Figure S1



Figure S1. The *EMILIN-2* **gene is methylated in CRC.** Epigenetic landscape of the *EMILIN-2* gene and clinical and molecular parameters characterizing the COAD cohort (477 colorectal cancer patients) from the Cancer Genome Atlas (TCGA), as assessed by MEXPRESS (accessed on 12 March 2021). The analyses are in relation to the levels of *EMILIN-2*. The Pearson correlation coefficients are reported on the right and highlight a significant correlation between the expression of the *EMILIN-2* gene, the methylation probes, and the corresponding clinical parameters.

Figure S2



EMILIN-2



Figure S2. The expression of EMILIN-2 is variable among CRC patients. Stratification of the patients of the TCGA COAD cohort based on the EMILIN-2 protein levels; molecular and clinical parameters are indicated and detailed on the bottom. The heat map shows the levels of the 2000 most variable genes.

Figure S3



Figure S3. The higher tumor rate in *Emilin-2^{-/-}* mice does not hinge on the activation of the Wnt/β-Catenin pathway. A, Representative Western blot analyses (left) and quantification (right) of β-catenin activation in the healthy (h) and tumoral (t) colonic mucosa of *wild type* (wt) and *Emilin-2^{-/-}* (E2^{-/-}) mice; n=3. **B**, Relative expression levels of c-Myc (left) and Cyclin D1 (CycD1, right) in the healthy and tumoral colonic mucosa of *wild type* (wt) and *Emilin-2^{-/-}* (E2^{-/-}) mice. **C**, Representative images (left) and quantification (right) of the Ki67 stainings performed on adenomas developed in *wild type* (wt) and *Emilin-2^{-/-}* (E2^{-/-}) mice. Blue: nuclei; green: Ki67, scale bar=50 µm. Graphs represent the mean \pm SD of at least three independent experiments; in A and B, *P* values were obtained using the one-way ANOVA test and in C the paired Student's t-test; **P*<0.05, ***P*<0.01, n.s.: *P*>0.05.