Title: Analysis of colorectal cancer microenvironment in the FinCRC cohort

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Abstract

Colorectal cancer (CRC) is the third most common and the second most lethal cancer in the world. Despite curative-intent surgery of localized stage I-III cancer, 5-33% of CRCs get a local recurrence or distant metastases. The CRC tumor microenvironment (TME) contains different cell types and structures, and actively affects the behavior of the disease. Previous data show differences in respect to tumor and lymph node status, mismatch repair, and tumor location (right-sided colon, left-sided colon or rectum, respectively). In this project, we study how the TME is associated with these factors in the Finnish CRC study.

We stained in total 531 tissue microarray (TMA) cores from 81 curatively resected patients and from metachronous metastases of 6 relapses with multiplex immunohistochemistry. Staining data of 14 protein markers from each tissue section was used to identify cancer cells and 11 different non-malignant cell types with a machine learning-based cell classifier.

Results show the TME differing based on the original tumor location. Primaries located on the right side have a higher density of CD163- macrophages compared to that of the left side and rectum ($p<0.05$ and $p<0.01$ Wilcoxon, respectively). Cell distance analysis showed that the

CD163- macrophages in the tumors originating from the right side interact more with CD8+ T-cells, compared to those located on the left side and rectum (both $p<0.05$, Wilcoxon). Analyses of larger cellular neighborhoods are still ongoing to discover new prognostic and predictive tools for clinical practice.