

New paper in GigaScience: sequencing and the single-cell

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Feature Image

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Single Cell SequencingThe precipitous [drop in the price](#) of next generation sequencing coupled with its increasing sensitivity has opened up whole new areas of research, one of the most interesting in recent years being the advent of single-cell sequencing. [Combining advances](#) in flow-sorting of cells, whole genome amplification and the latest sequencing technologies is now allowing researchers to study tumor evolution on a single-cell level. As cancers develop from a growing mass of mutated heterogeneous cells, this new technique allows novel insight into a cancer's developmental history, and importantly for the patient, development of drug resistance. Throwing light on previously unstudied aspects of cancer biology and the huge potential this has for novel and targeted therapies has lead to a huge amount of recent interest, very clearly seen at the recent Biology of Genomes meeting (see [this](#) write-up in *Science*), and by the NIH planning a [Single Cell Analysis](#) roadmap initiative that will spur more researchers to join the field.

Being so topical we are pleased this week to [publish](#) our first single-cell analysis study, on single-cell deep exome sequencing of 66 tumor cells from a muscle-invasive bladder transitional cell carcinoma. Following from their recent single-cell studies of [kidney](#) and [bone-marrow](#) cancers published in *Cell*, Yingrui Li and colleagues present a new method for assessing bladder cancer evolution at a cell-population level for our journal, the first time a single-cell genome analysis of bladder cancer has been published. Demonstrating a new method for assessing bladder cancer evolution at a cell-population level, unlike *Cell*, who are one of the [few journals](#) to have raised objections about pre-publication release of citable data, to maximize the reproducibility and reuse of the data in this study immediately after passing peer-review we [published](#) 267GB of the supporting data in our [GigaDB](#) database (on top of the raw data submitted to the SRA) via a DOI that was then integrated and cited in the paper. Further promoting transparency all of the peer-reviewed reports are available for view from the [pre-publication history](#) link associated with the article. Following our [launch](#) last month, if you have a similar scale or scope of research you would like us to consider, BGI is generously [covering](#) the open [access article processing charges](#) for the journal's first year, so please contact us at editorial@gigasciencejournal.com or alternatively submit a manuscript [here](#).

Further Reading

1. Li, Y et al., Single-cell sequencing analysis characterizes common and cell-lineage-specific mutations in a muscle-invasive bladder cancer *GigaScience* 2012, **1**:12

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