to better assess cell lines' validity for future use in this and in other types of cancer research.

Computational biologists Nikolaus Schultz and Rileen Sinha, and biochemist Silvia Domcke, focused their review on high-grade serous ovarian cancer (HGSOC), the most commonly diagnosed and frequently studied subtype of ovarian cancer. Using datasets from The Cancer Genome Atlas and the Cancer Cell Line Encyclopedia, which detail and define the genomic features of numerous clinical samples and cell lines, the team analyzed and then ranked several cell lines by their genomic similarities to tissue samples and, in doing so, uncovered multiple discrepancies between the cell lines and actual human tumors.

"Our review showed that the two most utilized cell lines, accounting for almost 60 percent of all published research studies, do not resemble HGSOC well at all," explained Dr. Schultz, the paper's lead author. "The problem with this is, investigators assumed they were studying high-grade serous ovarian cancer, when in reality they were looking at something else. So conclusions drawn from this work might be misleading."

Cancer cell lines are generated and grown indefinitely in laboratories around the world, but are ultimately derived from human tumors. For the past several decades, they have been the most popular model for the

study of cancer because they are inexpensive and easy to replicate. However, the origin of some cell lines is not well established, and through years in culture, they can acquire additional changes, making them less desirable.

“With the explosion of genomic data now at our fingertips and the potential for more to become available, it’s our hope that this approach can be used by our colleagues to choose optimal cell lines, as we do expect similar discrepancies in other tumor types,” said Dr. Schultz. “Overall, we believe these findings should greatly benefit the study of cancer.”

The study’s co-authors are Silvia Domcke, Rileen Sinha, Douglas Levine, Chris Sander, and Nikolaus Schultz. The work was supported in part by a grant from the National Cancer Institute under award number NCI-U24CA143840.