

Results: “Gene’s” metrics are tracked, including total unique users, users by relationship to AS, users by country, thumbs up/down feedback, returning users, and conversion rate for other activities within the website, such as newsletter sign up, scheduling genetic counseling, or clicking on hyperlinks to newsletters or emails.

Between July and November 2025, “Gene” had 41 users in 16 different countries, with 25% of users in the USA. During this interval, users submitted 160 questions addressing a range of themes. Analysis showed that caregivers most frequently asked about the development of potential therapeutics for AS (30%), followed by inquiries about general AS characteristics (13%), FAST programs and events (17%), and genotype-specific topics (14%). Further evaluation of user engagement, question themes, and “Gene’s” impact is planned post-pilot at year’s end.

Conclusion: While “Gene” was created to deliver timely, trustworthy information to the AS community, uptake has been lower than anticipated. Barriers may include the requirements to register, compared with the ease of using general AI tools like ChatGPT and Google. Future use of AI within the website may incorporate deidentified registry data or other unique data sources to improve its benefit to caregivers.

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GraTeFUL Project: Genetic testing follow up quality project

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Introduction: Genetic testing technology has improved rapidly in the past 10 years. The breast cancer team (medical oncology, surgical breast oncology) at Henry Ford St. John Hospital in Detroit sees many patients who had genetic testing originally performed between 1998-2010, at the time of their initial cancer diagnosis. Broader multi-gene panel testing began to be offered around 2014 with more expansive gene interrogation. NCCN guidelines Version 1.2026 for breast cancers now include recommendations for patients to have updated multi-gene panel testing if they had single gene or limited testing in the past. A retrospective chart review done by our team in 2025 identified only 2.4% of patients had updated genetic testing. The objective of this quality improvement project was to improve physician awareness about updated recommendations for multi-gene panel testing in patients who previously tested negative.

Methods: An eight-question survey was administered at pre- and post-educational lectures. The survey assessed provider role (eg, oncology fellow, oncologist, breast surgeon, radiation oncologist, nurse practitioner, etc). Other questions evaluated which factors were reviewed when the provider saw a cancer patient for follow up, such as changes to their family history, advancements in genetic testing, and how likely a provider would refer a patient for updated genetic testing. An educational lecture with a slide deck overviews multigene testing advances, and pearls from clinical cases was given at the community hospital’s Breast Tumor Board, GI Tumor Board, Oncology Tumor Board, and Oncology Fellows Didactic Lecture. A Fact Sheet on Updated testing was also disseminated to clinical practices at our cancer center.

Results: Overall, 53 participants participated in this study including surgeons, oncologists, radiation oncologists, oncology fellows, surgical residents, and nurse practitioners/nurse navigators. Paired pre-post survey data were available for 21 participants. The following analysis is on the 21 participants; the McNemar chi-squared test was used.

Question 2 on the survey asked: “when seeing a patient with a personal history of cancer, which factors do you review?” Almost all participants checked a new cancer diagnosis for pre-post (20, 1 missing). After the lecture 5 out of 6 participants who did not check family history initially, did check this as a factor they would review, suggesting that the lecture impressed on participants the importance of reviewing family history. Advancements in genetic technology did not impress the participants given 12 did not check this as a factor before the lecture, and 10 did not check this following the lecture. Question 4 asked “do you counsel patients on updated genetic testing?” before the lecture 10 participants said NO, four of these participants checked yes after the educational lecture suggesting that the lectures were impactful for a provider/patient conversation on updates in genetics for their care. Question 6 asked do you provide patients with information (handout): Pre-survey 14 participants said no, after which 6 said yes and 8 still said no. The genetics team had provided a FACT sheet which may have contributed to more participants saying yes.

Conclusion: Updated genetic testing may identify new actionable genetic findings that can impact patients and their families. Ongoing education with providers is important so that in follow-up encounters they bring up the value of multigene testing to patients who had previously limited genetic testing. Because of the small sample size, generalizations are challenging, but continued education of providers on updates in genetic testing may be of value and potentially providing providers with handouts to serve as an icebreaker to discuss updated genetic testing for them and their families by be useful. The genetics team will continue to work on handouts that can be given to patients to aid in educating them about updated genetic testing.

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Building a natural history and patient registry platform for Coffin-Lowry syndrome (CLS): A roadmap for therapeutic readiness

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Introduction: Coffin-Lowry Syndrome (CLS) is a rare X-linked neurodevelopmental disorder caused by pathogenic variants in the RPS6KA3 gene, characterized by severe intellectual disability, distinctive craniofacial and skeletal findings, sensorineural hearing loss, and stimulus-induced drop attacks. No approved therapies exist, and natural-history data remains limited. The absence of a comprehensive, CLS-specific registry restricts progress toward therapeutic readiness and hinders the development of measurable clinically meaningful endpoints. To address this unmet need, a multi-partner initiative was undertaken to integrate existing datasets, establish a scalable registry framework, and define priority data elements to support future interventional trials.

Methods: A structured natural-history and registry development framework was derived from prior rare-disease registry models and expanded using multiple data sources. Foundational demographic information was provided by the Coffin-Lowry Syndrome Foundation (CLSF), which reported 295 families with CLS in the United States. Molecular data were incorporated from GeneDx, which contributed 196 genetically confirmed, de-identified cases. Additional genomic datasets from collaborating laboratories and clinical programs will be integrated as data-sharing agreements are finalized.

Coordination of Rare Diseases at Sanford (CoRDS), Sanford Research, Sioux Falls, South Dakota, agreed to contribute its CLS-related dataset and to participate as a registry-design partner. CoRDS data elements and infrastructure were reviewed to promote harmonization, allow linkage with external datasets, and accelerate development of a unified, patient-centric platform.

The proposed registry design incorporates both clinician-entered and patient/caregiver-reported data modules. Baseline data elements include demographics, genotype, developmental history, functional status, hearing and orthopedic assessments, history of stimulus-induced drop episodes, quality-of-life measures, and caregiver burden. Longitudinal follow-up options are structured as in-person or remote visits with interim digital diaries for high-burden features. Governance elements include a multi-stakeholder steering committee, standardized electronic case-report forms, a shared data dictionary, and harmonized outcome domains aligned with contemporary neurodevelopmental-disorder consensus recommendations.

Results: Initial aggregated data indicate a sizeable US CLS population suitable for registry-based natural-history characterization and eventual targets for trial recruitment. The 295 families reported by the CLSF demonstrate broad geographic distribution and high caregiver engagement, supporting feasibility of remote-first data capture. The 196 molecularly confirmed cases contributed by GeneDx provide an initial genotype reference dataset spanning a range of RPS6KA3 pathogenic variants. CoRDS contribution of CLS data allows evaluation of pre-existing patient-reported outcomes, diagnostic histories, and longitudinal information, supporting early harmonization of outcome measures and alignment of consent structures.

Next steps for registry development includes the formation of a steering committee including CLS families, industry, advocacy, and research scientists. A governance charter will be drafted to define the core and operational modules. This platform will allow quantification of disease progression, genotype-phenotype correlations, establishment of meaningful outcome measures, and a ready-to-go cohort for trial recruitment and external controls. The partnership model with advocacy organizations ensures the patient/family voice is central, enhances enrollment and retention, and promotes global reach. Ultimately, this roadmap positions CLS for therapeutic trial readiness, and serves as a blueprint for other ultra-rare neurodevelopmental disorders.

Conclusion: The unmet medical need in CLS: no approved therapies, limited natural-history data, heterogeneity of phenotype - makes the creation of a dedicated natural-history and registry platform essential. The proposed design, combined with strategic collaborations (CLSF, CoRDS, Sanford, CURE NDD, GeneDx), offers a feasible and impactful framework. Advancing this platform will enable the CLS community to move from descriptive science to interventional readiness and, ultimately, to improved outcomes for individuals and families. This registry framework will enable more rigorous natural-history definition, support early-phase clinical-trial design, and accelerate therapeutic development for individuals with Coffin-Lowry Syndrome.

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Impact of a research resource: A 5-year review of peer-reviewed publications utilizing samples from the NIGMS Human Genetic Cell Repository

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Introduction: The NIGMS Human Genetic Cell Repository (HGCR) was established by the NIGMS at the Coriell Institute for Medical Research in 1972 and it stores, processes, and distributes cell lines and DNA samples to researchers around the world. The HGCR collection currently comprises more than 12,000 fibroblast and lymphoblastoid cell lines, over 6,500 DNA samples, and almost 200 induced pluripotent stem cell lines. The primary goal of the HGCR is to stimulate and facilitate biomedical research, teaching, and diagnosis and prevention of human genetic diseases by establishing, maintaining, and distributing a repository of high quality, uncontaminated, well-characterized, and clinically documented cell lines and DNA from individuals with genetic disorders and chromosomal abnormalities, and from individuals from various geographical locations for studies on human diversity.

Methods: To better understand the specific uses of these specimens, we surveyed the peer-reviewed literature that cited the use of samples from the HGCR in studies published from 2019 until the present. Publications were identified for review by keyword search from the Google Scholar index and filtered for inclusion based on an explicit citation of an HGCR ID. Publication metadata that was analyzed was gathered from the article text, article keywords, and the content of the abstract.

Results: We identified over 1,800 publications, referencing HGCR samples more than 6,000 times. These publications originated from research groups in over 60 countries, representing both the academic and commercial sectors. They included research applications that ranged from technological improvements to basic science investigations, while also highlighting significant therapeutic and clinical breakthroughs, including the development of novel disease models, identification of molecular targets, and validation of potential treatment strategies.

Conclusion: Over time, these analyses will provide metrics on the value and impact of this resource and highlight evolving trends in research that utilize NIGMS HGCR samples. Understanding the research impact of its samples provides an opportunity to improve the HGCR and the diversity of samples in the collection with the aim of promoting impactful research and stimulating the advancement of scientific knowledge.

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