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Reporting Summary

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For	ali statistical an	alyses, confirm that the following litems are present in the figure legend, table legend, main text, or Methods section.		
n/a	Confirmed			
	The exact	sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement		
	A stateme	ent on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly		
	The statistical test(s) used AND whether they are one- or two-sided Only common tests should be described solely by name; describe more complex techniques in the Methods section.			
	A descript	ion of all covariates tested		
	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons			
	A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)			
	For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted Give <i>P</i> values as exact values whenever suitable.			
	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings			
\boxtimes	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes			
	\square Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated			
	'	Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.		
So	ftware an	d code		
Polic	cy information	about <u>availability of computer code</u>		
Da	ata collection	FreeSurfer (v 5.3.) cortical reconstruction was used to derive measures of cortical thickness and surface area.		
Da	ata analysis	All analyses were performed in R version 3.6.2.		
For m	nanuscripts utilizing	custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and		

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

The summary statistics are available within the article and its data supplement. The individual level participant data analyzed in this study are available by application from the Saguenay Youth Study.

Field-spe	ecific reporting			
Please select the o	ne below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.			
\(\sum_\) Life sciences	Behavioural & social sciences Ecological, evolutionary & environmental sciences			
For a reference copy of	the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf			
Life scier	nces study design			
All studies must dis	sclose on these points even when the disclosure is negative.			
Sample size	e used the maximal sample size (individuals with full data) available in our cohort, Saguenay Youth Study.			
Data exclusions	As lipid-lowering medications have robust effect on circulating triglyceride levels, we excluded individuals using any lipid-lowering medications.			
Replication	We have not found a collaborator with suitable brain MRI data and blood triglycerides quantified with Metabolon's Complex Lipid platform - hus, we have not been able to replicate our findings.			
Randomization	We don't have multiple experimental groups, and thus we have not performed randomization. We have adjusted our analyses for age and sex, and in addition for APOE alleles, as these all are potential confounding factors influencing both lipid and brain phenotypes.			
Blinding	We don't have multiple experimental groups nor randomization, and therefore blinding is not relevant in our study.			
We require informatis system or method lis Materials & ex n/a Involved in the Antibodies Eukaryotic Palaeonto Animals ar	ChIP-seq cell lines ChIP-seq logy and archaeology MRI-based neuroimaging and other organisms search participants ta			
Human rese	arch participants			
Policy information	about studies involving human research participants			
Population chara	Our study population consisted of 441 middle-aged adults from the Saguenay Youth Study (males 43%, average age 49 years, mean BMI 27.6). Study participants are generally healthy. Individuals on lipid-lowering medications were excluded.			
Recruitment	The Saguenay Youth Study is a family-based study, including 1029 adolescents and their 962 parents. The study was recruited via adolescents attending high schools in the Saguenay-Lac-Saint-Jean region of Quebec, Canada. Both maternal and paternal grandparents of the adolescents were required to be of French-Canadian ancestry and born in the region; as such, all adolescents and their parents are of a single ethnicity (European ancestry).			
Ethics oversight	The study was approved by the research ethics committees of Chicoutimi Hospital (Chicoutimi, QC, Canada) and the Hospital for Sick Children (Toronto, ON, Canada).			
Note that full inform	ation on the approval of the study protocol must also be provided in the manuscript.			
Magnetic re	sonance imaging			
Experimental d				
Design type	N/A			

Design specifications	N/A			
Behavioral performance measure	res N/A			
Acquisition				
Imaging type(s)	Structural T1-weighted images			
Field strength	1.5T			
Sequence & imaging parameters	3D Magnetization Prepared Rapid Gradient Echo sequence with 176 sagittal slices (1-mm isotropic resolution, TR = 2.400ms, TE = 2.65ms, TI = 1000ms, and flip angle = 8°).			
Area of acquisition	Whole brain			
Diffusion MRI Used	Not used ■ Not used			
Preprocessing				
Preprocessing software	T1W images processed with FreeSurfer, version 5.3			
Normalization	FreeSurfer, version 5.3			
Normalization template	FreeSurfer, version 5.3			
Noise and artifact removal	N/A			
Volume censoring	N/A			
Statistical modeling & infere	nce			
Model type and settings	N/A			
Effect(s) tested	N/A			
Specify type of analysis: Whole brain ROI-based Both				
Anatomical location(s) 34 regions (per hemisphere), as segmented using the Desikan-Killiany atlas				
Statistic type for inference (See Eklund et al. 2016)	N/A			
Correction	N/A			
Models & analysis				
n/a Involved in the study Functional and/or effective connectivity Graph analysis Multivariate modeling or predictive analysis				