

positive for ANDV. Patient 8, a passenger who disembarked in Tristan da Cunha, began to have symptoms on April 28 and is currently receiving medical care; the illness in this patient is considered a probable case because of limited access to testing. Two additional confirmed cases (in France and Spain) were detected among persons evacuated from the ship in Tenerife, Spain; symptoms developed in these patients after they had disembarked from the ship — one on May 10 (Patient 9) and the other on May 12 (Patient 10). PCR testing in the patients in this outbreak has been performed in different laboratories with the use of locally validated assays in the respective countries.

Early sequencing of ANDV from the patients showed a high degree of similarity to previously reported sequences from Argentina. An initial zoonotic introduction before the departure of the ship from Argentina on April 1 is likely, because symptoms developed in Patient 1 on April 3, and he had a 3-month travel history to regions with known enzootic circulation of ANDV. No samples were available from this patient. Sequencing of samples from the subsequent patients showed a high level of genetic similarity, with a maximum of one detected single-nucleotide polymorphism per patient.³ Further epidemiologic analysis is needed to determine whether this outbreak resulted from one or more zoonotic spillover events or from human-to-human transmission, as was seen in the 2018 outbreak, which showed similar clustering and absence of viral genetic diversity.⁵

The situation is evolving, and the World Health Organization and European Center for Disease

Prevention and Control assess the global risk as low. The primary source of the outbreak is under active investigation, and experts who have experience with ANDV are collaborating to focus on exposures to South American rodents that occurred before the departure of the ship.

Andes Virus Outbreak Working Group*

Nazir Ahmed Ismail can be contacted at naziri@nicd.ac.za.

*The authors' full names, academic degrees, and affiliations are listed in the Supplementary Appendix, available at NEJM.org.

Disclosure forms provided by the authors are available with the full text of this letter at NEJM.org.

This letter was published on May 20, 2026, and updated on May 21, 2026, at NEJM.org. It was also published in Public Health Alerts at evidence.NEJM.org.

1. South African National Department of Health. Health Department confirms the deaths of tourists from severe acute respiratory infection. May 4, 2026 (<https://www.health.gov.za/wp-content/uploads/2026/05/Health-Department-confirms-the-deaths-of-international-tourists-from-severe-acute-respiratory-infection-04-May-2026.pdf>).
2. World Health Organization. Disease outbreak news: hanta-virus cluster linked to cruise ship travel, multi-country. May 8, 2026 (<https://www.who.int/emergencies/disease-outbreak-news/item/2026-DON600>).
3. Palacios G, Hoxha A, Oude Munnink B, et al. Preliminary analysis of Orthohantavirus andesense virus sequences from a cruise-ship related cluster, May 2026. *Virological*, May 10, 2026 (<https://virological.org/t/preliminary-analysis-of-orthohantavirus-andesense-virus-sequences-from-a-cruise-ship-related-cluster-may-2026/1029>).
4. World Health Organization. Disease outbreak news: hanta-virus cluster linked to cruise ship travel, multi-country. May 13, 2026 (<https://www.who.int/emergencies/disease-outbreak-news/item/2026-DON601>).
5. Martínez VP, Di Paola N, Alonso DO, et al. "Super-spreaders" and person-to-person transmission of Andes virus in Argentina. *N Engl J Med* 2020;383:2230-41.

DOI: 10.1056/NEJMc2606496

Clusters of Concern — Spatial Link between Childhood Undervaccination and Measles Outbreaks in South Carolina

TO THE EDITOR: Vaccination coverage in South Carolina has declined over the past 5 years, a reduction that has increased concern about susceptibility to outbreaks of vaccine-preventable disease. During the 2025–2026 school year, the state has had the largest measles outbreak since the elimination of measles in the United States was declared in 2000.¹ As of April 8, 2026, South Carolina had 997 confirmed cases of measles, of which 95.3% were reported to be among unvaccinated residents.² Of these cases, 90.8% occurred

in children (<18 years of age).² Thus, school-based vaccination patterns provide a reasonable indicator of local pediatric susceptibility in the communities where transmission has occurred.

In the United States, two-dose MMR (measles, mumps, and rubella) vaccination coverage above 95% is considered necessary for community protection against measles. We conducted a spatial analysis to identify clusters of undervaccinated students (i.e., those who had no documentation of having received the required school-entry vaccines)

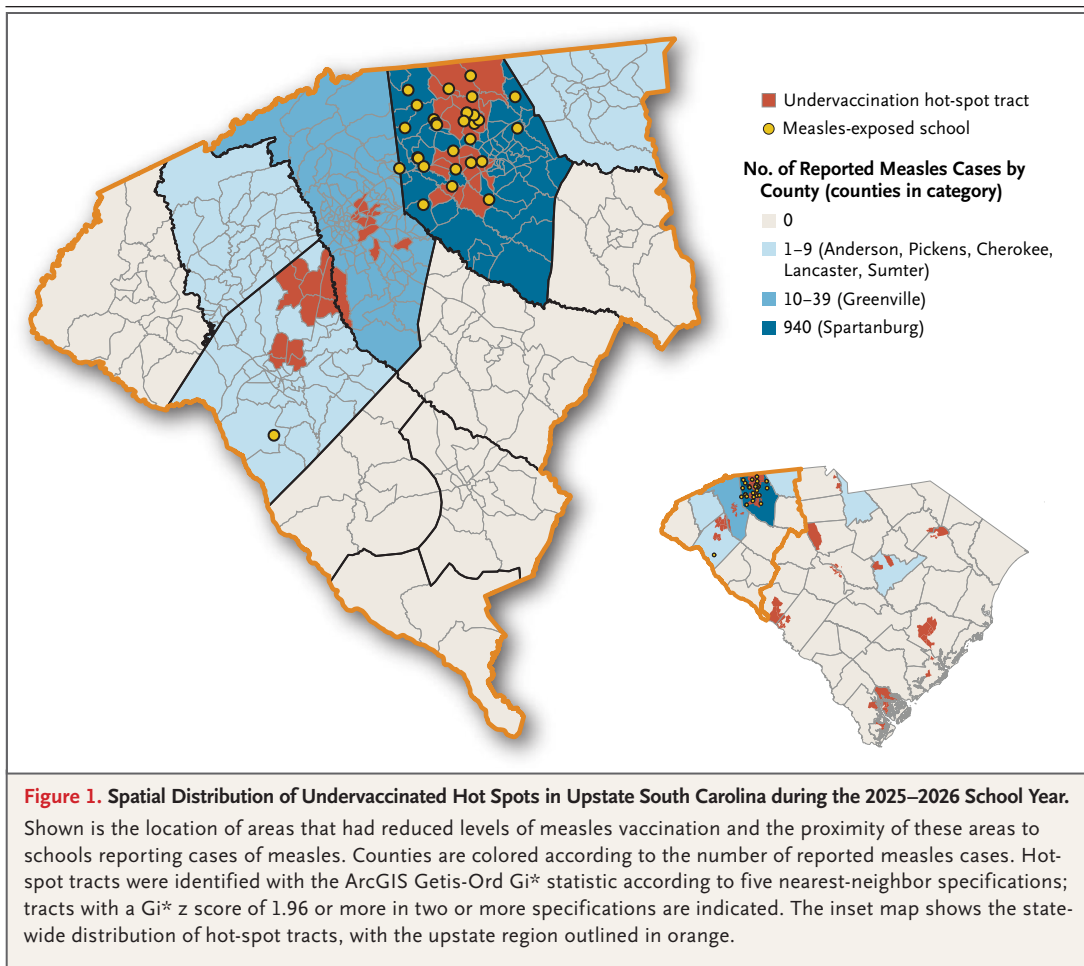
and assessed the geographic overlap between the identified clusters and schools with documented measles exposures.

Using school immunization data from the 2025–2026 school year, we estimated the number of undervaccinated students in each census tract, with spatial hot spots identified with the ArcGIS Getis-Ord G_i^* statistic, which is used to calculate a z score for each grid cell or unit of spatial analysis. Analyses were repeated across five nearest-neighbor specifications, with tracts exceeding the prespecified threshold (G_i^* z score, ≥ 1.96) in two or more specifications classified as hot spots. Details regarding the methods that were used in this study are provided in the Supplementary Appendix, available with the full text of this letter at NEJM.org.

The local Getis-Ord G_i^* analysis identified 109 of 1319 census tracts (8.3%) as hot spots (Fig. 1). The number of census tracts that were identified as persistent hot spots increased from 106 in

2024–2025 to 109 in 2025–2026. Spartanburg County (population, 380,000) was identified as the dominant cluster, containing 27 of 109 hot-spot tracts (24.8%). Of the 997 reported measles cases in the state, 940 (94.3%) occurred in Spartanburg County; of the 30 schools statewide with documented measles exposures, 28 (93%) were in Spartanburg County. The mean vaccination coverage was lower in the schools with reported measles cases (coverage, 83.9%) than in those with no reported cases (coverage, 92.9%), a mean difference of 9 percentage points (95% confidence interval [CI], 4.0 to 14). The locations of the 30 schools with measles exposure were not uniformly distributed: 26 (87%) were located within or adjacent to undervaccinated hot-spot tracts (Fig. 1).

These findings indicate that undervaccination in South Carolina is concentrated in geographic clusters. The spatial alignment between hot-spot tracts and measles-exposed schools suggests that



geographic clustering of undervaccinated students may serve as a precursor to outbreak activity. The concentration of documented measles exposures in Spartanburg County may reflect the geographic overlap between clusters of undervaccination and a close-knit community that is concentrated in that area, whereas the geographic separation of other undervaccinated hot spots from the Spartanburg cluster may have prevented measles from spreading more broadly. Other possible contributors to geographic containment (e.g., public health response) were not examined. With measles outbreaks active in multiple states, proactive spatial surveillance of high-risk clusters may support earlier, more targeted public health interventions to reduce barriers to immunization,³ prevent further clustering,⁴ and enhance outbreak-control efficiency.⁵

Emily A. Serman, Ph.D.,¹ Brian Witrick, Ph.D.,¹ and Lior Rennert, Ph.D.¹

¹Clemson University, Clemson, SC.

Lior Rennert can be contacted at liorr@clemson.edu.

Supported by a grant (NU38FT000011) from the Center for Forecasting and Outbreak Analytics of the Centers for Disease Control and Prevention and by a grant (R01LM014193) from the National Library of Medicine of the National Institutes of Health.

Disclosure forms provided by the authors are available with the full text of this letter at [NEJM.org](https://www.nejm.org).

Data for South Carolina School Vaccination Coverage are available from the South Carolina Department of Public Health at https://dph.sc.gov/sites/scdph/files/2025-12/45_Day_Report_25-26_20251230.pdf. Data regarding measles-exposed schools are available from the authors upon request.

This letter was published on May 20, 2026, at [NEJM.org](https://www.nejm.org).

- Centers for Disease Control and Prevention. History of measles — measles elimination in the United States. May 9, 2024 (<https://www.cdc.gov/measles/about/history-of-measles.html>).
- South Carolina Department of Public Health. Measles dashboard. April 2026 (<https://dph.sc.gov/diseases-conditions/infectious-diseases/measles-rubeola/measles-dashboard>).
- Albers AN, Thaker J, Newcomer SR. Barriers to and facilitators of early childhood immunization in rural areas of the United States: a systematic review of the literature. *Prev Med Rep* 2022;27:101804.
- Gromis A, Liu K-Y. Spatial clustering of vaccine exemptions on the risk of a measles outbreak. *Pediatrics* 2022;149(1):e2021050971.
- Gastañaduy PA, Banerjee E, DeBolt C, et al. Public health responses during measles outbreaks in elimination settings: strategies and challenges. *Hum Vaccin Immunother* 2018;14:2222-38.

DOI: 10.1056/NEJMc2604004

Response to Crizotinib in Infantile Fibrosarcoma with *TFG::MET* Gene Fusion

TO THE EDITOR: Infantile fibrosarcoma is a rare pediatric soft-tissue sarcoma of early childhood, driven mostly by *ETV6::NTRK3* fusion.¹ We report a locally invasive case in the left scapula and forearm without an upfront limb-sparing surgical option. A *TFG::MET* fusion was present, a finding that expands the known genomic landscape of infantile fibrosarcoma. Our case highlights the diagnostic importance of comprehensive molecular profiling and the therapeutic potential of tyrosine kinase inhibitors (TKIs).

An otherwise healthy male infant was antenatally diagnosed with a left scapular lesion at 29 weeks' gestation. Postnatal imaging showed a localized large, lobulated, soft-tissue lesion with ¹⁸F-fluorodeoxyglucose (FDG) avidity (Fig. 1A, 1C, and 1E). Histopathological analysis showed a highly cellular spindle-cell neoplasm that lacked the characteristic immunophenotypic profile of infantile fibrosarcoma (Fig. 1B), and fluorescence in situ hybridization was negative for *ETV6* rearrangement. RNA sequencing detected a 5'-to-3' in-frame fusion of *TFG* exon 4 to *MET* exon

15, which confirmed the diagnosis of *TFG::MET* fusion-positive infantile fibrosarcoma (Fig. 1D).

Given the need for a forequarter amputation to achieve a resection with microscopically clear margins (R0), chemotherapy (vincristine-dactinomycin) was initiated, with progression after three cycles. Cyclophosphamide was added, with minimal benefit; interval-compressed (dose-dense) chemotherapy with vincristine, doxorubicin, and cyclophosphamide alternating with ifosfamide and etoposide did not lead to an adequate response for limb-sparing surgery. Compassionate access to crizotinib, a multitargeted TKI that inhibits anaplastic lymphoma kinase (ALK), mesenchymal-epithelial transition factor (MET), and ROS1, was obtained. Treatment with crizotinib was administered for 10 months and resulted in a rapid tumor response, which was followed by limb-sparing surgery that achieved complete resection of the remaining 2-cm lesion. Treatment with crizotinib was not restarted postoperatively, and a sustained remission was shown at 12 months after resection (Fig. 1F).