**Supplementary Figure:**

**Supplementary Figure 1 : Design and use of the Microenvironment Cell Populations (MCP)-counter algorithm**

**a)** Heatmap representation of the expression of selected transcriptomic markers underlying MCP-counter scores in transcriptomic profiles corresponding to microenvironment cell populations. These scores have been quantitatively validated for their ability to predict the abundance of the corresponding cell population from the gene expression profile of a cellularly heterogeneous sample. **b)** MCP-counter is implemented as an R package, which takes as input transcriptomic profiles of cellularly heterogeneous tissues, such as tumors. It first maps the previously-identified transcriptomic markers to the assayed gene-expression features (as illustrated here for the ‘discovery’ CIT CRC cohort, and summarize them to output a score per cell population per sample. These scores can then be used to compare samples against each-others and to determine whether a group of samples is more highly infiltrated by a given cell type than another group of samples.

**Supplementary Tables:**

**Table S1 : Immune, and other stromal samples analyzed**

**Table S2 : Colorectal cancer samples constituting the 3 cohorts analyzed, along with their molecular subgroups**

**Table S3 : Samples from the Cancer Cell Line Encyclopedia**

**Table S4 : Antibodies used for immunohistochemical analyses**

**Table S5 : Consensus Molecular Subgroup-level statistics on each MCP-counter abundance estimates**

**Table S6 : Levels of expression of genes related to inflammation, angiogenesis and immunomodulation in CRC cohorts**