# Sets of Co-regulated Serum Lipids are Associated with Alzheimer Disease Pathophysiology

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#### 49 ABSTRACT

- 50 **INTRODUCTION:** Altered regulation of lipid metabolism in Alzheimer disease (AD) can
  51 be characterized using lipidomic profiling.
- 52 **METHOD:** 349 serum lipids were measured in 806 participants enrolled in the

53 Alzheimer Disease Neuroimaging Initiative Phase 1 (ADNI1) cohort and analysed using

54 lipid regression models and lipid set enrichment statistics.

55 **RESULTS:** AD diagnosis was associated with 7 of 28 lipid sets of which four also

56 correlated with cognitive decline, including polyunsaturated fatty acids. CSF amyloid

- 57 beta Aβ<sub>1-42</sub> correlated with glucosylceramides, lysophosphatidyl cholines and
- 58 unsaturated triacylglycerides; CSF total tau and brain atrophy correlated with
- 59 monounsaturated sphingomyelins and ceramides, in addition to EPA-containing lipids.

60 **DISCUSSION:** Lipid desaturation, elongation and acyl chain remodeling are

61 dysregulated across the spectrum of AD pathogenesis. Monounsaturated lipids were

62 important in early stages of AD, while polyunsaturated lipid metabolism was associated

63 with later stages of AD.

#### 64 SIGNFICANCE

Both metabolic genes and co-morbidity with metabolic diseases indicate that lipid metabolism is critical in the etiology of Alzheimer's disease (AD). For 800 subjects, we found that sets of blood lipids were associated with current AD-biomarkers and with AD clinical symptoms. Our study highlights the role of disturbed acyl chain lipid remodelling in several lipid classes. Our work has significant implications on finding a cure for AD. Depending on subject age, human blood lipids may have different effects on AD development. Remodelling of acyl chains needs to be studied in relation to genetic

- variants and environmental factors. Specifically, the impact of dietary supplements and
- 73 drugs on lipid remodelling must be investigated.

# 74 ABBREVIATIONS

- FA fatty acids
- 76 AC acetyl carnitine
- 77 PC phosphatidylcholine
- 78 CE cholesteryl esters
- 79 SM sphingomyelins
- 80 Cer Ceramide
- 81 PE phosphatidylethanolamine
- 82 TG triacylglycerol
- 83 PI phosphatidylinositol
- 84 DG diacylglycerol
- 85 LPC lysophosphatidylcholine
- 86  $A\beta$  Amyloid Beta
- 87 SPARE-AD Spatial Pattern of Abnormality for Recognition of Early Alzheimer's
- 88 disease
- 89 LCRS Lipid Co-Regulatory Set
- 90 MUFA mono unsaturated fatty acid
- 91 PUFA poly unsaturated fatty acid
- 92 ADASCog13 Alzheimer's Disease Assessment Scale–Cognitive subscale
- 93 ADNI Alzheimer's disease neuroimaging initiative
- 94 EPA eicosapentaenoic acid

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#### 95 DHA – docosahexaenoic acid

#### 96 CSF – cerebrospinal fluid

#### 97 **1. Introduction**

The failure of clinical trials of disease modifying agents in Alzheimer's disease (AD) 98 99 highlights our limited knowledge about underlying pathophysiological mechanisms. AD often presents with diabetes co-morbidity and a wide range of metabolic perturbations 100 101 occurring early in the disease process (1). APOE- $\varepsilon$ 4 is by far the strongest single gene 102 variant contributing to increased AD risk and plays key roles in lipid transport and metabolism. Presence of the APOE-E4 variant is correlated with higher cholesterol levels 103 104 in the blood (2). More than twenty additional genes have recently been implicated in AD with functional roles in lipid processing, immune regulation and phagocytosis. Hence, 105 both co-morbidities and known gene variants support the idea that metabolic 106 107 dysfunctions may contribute to AD onset and progression.

Lipidomics methods using liquid chromatography and mass spectrometry (LC/MS) yield reliable measurements of hundreds of lipids in biological samples. LC/MS methods have been used in AD studies in attempts to define possible risk factors (3-7), diagnostic markers (8) and for highlighting novel drug targets (9-11). Perturbations in ceramides and related sphingomyelin metabolism (4, 7) were noted in many of these studies pointing towards a possible role of these lipids in aberrant signalling pathways, membrane remodelling, and apoptotic cascades during AD progression.

115 Changes in phosphatidylcholines were observed in several studies (11-13) pointing to a 116 possible role for phospholipid metabolism in AD pathogenesis. Yet, AD risk prediction 117 failed to replicate using a phosphatidylcholine (PC) biomarker panel(11, 14). Partial 118 correlation network analysis indicated early AD biomarker A $\beta_{1-42}$  was associated with PC 119 and sphingomyelin (SM) (11). These studies support our hypothesis that distinct lipid biochemical pathways were dysregulated in early and late phase of AD. Here, we used
LC-MS/MS based serum lipidomics analysis measured in the ADNI I cohort to define the
lipid co-regulatory network of AD phenotypes, a statistical analysis tool that previously
has been successfully used in the analysis of transcriptomic data (15). We investigated
correlation of lipid sets with (1) Disease diagnosis, (2) CSF markers of disease Aβ<sub>1-42</sub>,
CSF total tau and (3) cognitive decline and brain atrophy.

#### 126 **2. Material and methods**

# 127 2.1. Study cohort

Data used in the preparation of this article were obtained from the Alzheimer's Disease 128 129 Neuroimaging Initiative (ADNI) database (adni.loni.usc.edu). The ADNI was launched in 2003 as a public-private partnership, led by Principal Investigator Michael W. Weiner, 130 131 MD. The primary goal of ADNI has been to test whether serial magnetic resonance 132 imaging (MRI), positron emission tomography (PET), other biological markers, and 133 clinical and neuropsychological assessment can be combined to measure the 134 progression of mild cognitive impairment (MCI) and early Alzheimer's disease (AD). For 135 up-to-date information, see www.adni-info.org.

The ADNI cohort information was downloaded from the ADNI data repository 136 137 (http://adni.loni.ucla.edu/), supplying all the demographic information, neuropsychological and clinical assessment data, and diagnostic information that was 138 139 previously published (16). Prior Institutional Review Board approval was obtained at each participating institution and written informed consent was obtained for all 140 141 participants. Information about the ADNI project is provided on http://www.adni-info.org/ and the associated publication (17). 142

# 143 **2.2. Pathology, clinical and lipidomics data**

144 Untargeted lipidomics, AD diagnosis, CSF biomarkers including Total Tau (t-tau) and 145 amyloid beta (A $\beta_{1-42}$ ), cognitive decline (ADAScog13), brain atrophy represented by 146 Spatial Pattern of Abnormality for Recognition of Early Alzheimer's disease (SPARE-AD)(17) 147 data were obtained from the ADNI repository (<u>http://www.adni-info.org/</u>). Generation and 148 quality control of lipidomics data have been described in (18).

# 149 **2.3. Detection of sets of co-regulated lipids**

A pair-wise Spearman-rank correlation matrix was generated for lipids using the R function cor.test. The matrix was converted to a hierarchical tree model using the hclust function in R with the ward linkage method. The resulting tree model was divided into clusters using the tree cutting algorithm dynamicTreeCut (19). We used a minimum cluster size of three and a split depth of four in the tree cutting method.

# 155 2.4. Association modeling

156 Linear regression models were established for association of serum lipid abundances and CSF biomarkers and indices for cognitive decline and brain atrophy. No confounding 157 158 variables were included in the regression models. Logistic regression models were calculated to associate serum lipids with AD diagnosis. Lipid abundances were scaled 159 160 by the mean substracting approach. All models were unadjusted to identify all the lipid co-regulatory sets that were associated specifically with only AD or with AD and other 161 162 demographics or confounding factors. Data from all ADNI-1 participants were included 163 in the analysis.

# 164 2.5. Lipid set enrichment analysis

165 Co-regulatory lipid sets detected by the dynamicTreeCut method (19) were used as an 166 input for cluster enrichment analysis using the Kolmogorov–Smirnov test as described 167 in the ChemRICH method (20). In this test, the distribution of p-values was assumed to 168 be uniform under a null hypothesis for a lipid cluster. Raw p-values obtained from the bioRxiv preprint doi: https://doi.org/10.1101/550723; this version posted February 18, 2019. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under a CC-BY-NC-ND 4.0 International license.

169	linear and logistic models were used as input for computing the enrichment statistics by
170	comparing the experimental p-values with the uniform distribution. Set level p-values
171	were adjusted for false discovery rate using the Benjamini–Hochberg method.

# 172 **2.6. Source code**

- 173 All statistical analyses were performed in R programming language version 3.4.0.
- 174 The R-script is available at <u>http://github.com/barupal/ADNI</u>

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# 176 **3. Results**

The main objective of the study was to identify lipid co-regulatory modules that were associated with AD diagnosis and its clinical and pathological features. In this direction, we first computed univariate association models and obtained raw p-values for each lipid. Next, we identified lipid co-regulatory modules, which were then used as setdefinitions for a lipid-set enrichment analysis using the raw p-values for lipids. To minimize the false-negative rate on the set-level statistics, univariate p-values were not corrected for the multiple hypothesis testing.

# 184 **3.1. Subject cohort and lipidomics details**

Supplement Table 1 summarizes the details for the 806 ADNI participants at baseline
included in the present study. The baseline ADNI1 serum lipidomics dataset contained
16 different lipid chemical classes summarizing 349 annotated lipids (Table 1).

# 188 **3.2. Regression models for individual lipids**

We first tested all individual lipids for their association with both early and late AD pathogenic markers and cognitive changes (Supplement Table S2). Raw p-values from these association models will be used as an input for the lipid set enrichment analysis in the following section. Figure 1 shows the number of significantly associated lipids in these regression models. A total of 168 lipids were found to be significant in at least one

194 regression model (raw p-value < 0.05), making it difficult to biologically interpret them on 195 individual lipid level. Two AD phenotypes showed strong positive associations with individual serum lipids, CSF Total tau and SPARE AD. Conversely, three phenotypes 196 197 were mostly negatively associated with individual blood lipids, including the two related 198 phentoypes AD diagnosis and its major contributor, ADASCog13. Overall, AD diagnosis 199 was associated with a decline in many lipid levels which could point to lower metabolic 200 activity in specific lipid metabolic pathways. When analyzing all individual lipids that were 201 associated with at least one AD-phenotype, we found a very high specificity of lipid 202 associations with a particular AD-phenotype (Figure 2 and Table S3). 48% (168/349) of all lipids were associated with at least one AD-phenotype (Table S3). Specifically, for 203 204 known lipids, 63% of all AD-phenotype associated lipids were specific to only one 205 phenotype and not shared with others (Figure 3). 28 % of the detected associations of 206 known lipids were shared between two phenotypes, driven by lipids shared between the 207 two related phentoypes AD diagnosis and its major contributor, ADASCog13, in addition 208 to lipids shared between total tau and SPARE-AD. Conversely, Abeta142 showed few shared lipids. Importantly, there was no identified lipid that was shared between four 209 210 phenotypes, and only one lipid that was associated with all AD-phenotypes (arachidonyl-211 lysophosphatidylethanolamine; LPE C20:4). Many lipids are co-regulated by the activity 212 of specific lipases or other enzymes involved in lipid remodeling. Identifying 213 commonalities of biochemical mechanisms may lead to underlying genetic drivers or 214 environmental factors implicated in AD-etiology. Therefore, we next focused on 215 identifying sets of co-regulated lipids associated with AD pathophysiology rather than 216 interpreting individual lipids.

#### **3.3. Identifying sets of co-regulated lipids**

218 Lipid classification often uses chemical structure as the only criterion. To specify the 219 biochemical relationships between circulating blood lipids, we instead used correlation analysis to determine sets of lipids. A pair-wise Spearman correlation matrix followed by 220 221 hierarchical clustering with the DynamicTreeCut dendrogram cutting method (19) yielded 222 a total of 28 co-regulated lipid sets in the ADNI1 dataset (Figure 3). The mean size was 223 12.5 lipids per set, ranging from 4 to 28 members. These lipid sets (LM) were named 224 LM1 to LM28. The average Spearman correlation coefficient *rho* across sets was 0.63 225 with a range of 0.19 < rho < 0.82. Figure 3 and Supplemental Table S2 show that some 226 lipid co-regulatory sets were composed of lipids from the same chemical classes (such as Set-17 for free fatty acids, Set-1 for triacylglycerides and Set-14 for ceramides) 227 228 whereas other sets were heterogeneous (such as Set-3 consisting of ceramides and 229 sphingomyelins, or Set-7 that includes phosphatidylinositols and phosphatidylcholines). 230 Interestingly, several classes of lipids were found with distinct co-regulation within each 231 class. For example, triacylglycerides were not found as one large group of co-regulated 232 species, but clustered in three specific sets, and similarly, free fatty acids were found in two different sets, Set-9 consisting only of saturated fatty acids and Set-17 comprised 233 234 only of unsaturated fatty acids. Similarly, other lipid classes were distributed across different sets, too. For example, phosphatidylcholines were found in five sets and 235 236 sphingomyelins were co-regulated in three sets, indicating downstream regulation of lipid 237 biochemistry by specific elongases, desaturases, lipases, acyl-transferases within each lipid class (Figure 2). 238

**3.4 Associating lipid sets with AD-phenotypes** 

These lipid groups served as input for a lipid-set enrichment analysis (LSEA)(20) along with the p-value and beta coefficient results from the regression models. Overall, 19 out of 28 lipid sets were significantly associated with at least one AD-phenotype (Figure 4, 243 Table S3) using the Kolmogorov-Smirnoff statistical test with FDR-corrections. Eight sets 244 were uniquely associated with only one specific AD-phenotype, but only one set was associated with four phenotypes, Set-11, consisting primarily of ceramides and 245 246 phosphatidylcholines. Set-11 did not include polyunsaturated acyl chains with three or 247 more double bonds. Six sets were associated with two AD-phenotypes and four sets were correlated with three AD-phenotypes, but no set correlated with all five phenotypes. 248 249 More than two-thirds of all associations were positively correlated between lipid sets and 250 phenotypes, mostly driven by the t-tau phenotype that also had the highest number of 251 correlated lipid sets. Conversely, ADASCog13 showed the highest number of negative 252 associations with lipid sets. We therefore investigated the individual phenotypes with respect to the composition of their associated lipid sets. 253

#### 254 **3.4.1. Lipid sets associated with AD diagnosis**

255 AD-diagnosis was significantly associated with seven distinct lipid sets (Figure 4) after 256 FDR correction. Specifically, the phenotype was highly significantly negatively correlated 257 with lipid Set-26 and Set-4. Both sets were comprised of acyl chains with at least one polyunsaturated fatty acyl chain (PUFA) (see Table S2), either eicosapentaenoic acid 258 (EPA), docosahexaenoic acid (DHA) or arachidonic acid (AA). Set-26 consisted 259 260 exclusively of triacylglycerides that also contained either EPA or DHA, but not a single 261 saturated fatty acid. Set-4 was mixed between different phospholipid head groups, cholesteryl esters and free fatty acids, indicating that the co-regulation mechanisms 262 focused on the modulation and incorporation of acyl chains irrespective of the lipid class. 263 Set-23 was also negatively correlated with AD-diagnosis and comprised of DHA-264 containing choline- and ethanolamine-plasmalogens. Conversely, two other sets of lipids 265 266 were positively associated with AD-diagnosis, most significantly for Set-5 and Set-20, and less significantly with Set-11 and Set-12. Set-5 contained co-regulated di- and 267

triacylglycerols with acyl groups that did not contain any PUFA with four or more double
bonds, and only one single lipid with linolenic acid (C18:3). Set-20 was exclusively
composed of unsaturated choline-plasmalogens, but not containing any EPA or DHA
acyl chain.

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# 273 3.4.2 Lipid sets associated with CSF Aβ1-42

CSF A<sub>β1-42</sub> was significantly associated with four lipid sets (Figure 4). Three sets were 274 275 negatively correlated, Set-11, Set-7 and Set-8. Set-7 was the only lipid set that contained 276 phosphatidylinositols, in addition to phosphatidyl cholines. Acyl chains were primarily saturated or mono- and di-unsaturated. Similarly, Set-8, consisted mostly of desaturated 277 acyl groups with less than four double bonds, exclusively found as lyso-278 279 phosphatidylcholines. In the same way, no PUFA-acyl chains were found in Set-11, a 280 heterogenous set of ceramides and choline-plasmalogens. Importantly, the only positive association of a lipid set with CSF AB1-42 was Set-26 that was completely made of PUFA-281 282 triacylglycerides.

283

# 284 3.4.3 Lipid sets associated with CSF tau

CSF total tau correlated with 12 lipid sets, the highest number of associated lipid sets 285 286 among all phenotypes (Figure 4). All sets except Set-1 were positively correlated with 287 CSF-total tau. Three unique sets that were not shared with other phenotypes. Set-16 288 was composed of acylcarnitines with increasing degree of desaturation, and Set-17 was 289 a set of monounsaturated fatty acids. Set-1 was less significant in comparison to other 290 set associations. Four sets were shared with brain atrophy, four sets were shared with AD-diagnosis, two sets with amyloid beta and four lipid sets were shared with cognitive 291 292 decline. Notably, set-19 was also associated with brain atrophy and contained mostly 293 EPA-side chain phosphatidylcholines. Set-3 was composed of sphingomyelins and 294 ceramides that were not associated with diagnosis or amyloid beta, but instead was also 295 linked with cognitive decline and SPARE-AD.

296

# 297 **3.4.4 Lipid sets associated with Brain atrophy (SPARE-AD)**

Brain atrophy was most significantly associated with Set 27, 19, 11 and 2 (Figure 4). Three sets (Set 2, Set 11, Set 27) were void of PUFA-side chains with either phosphoplipid or sphingolipid head groups. Conversely, Set 19 contained mostly EPAside chain phosphatidylcholines and was further associated with CSF total tau. Similarly, Set 21 was associated with both phenotypes, containing phospholipids and their lysoforms with the PUFA acyl chain arachidonic acid.

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# 305 **3.4.5 Lipid sets associated with cognitive functions**

Most of the lipid sets associated with cognitive decline were also associated with AD diagnosis (Figure 4). Additionally, it was negatively associated with set Set-22 which consisted of ethanolamine-plasmalogens.

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#### 310 **4. Discussion**

We here focused on associations between blood lipids and five AD-phenotypes guided by known contributions of lipids and metabolic co-morbidities to Alzheimer's disease. We systematically tested both the association of individual lipids and the association with sets of co-regulated lipids. This approach showed an important advantages over previous "feature" based lipidomics-AD studies (9), (21) that did not focus on specific lipid groups, their side chains or their biological regulation. Without clear lipid identification, feature-based associations miss biological insights and have a high risk of 318 not being validated in subsequent studies because each individual lipid may cause more 319 than one feature in LC-MS based lipidomics(21, 22). Instead we used the largest published AD-lipidomics data set (18) to date with 349 identified lipids belonging to 13 320 321 major lipid classes, identified by extensive MS/MS fragmentation analysis (23) and enabling analyses reaching to the level of acyl chains. A second difference to previous 322 323 efforts was a focus on summarizing lipids by statistical co-regulation instead of only 324 relying on univariate analysis or grouping by lipid head groups. This expansion of classic 325 statistical analysis was critical to extend from diagnostic biomarkers (that need 326 correctiong for multiple testing using false discovery rate (FDR) adjustments) to revealing underlying biological mechanisms. The axiom of univariate analyses, the mutual 327 328 independence of variables, is untrue in lipid biology. Moreover, stringent FDR corrections 329 lead to an increased number of false negative results and compromise the statistical 330 power to investigate the biological mechanisms and pathways. As lipids are poorly 331 presented in biochemical pathway databases (20), classic metabolic pathway 332 enrichment analysis (24) ignores a majority of detected lipids and is unsuitable for lipidomics. Instead, Spearman-rank correlation based matrices yielded specific clusters 333 334 of lipids associated with Alzheimer's disease phenotypes by using the robust 335 Kolmogorov-Smirnov test for *p*-value distributions. These lipid sets showed very distinct 336 metabolic features that we identified as preferential use of specific polyunsaturated fatty 337 acids that replaced saturated or monounsaturated fatty acids for distinct lipid classes. These mechanisms of lipid desaturation, elongation, and acyl-chain remodeling were 338 339 disturbed in early and later stages of Alzheimer disease. A minimal overlap among lipid 340 sets was observed (Figure 3) with respect to statistical associations with AD phenotypes, indicating that quite distinct lipid biochemical processes were involved in the early and 341 342 later stages of AD. Lipid metabolic pathways associated with the early stage, in 343 particular, may provide new therapeutic targets to stop AD progression. MUFA-344 containing lipids were positively associated with the brain atrophy and tau accumulation 345 whereas PUFA-containing lipids were negatively associated with AD diagnosis and 346 cognitive decline. Therapeutic strategies targeting MUFA lipid pathways at the early 347 stages of AD could therefore be potentially more effective in delaying the progression of 348 the disease.

#### 349 **4.1 Lipids linked to the amyloid beta clearance pathway**

A decrease in the CSF AB1-42 peptide marker is indicating a poor clearance of the peptide 350 351 in the brain, leading to its extra-neuronal accumulation. In our study, poor clearance was 352 indicated by negative associations with lipids sets, including sets that contained phosphatidylinositols, lysoPCs, ceramides and choline-plasmalogens and PUFA TGs. 353 354 The amyloid  $\beta$  peptide is known to cause mitochondrial dysfunction (25) which can lead 355 to neurodegeneration via autophagic cascades (26, 27). The associated lipids, specifically ceramides and phosphatidylinositols and lysoPCs have been linked with cell 356 357 death and may also contribute in the Amyloid Beta mediated toxicity in neurons (28-30). 358 Higher levels of ceramides containing oleic acid (C18:1) have been shown to increase AD risk (4, 5). We validate this finding in our study and also observed lower levels of 359 phosphoinositols containing polyunsaturated fatty acids to correlate with poor Amyloid-360 361 beta clearance. An alternative explanation to our data is an impaired amyloid beta 362 clearance in the liver(31)that subsequently leads to dysregulation of lipid metabolism in 363 the liver. Overall, our data suggest that these lipid sets can serve as serum biomarkers for disturbed Amyloid beta pathway regulation in brain and can complement Amyloid 364 365 beta imaging assays.

366

#### 367 4.2 Cerebrospinal fluid total tau

368 CSF tau is a marker for accumulating tau tangles in the brain tissues, causing 369 neurodegeneration. We found that the total CSF tau marker was significantly associated with lipid sets enriched in monounsaturated fatty acids, acyl-carnitines, ceramides, 370 371 sphingomyelins, and EPA containing phosphatidylcholines. Increased fatty acids and acyl-carnitines are known markers of impaired fatty acid beta oxidation in 372 mitochondria(32), specially during metabolic diseases such as diabetes and obesity(33, 373 34). We found free fatty acids and acylcarnitines to be positively correlated with total tau, 374 supporting the notion of tau mediated neurodegeneration and mitochondrial 375 376 dysfunctions. Mitochondrial impairment was further evidenced by positive associations 377 of total tau with sets of ceramides, because accumulating ceramide are known to induce cell death and to increase the AD risk in normal subjects (5) Rozen et al. 2011. Higher 378 379 ceramide levels were also reported for early stage Alzheimer's disease (35-37). These 380 findings indicate that these lipids may be involved in early neurodegenerative pathways, and their underlying pathways might lead to candidates for new therapeutic strategies. 381

382

# 383 **4.3 Lipid sets linked with brain atrophy**

384 SPARE-AD is a composite index of brain atrophy and indicates the neurodegeneration 385 magnitude. We found a high overlap of lipid sets that were associated with both SPARE-AD and 386 total tau, reinforcing the usability of these serum lipids as biomarkers for neurodegeneration. 387 These lipid sets included phosphatidylcholines and sphingolipids that were enriched in polyunsaturated fatty acyls (PUFA) eicosapentaenoic acid and arachidonic acid (EPA, AA). 388 389 These fatty acids are main components of brain lipids (38, 39). The loss of brain tissue may cause 390 an increase in levels of serum lipids that include EPA and AA as acyl groups through lipid 391 remodelling (40, 41). We here identify lipid pathways associated with tau-mediated brain atrophy 392 that eventually contributes to AD.

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## 394 **4.4 AD diagnosis and cognitive decline**

395 Previous publications reported that lower levels of PUFA in AD subjects across multiple lipid classes, along with higher levels of monounsaturated lipids (4, 8, 9, 42-46). We 396 397 found numerous, very significant associations of omega-3 and omega-6 containing complex lipids with AD diagnosis and cognitive functions. Our analysis is consistent with 398 these results as shown by AD associated lipids in Set-4, Set-20, Set-23 (Figure 4). We 399 here specify that the major difference is not related to total levels of mono- or 400 401 polyunsaturated fatty acids, but the extent at which these fatty acids are incorporated 402 into different complex lipids. Clear differences in circulating PUFA phospholipid and PUFA triacylglycerol levels in AD subjects in comparison to normal subjects were 403 404 observed, likely due to dysregulation of biosynthesis in liver. Here, substrate preference 405 of MGAT and DGAT enzymes in the liver may play an important role, but the exact specificities of acyltransferase enzymes (and their corresponding lipase enzymes) are 406 407 not well studied. Levels of anti-inflammatory plasmalogens (47), important lipids for brain 408 membrane functions (45, 48), were decreased in AD patients in comparison to cognitively normal subjects. Lower levels of plasmalogens have been linked to AD (45). 409 410 However, in clinical trials, EPA and DHA supplementation do not improve the cognitive 411 function of AD subjects (49). Nutritional intervention trials such as the European 412 LipiDiDiet have failed to show any cognitive improvement in AD subjects. A broad-413 spectrum effect of FOS on additional lipid pathways may explain the failure of this trial and warrants further lipidomics studies for serum specimens of this trial's participants. It 414 was observed that the incorporation of omega-6 fatty acids was increased in AD 415 416 subjects. These fatty acids are well-known precursors to pro-inflammatory molecules such as leukotrienes. Further studies are needed to test if post-mortem brain tissues of 417

AD subjects show similar disruption in fatty acid incorporation and if these patternscorrelate with AD severity or other AD phenotypes.

420

# 421 **5. Conclusions**

Using co-regulated sets of lipids enabled us to find significant associations of lipids with Alzheimer's disease that led to biochemical mechanisms. Across the spectrum of AD progression, pathways were dysregulated that pointed to lipid desaturation, elongation and remodelling. These pathways provide new targets as well candidate biomarkers for the population screening for AD prevention. Future studies are needed to tease out the roles of genetic variations, drug, and diet the metabolism of MUFA and PUFAs and their complex lipids and their roles in AD.

429

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# 454 Author's contribution

DKB and OF generated the lipidomics dataset. DKB, RB, RKD and OF design the study.
DKB and SF performed the statistical analyses. AJS, PJM, MA and KN contributed in
data interpretation. All author contributed in the manuscript writing.

Transparency declaration: Authors affirms that the manuscript is an honest, accurate, and transparent account of the study being reported; no important aspects of the study have been omitted; and any discrepancies from the study as planned have been explained.

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## 463 Figure legends

- 464 Figure 1. Co-regulated sets of serum lipids in the ADNI lipidomics dataset. Sets
- were detected by the dynamicTreeCut algorithm (see method). Node colors show
- 466 different chemical classes. FA fatty acids, AC acyl carnitines, PC
- 467 phosphatidylcholines, CE cholesteryl esters, SM sphingomyelins, Cer ceramides,
- 468 PE phosphatidylethanolamines, TG triacylglycerols, PI phosphatidylinositols, DG
- 469 diacylglycerols, LPC lysophosphatidylcholines.

# 470 Figure 2. Number of significantly different lipids with AD phenotypes in

- 471 univariate statistics. Directions of beta coefficients in regression models are given by
- 472 colors as blue (negative) and red (positive) associations using uncorrected p < 0.05
- 473 values. CN : cognitively normal, LMCI : late mild cognitive impairment, AD : Alzheimer's
- 474 disease. DIAG : linear models for diagnosis, tau linear model for tau,  $A\beta_{1-42}$  linear
- 475 model for amyloid beta peptide 42, SPARE-AD linear model for Spatial Pattern of
- 476 Abnormality for Recognition of Early Alzheimer's disease index, ADASCog13 -
- 477 Cognitive Subscale of the Alzheimer's Disease Assessment Scale index.

478

# 479 Figure 3. Number of significantly associated lipids across AD-phenotypes.

- 480 Uncorrected p<0.05 values for five AD-phenotypes. DIAG : linear models for
- 481 diagnosis, tau linear model for tau, ABETA142 linear model for amyloid beta
- 482 peptide 42, SPARE-AD linear model for Spatial Pattern of Abnormality for
- 483 Recognition of Early Alzheimer's disease index, ADASCog13 Cognitive Subscale of
- the Alzheimer's Disease Assessment Scale index.

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# 485 Figure 4. Co-regulated sets of lipids significantly associated with AD-

- 486 **phenotypes.** Direction of associations is given by red (positive) and blue (negative)
- 487 edge colors. Line thickness indicates the significance of associations (see
- 488 Supplementary Table 4 for details). Lipid compositions for each set are shown in
- Figure 1 and Supplementary Table S1. DIAG : linear models for diagnosis, tau linear
- 490 model for tau, ABETA142 linear model for amyloid beta peptide 42, SPARE-AD –
- 491 linear model for Spatial Pattern of Abnormality for Recognition of Early Alzheimer's
- disease index, ADASCog13 Cognitive Subscale of the Alzheimer's Disease
- 493 Assessment Scale index.

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# 495 Tables

# 496 Table 1. Lipid classes and sub-classes in the ADNI serum lipidomics untargeted

#### 497 dataset

Class	Subclass	Count
Acylcarnitine (AC)	Acylcarnitine	9
Free fatty acid (FA)	Fatty acid	29
Sterol lipids	Cholesterol	1
	Cholesteroyl ester (CE)	8
Phospholipid	Lysophosphatidylcholine (LPC)	22
	Lysophosphatidylethanolamine (LPE)	4
	Phosphatidylcholine (PC)	53
	Phosphatidylethanolamine (PE)	11
	Phosphatidylinositol (PI)	11
	Plasmalogen phosphatidylcholine (p-PC)	28
	Plasmalogen phosphatidylethanolamine (p-PE)	15
Sphingolipid	Ceramide (CER)	19
	Glucosylceramide (GluCer)	8
	Sphingomyelin (SM)	34
Acylglycerols	Diacylglycerol (DG)	13
	Triacylglycerol (TG)	84

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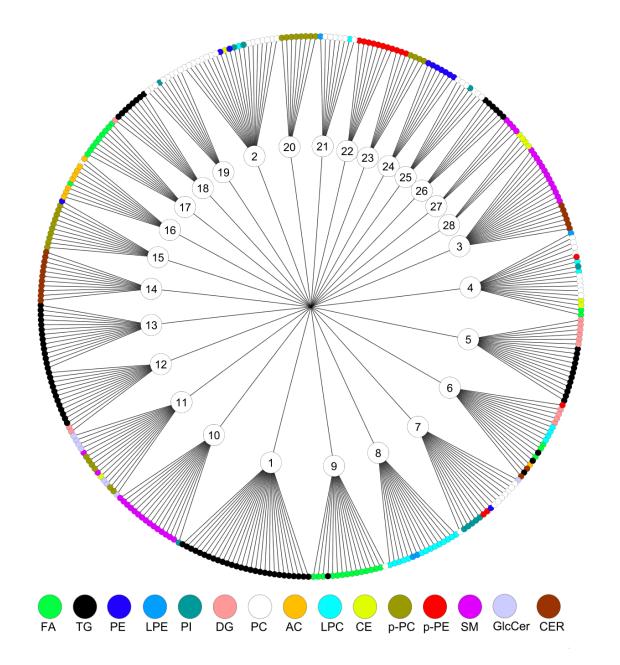
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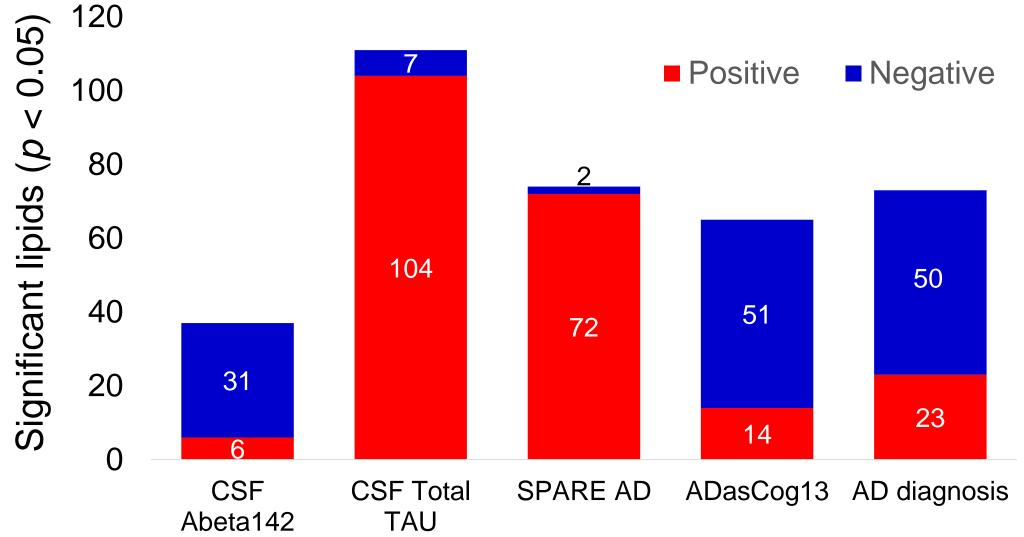
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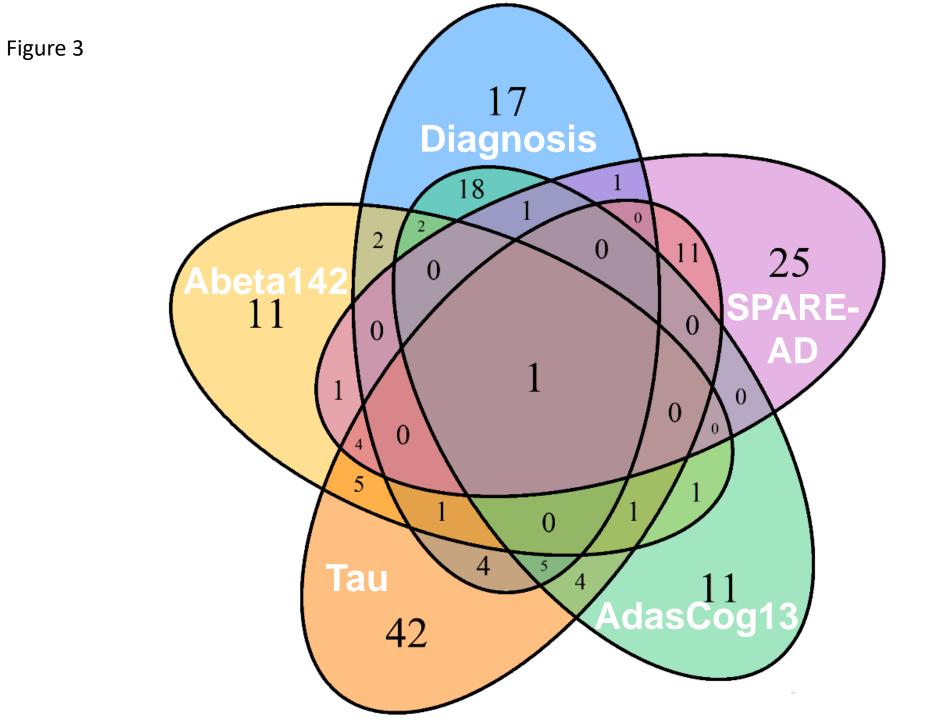
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Figure 1



# Figure 2





# Figure 4

