iProFun:

**An *i*ntegrative analysis tool to screen for *Pro*teogenomic *Fun*ctional traits perturbed by DNA copy number alterations (CNA) and DNA methylation**

The goal of **iProFun** is to

* characterize functional consequences of DNA copy number and methylation alterations in tumors
* facilitate screening for cancer drivers contributing to tumor initiation and progression, since CNAs and DNA methylations that preserve functional consequences are more likely to be cancer drivers.

This package implement iProFun using 2 main functions. The primary function is (surprise!) iProFun, which first fit gene-level multiple linear regression to obtain summary statistics and then run Primo for detecting joint associations of DNA alternations with multi-omics traits. False discovery rate assessment is supported by iProFun\_permutate function. A full description of the method can be found in our [paper](https://www.biorxiv.org/content/early/2018/12/06/488833).

Reference:

Contact:

Acknowledgement: