Karolinska University hospital is associated with Karolinska Institute, which is one of the leading biomedical universities in the world (see, for instance, QS ranking). The hospital and the institute perform basic and translational research in a wide array of diseases using state-of-the-art technologies.

I am associated with Radiumhemmet, which is the cancer treatment and radiotherapy research institution within the hospital. My postdoctoral research is funded by Wallenberg Foundation and Cancerfonden Association. I am part of Prof. Jonas Bergh group (http://ki.se/en/onkpat/jonas-berghs-group), which is one of the leading breast cancer groups in the EU, performing cutting-edge research in both basic and translational breast cancer.

My main research deals with analyzing tumor evolution patterns in metastatic breast cancer using next generation DNA- and RNA-sequencing data extracted from patient material. I, along with my colleagues, have demonstrated using genomic data that the route to distant metastasis is pre-dominantly via hematogenous route and that axillary lymph node has minimal role in seeding distant metastasis. Our findings have been accepted in Journal of Clinical Oncology. Currently, I am looking into intra-tumor heterogeneity patterns within different metastatic lesions in breast cancer and its implications for targeted therapy in terms of actionable mutations. Moreover, I am also assisting my team-members and collaborators in statistical analysis and visualization of their biomedical data related to precision medicine, drug development and in-situ measurement of drug target engagement.

Following are some of the accepted papers from above research. My previous research papers can be found at my Google Scholar page (https://scholar.google.se/citations?user=HjM0XDoAAAAJ)

1. Ikram Ullah, Govindasamy-Muralidharan Karthik, Amjad Alkodsi, Una Kjallquist, Gustav Stalhammar, John Lovrot, Nelson-Fuentes Martinez, Jens Lagergren, Sampsa Hautaniemi, Johan Hartman, and Jonas Bergh. Evolutionary history of metastatic breast cancer reveals minimal seeding from axillary lymph-nodes – accepted in Journal of Clinical Investigation (JCI) (impact factor 12.784)
2. Una Kjallquist, Rikard Erlandsson, Nicholas P Tobin, Amjad Alkodsi, Ikram Ullah, Gustav Stalhammar, Eva Karlsson, Thomas Hatschek, Johan Hartman, Sten Linnarsson, Jonas Bergh. Exome sequencing of primary breast cancers with paired metastatic lesions reveals metastasis-enriched mutations in the A-kinase anchoring protein family (AKAPs) – accepted in BMC Cancer (impact factor 3.288)
3. Karthik Govindasamy Muralidharan, Mattias Rantalainen, Gustav Stalhammar, John Lovrot, Ikram Ullah, Amjad Alkodsi, Ran Ma, Lena Wedlund, Johan Lindberg, Jan Frisell, Jonas Bergh, Johan Hartman. Intra-tumor heterogeneity in breast cancer has limited impact on transcriptomic-based molecular profiling – accepted in BMC Cancer (impact factor 3.288)