We are interested in DNA repair and its link to tumorigenesis.

In particular, we study BRCA2, a tumor suppressor involved in DNA repair by Homologous Recombination. Mutations in this gene cause susceptibility to breast and ovarian cancer.

**Homologous Recombination**

In humans, the central player of the HR process is RAD51; it catalyzes the homology search in the intact copy of the sister chromatid and the strand exchange required to repair the DNA lesion. Through its interaction with RAD51, BRCA2 controls RAD51 function by locating it to the DSB (Figure 1). Thus, defects in BRCA2 lead to genomic instability, a hallmark of tumorigenesis.

**Figure 1: Our current model for the role of BRCA2 in homologous recombination**

We use biochemical, cell biology and recently also genomic and proteomics approaches to understand BRCA2’s function in HR and other pathways. Our approach consists on searching for new BRCA2 protein partners and studying the phenotype of BRCA2 mutations identified in breast cancer patients to elucidate the mechanisms that contribute to tumorigenesis in a BRCA2 or HR defective background.

The main projects of the lab include:

1) **Identifying new functional domains of BRCA2**: BRCA2 comprises 3,418 aa. This protein is known to interact with several partners such as RAD51 or PALB2 however; there are a priori “unstructured” regions of the protein that are mostly unexplored. We have used a proteomic approach to identify novel interacting partners of the unstructured part of the protein, the N-terminal region, enriched under DNA damage. This strategy can reveal functions in other RH related processes such as cell cycle regulation, chromatin remodeling, etc.
Importantly, these interactions may be used as targets to develop new anticancer therapy tools, which we also plan to exploit.

We have recently revealed a second DNA binding site in BRCA2 that promotes the recombination activity of RAD51 (**Figure 2**). This study opens new questions about the interplay of the two DNA binding domains in cells.

**Figure 2.** Working model for the role of the N-terminal DNA binding domain of BRCA2 (NTD).

2) **Functional characterization of BRCA2 missense variants identified in breast cancer patients.** Using an interdisciplinary and systematic approach our goal is to accurately evaluate the impact of variant of missense variants of unknown clinical significance (VUS) on BRCA2 function and to determine their clinical relevance for the benefit of patients. For example, in a collaborative work, we have identified BRCA2 hypomorphic mutations that confer moderate risk of breast cancer. In turn, studying the phenotype of these variants will also serve to find new functions of BRCA2 protein (objective 1).

3) **BRCA2 haploinsufficiency and cancer predisposition**

Inactivating germline monoallelic mutations in the BRCA2 gene are associated with an increase risk in breast cancer. However, the precise link between BRCA2 mutation and tumorigenesis remains elusive. We are trying to address this question using functional genomics.

Thus, we expect to contribute to identify the genetic signature(s) that predispose to tumour formation in a BRCA2-mutation context.

In addition, as part of the PanCanRisk consortium, we plan on using the same tools to uncover
variants predisposing to cancer in other genes and regulatory regions.