**The role of methylation in promoter regions of tumor suppressor genes in chemotherapy response.**

DNA methylation is an epigenetic mechanism that can alternate gene expression, acting exclusively at CpG dinucleotides. Most of these dinucleotides have been depleted from the mammal genome over evolution, but short regions called CpG islands, can be found in the promotor regions of almost half of the genes. Whilst normally unmethylated, hypermethylation of these regions in cancer can lead to inactivation of tumor suppressor genes and thereby tumor progression.

Our aim is to explore the potential epigenetic events that can contribute to the acquired resistance to chemotherapy. In the present projects, we used massive parallel sequencing and in-house methylation sequencing bioinformatics pipeline to analyze promoter regions of 283 selected tumor suppressor genes. We studied the differentially methylated CpG’s in these regions under different treatment regiments to assess the potential effect of these drugs on methylation profiles. By combining sequencing data, gene expression data and methylation profiles we can further explore, if methylation can be the cause of drug resistance/sensitivity in samples, where there’s no obvious explanation among the detected genetic mutations.

The role of genetic and epigenetic alternations in expression of tumor suppressor genes during cancer progression can help us better understand the mechanisms by which tumor cells develop resistance to drugs and thus better approach towards cancer therapy.