1130    1.81e-03      23.1   0.057700      0.3060
## TG(52:2)                -0.042800   -0.0880    2.42e-03      22.6   0.063500      0.3180
## SM(d38:2)               -0.060100   -0.1240    4.18e-03      21.3   0.066800      0.3180
## TG(52:3)                -0.049600   -0.1030    3.89e-03      22.3   0.069100      0.3180
## TG(53:2)                -0.102000   -0.2160    1.22e-02      20.7   0.080100      0.3460
## TG(48:3)                 0.159000   -0.0200    3.38e-01      20.6   0.081600      0.3460
## LPC(18:0)               -0.056900   -0.1220    8.08e-03      24.0   0.086000      0.3510
## TG(53:3)                -0.096100   -0.2080    1.59e-02      20.7   0.092400      0.3630
## PC(O-38:5)              -0.060600   -0.1320    1.12e-02      22.7   0.097900      0.3710
## TG(18:1/18:1/16:0)      -0.082200   -0.1840    1.91e-02      25.6   0.112000      0.4080
## TG(56:6)                -0.076800   -0.1730    1.98e-02      19.9   0.119000      0.4200
## PC(O-36:5)              -0.062100   -0.1420    1.80e-02      22.3   0.129000      0.4230
## TG(18:2/18:1/16:0)      -0.068100   -0.1570    2.05e-02      25.3   0.132000      0.4230
## SM(d16:1/18:1)          -0.036900   -0.0857    1.18e-02      22.8   0.137000      0.4230
## TG(18:1/12:0/18:1)       0.090500   -0.0307    2.12e-01      22.5   0.143000      0.4230
## PC(38:4)                -0.039300   -0.0922    1.37e-02      25.2   0.146000      0.4230
## SM(d39:1)               -0.067100   -0.1590    2.44e-02      21.1   0.151000      0.4230
## TG(46:1)                 0.105000   -0.0382    2.48e-01      21.3   0.151000      0.4230
## PC(O-36:4)              -0.062000   -0.1470    2.28e-02      22.9   0.152000      0.4230
```

```
## TG(16:0/18:2/18:2)     -0.080700  -0.1930  3.13e-02     24.5  0.158000      0.4260
## LPC(16:0)              -0.025200  -0.0608  1.04e-02     25.3  0.165000      0.4260
## PC(O-36:2)             -0.058300  -0.1410  2.43e-02     20.5  0.166000      0.4260
## TG(45:0)               -0.023900  -0.0581  1.03e-02     23.1  0.170000      0.4260
## PC(32:2)                0.085000  -0.0373  2.07e-01     20.8  0.173000      0.4260
## PC(O-36:3)             -0.058000  -0.1450  2.88e-02     20.4  0.190000      0.4430
## PC(O-38:4)             -0.063100  -0.1580  3.14e-02     21.7  0.190000      0.4430
## TG(56:3)               -0.077500  -0.1950  4.00e-02     19.9  0.196000      0.4430
## TG(16:0/18:2/18:3)     -0.122000  -0.3070  6.32e-02     22.0  0.196000      0.4430
## TG(16:0/18:0/18:1)     -0.101000  -0.2580  5.59e-02     23.1  0.207000      0.4450
## TG(46:2)                0.093400  -0.0529  2.40e-01     20.1  0.211000      0.4450
## TG(18:0/18:1/20:4)     -0.111000  -0.2850  6.31e-02     21.3  0.211000      0.4450
## TG(53:4)               -0.086100  -0.2220  4.98e-02     19.7  0.214000      0.4450
## TG(50:2)                0.042400  -0.0260  1.11e-01     21.2  0.224000      0.4560
## PC(36:4)               -0.025700  -0.0724  2.10e-02     26.0  0.280000      0.5410
## TG(56:7)               -0.064300  -0.1810  5.28e-02     19.6  0.281000      0.5410
## SM(d40:2)              -0.028200  -0.0795  2.31e-02     23.7  0.282000      0.5410
## PC(34:2)                0.076000  -0.0637  2.16e-01     26.0  0.286000      0.5410
## TG(52:4)               -0.045400  -0.1310  4.06e-02     21.7  0.300000      0.5440
## TG(47:1)               -0.078000  -0.2270  7.05e-02     19.6  0.303000      0.5440
## PC(32:1)                0.071000  -0.0660  2.08e-01     23.3  0.309000      0.5440
## TG(16:0/18:2/22:6)     -0.144000  -0.4240  1.35e-01     21.0  0.310000      0.5440
## TG(18:1/18:1/22:6)     -0.131000  -0.3890  1.27e-01     20.7  0.320000      0.5440
## PC(40:5)               -0.043700  -0.1300  4.29e-02     22.0  0.322000      0.5440
## PC(38:5)               -0.024300  -0.0725  2.40e-02     24.5  0.324000      0.5440
## SM(d41:2)              -0.034000  -0.1030  3.47e-02     22.5  0.331000      0.5490
## SM(d33:1)              -0.031600  -0.0984  3.53e-02     21.3  0.354000      0.5690
## TG(51:1)               -0.055500  -0.1730  6.21e-02     20.3  0.355000      0.5690
## PC(16:0e/18:1(9Z)      -0.032700  -0.1030  3.77e-02     21.8  0.362000      0.5710
## PC(40:6)               -0.044400  -0.1410  5.26e-02     23.9  0.369000      0.5710
## TG(14:0/18:1/18:1)      0.036400  -0.0436  1.16e-01     24.4  0.372000      0.5710
## PC(38:6)               -0.029300  -0.0954  3.67e-02     25.3  0.384000      0.5810
## TG(50:0)               -0.070200  -0.2310  9.10e-02     20.8  0.393000      0.5860
## TG(58:9)               -0.111000  -0.3710  1.49e-01     19.9  0.402000      0.5920
## TG(14:0/16:0/18:1)      0.053000  -0.0746  1.81e-01     22.8  0.415000      0.6020
## TG(18:2/22:5/16:0)     -0.081700  -0.2840  1.20e-01     22.1  0.427000      0.6110
## PC(O-34:3)             -0.032100  -0.1140  5.02e-02     21.9  0.444000      0.6280
## TG(18:2/18:2/18:2)     -0.055400  -0.2020  9.07e-02     22.1  0.457000      0.6370
## TG(51:2)               -0.034000  -0.1290  6.07e-02     21.6  0.481000      0.6560
## PC(35:1)               -0.028500  -0.1080  5.12e-02     21.8  0.483000      0.6560
## PC(36:2)               -0.020600  -0.0809  3.97e-02     26.1  0.502000      0.6740
## PC(34:1)                0.022400  -0.0488  9.36e-02     25.9  0.537000      0.7110
## PC(O-34:2)             -0.033900  -0.1460  7.78e-02     21.5  0.551000      0.7150
## TG(46:0)                0.042100  -0.0973  1.81e-01     20.4  0.553000      0.7150
## TG(52:5)               -0.046200  -0.2050  1.13e-01     19.8  0.568000      0.7260
## SM(d34:1)              -0.008390  -0.0388  2.20e-02     24.9  0.589000      0.7350
## SM(42:2)               -0.013500  -0.0624  3.55e-02     25.2  0.590000      0.7350
## TG(51:3)               -0.028900  -0.1400  8.23e-02     20.7  0.610000      0.7460
## PC(33:1)                0.024000  -0.0688  1.17e-01     20.9  0.612000      0.7460
## PC(32:0)                0.010800  -0.0364  5.80e-02     22.5  0.654000      0.7800
## SM(d32:1)               0.014200  -0.0480  7.63e-02     22.3  0.655000      0.7800
## PC(38:3)               -0.014800  -0.0914  6.18e-02     24.0  0.705000      0.8300
## PC(36:5)               -0.028300  -0.1820  1.25e-01     24.3  0.717000      0.8350
## PC(38:2)                0.011600  -0.0590  8.22e-02     21.3  0.748000      0.8610
```

```
## TG(49:2)                 0.013700   -0.0791   1.06e-01      20.4   0.772000      0.8800
## PC(40:7)                -0.012500   -0.1090   8.45e-02      21.4   0.801000      0.9030
## PC(37:2)                -0.009400   -0.1190   1.00e-01      19.3   0.867000      0.9610
## TG(14:0/18:2/18:2)      -0.011200   -0.1470   1.25e-01      21.2   0.872000      0.9610
## LPC(16:1)                0.008170   -0.1000   1.17e-01      20.0   0.882000      0.9610
## TG(50:1)                 0.008810   -0.1150   1.32e-01      24.3   0.889000      0.9610
## TG(50:3)                 0.004710   -0.0734   8.28e-02      23.5   0.906000      0.9670
## PC(34:3)                 0.007930   -0.1330   1.49e-01      22.5   0.912000      0.9670
## SM(d18:2/24:1)          -0.002360   -0.0589   5.42e-02      24.0   0.935000      0.9750
## PC(36:3)                 0.002540   -0.0751   8.01e-02      25.6   0.949000      0.9750
## TG(54:6)                 0.005130   -0.1540   1.64e-01      19.5   0.949000      0.9750
## TG(49:3)                 0.000334   -0.0140   1.47e-02      20.7   0.963000      0.9750
## PC(35:2)                -0.001960   -0.0923   8.83e-02      21.8   0.966000      0.9750
## TG(49:1)                -0.001130   -0.1070   1.04e-01      20.9   0.983000      0.9830
##
##
## Table: Coefficients for GroupT1D Macro
## Results of the adjusted model for albuminuria group variable.
## Shown in the table are name of the lipid (Name),
## model coefficient (Coefficient),
## its lower and upper confidence intervals (CI.L, CL.R),
## average value of the variable (AveExpr),
## p-value of the coefficient (P.Value) and
## the p-value after correction for multiple testing (adj.P.Val).
## The rows of the table are shown in an increasing order by the respective p-value.
##
## Name                    Coefficient        CI.L        CI.R   AveExpr     P.Value   adj.P.Val
## -------------------  ------------  ---------  ---------  --------  ---------  ----------
## SM(d40:1)                 -0.15600   -0.22000   -0.09170      24.0   2.20e-06    0.000228
## SM(d18:1/24:0)            -0.15300   -0.22300   -0.08330      23.6   1.95e-05    0.001030
## SM(d41:1)                 -0.17000   -0.25000   -0.08920      22.7   3.93e-05    0.001390
## SM(d38:1)                 -0.13100   -0.19400   -0.06700      23.1   6.16e-05    0.001630
## SM(d40:2)                 -0.11200   -0.16900   -0.05470      23.7   1.29e-04    0.002740
## TG(54:2)                  -0.19600   -0.30500   -0.08640      23.4   4.72e-04    0.008340
## SM(d38:2)                 -0.12400   -0.19500   -0.05220      21.3   7.12e-04    0.009630
## SM(d39:1)                 -0.17600   -0.27700   -0.07400      21.1   7.27e-04    0.009630
## PC(O-34:3)                -0.14700   -0.23800   -0.05570      21.9   1.65e-03    0.019400
## TG(52:2)                  -0.07900   -0.12900   -0.02880      22.6   2.08e-03    0.022000
## PC(O-36:2)                -0.14100   -0.23300   -0.04940      20.5   2.62e-03    0.024600
## SM(d36:2)                 -0.09670   -0.16000   -0.03350      21.4   2.78e-03    0.024600
## TG(52:3)                  -0.08990   -0.14900   -0.03050      22.3   3.07e-03    0.025000
## SM(d36:1)                 -0.08050   -0.13600   -0.02490      23.4   4.60e-03    0.034800
## SM(d41:2)                 -0.10700   -0.18300   -0.03040      22.5   6.21e-03    0.043900
## TG(54:3)                  -0.10600   -0.18300   -0.02850      21.7   7.32e-03    0.047100
## TG(53:2)                  -0.17300   -0.29900   -0.04620      20.7   7.55e-03    0.047100
## PC(O-38:6)                -0.10900   -0.19100   -0.02650      20.4   9.58e-03    0.054300
## SM(d16:1/18:1)            -0.07150   -0.12600   -0.01740      22.8   9.72e-03    0.054300
## PC(O-38:4)                -0.13400   -0.23900   -0.02890      21.7   1.25e-02    0.064900
## PC(O-36:5)                -0.11300   -0.20200   -0.02400      22.3   1.29e-02    0.064900
## PC(O-36:3)                -0.12100   -0.21700   -0.02450      20.4   1.40e-02    0.066800
## TG(18:2/18:1/18:1)        -0.14500   -0.26100   -0.02880      24.4   1.46e-02    0.066800
## TG(18:1/18:1/18:1)        -0.13700   -0.24700   -0.02650      24.8   1.51e-02    0.066800
## TG(56:5)                  -0.13900   -0.25900   -0.01850      20.3   2.38e-02    0.101000
## TG(16:0/22:5/18:1)        -0.13800   -0.25900   -0.01760      22.7   2.47e-02    0.101000
```

```
## TG(54:4)                 -0.11400   -0.21600   -0.01120      21.4   2.97e-02    0.117000
## TG(56:6)                 -0.10900   -0.21700   -0.00229      19.9   4.53e-02    0.172000
## PC(35:1)                 -0.08650   -0.17500    0.00197      21.8   5.53e-02    0.198000
## TG(51:1)                 -0.12700   -0.25800    0.00326      20.3   5.60e-02    0.198000
## TG(16:0/18:0/18:1)       -0.15600   -0.33000    0.01800      23.1   7.89e-02    0.263000
## SM(d33:1)                -0.06590   -0.14000    0.00828      21.3   8.16e-02    0.263000
## TG(16:0/18:2/18:2)       -0.11000   -0.23500    0.01400      24.5   8.20e-02    0.263000
## TG(50:0)                 -0.15700   -0.33600    0.02190      20.8   8.54e-02    0.266000
## PC(34:2)                  0.13500   -0.02000    0.29000      26.0   8.78e-02    0.266000
## PC(35:2)                 -0.08590   -0.18600    0.01430      21.8   9.28e-02    0.267000
## TG(52:4)                 -0.08160   -0.17700    0.01390      21.7   9.37e-02    0.267000
## TG(53:3)                 -0.10600   -0.23000    0.01870      20.7   9.56e-02    0.267000
## PC(38:3)                 -0.07020   -0.15500    0.01490      24.0   1.06e-01    0.284000
## TG(50:3)                 -0.07080   -0.15800    0.01590      23.5   1.09e-01    0.284000
## PC(36:3)                 -0.07010   -0.15600    0.01600      25.6   1.10e-01    0.284000
## TG(18:0/18:1/20:4)       -0.15600   -0.34900    0.03690      21.3   1.13e-01    0.284000
## PC(38:4)                 -0.04720   -0.10600    0.01160      25.2   1.15e-01    0.284000
## PC(16:0e/18:1(9Z)        -0.06180   -0.14000    0.01630      21.8   1.21e-01    0.289000
## TG(56:4)                 -0.12400   -0.28100    0.03340      20.0   1.23e-01    0.289000
## TG(51:2)                 -0.08060   -0.18600    0.02450      21.6   1.33e-01    0.304000
## TG(18:1/18:2/18:2)       -0.11200   -0.25800    0.03480      23.6   1.35e-01    0.304000
## PC(O-36:4)               -0.06740   -0.16200    0.02680      22.9   1.61e-01    0.355000
## TG(54:5)                 -0.09120   -0.22300    0.04010      20.6   1.73e-01    0.374000
## TG(53:4)                 -0.10300   -0.25400    0.04760      19.7   1.79e-01    0.380000
## PC(O-38:5)               -0.05360   -0.13300    0.02610      22.7   1.87e-01    0.389000
## PC(38:5)                 -0.03420   -0.08780    0.01930      24.5   2.10e-01    0.428000
## LPC(20:4)                -0.07590   -0.19800    0.04620      21.4   2.23e-01    0.445000
## TG(51:3)                 -0.07460   -0.19800    0.04890      20.7   2.36e-01    0.459000
## PC(36:5)                 -0.10200   -0.27300    0.06800      24.3   2.38e-01    0.459000
## LPC(18:2)                -0.07270   -0.19600    0.05020      24.0   2.46e-01    0.459000
## TG(18:2/18:1/16:0)       -0.05800   -0.15600    0.04040      25.3   2.48e-01    0.459000
## LPC(16:1)                 0.06960   -0.05080    0.19000      20.0   2.57e-01    0.459000
## TG(18:1/18:1/16:0)       -0.06500   -0.17800    0.04750      25.6   2.57e-01    0.459000
## TG(49:1)                 -0.06720   -0.18400    0.04980      20.9   2.60e-01    0.459000
## TG(56:3)                 -0.06900   -0.19900    0.06140      19.9   2.99e-01    0.520000
## TG(14:0/18:1/18:1)       -0.04600   -0.13500    0.04280      24.4   3.10e-01    0.529000
## TG(16:0/18:2/22:6)       -0.15400   -0.46400    0.15600      21.0   3.29e-01    0.554000
## TG(49:3)                  0.00773   -0.00817    0.02360      20.7   3.40e-01    0.563000
## SM(42:2)                 -0.02470   -0.07900    0.02970      25.2   3.73e-01    0.608000
## PC(33:1)                 -0.04620   -0.14900    0.05680      20.9   3.79e-01    0.609000
## TG(14:0/18:2/18:2)       -0.06500   -0.21600    0.08580      21.2   3.98e-01    0.621000
## SM(d18:2/24:1)           -0.02680   -0.08950    0.03600      24.0   4.03e-01    0.621000
## TG(50:1)                 -0.05820   -0.19500    0.07880      24.3   4.04e-01    0.621000
## TG(49:2)                 -0.04150   -0.14400    0.06150      20.4   4.29e-01    0.650000
## PC(37:2)                 -0.04710   -0.16900    0.07480      19.3   4.48e-01    0.669000
## PC(40:5)                 -0.03600   -0.13200    0.06010      22.0   4.62e-01    0.680000
## SM(d32:1)                -0.02510   -0.09410    0.04400      22.3   4.76e-01    0.691000
## TG(45:0)                  0.01350   -0.02450    0.05140      23.1   4.86e-01    0.696000
## PC(32:0)                  0.01720   -0.03520    0.06960      22.5   5.20e-01    0.735000
## PC(38:6)                 -0.02340   -0.09680    0.04990      25.3   5.31e-01    0.740000
## PC(36:2)                 -0.02050   -0.08750    0.04640      26.1   5.48e-01    0.754000
## PC(40:6)                 -0.03230   -0.14000    0.07540      23.9   5.56e-01    0.755000
## TG(50:2)                 -0.02210   -0.09790    0.05380      21.2   5.68e-01    0.763000
## TG(18:2/18:2/18:2)       -0.04380   -0.20600    0.11800      22.1   5.96e-01    0.782000
```

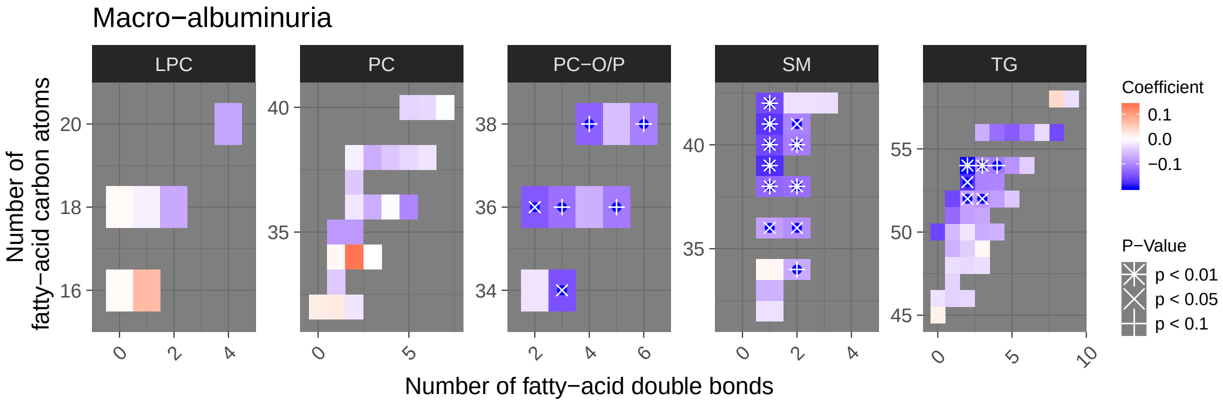
```
## TG(52:5)                 -0.04690   -0.22300    0.13000      19.8   6.02e-01    0.782000
## SM(d34:1)                 0.00869   -0.02510    0.04250      24.9   6.14e-01    0.782000
## TG(46:1)                 -0.03820   -0.19700    0.12000      21.3   6.36e-01    0.782000
## TG(16:0/18:2/18:3)       -0.04950   -0.25500    0.15600      22.0   6.37e-01    0.782000
## TG(56:7)                 -0.03090   -0.16100    0.09920      19.6   6.41e-01    0.782000
## TG(18:1/12:0/18:1)       -0.03200   -0.16700    0.10300      22.5   6.41e-01    0.782000
## TG(54:6)                 -0.04180   -0.21800    0.13500      19.5   6.42e-01    0.782000
## TG(47:1)                 -0.03710   -0.20200    0.12800      19.6   6.59e-01    0.794000
## TG(46:2)                 -0.03420   -0.19700    0.12800      20.1   6.79e-01    0.809000
## TG(14:0/16:0/18:1)       -0.02720   -0.16900    0.11400      22.8   7.07e-01    0.832000
## PC(O-34:2)               -0.02290   -0.14700    0.10100      21.5   7.17e-01    0.835000
## PC(38:2)                 -0.01340   -0.09180    0.06500      21.3   7.37e-01    0.849000
## PC(32:2)                 -0.02220   -0.15800    0.11400      20.8   7.48e-01    0.851000
## TG(46:0)                 -0.02410   -0.17900    0.13100      20.4   7.60e-01    0.851000
## TG(18:2/22:5/16:0)       -0.03340   -0.25700    0.19100      22.1   7.70e-01    0.851000
## PC(32:1)                  0.02230   -0.13000    0.17400      23.3   7.74e-01    0.851000
## TG(48:3)                 -0.02680   -0.22600    0.17200      20.6   7.91e-01    0.851000
## TG(18:1/18:1/22:6)        0.03850   -0.24800    0.32500      20.7   7.92e-01    0.851000
## LPC(18:1)                -0.01240   -0.10600    0.08140      23.7   7.95e-01    0.851000
## LPC(16:0)                 0.00421   -0.03530    0.04370      25.3   8.34e-01    0.884000
## TG(58:9)                 -0.02750   -0.31600    0.26100      19.9   8.52e-01    0.886000
## PC(34:1)                  0.00749   -0.07160    0.08660      25.9   8.52e-01    0.886000
## LPC(18:0)                 0.00534   -0.06680    0.07750      24.0   8.85e-01    0.910000
## PC(36:4)                 -0.00304   -0.05490    0.04880      26.0   9.08e-01    0.926000
## PC(40:7)                 -0.00257   -0.11000    0.10500      21.4   9.63e-01    0.972000
## PC(34:3)                 -0.00029   -0.15700    0.15600      22.5   9.97e-01    0.997000
##
##
## Table: Coefficients for GroupHealthy Control
## Results of the adjusted model for albuminuria group variable.
## Shown in the table are name of the lipid (Name),
## model coefficient (Coefficient),
## its lower and upper confidence intervals (CI.L, CL.R),
## average value of the variable (AveExpr),
## p-value of the coefficient (P.Value) and
## the p-value after correction for multiple testing (adj.P.Val).
## The rows of the table are shown in an increasing order by the respective p-value.
##
## Name                  Coefficient        CI.L       CI.R   AveExpr    P.Value   adj.P.Val
## -------------------  ------------  ----------  ---------  --------  ---------  ----------
## LPC(18:1)               -0.432000   -0.584000   -0.27900      23.7   0.00e+00    4.40e-06
## PC(16:0e/18:1(9Z)       -0.316000   -0.443000   -0.18900      21.8   1.30e-06    6.70e-05
## PC(32:0)                -0.189000   -0.274000   -0.10300      22.5   1.62e-05    4.99e-04
## PC(O-36:3)              -0.344000   -0.501000   -0.18700      20.4   1.88e-05    4.99e-04
## LPC(18:2)               -0.426000   -0.626000   -0.22500      24.0   3.36e-05    7.13e-04
## PC(38:5)                -0.179000   -0.266000   -0.09200      24.5   6.07e-05    1.07e-03
## PC(O-36:2)              -0.299000   -0.449000   -0.15000      20.5   9.08e-05    1.26e-03
## PC(38:3)                 0.277000    0.138000    0.41500      24.0   9.54e-05    1.26e-03
## PC(40:7)                -0.333000   -0.508000   -0.15800      21.4   2.06e-04    2.43e-03
## PC(O-34:3)              -0.277000   -0.425000   -0.12800      21.9   2.80e-04    2.97e-03
## PC(O-38:5)              -0.236000   -0.366000   -0.10700      22.7   3.73e-04    3.60e-03
## TG(50:3)                 0.249000    0.108000    0.39000      23.5   5.58e-04    4.93e-03
## PC(36:2)                -0.185000   -0.294000   -0.07580      26.1   9.18e-04    7.49e-03
## PC(O-38:6)              -0.223000   -0.357000   -0.08960      20.4   1.09e-03    8.25e-03
```

```
## TG(16:0/18:2/18:2)     0.327000   0.124000   0.52900     24.5  1.58e-03  1.12e-02
## TG(51:3)               0.309000   0.108000   0.51000     20.7  2.59e-03  1.72e-02
## TG(53:3)               0.304000   0.102000   0.50600     20.7  3.27e-03  2.04e-02
## SM(d16:1/18:1)        -0.131000  -0.219000  -0.04300     22.8  3.59e-03  2.11e-02
## TG(52:4)               0.226000   0.070400   0.38100     21.7  4.46e-03  2.40e-02
## TG(14:0/18:2/18:2)     0.356000   0.111000   0.60200     21.2  4.53e-03  2.40e-02
## SM(d39:1)              0.229000   0.063300   0.39400     21.1  6.79e-03  3.04e-02
## TG(51:2)               0.236000   0.065100   0.40700     21.6  6.89e-03  3.04e-02
## TG(53:4)               0.338000   0.092500   0.58400     19.7  7.04e-03  3.04e-02
## SM(42:2)              -0.122000  -0.210000  -0.03330     25.2  7.05e-03  3.04e-02
## TG(45:0)              -0.084900  -0.147000  -0.02310     23.1  7.17e-03  3.04e-02
## TG(53:2)               0.281000   0.074400   0.48700     20.7  7.71e-03  3.14e-02
## TG(52:5)               0.387000   0.099900   0.67400     19.8  8.32e-03  3.22e-02
## PC(38:2)              -0.172000  -0.299000  -0.04390     21.3  8.49e-03  3.22e-02
## TG(16:0/18:2/18:3)     0.440000   0.105000   0.77500     22.0  1.01e-02  3.69e-02
## TG(52:3)               0.122000   0.025700   0.21900     22.3  1.32e-02  4.67e-02
## TG(18:2/18:2/18:2)     0.328000   0.064300   0.59200     22.1  1.49e-02  5.09e-02
## SM(d36:2)              0.125000   0.022400   0.22800     21.4  1.71e-02  5.66e-02
## SM(d18:2/24:1)        -0.122000  -0.224000  -0.02010     24.0  1.91e-02  6.01e-02
## PC(37:2)              -0.237000  -0.436000  -0.03870     19.3  1.93e-02  6.01e-02
## LPC(16:0)             -0.073200  -0.138000  -0.00888     25.3  2.58e-02  7.81e-02
## PC(O-34:2)            -0.228000  -0.430000  -0.02640     21.5  2.67e-02  7.87e-02
## LPC(16:1)             -0.208000  -0.404000  -0.01220     20.0  3.74e-02  1.07e-01
## TG(16:0/18:2/22:6)     0.514000   0.009420   1.02000     21.0  4.59e-02  1.28e-01
## TG(14:0/18:1/18:1)     0.145000   0.000898   0.29000     24.4  4.86e-02  1.32e-01
## SM(d41:1)              0.130000  -0.000909   0.26100     22.7  5.16e-02  1.37e-01
## TG(52:2)               0.077800  -0.003870   0.16000     22.6  6.19e-02  1.54e-01
## PC(O-36:4)            -0.146000  -0.299000   0.00775     22.9  6.27e-02  1.54e-01
## PC(36:5)              -0.263000  -0.540000   0.01450     24.3  6.32e-02  1.54e-01
## TG(48:3)               0.306000  -0.017700   0.63000     20.6  6.39e-02  1.54e-01
## PC(34:2)               0.234000  -0.018300   0.48600     26.0  6.90e-02  1.63e-01
## PC(40:5)              -0.144000  -0.301000   0.01240     22.0  7.11e-02  1.64e-01
## TG(18:2/22:5/16:0)     0.334000  -0.030900   0.69800     22.1  7.28e-02  1.64e-01
## TG(16:0/22:5/18:1)     0.178000  -0.018500   0.37400     22.7  7.58e-02  1.67e-01
## TG(56:5)               0.170000  -0.026100   0.36500     20.3  8.93e-02  1.93e-01
## TG(18:2/18:1/16:0)     0.138000  -0.022400   0.29800     25.3  9.18e-02  1.95e-01
## PC(33:1)              -0.141000  -0.309000   0.02640     20.9  9.86e-02  2.03e-01
## PC(38:4)               0.080000  -0.015700   0.17600     25.2  1.01e-01  2.03e-01
## TG(46:0)              -0.210000  -0.462000   0.04170     20.4  1.02e-01  2.03e-01
## SM(d38:1)              0.085800  -0.017700   0.18900     23.1  1.04e-01  2.04e-01
## TG(56:3)              -0.173000  -0.386000   0.03900     19.9  1.09e-01  2.11e-01
## TG(54:6)               0.221000  -0.065800   0.50800     19.5  1.31e-01  2.47e-01
## PC(34:3)              -0.195000  -0.450000   0.05960     22.5  1.33e-01  2.47e-01
## PC(32:1)              -0.188000  -0.435000   0.06000     23.3  1.37e-01  2.51e-01
## TG(18:1/12:0/18:1)     0.164000  -0.055100   0.38300     22.5  1.42e-01  2.55e-01
## PC(35:1)              -0.106000  -0.250000   0.03810     21.8  1.49e-01  2.64e-01
## PC(38:6)              -0.084200  -0.204000   0.03530     25.3  1.67e-01  2.89e-01
## TG(18:1/18:1/16:0)     0.128000  -0.054700   0.31200     25.6  1.69e-01  2.89e-01
## TG(18:1/18:2/18:2)     0.156000  -0.082800   0.39400     23.6  2.00e-01  3.37e-01
## TG(54:3)              -0.080400  -0.206000   0.04510     21.7  2.09e-01  3.46e-01
## TG(56:7)               0.132000  -0.079900   0.34300     19.6  2.22e-01  3.62e-01
## TG(18:0/18:1/20:4)     0.193000  -0.122000   0.50700     21.3  2.29e-01  3.68e-01
## PC(O-36:5)            -0.085700  -0.230000   0.05900     22.3  2.45e-01  3.88e-01
## TG(50:2)               0.068100  -0.055400   0.19200     21.2  2.79e-01  4.35e-01
```

```
## TG(51:1)                 0.109000   -0.103000    0.32200      20.3   3.13e-01    4.81e-01
## LPC(18:0)               -0.058000   -0.175000    0.05940      24.0   3.32e-01    5.03e-01
## PC(35:2)                -0.078600   -0.242000    0.08450      21.8   3.44e-01    5.08e-01
## SM(d36:1)                0.043600   -0.046900    0.13400      23.4   3.45e-01    5.08e-01
## SM(d41:2)                0.058600   -0.065600    0.18300      22.5   3.55e-01    5.15e-01
## TG(49:2)                 0.076100   -0.091500    0.24400      20.4   3.73e-01    5.34e-01
## TG(49:3)                -0.011300   -0.037200    0.01460      20.7   3.92e-01    5.54e-01
## TG(56:4)                -0.110000   -0.365000    0.14600      20.0   4.00e-01    5.58e-01
## LPC(20:4)               -0.080700   -0.279000    0.11800      21.4   4.25e-01    5.84e-01
## SM(d40:1)                0.041900   -0.062100    0.14600      24.0   4.29e-01    5.84e-01
## TG(58:9)                 0.182000   -0.288000    0.65300      19.9   4.47e-01    5.99e-01
## TG(47:1)                -0.097400   -0.366000    0.17100      19.6   4.77e-01    6.32e-01
## TG(14:0/16:0/18:1)       0.075300   -0.155000    0.30600      22.8   5.21e-01    6.82e-01
## TG(50:1)                 0.070700   -0.152000    0.29400      24.3   5.34e-01    6.83e-01
## PC(36:3)                 0.044300   -0.095900    0.18500      25.6   5.35e-01    6.83e-01
## TG(54:5)                 0.064500   -0.149000    0.27800      20.6   5.53e-01    6.98e-01
## TG(18:2/18:1/18:1)       0.049600   -0.140000    0.23900      24.4   6.07e-01    7.39e-01
## PC(O-38:4)              -0.044100   -0.215000    0.12700      21.7   6.13e-01    7.39e-01
## TG(56:6)                 0.044900   -0.130000    0.21900      19.9   6.13e-01    7.39e-01
## PC(36:4)                 0.021700   -0.062700    0.10600      26.0   6.14e-01    7.39e-01
## TG(18:1/18:1/18:1)      -0.043200   -0.223000    0.13600      24.8   6.37e-01    7.58e-01
## TG(54:2)                -0.041900   -0.220000    0.13600      23.4   6.45e-01    7.59e-01
## TG(50:0)                -0.051900   -0.343000    0.23900      20.8   7.26e-01    8.46e-01
## PC(32:2)                 0.035500   -0.186000    0.25700      20.8   7.53e-01    8.67e-01
## SM(d34:1)               -0.008540   -0.063500    0.04650      24.9   7.61e-01    8.67e-01
## SM(d40:2)                0.012200   -0.080500    0.10500      23.7   7.96e-01    8.98e-01
## PC(40:6)                 0.016400   -0.159000    0.19200      23.9   8.54e-01    9.53e-01
## SM(d18:1/24:0)          -0.009170   -0.123000    0.10500      23.6   8.74e-01    9.66e-01
## PC(34:1)                -0.009240   -0.138000    0.11900      25.9   8.88e-01    9.70e-01
## TG(46:1)                -0.016800   -0.275000    0.24100      21.3   8.99e-01    9.72e-01
## TG(18:1/18:1/22:6)       0.025400   -0.441000    0.49200      20.7   9.15e-01    9.79e-01
## SM(d38:2)               -0.004960   -0.121000    0.11100      21.3   9.33e-01    9.80e-01
## TG(46:2)                 0.011200   -0.253000    0.27600      20.1   9.34e-01    9.80e-01
## TG(54:4)                -0.005690   -0.173000    0.16100      21.4   9.47e-01    9.81e-01
## TG(16:0/18:0/18:1)       0.007630   -0.276000    0.29100      23.1   9.58e-01    9.81e-01
## SM(d33:1)               -0.002860   -0.124000    0.11800      21.3   9.63e-01    9.81e-01
## SM(d32:1)                0.001890   -0.110000    0.11400      22.3   9.74e-01    9.83e-01
## TG(49:1)                -0.000983   -0.191000    0.19000      20.9   9.92e-01    9.92e-01
```

1.1.1.2.2 Heatmaps

```
## [1] "map_lipid_names has been created by Tommi Suvitaival"
## [1] "tommi.raimo.leo.suvitaival@regionh.dk"
## [1] "2019-05-06"
```



```
##   Label Relation p.adj
## 1     #  p.adj <  0.01
## 2     x  p.adj <  0.05
## 3     *  p.adj <  0.10
```

```
##   Label Relation p.adj
## 1     #  p.adj <  0.01
## 2     x  p.adj <  0.05
## 3     *  p.adj <  0.10
```

```
##   Label Relation p.adj
## 1     #  p.adj <  0.01
## 2     x  p.adj <  0.05
## 3     *  p.adj <  0.10
```

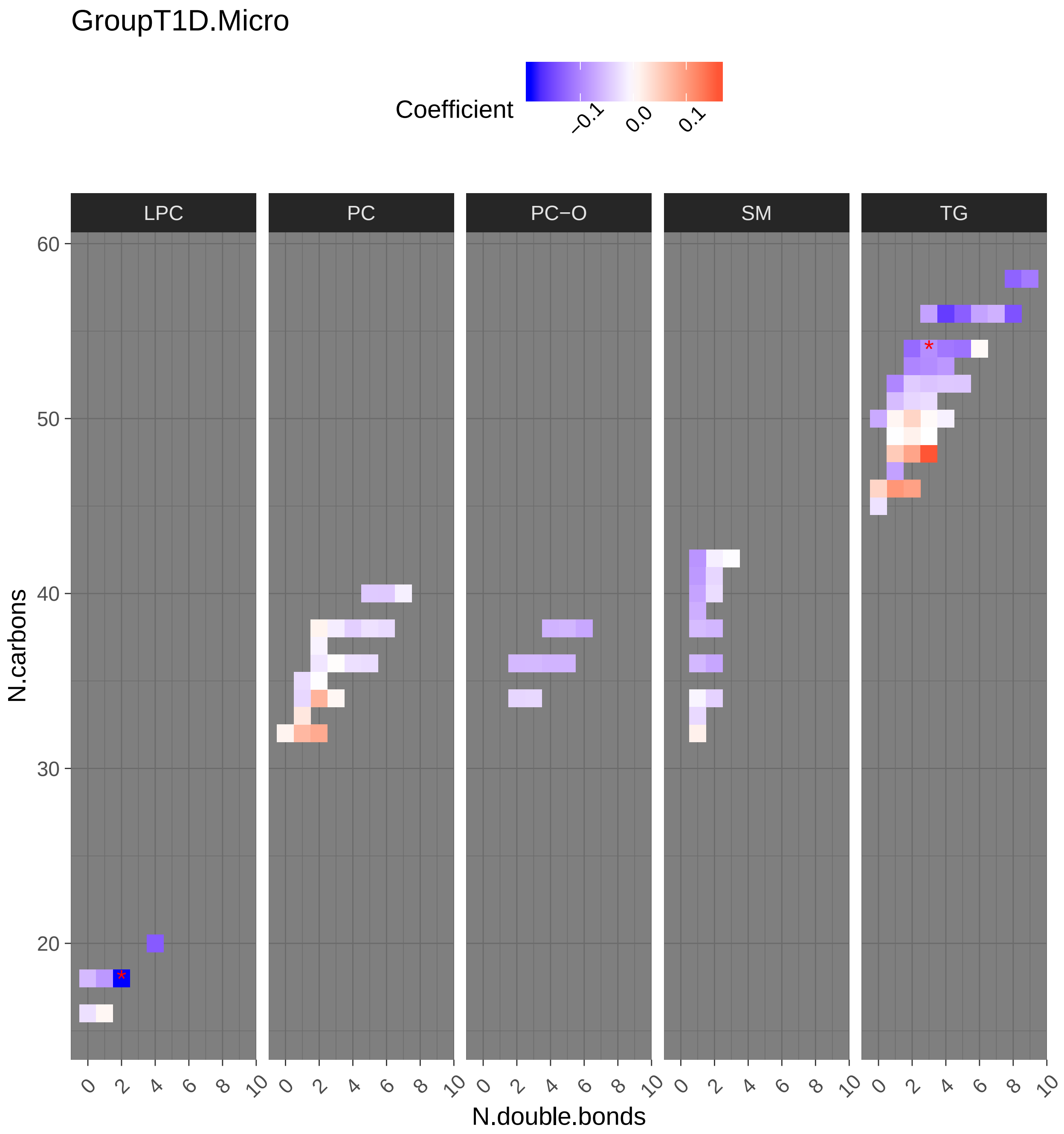


Figure 4: Heatmap of the lipid-specific model coefficents from the adjusted model for albuminuria groups. The name of the group is shown in the title of the figure in the top-left corner. Lipids are organized into panels (columns) by their class (from LPC to TG). One colored rectangle corresponds to one lipid species, where the coordinates in the x-axis and y-axis, respectively, show the number of double bonds (N.double.bonds) and the number of carbon atoms (N.carbons) in the fatty acid chains of the lipid. The number of double bonds corresponds to the number of unsaturated bonds in the fatty acid chains, and the number of carbon atoms corresponds to the length of the fatty acid chains and, thus, the size of the lipid. The magnitude of the lipid-specifc model coefficient is shown as the color of the rectangle (blue: negative; red: positive). Coefficient with statistical significance are annotated with symbols #, x and *, respectively, corresponding to $p < 0.01$, $p < 0.05$ and $p < 0.1$.

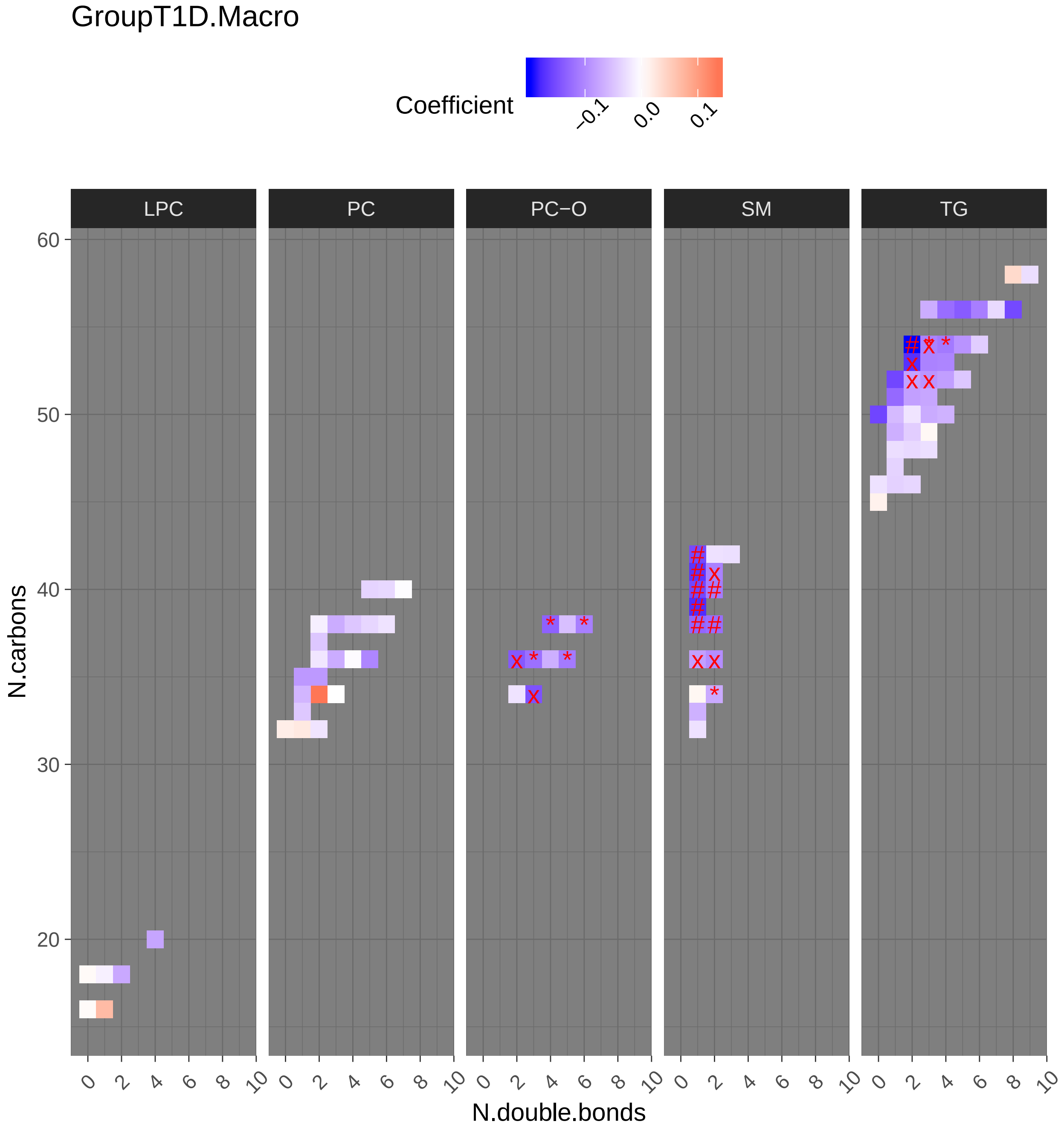


Figure 5: Heatmap of the lipid-specific model coefficents from the adjusted model for albuminuria groups. The name of the group is shown in the title of the figure in the top-left corner. Lipids are organized into panels (columns) by their class (from LPC to TG). One colored rectangle corresponds to one lipid species, where the coordinates in the x-axis and y-axis, respectively, show the number of double bonds (N.double.bonds) and the number of carbon atoms (N.carbons) in the fatty acid chains of the lipid. The number of double bonds corresponds to the number of unsaturated bonds in the fatty acid chains, and the number of carbon atoms corresponds to the length of the fatty acid chains and, thus, the size of the lipid. The magnitude of the lipid-specifc model coefficient is shown as the color of the rectangle (blue: negative; red: positive). Coefficient with statistical significance are annotated with symbols #, x and *, respectively, corresponding to $p < 0.01$, $p < 0.05$ and $p < 0.1$.

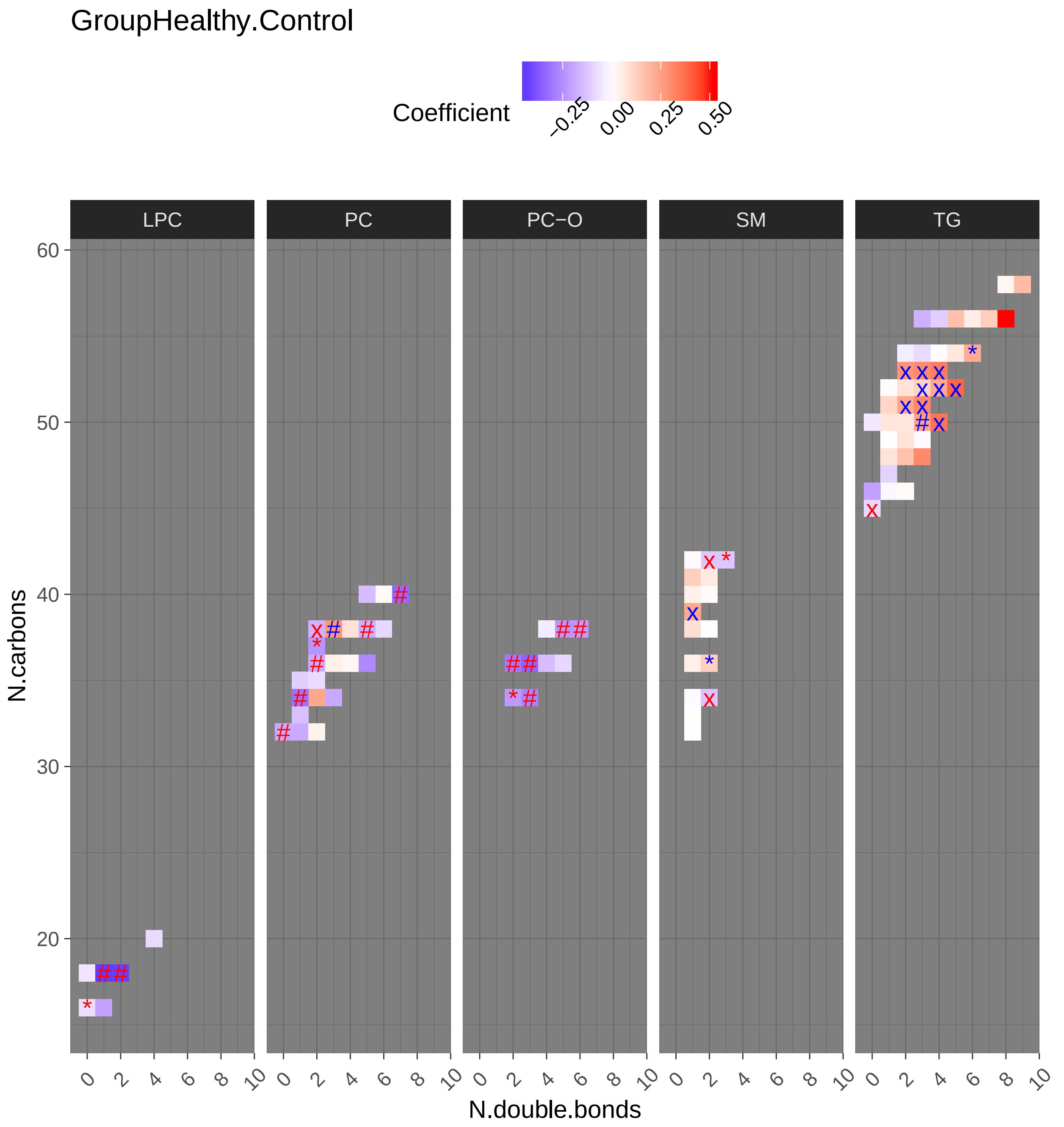


Figure 6: Heatmap of the lipid-specific model coefficents from the adjusted model for albuminuria groups. The name of the group is shown in the title of the figure in the top-left corner. Lipids are organized into panels (columns) by their class (from LPC to TG). One colored rectangle corresponds to one lipid species, where the coordinates in the x-axis and y-axis, respectively, show the number of double bonds (N.double.bonds) and the number of carbon atoms (N.carbons) in the fatty acid chains of the lipid. The number of double bonds corresponds to the number of unsaturated bonds in the fatty acid chains, and the number of carbon atoms corresponds to the length of the fatty acid chains and, thus, the size of the lipid. The magnitude of the lipid-specifc model coefficient is shown as the color of the rectangle (blue: negative; red: positive). Coefficient with statistical significance are annotated with symbols #, x and *, respectively, corresponding to $p < 0.01$, $p < 0.05$ and $p < 0.1$.

1.1.2 eGFR

1.1.2.1 Crude Model

1.1.2.1.1 Table

```
##
##
## Table: egfr.intervals
##
## Name                   Coefficient        CI.L        CI.R   AveExpr    P.Value   adj.P.Val
## -------------------  ------------  ----------  ----------  --------  ---------  ----------
## SM(d18:1/24:0)           4.99e-02    0.027900    0.071800      23.5   9.50e-06     0.00101
## SM(d36:2)               -3.95e-02   -0.057600   -0.021400      21.4   2.07e-05     0.00110
## SM(d34:1)               -1.75e-02   -0.026800   -0.008130      24.9   2.59e-04     0.00914
## SM(d40:1)                3.75e-02    0.016600    0.058400      23.9   4.63e-04     0.01230
## LPC(18:2)                5.60e-02    0.024000    0.088100      24.0   6.30e-04     0.01340
## TG(18:0/18:1/20:4)      -8.50e-02   -0.136000   -0.034500      21.3   1.01e-03     0.01780
## PC(38:4)                -2.52e-02   -0.040700   -0.009640      25.2   1.53e-03     0.02320
## SM(d32:1)               -3.35e-02   -0.054500   -0.012600      22.3   1.78e-03     0.02360
## SM(d16:1/18:1)          -2.97e-02   -0.048800   -0.010600      22.8   2.37e-03     0.02790
## PC(32:2)                 5.74e-02    0.019900    0.094900      20.7   2.76e-03     0.02930
## LPC(16:0)                1.55e-02    0.004800    0.026100      25.3   4.53e-03     0.04370
## PC(O-34:3)               3.81e-02    0.011300    0.064800      21.9   5.34e-03     0.04720
## TG(54:3)                -3.88e-02   -0.066500   -0.011000      21.7   6.28e-03     0.05120
## SM(d33:1)               -2.98e-02   -0.051500   -0.008060      21.3   7.29e-03     0.05520
## SM(d18:2/24:1)          -2.58e-02   -0.044800   -0.006820      24.0   7.81e-03     0.05520
## TG(53:2)                -6.54e-02   -0.115000   -0.015700      20.7   1.01e-02     0.06670
## SM(d41:1)                3.23e-02    0.007470    0.057100      22.7   1.08e-02     0.06760
## TG(52:3)                -2.53e-02   -0.047600   -0.003000      22.3   2.62e-02     0.14700
## TG(54:4)                -3.64e-02   -0.068400   -0.004300      21.4   2.63e-02     0.14700
## TG(52:2)                -2.30e-02   -0.043900   -0.002020      22.6   3.17e-02     0.16600
## TG(53:3)                -5.03e-02   -0.097100   -0.003530      20.7   3.51e-02     0.16600
## TG(56:3)                -5.03e-02   -0.097200   -0.003300      20.0   3.60e-02     0.16600
## TG(53:4)                -5.46e-02   -0.106000   -0.003390      19.7   3.67e-02     0.16600
## TG(18:2/18:1/18:1)      -3.95e-02   -0.077200   -0.001880      24.4   3.96e-02     0.16600
## TG(56:4)                -5.62e-02   -0.110000   -0.002470      20.0   4.04e-02     0.16600
## TG(52:4)                -3.46e-02   -0.067800   -0.001460      21.6   4.08e-02     0.16600
## PC(34:2)                -3.92e-02   -0.077200   -0.001170      26.0   4.34e-02     0.17000
## LPC(18:1)                2.42e-02    0.000366    0.048000      23.7   4.66e-02     0.17600
## TG(51:2)                -4.37e-02   -0.088300    0.000787      21.6   5.42e-02     0.19800
## PC(36:5)                 4.60e-02   -0.001160    0.093200      24.3   5.59e-02     0.19800
## TG(54:2)                -4.29e-02   -0.088600    0.002750      23.4   6.54e-02     0.22400
## TG(45:0)                 1.55e-02   -0.001290    0.032300      23.1   7.03e-02     0.23300
## LPC(16:1)                2.76e-02   -0.003240    0.058400      20.0   7.93e-02     0.25500
## TG(18:1/18:1/18:1)      -3.19e-02   -0.067900    0.004160      24.8   8.29e-02     0.25800
## TG(56:6)                -2.72e-02   -0.058700    0.004350      19.9   9.11e-02     0.27300
## LPC(18:0)                1.63e-02   -0.002830    0.035400      23.9   9.48e-02     0.27300
## TG(18:1/18:1/16:0)      -2.41e-02   -0.052500    0.004360      25.6   9.68e-02     0.27300
## TG(16:0/22:5/18:1)      -3.28e-02   -0.071700    0.006050      22.7   9.78e-02     0.27300
## PC(O-36:5)               1.84e-02   -0.003820    0.040700      22.3   1.04e-01     0.28300
## TG(16:0/18:2/18:2)      -3.66e-02   -0.081400    0.008260      24.5   1.10e-01     0.28900
## PC(34:3)                 3.43e-02   -0.007980    0.076600      22.5   1.12e-01     0.28900
## TG(51:3)                -3.67e-02   -0.082600    0.009220      20.7   1.17e-01     0.29500
## PC(38:6)                 1.61e-02   -0.004440    0.036700      25.3   1.24e-01     0.30400
## SM(d41:2)               -1.80e-02   -0.041200    0.005090      22.5   1.26e-01     0.30400
## PC(O-34:2)               2.37e-02   -0.008900    0.056300      21.5   1.54e-01     0.36200
## TG(16:0/18:2/18:3)      -4.74e-02   -0.114000    0.018600      22.0   1.59e-01     0.36700
```

```
## PC(32:0)              1.01e-02  -0.004620  0.024800     22.5 1.78e-01    0.40300
## PC(38:2)              1.49e-02  -0.007570  0.037300     21.2 1.94e-01    0.42800
## PC(32:1)              2.73e-02  -0.014500  0.069200     23.3 2.00e-01    0.43100
## TG(50:3)             -2.68e-02  -0.068200  0.014700     23.5 2.06e-01    0.43100
## TG(18:2/18:1/16:0)   -1.62e-02  -0.041700  0.009230     25.3 2.11e-01    0.43100
## TG(52:5)             -3.37e-02  -0.087100  0.019800     19.8 2.16e-01    0.43100
## SM(d38:2)            -1.32e-02  -0.034100  0.007770     21.3 2.17e-01    0.43100
## SM(d36:1)            -1.06e-02  -0.027400  0.006320     23.4 2.20e-01    0.43100
## TG(56:5)             -2.50e-02  -0.065200  0.015300     20.3 2.24e-01    0.43200
## TG(54:5)             -2.39e-02  -0.063100  0.015400     20.6 2.33e-01    0.43600
## SM(d38:1)             1.18e-02  -0.007730  0.031400     23.1 2.35e-01    0.43600
## TG(18:1/18:2/18:2)   -2.78e-02  -0.074200  0.018500     23.6 2.39e-01    0.43600
## TG(51:1)             -2.81e-02  -0.075600  0.019300     20.3 2.45e-01    0.44000
## SM(d40:2)            -1.06e-02  -0.029000  0.007800     23.7 2.58e-01    0.45600
## PC(37:2)              1.93e-02  -0.014700  0.053300     19.3 2.66e-01    0.46200
## TG(14:0/18:1/18:1)   -2.09e-02  -0.059400  0.017600     24.4 2.87e-01    0.49000
## TG(49:2)             -1.72e-02  -0.051400  0.016900     20.4 3.22e-01    0.54000
## TG(49:1)             -1.90e-02  -0.056900  0.018900     20.9 3.26e-01    0.54000
## TG(50:2)             -1.54e-02  -0.047100  0.016300     21.1 3.40e-01    0.55400
## TG(18:1/18:1/22:6)    3.08e-02  -0.044000  0.106000     20.7 4.19e-01    0.67300
## TG(14:0/18:2/18:2)   -2.39e-02  -0.083300  0.035500     21.2 4.30e-01    0.67500
## TG(56:7)             -1.43e-02  -0.050400  0.021800     19.6 4.36e-01    0.67500
## PC(38:5)             -5.68e-03  -0.020100  0.008740     24.6 4.39e-01    0.67500
## PC(O-38:5)           -7.79e-03  -0.027800  0.012300     22.8 4.46e-01    0.67500
## PC(O-36:4)            8.91e-03  -0.014800  0.032600     22.9 4.61e-01    0.68900
## TG(46:0)              1.66e-02  -0.030300  0.063500     20.4 4.88e-01    0.70800
## PC(O-36:3)            1.00e-02  -0.018400  0.038400     20.4 4.88e-01    0.70800
## PC(35:1)             -8.50e-03  -0.033700  0.016700     21.8 5.08e-01    0.72700
## TG(50:1)             -1.63e-02  -0.066100  0.033400     24.3 5.19e-01    0.72700
## TG(47:1)             -1.33e-02  -0.054100  0.027500     19.6 5.21e-01    0.72700
## LPC(20:4)             9.80e-03  -0.021700  0.041300     21.4 5.41e-01    0.74500
## PC(33:1)              8.44e-03  -0.021000  0.037900     20.9 5.74e-01    0.78000
## TG(16:0/18:0/18:1)   -1.75e-02  -0.080000  0.045100     23.1 5.84e-01    0.78300
## PC(34:1)             -4.92e-03  -0.024400  0.014600     26.0 6.20e-01    0.82200
## PC(40:6)              7.53e-03  -0.023500  0.038500     23.9 6.33e-01    0.82900
## PC(36:3)              5.14e-03  -0.017800  0.028000     25.6 6.60e-01    0.85300
## TG(58:9)              1.56e-02  -0.058800  0.090000     19.9 6.81e-01    0.86900
## TG(16:0/18:2/22:6)    1.68e-02  -0.065700  0.099300     21.0 6.90e-01    0.87100
## PC(O-38:6)            4.03e-03  -0.017900  0.026000     20.4 7.18e-01    0.89600
## SM(d39:1)             4.24e-03  -0.024600  0.033100     21.1 7.73e-01    0.94500
## PC(16:0e/18:1(9Z)    -3.23e-03  -0.025500  0.019000     21.8 7.75e-01    0.94500
## PC(36:2)              1.82e-03  -0.012500  0.016100     26.1 8.02e-01    0.94900
## TG(54:6)             -6.60e-03  -0.059300  0.046100     19.5 8.06e-01    0.94900
## TG(18:1/12:0/18:1)   -6.27e-03  -0.056300  0.043800     22.5 8.06e-01    0.94900
## TG(48:3)             -7.66e-03  -0.074700  0.059400     20.5 8.23e-01    0.95500
## TG(46:2)             -5.66e-03  -0.059000  0.047700     20.1 8.35e-01    0.95500
## PC(O-36:2)           -2.65e-03  -0.028100  0.022800     20.5 8.38e-01    0.95500
## PC(40:5)              2.60e-03  -0.024500  0.029700     22.0 8.50e-01    0.95900
## PC(40:7)              2.19e-03  -0.028100  0.032400     21.4 8.87e-01    0.98700
## TG(14:0/16:0/18:1)    3.42e-03  -0.046800  0.053700     22.8 8.94e-01    0.98700
## PC(O-38:4)           -1.34e-03  -0.028000  0.025400     21.7 9.22e-01    0.99900
## TG(50:0)             -1.95e-03  -0.058700  0.054800     20.8 9.46e-01    0.99900
## SM(42:2)             -4.21e-04  -0.016800  0.016000     25.2 9.60e-01    0.99900
## PC(35:2)             -6.49e-04  -0.027700  0.026400     21.8 9.63e-01    0.99900
```

```
## PC(38:3)              -5.76e-04   -0.025300    0.024100      24.0   9.63e-01     0.99900
## TG(49:3)              -4.00e-05   -0.005670    0.005590      20.7   9.89e-01     0.99900
## PC(36:4)               6.80e-05   -0.012600    0.012700      25.9   9.92e-01     0.99900
## TG(46:1)               2.32e-04   -0.049500    0.050000      21.3   9.93e-01     0.99900
## TG(18:2/22:5/16:0)    -2.18e-04   -0.064100    0.063700      22.1   9.95e-01     0.99900
## TG(18:2/18:2/18:2)     2.08e-05   -0.051000    0.051000      22.1   9.99e-01     0.99900
##
##
## Table: Results of the crude model for eGFR variable.
## Shown in the table are name of the lipid (Name),
## model coefficient (Coefficient),
## its lower and upper confidence intervals (CI.L, CL.R),
## average value of the variable (AveExpr),
## p-value of the coefficient (P.Value) and
## the p-value after correction for multiple testing (adj.P.Val).
## The rows of the table are shown in an increasing order by the respective p-value.
##
## Name                   Coefficient        CI.L        CI.R   AveExpr    P.Value   adj.P.Val
## -------------------  ------------  ----------  ----------  --------  ---------  ----------
## SM(d18:1/24:0)          4.99e-02    0.027900    0.071800      23.5   9.50e-06     0.00101
## SM(d36:2)              -3.95e-02   -0.057600   -0.021400      21.4   2.07e-05     0.00110
## SM(d34:1)              -1.75e-02   -0.026800   -0.008130      24.9   2.59e-04     0.00914
## SM(d40:1)               3.75e-02    0.016600    0.058400      23.9   4.63e-04     0.01230
## LPC(18:2)               5.60e-02    0.024000    0.088100      24.0   6.30e-04     0.01340
## TG(18:0/18:1/20:4)     -8.50e-02   -0.136000   -0.034500      21.3   1.01e-03     0.01780
## PC(38:4)               -2.52e-02   -0.040700   -0.009640      25.2   1.53e-03     0.02320
## SM(d32:1)              -3.35e-02   -0.054500   -0.012600      22.3   1.78e-03     0.02360
## SM(d16:1/18:1)         -2.97e-02   -0.048800   -0.010600      22.8   2.37e-03     0.02790
## PC(32:2)                5.74e-02    0.019900    0.094900      20.7   2.76e-03     0.02930
## LPC(16:0)               1.55e-02    0.004800    0.026100      25.3   4.53e-03     0.04370
## PC(O-34:3)              3.81e-02    0.011300    0.064800      21.9   5.34e-03     0.04720
## TG(54:3)               -3.88e-02   -0.066500   -0.011000      21.7   6.28e-03     0.05120
## SM(d33:1)              -2.98e-02   -0.051500   -0.008060      21.3   7.29e-03     0.05520
## SM(d18:2/24:1)         -2.58e-02   -0.044800   -0.006820      24.0   7.81e-03     0.05520
## TG(53:2)               -6.54e-02   -0.115000   -0.015700      20.7   1.01e-02     0.06670
## SM(d41:1)               3.23e-02    0.007470    0.057100      22.7   1.08e-02     0.06760
## TG(52:3)               -2.53e-02   -0.047600   -0.003000      22.3   2.62e-02     0.14700
## TG(54:4)               -3.64e-02   -0.068400   -0.004300      21.4   2.63e-02     0.14700
## TG(52:2)               -2.30e-02   -0.043900   -0.002020      22.6   3.17e-02     0.16600
## TG(53:3)               -5.03e-02   -0.097100   -0.003530      20.7   3.51e-02     0.16600
## TG(56:3)               -5.03e-02   -0.097200   -0.003300      20.0   3.60e-02     0.16600
## TG(53:4)               -5.46e-02   -0.106000   -0.003390      19.7   3.67e-02     0.16600
## TG(18:2/18:1/18:1)     -3.95e-02   -0.077200   -0.001880      24.4   3.96e-02     0.16600
## TG(56:4)               -5.62e-02   -0.110000   -0.002470      20.0   4.04e-02     0.16600
## TG(52:4)               -3.46e-02   -0.067800   -0.001460      21.6   4.08e-02     0.16600
## PC(34:2)               -3.92e-02   -0.077200   -0.001170      26.0   4.34e-02     0.17000
## LPC(18:1)               2.42e-02    0.000366    0.048000      23.7   4.66e-02     0.17600
## TG(51:2)               -4.37e-02   -0.088300    0.000787      21.6   5.42e-02     0.19800
## PC(36:5)                4.60e-02   -0.001160    0.093200      24.3   5.59e-02     0.19800
## TG(54:2)               -4.29e-02   -0.088600    0.002750      23.4   6.54e-02     0.22400
## TG(45:0)                1.55e-02   -0.001290    0.032300      23.1   7.03e-02     0.23300
## LPC(16:1)               2.76e-02   -0.003240    0.058400      20.0   7.93e-02     0.25500
## TG(18:1/18:1/18:1)     -3.19e-02   -0.067900    0.004160      24.8   8.29e-02     0.25800
## TG(56:6)               -2.72e-02   -0.058700    0.004350      19.9   9.11e-02     0.27300
```

```
## LPC(18:0)                1.63e-02   -0.002830    0.035400      23.9   9.48e-02     0.27300
## TG(18:1/18:1/16:0)      -2.41e-02   -0.052500    0.004360      25.6   9.68e-02     0.27300
## TG(16:0/22:5/18:1)      -3.28e-02   -0.071700    0.006050      22.7   9.78e-02     0.27300
## PC(O-36:5)               1.84e-02   -0.003820    0.040700      22.3   1.04e-01     0.28300
## TG(16:0/18:2/18:2)      -3.66e-02   -0.081400    0.008260      24.5   1.10e-01     0.28900
## PC(34:3)                 3.43e-02   -0.007980    0.076600      22.5   1.12e-01     0.28900
## TG(51:3)                -3.67e-02   -0.082600    0.009220      20.7   1.17e-01     0.29500
## PC(38:6)                 1.61e-02   -0.004440    0.036700      25.3   1.24e-01     0.30400
## SM(d41:2)               -1.80e-02   -0.041200    0.005090      22.5   1.26e-01     0.30400
## PC(O-34:2)               2.37e-02   -0.008900    0.056300      21.5   1.54e-01     0.36200
## TG(16:0/18:2/18:3)      -4.74e-02   -0.114000    0.018600      22.0   1.59e-01     0.36700
## PC(32:0)                 1.01e-02   -0.004620    0.024800      22.5   1.78e-01     0.40300
## PC(38:2)                 1.49e-02   -0.007570    0.037300      21.2   1.94e-01     0.42800
## PC(32:1)                 2.73e-02   -0.014500    0.069200      23.3   2.00e-01     0.43100
## TG(50:3)                -2.68e-02   -0.068200    0.014700      23.5   2.06e-01     0.43100
## TG(18:2/18:1/16:0)      -1.62e-02   -0.041700    0.009230      25.3   2.11e-01     0.43100
## TG(52:5)                -3.37e-02   -0.087100    0.019800      19.8   2.16e-01     0.43100
## SM(d38:2)               -1.32e-02   -0.034100    0.007770      21.3   2.17e-01     0.43100
## SM(d36:1)               -1.06e-02   -0.027400    0.006320      23.4   2.20e-01     0.43100
## TG(56:5)                -2.50e-02   -0.065200    0.015300      20.3   2.24e-01     0.43200
## TG(54:5)                -2.39e-02   -0.063100    0.015400      20.6   2.33e-01     0.43600
## SM(d38:1)                1.18e-02   -0.007730    0.031400      23.1   2.35e-01     0.43600
## TG(18:1/18:2/18:2)      -2.78e-02   -0.074200    0.018500      23.6   2.39e-01     0.43600
## TG(51:1)                -2.81e-02   -0.075600    0.019300      20.3   2.45e-01     0.44000
## SM(d40:2)               -1.06e-02   -0.029000    0.007800      23.7   2.58e-01     0.45600
## PC(37:2)                 1.93e-02   -0.014700    0.053300      19.3   2.66e-01     0.46200
## TG(14:0/18:1/18:1)      -2.09e-02   -0.059400    0.017600      24.4   2.87e-01     0.49000
## TG(49:2)                -1.72e-02   -0.051400    0.016900      20.4   3.22e-01     0.54000
## TG(49:1)                -1.90e-02   -0.056900    0.018900      20.9   3.26e-01     0.54000
## TG(50:2)                -1.54e-02   -0.047100    0.016300      21.1   3.40e-01     0.55400
## TG(18:1/18:1/22:6)       3.08e-02   -0.044000    0.106000      20.7   4.19e-01     0.67300
## TG(14:0/18:2/18:2)      -2.39e-02   -0.083300    0.035500      21.2   4.30e-01     0.67500
## TG(56:7)                -1.43e-02   -0.050400    0.021800      19.6   4.36e-01     0.67500
## PC(38:5)                -5.68e-03   -0.020100    0.008740      24.6   4.39e-01     0.67500
## PC(O-38:5)              -7.79e-03   -0.027800    0.012300      22.8   4.46e-01     0.67500
## PC(O-36:4)               8.91e-03   -0.014800    0.032600      22.9   4.61e-01     0.68900
## TG(46:0)                 1.66e-02   -0.030300    0.063500      20.4   4.88e-01     0.70800
## PC(O-36:3)               1.00e-02   -0.018400    0.038400      20.4   4.88e-01     0.70800
## PC(35:1)                -8.50e-03   -0.033700    0.016700      21.8   5.08e-01     0.72700
## TG(50:1)                -1.63e-02   -0.066100    0.033400      24.3   5.19e-01     0.72700
## TG(47:1)                -1.33e-02   -0.054100    0.027500      19.6   5.21e-01     0.72700
## LPC(20:4)                9.80e-03   -0.021700    0.041300      21.4   5.41e-01     0.74500
## PC(33:1)                 8.44e-03   -0.021000    0.037900      20.9   5.74e-01     0.78000
## TG(16:0/18:0/18:1)      -1.75e-02   -0.080000    0.045100      23.1   5.84e-01     0.78300
## PC(34:1)                -4.92e-03   -0.024400    0.014600      26.0   6.20e-01     0.82200
## PC(40:6)                 7.53e-03   -0.023500    0.038500      23.9   6.33e-01     0.82900
## PC(36:3)                 5.14e-03   -0.017800    0.028000      25.6   6.60e-01     0.85300
## TG(58:9)                 1.56e-02   -0.058800    0.090000      19.9   6.81e-01     0.86900
## TG(16:0/18:2/22:6)       1.68e-02   -0.065700    0.099300      21.0   6.90e-01     0.87100
## PC(O-38:6)               4.03e-03   -0.017900    0.026000      20.4   7.18e-01     0.89600
## SM(d39:1)                4.24e-03   -0.024600    0.033100      21.1   7.73e-01     0.94500
## PC(16:0e/18:1(9Z)       -3.23e-03   -0.025500    0.019000      21.8   7.75e-01     0.94500
## PC(36:2)                 1.82e-03   -0.012500    0.016100      26.1   8.02e-01     0.94900
## TG(54:6)                -6.60e-03   -0.059300    0.046100      19.5   8.06e-01     0.94900
```

```
## TG(18:1/12:0/18:1)      -6.27e-03   -0.056300    0.043800       22.5   8.06e-01       0.94900
## TG(48:3)                -7.66e-03   -0.074700    0.059400       20.5   8.23e-01       0.95500
## TG(46:2)                -5.66e-03   -0.059000    0.047700       20.1   8.35e-01       0.95500
## PC(O-36:2)              -2.65e-03   -0.028100    0.022800       20.5   8.38e-01       0.95500
## PC(40:5)                 2.60e-03   -0.024500    0.029700       22.0   8.50e-01       0.95900
## PC(40:7)                 2.19e-03   -0.028100    0.032400       21.4   8.87e-01       0.98700
## TG(14:0/16:0/18:1)       3.42e-03   -0.046800    0.053700       22.8   8.94e-01       0.98700
## PC(O-38:4)              -1.34e-03   -0.028000    0.025400       21.7   9.22e-01       0.99900
## TG(50:0)                -1.95e-03   -0.058700    0.054800       20.8   9.46e-01       0.99900
## SM(42:2)                -4.21e-04   -0.016800    0.016000       25.2   9.60e-01       0.99900
## PC(35:2)                -6.49e-04   -0.027700    0.026400       21.8   9.63e-01       0.99900
## PC(38:3)                -5.76e-04   -0.025300    0.024100       24.0   9.63e-01       0.99900
## TG(49:3)                -4.00e-05   -0.005670    0.005590       20.7   9.89e-01       0.99900
## PC(36:4)                 6.80e-05   -0.012600    0.012700       25.9   9.92e-01       0.99900
## TG(46:1)                 2.32e-04   -0.049500    0.050000       21.3   9.93e-01       0.99900
## TG(18:2/22:5/16:0)      -2.18e-04   -0.064100    0.063700       22.1   9.95e-01       0.99900
## TG(18:2/18:2/18:2)       2.08e-05   -0.051000    0.051000       22.1   9.99e-01       0.99900
```

1.1.2.1.2 Heatmaps

```
##   Label Relation p.adj
## 1     #  p.adj <  0.01
## 2     x  p.adj <  0.05
## 3     *  p.adj <  0.10
```

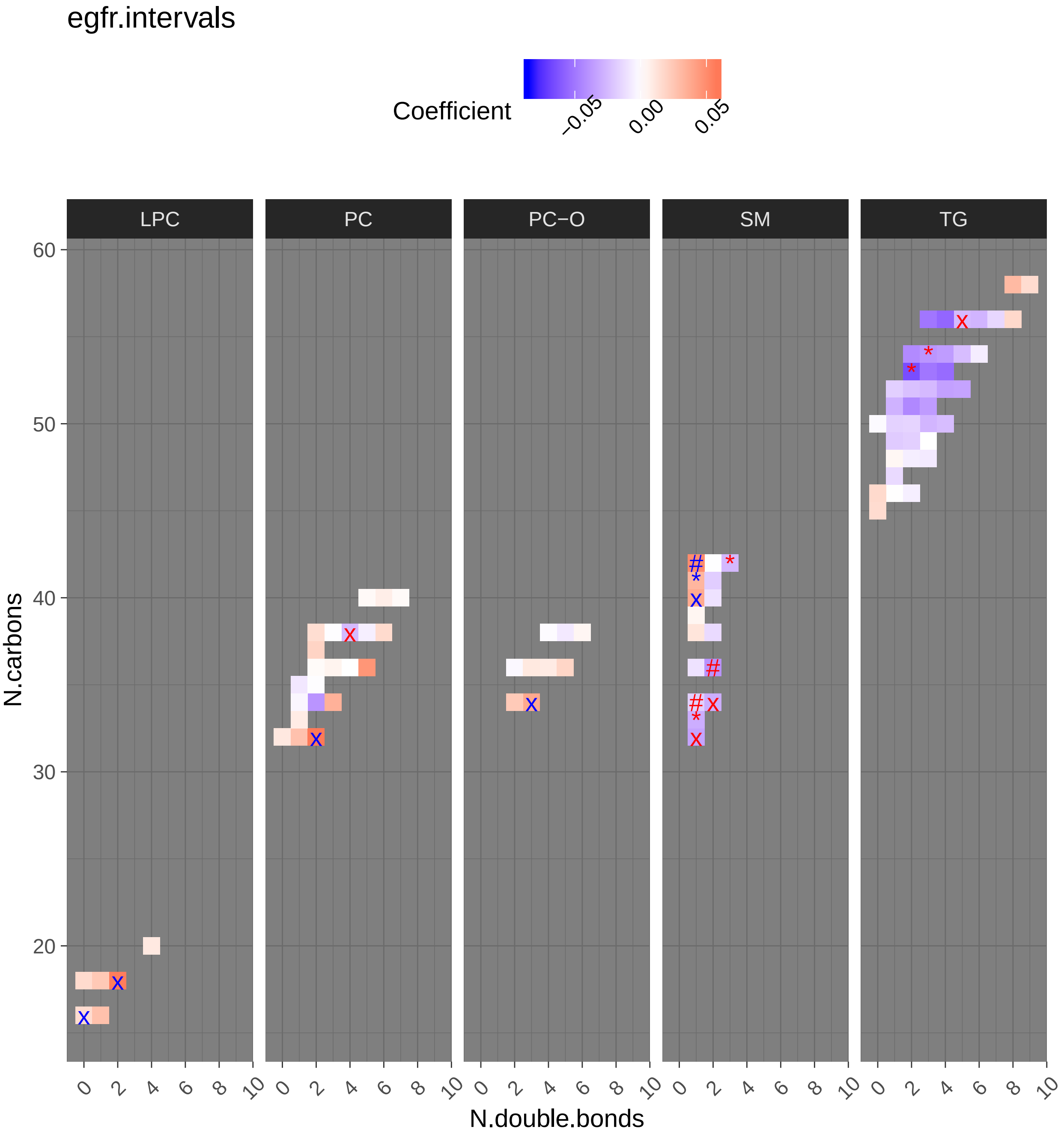


Figure 7: Heatmap of the lipid-specific model coefficents from the crude model for eGFR. Lipids are organized into panels (columns) by their class (from LPC to TG). One colored rectangle corresponds to one lipid species, where the coordinates in the x-axis and y-axis, respectively, show the number of double bonds (N.double.bonds) and the number of carbon atoms (N.carbons) in the fatty acid chains of the lipid. The number of double bonds corresponds to the number of unsaturated bonds in the fatty acid chains, and the number of carbon atoms corresponds to the length of the fatty acid chains and, thus, the size of the lipid. The magnitude of the lipid-specifc model coefficient is shown as the color of the rectangle (blue: negative; red: positive). Coefficient with statistical significance are annotated with symbols #, x and *, respectively, corresponding to $p < 0.01$, $p < 0.05$ and $p < 0.1$.

1.1.2.2 Adjusted Model

1.1.2.2.1 Table

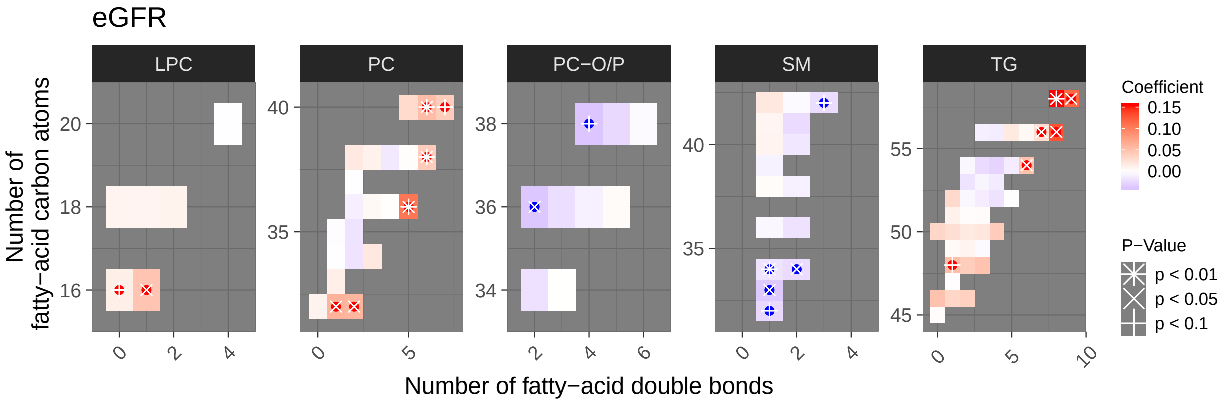
```
##
##
## Table: Results of the adjustred model for eGFR variable.
## Shown in the table are name of the lipid (Name),
## model coefficient (Coefficient),
## its lower and upper confidence intervals (CI.L, CL.R),
## average value of the variable (AveExpr),
## p-value of the coefficient (P.Value) and
## the p-value after correction for multiple testing (adj.P.Val).
## The rows of the table are shown in an increasing order by the respective p-value.
##
## Name                  Coefficient        CI.L        CI.R   AveExpr    P.Value   adj.P.Val
## -------------------  ------------  ----------  ----------  --------  ---------  ----------
## PC(36:5)                 0.106000    0.059400    0.153000      24.3   1.05e-05     0.00112
## PC(38:6)                 0.041800    0.021400    0.062100      25.3   6.17e-05     0.00327
## TG(18:1/18:1/22:6)       0.154000    0.075800    0.233000      20.7   1.25e-04     0.00442
## SM(d34:1)               -0.017800   -0.027300   -0.008350      24.9   2.39e-04     0.00633
## PC(40:6)                 0.053700    0.023800    0.083600      23.9   4.49e-04     0.00951
## SM(d33:1)               -0.035100   -0.056200   -0.014000      21.3   1.16e-03     0.01920
## TG(18:2/18:2/18:2)       0.074600    0.029400    0.120000      22.1   1.27e-03     0.01920
## PC(32:2)                 0.058400    0.020400    0.096500      20.7   2.66e-03     0.03070
## TG(18:2/22:5/16:0)       0.095600    0.033200    0.158000      22.1   2.74e-03     0.03070
## TG(16:0/18:2/22:6)       0.128000    0.043500    0.213000      21.0   3.08e-03     0.03070
## SM(d16:1/18:1)          -0.023000   -0.038300   -0.007750      22.8   3.19e-03     0.03070
## TG(58:9)                 0.117000    0.036800    0.196000      19.9   4.25e-03     0.03760
## PC(O-36:2)              -0.037000   -0.062700   -0.011300      20.5   4.81e-03     0.03920
## PC(32:1)                 0.061200    0.018300    0.104000      23.3   5.24e-03     0.03960
## LPC(16:1)                0.046500    0.012800    0.080300      20.0   6.91e-03     0.04880
## PC(40:7)                 0.040600    0.010600    0.070600      21.4   8.02e-03     0.05320
## TG(14:0/16:0/18:1)       0.052500    0.013200    0.091800      22.8   8.93e-03     0.05570
## PC(O-38:4)              -0.037400   -0.066500   -0.008220      21.7   1.21e-02     0.07030
## SM(d18:2/24:1)          -0.022500   -0.040300   -0.004800      24.0   1.28e-02     0.07030
## SM(d32:1)               -0.024700   -0.044300   -0.005180      22.3   1.33e-02     0.07030
## LPC(16:0)                0.013100    0.002090    0.024100      25.3   1.98e-02     0.09980
## TG(46:0)                 0.049100    0.006210    0.091900      20.4   2.49e-02     0.12000
## PC(40:5)                 0.029400    0.003180    0.055700      22.0   2.81e-02     0.12500
## PC(O-38:5)              -0.024600   -0.046600   -0.002610      22.8   2.84e-02     0.12500
## TG(18:1/12:0/18:1)       0.040200    0.002350    0.078100      22.5   3.74e-02     0.15200
## TG(54:3)                -0.022600   -0.044000   -0.001290      21.7   3.77e-02     0.15200
## SM(d36:2)               -0.018800   -0.036600   -0.000984      21.4   3.86e-02     0.15200
## SM(d41:2)               -0.022700   -0.044600   -0.000879      22.5   4.15e-02     0.15700
## PC(16:0e/18:1(9Z)       -0.022100   -0.043700   -0.000456      21.8   4.54e-02     0.16600
## TG(54:6)                 0.049500    0.000222    0.098800      19.5   4.90e-02     0.17300
## SM(d40:2)               -0.015800   -0.032000    0.000265      23.7   5.39e-02     0.17700
## TG(54:4)                -0.027900   -0.056300    0.000512      21.4   5.43e-02     0.17700
## SM(d18:1/24:0)           0.019000   -0.000487    0.038500      23.5   5.60e-02     0.17700
## TG(14:0/18:2/18:2)       0.041000   -0.001180    0.083200      21.2   5.67e-02     0.17700
## TG(49:3)                -0.004000   -0.008450    0.000451      20.7   7.81e-02     0.23700
## PC(38:4)                -0.014600   -0.030900    0.001830      25.2   8.15e-02     0.24000
## TG(48:3)                 0.048200   -0.006770    0.103000      20.5   8.56e-02     0.24500
## TG(46:2)                 0.037200   -0.007500    0.081800      20.1   1.03e-01     0.27800
## TG(14:0/18:1/18:1)       0.020600   -0.004450    0.045700      24.4   1.07e-01     0.27800
```

```
## TG(50:2)              0.017400  -0.003920   0.038800      21.1   1.09e-01     0.27800
## PC(38:2)              0.017700  -0.003980   0.039300      21.2   1.10e-01     0.27800
## PC(O-36:3)           -0.021900  -0.048800   0.004980      20.4   1.10e-01     0.27800
## TG(50:3)              0.019400  -0.004770   0.043500      23.5   1.16e-01     0.28500
## TG(18:0/18:1/20:4)   -0.037700  -0.087500   0.012200      21.3   1.39e-01     0.33400
## TG(56:7)              0.026500  -0.009270   0.062300      19.6   1.46e-01     0.34000
## TG(46:1)              0.032600  -0.011600   0.076800      21.3   1.48e-01     0.34000
## TG(52:4)             -0.019100  -0.045500   0.007360      21.6   1.57e-01     0.35100
## TG(52:3)             -0.011900  -0.028500   0.004680      22.3   1.59e-01     0.35100
## TG(50:1)              0.025900  -0.012800   0.064500      24.3   1.89e-01     0.40300
## TG(18:2/18:1/18:1)   -0.021700  -0.054300   0.011000      24.4   1.93e-01     0.40300
## PC(32:0)              0.009630  -0.005010   0.024300      22.5   1.97e-01     0.40300
## PC(36:2)             -0.010600  -0.026900   0.005590      26.1   1.99e-01     0.40300
## TG(50:0)              0.032100  -0.017200   0.081300      20.8   2.02e-01     0.40300
## PC(35:2)             -0.017800  -0.045800   0.010200      21.8   2.13e-01     0.41900
## TG(16:0/18:0/18:1)    0.030600  -0.018400   0.079700      23.1   2.21e-01     0.42600
## PC(O-34:2)           -0.019400  -0.053600   0.014700      21.5   2.64e-01     0.50100
## TG(56:5)              0.017400  -0.015500   0.050200      20.3   3.00e-01     0.55900
## SM(d40:1)             0.009320  -0.008600   0.027200      23.9   3.08e-01     0.56200
## TG(53:2)             -0.017800  -0.053700   0.018000      20.7   3.29e-01     0.59000
## PC(38:3)              0.011000  -0.012700   0.034800      24.0   3.63e-01     0.63300
## PC(33:1)              0.013300  -0.015500   0.042100      20.9   3.64e-01     0.63300
## LPC(18:0)             0.008960  -0.011200   0.029100      23.9   3.83e-01     0.64500
## PC(34:2)             -0.018500  -0.060700   0.023700      26.0   3.89e-01     0.64500
## SM(d38:2)            -0.008840  -0.029000   0.011300      21.3   3.90e-01     0.64500
## PC(34:3)              0.018300  -0.025000   0.061500      22.5   4.06e-01     0.66300
## PC(O-36:4)           -0.009480  -0.035700   0.016700      22.9   4.77e-01     0.76300
## TG(52:2)             -0.004980  -0.019000   0.009050      22.6   4.86e-01     0.76300
## SM(d41:1)             0.007760  -0.015100   0.030700      22.7   5.06e-01     0.76300
## TG(54:5)             -0.012000  -0.048000   0.024000      20.6   5.14e-01     0.76300
## LPC(18:1)             0.008550  -0.017300   0.034400      23.7   5.16e-01     0.76300
## SM(d36:1)            -0.005100  -0.020700   0.010500      23.4   5.20e-01     0.76300
## TG(53:4)             -0.013200  -0.055900   0.029500      19.7   5.44e-01     0.76300
## TG(51:1)              0.010900  -0.024800   0.046500      20.3   5.50e-01     0.76300
## SM(d39:1)            -0.008770  -0.037700   0.020200      21.1   5.52e-01     0.76300
## TG(49:2)              0.008660  -0.020000   0.037300      20.4   5.54e-01     0.76300
## LPC(18:2)             0.010100  -0.024600   0.044800      24.0   5.68e-01     0.76300
## TG(16:0/22:5/18:1)    0.009550  -0.023600   0.042700      22.7   5.71e-01     0.76300
## TG(56:3)             -0.010500  -0.047000   0.026000      20.0   5.72e-01     0.76300
## TG(56:4)             -0.012500  -0.056200   0.031200      20.0   5.74e-01     0.76300
## TG(18:1/18:1/18:1)   -0.008830  -0.039800   0.022200      24.8   5.76e-01     0.76300
## SM(42:2)             -0.004040  -0.019200   0.011100      25.2   6.01e-01     0.78600
## TG(45:0)              0.002500  -0.008120   0.013100      23.1   6.45e-01     0.83300
## PC(36:3)              0.005020  -0.019100   0.029200      25.6   6.83e-01     0.87200
## TG(53:3)             -0.006790  -0.041900   0.028300      20.7   7.04e-01     0.88900
## TG(54:2)             -0.005460  -0.035700   0.024700      23.4   7.23e-01     0.89900
## TG(56:6)              0.005100  -0.023900   0.034100      19.9   7.30e-01     0.89900
## PC(O-38:6)           -0.003680  -0.026300   0.018900      20.4   7.49e-01     0.89900
## TG(18:2/18:1/16:0)    0.004320  -0.023200   0.031800      25.3   7.58e-01     0.89900
## SM(d38:1)             0.002780  -0.015100   0.020600      23.1   7.60e-01     0.89900
## TG(16:0/18:2/18:2)   -0.004980  -0.040000   0.030000      24.5   7.80e-01     0.89900
## TG(18:1/18:1/16:0)   -0.004410  -0.035400   0.026600      25.6   7.80e-01     0.89900
## PC(O-36:5)            0.003480  -0.021000   0.028000      22.3   7.81e-01     0.89900
## PC(38:5)              0.001830  -0.012800   0.016500      24.6   8.06e-01     0.90900
```

```
## TG(49:1)                 0.004060   -0.028500    0.036600       20.9   8.07e-01       0.90900
## TG(18:1/18:2/18:2)      -0.003850   -0.044700    0.037000       23.6   8.53e-01       0.95200
## TG(51:3)                 0.002930   -0.031600    0.037400       20.7   8.68e-01       0.95300
## TG(51:2)                 0.002370   -0.027000    0.031800       21.6   8.74e-01       0.95300
## PC(35:1)                -0.001730   -0.026500    0.023000       21.8   8.91e-01       0.95300
## PC(36:4)                 0.000956   -0.013300    0.015300       25.9   8.96e-01       0.95300
## TG(16:0/18:2/18:3)       0.003450   -0.054300    0.061200       22.0   9.07e-01       0.95300
## PC(34:1)                -0.001310   -0.023600    0.021000       26.0   9.08e-01       0.95300
## LPC(20:4)               -0.001550   -0.036000    0.032900       21.4   9.30e-01       0.96600
## PC(37:2)                -0.001130   -0.035400    0.033200       19.3   9.48e-01       0.97100
## TG(47:1)                 0.001390   -0.044700    0.047500       19.6   9.53e-01       0.97100
## PC(O-34:3)               0.000326   -0.025000    0.025700       21.9   9.80e-01       0.98400
## TG(52:5)                 0.000486   -0.048400    0.049400       19.8   9.84e-01       0.98400
```

1.1.2.2.2 Heatmaps

```
## [1] "map_lipid_names has been created by Tommi Suvitaival"
## [1] "tommi.raimo.leo.suvitaival@regionh.dk"
## [1] "2019-05-06"
```



1.1.3 logUAER – Continuous Albuminuria

1.1.3.1 Crude Model

1.1.3.1.1 Table

```
##
##
## Table: Results of the crude model for continuous albuminuria variable (logUAER).
## Shown in the table are name of the lipid (Name),
## model coefficient (Coefficient),
## its lower and upper confidence intervals (CI.L, CL.R),
## average value of the variable (AveExpr),
## p-value of the coefficient (P.Value) and
## the p-value after correction for multiple testing (adj.P.Val).
## The rows of the table are shown in an increasing order by the respective p-value.
##
## Name                  Coefficient        CI.L        CI.R   AveExpr    P.Value   adj.P.Val
## -------------------  ------------  ----------  ----------  --------  ---------  ----------
## PC(O-34:3)              -0.047000   -6.39e-02   -0.030000      21.9   1.00e-07    7.90e-06
## PC(O-36:3)              -0.041900   -5.99e-02   -0.023900      20.4   5.80e-06    3.09e-04
## PC(O-38:6)              -0.026600   -4.06e-02   -0.012600      20.4   2.03e-04    5.62e-03
## PC(O-36:2)              -0.030800   -4.70e-02   -0.014600      20.5   2.12e-04    5.62e-03
## TG(53:2)                 0.058900    2.70e-02    0.090800      20.7   3.13e-04    5.65e-03
## TG(45:0)                -0.019700   -3.05e-02   -0.008970      23.1   3.39e-04    5.65e-03
## TG(52:2)                 0.024400    1.10e-02    0.037800      22.6   3.73e-04    5.65e-03
## TG(51:2)                 0.048400    1.99e-02    0.077000      21.6   9.03e-04    1.10e-02
## TG(56:3)                 0.051000    2.09e-02    0.081100      20.0   9.38e-04    1.10e-02
## SM(d18:1/24:0)          -0.023500   -3.77e-02   -0.009240      23.5   1.27e-03    1.29e-02
## TG(54:2)                 0.048000    1.88e-02    0.077300      23.4   1.34e-03    1.29e-02
## PC(O-34:2)              -0.033900   -5.48e-02   -0.013100      21.5   1.48e-03    1.31e-02
## PC(16:0e/18:1(9Z)       -0.022200   -3.64e-02   -0.007930      21.8   2.32e-03    1.89e-02
## TG(53:3)                 0.045500    1.55e-02    0.075500      20.7   3.05e-03    2.31e-02
## SM(d41:1)               -0.023200   -3.92e-02   -0.007250      22.7   4.43e-03    3.13e-02
## SM(d40:1)               -0.018800   -3.24e-02   -0.005290      23.9   6.48e-03    4.27e-02
## TG(56:4)                 0.047700    1.32e-02    0.082200      20.0   6.85e-03    4.27e-02
## TG(54:3)                 0.024300    6.45e-03    0.042200      21.7   7.73e-03    4.55e-02
## TG(50:2)                 0.026900    6.59e-03    0.047200      21.1   9.51e-03    4.99e-02
## TG(14:0/18:1/18:1)       0.032500    7.84e-03    0.057200      24.4   9.89e-03    4.99e-02
## TG(50:1)                 0.041900    1.01e-02    0.073800      24.3   1.00e-02    4.99e-02
## TG(56:6)                 0.026300    6.07e-03    0.046600      19.9   1.09e-02    4.99e-02
## PC(32:0)                -0.012200   -2.17e-02   -0.002800      22.5   1.11e-02    4.99e-02
## TG(51:1)                 0.039400    8.95e-03    0.069800      20.3   1.13e-02    4.99e-02
## TG(52:3)                 0.018200    3.86e-03    0.032500      22.3   1.29e-02    5.30e-02
## TG(16:0/22:5/18:1)       0.031700    6.71e-03    0.056700      22.7   1.30e-02    5.30e-02
## TG(16:0/18:0/18:1)       0.050300    1.01e-02    0.090400      23.1   1.41e-02    5.55e-02
## TG(52:4)                 0.026500    5.17e-03    0.047900      21.6   1.50e-02    5.64e-02
## TG(54:6)                 0.041800    8.00e-03    0.075600      19.5   1.54e-02    5.64e-02
## TG(51:3)                 0.036000    6.45e-03    0.065500      20.7   1.70e-02    6.01e-02
## TG(18:1/18:1/16:0)       0.022000    3.71e-03    0.040300      25.6   1.85e-02    6.32e-02
## TG(56:5)                 0.030700    4.84e-03    0.056600      20.3   2.01e-02    6.65e-02
## PC(O-36:5)              -0.016300   -3.06e-02   -0.001960      22.3   2.59e-02    8.32e-02
## TG(50:3)                 0.029700    3.09e-03    0.056400      23.5   2.88e-02    8.98e-02
## TG(18:2/18:2/18:2)       0.035900    3.21e-03    0.068700      22.1   3.15e-02    9.52e-02
## PC(32:2)                -0.026500   -5.08e-02   -0.002240      20.7   3.24e-02    9.53e-02
## PC(40:7)                -0.020300   -3.98e-02   -0.000904      21.4   4.03e-02    1.15e-01
## LPC(18:2)               -0.021600   -4.23e-02   -0.000798      24.0   4.18e-02    1.17e-01
## PC(34:2)                 0.024400   -9.28e-05    0.048900      26.0   5.09e-02    1.37e-01
```

```
## TG(18:2/22:5/16:0)     0.040700  -3.06e-04   0.081800     22.1  5.17e-02   1.37e-01
## TG(16:0/18:2/18:2)     0.028300  -5.36e-04   0.057200     24.5  5.44e-02   1.41e-01
## TG(18:1/18:1/18:1)     0.022400  -7.57e-04   0.045600     24.8  5.79e-02   1.44e-01
## TG(49:1)               0.023500  -8.22e-04   0.047900     20.9  5.82e-02   1.44e-01
## TG(53:4)               0.030900  -2.06e-03   0.063900     19.7  6.61e-02   1.57e-01
## TG(14:0/16:0/18:1)     0.030200  -2.09e-03   0.062500     22.8  6.67e-02   1.57e-01
## TG(18:0/18:1/20:4)     0.030400  -2.37e-03   0.063200     21.3  6.90e-02   1.59e-01
## TG(56:7)               0.021200  -1.97e-03   0.044500     19.6  7.28e-02   1.64e-01
## TG(49:3)              -0.003280  -6.89e-03   0.000341     20.7  7.58e-02   1.67e-01
## PC(37:2)              -0.019400  -4.13e-02   0.002520     19.3  8.27e-02   1.78e-01
## TG(16:0/18:2/18:3)     0.037500  -5.06e-03   0.080100     22.0  8.41e-02   1.78e-01
## TG(52:5)               0.029600  -4.75e-03   0.064000     19.8  9.11e-02   1.89e-01
## SM(d39:1)             -0.015900  -3.45e-02   0.002650     21.1  9.28e-02   1.89e-01
## TG(14:0/18:2/18:2)     0.032500  -5.69e-03   0.070700     21.2  9.52e-02   1.89e-01
## TG(18:1/12:0/18:1)     0.027300  -4.87e-03   0.059500     22.5  9.61e-02   1.89e-01
## PC(38:4)               0.008360  -1.71e-03   0.018400     25.2  1.04e-01   2.00e-01
## PC(38:6)              -0.010900  -2.42e-02   0.002350     25.3  1.07e-01   2.02e-01
## TG(18:2/18:1/18:1)     0.019200  -5.06e-03   0.043500     24.4  1.20e-01   2.24e-01
## TG(49:2)               0.017000  -5.01e-03   0.038900     20.4  1.30e-01   2.38e-01
## TG(54:4)               0.014900  -5.80e-03   0.035600     21.4  1.58e-01   2.83e-01
## SM(d41:2)             -0.010400  -2.53e-02   0.004500     22.5  1.71e-01   3.00e-01
## SM(d34:1)              0.004200  -1.87e-03   0.010300     24.9  1.75e-01   3.00e-01
## PC(35:2)              -0.012000  -2.94e-02   0.005430     21.8  1.77e-01   3.00e-01
## SM(d38:2)             -0.009200  -2.27e-02   0.004300     21.3  1.81e-01   3.00e-01
## PC(36:5)              -0.020800  -5.12e-02   0.009700     24.3  1.81e-01   3.00e-01
## PC(36:2)              -0.006110  -1.53e-02   0.003070     26.1  1.92e-01   3.13e-01
## TG(46:2)               0.022200  -1.21e-02   0.056600     20.1  2.04e-01   3.28e-01
## SM(d38:1)             -0.007900  -2.05e-02   0.004710     23.1  2.19e-01   3.45e-01
## LPC(20:4)              0.012600  -7.63e-03   0.032900     21.4  2.21e-01   3.45e-01
## SM(d40:2)             -0.007170  -1.90e-02   0.004690     23.7  2.36e-01   3.62e-01
## TG(50:0)               0.021500  -1.50e-02   0.058000     20.8  2.47e-01   3.72e-01
## TG(18:1/18:1/22:6)     0.028200  -2.00e-02   0.076300     20.7  2.51e-01   3.72e-01
## TG(54:5)               0.014700  -1.05e-02   0.040000     20.6  2.52e-01   3.72e-01
## PC(38:3)               0.009080  -6.82e-03   0.025000     24.0  2.63e-01   3.81e-01
## PC(40:6)              -0.011200  -3.11e-02   0.008770     23.9  2.72e-01   3.89e-01
## TG(48:3)               0.023700  -1.94e-02   0.066900     20.5  2.81e-01   3.95e-01
## TG(46:1)               0.017500  -1.45e-02   0.049500     21.3  2.83e-01   3.95e-01
## SM(d32:1)              0.007230  -6.39e-03   0.020800     22.3  2.97e-01   4.07e-01
## TG(18:1/18:2/18:2)     0.015800  -1.41e-02   0.045600     23.6  3.00e-01   4.07e-01
## TG(18:2/18:1/16:0)     0.007520  -8.91e-03   0.023900     25.3  3.69e-01   4.95e-01
## PC(34:1)               0.005490  -7.07e-03   0.018000     26.0  3.91e-01   5.18e-01
## PC(O-38:5)            -0.005040  -1.80e-02   0.007870     22.8  4.44e-01   5.80e-01
## SM(d18:2/24:1)        -0.004320  -1.66e-02   0.007990     24.0  4.91e-01   6.34e-01
## PC(36:4)               0.002820  -5.35e-03   0.011000     25.9  4.98e-01   6.35e-01
## PC(38:5)              -0.003130  -1.24e-02   0.006160     24.6  5.08e-01   6.35e-01
## SM(d36:2)              0.003980  -7.85e-03   0.015800     21.4  5.09e-01   6.35e-01
## SM(42:2)              -0.003370  -1.39e-02   0.007190     25.2  5.31e-01   6.54e-01
## TG(46:0)               0.008220  -2.20e-02   0.038500     20.4  5.93e-01   7.23e-01
## TG(58:9)               0.010900  -3.71e-02   0.058800     19.9  6.56e-01   7.90e-01
## TG(16:0/18:2/22:6)     0.011000  -4.21e-02   0.064200     21.0  6.84e-01   8.15e-01
## PC(O-38:4)            -0.003460  -2.07e-02   0.013700     21.7  6.93e-01   8.17e-01
## TG(47:1)              -0.004750  -3.11e-02   0.021600     19.6  7.23e-01   8.33e-01
## SM(d16:1/18:1)        -0.002230  -1.46e-02   0.010200     22.8  7.23e-01   8.33e-01
## PC(38:2)              -0.002440  -1.69e-02   0.012000     21.2  7.41e-01   8.44e-01
```

```
## SM(d33:1)                 -0.002270   -1.64e-02    0.011800      21.3   7.52e-01    8.48e-01
## PC(34:3)                   0.004120   -2.32e-02    0.031400      22.5   7.67e-01    8.56e-01
## PC(35:1)                   0.002320   -1.39e-02    0.018600      21.8   7.79e-01    8.60e-01
## LPC(18:0)                 -0.001360   -1.37e-02    0.011000      23.9   8.28e-01    9.02e-01
## LPC(18:1)                  0.001640   -1.38e-02    0.017100      23.7   8.34e-01    9.02e-01
## PC(36:3)                  -0.001290   -1.60e-02    0.013500      25.6   8.64e-01    9.23e-01
## PC(32:1)                   0.002220   -2.48e-02    0.029200      23.3   8.72e-01    9.23e-01
## LPC(16:0)                 -0.000536   -7.44e-03    0.006370      25.3   8.79e-01    9.23e-01
## PC(40:5)                  -0.001080   -1.85e-02    0.016400      22.0   9.03e-01    9.36e-01
## LPC(16:1)                  0.001060   -1.88e-02    0.021000      20.0   9.17e-01    9.36e-01
## SM(d36:1)                 -0.000566   -1.15e-02    0.010300      23.4   9.19e-01    9.36e-01
## PC(33:1)                   0.000188   -1.88e-02    0.019200      20.9   9.85e-01    9.85e-01
## PC(O-36:4)                 0.000145   -1.52e-02    0.015400      22.9   9.85e-01    9.85e-01
```

1.1.3.1.2 Heatmaps

```
##   Label Relation p.adj
## 1     #  p.adj <  0.01
## 2     x  p.adj <  0.05
## 3     *  p.adj <  0.10
```

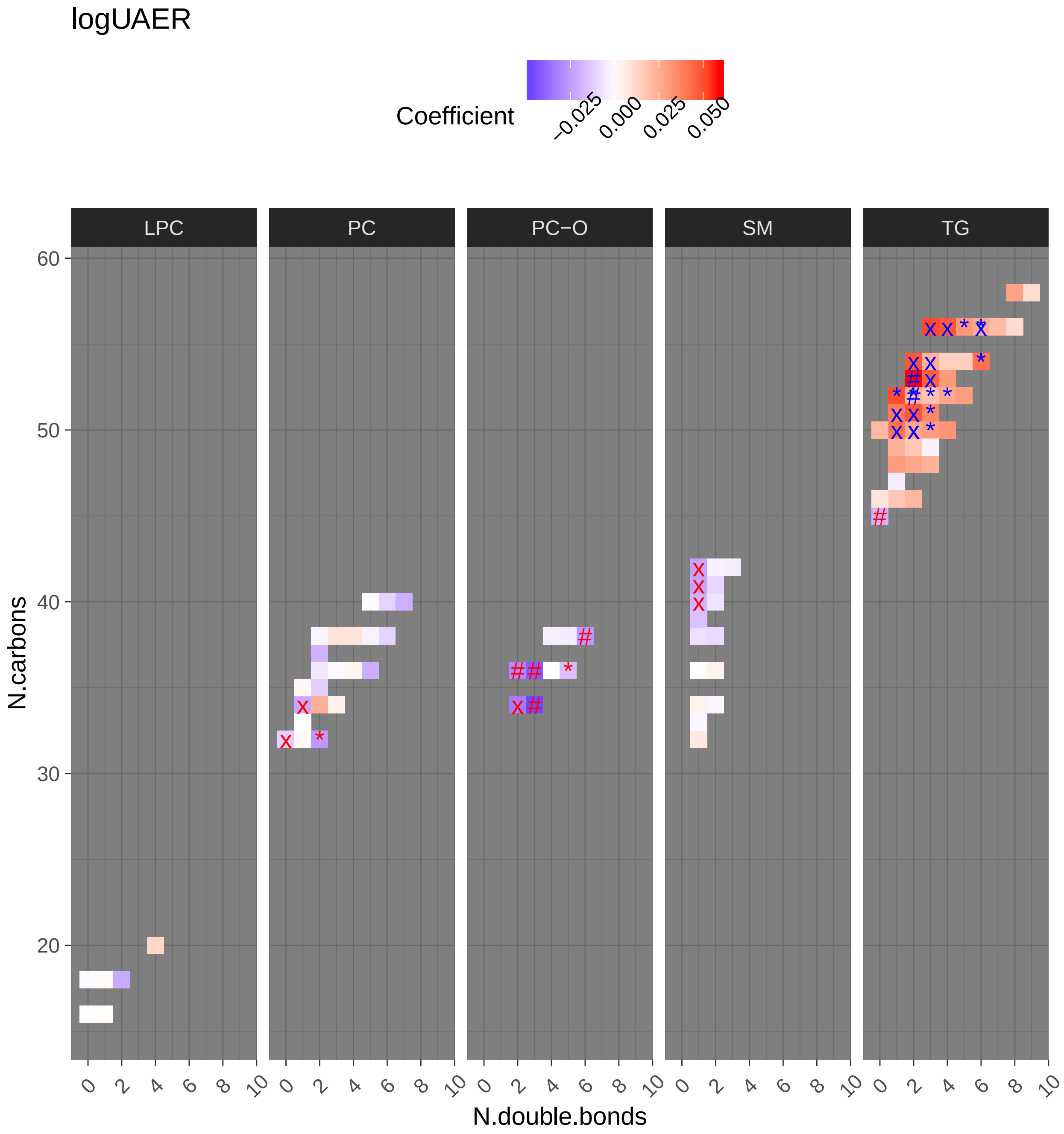


Figure 8: Heatmap of the lipid-specific model coefficents from the crude model for continuous albuminuria (logUAER). The name of the group is shown in the title of the figure in the top-left corner. Lipids are organized into panels (columns) by their class (from LPC to TG). One colored rectangle corresponds to one lipid species, where the coordinates in the x-axis and y-axis, respectively, show the number of double bonds (N.double.bonds) and the number of carbon atoms (N.carbons) in the fatty acid chains of the lipid. The number of double bonds corresponds to the number of unsaturated bonds in the fatty acid chains, and the number of carbon atoms corresponds to the length of the fatty acid chains and, thus, the size of the lipid. The magnitude of the lipid-specifc model coefficient is shown as the color of the rectangle (blue: negative; red: positive). Coefficient with statistical significance are annotated with symbols #, x and *, respectively, corresponding to $p < 0.01$, $p < 0.05$ and $p < 0.1$.

1.1.3.2 Adjusted Model

1.1.3.2.1 Table

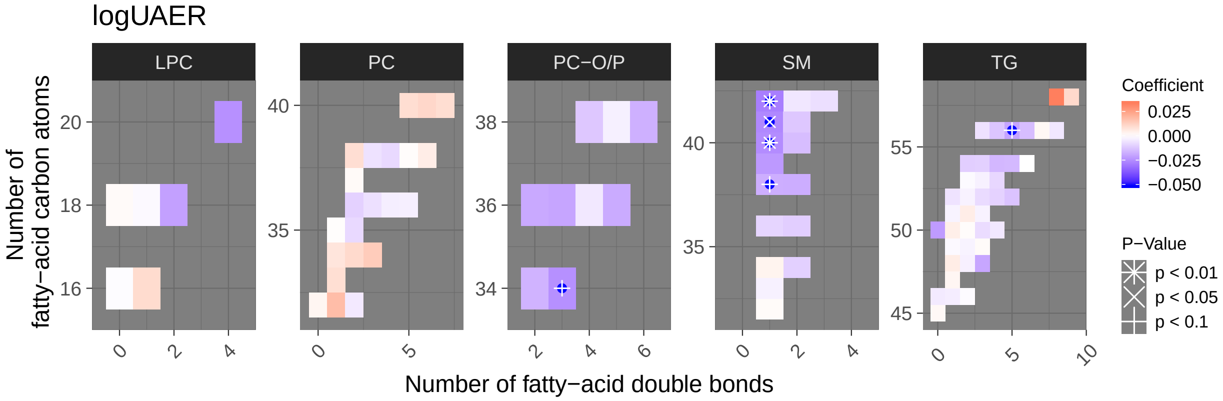
```
##
##
## Table: Results of the adjusted model for the continuous albuminuria variable (logUAER).
## Shown in the table are name of the lipid (Name),
## model coefficient (Coefficient),
## its lower and upper confidence intervals (CI.L, CL.R),
## average value of the variable (AveExpr),
## p-value of the coefficient (P.Value) and
## the p-value after correction for multiple testing (adj.P.Val).
## The rows of the table are shown in an increasing order by the respective p-value.
##
## Name                   Coefficient       CI.L        CI.R   AveExpr    P.Value   adj.P.Val
## -------------------  ------------  ---------  ----------  --------  ---------  ----------
## SM(d18:1/24:0)           -2.84e-02   -0.04170   -0.015200      23.5   2.95e-05     0.00264
## SM(d40:1)                -2.53e-02   -0.03750   -0.013200      23.9   4.97e-05     0.00264
## SM(d41:1)                -2.63e-02   -0.04180   -0.010800      22.7   9.32e-04     0.03290
## TG(18:0/18:1/20:4)       -5.12e-02   -0.08500   -0.017300      21.3   3.09e-03     0.08180
## SM(d38:1)                -1.77e-02   -0.02980   -0.005630      23.1   4.14e-03     0.08770
## PC(O-34:3)               -2.45e-02   -0.04170   -0.007370      21.9   5.16e-03     0.09110
## SM(d38:2)                -1.80e-02   -0.03160   -0.004340      21.3   9.85e-03     0.13100
## SM(d40:2)                -1.43e-02   -0.02520   -0.003460      23.7   9.89e-03     0.13100
## SM(d39:1)                -2.26e-02   -0.04220   -0.002950      21.1   2.43e-02     0.27100
## PC(O-38:6)               -1.74e-02   -0.03270   -0.002100      20.4   2.59e-02     0.27100
## PC(O-36:5)               -1.85e-02   -0.03520   -0.001920      22.3   2.89e-02     0.27100
## PC(O-36:3)               -1.99e-02   -0.03800   -0.001670      20.4   3.25e-02     0.27100
## PC(O-36:2)               -1.88e-02   -0.03610   -0.001500      20.5   3.32e-02     0.27100
## LPC(20:4)                -2.44e-02   -0.04770   -0.001010      21.4   4.09e-02     0.31000
## SM(d16:1/18:1)           -1.02e-02   -0.02060    0.000109      22.8   5.25e-02     0.37100
## PC(36:2)                 -9.97e-03   -0.02090    0.001000      26.1   7.49e-02     0.46300
## LPC(18:2)                -2.08e-02   -0.04440    0.002760      24.0   8.35e-02     0.46300
## TG(56:5)                 -1.97e-02   -0.04200    0.002640      20.3   8.38e-02     0.46300
## SM(d36:2)                -1.06e-02   -0.02260    0.001440      21.4   8.43e-02     0.46300
## SM(d36:1)                -9.20e-03   -0.01980    0.001350      23.4   8.73e-02     0.46300
## TG(18:2/18:1/18:1)       -1.86e-02   -0.04070    0.003430      24.4   9.78e-02     0.49000
## SM(d41:2)                -1.22e-02   -0.02690    0.002600      22.5   1.06e-01     0.49000
## TG(54:4)                 -1.58e-02   -0.03510    0.003390      21.4   1.06e-01     0.49000
## PC(38:4)                 -8.23e-03   -0.01930    0.002840      25.2   1.45e-01     0.63600
## TG(56:6)                 -1.43e-02   -0.03400    0.005380      19.9   1.54e-01     0.63600
## PC(O-34:2)               -1.66e-02   -0.03970    0.006510      21.5   1.59e-01     0.63600
## TG(54:3)                 -1.03e-02   -0.02480    0.004150      21.7   1.62e-01     0.63600
## TG(16:0/22:5/18:1)       -1.56e-02   -0.03810    0.006880      22.7   1.74e-01     0.64400
## TG(52:3)                 -7.75e-03   -0.01900    0.003490      22.3   1.76e-01     0.64400
## TG(18:1/18:2/18:2)       -1.84e-02   -0.04610    0.009340      23.6   1.93e-01     0.66500
## TG(50:0)                 -2.21e-02   -0.05550    0.011400      20.8   1.95e-01     0.66500
## TG(18:1/18:1/18:1)       -1.37e-02   -0.03470    0.007350      24.8   2.02e-01     0.66500
## TG(54:5)                 -1.53e-02   -0.03980    0.009090      20.6   2.18e-01     0.66500
## PC(O-38:4)               -1.22e-02   -0.03190    0.007480      21.7   2.24e-01     0.66500
## TG(18:1/18:1/22:6)        3.32e-02   -0.02030    0.086700      20.7   2.24e-01     0.66500
## TG(16:0/18:2/18:2)       -1.47e-02   -0.03840    0.009090      24.5   2.26e-01     0.66500
## PC(32:1)                  1.76e-02   -0.01150    0.046600      23.3   2.36e-01     0.67500
## PC(38:2)                  8.75e-03   -0.00596    0.023500      21.2   2.43e-01     0.67800
## SM(d18:2/24:1)           -7.03e-03   -0.01900    0.004950      24.0   2.50e-01     0.67800
```

```
## TG(18:1/18:1/16:0)       1.22e-02   -0.00887    0.033300       25.6   2.56e-01       0.67900
## TG(52:4)                -9.75e-03   -0.02760    0.008140       21.6   2.85e-01       0.73700
## TG(48:3)                -1.97e-02   -0.05690    0.017600       20.5   3.00e-01       0.73900
## TG(54:2)                -1.07e-02   -0.03120    0.009810       23.4   3.06e-01       0.73900
## PC(40:6)                 1.06e-02   -0.00976    0.031000       23.9   3.07e-01       0.73900
## TG(18:2/22:5/16:0)       2.16e-02   -0.02080    0.064000       22.1   3.18e-01       0.74000
## SM(42:2)                -5.15e-03   -0.01540    0.005120       25.2   3.25e-01       0.74000
## PC(40:5)                 8.90e-03   -0.00896    0.026800       22.0   3.28e-01       0.74000
## SM(d34:1)                3.05e-03   -0.00338    0.009480       24.9   3.52e-01       0.76500
## TG(50:3)                -7.59e-03   -0.02400    0.008780       23.5   3.63e-01       0.76500
## PC(34:3)                 1.35e-02   -0.01580    0.042900       22.5   3.65e-01       0.76500
## PC(34:1)                 6.94e-03   -0.00819    0.022100       26.0   3.68e-01       0.76500
## PC(33:1)                 8.63e-03   -0.01090    0.028200       20.9   3.87e-01       0.77000
## PC(35:2)                -8.36e-03   -0.02730    0.010600       21.8   3.87e-01       0.77000
## PC(40:7)                 8.86e-03   -0.01160    0.029300       21.4   3.95e-01       0.77000
## TG(56:4)                -1.27e-02   -0.04230    0.016900       20.0   3.99e-01       0.77000
## PC(36:3)                -6.78e-03   -0.02320    0.009610       25.6   4.17e-01       0.77800
## LPC(16:1)                9.42e-03   -0.01340    0.032200       20.0   4.18e-01       0.77800
## TG(52:5)                -1.31e-02   -0.04630    0.020100       19.8   4.38e-01       0.79600
## PC(38:3)                -6.30e-03   -0.02240    0.009830       24.0   4.43e-01       0.79600
## PC(36:4)                -3.72e-03   -0.01340    0.005990       25.9   4.52e-01       0.79900
## TG(49:3)                 1.08e-03   -0.00194    0.004100       20.7   4.84e-01       0.84100
## PC(34:2)                 9.87e-03   -0.01880    0.038500       26.0   4.98e-01       0.84100
## PC(38:6)                 4.76e-03   -0.00910    0.018600       25.3   5.00e-01       0.84100
## TG(53:4)                -8.61e-03   -0.03750    0.020300       19.7   5.59e-01       0.92000
## TG(52:2)                -2.80e-03   -0.01230    0.006730       22.6   5.64e-01       0.92000
## PC(O-36:4)              -4.97e-03   -0.02270    0.012800       22.9   5.82e-01       0.93500
## TG(56:3)                -6.53e-03   -0.03130    0.018200       20.0   6.04e-01       0.94700
## TG(45:0)                 1.85e-03   -0.00534    0.009050       23.1   6.14e-01       0.94700
## PC(32:0)                 2.54e-03   -0.00740    0.012500       22.5   6.16e-01       0.94700
## TG(16:0/18:2/18:3)      -9.63e-03   -0.04880    0.029600       22.0   6.30e-01       0.95200
## TG(51:2)                 4.73e-03   -0.01520    0.024700       21.6   6.42e-01       0.95200
## PC(O-38:5)              -3.25e-03   -0.01810    0.011600       22.8   6.68e-01       0.95200
## TG(18:2/18:1/16:0)       3.95e-03   -0.01470    0.022600       25.3   6.78e-01       0.95200
## SM(d33:1)               -2.99e-03   -0.01730    0.011300       21.3   6.81e-01       0.95200
## TG(14:0/16:0/18:1)       4.95e-03   -0.02160    0.031500       22.8   7.15e-01       0.95200
## PC(16:0e/18:1(9Z)       -2.72e-03   -0.01740    0.011900       21.8   7.15e-01       0.95200
## TG(58:9)                 1.01e-02   -0.04420    0.064400       19.9   7.16e-01       0.95200
## TG(16:0/18:0/18:1)      -6.11e-03   -0.03940    0.027200       23.1   7.19e-01       0.95200
## PC(32:2)                -4.70e-03   -0.03050    0.021100       20.7   7.20e-01       0.95200
## TG(14:0/18:2/18:2)      -5.05e-03   -0.03370    0.023600       21.2   7.29e-01       0.95200
## TG(50:1)                 4.37e-03   -0.02180    0.030600       24.3   7.43e-01       0.95200
## TG(46:0)                -4.62e-03   -0.03360    0.024400       20.4   7.55e-01       0.95200
## TG(18:2/18:2/18:2)      -4.63e-03   -0.03550    0.026200       22.1   7.68e-01       0.95200
## TG(49:2)                -2.66e-03   -0.02210    0.016800       20.4   7.88e-01       0.95200
## TG(14:0/18:1/18:1)      -2.28e-03   -0.01930    0.014700       24.4   7.92e-01       0.95200
## TG(46:1)                -3.95e-03   -0.03390    0.026000       21.3   7.95e-01       0.95200
## TG(53:3)                -3.11e-03   -0.02690    0.020700       20.7   7.98e-01       0.95200
## TG(18:1/12:0/18:1)      -3.15e-03   -0.02880    0.022500       22.5   8.09e-01       0.95200
## TG(51:3)                -2.84e-03   -0.02630    0.020600       20.7   8.12e-01       0.95200
## TG(51:1)                -2.65e-03   -0.02690    0.021600       20.3   8.30e-01       0.95200
## PC(36:5)                -3.35e-03   -0.03550    0.028800       24.3   8.38e-01       0.95200
## LPC(16:0)               -7.46e-04   -0.00821    0.006720       25.3   8.44e-01       0.95200
## LPC(18:0)                1.24e-03   -0.01240    0.014900       23.9   8.59e-01       0.95200
```

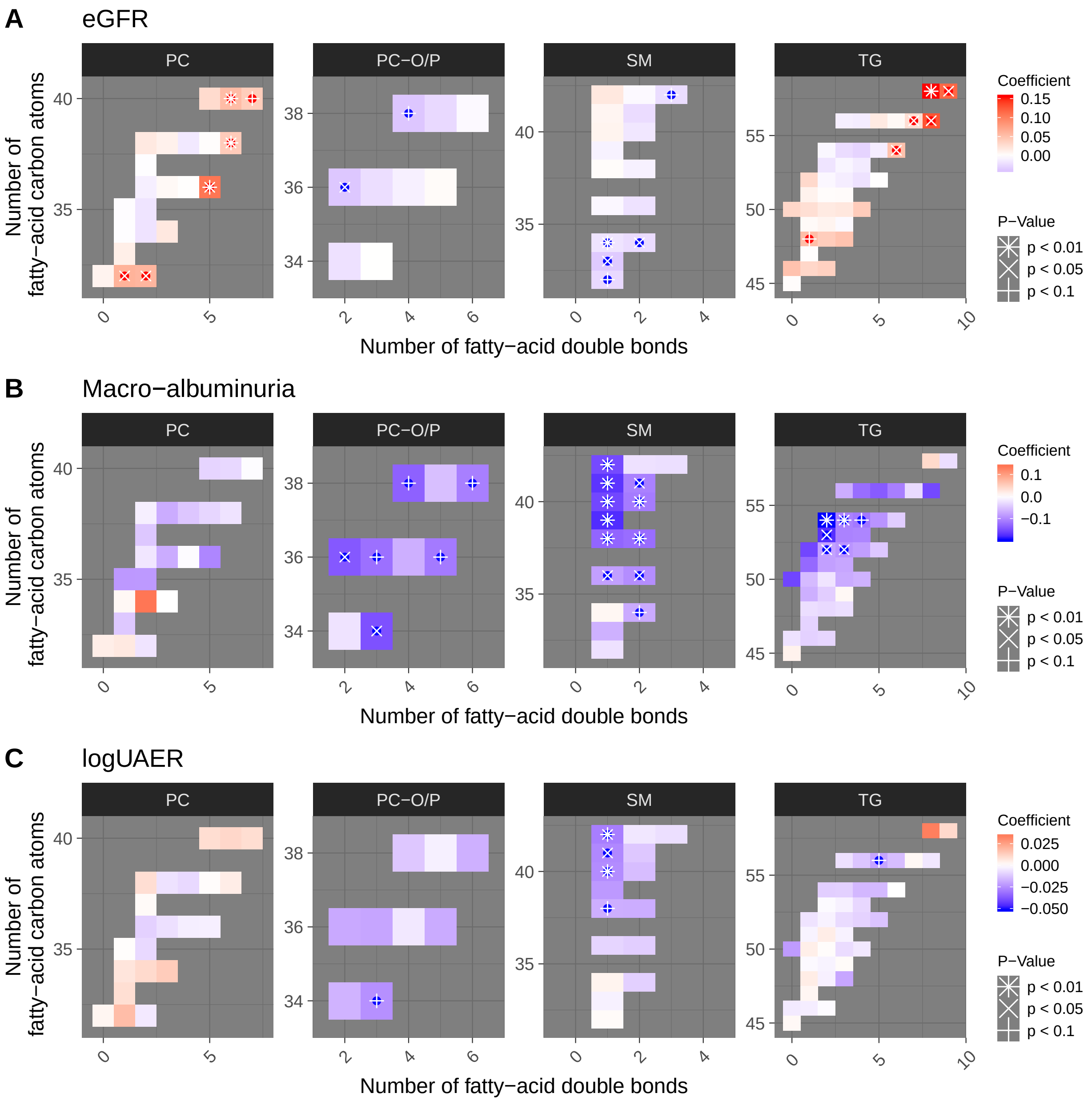
```
## TG(16:0/18:2/22:6)       -5.16e-03   -0.06280    0.052500       21.0   8.61e-01      0.95200
## PC(38:5)                  8.69e-04   -0.00909    0.010800       24.6   8.64e-01      0.95200
## SM(d32:1)                 1.11e-03   -0.01220    0.014400       22.3   8.69e-01      0.95200
## TG(56:7)                  1.92e-03   -0.02240    0.026200       19.6   8.77e-01      0.95200
## TG(47:1)                  2.39e-03   -0.02890    0.033700       19.6   8.81e-01      0.95200
## LPC(18:1)                -1.20e-03   -0.01870    0.016300       23.7   8.93e-01      0.95200
## PC(37:2)                  1.44e-03   -0.02180    0.024700       19.3   9.03e-01      0.95200
## TG(49:1)                 -1.31e-03   -0.02340    0.020800       20.9   9.07e-01      0.95200
## TG(50:2)                  7.19e-04   -0.01370    0.015200       21.1   9.22e-01      0.95800
## TG(53:2)                 -9.74e-04   -0.02520    0.023300       20.7   9.37e-01      0.96200
## PC(35:1)                  5.15e-04   -0.01630    0.017300       21.8   9.52e-01      0.96200
## TG(46:2)                 -9.01e-04   -0.03110    0.029300       20.1   9.53e-01      0.96200
## TG(54:6)                 -6.16e-05   -0.03360    0.033500       19.5   9.97e-01      0.99700
```

1.1.3.2.2 Heatmaps

```
## [1] "map_lipid_names has been created by Tommi Suvitaival"
## [1] "tommi.raimo.leo.suvitaival@regionh.dk"
## [1] "2019-05-06"
```



1.1.4 Combined Heatmaps from Adjusted Cross-sectional Analyses


A
eGFR
B
Macro−albuminuria
C
logUAER
PC
PC−O/P
SM
TG
Number of fatty−acid carbon atoms
Number of fatty−acid double bonds
40
35
38
36
34
55
50
45
0
2
4
5
6
10
Coefficient
0.15
0.10
0.05
0.00
0.1
0.0
−0.1
0.025
0.000
−0.025
−0.050
P−Value
p < 0.01
p < 0.05
p < 0.1

1.2 Step 1B: Crude Associations of All Lipids to Clinical Changes Over Time

1.2.1 eGFR Slope

1.2.1.1 Table

```
##
##
## Table: Results of the crude model for the eGFR slope.
## Shown in the table are name of the lipid (Name),
## model coefficient (Coefficient),
## its lower and upper confidence intervals (CI.L, CL.R),
## average value of the variable (AveExpr),
## p-value of the coefficient (P.Value) and
## the p-value after correction for multiple testing (adj.P.Val).
## The rows of the table are shown in an increasing order by the respective p-value.
##
## Name                  Coefficient        CI.L        CI.R   AveExpr    P.Value   adj.P.Val
## -------------------  ------------  ----------  ----------  --------  ---------  ----------
## PC(36:4)                -0.012800   -0.018600   -0.006930      26.0   2.14e-05     0.00227
## TG(14:0/16:0/18:1)      -0.035400   -0.058100   -0.012700      22.8   2.26e-03     0.06860
## LPC(16:0)               -0.007400   -0.012200   -0.002640      25.3   2.35e-03     0.06860
## PC(O-38:6)               0.015000    0.005030    0.024900      20.4   3.22e-03     0.06860
## TG(51:3)                -0.030200   -0.050700   -0.009640      20.7   4.04e-03     0.06860
## TG(51:2)                -0.029400   -0.049700   -0.009180      21.5   4.47e-03     0.06860
## TG(50:2)                -0.021000   -0.035600   -0.006330      21.1   5.08e-03     0.06860
## TG(14:0/18:1/18:1)      -0.025000   -0.042500   -0.007520      24.4   5.18e-03     0.06860
## TG(50:0)                -0.035200   -0.061500   -0.008980      20.8   8.62e-03     0.08520
## TG(18:2/18:2/18:2)      -0.031500   -0.055300   -0.007820      22.1   9.27e-03     0.08520
## TG(51:1)                -0.028700   -0.050300   -0.007010      20.3   9.59e-03     0.08520
## TG(46:0)                -0.027600   -0.048600   -0.006740      20.4   9.64e-03     0.08520
## TG(50:3)                -0.023500   -0.042700   -0.004340      23.4   1.64e-02     0.13100
## TG(52:2)                -0.012000   -0.021800   -0.002120      22.6   1.74e-02     0.13100
## TG(49:1)                -0.021000   -0.038500   -0.003490      20.8   1.88e-02     0.13300
## TG(18:1/12:0/18:1)      -0.027400   -0.050700   -0.004130      22.4   2.11e-02     0.14000
## PC(32:1)                -0.022500   -0.042100   -0.002910      23.3   2.45e-02     0.15000
## TG(46:1)                -0.026100   -0.049000   -0.003210      21.2   2.55e-02     0.15000
## TG(50:1)                -0.026100   -0.049400   -0.002820      24.3   2.81e-02     0.15000
## TG(16:0/18:0/18:1)      -0.033000   -0.062800   -0.003200      23.1   3.01e-02     0.15000
## PC(38:3)                -0.012400   -0.023800   -0.001050      24.0   3.23e-02     0.15000
## TG(14:0/18:2/18:2)      -0.029900   -0.057400   -0.002490      21.1   3.26e-02     0.15000
## PC(O-36:2)               0.012600    0.001040    0.024100      20.5   3.26e-02     0.15000
## TG(49:2)                -0.016800   -0.032400   -0.001220      20.4   3.47e-02     0.15200
## TG(53:2)                -0.024500   -0.047500   -0.001620      20.6   3.60e-02     0.15200
## TG(48:3)                -0.032900   -0.064000   -0.001720      20.5   3.87e-02     0.15600
## TG(56:5)                -0.019500   -0.038200   -0.000833      20.3   4.07e-02     0.15600
## PC(36:3)                -0.011100   -0.021700   -0.000450      25.6   4.11e-02     0.15600
## PC(33:1)                -0.014400   -0.028400   -0.000378      20.8   4.42e-02     0.15800
## TG(16:0/22:5/18:1)      -0.018700   -0.036900   -0.000453      22.7   4.46e-02     0.15800
## TG(46:2)                -0.024800   -0.049400   -0.000318      20.1   4.71e-02     0.16100
## TG(53:3)                -0.019900   -0.041300    0.001400      20.7   6.70e-02     0.22200
## LPC(16:1)               -0.013100   -0.027400    0.001300      20.0   7.45e-02     0.23900
## PC(34:3)                -0.017700   -0.037700    0.002240      22.4   8.17e-02     0.24700
## PC(O-38:5)               0.008360   -0.001100    0.017800      22.8   8.30e-02     0.24700
## TG(18:2/22:5/16:0)      -0.026400   -0.056300    0.003540      22.1   8.39e-02     0.24700
## PC(32:2)                -0.015500   -0.033200    0.002220      20.7   8.64e-02     0.24700
## TG(52:3)                -0.008570   -0.018900    0.001720      22.3   1.03e-01     0.28100
## TG(18:0/18:1/20:4)      -0.020000   -0.044400    0.004420      21.3   1.08e-01     0.28100
```

```
## TG(45:0)                0.006260   -0.001450    0.014000       23.1   1.11e-01      0.28100
## PC(O-34:3)              0.009890   -0.002290    0.022100       21.9   1.11e-01      0.28100
## PC(36:2)               -0.006190   -0.013900    0.001470       26.1   1.13e-01      0.28100
## TG(49:3)                0.002120   -0.000512    0.004760       20.7   1.14e-01      0.28100
## TG(54:2)               -0.017100   -0.038800    0.004580       23.4   1.22e-01      0.29300
## PC(O-34:2)              0.011200   -0.003900    0.026300       21.5   1.46e-01      0.34300
## TG(16:0/18:2/18:2)     -0.014900   -0.035500    0.005600       24.5   1.54e-01      0.35400
## PC(16:0e/18:1(9Z)       0.007230   -0.002810    0.017300       21.8   1.58e-01      0.35600
## TG(52:5)               -0.017100   -0.041200    0.006940       19.8   1.63e-01      0.36000
## TG(56:6)               -0.010400   -0.025100    0.004430       19.9   1.69e-01      0.36600
## TG(56:7)               -0.010700   -0.027500    0.006090       19.6   2.11e-01      0.44700
## LPC(18:0)              -0.005540   -0.014300    0.003240       24.0   2.16e-01      0.44800
## TG(18:1/18:1/16:0)     -0.007830   -0.021000    0.005300       25.6   2.42e-01      0.48800
## TG(54:6)               -0.015200   -0.040900    0.010400       19.5   2.44e-01      0.48800
## PC(40:7)                0.007890   -0.005830    0.021600       21.4   2.59e-01      0.50300
## PC(34:1)                0.005220   -0.003920    0.014400       25.9   2.63e-01      0.50300
## SM(d41:2)               0.006020   -0.004590    0.016600       22.5   2.66e-01      0.50300
## PC(40:5)               -0.006980   -0.019600    0.005660       22.0   2.79e-01      0.51800
## SM(d39:1)               0.007040   -0.005970    0.020000       21.1   2.88e-01      0.52200
## PC(35:1)               -0.006450   -0.018400    0.005530       21.8   2.91e-01      0.52200
## TG(16:0/18:2/18:3)     -0.016500   -0.047600    0.014600       22.0   2.98e-01      0.52600
## LPC(18:1)              -0.005800   -0.017100    0.005520       23.7   3.15e-01      0.54700
## TG(18:1/18:1/22:6)     -0.017200   -0.051300    0.017000       20.7   3.23e-01      0.55200
## SM(d41:1)               0.005540   -0.005750    0.016800       22.7   3.35e-01      0.56400
## PC(O-36:3)              0.006160   -0.006810    0.019100       20.4   3.51e-01      0.57500
## TG(53:4)               -0.010900   -0.034100    0.012300       19.7   3.58e-01      0.57500
## PC(35:2)                0.005610   -0.006570    0.017800       21.8   3.66e-01      0.57500
## PC(O-36:5)              0.004720   -0.005550    0.015000       22.3   3.67e-01      0.57500
## SM(d32:1)              -0.004430   -0.014100    0.005260       22.3   3.69e-01      0.57500
## PC(38:4)               -0.003100   -0.010100    0.003920       25.2   3.86e-01      0.58400
## TG(52:4)               -0.006750   -0.022200    0.008660       21.6   3.90e-01      0.58400
## PC(38:5)               -0.002930   -0.009650    0.003780       24.6   3.91e-01      0.58400
## SM(d34:1)               0.001860   -0.002470    0.006190       24.9   3.99e-01      0.58700
## SM(d33:1)               0.004150   -0.005770    0.014100       21.3   4.12e-01      0.59800
## TG(56:3)               -0.008500   -0.030900    0.013900       20.0   4.56e-01      0.65300
## TG(18:1/18:1/18:1)     -0.006390   -0.023600    0.010800       24.8   4.65e-01      0.65600
## TG(16:0/18:2/22:6)     -0.014200   -0.053100    0.024700       21.0   4.74e-01      0.65600
## TG(54:3)               -0.004750   -0.017900    0.008360       21.7   4.77e-01      0.65600
## PC(38:2)               -0.003190   -0.013500    0.007130       21.3   5.44e-01      0.73900
## PC(40:6)                0.004160   -0.009910    0.018200       23.9   5.62e-01      0.75400
## TG(58:9)               -0.009850   -0.044500    0.024800       19.9   5.76e-01      0.75500
## SM(d18:2/24:1)          0.002410   -0.006080    0.010900       24.0   5.77e-01      0.75500
## TG(18:2/18:1/18:1)     -0.004280   -0.021500    0.013000       24.4   6.27e-01      0.80100
## SM(d40:2)               0.002030   -0.006190    0.010300       23.7   6.28e-01      0.80100
## SM(d38:1)               0.002100   -0.006660    0.010900       23.1   6.38e-01      0.80500
## TG(18:1/18:2/18:2)     -0.004810   -0.026700    0.017000       23.6   6.65e-01      0.81300
## PC(O-38:4)             -0.002830   -0.015700    0.010000       21.7   6.65e-01      0.81300
## SM(d38:2)               0.002040   -0.007320    0.011400       21.4   6.68e-01      0.81300
## SM(42:2)                0.001580   -0.005800    0.008960       25.2   6.75e-01      0.81300
## PC(38:6)                0.001880   -0.007210    0.011000       25.3   6.85e-01      0.81600
## SM(d40:1)               0.001860   -0.007510    0.011200       24.0   6.97e-01      0.82100
## SM(d36:2)               0.001370   -0.006720    0.009450       21.4   7.40e-01      0.86100
## PC(34:2)                0.003020   -0.015400    0.021400       26.0   7.48e-01      0.86100
## TG(47:1)               -0.002760   -0.021900    0.016400       19.5   7.78e-01      0.88600
```

```
## LPC(20:4)               -0.002000   -0.016700    0.012700      21.4   7.89e-01     0.89000
## SM(d18:1/24:0)          -0.001260   -0.011200    0.008640      23.6   8.03e-01     0.89100
## TG(54:5)                 0.002260   -0.016100    0.020600      20.6   8.09e-01     0.89100
## SM(d16:1/18:1)          -0.001010   -0.009550    0.007530      22.8   8.16e-01     0.89100
## PC(32:0)                 0.000682   -0.005980    0.007340      22.5   8.41e-01     0.90900
## PC(36:5)                -0.002100   -0.024300    0.020100      24.3   8.52e-01     0.91300
## SM(d36:1)               -0.000595   -0.008270    0.007080      23.4   8.79e-01     0.93200
## TG(56:4)                -0.001740   -0.026800    0.023300      20.0   8.92e-01     0.93600
## LPC(18:2)               -0.000865   -0.015500    0.013800      24.0   9.08e-01     0.94300
## PC(37:2)                 0.000590   -0.015200    0.016300      19.3   9.41e-01     0.95500
## TG(18:2/18:1/16:0)       0.000421   -0.011600    0.012500      25.3   9.45e-01     0.95500
## PC(O-36:4)              -0.000376   -0.011400    0.010600      22.9   9.46e-01     0.95500
## TG(54:4)                -0.000244   -0.015300    0.014800      21.4   9.75e-01     0.97500
##
##
## Table: Results of the crude model for the eGFR slope.
## Shown in the table are name of the lipid (Name),
## model coefficient (Coefficient),
## its lower and upper confidence intervals (CI.L, CL.R),
## average value of the variable (AveExpr),
## p-value of the coefficient (P.Value) and
## the p-value after correction for multiple testing (adj.P.Val).
## The rows of the table are shown in an increasing order by the respective p-value.
##
## Name                  Coefficient        CI.L        CI.R   AveExpr    P.Value   adj.P.Val
## -------------------  ------------  ----------  ----------  --------  ---------  ----------
## SM(d36:2)               -3.15e-03   -4.22e-03   -2.08e-03      21.4   0.00e+00    1.30e-06
## SM(d34:1)               -1.37e-03   -1.94e-03   -7.96e-04      24.9   3.40e-06    1.36e-04
## SM(d16:1/18:1)          -2.68e-03   -3.81e-03   -1.55e-03      22.8   3.90e-06    1.36e-04
## PC(38:4)                -2.12e-03   -3.05e-03   -1.19e-03      25.2   8.70e-06    2.31e-04
## TG(18:0/18:1/20:4)      -6.80e-03   -1.00e-02   -3.58e-03      21.3   3.98e-05    8.44e-04
## SM(d18:2/24:1)          -2.31e-03   -3.43e-03   -1.18e-03      24.0   6.19e-05    1.09e-03
## LPC(18:2)                3.87e-03    1.94e-03    5.80e-03      24.0   9.59e-05    1.45e-03
## SM(d32:1)               -2.45e-03   -3.73e-03   -1.17e-03      22.3   1.89e-04    2.51e-03
## SM(d18:1/24:0)           2.20e-03    8.95e-04    3.51e-03      23.6   1.00e-03    1.18e-02
## SM(d33:1)               -2.08e-03   -3.39e-03   -7.67e-04      21.3   1.95e-03    2.06e-02
## SM(d38:2)               -1.87e-03   -3.11e-03   -6.36e-04      21.4   3.08e-03    2.96e-02
## LPC(16:0)                9.24e-04    2.95e-04    1.55e-03      25.3   4.06e-03    3.59e-02
## SM(d36:1)               -1.39e-03   -2.41e-03   -3.77e-04      23.4   7.27e-03    5.93e-02
## PC(32:2)                 3.10e-03    7.61e-04    5.44e-03      20.7   9.49e-03    7.18e-02
## SM(d41:2)               -1.69e-03   -3.09e-03   -2.87e-04      22.5   1.83e-02    1.29e-01
## SM(d40:2)               -1.26e-03   -2.35e-03   -1.78e-04      23.7   2.26e-02    1.47e-01
## SM(d40:1)                1.43e-03    1.94e-04    2.67e-03      24.0   2.35e-02    1.47e-01
## TG(53:2)                -3.20e-03   -6.23e-03   -1.75e-04      20.6   3.82e-02    2.15e-01
## PC(38:5)                -9.37e-04   -1.82e-03   -4.94e-05      24.6   3.86e-02    2.15e-01
## TG(16:0/22:5/18:1)      -2.45e-03   -4.86e-03   -4.27e-05      22.7   4.61e-02    2.44e-01
## TG(56:6)                -1.93e-03   -3.89e-03    2.04e-05      19.9   5.24e-02    2.65e-01
## TG(52:2)                -1.24e-03   -2.54e-03    6.17e-05      22.6   6.19e-02    2.89e-01
## LPC(18:1)                1.42e-03   -7.53e-05    2.92e-03      23.7   6.27e-02    2.89e-01
## LPC(18:0)                1.07e-03   -8.74e-05    2.23e-03      24.0   6.99e-02    3.09e-01
## TG(56:5)                -2.23e-03   -4.70e-03    2.39e-04      20.3   7.66e-02    3.14e-01
## PC(O-34:3)               1.45e-03   -1.58e-04    3.06e-03      21.9   7.70e-02    3.14e-01
## PC(16:0e/18:1(9Z)       -1.18e-03   -2.51e-03    1.43e-04      21.8   8.01e-02    3.15e-01
## PC(40:6)                -1.64e-03   -3.50e-03    2.19e-04      23.9   8.36e-02    3.16e-01
```

```
## PC(38:3)             -1.27e-03 -2.78e-03 2.30e-04   24.0 9.66e-02 3.43e-01
## TG(54:3)             -1.47e-03 -3.20e-03 2.67e-04   21.7 9.72e-02 3.43e-01
## PC(40:5)             -1.37e-03 -3.05e-03 2.97e-04   22.0 1.07e-01 3.56e-01
## PC(35:1)             -1.30e-03 -2.88e-03 2.84e-04   21.8 1.08e-01 3.56e-01
## TG(51:2)             -2.12e-03 -4.80e-03 5.57e-04   21.5 1.20e-01 3.87e-01
## TG(54:2)             -2.23e-03 -5.10e-03 6.33e-04   23.4 1.26e-01 3.92e-01
## SM(d41:1)             1.14e-03 -3.49e-04 2.64e-03   22.7 1.33e-01 3.92e-01
## PC(37:2)              1.59e-03 -4.87e-04 3.68e-03   19.3 1.33e-01 3.92e-01
## PC(O-38:6)           -9.80e-04 -2.29e-03 3.32e-04   20.4 1.43e-01 4.07e-01
## PC(34:2)             -1.80e-03 -4.23e-03 6.29e-04   26.0 1.46e-01 4.07e-01
## TG(56:3)             -2.11e-03 -5.07e-03 8.48e-04   20.0 1.62e-01 4.36e-01
## TG(45:0)              7.22e-04 -2.96e-04 1.74e-03   23.1 1.64e-01 4.36e-01
## SM(42:2)             -6.60e-04 -1.64e-03 3.15e-04   25.2 1.84e-01 4.66e-01
## TG(52:3)             -9.16e-04 -2.28e-03 4.44e-04   22.3 1.86e-01 4.66e-01
## PC(34:3)              1.77e-03 -8.73e-04 4.41e-03   22.4 1.89e-01 4.66e-01
## PC(35:2)              1.01e-03 -5.97e-04 2.62e-03   21.8 2.17e-01 5.16e-01
## TG(53:3)             -1.77e-03 -4.58e-03 1.05e-03   20.7 2.19e-01 5.16e-01
## TG(51:1)             -1.75e-03 -4.61e-03 1.11e-03   20.3 2.31e-01 5.31e-01
## LPC(16:1)             1.14e-03 -7.56e-04 3.04e-03   20.0 2.37e-01 5.35e-01
## TG(49:3)              2.00e-04 -1.48e-04 5.48e-04   20.7 2.60e-01 5.39e-01
## TG(53:4)             -1.76e-03 -4.83e-03 1.31e-03   19.7 2.60e-01 5.39e-01
## TG(18:1/18:1/16:0)   -9.35e-04 -2.67e-03 8.01e-04   25.6 2.90e-01 5.39e-01
## TG(50:2)             -1.04e-03 -2.97e-03 8.94e-04   21.1 2.91e-01 5.39e-01
## TG(54:4)             -1.06e-03 -3.04e-03 9.26e-04   21.4 2.95e-01 5.39e-01
## PC(36:4)             -4.13e-04 -1.19e-03 3.61e-04   26.0 2.95e-01 5.39e-01
## TG(18:1/18:1/18:1)   -1.21e-03 -3.48e-03 1.06e-03   24.8 2.96e-01 5.39e-01
## PC(O-34:2)            1.06e-03 -9.36e-04 3.05e-03   21.5 2.98e-01 5.39e-01
## PC(O-38:5)           -6.62e-04 -1.91e-03 5.88e-04   22.8 2.99e-01 5.39e-01
## TG(52:4)             -1.08e-03 -3.12e-03 9.59e-04   21.6 2.99e-01 5.39e-01
## PC(O-36:2)           -8.03e-04 -2.33e-03 7.21e-04   20.5 3.01e-01 5.39e-01
## TG(14:0/18:1/18:1)   -1.22e-03 -3.53e-03 1.10e-03   24.4 3.02e-01 5.39e-01
## TG(56:7)             -1.16e-03 -3.38e-03 1.06e-03   19.6 3.05e-01 5.39e-01
## TG(18:2/18:2/18:2)   -1.51e-03 -4.65e-03 1.62e-03   22.1 3.43e-01 5.96e-01
## TG(16:0/18:0/18:1)   -1.79e-03 -5.72e-03 2.15e-03   23.1 3.73e-01 6.35e-01
## TG(18:2/22:5/16:0)   -1.78e-03 -5.73e-03 2.18e-03   22.1 3.78e-01 6.35e-01
## TG(49:1)             -9.96e-04 -3.31e-03 1.32e-03   20.8 3.97e-01 6.35e-01
## TG(51:3)             -1.17e-03 -3.88e-03 1.54e-03   20.7 3.98e-01 6.35e-01
## TG(49:2)             -8.76e-04 -2.93e-03 1.18e-03   20.4 4.03e-01 6.35e-01
## PC(O-38:4)           -7.19e-04 -2.41e-03 9.76e-04   21.7 4.05e-01 6.35e-01
## TG(18:2/18:1/18:1)   -9.62e-04 -3.24e-03 1.32e-03   24.4 4.08e-01 6.35e-01
## TG(18:2/18:1/16:0)   -6.62e-04 -2.25e-03 9.29e-04   25.3 4.14e-01 6.36e-01
## TG(16:0/18:2/18:2)   -1.08e-03 -3.80e-03 1.63e-03   24.5 4.33e-01 6.56e-01
## TG(50:3)             -9.59e-04 -3.49e-03 1.58e-03   23.4 4.58e-01 6.58e-01
## PC(40:7)             -6.86e-04 -2.50e-03 1.13e-03   21.4 4.58e-01 6.58e-01
## PC(33:1)             -7.00e-04 -2.55e-03 1.15e-03   20.8 4.58e-01 6.58e-01
## TG(56:4)             -1.23e-03 -4.54e-03 2.09e-03   20.0 4.67e-01 6.58e-01
## TG(50:1)             -1.14e-03 -4.21e-03 1.94e-03   24.3 4.69e-01 6.58e-01
## PC(32:0)             -3.23e-04 -1.20e-03 5.57e-04   22.5 4.72e-01 6.58e-01
## TG(54:6)             -1.21e-03 -4.60e-03 2.18e-03   19.5 4.83e-01 6.64e-01
## TG(16:0/18:2/18:3)   -1.39e-03 -5.50e-03 2.72e-03   22.0 5.07e-01 6.81e-01
## TG(50:0)             -1.17e-03 -4.64e-03 2.30e-03   20.8 5.08e-01 6.81e-01
## PC(36:3)             -4.38e-04 -1.84e-03 9.66e-04   25.6 5.40e-01 7.16e-01
## PC(34:1)             -3.59e-04 -1.57e-03 8.49e-04   25.9 5.60e-01 7.32e-01
## TG(16:0/18:2/22:6)   -1.40e-03 -6.55e-03 3.74e-03   21.0 5.92e-01 7.64e-01
```

```
## PC(38:6)               -3.22e-04  -1.52e-03   8.79e-04      25.3  5.99e-01   7.64e-01
## TG(52:5)               -7.78e-04  -3.96e-03   2.40e-03      19.8  6.31e-01   7.96e-01
## SM(d39:1)              -3.73e-04  -2.09e-03   1.35e-03      21.1  6.70e-01   8.28e-01
## TG(47:1)               -5.48e-04  -3.08e-03   1.99e-03      19.5  6.72e-01   8.28e-01
## TG(18:1/18:2/18:2)     -5.41e-04  -3.43e-03   2.35e-03      23.6  7.13e-01   8.69e-01
## PC(32:1)               -4.67e-04  -3.06e-03   2.12e-03      23.3  7.23e-01   8.71e-01
## TG(54:5)               -3.04e-04  -2.73e-03   2.12e-03      20.6  8.06e-01   9.60e-01
## TG(14:0/16:0/18:1)     -3.46e-04  -3.34e-03   2.65e-03      22.8  8.20e-01   9.63e-01
## LPC(20:4)               2.17e-04  -1.72e-03   2.16e-03      21.4  8.26e-01   9.63e-01
## PC(O-36:3)             -1.80e-04  -1.89e-03   1.53e-03      20.4  8.37e-01   9.64e-01
## TG(48:3)                3.90e-04  -3.73e-03   4.51e-03      20.5  8.53e-01   9.72e-01
## PC(36:5)               -2.48e-04  -3.18e-03   2.68e-03      24.3  8.68e-01   9.79e-01
## TG(46:0)                1.58e-04  -2.61e-03   2.92e-03      20.4  9.11e-01   9.92e-01
## TG(18:1/18:1/22:6)     -2.27e-04  -4.74e-03   4.28e-03      20.7  9.21e-01   9.92e-01
## TG(58:9)                2.28e-04  -4.35e-03   4.80e-03      19.9  9.22e-01   9.92e-01
## TG(18:1/12:0/18:1)     -9.00e-05  -3.17e-03   2.99e-03      22.4  9.54e-01   9.92e-01
## SM(d38:1)               3.02e-05  -1.13e-03   1.19e-03      23.1  9.59e-01   9.92e-01
## TG(14:0/18:2/18:2)     -9.44e-05  -3.72e-03   3.53e-03      21.1  9.59e-01   9.92e-01
## PC(36:2)                2.17e-05  -9.91e-04   1.03e-03      26.1  9.66e-01   9.92e-01
## PC(38:2)               -2.20e-05  -1.39e-03   1.34e-03      21.3  9.75e-01   9.92e-01
## PC(O-36:5)             -1.46e-05  -1.37e-03   1.34e-03      22.3  9.83e-01   9.92e-01
## PC(O-36:4)              8.80e-06  -1.45e-03   1.46e-03      22.9  9.90e-01   9.92e-01
## TG(46:1)               -1.82e-05  -3.05e-03   3.01e-03      21.2  9.91e-01   9.92e-01
## TG(46:2)               -1.67e-05  -3.26e-03   3.22e-03      20.1  9.92e-01   9.92e-01
```

1.2.1.2 Heatmaps

```
##   Label Relation p.adj
## 1     #  p.adj <  0.01
## 2     x  p.adj <  0.05
## 3     *  p.adj <  0.10
```

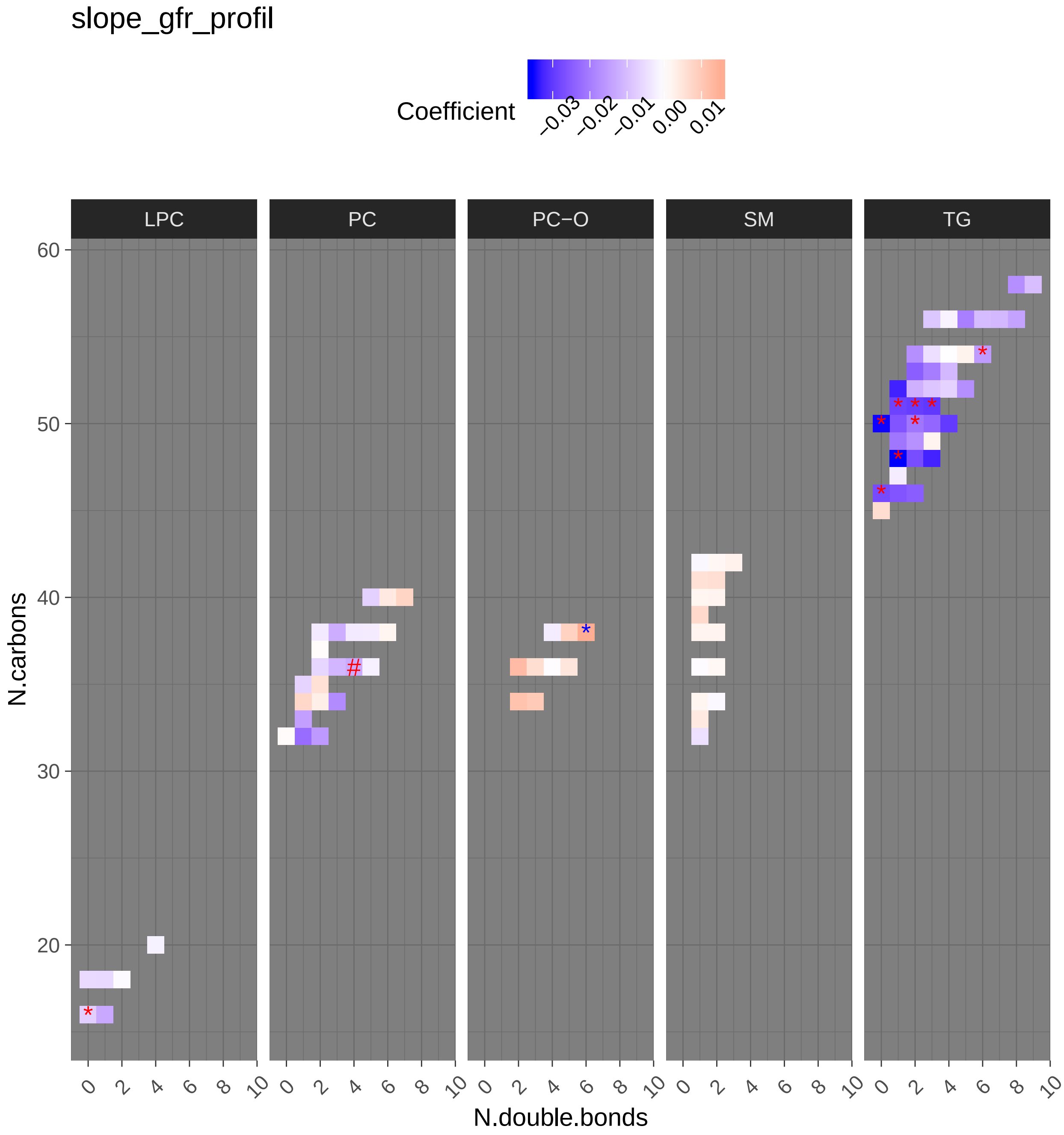


Figure 9: Heatmap of the lipid-specific model coefficents from the crude model for eGFR slope. The name of the group is shown in the title of the figure in the top-left corner. Lipids are organized into panels (columns) by their class (from LPC to TG). One colored rectangle corresponds to one lipid species, where the coordinates in the x-axis and y-axis, respectively, show the number of double bonds (N.double.bonds) and the number of carbon atoms (N.carbons) in the fatty acid chains of the lipid. The number of double bonds corresponds to the number of unsaturated bonds in the fatty acid chains, and the number of carbon atoms corresponds to the length of the fatty acid chains and, thus, the size of the lipid. The magnitude of the lipid-specifc model coefficient is shown as the color of the rectangle (blue: negative; red: positive). Coefficient with statistical significance are annotated with symbols #, x and *, respectively, corresponding to $p < 0.01$, $p < 0.05$ and $p < 0.1$.

1.2.2 Albuminuria Slope

1.2.2.1 Table

```
##
##
## Table: Results of the crude model for the continuous albuminuria (logUAER) slope.
## Shown in the table are name of the lipid (Name),
## model coefficient (Coefficient),
## its lower and upper confidence intervals (CI.L, CL.R),
## average value of the variable (AveExpr),
## p-value of the coefficient (P.Value) and
## the p-value after correction for multiple testing (adj.P.Val).
## The rows of the table are shown in an increasing order by the respective p-value.
##
## Name                  Coefficient      CI.L        CI.R   AveExpr    P.Value   adj.P.Val
## -------------------  ------------  --------  ----------  --------  ---------  ----------
## LPC(18:2)               -0.297000   -0.4640   -0.130000      24.0   0.000511      0.0315
## PC(O-36:5)              -0.193000   -0.3030   -0.083500      22.3   0.000595      0.0315
## PC(O-36:4)              -0.201000   -0.3200   -0.081300      22.9   0.001030      0.0364
## PC(O-38:5)              -0.164000   -0.2680   -0.060700      22.8   0.001940      0.0505
## PC(O-38:6)              -0.167000   -0.2760   -0.058800      20.4   0.002570      0.0505
## PC(O-38:4)              -0.210000   -0.3490   -0.071200      21.7   0.003090      0.0505
## SM(d18:1/24:0)          -0.168000   -0.2800   -0.056000      23.6   0.003340      0.0505
## PC(O-34:3)              -0.188000   -0.3190   -0.056700      21.9   0.005100      0.0676
## PC(O-34:2)              -0.232000   -0.3990   -0.066400      21.5   0.006180      0.0728
## SM(d40:1)               -0.138000   -0.2450   -0.031400      24.0   0.011300      0.1200
## LPC(20:4)               -0.200000   -0.3660   -0.034300      21.4   0.018200      0.1750
## SM(d38:1)               -0.113000   -0.2130   -0.012100      23.1   0.028200      0.2490
## LPC(18:1)               -0.137000   -0.2640   -0.009630      23.7   0.035000      0.2860
## SM(d41:1)               -0.129000   -0.2560   -0.000812      22.7   0.048600      0.3680
## LPC(16:0)               -0.049600   -0.1050    0.005320      25.3   0.076600      0.5130
## LPC(18:0)               -0.089500   -0.1890    0.009880      24.0   0.077400      0.5130
## SM(d39:1)               -0.130000   -0.2810    0.020500      21.1   0.090200      0.5630
## PC(O-36:3)              -0.112000   -0.2540    0.030700      20.4   0.124000      0.7310
## PC(36:2)                -0.059700   -0.1390    0.019400      26.1   0.139000      0.7740
## PC(32:1)                 0.160000   -0.0605    0.381000      23.3   0.154000      0.8040
## TG(54:6)                 0.202000   -0.0843    0.489000      19.5   0.166000      0.8040
## TG(49:3)                -0.021900   -0.0530    0.009180      20.7   0.167000      0.8040
## PC(32:0)                 0.051700   -0.0235    0.127000      22.5   0.177000      0.8040
## PC(34:1)                -0.074200   -0.1830    0.034900      25.9   0.182000      0.8040
## PC(37:2)                -0.118000   -0.2960    0.060600      19.3   0.195000      0.8050
## TG(50:2)                 0.110000   -0.0574    0.277000      21.1   0.197000      0.8050
## TG(14:0/18:1/18:1)       0.122000   -0.0781    0.323000      24.4   0.231000      0.8930
## PC(38:5)                -0.045300   -0.1200    0.029700      24.6   0.236000      0.8930
## SM(d38:2)               -0.063700   -0.1710    0.043900      21.4   0.245000      0.8960
## SM(d32:1)                0.061500   -0.0491    0.172000      22.3   0.275000      0.9570
## TG(50:0)                 0.160000   -0.1390    0.460000      20.8   0.293000      0.9570
## TG(14:0/16:0/18:1)       0.136000   -0.1230    0.395000      22.8   0.303000      0.9570
## TG(18:1/18:1/16:0)       0.076300   -0.0735    0.226000      25.6   0.317000      0.9570
## PC(O-36:2)              -0.065000   -0.1940    0.063700      20.5   0.322000      0.9570
## PC(36:3)                -0.058200   -0.1770    0.060400      25.6   0.335000      0.9570
## TG(50:3)                 0.104000   -0.1160    0.323000      23.4   0.354000      0.9570
## SM(d40:2)               -0.043200   -0.1370    0.050500      23.7   0.366000      0.9570
## TG(14:0/18:2/18:2)       0.143000   -0.1710    0.457000      21.2   0.371000      0.9570
## SM(d18:2/24:1)           0.043600   -0.0538    0.141000      24.0   0.379000      0.9570
```

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## PC(35:2)                -0.061400   -0.1990    0.076600      21.8   0.383000      0.9570
## SM(d16:1/18:1)           0.043500   -0.0547    0.142000      22.8   0.385000      0.9570
## TG(18:1/12:0/18:1)       0.118000   -0.1490    0.385000      22.5   0.386000      0.9570
## TG(18:2/18:1/16:0)       0.059500   -0.0759    0.195000      25.3   0.388000      0.9570
## TG(56:7)                 0.078800   -0.1060    0.264000      19.6   0.403000      0.9570
## TG(18:2/18:2/18:2)       0.107000   -0.1590    0.373000      22.1   0.428000      0.9570
## SM(d34:1)                0.019400   -0.0300    0.068900      24.9   0.440000      0.9570
## TG(16:0/18:0/18:1)       0.132000   -0.2070    0.470000      23.1   0.444000      0.9570
## TG(18:0/18:1/20:4)       0.100000   -0.1680    0.369000      21.3   0.463000      0.9570
## TG(18:2/22:5/16:0)       0.125000   -0.2090    0.459000      22.1   0.464000      0.9570
## TG(49:2)                 0.066200   -0.1130    0.245000      20.4   0.469000      0.9570
## PC(40:7)                -0.054800   -0.2090    0.099600      21.4   0.486000      0.9570
## PC(16:0e/18:1(9Z)       -0.038200   -0.1510    0.074900      21.8   0.507000      0.9570
## TG(46:0)                 0.079600   -0.1610    0.320000      20.4   0.515000      0.9570
## LPC(16:1)                0.051300   -0.1130    0.215000      20.0   0.539000      0.9570
## PC(36:4)                -0.020300   -0.0874    0.046800      26.0   0.553000      0.9570
## PC(34:3)                -0.069400   -0.2990    0.160000      22.4   0.553000      0.9570
## TG(56:3)                 0.075500   -0.1770    0.328000      20.0   0.558000      0.9570
## TG(56:6)                -0.048600   -0.2120    0.115000      19.9   0.559000      0.9570
## TG(45:0)                -0.025900   -0.1130    0.061600      23.1   0.561000      0.9570
## TG(16:0/18:2/18:2)       0.066300   -0.1690    0.302000      24.5   0.581000      0.9570
## PC(33:1)                 0.044400   -0.1160    0.205000      20.9   0.587000      0.9570
## TG(48:3)                 0.097500   -0.2640    0.459000      20.5   0.596000      0.9570
## TG(52:5)                -0.075100   -0.3540    0.204000      19.8   0.598000      0.9570
## TG(16:0/18:2/22:6)       0.115000   -0.3190    0.548000      21.0   0.603000      0.9570
## PC(38:4)                -0.020300   -0.0993    0.058700      25.2   0.614000      0.9570
## PC(38:6)                -0.024700   -0.1250    0.075700      25.4   0.629000      0.9570
## SM(d41:2)               -0.029200   -0.1500    0.091900      22.5   0.636000      0.9570
## TG(51:1)                 0.059200   -0.1900    0.308000      20.3   0.641000      0.9570
## PC(40:6)                 0.037000   -0.1200    0.194000      24.0   0.643000      0.9570
## PC(35:1)                -0.032000   -0.1680    0.104000      21.8   0.645000      0.9570
## TG(18:1/18:2/18:2)       0.056600   -0.1900    0.304000      23.6   0.652000      0.9570
## TG(54:2)                 0.056100   -0.1890    0.302000      23.4   0.654000      0.9570
## TG(16:0/18:2/18:3)       0.079200   -0.2750    0.434000      22.0   0.661000      0.9570
## TG(51:2)                 0.049200   -0.1840    0.283000      21.5   0.679000      0.9570
## SM(d36:2)                0.019600   -0.0749    0.114000      21.4   0.683000      0.9570
## TG(46:1)                 0.052000   -0.2100    0.314000      21.2   0.697000      0.9570
## TG(53:4)                 0.051700   -0.2150    0.318000      19.7   0.704000      0.9570
## PC(38:2)                -0.022100   -0.1380    0.093800      21.3   0.708000      0.9570
## TG(54:3)                 0.027600   -0.1200    0.175000      21.7   0.714000      0.9570
## TG(46:2)                 0.049700   -0.2310    0.330000      20.1   0.728000      0.9570
## TG(54:4)                -0.029300   -0.1980    0.139000      21.4   0.733000      0.9570
## TG(54:5)                -0.033900   -0.2410    0.173000      20.6   0.747000      0.9570
## PC(32:2)                 0.031300   -0.1680    0.231000      20.7   0.758000      0.9570
## TG(49:1)                 0.030600   -0.1710    0.233000      20.9   0.766000      0.9570
## TG(52:4)                -0.025900   -0.2000    0.148000      21.6   0.769000      0.9570
## TG(56:4)                 0.041000   -0.2420    0.324000      20.0   0.776000      0.9570
## SM(d36:1)               -0.010700   -0.0989    0.077500      23.4   0.812000      0.9780
## TG(50:1)                 0.029100   -0.2350    0.293000      24.3   0.829000      0.9780
## TG(47:1)                 0.020700   -0.1990    0.240000      19.5   0.853000      0.9780
## PC(36:5)                -0.021000   -0.2650    0.223000      24.4   0.866000      0.9780
## TG(56:5)                 0.016400   -0.1940    0.227000      20.3   0.879000      0.9780
## TG(52:2)                 0.007520   -0.1030    0.118000      22.6   0.894000      0.9780
## PC(40:5)                 0.009250   -0.1320    0.150000      22.0   0.898000      0.9780
```

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## SM(d33:1)                0.007250   -0.1070    0.121000      21.3   0.901000      0.9780
## PC(34:2)                 0.012200   -0.1910    0.216000      26.0   0.906000      0.9780
## TG(58:9)                -0.021700   -0.4130    0.370000      19.9   0.913000      0.9780
## TG(52:3)                -0.005900   -0.1220    0.110000      22.3   0.921000      0.9780
## TG(18:2/18:1/18:1)       0.009110   -0.1870    0.205000      24.4   0.927000      0.9780
## TG(53:2)                 0.012000   -0.2510    0.275000      20.7   0.929000      0.9780
## TG(53:3)                -0.010800   -0.2560    0.235000      20.7   0.931000      0.9780
## SM(42:2)                 0.003660   -0.0801    0.087400      25.2   0.932000      0.9780
## TG(51:3)                -0.003930   -0.2420    0.234000      20.7   0.974000      0.9910
## TG(18:1/18:1/18:1)       0.002960   -0.1920    0.197000      24.8   0.976000      0.9910
## TG(18:1/18:1/22:6)       0.004370   -0.3760    0.385000      20.7   0.982000      0.9910
## TG(16:0/22:5/18:1)       0.002120   -0.2010    0.205000      22.7   0.984000      0.9910
## PC(38:3)                 0.000719   -0.1280    0.129000      24.0   0.991000      0.9910
##
##
## Table: Results of the crude model for the continuous albuminuria (logUAER) slope.
## Shown in the table are name of the lipid (Name),
## model coefficient (Coefficient),
## its lower and upper confidence intervals (CI.L, CL.R),
## average value of the variable (AveExpr),
## p-value of the coefficient (P.Value) and
## the p-value after correction for multiple testing (adj.P.Val).
## The rows of the table are shown in an increasing order by the respective p-value.
##
## Name                   Coefficient         CI.L         CI.R   AveExpr     P.Value    adj.P.Val
## -------------------  ------------  -----------  -----------  --------  ----------  -----------
## PC(O-34:3)              -5.47e-02    -0.073200    -0.036100      21.9    0.00e+00     1.40e-06
## PC(O-36:3)              -4.66e-02    -0.066700    -0.026500      20.4    6.80e-06     3.62e-04
## PC(O-36:2)              -3.84e-02    -0.056700    -0.020200      20.5    3.96e-05     1.40e-03
## PC(O-34:2)              -4.72e-02    -0.070700    -0.023700      21.5    9.11e-05     2.41e-03
## TG(45:0)                -2.30e-02    -0.035300    -0.010600      23.1    3.00e-04     6.35e-03
## SM(d18:1/24:0)          -2.65e-02    -0.042300    -0.010700      23.6    1.07e-03     1.89e-02
## TG(52:2)                 2.58e-02     0.010100     0.041500      22.6    1.32e-03     2.00e-02
## SM(d41:1)               -2.91e-02    -0.047200    -0.011000      22.7    1.67e-03     2.22e-02
## SM(d40:1)               -2.35e-02    -0.038600    -0.008370      24.0    2.40e-03     2.82e-02
## TG(14:0/18:1/18:1)       4.16e-02     0.013200     0.069900      24.4    4.14e-03     4.13e-02
## TG(50:2)                 3.43e-02     0.010600     0.057900      21.1    4.57e-03     4.13e-02
## PC(16:0e/18:1(9Z)       -2.31e-02    -0.039200    -0.007140      21.8    4.68e-03     4.13e-02
## LPC(18:2)               -3.32e-02    -0.056800    -0.009560      24.0    5.99e-03     4.61e-02
## PC(O-38:6)              -2.15e-02    -0.036900    -0.006170      20.4    6.09e-03     4.61e-02
## TG(56:3)                 4.96e-02     0.013900     0.085400      20.0    6.63e-03     4.69e-02
## TG(49:3)                -5.97e-03    -0.010400    -0.001580      20.7    7.85e-03     5.05e-02
## TG(53:2)                 5.03e-02     0.013100     0.087600      20.7    8.19e-03     5.05e-02
## TG(51:2)                 4.41e-02     0.011100     0.077100      21.5    8.99e-03     5.05e-02
## TG(18:2/22:5/16:0)       6.30e-02     0.015800     0.110000      22.1    9.06e-03     5.05e-02
## TG(54:6)                 5.34e-02     0.012800     0.093900      19.5    9.97e-03     5.17e-02
## TG(56:6)                 3.01e-02     0.007050     0.053200      19.9    1.06e-02     5.17e-02
## TG(54:2)                 4.53e-02     0.010500     0.080000      23.4    1.07e-02     5.17e-02
## TG(18:1/18:1/16:0)       2.74e-02     0.006170     0.048500      25.6    1.15e-02     5.29e-02
## TG(56:7)                 3.32e-02     0.006980     0.059300      19.6    1.32e-02     5.81e-02
## TG(18:2/18:2/18:2)       4.69e-02     0.009230     0.084500      22.1    1.48e-02     6.26e-02
## TG(56:5)                 3.61e-02     0.006300     0.066000      20.3    1.77e-02     7.21e-02
## PC(37:2)                -3.02e-02    -0.055500    -0.005020      19.3    1.89e-02     7.41e-02
## SM(d39:1)               -2.52e-02    -0.046600    -0.003880      21.1    2.07e-02     7.48e-02
```

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## PC(36:2)              -1.32e-02   -0.024400   -0.002010      26.1   2.08e-02    7.48e-02
## PC(38:4)               1.32e-02    0.001980    0.024300      25.2   2.12e-02    7.48e-02
## PC(35:2)              -2.28e-02   -0.042300   -0.003280      21.8   2.22e-02    7.58e-02
## TG(50:1)               4.24e-02    0.005050    0.079700      24.3   2.62e-02    8.47e-02
## TG(16:0/22:5/18:1)     3.26e-02    0.003850    0.061400      22.7   2.64e-02    8.47e-02
## TG(50:3)               3.44e-02    0.003410    0.065500      23.4   2.97e-02    9.25e-02
## TG(16:0/18:0/18:1)     5.28e-02    0.004870    0.101000      23.1   3.09e-02    9.36e-02
## TG(54:3)               2.25e-02    0.001580    0.043400      21.7   3.51e-02    1.03e-01
## PC(32:2)              -2.95e-02   -0.057700   -0.001290      20.7   4.04e-02    1.15e-01
## TG(51:1)               3.67e-02    0.001470    0.072000      20.3   4.12e-02    1.15e-01
## PC(40:7)              -2.22e-02   -0.044000   -0.000309      21.4   4.69e-02    1.27e-01
## TG(53:3)               3.44e-02   -0.000368    0.069200      20.7   5.25e-02    1.39e-01
## TG(14:0/16:0/18:1)     3.59e-02   -0.000813    0.072500      22.8   5.53e-02    1.43e-01
## TG(52:3)               1.57e-02   -0.000783    0.032100      22.3   6.19e-02    1.55e-01
## TG(18:1/12:0/18:1)     3.58e-02   -0.001920    0.073600      22.5   6.28e-02    1.55e-01
## SM(d36:2)              1.21e-02   -0.001220    0.025500      21.4   7.49e-02    1.78e-01
## TG(56:4)               3.63e-02   -0.003790    0.076400      20.0   7.59e-02    1.78e-01
## TG(52:4)               2.21e-02   -0.002430    0.046700      21.6   7.73e-02    1.78e-01
## TG(18:0/18:1/20:4)     3.31e-02   -0.004890    0.071200      21.3   8.75e-02    1.97e-01
## SM(d38:1)             -1.23e-02   -0.026500    0.001910      23.1   8.96e-02    1.97e-01
## PC(38:3)               1.57e-02   -0.002520    0.033800      24.0   9.13e-02    1.97e-01
## TG(49:1)               2.42e-02   -0.004330    0.052800      20.9   9.62e-02    2.04e-01
## PC(O-36:5)            -1.29e-02   -0.028500    0.002630      22.3   1.03e-01    2.14e-01
## SM(d34:1)              5.65e-03   -0.001340    0.012600      24.9   1.13e-01    2.28e-01
## LPC(20:4)              1.89e-02   -0.004560    0.042400      21.4   1.14e-01    2.28e-01
## SM(d41:2)             -1.37e-02   -0.030800    0.003430      22.5   1.17e-01    2.29e-01
## TG(49:2)               2.02e-02   -0.005190    0.045600      20.4   1.19e-01    2.29e-01
## TG(50:0)               3.31e-02   -0.009280    0.075400      20.8   1.26e-01    2.36e-01
## TG(51:3)               2.62e-02   -0.007450    0.059800      20.7   1.27e-01    2.36e-01
## PC(32:0)              -8.09e-03   -0.018700    0.002550      22.5   1.36e-01    2.48e-01
## PC(34:2)               2.17e-02   -0.007100    0.050400      26.0   1.40e-01    2.51e-01
## TG(46:2)               2.79e-02   -0.011700    0.067600      20.1   1.67e-01    2.95e-01
## TG(46:1)               2.53e-02   -0.011800    0.062300      21.2   1.81e-01    3.14e-01
## TG(46:0)               2.27e-02   -0.011300    0.056700      20.4   1.90e-01    3.25e-01
## PC(38:6)              -9.29e-03   -0.023500    0.004910      25.4   1.99e-01    3.35e-01
## SM(d40:2)             -8.41e-03   -0.021700    0.004850      23.7   2.13e-01    3.53e-01
## LPC(16:1)              1.39e-02   -0.009360    0.037100      20.0   2.41e-01    3.94e-01
## TG(14:0/18:2/18:2)     2.63e-02   -0.018100    0.070700      21.2   2.45e-01    3.94e-01
## SM(d33:1)             -9.27e-03   -0.025400    0.006890      21.3   2.60e-01    4.11e-01
## TG(16:0/18:2/18:2)     1.90e-02   -0.014400    0.052300      24.5   2.64e-01    4.11e-01
## PC(O-38:5)            -7.95e-03   -0.022600    0.006720      22.8   2.87e-01    4.42e-01
## PC(32:1)               1.67e-02   -0.014600    0.047900      23.3   2.96e-01    4.46e-01
## TG(16:0/18:2/18:3)     2.66e-02   -0.023600    0.076700      22.0   2.99e-01    4.46e-01
## PC(O-38:4)            -1.03e-02   -0.029900    0.009370      21.7   3.05e-01    4.49e-01
## SM(d38:2)             -7.68e-03   -0.022900    0.007550      21.4   3.22e-01    4.68e-01
## TG(48:3)               2.44e-02   -0.026600    0.075500      20.5   3.48e-01    4.98e-01
## PC(40:5)               9.34e-03   -0.010600    0.029300      22.0   3.58e-01    5.06e-01
## TG(18:1/18:1/22:6)     2.47e-02   -0.029100    0.078500      20.7   3.67e-01    5.12e-01
## TG(53:4)               1.70e-02   -0.020700    0.054700      19.7   3.77e-01    5.19e-01
## TG(18:1/18:1/18:1)     1.17e-02   -0.015800    0.039200      24.8   4.04e-01    5.50e-01
## TG(52:5)               1.57e-02   -0.023800    0.055200      19.8   4.34e-01    5.83e-01
## PC(36:5)              -1.26e-02   -0.047100    0.022000      24.4   4.74e-01    6.28e-01
## SM(d32:1)              5.53e-03   -0.010100    0.021200      22.3   4.88e-01    6.38e-01
## TG(54:4)               7.72e-03   -0.016100    0.031600      21.4   5.25e-01    6.79e-01
```

```
## TG(54:5)                 8.30e-03   -0.020900    0.037500       20.6   5.77e-01    7.37e-01
## TG(18:2/18:1/18:1)       5.40e-03   -0.022400    0.033200       24.4   7.03e-01    8.70e-01
## TG(16:0/18:2/22:6)       1.18e-02   -0.049500    0.073100       21.0   7.05e-01    8.70e-01
## PC(38:2)                -3.07e-03   -0.019500    0.013300       21.3   7.13e-01    8.70e-01
## LPC(18:1)                3.32e-03   -0.014700    0.021300       23.7   7.17e-01    8.70e-01
## PC(34:3)                -5.83e-03   -0.038300    0.026700       22.4   7.25e-01    8.70e-01
## SM(d36:1)                2.19e-03   -0.010300    0.014700       23.4   7.30e-01    8.70e-01
## SM(d16:1/18:1)           2.20e-03   -0.011700    0.016100       22.8   7.56e-01    8.83e-01
## TG(18:1/18:2/18:2)       5.47e-03   -0.029500    0.040400       23.6   7.58e-01    8.83e-01
## SM(42:2)                -1.63e-03   -0.013500    0.010200       25.2   7.88e-01    8.94e-01
## PC(36:4)                 1.20e-03   -0.008290    0.010700       26.0   8.04e-01    8.94e-01
## PC(38:5)                -1.30e-03   -0.011900    0.009310       24.6   8.10e-01    8.94e-01
## TG(47:1)                -3.70e-03   -0.034800    0.027400       19.5   8.15e-01    8.94e-01
## PC(34:1)                 1.74e-03   -0.013700    0.017200       25.9   8.25e-01    8.94e-01
## TG(58:9)                 6.24e-03   -0.049200    0.061600       19.9   8.25e-01    8.94e-01
## PC(36:3)                -1.84e-03   -0.018600    0.015000       25.6   8.30e-01    8.94e-01
## LPC(16:0)                8.10e-04   -0.006960    0.008580       25.3   8.38e-01    8.94e-01
## LPC(18:0)               -1.41e-03   -0.015500    0.012700       24.0   8.44e-01    8.94e-01
## PC(40:6)                -1.74e-03   -0.023900    0.020400       24.0   8.78e-01    9.14e-01
## TG(18:2/18:1/16:0)      -1.48e-03   -0.020600    0.017700       25.3   8.79e-01    9.14e-01
## PC(O-36:4)              -1.04e-03   -0.017900    0.015900       22.9   9.04e-01    9.30e-01
## PC(33:1)                 9.94e-04   -0.021700    0.023700       20.9   9.32e-01    9.46e-01
## SM(d18:2/24:1)           5.51e-04   -0.013200    0.014300       24.0   9.37e-01    9.46e-01
## PC(35:1)                -1.71e-05   -0.019300    0.019300       21.8   9.99e-01    9.99e-01
```

1.2.2.2 Heatmaps

```
##   Label Relation p.adj
## 1     #  p.adj <  0.01
## 2     x  p.adj <  0.05
## 3     *  p.adj <  0.10
```

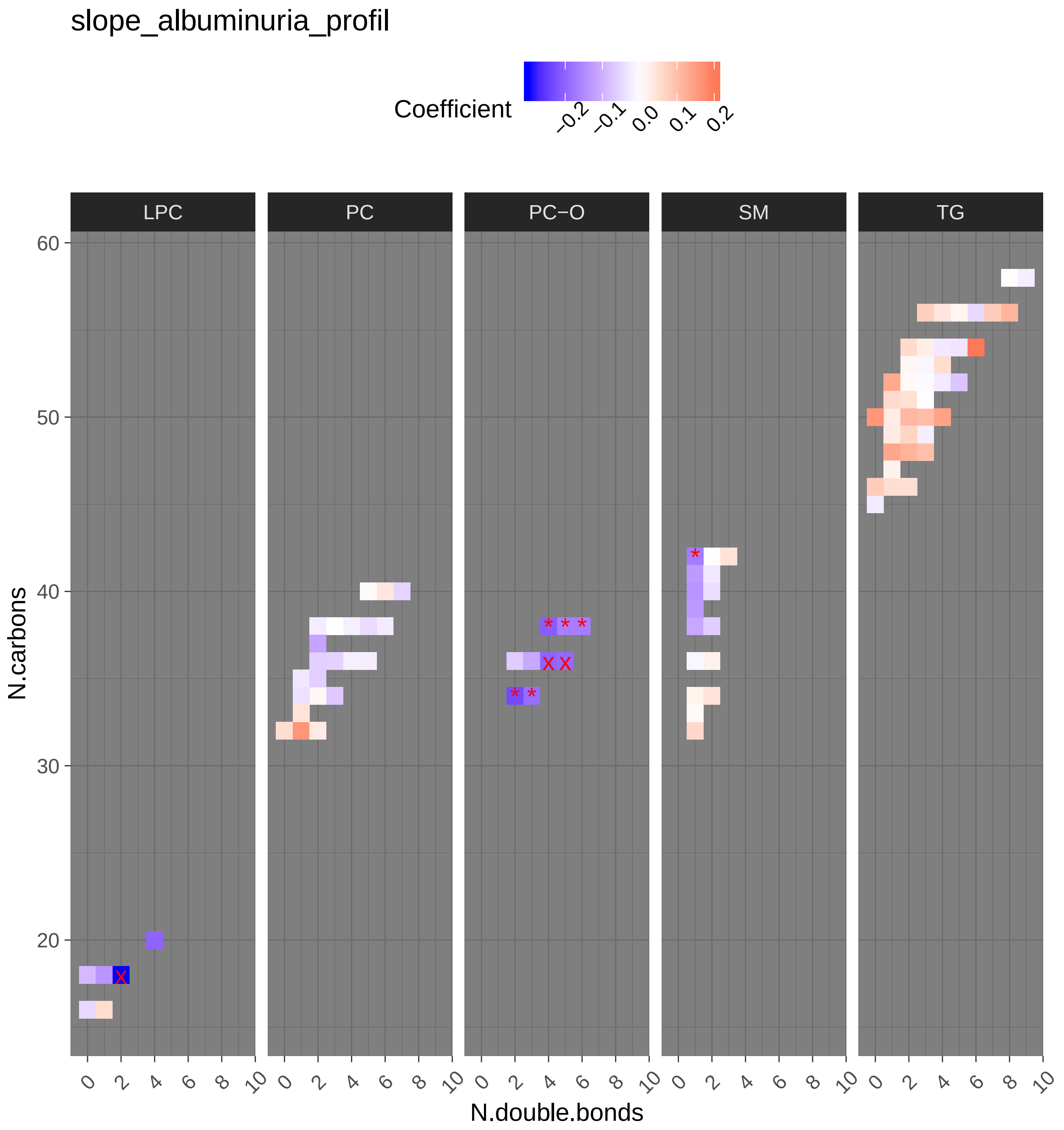


Figure 10: Heatmap of the lipid-specific model coefficents from the crude model for albuminuria (logUAER) slope. The name of the group is shown in the title of the figure in the top-left corner. Lipids are organized into panels (columns) by their class (from LPC to TG). One colored rectangle corresponds to one lipid species, where the coordinates in the x-axis and y-axis, respectively, show the number of double bonds (N.double.bonds) and the number of carbon atoms (N.carbons) in the fatty acid chains of the lipid. The number of double bonds corresponds to the number of unsaturated bonds in the fatty acid chains, and the number of carbon atoms corresponds to the length of the fatty acid chains and, thus, the size of the lipid. The magnitude of the lipid-specifc model coefficient is shown as the color of the rectangle (blue: negative; red: positive). Coefficient with statistical significance are annotated with symbols #, x and *, respectively, corresponding to $p < 0.01$, $p < 0.05$ and $p < 0.1$.

1.3 Combined Heatmaps from Crude Models for Slopes

```
##   Label Relation p.adj
## 1     #  p.adj <  0.01
## 2     x  p.adj <  0.05
## 3     *  p.adj <  0.10
```

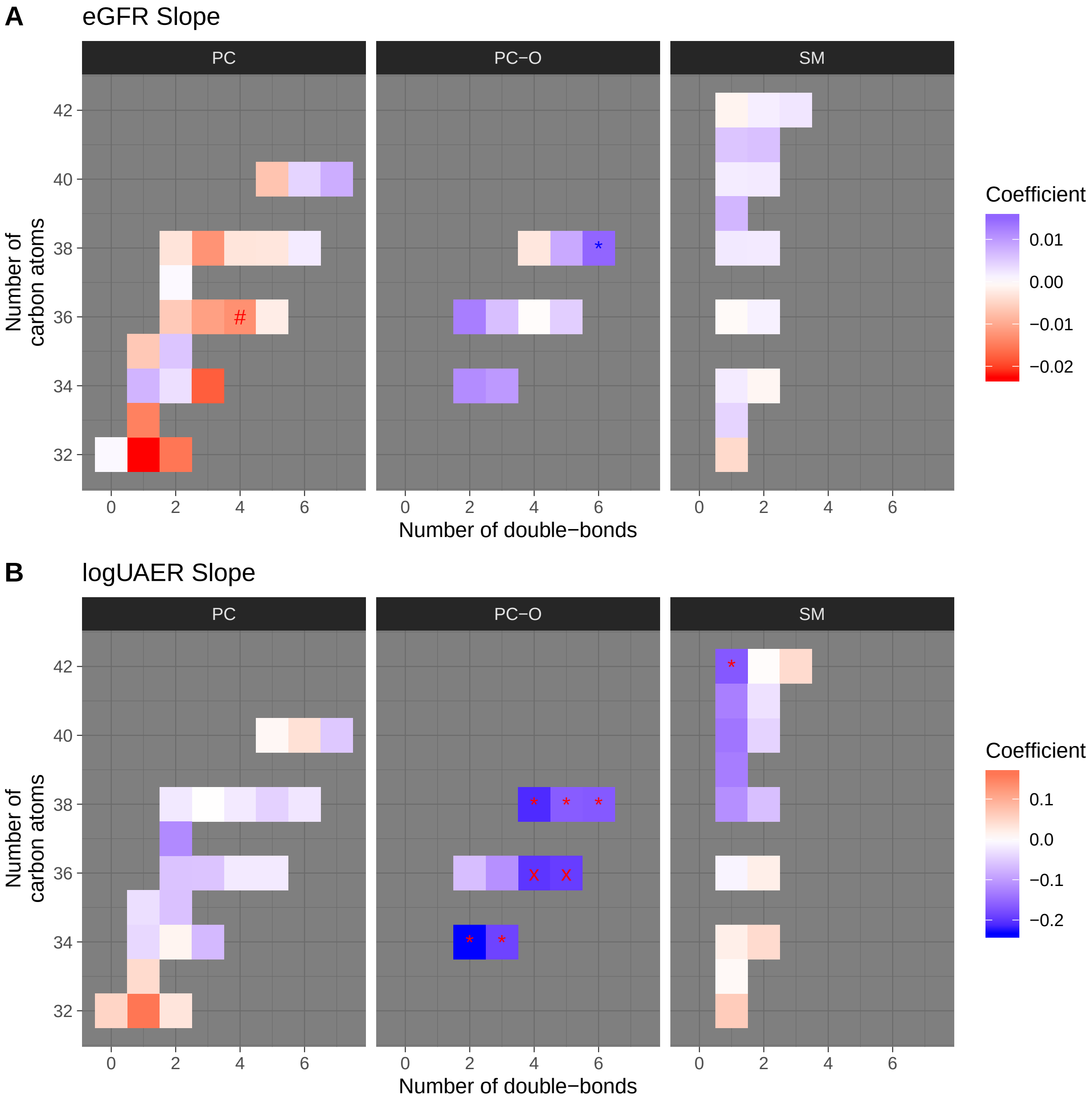


Figure 11: Heatmap of the lipid-specific model coefficents from the crude models for eGFR slope (A) and albuminuria (logUAER) slope (B). The name of the group is shown in the title of the figure in the top-left corner. Lipids are organized into panels (columns) by their class (from PC to SM). One colored rectangle corresponds to one lipid species, where the coordinates in the x-axis and y-axis, respectively, show the number of double bonds (N.double.bonds) and the number of carbon atoms (N.carbons) in the fatty acid chains of the lipid. The number of double bonds corresponds to the number of unsaturated bonds in the fatty acid chains, and the number of carbon atoms corresponds to the length of the fatty acid chains and, thus, the size of the lipid. The magnitude of the lipid-specifc model coefficient is shown as the color of the rectangle (blue: negative; red: positive). Coefficient with statistical significance are annotated with symbols #, x and *, respectively, corresponding to $p < 0.01$, $p < 0.05$ and $p < 0.1$.

2 Step 2: Adjusted Associations to Clinical Changes Over Time with Prioritized Lipids from Steps 1A-B

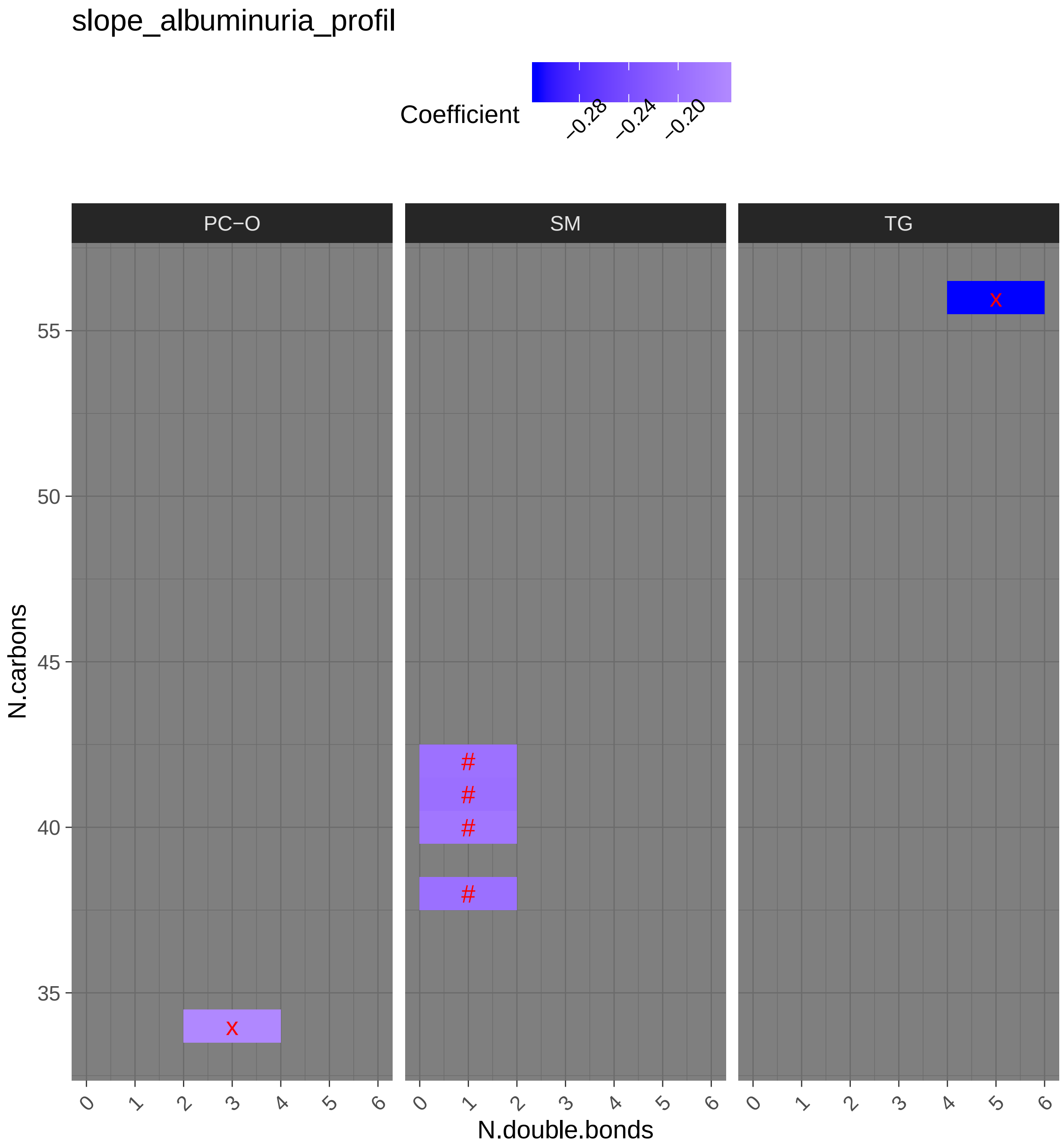
2.1 Step 2A: Adjusted Model for Prioritized Lipids from the Adjusted Cross-Sectional Models

2.1.1 Albuminuria Slope

2.1.1.1 Table

```
##
##
## Table: Results of the adjusted model for the continuous albuminuria (logUAER) slope
## and with lipids prioritized from the cross-sectional models.
## Shown in the table are name of the lipid (Name),
## model coefficient (Coefficient),
## its lower and upper confidence intervals (CI.L, CL.R),
## average value of the variable (AveExpr),
## p-value of the coefficient (P.Value) and
## the p-value after correction for multiple testing (adj.P.Val).
## The rows of the table are shown in an increasing order by the respective p-value.
##
## Name                  Coefficient     CI.L      CI.R   AveExpr    P.Value   adj.P.Val
## -------------------  ------------  -------  --------  --------  ---------  ----------
## SM(d38:1)                  -0.195   -0.281   -0.1090      23.1   1.11e-05    6.67e-05
## SM(d40:1)                  -0.187   -0.272   -0.1010      24.0   2.36e-05    7.07e-05
## SM(d18:1/24:0)             -0.193   -0.286   -0.0992      23.6   5.93e-05    1.19e-04
## SM(d41:1)                  -0.196   -0.307   -0.0837      22.7   6.41e-04    9.62e-04
## PC(O-34:3)                 -0.161   -0.283   -0.0389      21.9   9.87e-03    1.18e-02
## TG(18:0/18:1/20:4)         -0.314   -0.563   -0.0656      21.3   1.33e-02    1.33e-02
```

2.1.1.2 Heatmaps



```
##   Label Relation p.adj
## 1     #  p.adj <  0.01
## 2     x  p.adj <  0.05
## 3     *  p.adj <  0.10
```

2.1.2 eGFR Slope

2.1.2.1 Table

```
##
##
## Table: Results of the adjusted model for the eGFR slope
## with lipids prioritized from the cross-sectional models.
## Shown in the table are name of the lipid (Name),
## model coefficient (Coefficient),
## its lower and upper confidence intervals (CI.L, CL.R),
## average value of the variable (AveExpr),
## p-value of the coefficient (P.Value) and
## the p-value after correction for multiple testing (adj.P.Val).
## The rows of the table are shown in an increasing order by the respective p-value.
##
## Name                   Coefficient       CI.L       CI.R   AveExpr   P.Value   adj.P.Val
## -------------------  ------------  ---------  ---------  --------  --------  ----------
## PC(32:2)                -0.016700   -0.03410   0.000693      20.7    0.0598       0.860
## LPC(16:0)               -0.004370   -0.00929   0.000556      25.3    0.0819       0.860
## TG(14:0/16:0/18:1)      -0.012700   -0.03000   0.004700      22.8    0.1530       0.984
## PC(32:1)                -0.012700   -0.03220   0.006850      23.3    0.2030       0.984
## LPC(16:1)               -0.008500   -0.02380   0.006850      20.0    0.2770       0.984
## SM(d34:1)                0.002180   -0.00218   0.006540      24.9    0.3260       0.984
## SM(d33:1)                0.004260   -0.00526   0.013800      21.3    0.3800       0.984
## PC(40:6)                 0.004770   -0.00845   0.018000      24.0    0.4790       0.984
## PC(O-36:2)               0.003420   -0.00813   0.015000      20.5    0.5610       0.984
## TG(18:2/18:2/18:2)      -0.006130   -0.02720   0.014900      22.1    0.5680       0.984
## PC(38:6)                 0.001860   -0.00682   0.010500      25.4    0.6730       0.984
## PC(O-38:4)              -0.002850   -0.01650   0.010800      21.7    0.6810       0.984
## TG(16:0/18:2/22:6)       0.005660   -0.03300   0.044300      21.0    0.7730       0.984
## PC(40:7)                 0.001840   -0.01130   0.015000      21.4    0.7840       0.984
## SM(d16:1/18:1)          -0.000797   -0.00778   0.006190      22.8    0.8230       0.984
## SM(d32:1)               -0.000827   -0.00982   0.008160      22.3    0.8570       0.984
## TG(18:1/18:1/22:6)      -0.002700   -0.03710   0.031700      20.7    0.8780       0.984
## SM(d18:2/24:1)           0.000381   -0.00745   0.008220      24.0    0.9240       0.984
## TG(58:9)                 0.000924   -0.03490   0.036800      19.9    0.9600       0.984
## TG(18:2/22:5/16:0)       0.000334   -0.02860   0.029300      22.1    0.9820       0.984
## PC(36:5)                 0.000226   -0.02140   0.021900      24.4    0.9840       0.984
```

2.1.2.2 Heatmaps

```
##   Label Relation p.adj
## 1     #  p.adj <  0.01
## 2     x  p.adj <  0.05
## 3     *  p.adj <  0.10
```

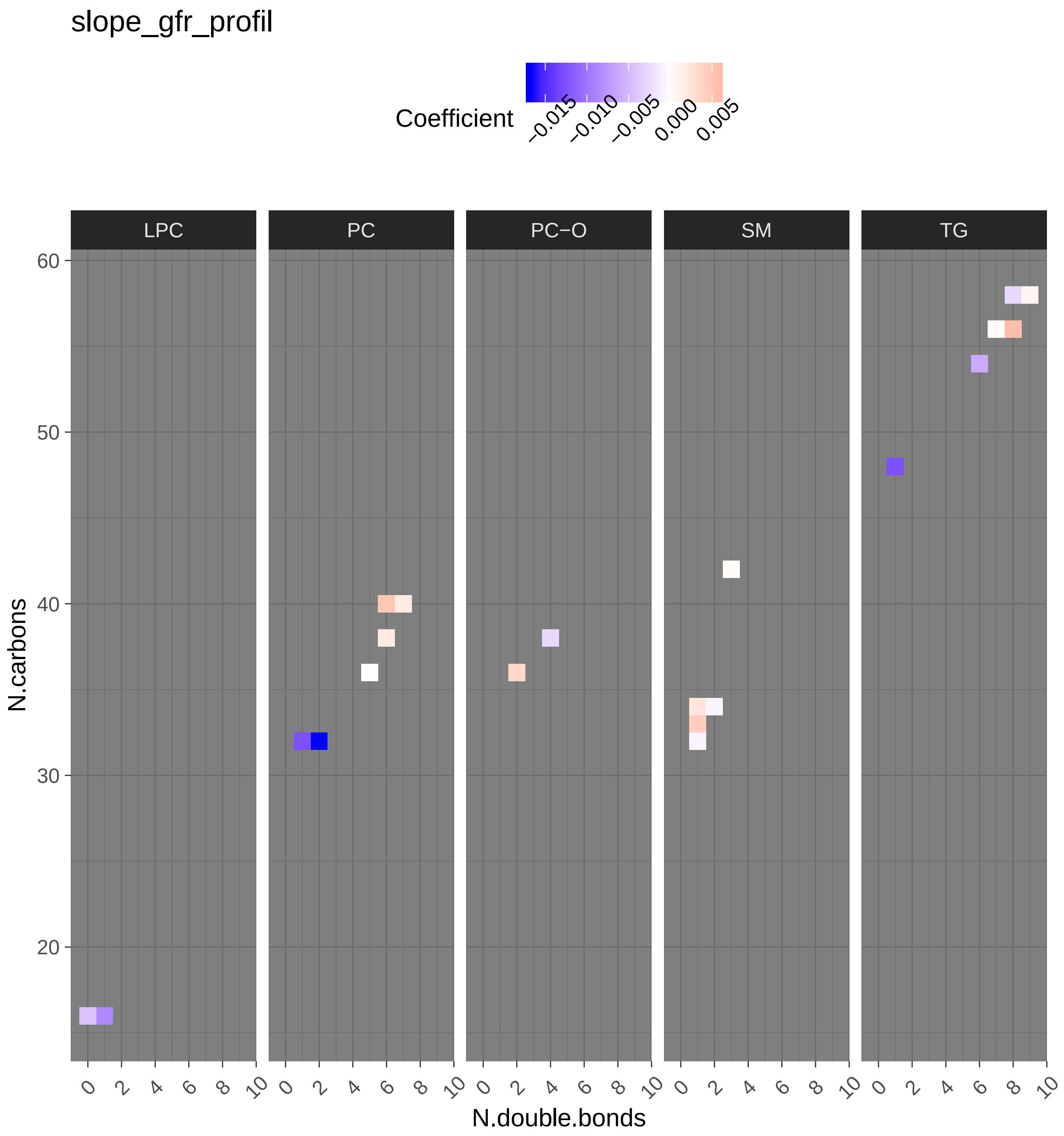


Figure 12: Heatmap of the lipid-specific model coefficents from the adjusted model for eGFR slope with lipids prioritized from the cross-sectional models. Lipids are organized into panels (columns) by their class (from LPC to TG). One colored rectangle corresponds to one lipid species, where the coordinates in the x-axis and y-axis, respectively, show the number of double bonds (N.double.bonds) and the number of carbon atoms (N.carbons) in the fatty acid chains of the lipid. The number of double bonds corresponds to the number of unsaturated bonds in the fatty acid chains, and the number of carbon atoms corresponds to the length of the fatty acid chains and, thus, the size of the lipid. The magnitude of the lipid-specifc model coefficient is shown as the color of the rectangle (blue: negative; red: positive). Coefficient with statistical significance are annotated with symbols #, x and *, respectively, corresponding to $p < 0.01$, $p < 0.05$ and $p < 0.1$.

2.2 Step 2B: Adjusted Model for Prioritized Lipids from the Crude Models for Slopes

2.2.1 eGFR Slope

2.2.1.1 Table

```
##
##
## Table: Results of the adjusted model for eGFR slope
## with the lipids prioritized from the crude slope models.
## Shown in the table are name of the lipid (Name),
## model coefficient (Coefficient),
## its lower and upper confidence intervals (CI.L, CL.R),
## average value of the variable (AveExpr),
## p-value of the coefficient (P.Value) and
## the p-value after correction for multiple testing (adj.P.Val).
## The rows of the table are shown in an increasing order by the respective p-value.
##
## Name                   Coefficient       CI.L         CI.R   AveExpr    P.Value   adj.P.Val
## -------------------  ------------  ---------  ----------  --------  ---------  ----------
## PC(36:4)                  -0.01400   -0.02060   -0.007370      26.0   3.79e-05    0.000455
## LPC(16:0)                 -0.00437   -0.00931    0.000576      25.3   8.32e-02    0.305000
## PC(O-38:6)                 0.00823   -0.00177    0.018200      20.4   1.06e-01    0.305000
## TG(51:3)                  -0.01250   -0.02780    0.002810      20.7   1.09e-01    0.305000
## TG(46:0)                  -0.01470   -0.03360    0.004220      20.4   1.28e-01    0.305000
## TG(14:0/16:0/18:1)        -0.01270   -0.03000    0.004690      22.8   1.52e-01    0.305000
## TG(51:2)                  -0.00629   -0.01980    0.007190      21.5   3.60e-01    0.617000
## TG(50:0)                  -0.00680   -0.02940    0.015800      20.8   5.54e-01    0.691000
## TG(18:2/18:2/18:2)        -0.00613   -0.02720    0.014900      22.1   5.68e-01    0.691000
## TG(51:1)                  -0.00463   -0.02090    0.011600      20.3   5.76e-01    0.691000
## TG(50:2)                  -0.00140   -0.01110    0.008270      21.1   7.76e-01    0.830000
## TG(14:0/18:1/18:1)        -0.00122   -0.01240    0.009910      24.4   8.30e-01    0.830000
```

2.2.1.2 Heatmaps

```
##   Label Relation p.adj
## 1     #  p.adj <  0.01
## 2     x  p.adj <  0.05
## 3     *  p.adj <  0.10
```

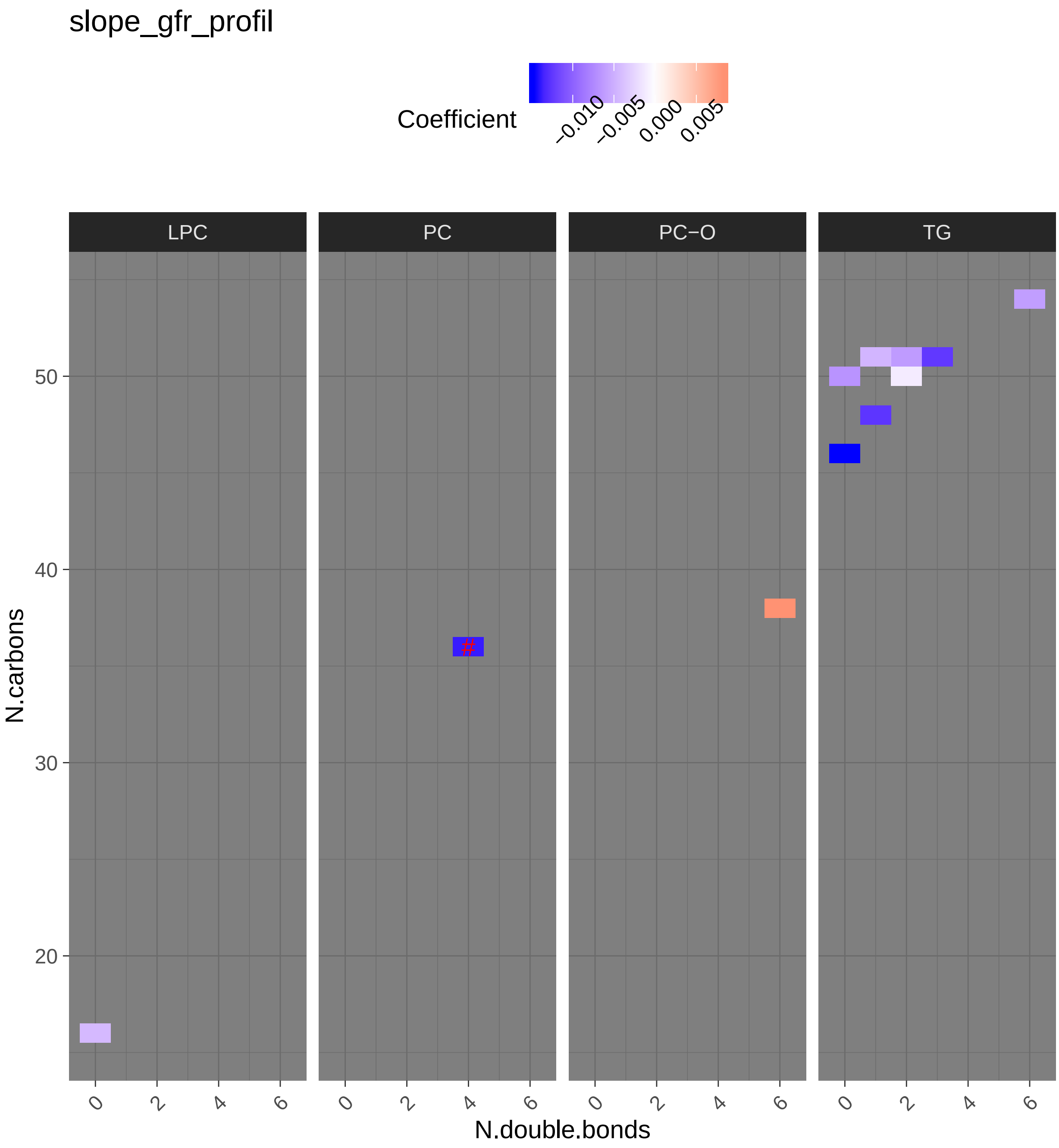


Figure 13: Heatmap of the lipid-specific model coefficents from the adjusted model for eGFR slope with lipids prioritized from the crude slope models. Lipids are organized into panels (columns) by their class (from LPC to TG). One colored rectangle corresponds to one lipid species, where the coordinates in the x-axis and y-axis, respectively, show the number of double bonds (N.double.bonds) and the number of carbon atoms (N.carbons) in the fatty acid chains of the lipid. The number of double bonds corresponds to the number of unsaturated bonds in the fatty acid chains, and the number of carbon atoms corresponds to the length of the fatty acid chains and, thus, the size of the lipid. The magnitude of the lipid-specifc model coefficient is shown as the color of the rectangle (blue: negative; red: positive). Coefficient with statistical significance are annotated with symbols #, x and *, respectively, corresponding to $p < 0.01$, $p < 0.05$ and $p < 0.1$.

2.2.2 Albuminuria Slope

2.2.2.1 Table

```
##
##
## Table: Results of the adjusted model for the continuous albuminuria (logUAER) slope
## with the lipids prioritized from the crude slope models.
## Shown in the table are name of the lipid (Name),
## model coefficient (Coefficient),
## its lower and upper confidence intervals (CI.L, CL.R),
## average value of the variable (AveExpr),
## p-value of the coefficient (P.Value) and
## the p-value after correction for multiple testing (adj.P.Val).
## The rows of the table are shown in an increasing order by the respective p-value.
##
## Name              Coefficient     CI.L      CI.R   AveExpr    P.Value   adj.P.Val
## ---------------  ------------  -------  --------  --------  ---------  ----------
## PC(O-38:6)             -0.229   -0.335   -0.1220      20.4   2.94e-05    0.000203
## PC(O-36:5)             -0.243   -0.359   -0.1270      22.3   4.66e-05    0.000203
## SM(d18:1/24:0)         -0.193   -0.287   -0.0984      23.6   6.75e-05    0.000203
## PC(O-36:4)             -0.225   -0.351   -0.0987      22.9   5.08e-04    0.001140
## PC(O-38:4)             -0.249   -0.394   -0.1050      21.7   7.28e-04    0.001310
## PC(O-38:5)             -0.173   -0.282   -0.0645      22.8   1.85e-03    0.002770
## PC(O-34:3)             -0.161   -0.284   -0.0388      21.9   9.94e-03    0.012800
## PC(O-34:2)             -0.188   -0.356   -0.0205      21.5   2.80e-02    0.031500
## LPC(18:2)              -0.134   -0.307    0.0387      24.0   1.28e-01    0.128000
```

2.2.2.2 Heatmaps

```
##   Label Relation p.adj
## 1     #  p.adj <  0.01
## 2     x  p.adj <  0.05
## 3     *  p.adj <  0.10
```

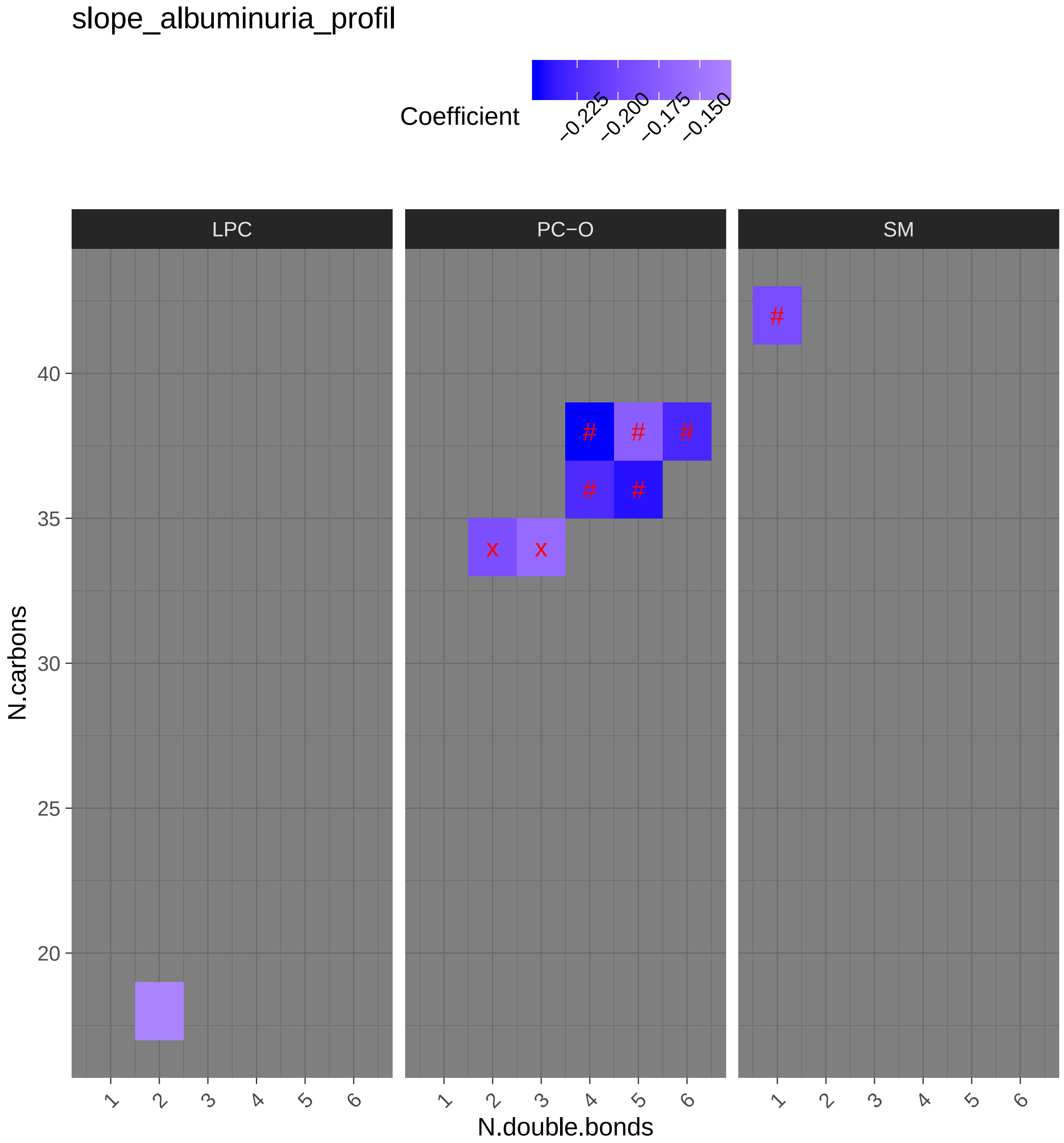


Figure 14: Heatmap of the lipid-specific model coefficents from the adjusted model for albuminuria (logUAER) slope with lipids prioritized from the crude slope models. Lipids are organized into panels (columns) by their class (from LPC to TG). One colored rectangle corresponds to one lipid species, where the coordinates in the x-axis and y-axis, respectively, show the number of double bonds (N.double.bonds) and the number of carbon atoms (N.carbons) in the fatty acid chains of the lipid. The number of double bonds corresponds to the number of unsaturated bonds in the fatty acid chains, and the number of carbon atoms corresponds to the length of the fatty acid chains and, thus, the size of the lipid. The magnitude of the lipid-specifc model coefficient is shown as the color of the rectangle (blue: negative; red: positive). Coefficient with statistical significance are annotated with symbols #, x and *, respectively, corresponding to $p < 0.01$, $p < 0.05$ and $p < 0.1$.

3 Step 3: Survival Analysis of Combined Renal Endpoint in Relation to Prioritized Lipids from Step 2A-B

3.1 Step 3A: Crude Model

```
## Warning in lapply(X = x, FUN = .Generic, ...): NaNs produced
```

3.1.1 Table

Table 1: Crude survival model for the combined renal endpoint. Shown in the table are the name of the lipid (Name), the hazard ratio (exp(coef)) and its lower and upper condidence intervals (lower .95 and upper .95, respectively), p-value of the coefficient (Pr(>|z|), and the p-value after correction for multiple testing (p.adj).

Name	exp(coef)	lower .95	upper .95	Pr(>|z|)	p.adj
PC(O-34:3)	0.404	0.289	0.566	1.00e-07	1.60e-06
PC(O-34:2)	0.583	0.441	0.770	1.47e-04	1.76e-03
SM(d41:1)	0.533	0.383	0.742	1.91e-04	2.10e-03
SM(d40:1)	0.472	0.308	0.724	5.79e-04	5.79e-03
SM(d18:1/24:0)	0.525	0.347	0.795	2.31e-03	2.08e-02
TG(18:0/18:1/20:4)	1.250	1.030	1.530	2.41e-02	1.93e-01
SM(d38:1)	0.615	0.384	0.983	4.22e-02	2.95e-01
PC(O-38:4)	0.738	0.526	1.040	7.83e-02	4.70e-01
PC(O-36:5)	0.704	0.466	1.060	9.53e-02	4.76e-01
PC(O-38:6)	0.737	0.483	1.120	1.57e-01	6.29e-01
PC(O-36:4)	0.791	0.535	1.170	2.40e-01	7.19e-01
PC(36:4)	1.620	0.709	3.700	2.52e-01	7.19e-01
PC(O-38:5)	0.866	0.548	1.370	5.37e-01	7.19e-01

3.1.2 Heatmaps

```
##   Label Relation p.adj
## 1     #  p.adj <  0.01
## 2     x  p.adj <  0.05
## 3     *  p.adj <  0.10
```

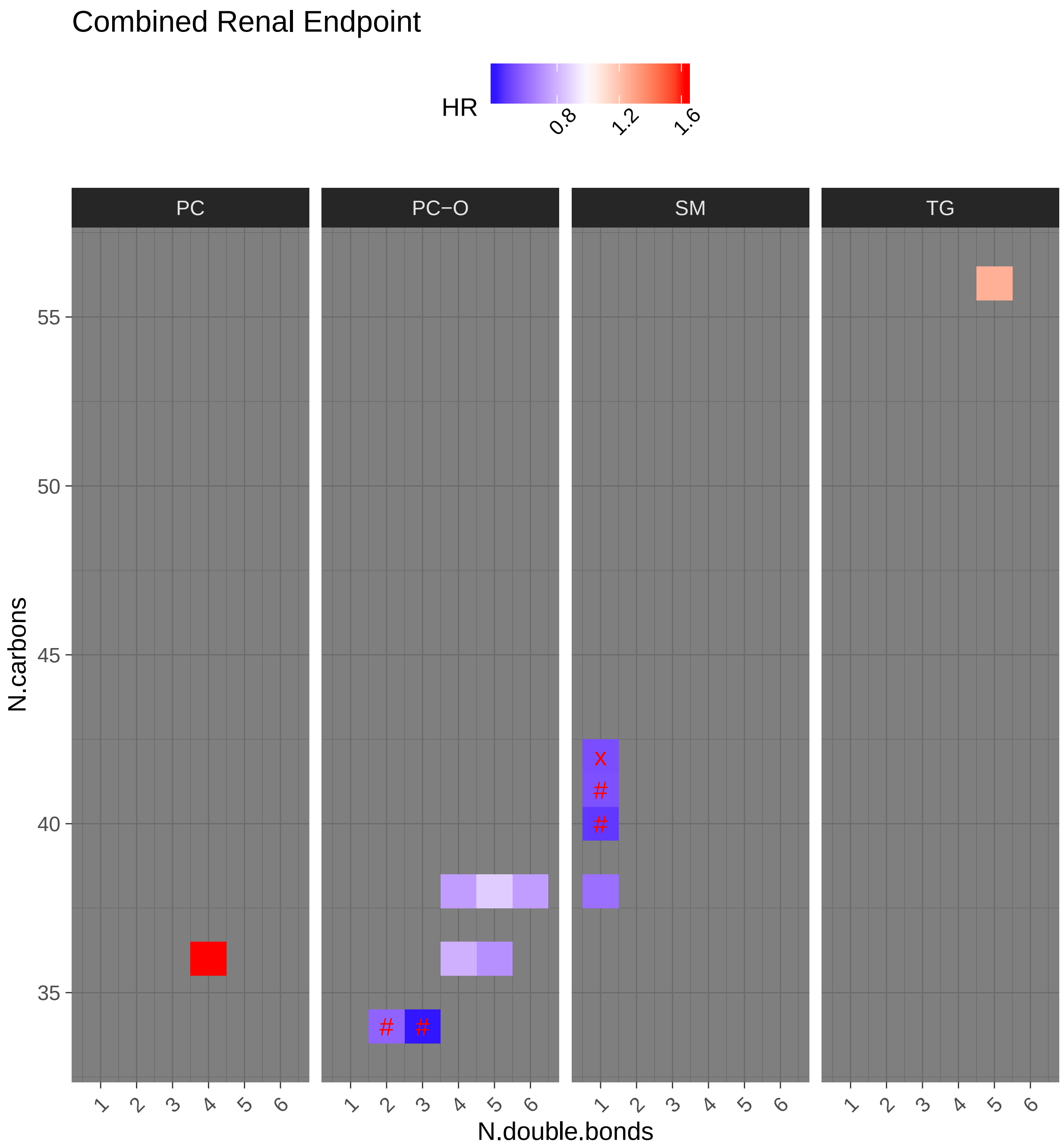


Figure 15: Heatmap of the lipid-specific hazard ratios (HRs) from the crude survival model for the combined renal endpoint. Lipids are organized into panels (columns) by their class (from PC to TG). One colored rectangle corresponds to one lipid species, where the coordinates in the x-axis and y-axis, respectively, show the number of double bonds (N.double.bonds) and the number of carbon atoms (N.carbons) in the fatty acid chains of the lipid. The number of double bonds corresponds to the number of unsaturated bonds in the fatty acid chains, and the number of carbon atoms corresponds to the length of the fatty acid chains and, thus, the size of the lipid. The magnitude of the lipid-specifc hazard ratio is shown as the color of the rectangle (blue: inverse association; red: positive association). Associations with statistical significance are annotated with symbols #, x and *, respectively, corresponding to $p < 0.01$, $p < 0.05$ and $p < 0.1$.

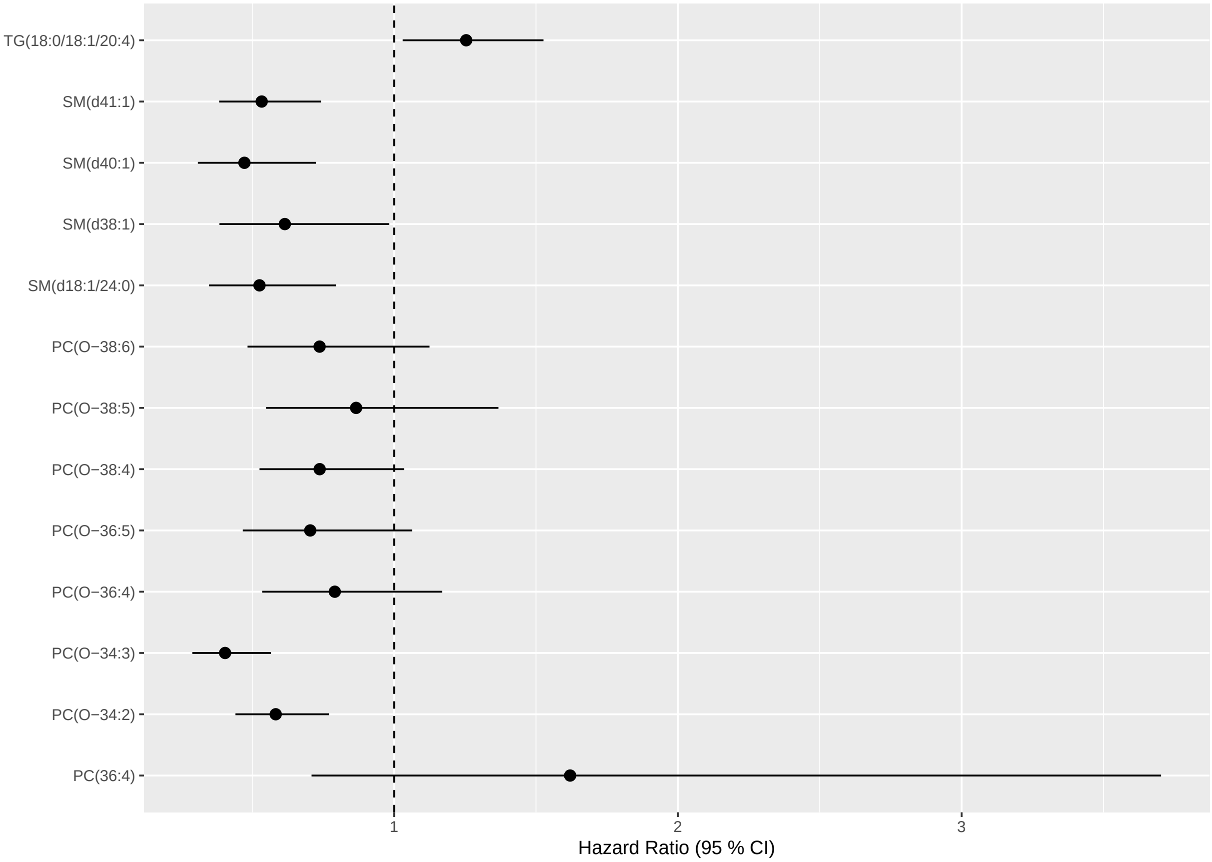


Figure 16: Forest plot of hazard ratios from the crude survival model for the combined renal event.

3.1.3 Forest Plot

3.2 Step 3B: Adjusted Model

```
## Warning in lapply(X = x, FUN = .Generic, ...): NaNs produced
```

3.2.1 Table

Table 2: Adjusted survival model for the combined renal endpoint. Shown in the table are the name of the lipid (Name), the hazard ratio (exp(coef)) and its lower and upper condidence intervals (lower .95 and upper .95, respectively), p-value of the coefficient (Pr(>|z|), and the p-value after correction for multiple testing (p.adj).

Name	exp(coef)	lower .95	upper .95	Pr(>|z|)	p.adj
SM(d38:1)	0.399	0.225	0.709	0.00173	0.0225
SM(d41:1)	0.490	0.303	0.791	0.00348	0.0418
SM(d40:1)	0.433	0.242	0.774	0.00477	0.0525
PC(O-34:3)	0.561	0.355	0.886	0.01310	0.1310
PC(O-38:4)	0.618	0.418	0.915	0.01620	0.1460
PC(O-34:2)	0.680	0.489	0.945	0.02170	0.1740
PC(O-36:4)	0.703	0.448	1.100	0.12500	0.8720
SM(d18:1/24:0)	0.682	0.395	1.180	0.17000	1.0000
PC(O-38:5)	0.742	0.437	1.260	0.26700	1.0000
TG(18:0/18:1/20:4)	0.914	0.722	1.160	0.45300	1.0000
PC(O-36:5)	0.835	0.513	1.360	0.47000	1.0000
PC(O-38:6)	0.898	0.533	1.510	0.68600	1.0000
PC(36:4)	1.120	0.545	2.300	0.75800	1.0000

3.2.2 Heatmaps

```
##   Label Relation p.adj
## 1     #  p.adj <  0.01
## 2     x  p.adj <  0.05
## 3     *  p.adj <  0.10
```

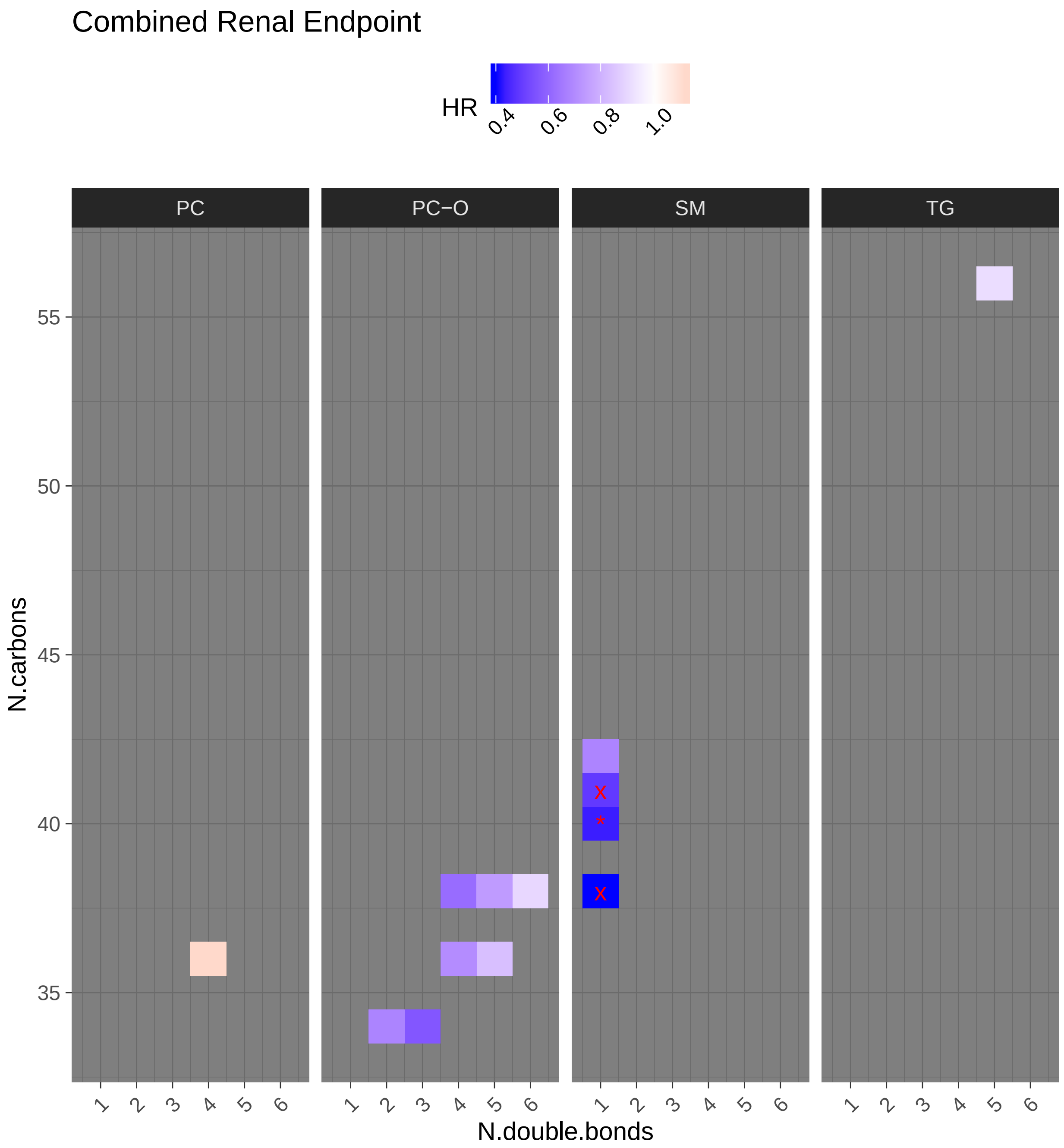


Figure 17: Heatmap of the lipid-specific hazard ratios (HRs) from the adjusted survival model for the combined renal endpoint. Lipids are organized into panels (columns) by their class (from PC to TG). One colored rectangle corresponds to one lipid species, where the coordinates in the x-axis and y-axis, respectively, show the number of double bonds (N.double.bonds) and the number of carbon atoms (N.carbons) in the fatty acid chains of the lipid. The number of double bonds corresponds to the number of unsaturated bonds in the fatty acid chains, and the number of carbon atoms corresponds to the length of the fatty acid chains and, thus, the size of the lipid. The magnitude of the lipid-specifc hazard ratio is shown as the color of the rectangle (blue: inverse association; red: positive association). Associations with statistical significance are annotated with symbols #, x and *, respectively, corresponding to $p < 0.01$, $p < 0.05$ and $p < 0.1$.

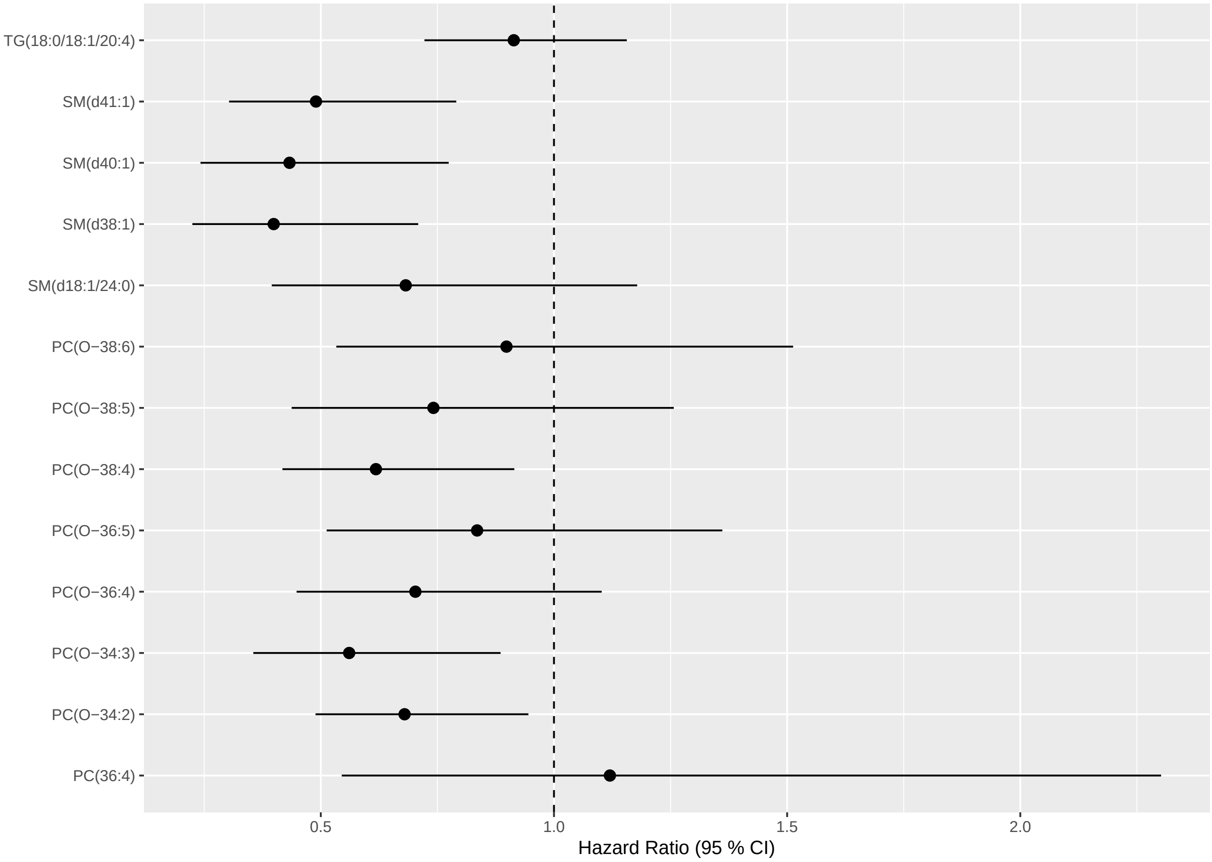
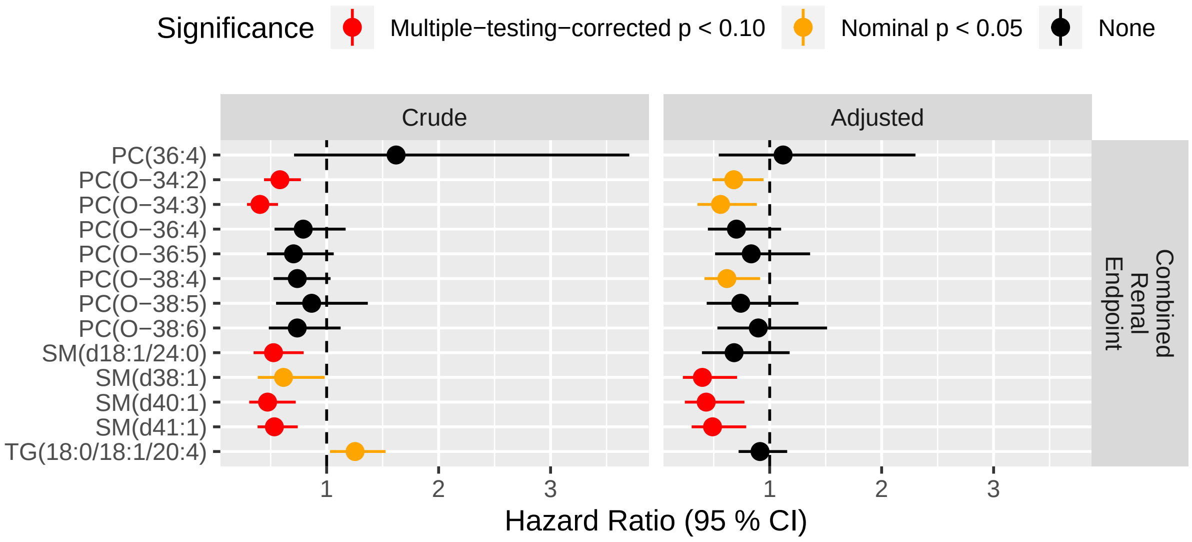


Figure 18: Forest plot of hazard ratios from the adjusted survival model for the combined renal event.

3.2.3 Forest Plot

3.3 Combined Forest Plot from Crude and Adjusted Models



4 Step 4: Survival Analysis of Specific Renal Endpoints in Relation to Prioritized Lipids from Step 3A

4.1 Step 4A: Albuminuria Group Progression

4.1.1 Crude Model

4.1.1.1 Table

Table 3: Crude survival model for albuminuria group progression. Shown in the table are the name of the lipid (Name), the hazard ratio (exp(coef)) and its lower and upper condidence intervals (lower .95 and upper .95, respectively), p-value of the coefficient (Pr(>|z|), and the p-value after correction for multiple testing (p.adj).

Name	exp(coef)	lower .95	upper .95	Pr(>|z|)	p.adj
SM(d18:1/24:0)	0.516	0.236	1.13	0.0981	0.491
SM(d40:1)	0.601	0.267	1.35	0.2190	0.874
SM(d41:1)	0.727	0.376	1.41	0.3440	1.000
PC(O-34:2)	0.873	0.517	1.47	0.6100	1.000
PC(O-34:3)	0.888	0.464	1.70	0.7200	1.000

4.1.1.2 Heatmaps

```
##   Label Relation p.adj
## 1     #  p.adj <  0.01
## 2     x  p.adj <  0.05
## 3     *  p.adj <  0.10
```

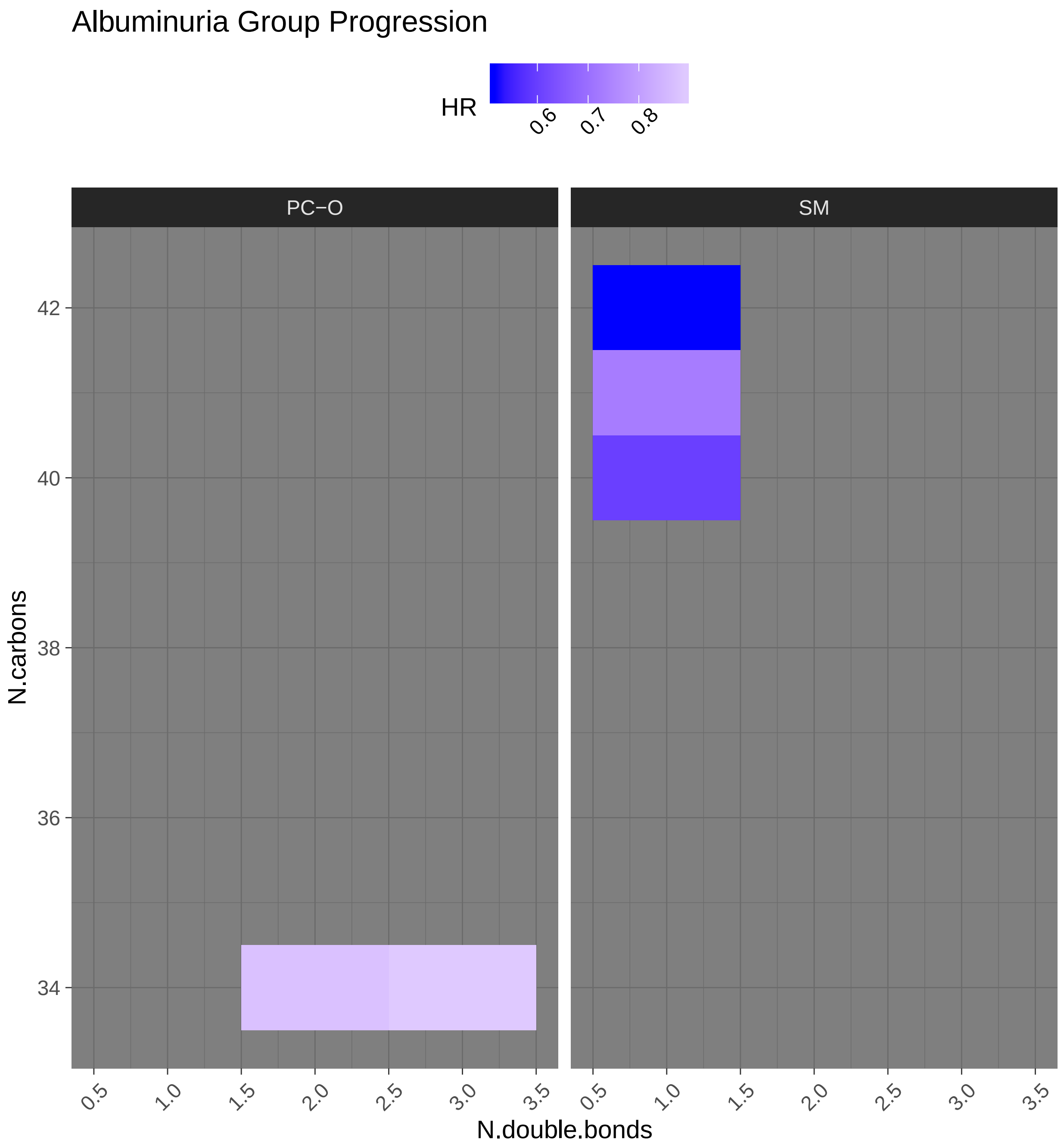


Figure 19: Heatmap of the lipid-specific hazard ratios (HRs) from the crude survival model for the albuminuria group progression. Lipids are organized into panels (columns) by their class (from PC-O to SM). One colored rectangle corresponds to one lipid species, where the coordinates in the x-axis and y-axis, respectively, show the number of double bonds (N.double.bonds) and the number of carbon atoms (N.carbons) in the fatty acid chains of the lipid. The number of double bonds corresponds to the number of unsaturated bonds in the fatty acid chains, and the number of carbon atoms corresponds to the length of the fatty acid chains and, thus, the size of the lipid. The magnitude of the lipid-specifc hazard ratio is shown as the color of the rectangle (blue: inverse association; red: positive association). Associations with statistical significance are annotated with symbols #, x and *, respectively, corresponding to $p < 0.01$, $p < 0.05$ and $p < 0.1$.

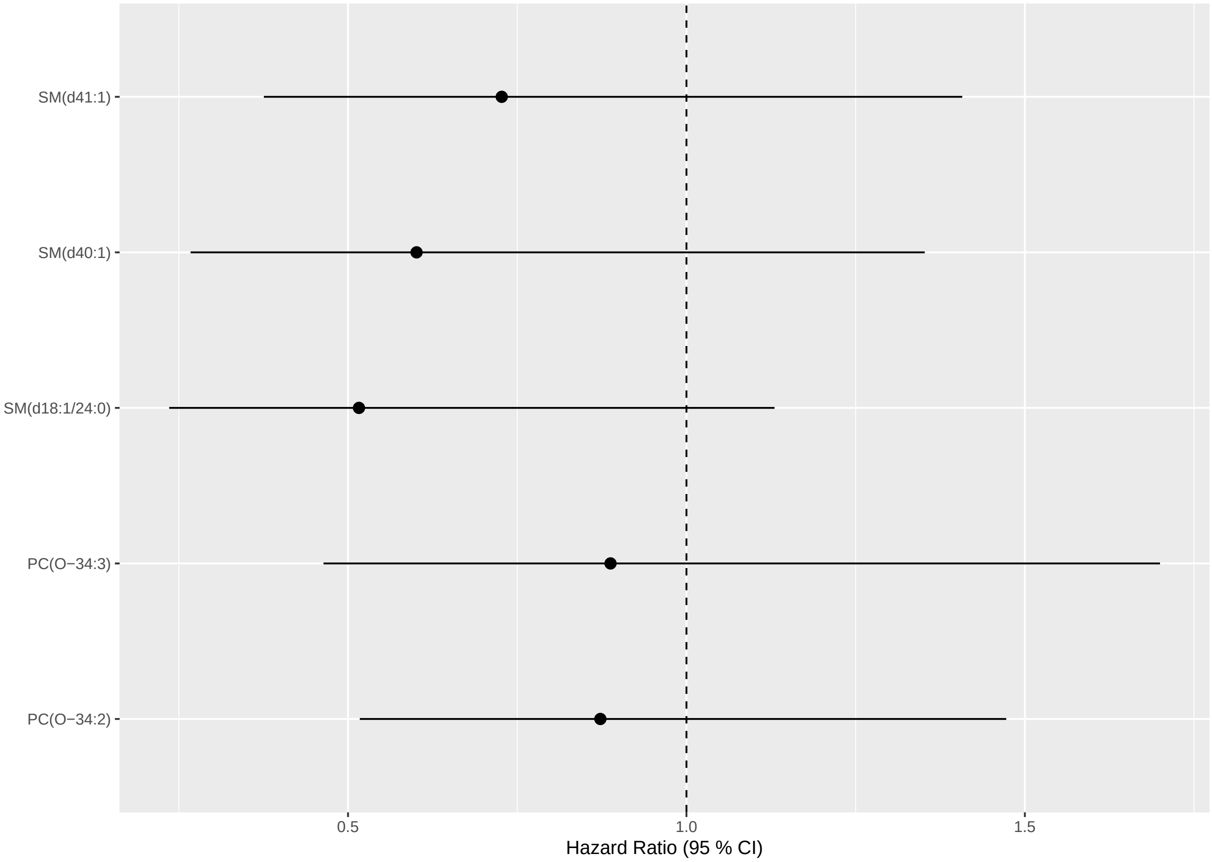


Figure 20: Forest plot of hazard ratios from the crude survival model for the albuminuria group progression. The hazard ratio and its 95 % confidence intervals (x-axis) are shown for each lipid (rows).

4.1.1.3 Forest Plot

4.1.2 Adjusted Model

4.1.2.1 Table

Table 4: Adjusted survival model for albuminuria group progression. Shown in the table are the name of the lipid (Name), the hazard ratio (exp(coef)) and its lower and upper condidence intervals (lower .95 and upper .95, respectively), p-value of the coefficient (Pr(>|z|), and the p-value after correction for multiple testing (p.adj).

Name	exp(coef)	lower .95	upper .95	Pr(>|z|)	p.adj
SM(d18:1/24:0)	0.270	0.0904	0.808	0.0191	0.0957
SM(d40:1)	0.286	0.0884	0.924	0.0365	0.1460
SM(d41:1)	0.480	0.1990	1.160	0.1040	0.3110
PC(O-34:3)	0.740	0.2960	1.850	0.5200	1.0000
PC(O-34:2)	0.854	0.4420	1.650	0.6400	1.0000

4.1.2.2 Heatmaps

```
##   Label Relation p.adj
## 1     #  p.adj <  0.01
## 2     x  p.adj <  0.05
## 3     *  p.adj <  0.10
```

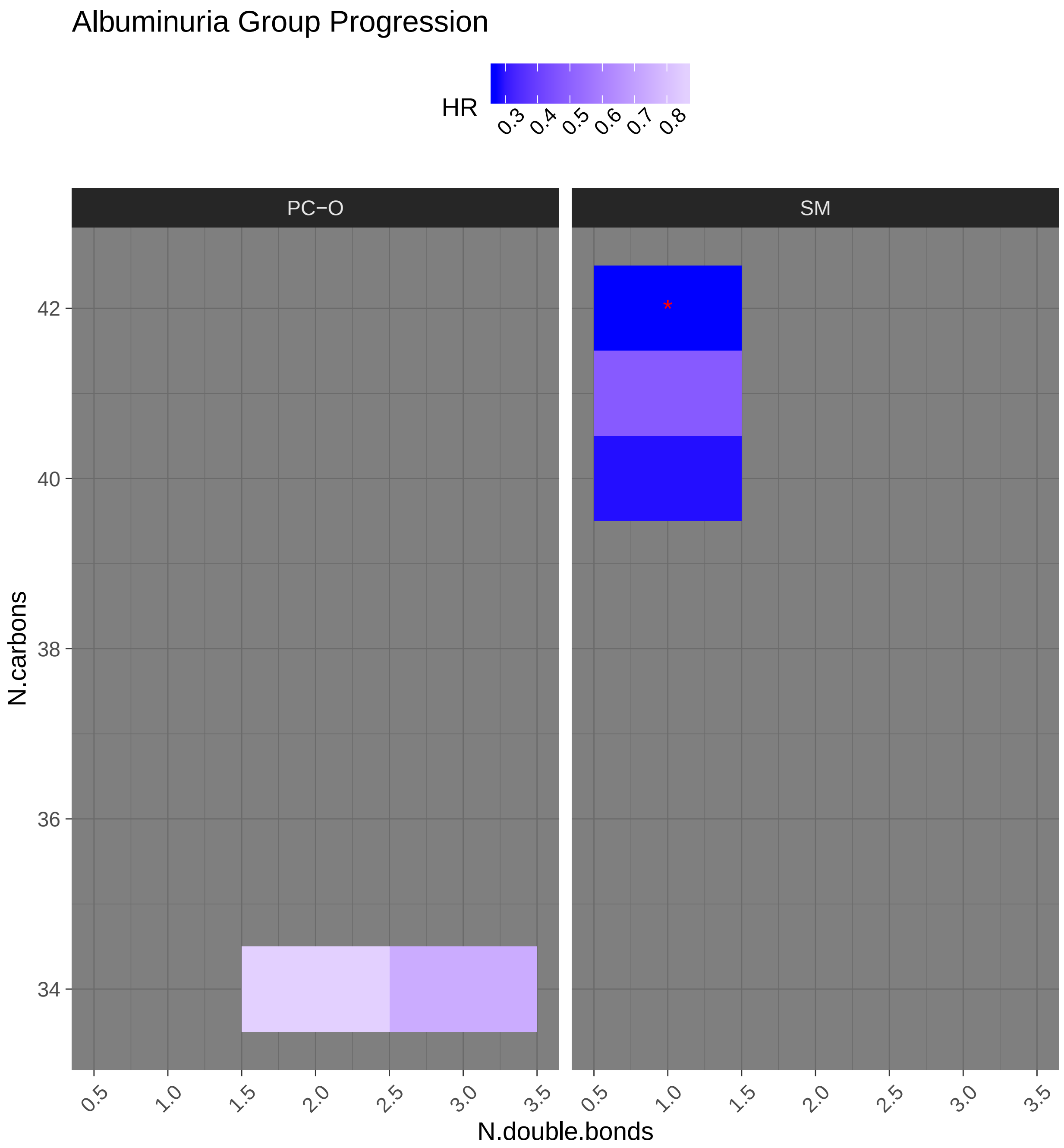


Figure 21: Heatmap of the lipid-specific hazard ratios (HRs) from the adjusted survival model for albuminuria group progression. Lipids are organized into panels (columns) by their class (from PC-O to SM). One colored rectangle corresponds to one lipid species, where the coordinates in the x-axis and y-axis, respectively, show the number of double bonds (N.double.bonds) and the number of carbon atoms (N.carbons) in the fatty acid chains of the lipid. The number of double bonds corresponds to the number of unsaturated bonds in the fatty acid chains, and the number of carbon atoms corresponds to the length of the fatty acid chains and, thus, the size of the lipid. The magnitude of the lipid-specifc hazard ratio is shown as the color of the rectangle (blue: inverse association; red: positive association). Associations with statistical significance are annotated with symbols #, x and *, respectively, corresponding to $p < 0.01$, $p < 0.05$ and $p < 0.1$.

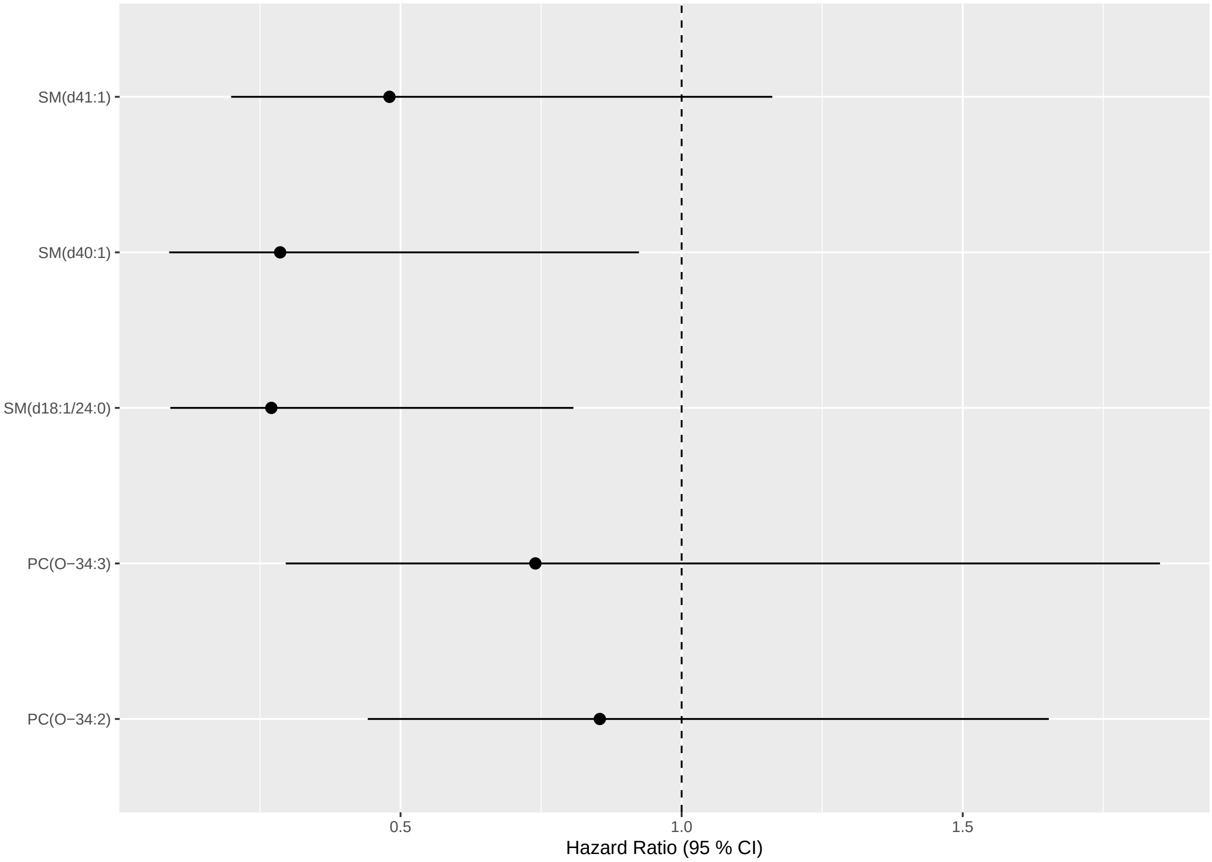


Figure 22: Forest plot of hazard ratios from the adjusted survival model for the albuminuria group progression. The hazard ratio and its 95 % confidence intervals (x-axis) are shown for each lipid (rows).

4.1.2.3 Forest Plot

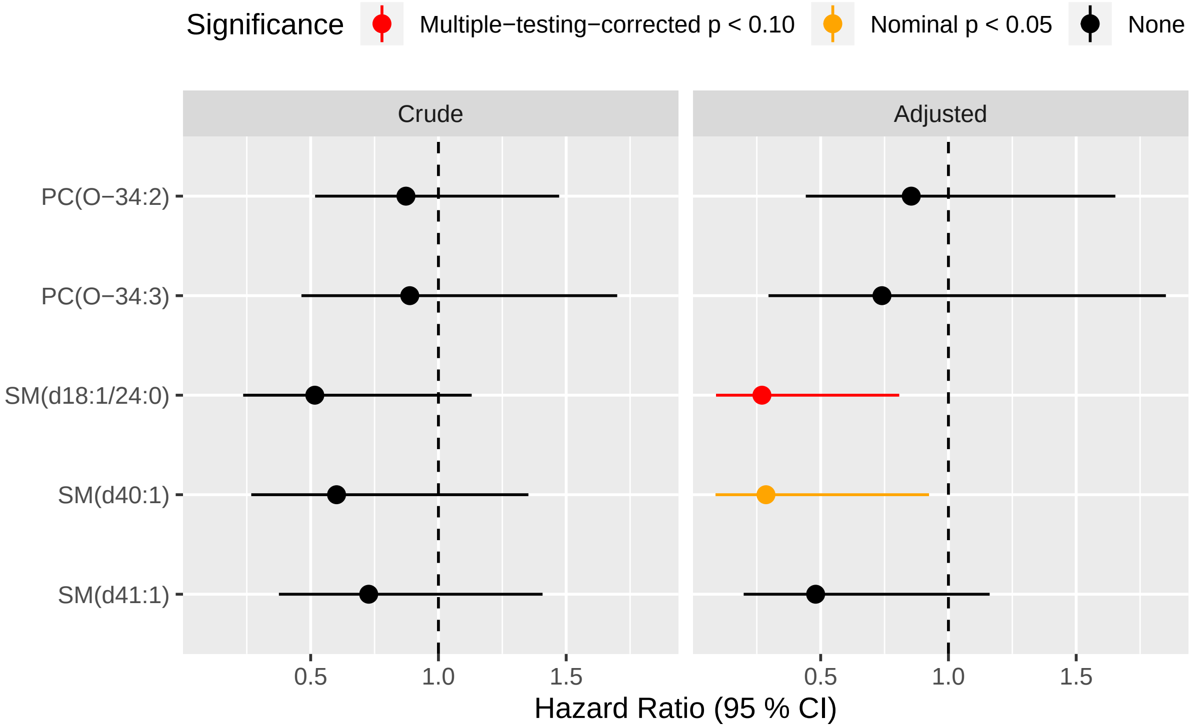


Figure 23: Combined Forest plot of hazard ratios from the crude and adjusted survival models (left and right, respectively) for the albuminuria group progression. The hazard ratio and its 95 % confidence intervals (x-axis) are shown for each lipid (rows).

4.1.3 Combined Forest Plot from Crude and Adjusted Models

4.2 Step 4B: All-Cause Mortality

4.2.1 Crude Model

4.2.1.1 Table

Table 5: Crude survival model for all-cause mortality. Shown in the table are the name of the lipid (Name), the hazard ratio (exp(coef)) and its lower and upper condidence intervals (lower .95 and upper .95, respectively), p-value of the coefficient (Pr(>|z|), and the p-value after correction for multiple testing (p.adj).

Name	exp(coef)	lower .95	upper .95	Pr(>|z|)	p.adj
SM(d41:1)	0.327	0.221	0.483	0.00e+00	1.00e-07
SM(d40:1)	0.232	0.130	0.416	9.00e-07	3.60e-06
PC(O-34:3)	0.364	0.223	0.592	4.67e-05	1.40e-04
SM(d18:1/24:0)	0.318	0.176	0.575	1.49e-04	2.99e-04
PC(O-34:2)	0.475	0.317	0.710	2.91e-04	2.99e-04

4.2.1.2 Heatmaps

```
##   Label Relation p.adj
## 1     #  p.adj <  0.01
## 2     x  p.adj <  0.05
## 3     *  p.adj <  0.10
```

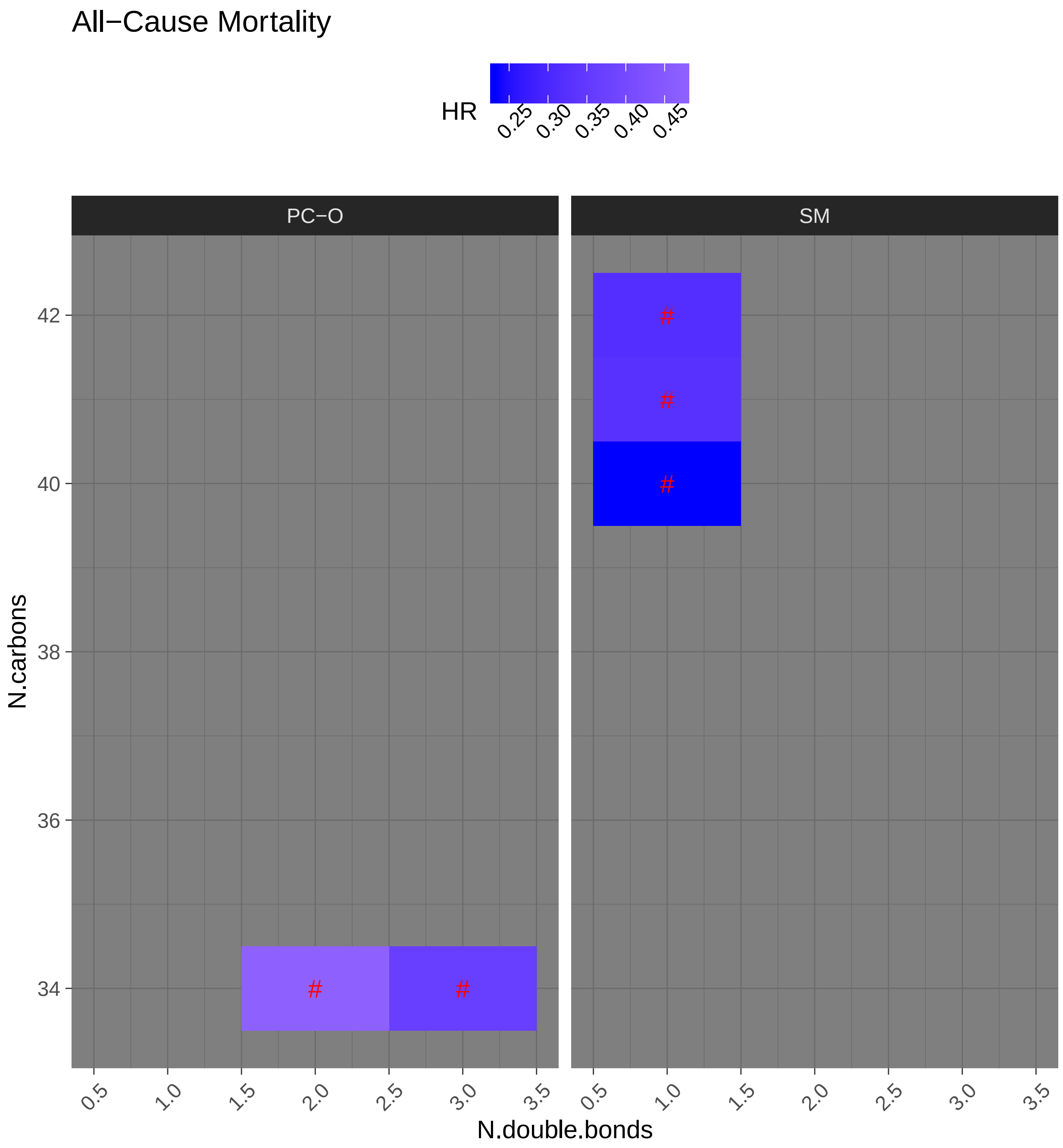


Figure 24: Heatmap of the lipid-specific hazard ratios (HRs) from the crude survival model for all-cause mortality. Lipids are organized into panels (columns) by their class (from PC-O to SM). One colored rectangle corresponds to one lipid species, where the coordinates in the x-axis and y-axis, respectively, show the number of double bonds (N.double.bonds) and the number of carbon atoms (N.carbons) in the fatty acid chains of the lipid. The number of double bonds corresponds to the number of unsaturated bonds in the fatty acid chains, and the number of carbon atoms corresponds to the length of the fatty acid chains and, thus, the size of the lipid. The magnitude of the lipid-specifc hazard ratio is shown as the color of the rectangle (blue: inverse association; red: positive association). Associations with statistical significance are annotated with symbols #, x and *, respectively, corresponding to $p < 0.01$, $p < 0.05$ and $p < 0.1$.

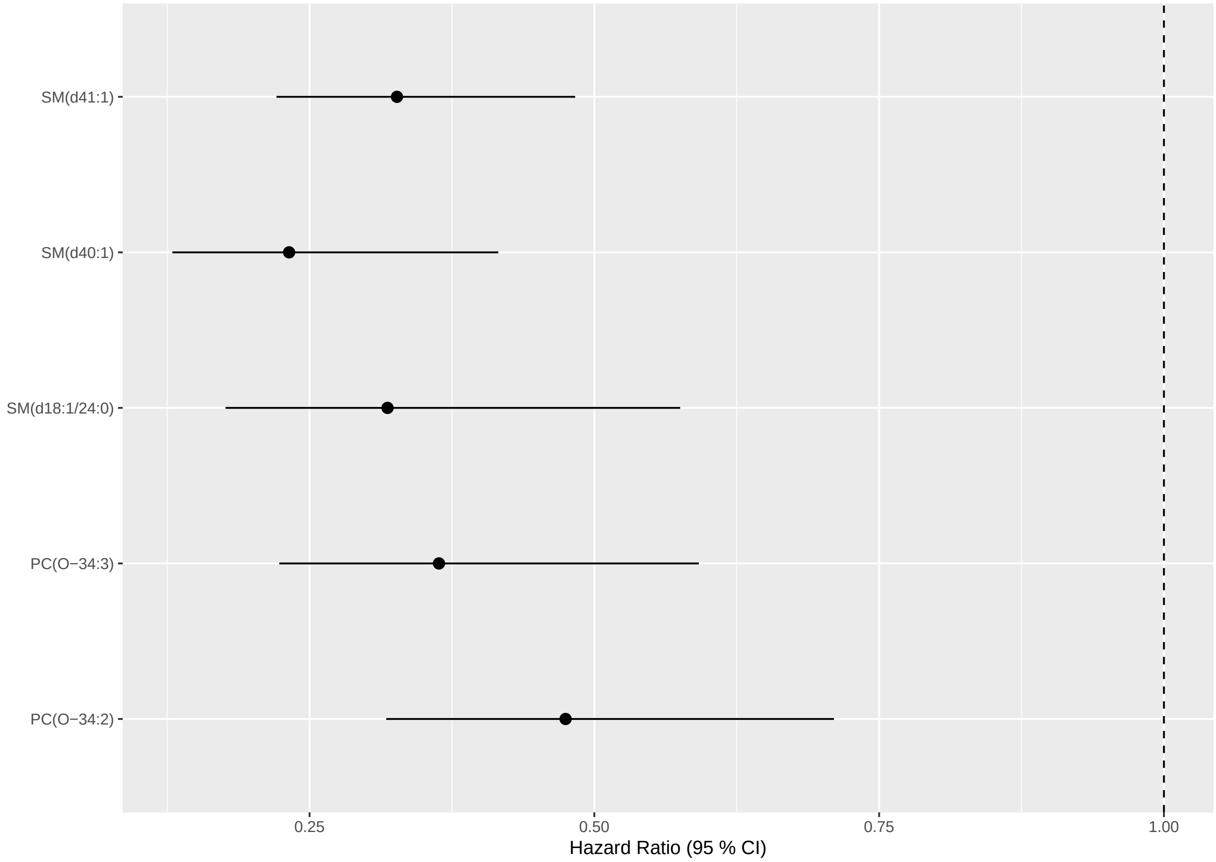


Figure 25: Forest plot of hazard ratios from the crude survival model for all-cause mortality. The hazard ratio and its 95 % confidence intervals (x-axis) are shown for each lipid (rows).

4.2.1.3 Forest Plot

4.2.2 Adjusted Model

4.2.2.1 Table

Table 6: Adjusted survival model for all-cause mortality. Shown in the table are the name of the lipid (Name), the hazard ratio (exp(coef)) and its lower and upper condidence intervals (lower .95 and upper .95, respectively), p-value of the coefficient (Pr(>|z|), and the p-value after correction for multiple testing (p.adj).

Name	exp(coef)	lower .95	upper .95	Pr(>|z|)	p.adj
SM(d41:1)	0.354	0.193	0.649	0.000803	0.00401
SM(d40:1)	0.327	0.143	0.747	0.008050	0.03220
PC(O-34:3)	0.469	0.239	0.920	0.027700	0.08310
PC(O-34:2)	0.623	0.385	1.010	0.053600	0.10700
SM(d18:1/24:0)	0.577	0.257	1.300	0.184000	0.18400

4.2.2.2 Heatmaps

```
##   Label Relation p.adj
## 1     #  p.adj <  0.01
## 2     x  p.adj <  0.05
## 3     *  p.adj <  0.10
```

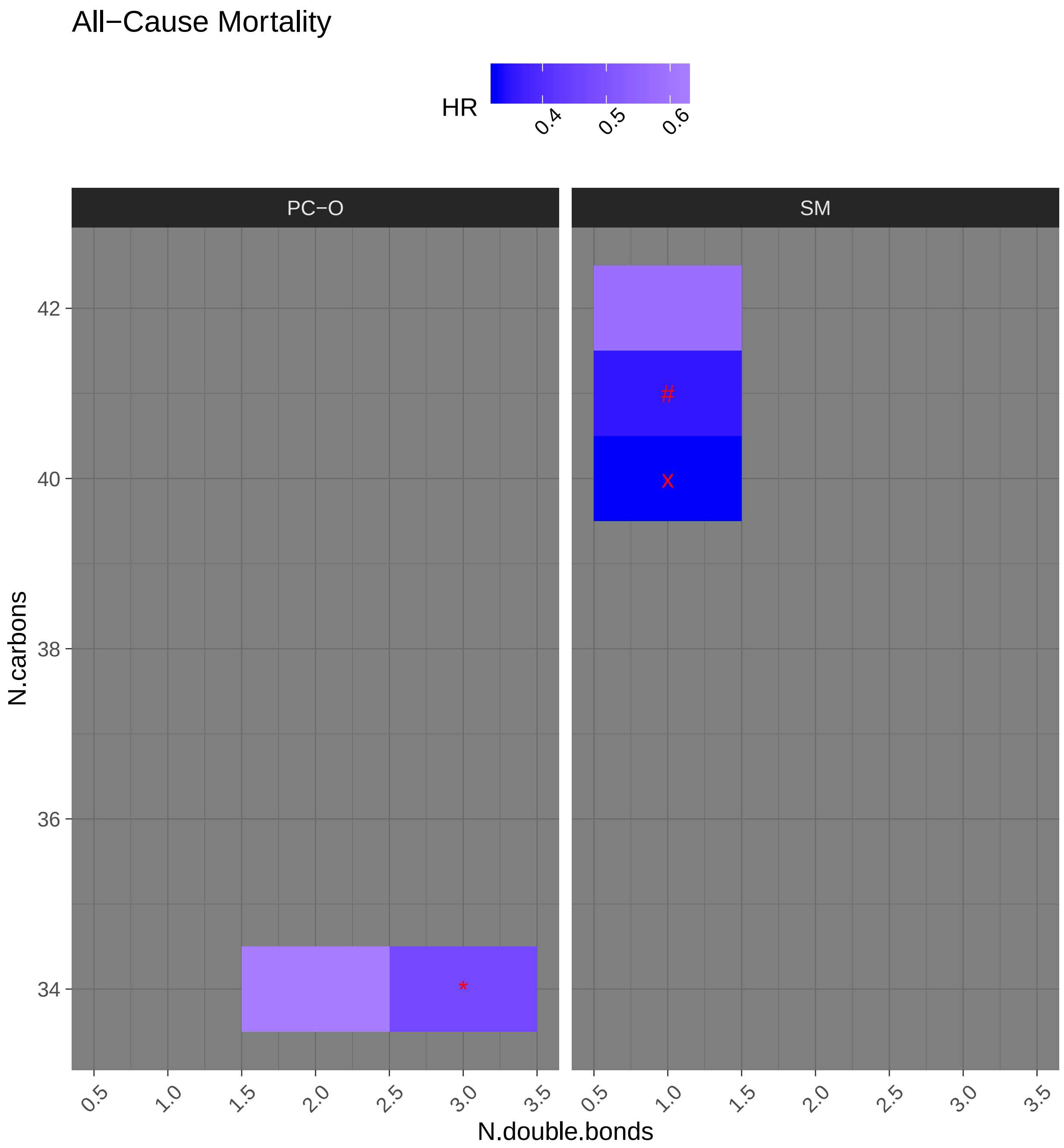


Figure 26: Heatmap of the lipid-specific hazard ratios (HRs) from the adjusted survival model for all-cause mortality. Lipids are organized into panels (columns) by their class (from PC-O to SM). One colored rectangle corresponds to one lipid species, where the coordinates in the x-axis and y-axis, respectively, show the number of double bonds (N.double.bonds) and the number of carbon atoms (N.carbons) in the fatty acid chains of the lipid. The number of double bonds corresponds to the number of unsaturated bonds in the fatty acid chains, and the number of carbon atoms corresponds to the length of the fatty acid chains and, thus, the size of the lipid. The magnitude of the lipid-specifc hazard ratio is shown as the color of the rectangle (blue: inverse association; red: positive association). Associations with statistical significance are annotated with symbols #, x and *, respectively, corresponding to $p < 0.01$, $p < 0.05$ and $p < 0.1$.

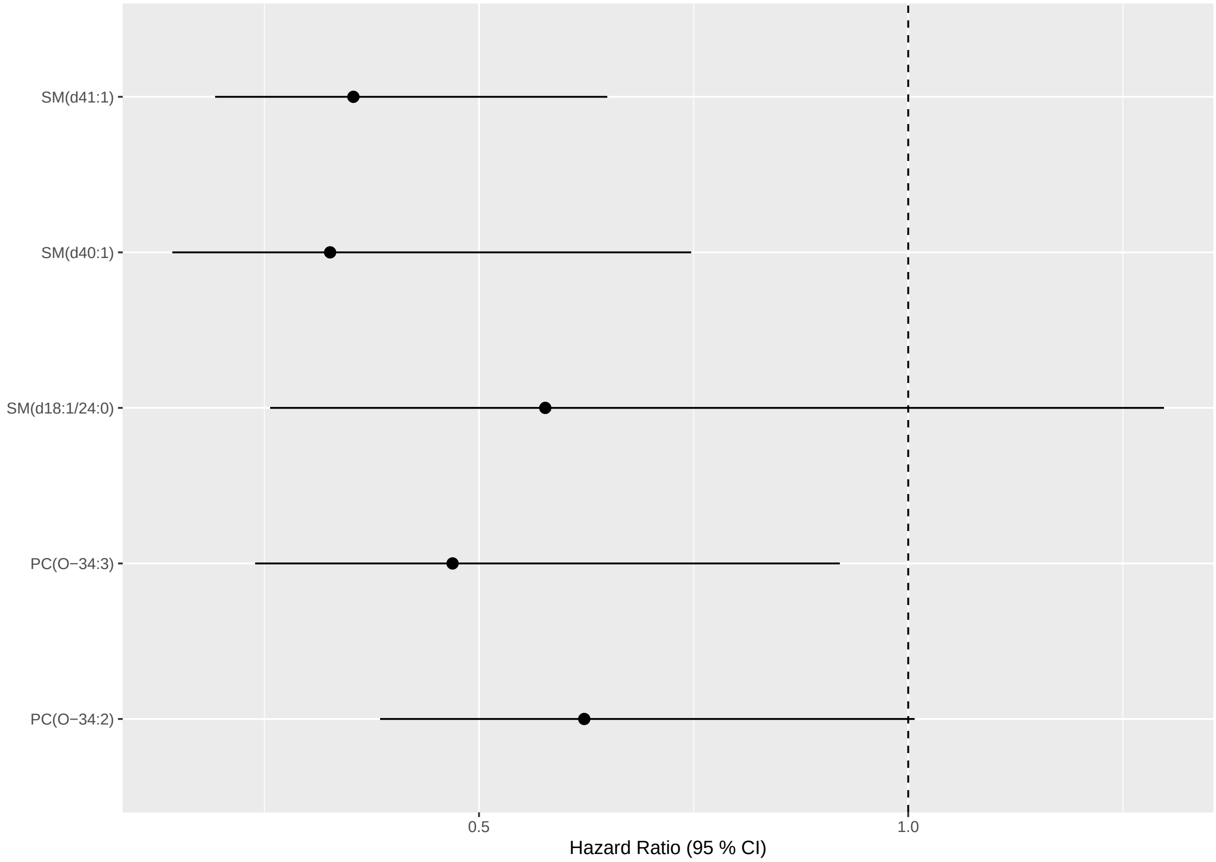


Figure 27: Forest plot of hazard ratios from the adjusted survival model for all-cause mortality. The hazard ratio and its 95 % confidence intervals (x-axis) are shown for each lipid (rows).

4.2.2.3 Forest Plot

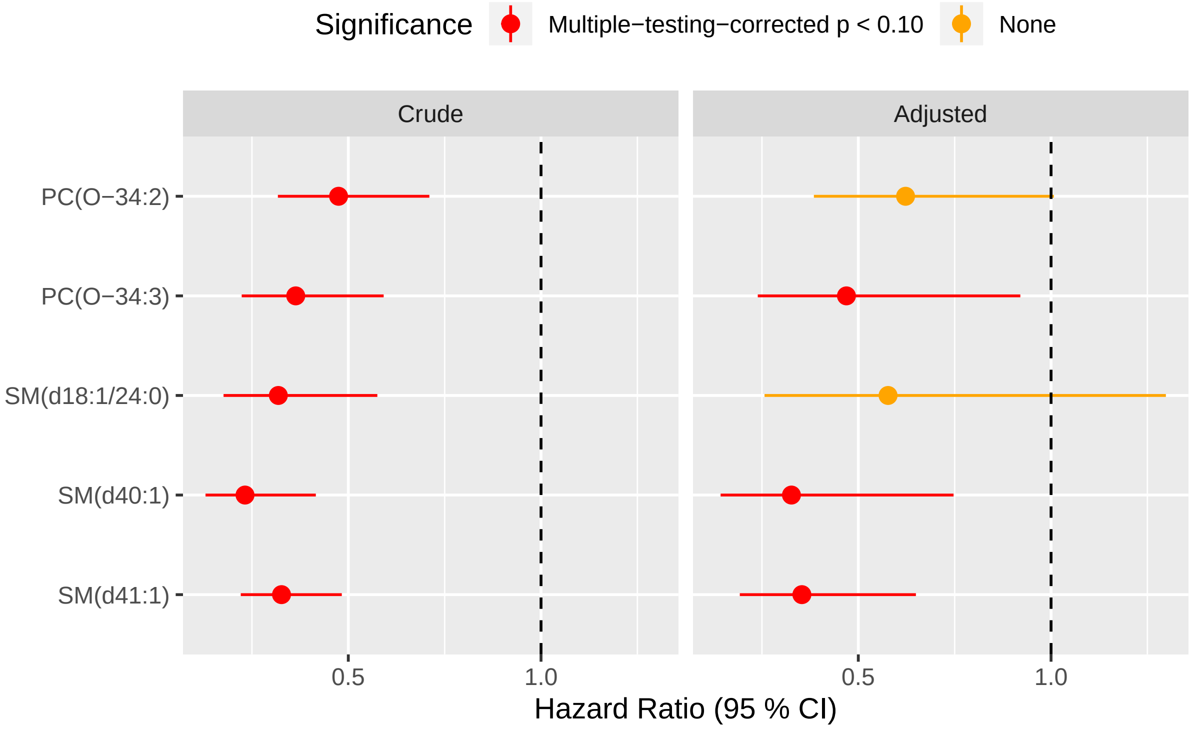


Figure 28: Combined forest plot of hazard ratios from the crude and adjusted survival models (left and right, respectively) for all-cause mortality. The hazard ratio and its 95 % confidence intervals (x-axis) are shown for each lipid (rows).

4.2.3 Combined Forest Plot

4.3 Step 4C: eGFR Decline > 30 %

4.3.1 Crude Model

4.3.1.1 Table

Table 7: Crude survival model for eGFR recline > 30 %. Shown in the table are the name of the lipid (Name), the hazard ratio (exp(coef)) and its lower and upper condidence intervals (lower .95 and upper .95, respectively), p-value of the coefficient (Pr(>|z|), and the p-value after correction for multiple testing (p.adj).

Name	exp(coef)	lower .95	upper .95	Pr(>|z|)	p.adj
PC(O-34:3)	0.544	0.363	0.817	0.00332	0.0166
PC(O-34:2)	0.722	0.521	1.000	0.04980	0.1990
SM(d40:1)	0.773	0.457	1.310	0.33800	1.0000
SM(d18:1/24:0)	0.794	0.482	1.310	0.36600	1.0000
SM(d41:1)	0.839	0.541	1.300	0.43300	1.0000

4.3.1.2 Heatmaps

```
##   Label Relation p.adj
## 1     #  p.adj <  0.01
## 2     x  p.adj <  0.05
## 3     *  p.adj <  0.10
```

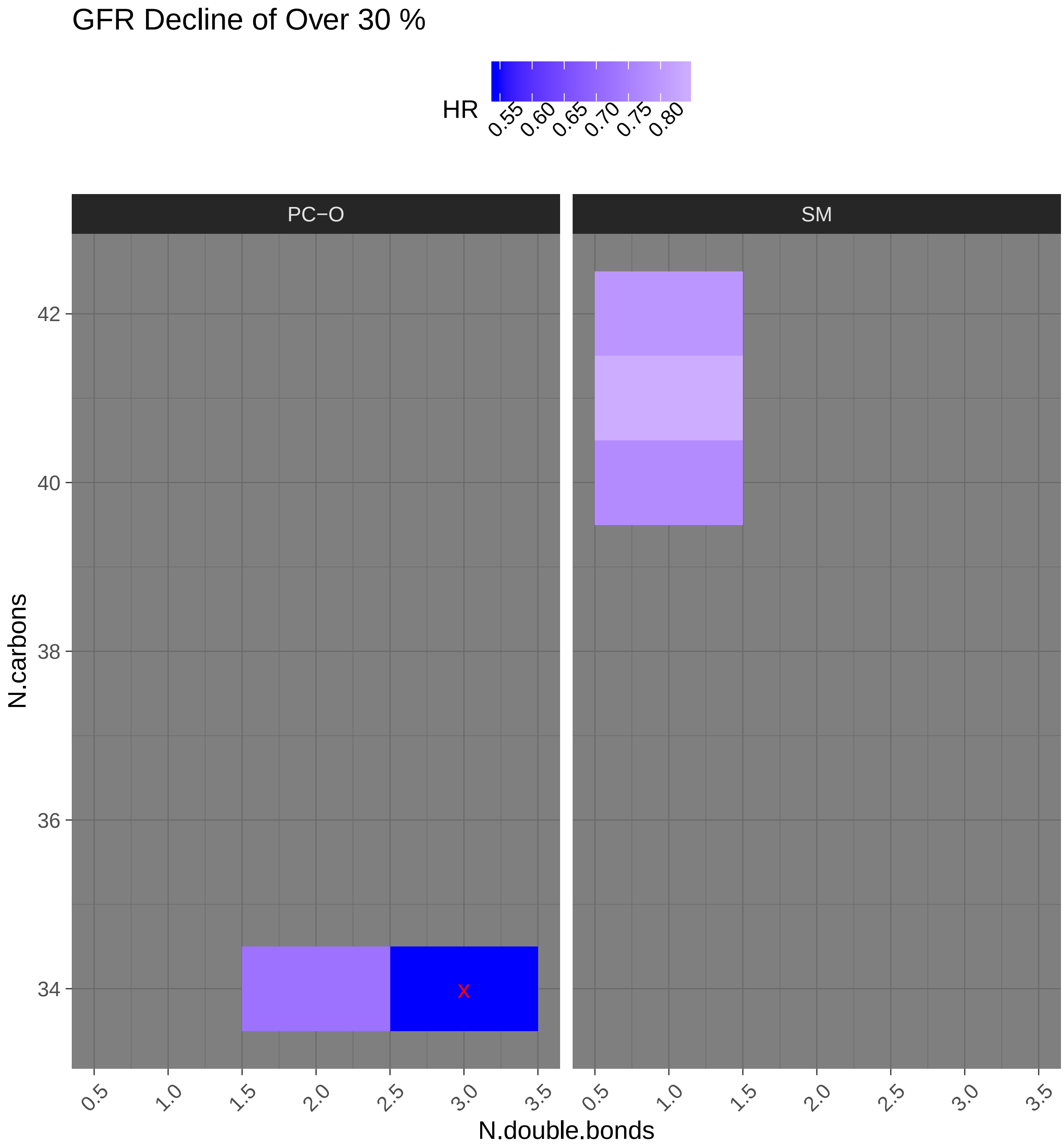


Figure 29: Heatmap of the lipid-specific hazard ratios (HRs) from the crude survival model for eGFR decline (> 30 %). Lipids are organized into panels (columns) by their class (from PC-O to SM). One colored rectangle corresponds to one lipid species, where the coordinates in the x-axis and y-axis, respectively, show the number of double bonds (N.double.bonds) and the number of carbon atoms (N.carbons) in the fatty acid chains of the lipid. The number of double bonds corresponds to the number of unsaturated bonds in the fatty acid chains, and the number of carbon atoms corresponds to the length of the fatty acid chains and, thus, the size of the lipid. The magnitude of the lipid-specifc hazard ratio is shown as the color of the rectangle (blue: inverse association; red: positive association). Associations with statistical significance are annotated with symbols #, x and *, respectively, corresponding to $p < 0.01$, $p < 0.05$ and $p < 0.1$.

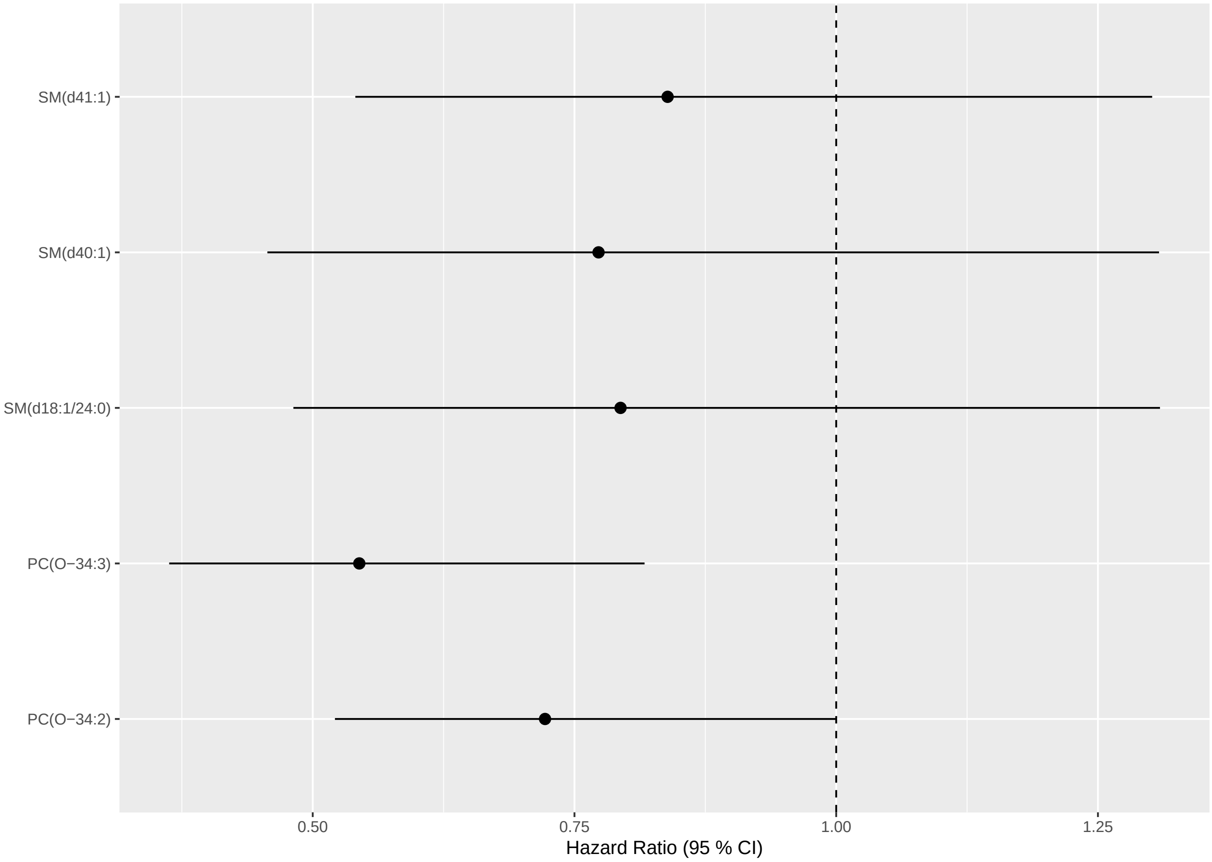


Figure 30: Forest plot of hazard ratios from the crude survival model for eGFR decline (> 30 %). The hazard ratio and its 95 % confidence intervals (x-axis) are shown for each lipid (rows).

4.3.1.3 Forest Plot

4.3.2 Adjusted Model

4.3.2.1 Table

Table 8: Adjusted survival model for eGFR decline > 30 %. Shown in the table are the name of the lipid (Name), the hazard ratio (exp(coef)) and its lower and upper condidence intervals (lower .95 and upper .95, respectively), p-value of the coefficient (Pr(>|z|), and the p-value after correction for multiple testing (p.adj).

Name	exp(coef)	lower .95	upper .95	Pr(>|z|)	p.adj
SM(d40:1)	0.598	0.293	1.22	0.159	0.794
PC(O-34:2)	0.866	0.597	1.26	0.448	1.000
SM(d18:1/24:0)	0.774	0.390	1.54	0.466	1.000
SM(d41:1)	0.819	0.455	1.47	0.506	1.000
PC(O-34:3)	0.909	0.547	1.51	0.714	1.000

4.3.2.2 Heatmaps

```
##   Label Relation p.adj
## 1     #  p.adj <  0.01
## 2     x  p.adj <  0.05
## 3     *  p.adj <  0.10
```

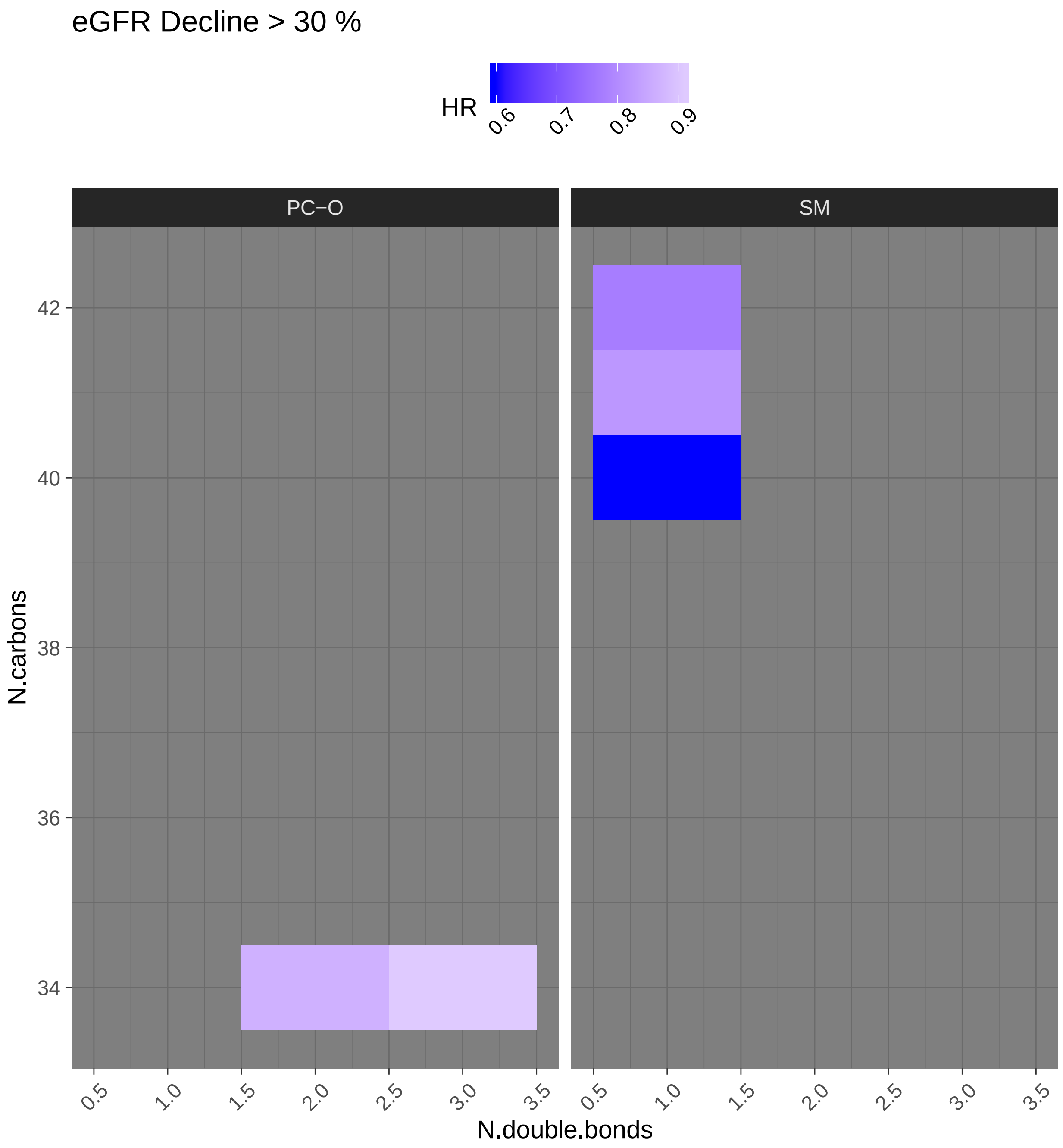


Figure 31: Heatmap of the lipid-specific hazard ratios (HRs) from the adjusted survival model for eGFR decline (> 30 %). Lipids are organized into panels (columns) by their class (from PC-O to SM). One colored rectangle corresponds to one lipid species, where the coordinates in the x-axis and y-axis, respectively, show the number of double bonds (N.double.bonds) and the number of carbon atoms (N.carbons) in the fatty acid chains of the lipid. The number of double bonds corresponds to the number of unsaturated bonds in the fatty acid chains, and the number of carbon atoms corresponds to the length of the fatty acid chains and, thus, the size of the lipid. The magnitude of the lipid-specifc hazard ratio is shown as the color of the rectangle (blue: inverse association; red: positive association). Associations with statistical significance are annotated with symbols #, x and *, respectively, corresponding to $p < 0.01$, $p < 0.05$ and $p < 0.1$.

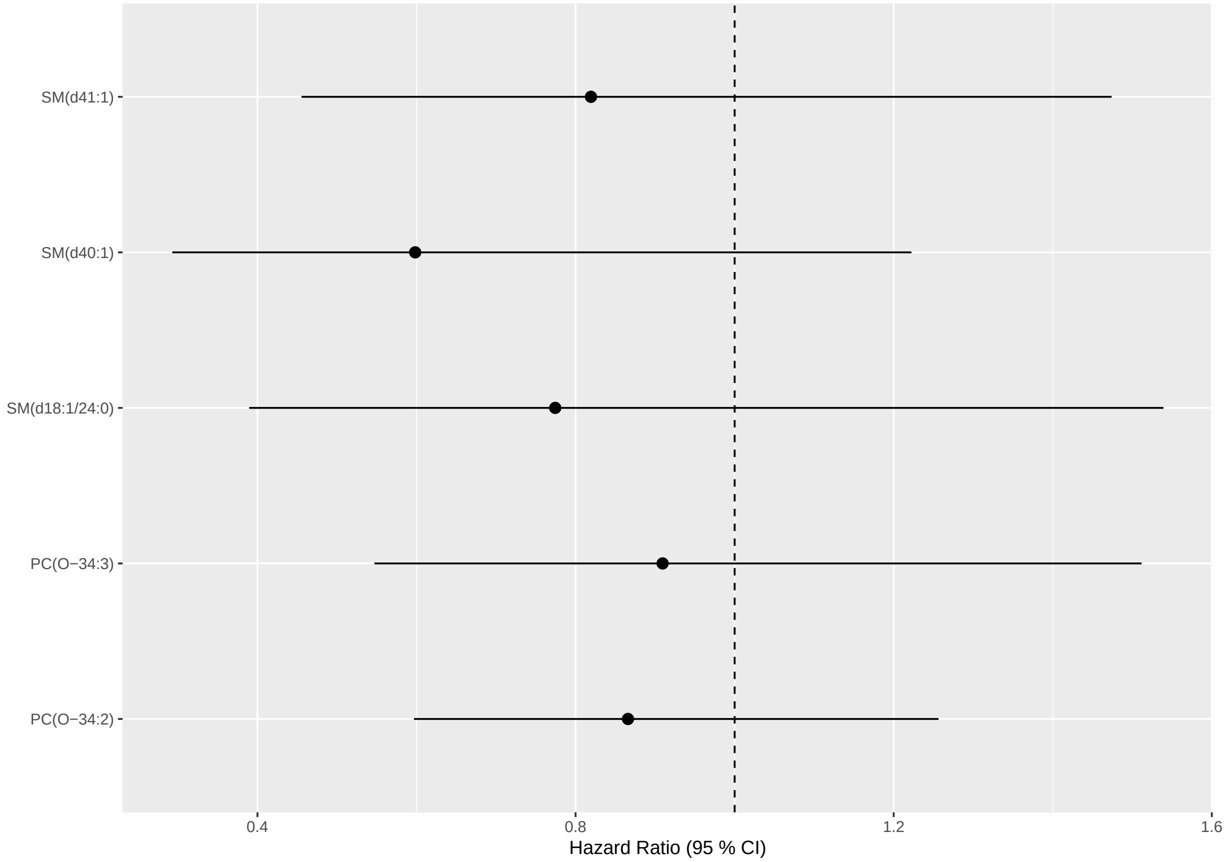


Figure 32: Forest plot of hazard ratios from the adjusted survival model for eGFR decline (> 30 %). The hazard ratio and its 95 % confidence intervals (x-axis) are shown for each lipid (rows).

4.3.2.3 Forest Plot

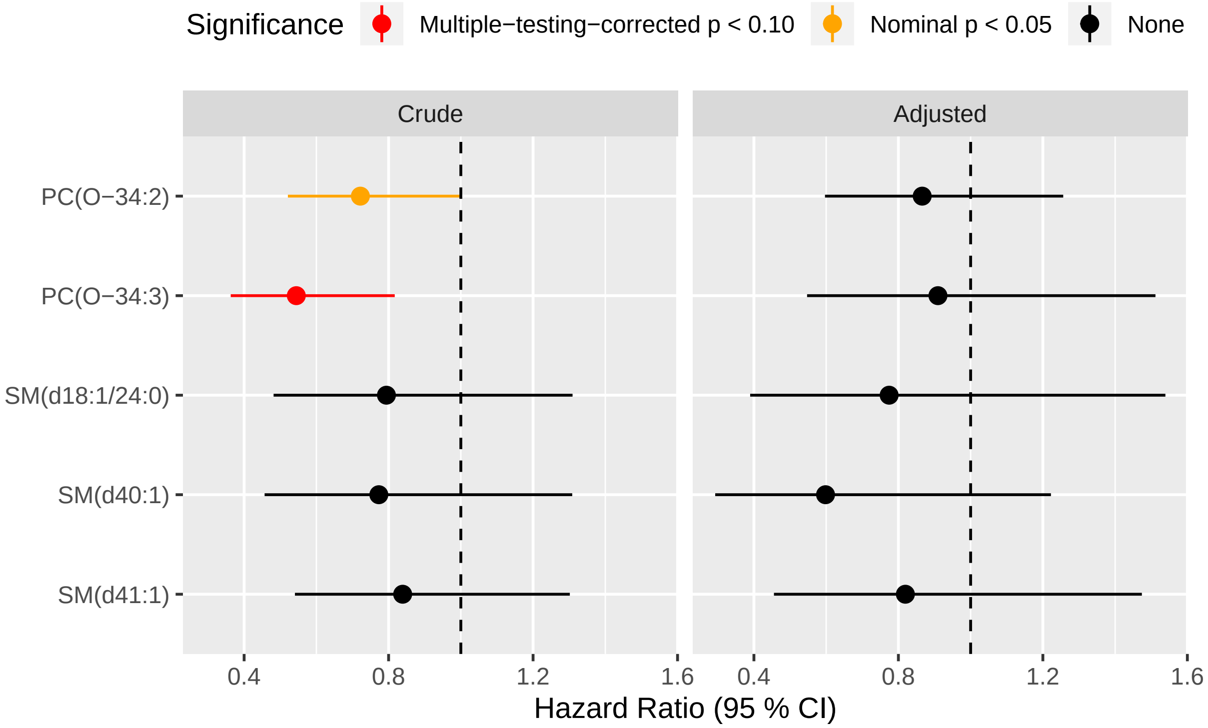


Figure 33: Combined forest plot of hazard ratios from the crude and adjusted survival models (left and right, respectively) for eGFR decline (>30 %). The hazard ratio and its 95 % confidence intervals (x-axis) are shown for each lipid (rows).

4.3.3 Combined Forest Plot from Crude and Adjusted Models

4.4 Step 4D: End-Stage Renal Disease

4.4.1 Crude Model

4.4.1.1 Table

Table 9: Crude survival model for end-stage renal disease. Shown in the table are the name of the lipid (Name), the hazard ratio (exp(coef)) and its lower and upper condidence intervals (lower .95 and upper .95, respectively), p-value of the coefficient (Pr(>|z|), and the p-value after correction for multiple testing (p.adj).

Name	exp(coef)	lower .95	upper .95	Pr(>|z|)	p.adj
PC(O-34:3)	0.192	0.0908	0.404	1.43e-05	7.15e-05
SM(d18:1/24:0)	0.203	0.0810	0.509	6.76e-04	2.70e-03
SM(d40:1)	0.279	0.1090	0.717	8.03e-03	2.41e-02
SM(d41:1)	0.404	0.2050	0.796	8.87e-03	2.41e-02
PC(O-34:2)	0.543	0.2850	1.040	6.36e-02	6.36e-02

4.4.1.2 Heatmaps

```
##   Label Relation p.adj
## 1     #  p.adj <  0.01
## 2     x  p.adj <  0.05
## 3     *  p.adj <  0.10
```

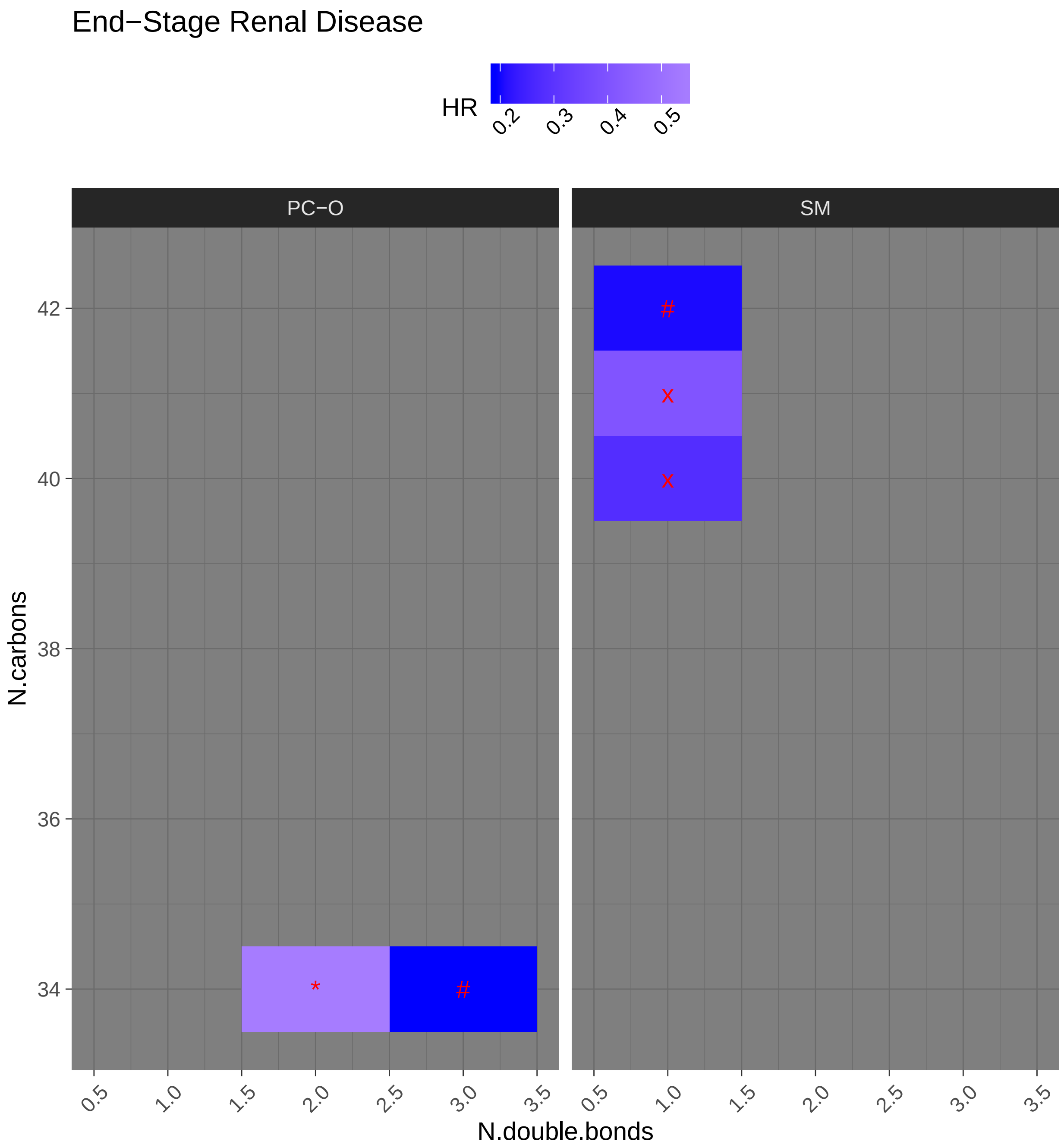


Figure 34: Heatmap of the lipid-specific hazard ratios (HRs) from the crude survival model for end-stage renal disease. Lipids are organized into panels (columns) by their class (from PC-O to SM). One colored rectangle corresponds to one lipid species, where the coordinates in the x-axis and y-axis, respectively, show the number of double bonds (N.double.bonds) and the number of carbon atoms (N.carbons) in the fatty acid chains of the lipid. The number of double bonds corresponds to the number of unsaturated bonds in the fatty acid chains, and the number of carbon atoms corresponds to the length of the fatty acid chains and, thus, the size of the lipid. The magnitude of the lipid-specifc hazard ratio is shown as the color of the rectangle (blue: inverse association; red: positive association). Associations with statistical significance are annotated with symbols #, x and *, respectively, corresponding to $p < 0.01$, $p < 0.05$ and $p < 0.1$.

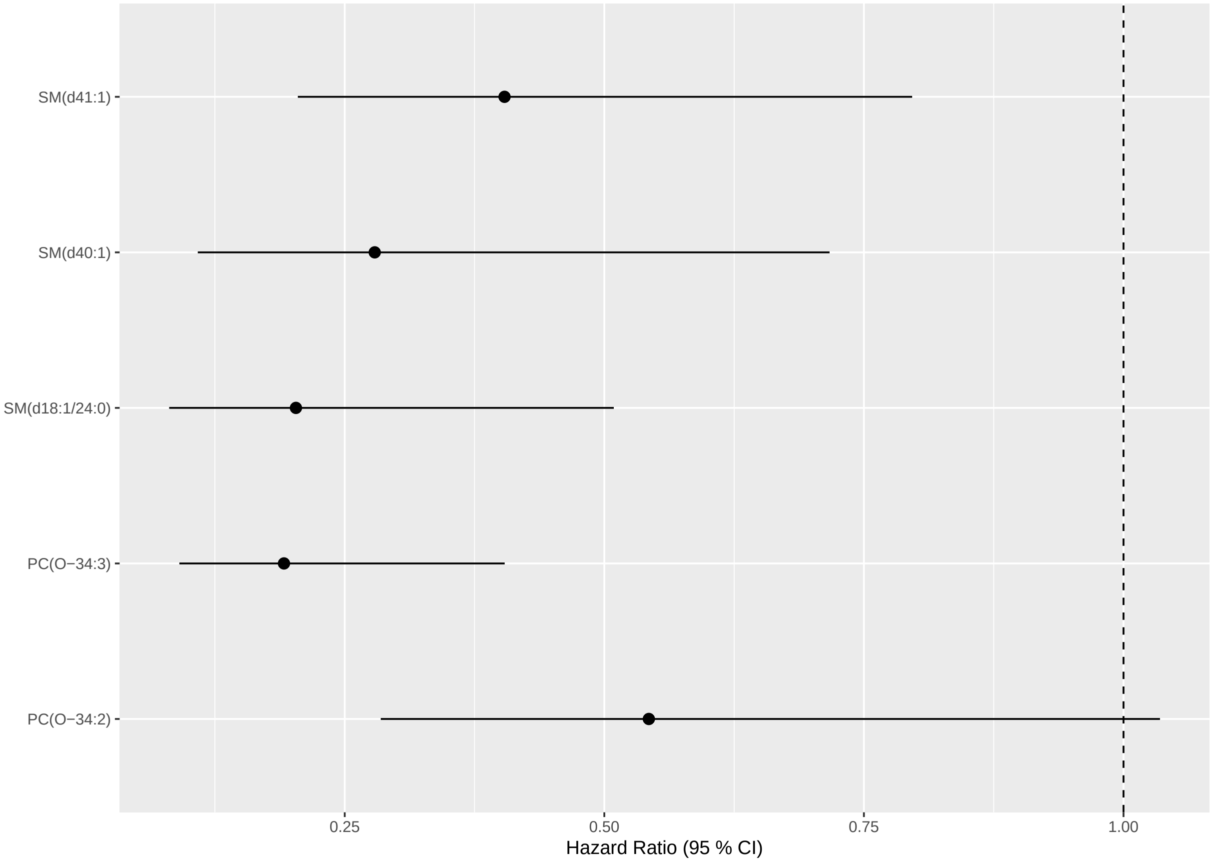


Figure 35: Forest plot of hazard ratios from the crude survival model for end-stage renal disease. The hazard ratio and its 95 % confidence intervals (x-axis) are shown for each lipid (rows).

4.4.1.3 Forest Plot

4.4.2 Adjusted Model

4.4.2.1 Table

Table 10: Adjusted survival model for end stage renal disease. Shown in the table are the name of the lipid (Name), the hazard ratio (exp(coef)) and its lower and upper condidence intervals (lower .95 and upper .95, respectively), p-value of the coefficient (Pr(>|z|), and the p-value after correction for multiple testing (p.adj).

Name	exp(coef)	lower .95	upper .95	Pr(>|z|)	p.adj
SM(d41:1)	0.531	0.147	1.92	0.335	1
SM(d40:1)	0.524	0.107	2.57	0.426	1
SM(d18:1/24:0)	0.687	0.178	2.66	0.586	1
PC(O-34:3)	0.785	0.251	2.45	0.676	1
PC(O-34:2)	0.917	0.389	2.16	0.842	1

4.4.2.2 Heatmaps

```
##   Label Relation p.adj
## 1     #  p.adj <  0.01
## 2     x  p.adj <  0.05
## 3     *  p.adj <  0.10
```

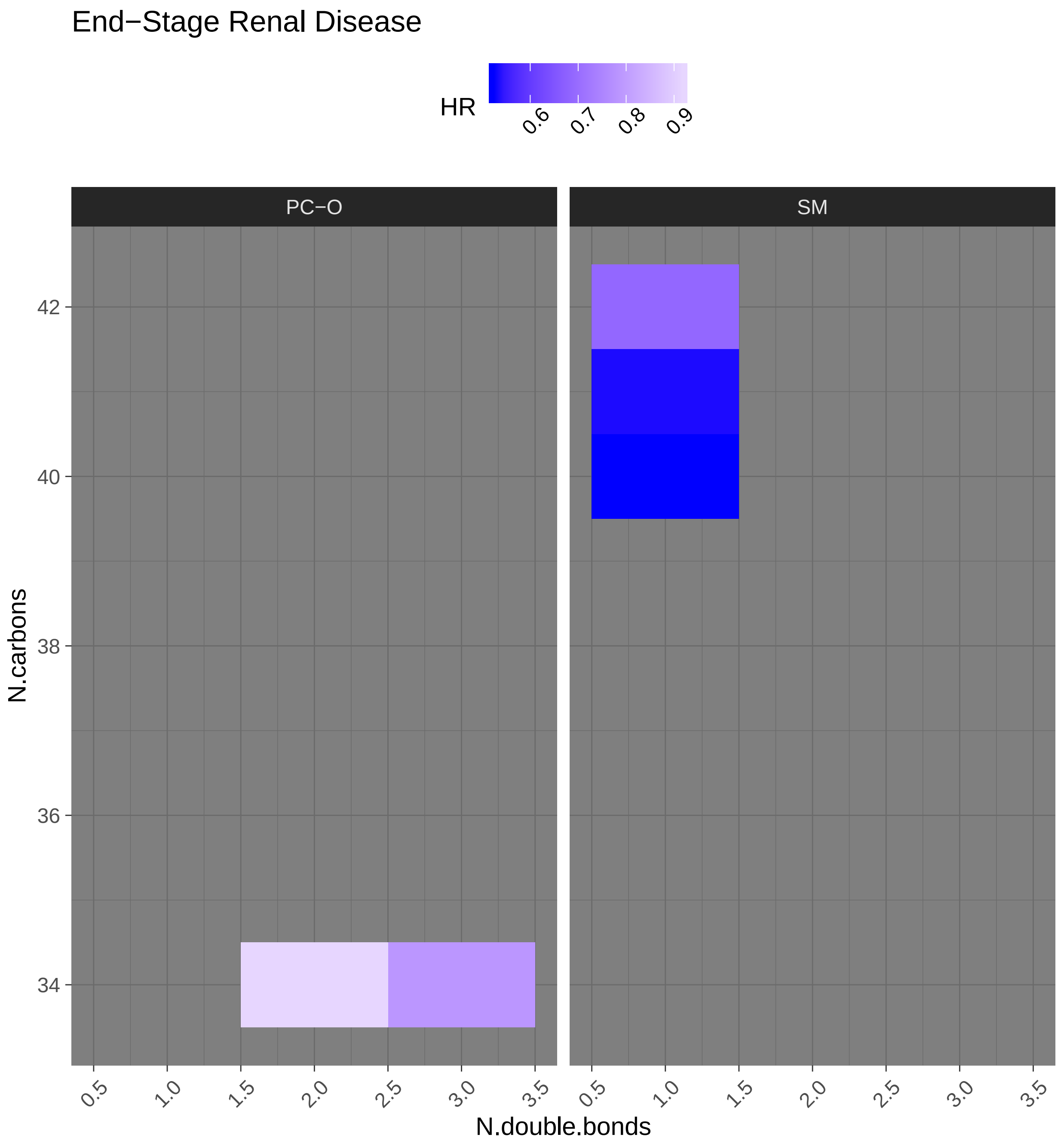


Figure 36: Heatmap of the lipid-specific hazard ratios (HRs) from the adjusted survival model for end-stage renal disease. Lipids are organized into panels (columns) by their class (from PC-O to SM). One colored rectangle corresponds to one lipid species, where the coordinates in the x-axis and y-axis, respectively, show the number of double bonds (N.double.bonds) and the number of carbon atoms (N.carbons) in the fatty acid chains of the lipid. The number of double bonds corresponds to the number of unsaturated bonds in the fatty acid chains, and the number of carbon atoms corresponds to the length of the fatty acid chains and, thus, the size of the lipid. The magnitude of the lipid-specifc hazard ratio is shown as the color of the rectangle (blue: inverse association; red: positive association). Associations with statistical significance are annotated with symbols #, x and *, respectively, corresponding to $p < 0.01$, $p < 0.05$ and $p < 0.1$.

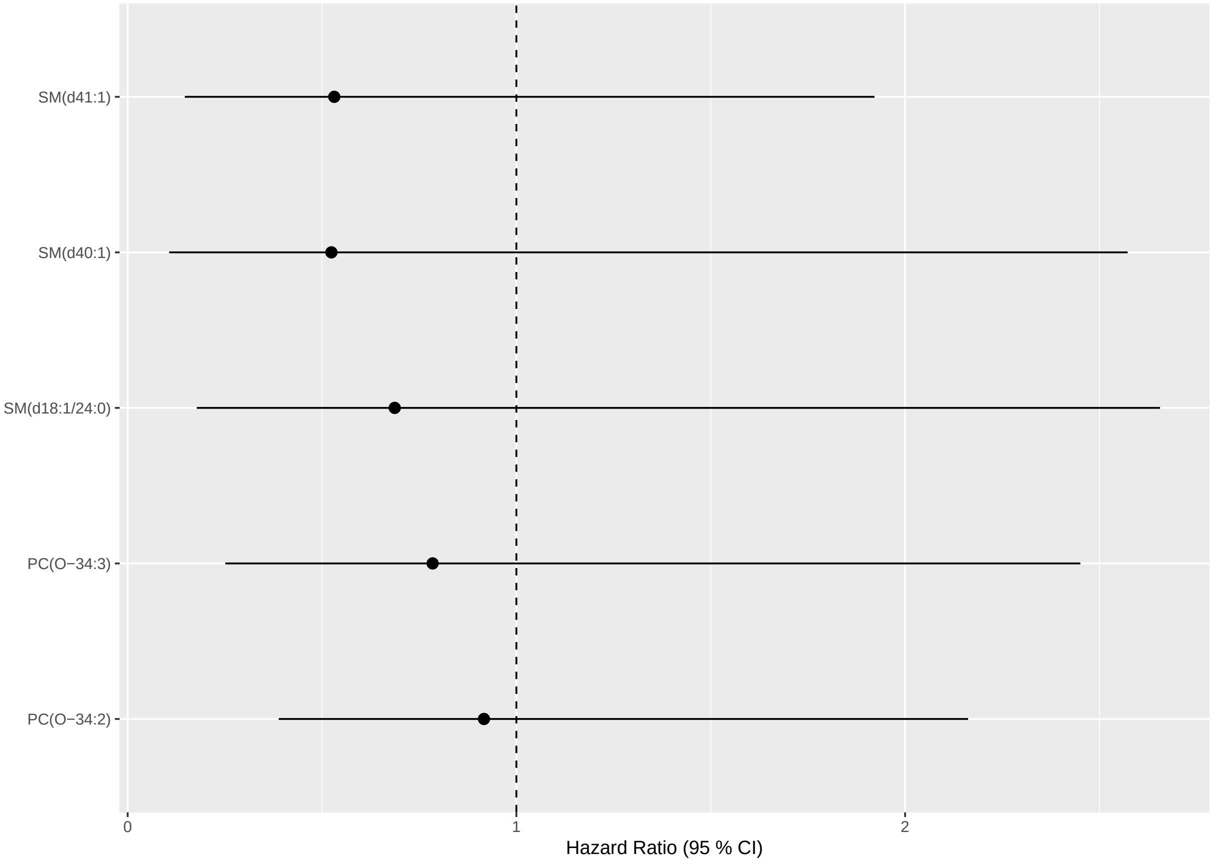


Figure 37: Forest plot of hazard ratios from the adjusted survival model for end-stage renal disease. The hazard ratio and its 95 % confidence intervals (x-axis) are shown for each lipid (rows).

4.4.2.3 Forest Plot

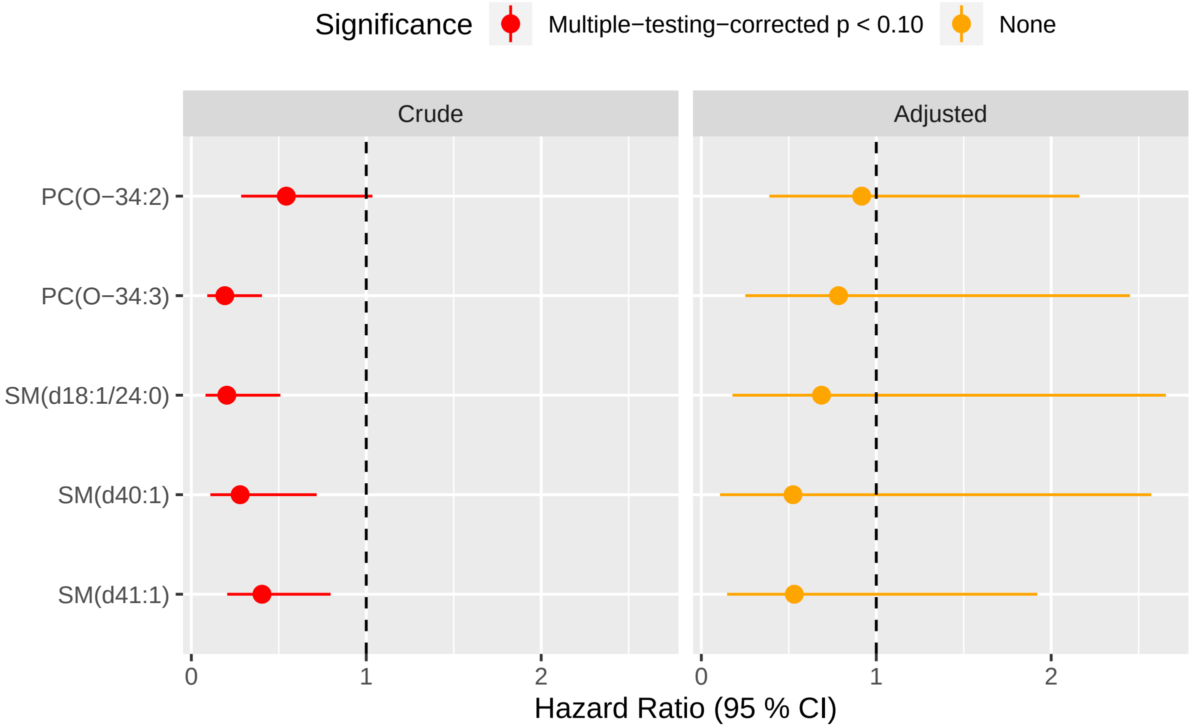


Figure 38: Combined forest plot of hazard ratios from the crude and adjusted survival models for end-stage renal disease. The hazard ratio and its 95 % confidence intervals (x-axis) are shown for each lipid (rows).

4.4.3 Combined Forest Plot from Crude and Adjusted Models

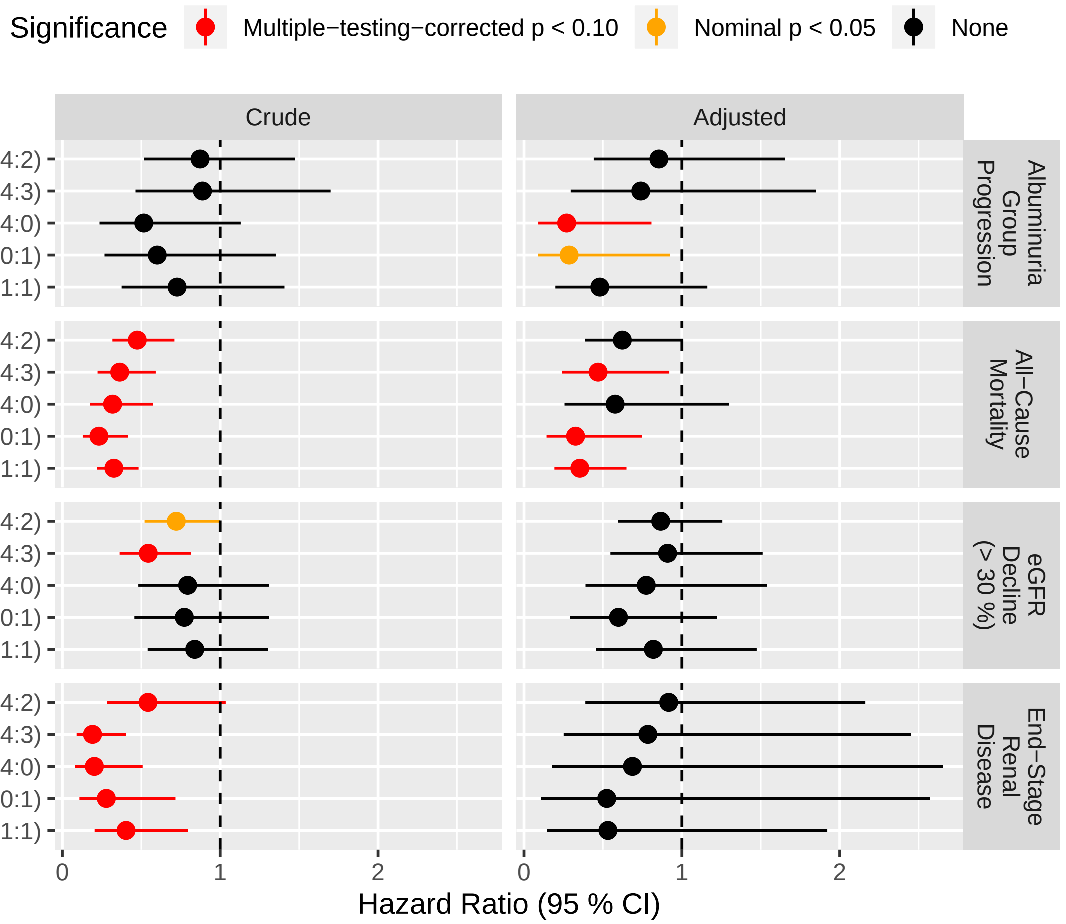


Figure 39: Compilation forest plot of hazard ratios from the crude and adjusted (left and right, respectively) survival models for the four endpoints (row-wise panels). The endpoints are albuminuria group progression, all-cause mortality, eGFR decline (> 30 %) and end-stage renal disease. The hazard ratio and its 95 % confidence intervals (x-axis) are shown for each lipid (rows).

4.5 Compilation Forest Plot from Steps 4A-D

5 Step 5: Detailed Assessment of the Top-Lipid in Relation to All-Cause Mortality

5.1 Step 5A: Analysis of Full Cohort

5.1.1 Survival Model with Details

```
## Call:
## survival::coxph(formula = survival::Surv(time = t_doed_profil,
##     event = censor_doed_profil.reversed.numeric) ~ SM.d41.1 +
##     Age + BMI + BP_Systolic + Cholesterol + eGFR + HbA1c + Medication_Statins +
##     Sex + Smoking + TG_total_log + UAER_log, data = data.survival)
##
##   n= 615, number of events= 54
##    (54 observations deleted due to missingness)
##
##                         coef exp(coef)  se(coef)      z Pr(>|z|)
## SM.d41.1           -1.039477  0.353639  0.310116 -3.352 0.000803 ***
## Age                 0.084875  1.088581  0.015360  5.526 3.28e-08 ***
## BMI                -0.075662  0.927129  0.040516 -1.867 0.061835 .
## BP_Systolic         0.001151  1.001152  0.008047  0.143 0.886259
## Cholesterol        -0.030785  0.969684  0.220076 -0.140 0.888753
## eGFR               -0.011654  0.988413  0.005703 -2.043 0.041009 *
## HbA1c               0.204795  1.227274  0.136686  1.498 0.134057
## Medication_Statins  0.229558  1.258044  0.356499  0.644 0.519624
## Sex                -0.062330  0.939573  0.322626 -0.193 0.846805
## Smoking             0.457539  1.580180  0.321395  1.424 0.154561
## TG_total_log        0.128373  1.136977  0.234372  0.548 0.583876
## UAER_log            0.116122  1.123133  0.069343  1.675 0.094013 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##                    exp(coef) exp(-coef) lower .95 upper .95
## SM.d41.1              0.3536     2.8277    0.1926    0.6494
## Age                   1.0886     0.9186    1.0563    1.1219
## BMI                   0.9271     1.0786    0.8564    1.0038
## BP_Systolic           1.0012     0.9988    0.9855    1.0171
## Cholesterol           0.9697     1.0313    0.6299    1.4927
## eGFR                  0.9884     1.0117    0.9774    0.9995
## HbA1c                 1.2273     0.8148    0.9388    1.6043
## Medication_Statins    1.2580     0.7949    0.6255    2.5302
## Sex                   0.9396     1.0643    0.4992    1.7683
## Smoking               1.5802     0.6328    0.8417    2.9667
## TG_total_log          1.1370     0.8795    0.7182    1.7999
## UAER_log              1.1231     0.8904    0.9804    1.2866
##
## Concordance= 0.824  (se = 0.04 )
## Rsquare= 0.123   (max possible= 0.669 )
## Likelihood ratio test= 80.61  on 12 df,   p=3.16e-12
## Wald test            = 65.62  on 12 df,   p=2.092e-09
## Score (logrank) test = 74.8  on 12 df,   p=4.002e-11
```

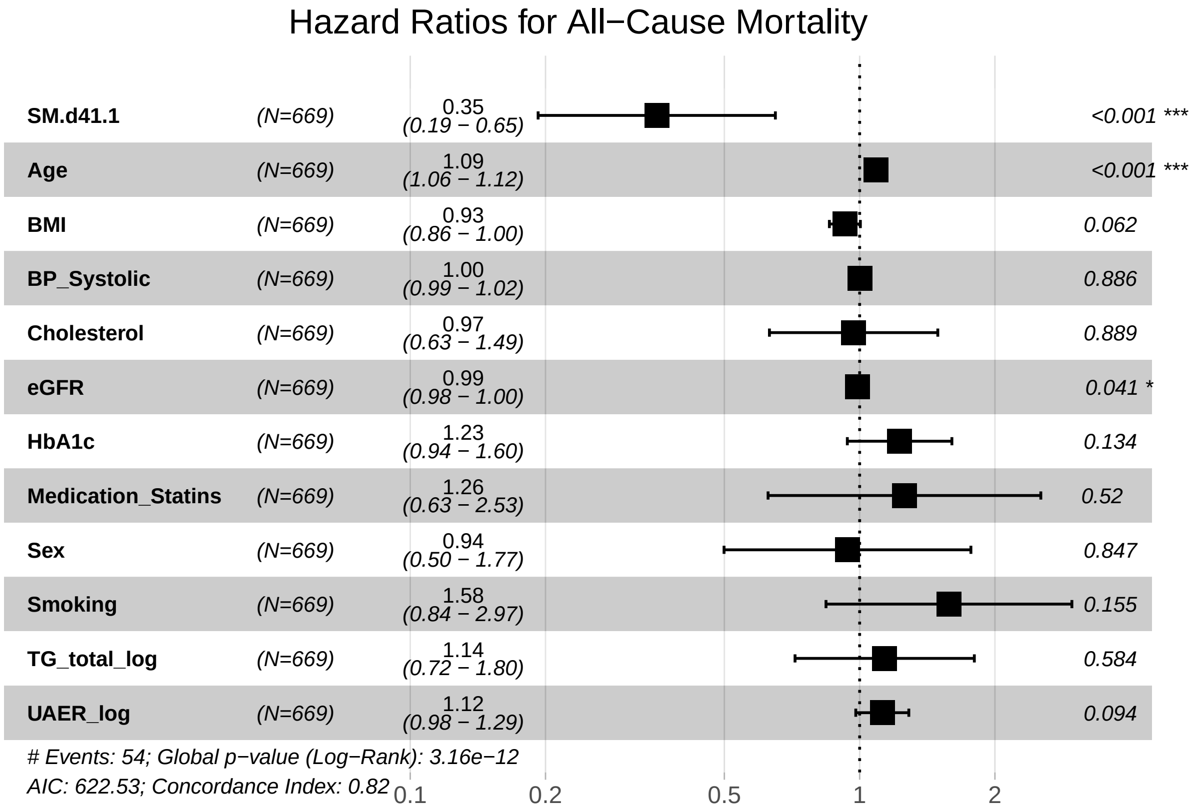
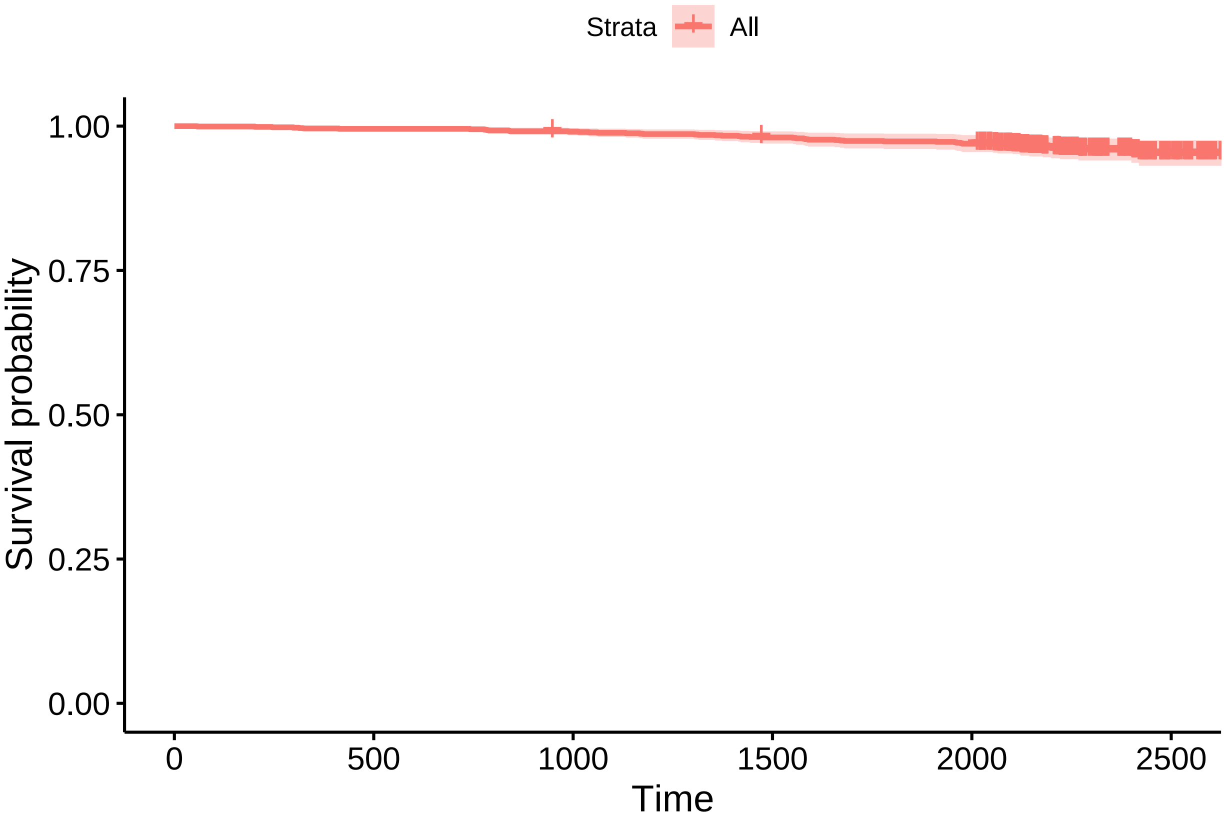


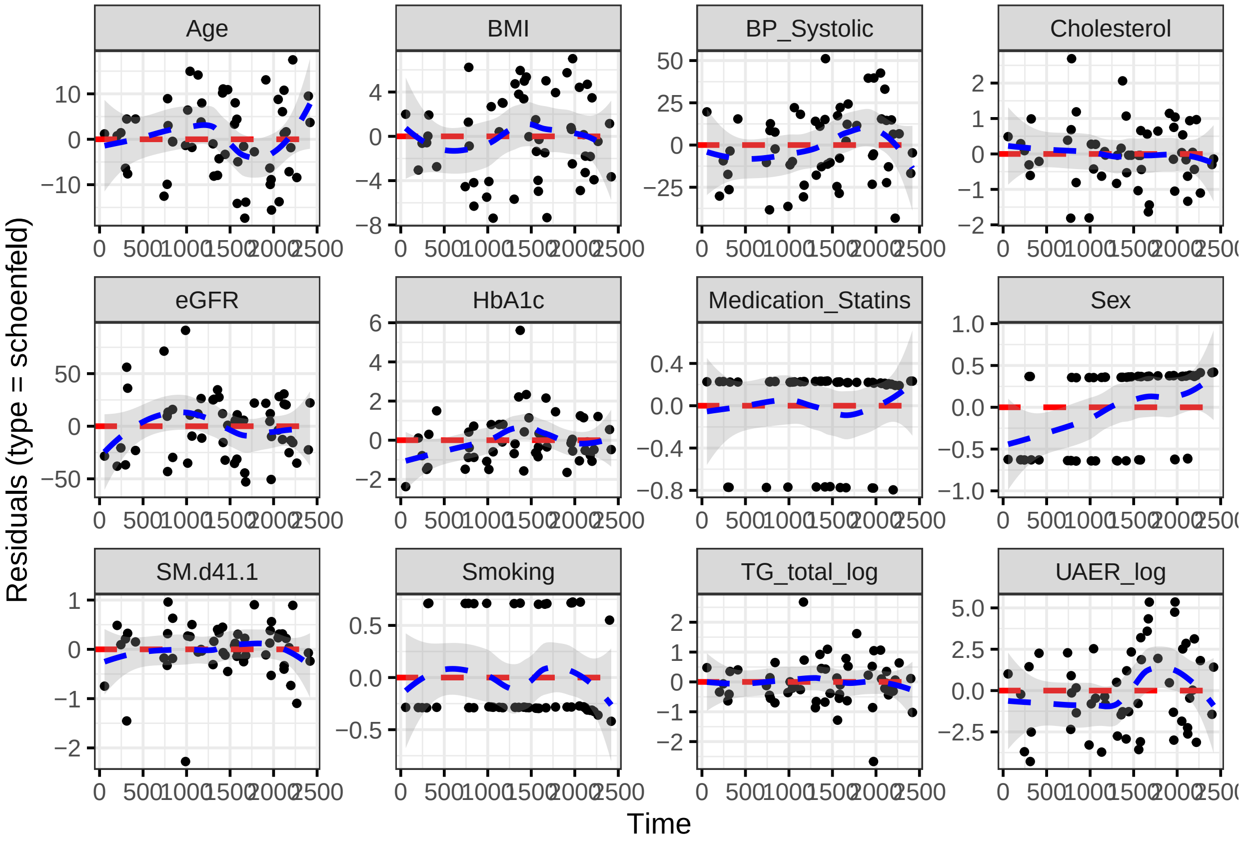
Figure 40: Forest plot of all the coefficients in the adjusted survival model for all-cause mortality. Shown in the figure are the name of the coefficient, number of observations (N), hazard ratio with 95 % confidence interval and the p-value of the association.

5.1.1.1 Forest Plot with Clinical Variables

5.1.1.2 Diagnostics of the Survival Model

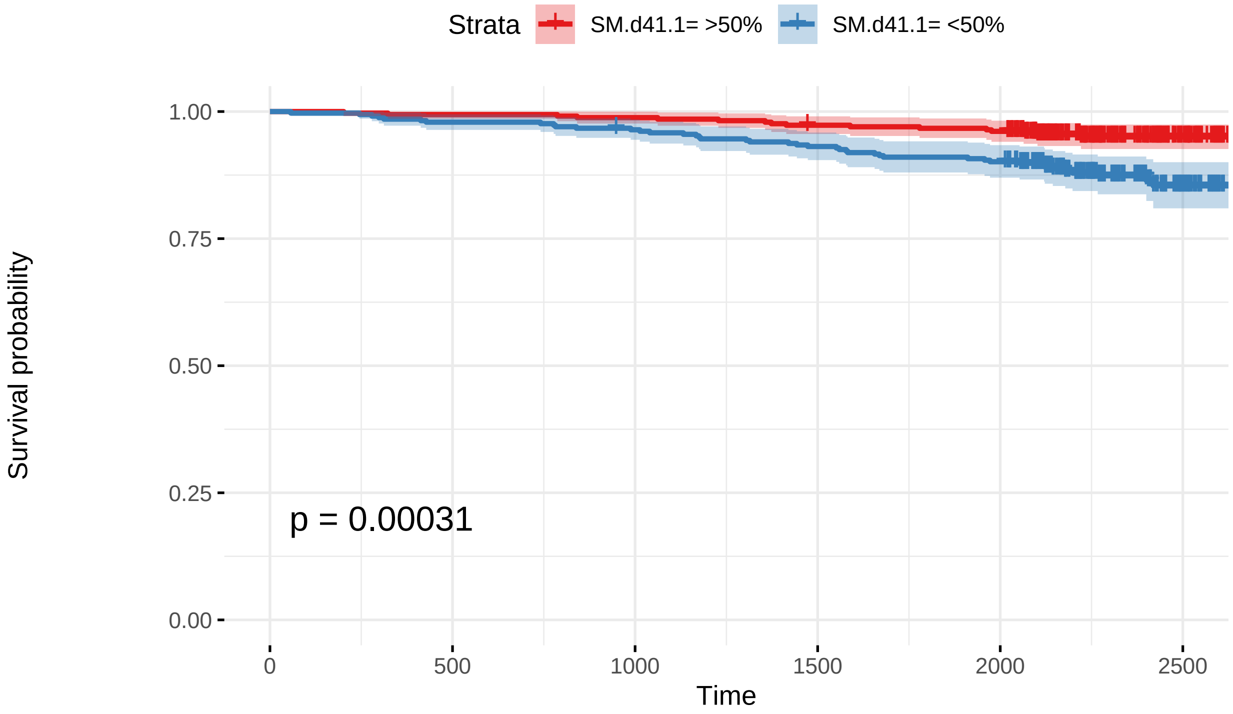


Strata
All
Survival probability
1.00
0.75
0.50
0.25
0.00
0
500
1000
1500
2000
2500
Time



Age
BMI
BP_Systolic
Cholesterol
eGFR
HbA1c
Medication_Statins
Sex
SM.d41.1
Smoking
TG_total_log
UAER_log
Residuals (type = schoenfeld)
Time
0
500
1000
1500
2000
2500

5.1.1.3 Kaplan-Maier Curve with Median Cutpoint



Number at risk

	0	500	1000	1500	2000	2500
SM.d41.1= >50%	334	332	330	324	320	64
SM.d41.1= <50%	335	328	322	311	301	45

Cumulative number of events

	0	500	1000	1500	2000	2500
SM.d41.1= >50%	0	2	4	9	13	16
SM.d41.1= <50%	0	7	12	23	33	42

Figure 41: Kaplan-Meier figure of all-cause mortality in participants with lipid SM(41:1) above or below its median level (red and blue curves, respectively). Time of follow-up and survival probablity, respectively, are shown on the x-axis and y-axis. Cumulative number of events and the number of remaining participants are shown for the two groups in the table below the figure.

5.1.2 Other Model Fits

```
## Call:
## survival::coxph(formula = survival::Surv(time = t_doed_profil,
##     event = censor_doed_profil.reversed.numeric) ~ SM.d41.1,
##     data = data.km)
##
##   n= 669, number of events= 58
##
##                  coef exp(coef) se(coef)     z Pr(>|z|)
## SM.d41.1 <50% 1.0152    2.7598   0.2939 3.454 0.000552 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##               exp(coef) exp(-coef) lower .95 upper .95
## SM.d41.1 <50%      2.76     0.3623     1.551      4.91
##
## Concordance= 0.614  (se = 0.033 )
## Rsquare= 0.02   (max possible= 0.669 )
## Likelihood ratio test= 13.41  on 1 df,   p=0.0002508
## Wald test            = 11.93  on 1 df,   p=0.0005523
## Score (logrank) test = 12.99  on 1 df,   p=0.0003135
```

```
##
## Call:
## glm(formula = censor_doed_profil.reversed.numeric ~ SM.d41.1 +
##     Age + BMI + BP_Systolic + Cholesterol + eGFR + HbA1c + Medication_Statins +
##     Sex + Smoking + TG_total_log + UAER_log, data = data.survival)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.33989  -0.13218  -0.06706   0.00555   0.95561
##
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)         2.1089761  0.6464134   3.263 0.001166 **
## SM.d41.1           -0.1003398  0.0294002  -3.413 0.000686 ***
## Age                 0.0047487  0.0010276   4.621 4.68e-06 ***
## BMI                -0.0055410  0.0029094  -1.904 0.057322 .
## BP_Systolic         0.0001645  0.0006808   0.242 0.809127
## Cholesterol        -0.0017448  0.0163895  -0.106 0.915254
## eGFR               -0.0008337  0.0004564  -1.827 0.068250 .
## HbA1c               0.0165920  0.0104610   1.586 0.113247
## Medication_Statins -0.0068740  0.0255750  -0.269 0.788192
## Sex                 0.0081634  0.0233883   0.349 0.727183
## Smoking             0.0365555  0.0276219   1.323 0.186195
## TG_total_log        0.0072646  0.0182897   0.397 0.691362
## UAER_log            0.0101679  0.0057618   1.765 0.078119 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.07223018)
##
##     Null deviance: 49.259  on 614  degrees of freedom
```

```
## Residual deviance: 43.483  on 602  degrees of freedom
##   (54 observations deleted due to missingness)
## AIC: 144
##
## Number of Fisher Scoring iterations: 2
```

```
##
## Call:
## lm(formula = SM.d41.1 ~ censor_doed_profil.reversed.numeric +
##     Age + BMI + BP_Systolic + Cholesterol + eGFR + HbA1c + Medication_Statins +
##     Sex + Smoking + TG_total_log + UAER_log, data = data.survival)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.36364 -0.19256  0.03596  0.22337  1.33335
##
## Coefficients:
##                                      Estimate Std. Error t value Pr(>|t|)
## (Intercept)                         21.3632619  0.2087609 102.334  < 2e-16
## censor_doed_profil.reversed.numeric -0.1891707  0.0554282  -3.413 0.000686
## Age                                 -0.0030716  0.0014304  -2.147 0.032158
## BMI                                 -0.0021123  0.0040059  -0.527 0.598183
## BP_Systolic                         -0.0002943  0.0009347  -0.315 0.752994
## Cholesterol                          0.3023688  0.0188298  16.058  < 2e-16
## eGFR                                -0.0006728  0.0006278  -1.072 0.284311
## HbA1c                                0.0522571  0.0142351   3.671 0.000263
## Medication_Statins                   0.0052398  0.0351176   0.149 0.881441
## Sex                                 -0.0754929  0.0319691  -2.361 0.018522
## Smoking                             -0.0448977  0.0379376  -1.183 0.237093
## TG_total_log                        -0.0260792  0.0250936  -1.039 0.299093
## UAER_log                            -0.0238898  0.0078718  -3.035 0.002510
##
## (Intercept)                         ***
## censor_doed_profil.reversed.numeric ***
## Age                                 *
## BMI
## BP_Systolic
## Cholesterol                         ***
## eGFR
## HbA1c                               ***
## Medication_Statins
## Sex                                 *
## Smoking
## TG_total_log
## UAER_log                            **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.369 on 602 degrees of freedom
##   (54 observations deleted due to missingness)
## Multiple R-squared:  0.3911, Adjusted R-squared:  0.379
## F-statistic: 32.23 on 12 and 602 DF,  p-value: < 2.2e-16
```

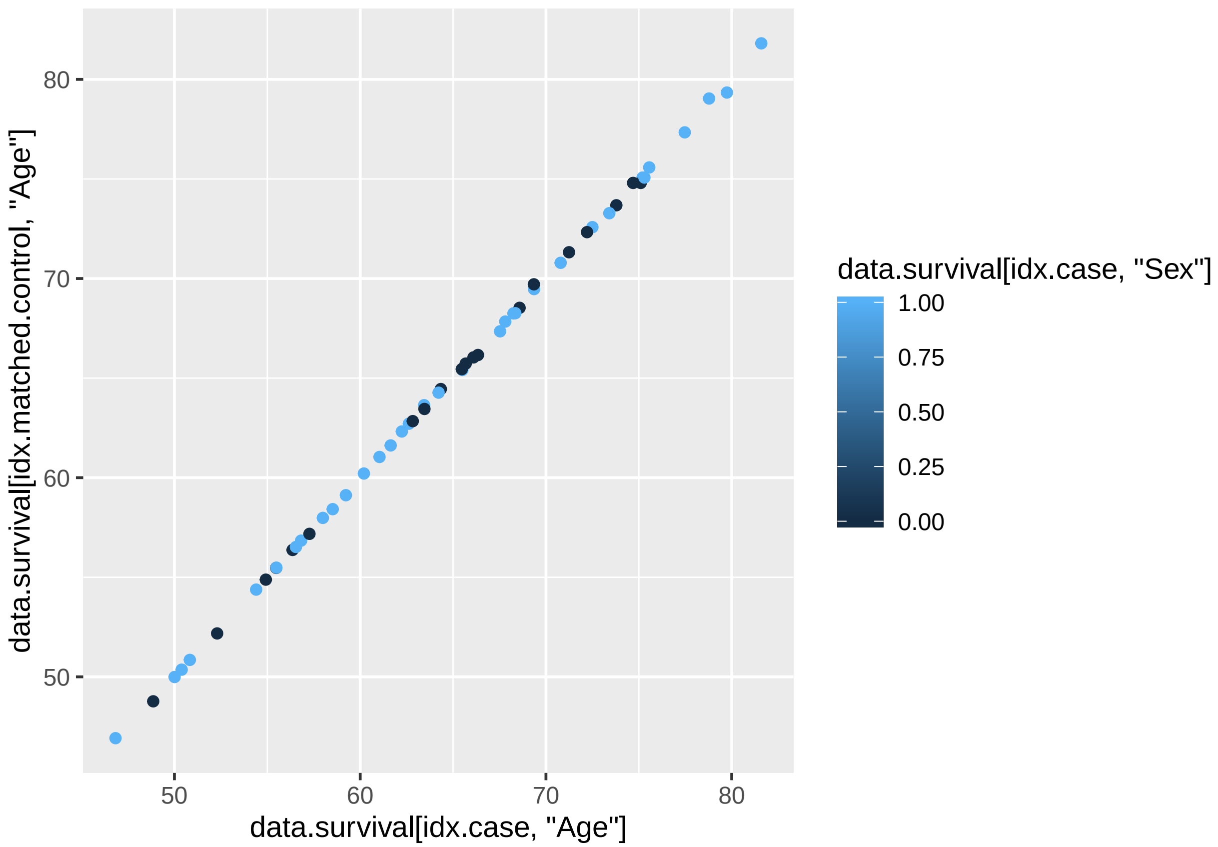


Figure 42: Quantile-quantile plot of the age of the sub-sampled cohort in persons with all-case mortality event (x-axis) and surviving persons without the event (y-axis). The two genders are shown in light and blue colors. Points falling on a diagonal line indicate a good age-matching in the two groups of the subcohort.

5.2 Step 5B: Analysis of an Age-and-Sex-Matched Subcohort

```
##
##  Paired t-test
##
## data:  data.survival[idx.case, "Age"] and data.survival[idx.matched.control, "Age"]
## t = 0.7071, df = 53, p-value = 0.4826
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.02278712  0.04760194
## sample estimates:
## mean of the differences
##              0.01240741
```

```
##
## Call:
## glm(formula = censor_doed_profil.reversed.numeric ~ SM.d41.1 +
##     Age + BMI + BP_Systolic + Cholesterol + eGFR + HbA1c + Medication_Statins +
##     Sex + Smoking + TG_total_log + UAER_log, data = data.survival.stratified)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
```

```
## -0.86519  -0.36291  -0.02769   0.34499   0.79471
##
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)         9.3731947  2.5000402   3.749 0.000305 ***
## SM.d41.1           -0.3877748  0.1146773  -3.381 0.001048 **
## Age                 0.0007879  0.0057495   0.137 0.891288
## BMI                -0.0083531  0.0147462  -0.566 0.572416
## BP_Systolic        -0.0012972  0.0027038  -0.480 0.632491
## Cholesterol         0.0425939  0.0716868   0.594 0.553813
## eGFR               -0.0041364  0.0018327  -2.257 0.026302 *
## HbA1c               0.0168307  0.0432329   0.389 0.697923
## Medication_Statins  0.1714852  0.1157483   1.482 0.141773
## Sex                -0.0771974  0.1072989  -0.719 0.473623
## Smoking             0.1191930  0.1197801   0.995 0.322216
## TG_total_log        0.0135161  0.0726105   0.186 0.852727
## UAER_log            0.0181071  0.0234331   0.773 0.441610
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.2133333)
##
##     Null deviance: 27.000  on 107  degrees of freedom
## Residual deviance: 20.267  on  95  degrees of freedom
## AIC: 153.79
##
## Number of Fisher Scoring iterations: 2
```

```
##
## Call:
## lm(formula = SM.d41.1 ~ censor_doed_profil.reversed.numeric +
##     Age + BMI + BP_Systolic + Cholesterol + eGFR + HbA1c + Medication_Statins +
##     Sex + Smoking + TG_total_log + UAER_log, data = data.survival.stratified)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.08663 -0.23451  0.00349  0.24801  0.80040
##
## Coefficients:
##                                      Estimate Std. Error t value Pr(>|t|)
## (Intercept)                         21.2477338  0.6114086  34.752  < 2e-16
## censor_doed_profil.reversed.numeric -0.2770409  0.0819297  -3.381  0.00105
## Age                                 -0.0050528  0.0048325  -1.046  0.29841
## BMI                                 -0.0165859  0.0123686  -1.341  0.18313
## BP_Systolic                          0.0002579  0.0022880   0.113  0.91051
## Cholesterol                          0.3859975  0.0460084   8.390 4.51e-13
## eGFR                                -0.0027896  0.0015641  -1.784  0.07770
## HbA1c                                0.0863963  0.0354810   2.435  0.01676
## Medication_Statins                   0.1604999  0.0975797   1.645  0.10331
## Sex                                 -0.1201282  0.0901014  -1.333  0.18564
## Smoking                             -0.1916226  0.0998527  -1.919  0.05798
## TG_total_log                        -0.0340404  0.0612853  -0.555  0.57990
## UAER_log                            -0.0143670  0.0198141  -0.725  0.47018
##
```

```
## (Intercept)                          ***
## censor_doed_profil.reversed.numeric **
## Age
## BMI
## BP_Systolic
## Cholesterol                          ***
## eGFR                                 .
## HbA1c                                *
## Medication_Statins
## Sex
## Smoking                              .
## TG_total_log
## UAER_log
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3904 on 95 degrees of freedom
## Multiple R-squared:  0.5687, Adjusted R-squared:  0.5142
## F-statistic: 10.44 on 12 and 95 DF,  p-value: 7.906e-13
```

5.2.1 Survival Model with Details

```
## Call:
## survival::coxph(formula = survival::Surv(time = t_doed_profil,
##     event = censor_doed_profil.reversed.numeric) ~ SM.d41.1 +
##     Age + BMI + BP_Systolic + Cholesterol + eGFR + HbA1c + Medication_Statins +
##     Sex + Smoking + TG_total_log + UAER_log, data = data.survival.stratified)
##
##   n= 108, number of events= 54
##
##                         coef exp(coef)  se(coef)      z Pr(>|z|)
## SM.d41.1           -1.245927  0.287674  0.373723 -3.334 0.000857 ***
## Age                 0.012702  1.012783  0.018732  0.678 0.497708
## BMI                 0.002475  1.002478  0.046936  0.053 0.957949
## BP_Systolic        -0.012498  0.987580  0.008782 -1.423 0.154694
## Cholesterol         0.192726  1.212551  0.255306  0.755 0.450319
## eGFR               -0.009692  0.990355  0.005628 -1.722 0.085052 .
## HbA1c              -0.038030  0.962684  0.147448 -0.258 0.796469
## Medication_Statins  0.844130  2.325953  0.413480  2.042 0.041199 *
## Sex                -0.655899  0.518975  0.361692 -1.813 0.069768 .
## Smoking             0.480851  1.617450  0.329439  1.460 0.144399
## TG_total_log        0.077683  1.080780  0.216428  0.359 0.719646
## UAER_log            0.055642  1.057219  0.070568  0.788 0.430408
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##                    exp(coef) exp(-coef) lower .95 upper .95
## SM.d41.1              0.2877     3.4762    0.1383    0.5984
## Age                   1.0128     0.9874    0.9763    1.0507
## BMI                   1.0025     0.9975    0.9144    1.0991
## BP_Systolic           0.9876     1.0126    0.9707    1.0047
## Cholesterol           1.2126     0.8247    0.7352    1.9999
## eGFR                  0.9904     1.0097    0.9795    1.0013
## HbA1c                 0.9627     1.0388    0.7211    1.2853
## Medication_Statins    2.3260     0.4299    1.0343    5.2307
## Sex                   0.5190     1.9269    0.2554    1.0544
## Smoking               1.6174     0.6183    0.8480    3.0850
## TG_total_log          1.0808     0.9253    0.7072    1.6518
## UAER_log              1.0572     0.9459    0.9207    1.2140
##
## Concordance= 0.697  (se = 0.041 )
## Rsquare= 0.232   (max possible= 0.986 )
## Likelihood ratio test= 28.45  on 12 df,   p=0.004748
## Wald test            = 27.6  on 12 df,   p=0.006318
## Score (logrank) test = 29.31  on 12 df,   p=0.00354
```

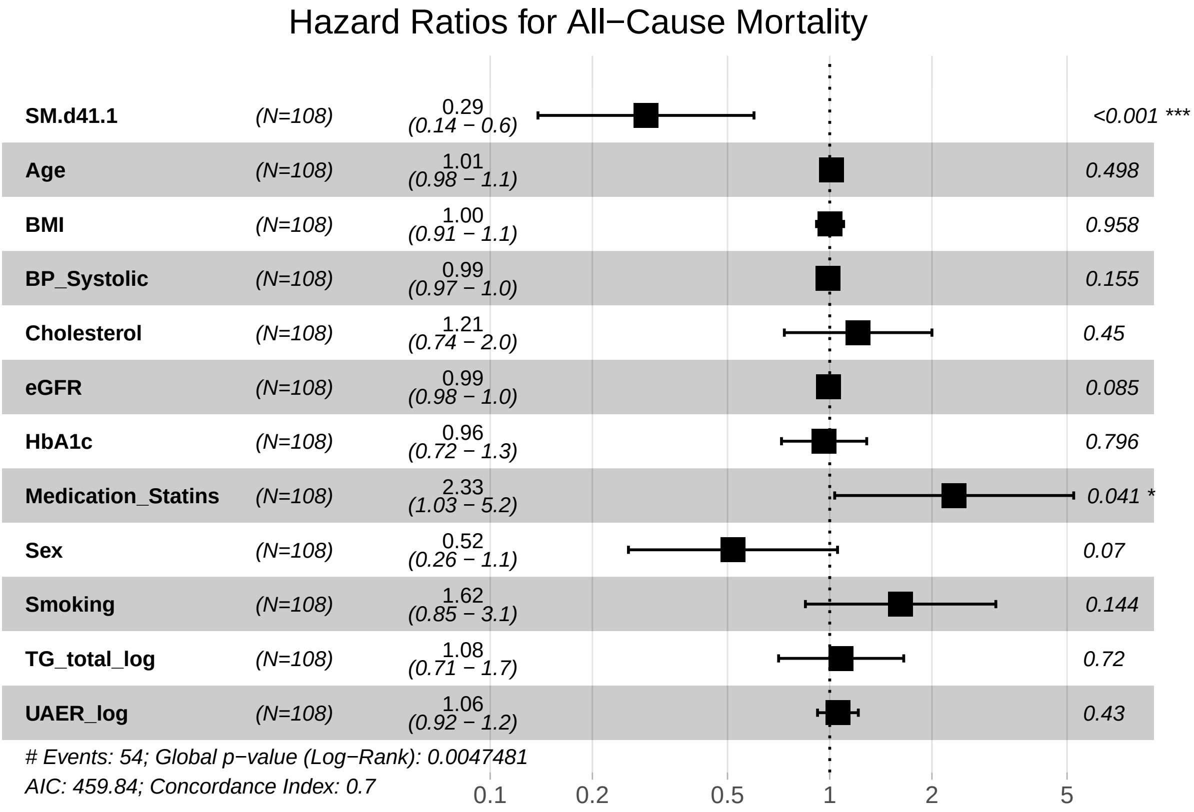
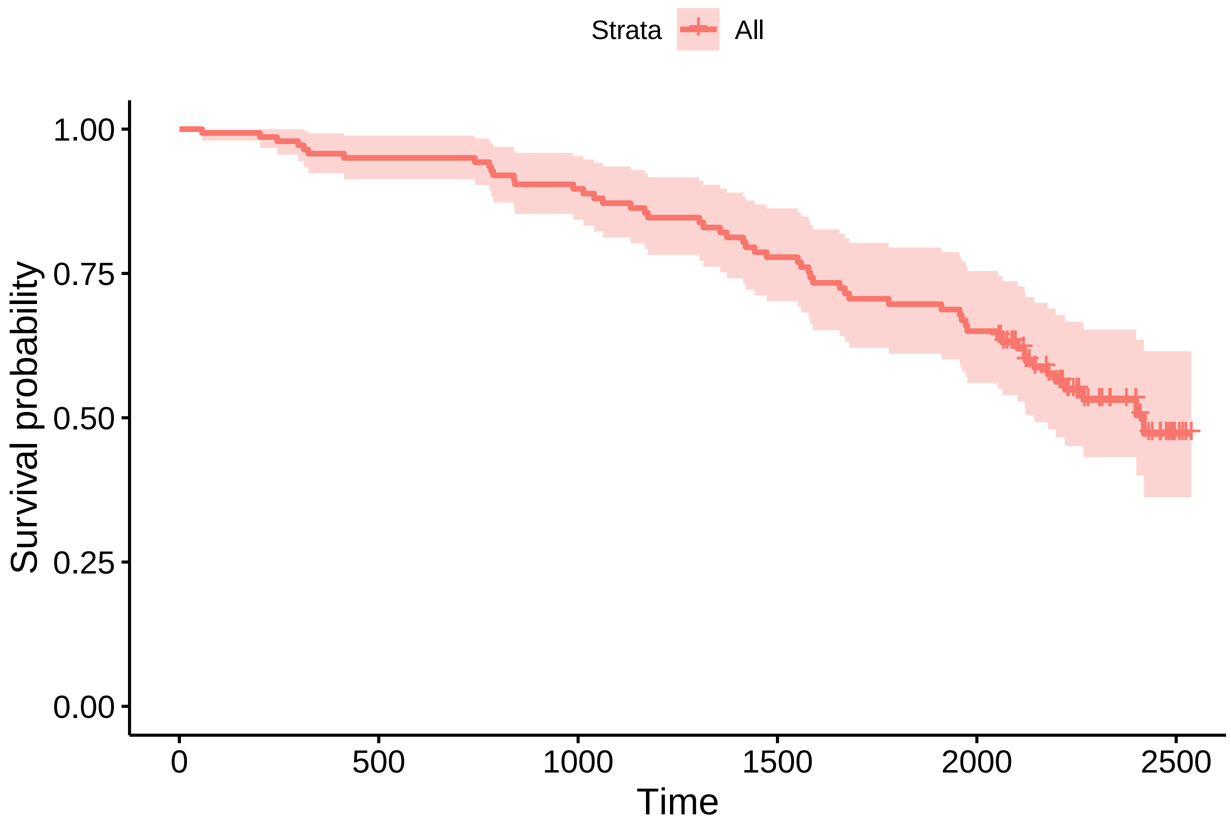
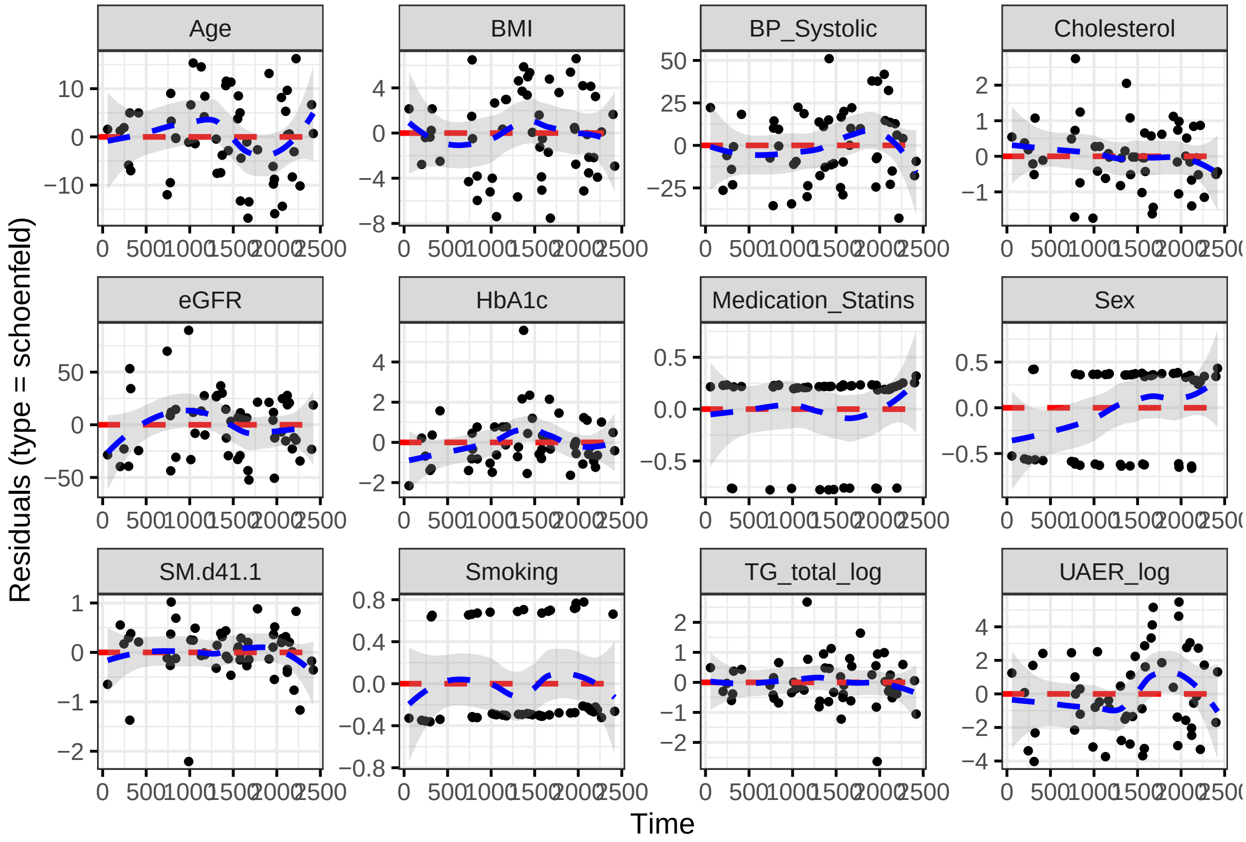


Figure 43: Forest plot of all the coefficients in the adjusted survival model for all-cause mortality. Shown in the figure are the name of the coefficient, number of observations (N), hazard ratio with 95 % confidence interval and the p-value of the association.

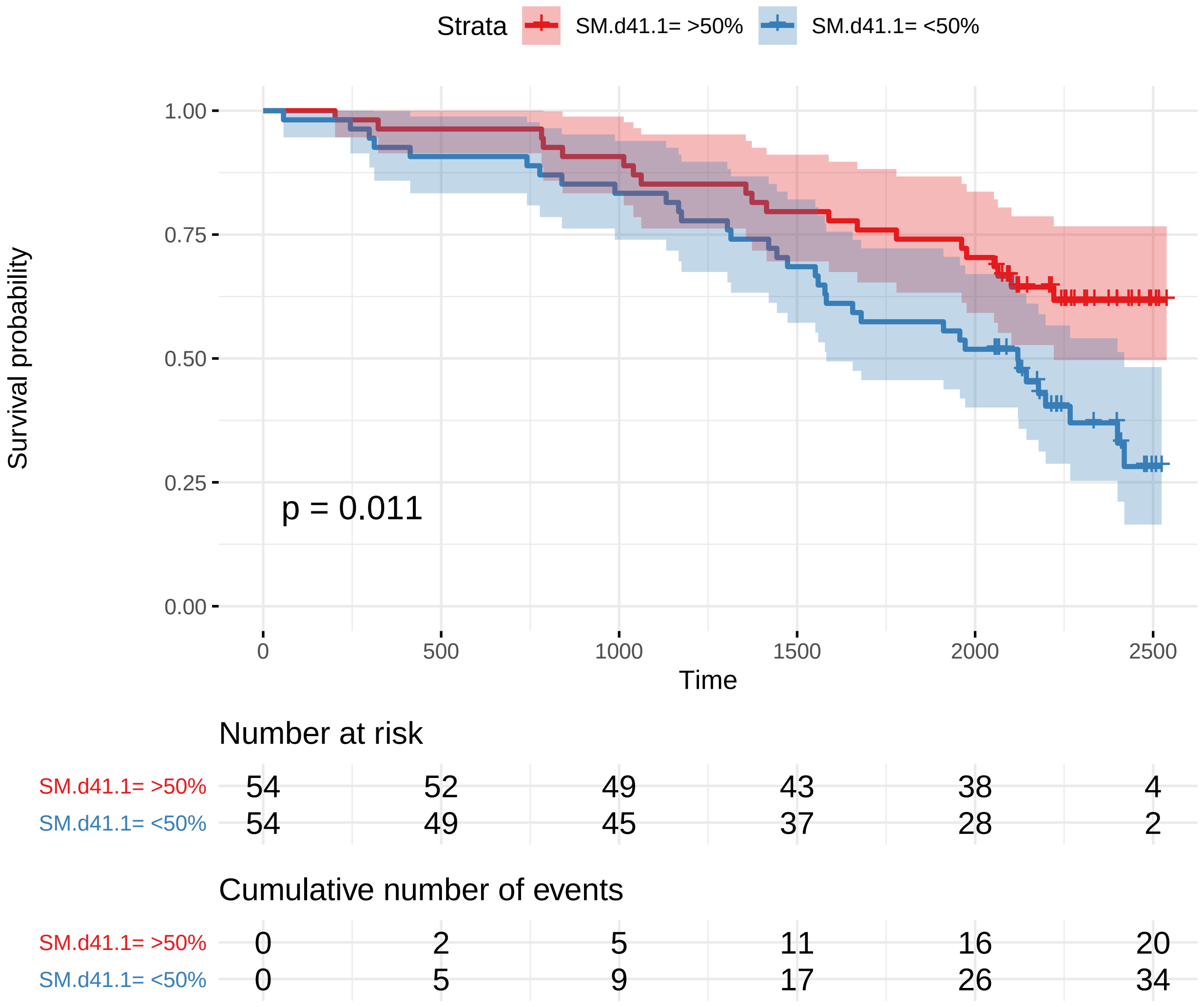
5.2.1.1 Forest Plot with Clinical Variables

5.2.1.2 Diagnostics of the Survival Model


Strata
All
Survival probability
1.00
0.75
0.50
0.25
0.00
0
500
1000
1500
2000
2500
Time


Residuals (type = schoenfeld)
Age
BMI
BP_Systolic
Cholesterol
eGFR
HbA1c
Medication_Statins
Sex
SM.d41.1
Smoking
TG_total_log
UAER_log
Time

5.2.1.3 Kaplan-Maier Curve with Median Cutpoint



Number at risk

	0	500	1000	1500	2000	2500
SM.d41.1= >50%	54	52	49	43	38	4
SM.d41.1= <50%	54	49	45	37	28	2

Cumulative number of events

	0	500	1000	1500	2000	2500
SM.d41.1= >50%	0	2	5	11	16	20
SM.d41.1= <50%	0	5	9	17	26	34

Figure 44: Kaplan-Meier figure of all-cause mortality in participants with lipid SM(41:1) above or below its median level (red and blue curves, respectively). Time of follow-up and survival probablity, respectively, are shown on the x-axis and y-axis. Cumulative number of events and the number of remaining participants are shown for the two groups in the table below the figure.

5.2.2 Other Model Fits

```
## Call:
## survival::coxph(formula = survival::Surv(time = t_doed_profil,
##     event = censor_doed_profil.reversed.numeric) ~ SM.d41.1,
##     data = data.km)
##
##   n= 108, number of events= 54
##
##                  coef exp(coef) se(coef)     z Pr(>|z|)
## SM.d41.1 <50% 0.7078    2.0296   0.2824 2.506   0.0122 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##               exp(coef) exp(-coef) lower .95 upper .95
## SM.d41.1 <50%      2.03     0.4927     1.167      3.53
##
## Concordance= 0.577  (se = 0.036 )
## Rsquare= 0.059   (max possible= 0.986 )
## Likelihood ratio test= 6.55  on 1 df,   p=0.01051
## Wald test            = 6.28  on 1 df,   p=0.01219
## Score (logrank) test = 6.55  on 1 df,   p=0.01051
```

```
##
## Call:
## glm(formula = censor_doed_profil.reversed.numeric ~ SM.d41.1 +
##     Age + BMI + BP_Systolic + Cholesterol + eGFR + HbA1c + Medication_Statins +
##     Sex + Smoking + TG_total_log + UAER_log, data = data.survival.stratified)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.86519  -0.36291  -0.02769   0.34499   0.79471
##
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)         9.3731947  2.5000402   3.749 0.000305 ***
## SM.d41.1           -0.3877748  0.1146773  -3.381 0.001048 **
## Age                 0.0007879  0.0057495   0.137 0.891288
## BMI                -0.0083531  0.0147462  -0.566 0.572416
## BP_Systolic        -0.0012972  0.0027038  -0.480 0.632491
## Cholesterol         0.0425939  0.0716868   0.594 0.553813
## eGFR               -0.0041364  0.0018327  -2.257 0.026302 *
## HbA1c               0.0168307  0.0432329   0.389 0.697923
## Medication_Statins  0.1714852  0.1157483   1.482 0.141773
## Sex                -0.0771974  0.1072989  -0.719 0.473623
## Smoking             0.1191930  0.1197801   0.995 0.322216
## TG_total_log        0.0135161  0.0726105   0.186 0.852727
## UAER_log            0.0181071  0.0234331   0.773 0.441610
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.2133333)
##
##     Null deviance: 27.000  on 107  degrees of freedom
```

```
## Residual deviance: 20.267  on  95  degrees of freedom
## AIC: 153.79
##
## Number of Fisher Scoring iterations: 2
```

```
##
## Call:
## lm(formula = SM.d41.1 ~ censor_doed_profil.reversed.numeric +
##     Age + BMI + BP_Systolic + Cholesterol + eGFR + HbA1c + Medication_Statins +
##     Sex + Smoking + TG_total_log + UAER_log, data = data.survival.stratified)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.08663 -0.23451  0.00349  0.24801  0.80040
##
## Coefficients:
##                                      Estimate Std. Error t value Pr(>|t|)
## (Intercept)                         21.2477338  0.6114086  34.752  < 2e-16
## censor_doed_profil.reversed.numeric -0.2770409  0.0819297  -3.381  0.00105
## Age                                 -0.0050528  0.0048325  -1.046  0.29841
## BMI                                 -0.0165859  0.0123686  -1.341  0.18313
## BP_Systolic                          0.0002579  0.0022880   0.113  0.91051
## Cholesterol                          0.3859975  0.0460084   8.390 4.51e-13
## eGFR                                -0.0027896  0.0015641  -1.784  0.07770
## HbA1c                                0.0863963  0.0354810   2.435  0.01676
## Medication_Statins                   0.1604999  0.0975797   1.645  0.10331
## Sex                                 -0.1201282  0.0901014  -1.333  0.18564
## Smoking                             -0.1916226  0.0998527  -1.919  0.05798
## TG_total_log                        -0.0340404  0.0612853  -0.555  0.57990
## UAER_log                            -0.0143670  0.0198141  -0.725  0.47018
##
## (Intercept)                         ***
## censor_doed_profil.reversed.numeric **
## Age
## BMI
## BP_Systolic
## Cholesterol                         ***
## eGFR                                .
## HbA1c                               *
## Medication_Statins
## Sex
## Smoking                             .
## TG_total_log
## UAER_log
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3904 on 95 degrees of freedom
## Multiple R-squared:  0.5687, Adjusted R-squared:  0.5142
## F-statistic: 10.44 on 12 and 95 DF,  p-value: 7.906e-13
```

6 Correlation Matrix

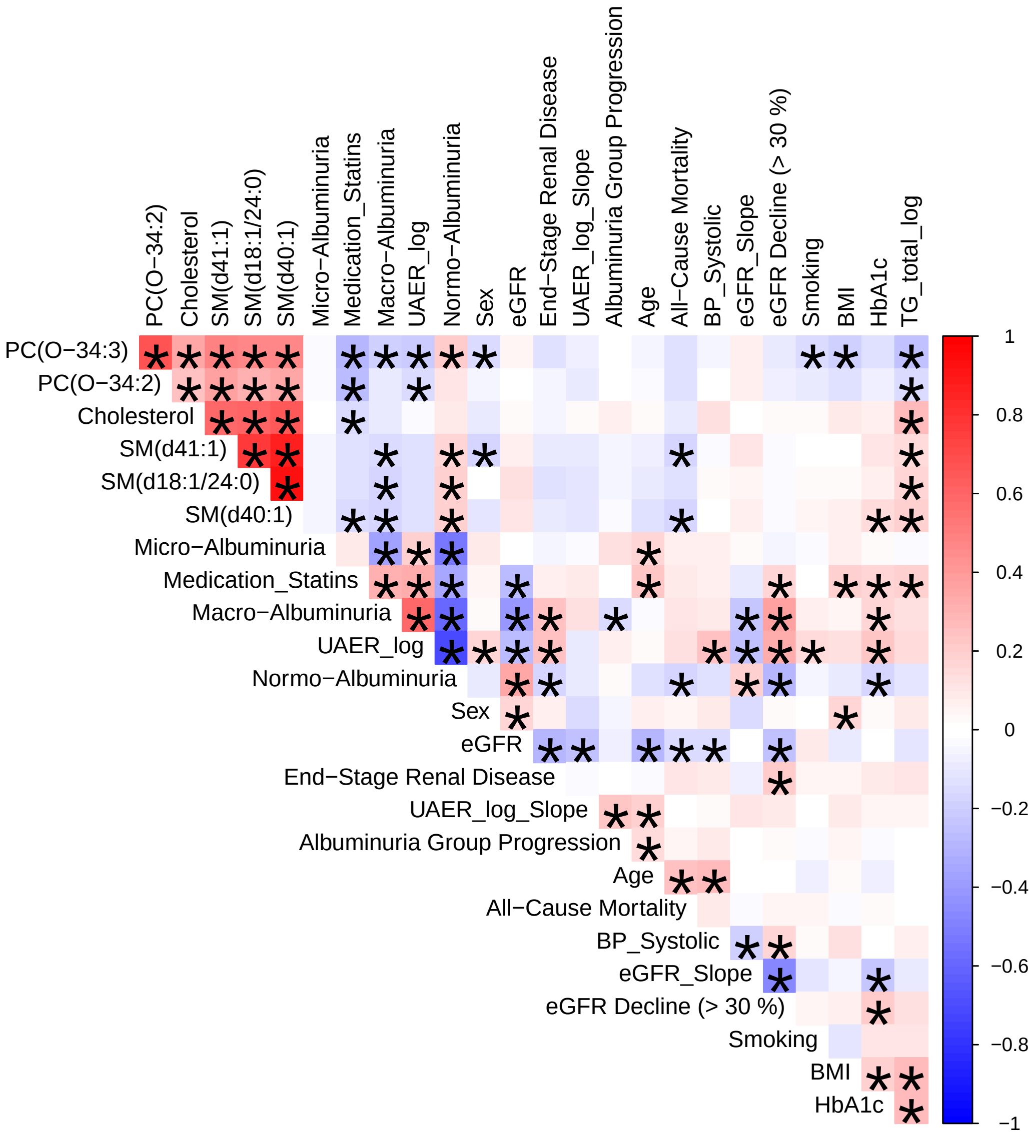


Figure 45: Correlation matrix of relevant variables. Variables are shown on the rows and columns. Spearman correlation of two variables is shown as the color of the square at the intersection of the row and column that corresponds to the two variables. Blue, red and white, respectively, indicate inverse, positive and no correlation. Correlations with statistical significance at $p < 0.05$ after correction for multiple testing are labeled with asterisk.

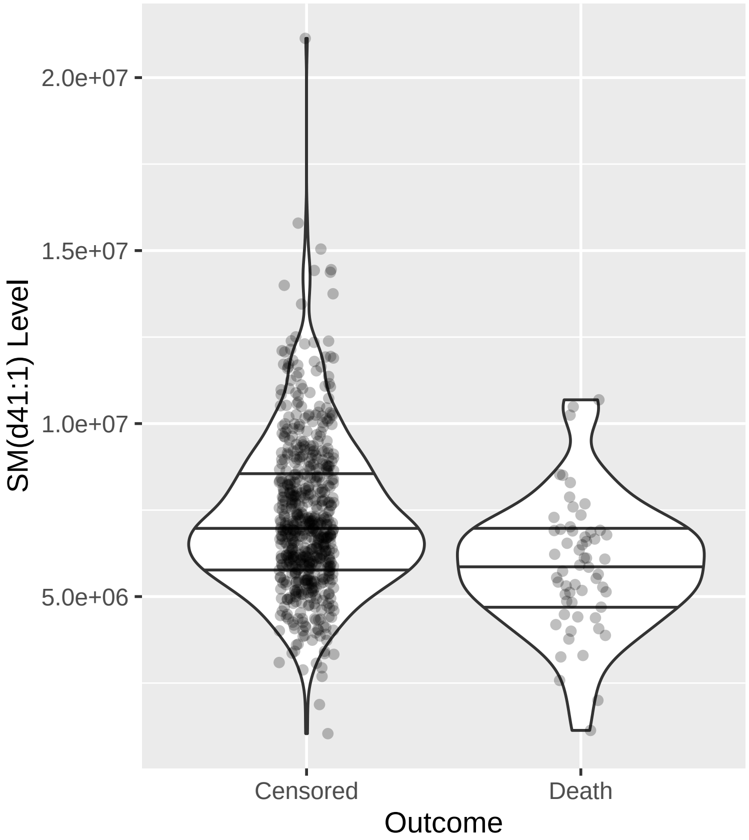


Figure 46: Violin plot of observations of the level of the lipid SM(d41:1). Subpopulations of the study are shown on the x-axis and the level of the lipid is shown on the y-axis. The density of the observations is shown in the shape of the violin and the quantiles of the distribution are shown as horizontal lines.

7 Boxplots

7.1 Entire Cohort

```
## [1] ""
```

```
## [1] ""
```

```
## [1] ""
```

```
## [1] ""
```

```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```

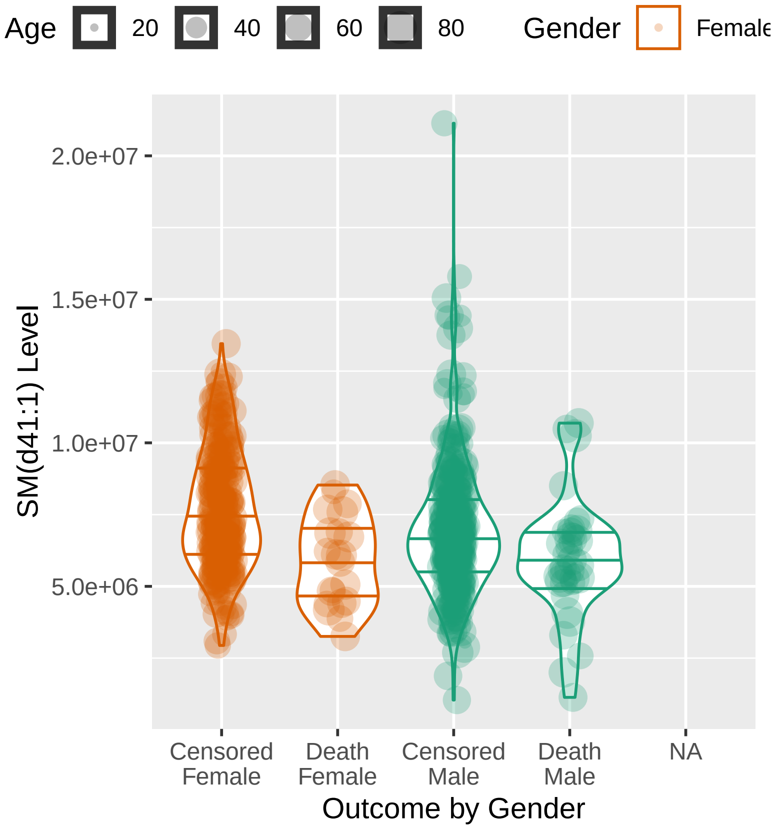


Figure 47: Violin plot of observations of the level of the lipid SM(d41:1). Subpopulations of the study are shown on the x-axis and the level of the lipid is shown on the y-axis. The density of the observations is shown in the shape of the violin and the quantiles of the distribution are shown as horizontal lines.

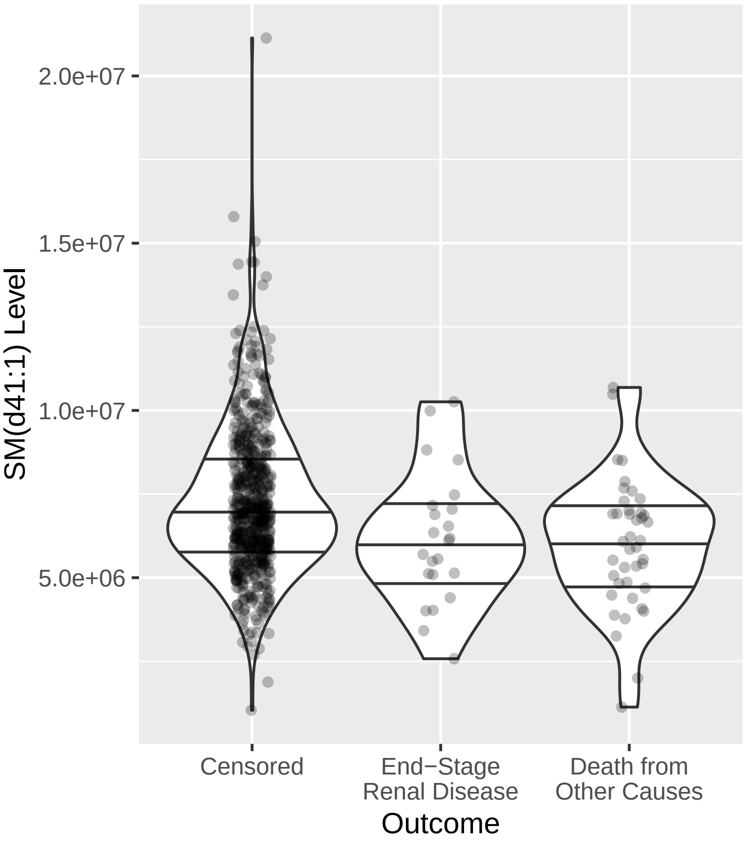


Figure 48: Violin plot of observations of the level of the lipid SM(d41:1). Subpopulations of the study are shown on the x-axis and the level of the lipid is shown on the y-axis. The density of the observations is shown in the shape of the violin and the quantiles of the distribution are shown as horizontal lines.

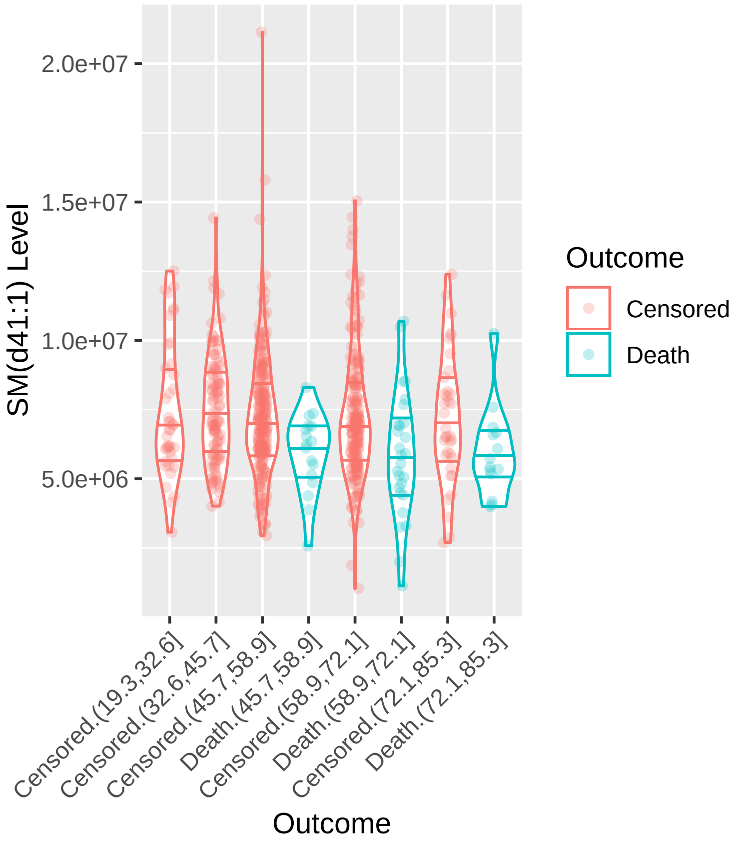


Figure 49: Violin plot of observations of the level of the lipid SM(d41:1). Subpopulations of the study are shown on the x-axis and the level of the lipid is shown on the y-axis. The density of the observations is shown in the shape of the violin and the quantiles of the distribution are shown as horizontal lines.

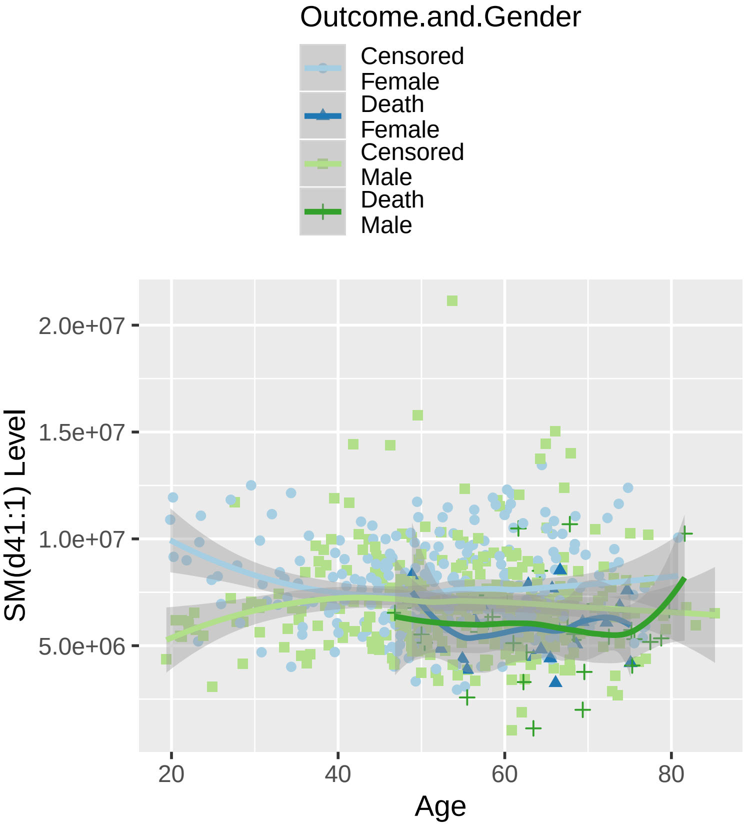


Figure 50: Observations of the level of the lipid SM(d41:1) against age. Subpopulations of the study are in different color. Possible trend in the observations is shown with a subgroup-specific nonlinear regression with the LOESS model.

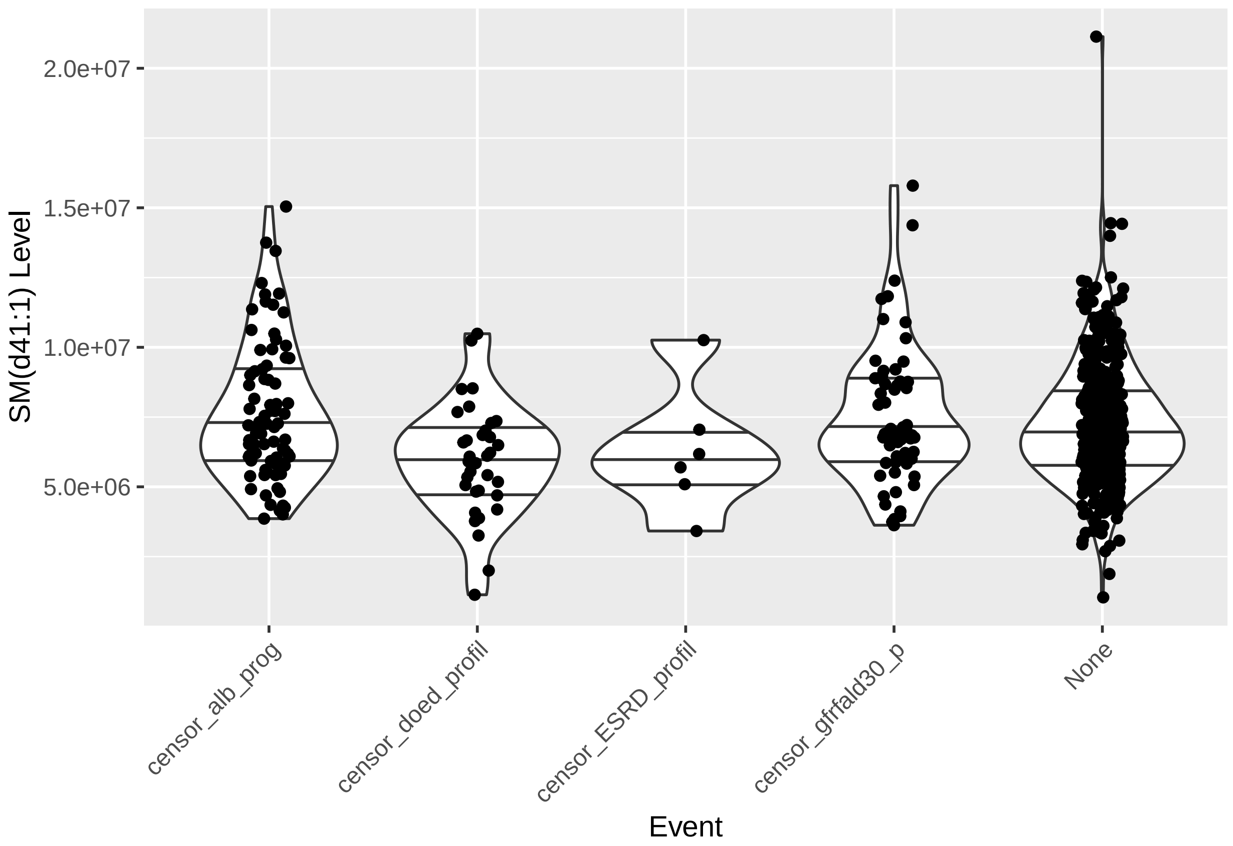


Figure 51: Violin plot of observations of the level of the lipid SM(d41:1). Subpopulations of the study are shown on the x-axis and the level of the lipid is shown on the y-axis. The density of the observations is shown in the shape of the violin and the quantiles of the distribution are shown as horizontal lines.

7.2 Age-and-Sex-Matched Subcohort

```
## [1] ""
```

```
## [1] ""
```

```
## [1] ""
```

```
## [1] ""
```

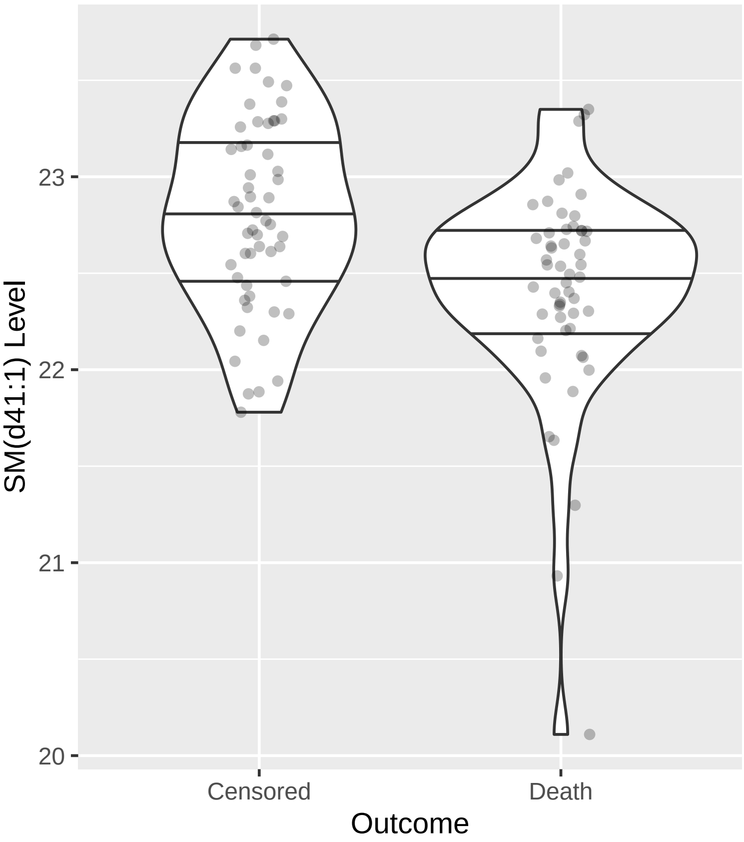


Figure 52: Violin plot of observations of the level of the lipid SM(d41:1). Subpopulations of the study are shown on the x-axis and the level of the lipid is shown on the y-axis. The density of the observations is shown in the shape of the violin and the quantiles of the distribution are shown as horizontal lines.

Figure 53: Violin plot of observations of the level of the lipid SM(d41:1). Subpopulations of the study are shown on the x-axis and the level of the lipid is shown on the y-axis. The density of the observations is shown in the shape of the violin and the quantiles of the distribution are shown as horizontal lines.

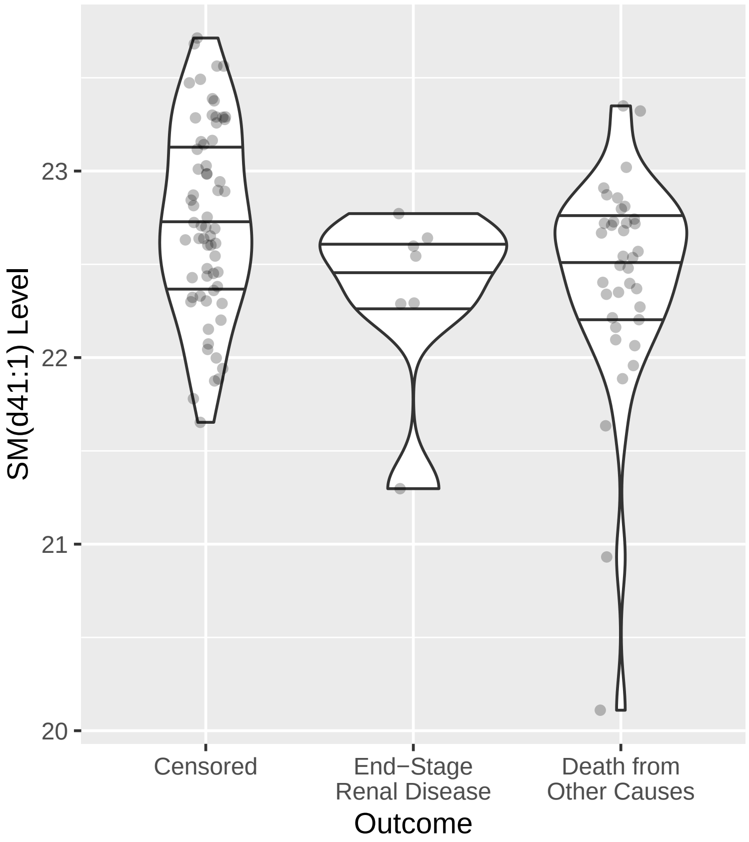


Figure 54: Violin plot of observations of the level of the lipid SM(d41:1). Subpopulations of the study are shown on the x-axis and the level of the lipid is shown on the y-axis. The density of the observations is shown in the shape of the violin and the quantiles of the distribution are shown as horizontal lines.

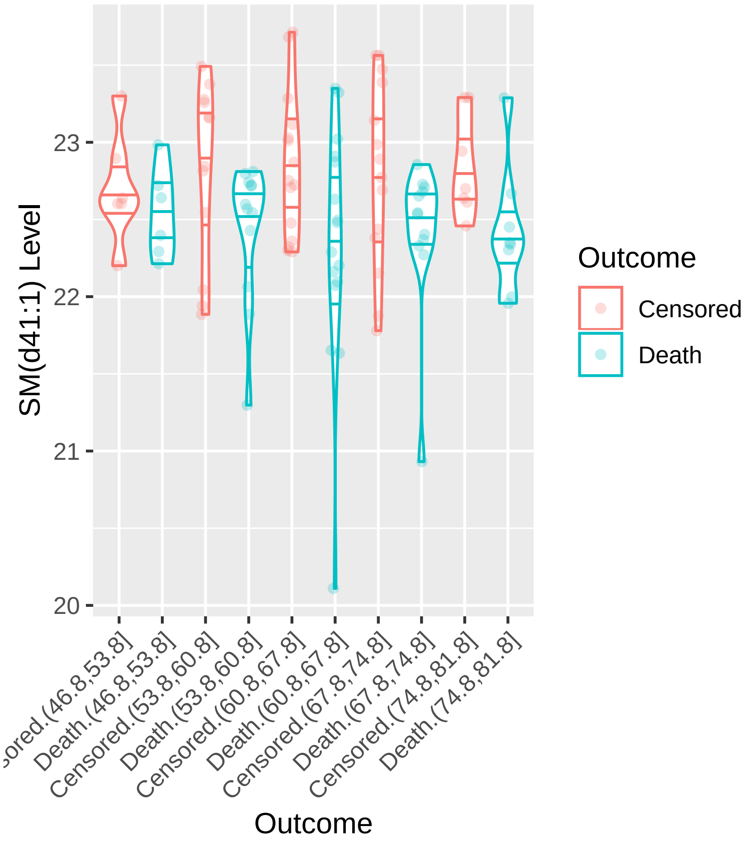


Figure 55: Violin plot of observations of the level of the lipid SM(d41:1). Subpopulations of the study are shown on the x-axis and the level of the lipid is shown on the y-axis. The density of the observations is shown in the shape of the violin and the quantiles of the distribution are shown as horizontal lines.

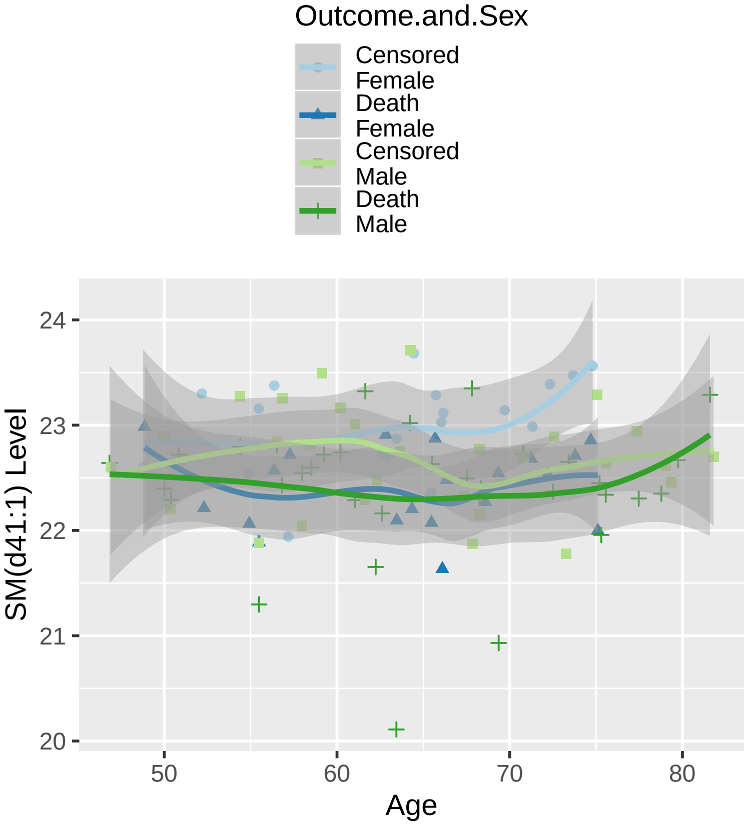


Figure 56: Observations of the level of the lipid SM(d41:1) against age. Subpopulations of the study are in different color. Possible trend in the observations is shown with a subgroup-specific nonlinear regression with the LOESS model.

```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```

8 Lipids' Proportion of the Total Amount of Lipid Class

```
##
##
## Table: List of lipids in the class LPC
## and the lipid's respective proportion of observed signal within the class.
## Shown are each lipid's rank (Rank),
## name (Name),
## class (Class) and
## proportion of the lipid in its class (Pcnt.of.Class; %).
##
##  Rank  Name        Class   Pcnt.of.Class
## -----  ----------  ------  --------------
##     1  LPC(16:0)   LPC     47
##     2  LPC(18:0)   LPC     20
##     3  LPC(18:2)   LPC     16
##     4  LPC(18:1)   LPC     13
##     5  LPC(20:4)   LPC     2.9
##     6  LPC(16:1)   LPC     1.2
##
##
## Table: List of lipids in the class PC
## and the lipid's respective proportion of observed signal within the class.
## Shown are each lipid's rank (Rank),
## name (Name),
## class (Class) and
## proportion of the lipid in its class (Pcnt.of.Class; %).
##
##  Rank  Name       Class   Pcnt.of.Class
## -----  ---------  ------  --------------
##     1  PC(34:2)   PC      13
##     2  PC(36:2)   PC      13
##     3  PC(36:4)   PC      12
##     4  PC(34:1)   PC      12
##     5  PC(36:3)   PC      10
##     6  PC(38:6)   PC      8.2
##     7  PC(38:4)   PC      7.3
##     8  PC(38:5)   PC      4.3
##     9  PC(36:5)   PC      4.1
##    10  PC(38:3)   PC      4
##    11  PC(40:6)   PC      3.5
##    12  PC(32:1)   PC      2.1
##    13  PC(34:3)   PC      1.2
##    14  PC(32:0)   PC      1
##    15  PC(40:5)   PC      0.85
##    16  PC(35:2)   PC      0.69
##    17  PC(35:1)   PC      0.66
##    18  PC(40:7)   PC      0.5
##    19  PC(38:2)   PC      0.48
##    20  PC(32:2)   PC      0.43
##    21  PC(33:1)   PC      0.37
##    22  PC(37:2)   PC      0.13
##
##
```

```
## Table: List of lipids in the class PC-O/P
## and the lipid's respective proportion of observed signal within the class.
## Shown are each lipid's rank (Rank),
## name (Name),
## class (Class) and
## proportion of the lipid in its class (Pcnt.of.Class; %).
##
##  Rank  Name         Class    Pcnt.of.Class
## -----  -----------  -------  --------------
##     1  PC(O-36:4)   PC-O/P   22
##     2  PC(O-38:5)   PC-O/P   19
##     3  PC(O-36:5)   PC-O/P   16
##     4  PC(O-34:3)   PC-O/P   12
##     5  PC(O-38:4)   PC-O/P   10
##     6  PC(O-34:2)   PC-O/P   9.1
##     7  PC(O-36:2)   PC-O/P   4
##     8  PC(O-38:6)   PC-O/P   3.9
##     9  PC(O-36:3)   PC-O/P   3.8
##
##
## Table: List of lipids in the class SM
## and the lipid's respective proportion of observed signal within the class.
## Shown are each lipid's rank (Rank),
## name (Name),
## class (Class) and
## proportion of the lipid in its class (Pcnt.of.Class; %).
##
##  Rank  Name             Class   Pcnt.of.Class
## -----  ---------------  ------  --------------
##     1  SM(42:2)         SM      20
##     2  SM(d34:1)        SM      16
##     3  SM(d40:1)        SM      9.6
##     4  SM(d18:2/24:1)   SM      8.6
##     5  SM(d40:2)        SM      7.6
##     6  SM(d18:1/24:0)   SM      7.3
##     7  SM(d36:1)        SM      6
##     8  SM(d38:1)        SM      5.3
##     9  SM(d41:1)        SM      4.3
##    10  SM(d16:1/18:1)   SM      3.7
##    11  SM(d41:2)        SM      3.3
##    12  SM(d32:1)        SM      2.7
##    13  SM(d36:2)        SM      1.5
##    14  SM(d38:2)        SM      1.5
##    15  SM(d39:1)        SM      1.4
##    16  SM(d33:1)        SM      1.4
##
##
## Table: List of lipids in the class TG
## and the lipid's respective proportion of observed signal within the class.
## Shown are each lipid's rank (Rank),
## name (Name),
## class (Class) and
## proportion of the lipid in its class (Pcnt.of.Class; %).
##
```

```
##  Rank  Name                 Class   Pcnt.of.Class
## -----  -------------------  ------  --------------
##     1  TG(18:1/18:1/16:0)   TG      12
##     2  TG(18:2/18:1/16:0)   TG      11
##     3  TG(16:0/18:2/18:2)   TG      7.4
##     4  TG(18:1/18:1/18:1)   TG      6.6
##     5  TG(14:0/18:1/18:1)   TG      6.4
##     6  TG(50:1)             TG      6.1
##     7  TG(18:2/18:1/18:1)   TG      5.6
##     8  TG(50:3)             TG      3.6
##     9  TG(18:1/18:2/18:2)   TG      3.5
##    10  TG(16:0/18:0/18:1)   TG      2.9
##    11  TG(54:2)             TG      2.8
##    12  TG(14:0/16:0/18:1)   TG      2.6
##    13  TG(18:1/12:0/18:1)   TG      2
##    14  TG(45:0)             TG      1.9
##    15  TG(16:0/22:5/18:1)   TG      1.8
##    16  TG(18:2/22:5/16:0)   TG      1.6
##    17  TG(16:0/18:2/18:3)   TG      1.6
##    18  TG(52:2)             TG      1.5
##    19  TG(18:2/18:2/18:2)   TG      1.4
##    20  TG(52:3)             TG      1.3
##    21  TG(51:2)             TG      1
##    22  TG(14:0/18:2/18:2)   TG      0.95
##    23  TG(16:0/18:2/22:6)   TG      0.94
##    24  TG(52:4)             TG      0.89
##    25  TG(46:1)             TG      0.83
##    26  TG(54:3)             TG      0.75
##    27  TG(48:3)             TG      0.65
##    28  TG(18:0/18:1/20:4)   TG      0.63
##    29  TG(54:4)             TG      0.62
##    30  TG(50:0)             TG      0.61
##    31  TG(50:2)             TG      0.61
##    32  TG(49:1)             TG      0.56
##    33  TG(51:3)             TG      0.56
##    34  TG(18:1/18:1/22:6)   TG      0.53
##    35  TG(53:2)             TG      0.51
##    36  TG(53:3)             TG      0.51
##    37  TG(51:1)             TG      0.43
##    38  TG(46:0)             TG      0.42
##    39  TG(46:2)             TG      0.41
##    40  TG(54:5)             TG      0.4
##    41  TG(49:2)             TG      0.4
##    42  TG(49:3)             TG      0.38
##    43  TG(56:5)             TG      0.35
##    44  TG(58:9)             TG      0.32
##    45  TG(52:5)             TG      0.31
##    46  TG(53:4)             TG      0.27
##    47  TG(56:4)             TG      0.25
##    48  TG(54:6)             TG      0.23
##    49  TG(56:3)             TG      0.23
##    50  TG(56:6)             TG      0.22
##    51  TG(47:1)             TG      0.21
##    52  TG(56:7)             TG      0.2
```

9 Quality Control Table of Lipid Measurements

Table 11: Coefficient of variation (CV; %; also called relative standard deviation) of the lipidomic features in quality control samples and study samples. Values are shown for pooled samples from the study (Pool.Study), NIST samples (NIST), long-term quality control samples from the clinic of Steno Diabetes Center Copenahgen (Pool.Clinic), and study samples (Sample). Additionally, the ratio of CVs in the study samples and in the pooled samples from the study are shown (Ratio.Sample.v.Pool). The rows of the table are sorted by this ratio.

Name	Pool.Study	NIST	Pool.Clinic	Sample	Ratio.Sample.v.Pool
PC(35:1)	4.58	21.11	13.10	31.49	6.87
SM(d36:1)	2.46	8.29	8.25	15.88	6.45
SM(d32:1)	4.60	14.49	8.78	25.76	5.60
SM(d38:1)	4.49	11.35	11.33	23.28	5.18
PC(33:1)	5.60	19.09	13.81	28.57	5.10
PC(36:5)	8.85	39.53	14.10	44.70	5.05
SM(d33:1)	4.96	16.28	8.29	24.68	4.97
PC(40:6)	5.81	18.49	11.81	28.71	4.94
PC(38:6)	5.35	18.32	8.66	26.04	4.87
TG(18:2/22:5/16:0)	9.52	52.28	13.35	45.18	4.75
SM(d41:2)	5.52	19.20	12.13	25.25	4.57
SM(d38:2)	3.98	8.20	9.05	18.00	4.52
PC(40:7)	5.98	25.03	14.38	26.59	4.44
SM(d40:2)	4.30	12.55	10.57	18.94	4.41
SM(d39:1)	6.26	18.70	12.79	26.75	4.28
SM(42:2)	5.23	16.82	9.95	21.87	4.18
TG(53:2)	8.85	25.11	14.95	36.78	4.16
TG(56:3)	8.19	24.92	16.42	33.19	4.05
SM(d18:2/24:1)	4.62	14.21	10.41	18.53	4.01
TG(54:2)	8.43	23.04	15.61	32.55	3.86
SM(d16:1/18:1)	3.59	13.45	9.34	13.76	3.83
TG(16:0/18:0/18:1)	7.96	25.73	15.81	30.28	3.80
TG(18:1/18:1/22:6)	13.71	66.72	19.28	49.94	3.64
TG(51:2)	9.02	25.03	14.04	30.22	3.35
TG(53:3)	8.08	22.50	14.99	26.78	3.31
PC(34:2)	4.12	12.86	17.26	13.66	3.31
PC(38:2)	5.92	18.78	13.49	19.50	3.29
PC(O-38:4)	5.36	17.02	18.24	16.83	3.14
TG(51:1)	10.96	22.86	15.11	32.90	3.00
TG(58:9)	14.28	39.16	22.76	42.32	2.96
TG(54:3)	5.81	12.24	8.64	17.04	2.93
PC(40:5)	6.92	17.63	14.21	20.13	2.91
TG(50:1)	7.94	16.60	13.24	22.98	2.89
TG(14:0/16:0/18:1)	8.72	18.91	13.83	25.00	2.87
SM(d40:1)	5.39	13.27	12.51	14.66	2.72
TG(46:1)	10.56	28.58	15.34	27.81	2.63
TG(18:1/18:1/18:1)	8.59	16.34	12.97	22.40	2.61
TG(49:1)	11.22	32.01	15.46	29.26	2.61
SM(d41:1)	7.17	17.41	13.91	18.49	2.58
PC(37:2)	11.27	30.48	17.21	28.68	2.54

Name	Pool.Study	NIST	Pool.Clinic	Sample	Ratio.Sample.v.Pool
TG(51:3)	9.13	24.67	15.63	23.12	2.53
PC(O-36:2)	6.98	18.49	14.84	17.32	2.48
TG(18:1/12:0/18:1)	9.46	22.90	14.15	23.42	2.48
TG(46:2)	11.11	25.71	18.43	27.42	2.47
TG(53:4)	8.52	19.69	17.40	20.76	2.44
TG(50:3)	6.00	17.88	11.92	14.38	2.40
TG(56:5)	11.32	22.83	15.72	27.03	2.39
TG(16:0/18:2/22:6)	22.15	55.17	23.12	52.39	2.37
PC(38:3)	4.94	13.44	11.56	11.65	2.36
PC(32:1)	6.60	10.31	14.00	15.42	2.34
TG(49:2)	9.96	24.15	15.98	22.42	2.25
TG(50:0)	14.25	29.08	24.34	31.64	2.22
PC(32:2)	8.10	23.93	14.89	17.94	2.22
TG(14:0/18:1/18:1)	7.11	15.29	10.51	15.67	2.20
PC(16:0e/18:1(9Z)	7.98	18.64	10.33	17.56	2.20
PC(34:1)	3.81	5.23	6.74	8.36	2.19
TG(52:2)	6.20	8.49	7.91	13.39	2.16
TG(56:7)	10.32	15.38	13.93	22.21	2.15
SM(d18:1/24:0)	7.42	17.68	14.58	15.88	2.14
TG(56:4)	14.65	18.86	17.96	30.45	2.08
TG(56:6)	10.49	13.29	12.89	21.69	2.07
TG(45:0)	4.35	5.83	7.68	8.93	2.05
PC(O-36:3)	10.22	21.62	13.02	20.89	2.04
PC(O-38:5)	6.62	16.21	11.95	13.42	2.03
TG(18:0/18:1/20:4)	17.37	20.86	24.04	35.02	2.02
TG(48:3)	14.00	31.86	23.28	28.16	2.01
TG(50:2)	6.64	11.62	8.90	13.15	1.98
TG(52:4)	5.77	9.58	9.03	11.30	1.96
TG(16:0/18:2/18:3)	10.31	25.12	17.29	19.53	1.89
TG(14:0/18:2/18:2)	9.76	23.95	16.77	18.11	1.86
PC(38:5)	4.66	9.84	8.25	8.41	1.81
PC(O-38:6)	6.84	13.50	10.21	12.33	1.80
TG(46:0)	11.75	22.81	13.95	20.93	1.78
PC(34:3)	21.13	37.19	24.31	37.18	1.76
TG(18:2/18:2/18:2)	15.81	26.85	16.17	27.46	1.74
TG(18:1/18:2/18:2)	8.62	18.14	15.07	14.70	1.71
LPC(18:1)	10.23	3.46	7.96	17.13	1.67
TG(54:6)	10.98	16.72	13.81	18.02	1.64
SM(d34:1)	4.28	4.32	6.66	7.01	1.64
TG(16:0/22:5/18:1)	15.96	16.91	17.01	26.06	1.63
PC(36:4)	7.56	6.28	14.96	12.35	1.63
TG(54:4)	6.03	10.07	9.33	9.81	1.63
TG(54:5)	7.22	11.02	9.98	11.74	1.63
TG(16:0/18:2/18:2)	7.35	13.21	14.55	11.91	1.62
TG(52:5)	12.90	19.07	16.36	20.56	1.59
PC(35:2)	16.03	20.39	24.54	25.13	1.57
LPC(16:0)	5.91	4.49	6.12	9.24	1.56
TG(49:3)	3.72	4.23	4.02	5.47	1.47
PC(38:4)	5.25	7.04	8.01	7.59	1.45
PC(O-36:5)	8.02	11.89	9.86	11.36	1.42
PC(36:2)	4.30	5.16	6.61	5.81	1.35
SM(d36:2)	5.59	6.27	8.14	7.51	1.34

Name	Pool.Study	NIST	Pool.Clinic	Sample	Ratio.Sample.v.Pool
LPC(18:0)	9.79	4.91	6.88	13.15	1.34
PC(32:0)	6.15	5.42	6.95	7.97	1.30
PC(O-36:4)	11.70	15.74	11.88	14.83	1.27
TG(47:1)	23.48	32.44	28.18	28.16	1.20
TG(52:3)	7.60	8.74	9.63	9.10	1.20
LPC(16:1)	9.77	5.90	11.40	10.54	1.08
PC(36:3)	10.12	9.17	11.57	10.82	1.07
PC(O-34:3)	15.20	15.27	10.86	15.98	1.05
LPC(20:4)	13.51	8.79	10.65	14.00	1.04
TG(18:2/18:1/18:1)	16.72	14.52	14.33	16.62	0.99
PC(O-34:2)	26.89	18.12	12.97	23.00	0.86
LPC(18:2)	10.68	6.03	9.06	9.01	0.84
TG(18:1/18:1/16:0)	31.60	13.28	22.78	25.92	0.82
TG(18:2/18:1/16:0)	33.75	19.63	24.84	26.83	0.79

10 Appendix

```
## R version 3.4.2 (2017-09-28)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 7 x64 (build 7601) Service Pack 1
##
## Matrix products: default
##
## locale:
## [1] LC_COLLATE=Danish_Denmark.1252  LC_CTYPE=Danish_Denmark.1252
## [3] LC_MONETARY=Danish_Denmark.1252 LC_NUMERIC=C
## [5] LC_TIME=Danish_Denmark.1252
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
## [1] stringr_1.2.0
##
## loaded via a namespace (and not attached):
##  [1] Rcpp_0.12.13       lattice_0.20-35     tidyr_0.8.0
##  [4] zoo_1.8-0          gtools_3.5.0        assertthat_0.2.0
##  [7] digest_0.6.12      psych_1.7.8         R6_2.2.2
## [10] survminer_0.4.2    plyr_1.8.4          evaluate_0.14
## [13] ggplot2_3.2.0      highr_0.6           gplots_3.0.1
## [16] rlang_0.3.4        lazyeval_0.2.0      data.table_1.10.4-3
## [19] gdata_2.18.0       Matrix_1.2-11       rmarkdown_1.13
## [22] labeling_0.3       splines_3.4.2       readr_1.1.1
## [25] foreign_0.8-69     munsell_0.5.0       broom_0.4.3
## [28] compiler_3.4.2     xfun_0.7            pkgconfig_2.0.1
## [31] mnormt_1.5-5       htmltools_0.3.6     tidyselect_0.2.3
## [34] tibble_1.3.4       gridExtra_2.3       km.ci_0.5-2
## [37] withr_2.0.0        dplyr_0.7.4         ggpubr_0.1.6
## [40] bitops_1.0-6       grid_3.4.2          nlme_3.1-131
## [43] xtable_1.8-2       gtable_0.2.0        magrittr_1.5
## [46] KMsurv_0.1-5       scales_1.0.0        KernSmooth_2.23-15
## [49] stringi_1.1.5      reshape2_1.4.2      bindrcpp_0.2
## [52] limma_3.32.10      survMisc_0.5.4      cowplot_0.9.2
## [55] RColorBrewer_1.1-2 tools_3.4.2         cmprsk_2.2-7
## [58] forcats_0.2.0      glue_1.2.0          purrr_0.2.4
## [61] hms_0.4.0          dummies_1.5.6       parallel_3.4.2
## [64] survival_2.41-3    yaml_2.2.0          colorspace_1.3-2
## [67] caTools_1.17.1     corrplot_0.84       knitr_1.23
## [70] bindr_0.1          haven_1.1.0
```