

Method to obtain useful data for the diagnosis, prediction or prognosis of colorectal cancer (SAS-FRD-SERGAS-USC-CIBER-UMA)

Obesity has been established as a relevant modifiable risk factor in the onset and progression of colorectal cancer (CRC). This relationship could be mediated by an epigenetic regulation.

The effects of excess body weight on the DNA methylation profile of CRC using a genome-wide DNA methylation approach and to identify an epigenetic signature of obesity-related CRC has been studied. The analysis has revealed statistically significant differences at 299 CpG sites, and they are mostly characterized as changes towards CpG hypermethylation occurring in the obese group. The 152 identified genes are involved in inflammatory and metabolic functional processes. Among these genes, novel genes have been identified as epigenetically regulated in CRC depending on adiposity.



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Relevant publications

Identification of an epesignature of human colorectal cancer associated with obesity by genome-wide DNA methylation analysis.

Int J Obes (Lond). 2018 May 1. doi: 10.1038/s41366-018-0065-6.

