Diagnostic to Predict Autism in Newborn Blood Spots

Tech ID: 34368 / UC Case 2025-558-0

ABSTRACT

Researchers at the University of California, Davis have developed a diagnostic screen using DNA methylation and genetic variant analysis from newborn blood spots that enables early prediction of autism spectrum disorder (ASD) risk.

FULL DESCRIPTION

This technology leverages sex-specific DNA methylation markers and adaptive long-read sequencing on the Oxford Nanopore platform to analyze targeted genomic regions associated with ASD. By integrating allele-specific genetic variants and methylation patterns, coupled with machine learning predictive models, the screen accurately distinguishes newborns at an increased likelihood for ASD from those with typical development. Utilizing widely banked newborn blood spots, the method offers a non-invasive, objective, and sensitive approach for early ASD risk detection, enabling timely intervention and treatment planning.

APPLICATIONS

- Newborn screening programs for early ASD risk identification.
- Clinical diagnostics for neurodevelopmental disorder risk stratification.
- Pharmaceutical development and personalized treatment planning for ASD.
- Research tools for studying epigenetic and genetic mechanisms in ASD and related disorders.
- Public health monitoring of environmental exposures linked to neurodevelopmental risks.
- Genetic counseling and family planning services.
- Development of companion diagnostics integrated with therapeutic interventions.

FEATURES/BENEFITS

- Improves prediction accuracy for both males and females by applying sex-stratified DNA methylation markers.
- Enriches targeted ASD-associated genomic regions to 20-40x coverage using adaptive sequencing.
- Enables simultaneous detection of DNA methylation and genetic polymorphisms through long-read sequencing.
- Enhances predictive power for ASD risk assessment with machine learning models.
- Utilizes non-invasive, routinely collected newborn blood spots.
- Assesses ASD severity and informs personalized therapeutic strategies.
- Delivers a scalable and integrative system for comprehensive epigenomic analysis associated with neurodevelopmental disorders.

CONTACT

Prabakaran Soundararajan
psoundararajan@ucdavis.edu
tel: .

INVENTORS

- LaSalle, Janine M.
- Mouat, Julia

OTHER INFORMATION

KEYWORDS

adaptive sequencing, allele-specific methylation, DNA methylation biomarkers, long-read sequencing, machine learning prediction, newborn screening, sex-specific markers, x-linked genes, zinc finger methylation, autism spectrum disorder

CATEGORIZED AS

- **Biotechnology**
  - Genomics
- **Medical**
  - Diagnostics

- Eliminates reliance on behavioral assessments that delay ASD diagnosis.
- Overcomes limitations of current genetic tests that explain only a small fraction of ASD risk.
- Addresses sex-specific differences in ASD biology and diagnosis bias.
- Enables early molecular biomarker-based screening at birth.
- Improves understanding of gene-environment interactions in ASD risk and progression.
- Facilitates non-invasive, high-throughput newborn screening at population scale.

- Screening

RELATED CASES

2025-558-0

University of California, Davis
Technology Transfer Office
1 Shields Avenue, Mrak Hall 4th Floor,
Davis,CA 95616

Tel:
530.754.8649
techtransfer@ucdavis.edu
https://research.ucdavis.edu/technology-transfer/
Fax:
530.754.7620