Ovarian cancer is the fifth largest cause of cancer-related deaths in women. The vast majority of ovarian cancers are epithelial ovarian cancers and high-grade serous carcinoma (HGSC) is the most common and most lethal epithelial ovarian cancer. In the last 10 years, it has been recognized that the cell of origin of most HGSCs is within the fallopian tube epithelium, instead of the ovarian surface epithelium. However, the early events in disease progression still remain poorly defined, because HGSC is usually diagnosed at advanced stages and lack of proper animal models recapitulating human disease progression. My group has recently developed a unique strategy for generating mouse ovarian cancer models, which is a combination of in vivo fallopian tube electroporation, Cre-mediated lineage tracing and CRISPR-mediated gene modifications. As proof-of-principle, we generated a highly metastatic HGSC model by targeting four tumor suppressor genes, Lkb1, Brca1, Tp53 and Pten. The female mice targeted these four genes generated ovarian tumors within 5 months after electroporation and peritoneal metastasis within 6 months. After 6 months, ascites formation was observed in two third of those females. Interestingly, similar to human ovarian cancer patients, we observed two metastatic patterns, miliary and non-miliary. Our unique strategy has several advantages over the current mouse cancer models; 1) Saving time and costs to generate mouse models because no breeding is required to generate cohorts; 2) High flexibility permitting many gene combinations/modifications and host genetic backgrounds to be tested; 3) control over the size and area of targeted cells (the low-frequency mosaic transfection pattern better recapitulates the sporadic nature of human tumorigenesis); 4) The ability to track genetically modified cells by fluorescent reporters, permitting analysis of tumor initiation and early metastasis; 5) Highly metastatic mouse models with immune competency.