

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 [Editorial Policies](#) and the [Editorial Policy Checklist](#).

Please do not complete any field with "not applicable" or n/a. Refer to the help text for what text to use if an item is not relevant to your study. For final submission: please carefully check your responses for accuracy; you will not be able to make changes later.

Statistics

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

- | n/a | Confirmed |
|--------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <input type="checkbox"/> | <input checked="" type="checkbox"/> The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> The statistical test(s) used AND whether they are one- or two-sided
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> A description of all covariates tested |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> 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) |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
<i>Give P values as exact values whenever suitable.</i> |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated |

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

Data collection

Data analysis

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 [data availability statement](#). 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 [policy](#)

As required by the National Institutes of Health, individual-level descriptive data from this study are deposited in the National Institute of Mental Health National Data Archive (NDA) using an NDA Global Unique Identifier (GUID) and made accessible to members of the research community according to provisions defined in the NDA Data Sharing Policy and Duke University Institutional Review Board.

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender

269 boys; 206 girls

Reporting on race, ethnicity, or other socially relevant groupings

425 Not Hispanic/Latino; 50 Hispanic/Latino; 4 American Indian/Alaska Native; 7 Asian; 54 Black or African American; 47 More than one race reported; 15 Not reported/Other

Population characteristics

Participants were patients at one of four Duke University Health System pediatrics primary care clinics who were 17-36 months of age and did not have significant sensory or motor impairments, were not ill, and whose parents spoke English or Spanish. Of the 475 participants, 49 were diagnosed with autism spectrum disorder, 98 with developmental or language delay without autism, and 328 were considered to have neurotypical development.

Recruitment

Parents or legal guardians of potential participants were approached by study staff during their child's well-child visit to a Duke University Health System (DUHS) pediatric primary care clinic and invited to participate in the present study. The clinic population roughly matches that of Durham, NC; approximately 86% of children living in Durham County, North Carolina, receive their primary care within the DUHS. Potential biases include exclusion of children with sensory and/or motor impairments and those whose parents did not speak English or Spanish. Racial and ethnic diversity of enrolled participants was greater for participants diagnosed with autism or developmental/language delay than for those with neurotypical development, with the clinical groups more closely matching the ethnic and racial distribution of the DUHS and Durham County, NC.

Ethics oversight

Duke University Institutional Review Board

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

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 sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size

Data exclusions

Replication

Randomization

Blinding

Behavioural & social sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description

Prospective, non-experimental study design based on quantitative data.

Research sample

The research sample was chosen based on the intended use of the SenseToKnow app as an autism screening tool administered as part of a child's routine 18-24 month well child visit in pediatric primary care. Participants were representative of patients at one of four Duke University Health System (DUHS) pediatrics primary care clinics who were 17-36 months of age and did not have significant sensory or motor impairments, were not ill, and whose parents spoke English or Spanish. Racial and ethnic diversity of enrolled participants was greater for participants diagnosed with autism or developmental/language delay than for those with neurotypical development, with the clinical groups more closely matching the ethnic and racial distribution of the DUHS and Durham County, NC.

Sampling strategy

Consecutive recruitment and enrollment of Duke University Health System patients in pediatric primary care clinics and sample size providing adequate statistical power to test of the hypothesis that the sensitivity and specificity of the SenseToKnow app for autism detection relative to expert clinical diagnosis are > 70% (alpha=0.05).

Data collection

Data were collected during a well-child visit to primary care. Parents held their child on their lap while brief, engaging movies were presented on an iPad set on a tripod approximately 60 cm away from the child. Parents were asked to refrain from talking during the movies. The front camera embedded in the device recorded the child's behavior at resolutions of 1280 x 720, 30 frames per second. While children were watching the movies, their name was called three times by an examiner standing behind them at pre-defined timestamps. The children then participated in a game using their finger to pop a set of colored bubbles that moved continuously across the screen. App completion took <10 minutes. Study staff responsible for app administration were blind to the child's diagnosis and clinicians responsible for making the child's clinical diagnosis were blind to the SenseToKnow app's diagnostic classification.

Timing

The study was conducted from December 2018 to March 2020.

Data exclusions

No data excluded.

Non-participation

754 patients invited to participate; 214 declined; 513 eligible and consented; 475 (93% of patients enrolled) completed study measures.

Randomization

Diagnostic classification was made naive to results of the autism screening app results. Children were administered the Modified Checklist for Autism in Toddlers (M-CHAT-R/F), a parent survey querying different autism signs. Children with a final M-CHAT-R/F score of >2 or whose parents and/or provider expressed any developmental concern were provided a gold standard autism diagnostic evaluation based on the Autism Diagnostic Observation Schedule—Second Edition (ADOS-2), DSM-5 criteria checklist, and Mullen Scales of Early Learning 3 conducted by a licensed, research-reliable psychologist who was blind with respect to app results. Mean duration between app screening and evaluation = 3.5 months, which is a similar or shorter duration compared to real-world settings. Diagnosis of autism spectrum disorder required meeting full DSM-5 diagnostic criteria. Diagnosis of developmental or language delay without autism (DD-LD) was defined as failing the M-CHAT-R/F and/or having provider or parent concerns and having been administered the ADOS-2 and Mullen Scales and determined by the psychologist not to meet diagnostic criteria for autism and exhibiting developmental and/or language delay based on the Mullen Scales (scoring > 9 points below the mean on at least one Mullen Scales subscale; SD=10).

In addition, each participant's Duke University Health System electronic health record (EHR) was monitored through age 4 years to confirm whether the child subsequently received a diagnosis of either autism spectrum disorder or DD-LD. Following validated methods used by Guthrie et al., children were classified as autistic or DD-LD based on their EHR record if an ICD-9/10 diagnostic code for autism spectrum disorder or DD-LD (without autism) appeared more than once or was provided by an autism specialty clinic. 4 if a child did not have an elevated M-CHAT-R/F score, no developmental concerns were raised by the provider or parents, and there were no autism or DD-LD diagnostic codes in the EHR through age four, they were considered neurotypical. There were 2 children classified as neurotypical who scored positive on the M-CHAT-R/F who were considered neurotypical based on expert diagnostic evaluation and had no autism or DD-LD EHR diagnostic codes. Based on these procedures, 49 children were diagnosed with autism spectrum disorder (6 based on EHR only), 98 children were diagnosed DD-LD without autism (78 based on EHR only), and 328 children were considered neurotypical.

Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	<input type="text"/>
Research sample	<input type="text"/>
Sampling strategy	<input type="text"/>
Data collection	<input type="text"/>
Timing and spatial scale	<input type="text"/>
Data exclusions	<input type="text"/>
Reproducibility	<input type="text"/>
Randomization	<input type="text"/>
Blinding	<input type="text"/>

Did the study involve field work? Yes No

Field work, collection and transport

Field conditions	<input type="text"/>
Location	<input type="text"/>
Access & import/export	<input type="text"/>
Disturbance	<input type="text"/>

Reporting for specific materials, systems and methods

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.

Materials & experimental systems

n/a	Involvement
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern
<input checked="" type="checkbox"/>	<input type="checkbox"/> Plants

Methods

n/a	Involvement
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

Antibodies

Antibodies used	<input type="text"/>
Validation	<input type="text"/>

Eukaryotic cell lines

Policy information about [cell lines and Sex and Gender in Research](#)

Cell line source(s)	<input type="text"/>
Authentication	<input type="text"/>
Mycoplasma contamination	<input type="text"/>
Commonly misidentified lines (See ICLAC register)	<input type="text"/>

Palaeontology and Archaeology

Specimen provenance	<input type="text"/>
Specimen deposition	<input type="text"/>
Dating methods	<input type="text"/>
<input type="checkbox"/> Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.	
Ethics oversight	<input type="text"/>

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Animals and other research organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research, and [Sex and Gender in Research](#)

Laboratory animals	<input type="text"/>
Wild animals	<input type="text"/>
Reporting on sex	<input type="text"/>
Field-collected samples	<input type="text"/>
Ethics oversight	<input type="text"/>

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Clinical data

Policy information about [clinical studies](#)

All manuscripts should comply with the ICMJE [guidelines for publication of clinical research](#) and a completed [CONSORT checklist](#) must be included with all submissions.

Clinical trial registration	DUHSPro00085434
Study protocol	Duke University Protocol # Pro00085434
Data collection	Data was collected in Duke Primary Care pediatric clinics from December 2018 through March 2020.
Outcomes	Outcome was a diagnostic classification of autism spectrum disorder (DSM-5 criteria), language or developmental delay without autism, or neurotypical development as assessed via expert clinical evaluation and/or diagnostic codes in the patient's electronic health record.

Dual use research of concern

Policy information about [dual use research of concern](#)

Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

- | No | Yes |
|--------------------------|-----------------------------------------------------|
| <input type="checkbox"/> | <input type="checkbox"/> Public health |
| <input type="checkbox"/> | <input type="checkbox"/> National security |
| <input type="checkbox"/> | <input type="checkbox"/> Crops and/or livestock |
| <input type="checkbox"/> | <input type="checkbox"/> Ecosystems |
| <input type="checkbox"/> | <input type="checkbox"/> Any other significant area |

Experiments of concern

Does the work involve any of these experiments of concern:

- | No | Yes |
|--------------------------|------------------------------------------------------------------------------------------------------|
| <input type="checkbox"/> | <input type="checkbox"/> Demonstrate how to render a vaccine ineffective |
| <input type="checkbox"/> | <input type="checkbox"/> Confer resistance to therapeutically useful antibiotics or antiviral agents |
| <input type="checkbox"/> | <input type="checkbox"/> Enhance the virulence of a pathogen or render a nonpathogen virulent |
| <input type="checkbox"/> | <input type="checkbox"/> Increase transmissibility of a pathogen |
| <input type="checkbox"/> | <input type="checkbox"/> Alter the host range of a pathogen |
| <input type="checkbox"/> | <input type="checkbox"/> Enable evasion of diagnostic/detection modalities |
| <input type="checkbox"/> | <input type="checkbox"/> Enable the weaponization of a biological agent or toxin |
| <input type="checkbox"/> | <input type="checkbox"/> Any other potentially harmful combination of experiments and agents |

Plants

- Seed stocks
- Novel plant genotypes
- Authentication

ChIP-seq

Data deposition

- Confirm that both raw and final processed data have been deposited in a public database such as [GEO](#).
- Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

- Data access links
May remain private before publication.
- Files in database submission
- Genome browser session
(e.g. [UCSC](#))

Methodology

- Replicates
- Sequencing depth
- Antibodies
- Peak calling parameters
- Data quality
- Software

Flow Cytometry

Plots

Confirm that:

- The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).
- The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).
- All plots are contour plots with outliers or pseudocolor plots.
- A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

- Sample preparation
- Instrument
- Software
- Cell population abundance
- Gating strategy

Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.

Magnetic resonance imaging

Experimental design

- Design type
- Design specifications
- Behavioral performance measures

- Imaging type(s)
- Field strength
- Sequence & imaging parameters
- Area of acquisition
- Diffusion MRI Used Not used

Preprocessing

- Preprocessing software
- Normalization
- Normalization template
- Noise and artifact removal
- Volume censoring

Statistical modeling & inference

- Model type and settings
- Effect(s) tested
- Specify type of analysis: Whole brain ROI-based Both

Statistic type for inference

(See [Eklund et al. 2016](#))

Correction

Models & analysis

n/a | Involved in the study

Functional and/or effective connectivity

Graph analysis

Multivariate modeling or predictive analysis

Functional and/or effective connectivity

Graph analysis

Multivariate modeling and predictive analysis

