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[OA]Open Access paper

Cover The SARS-CoV-2 outbreak in New York City in the spring of 2020 was notable for its rapid onset and extent, infecting over a fifth of the population in just a few months. The lack of large-scale diagnostic screening in February left unrecorded the origin and early progress of the outbreak, and fully 70% of tests in the region returned positive for the virus at the end of March, indicating an underestimate of outbreak extent. In this issue, sequencing 864 viral genomes from cases in the NYU Langone hospital system demonstrates that SARS-CoV-2 had been repeatedly introduced and was spreading widely throughout the region well in advance of its recognition. This work suggests that sequencing can play a key role in viral surveillance to avoid similarly underestimating future pandemics. (Cover artwork by Molly Ferguson, http://www.mollyfergusonart.com/. [For details, see Maurano et al., pp. 1781–1788.])