nature portfolio

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Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our <u>Editorial Policies</u> and the <u>Editorial Policy Checklist</u>.

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

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n/a	Confirmed
	The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
	A statement 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.
\boxtimes	A description of all covariates tested
\boxtimes	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 <i>Give P values as exact values whenever suitable.</i>
\boxtimes	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
	Estimates of effect sizes (e.g. Cohen's <i>d</i> , Pearson's <i>r</i>), indicating how they were calculated
	Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection

We used Oracle Software SQL Developer to execute the SQL code and extract the data from a copy of CLARITY database, which is an application of EPIC (electronic medical record software) that stores the patient data in a relational schema.

Data analysis

Data analysis was performed with Python software, version 3.7, with transformers and scikit-learn packages.

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

Data

Policy information about availability of data

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

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our <u>policy</u>

The datasets analyzed during the current study are not publicly available: due to reasonable privacy and security concerns, the underlying EHR data are not easily redistributable to researchers other than those engaged in the Institutional Review Board-approved research collaborations in the current project. The corresponding author may be contacted for access to EHR data for an IRB approved collaboration.

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Data exclusions

Randomization

Not applicable

Not applicable

Replication

Blinding

Policy information about studies involving human research participants and Sex and Gender in Research.

Reporting on sex a	No exclusions were made based on sex/gender. Of 56,530 patients included in our analysis, 22,233 (39.3%) were female based on self-reported electronic health record data. From this cohort, 34,234 patients had a statin prescription present and 12,179 (35.6%) were female. There were 22,296 patients without a statin prescription and 10,054 (45.1%) were female.	
Population charac	All patients included in the study cohort had an ASCVD diagnosis. Of patients with a statin prescription, the average age was 68.6 ± 11.6 years, and 55.7% were non-Hispanic White, 4.9% were non-Hispanic Black, 9.3% were Hispanic, and 16.2% were non-Hispanic Asian. Of patients without a statin prescription, the average age was 65.5 ± 14.7 years, and 58.4% were non-Hispanic White, 5.8% were non-Hispanic Black, 9.6% were Hispanic, and 13.6% were non-Hispanic Asian.	
Recruitment	Not applicable	
Ethics oversight	The study was approved by the Stanford University Institutional Review Board (Protocol 47644). Informed consent was waived under exemption 4: research on existing data.	
	cific reporting	
Please select the on	e below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.	
Life sciences For a reference copy of the	Behavioural & social sciences Ecological, evolutionary & environmental sciences e document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf	
Life scien	ces study design	
All studies must disc	lose on these points even when the disclosure is negative.	
	For NLP training, validation, and application, we included the entire local population of ASCVD patients who met our study criteria of missing statin prescriptions and the presence of statin discussions in their notes. No patients who met study criteria were excluded.	

Reporting for specific materials, systems and methods

No data were excluded from analysis in patients who met our study criteria.

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

We performed bootstrap resampling of 1000 iterations to repeatedly assess NLP performance and obtain uncertainty intervals.

Materials & experimental systems	Methods
n/a Involved in the study	n/a Involved in the study
Antibodies	ChIP-seq
Eukaryotic cell lines	Flow cytometry
Palaeontology and archaeology	MRI-based neuroimaging
Animals and other organisms	·
Clinical data	
Dual use research of concern	