Captions for Supplementary Tables for

“Patients with mesenchymal tumours and high

*Fusobacteriales* prevalence have worse prognosis in

colorectal cancer (CRC)”

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**Data and code availability:** Datasets and source code will be publicly available and archived upon publication at Zenodo ([https://10.5281/zenodo.4019142](https://10.5281/zenodo.4019142)).
Transcriptomic-dependent *Fn/Fusobacterales* impact.

**Supplementary Table 1.**

Clinico-pathological and demographic characteristics of the CRC patients included in this study (“Overall”) and grouped by cohort, namely “in house Taxonomy” and “TCGA-COAD-READ”. For continuous variables, median, interquartile range, and statistical significance (P-value) determined by Kruskal-Wallis tests are reported. For categorical values, number, and percentage of cases by level and statistical significance (P-value) determined by χ² tests are reported.

**Supplementary Table 2.**

Patient-level bacterium data for cases of the Taxonomy and TCGA-COAD-READ cohort. *Fn* load measured by qPCR for patients of the Taxonomy cohort is available in the sheet “Taxonomy cohort (n=140)”. Relative abundance of *Fusobacterales* and higher resolution taxonomic ranks (family, genus and species) including the *Fn* species for the patients in the TCGA-COAD-READ cohort is available in the sheet “TCGA-COAD-READ cohort (n=605)”. For the TCGA-COAD-READ cohort, genuses/species with an average relative abundance lower than 0.05 were aggregated as “Other”.

**Supplementary Table 3.**

Association between mutational status and *Fusobacterales* relative abundance in the TCGA-COAD-READ patients. Statistical significance was assessed by χ² independence tests and χ² statistics, unadjusted- and FDR-corrected mod-likelihood P-values are reported for each mutation that was either selected *a priori* or was found to be statistically significant altered when comparing *Fusobacterales*-low vs. -high patients (75th percentile cut-off) of the TCGA-COAD-READ cohort.

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**Supplementary Table 4.**

Association between recurrent copy number aberrations identified by GISTIC analysis when comparing *Fusobacteriales*-low vs. -high patients (75th percentile cut-off) of the TCGA-COAD-READ cohort.

**Supplementary Table 5.**

Association between gene expression profiles and *Fusobacteriales* relative abundance in the TCGA-COAD-READ patients was assessed by Spearman correlation. Correlation coefficient R, corresponding 95% confidence intervals, unadjusted- and FDR-corrected P-values are reported for each protein that was found to be statistically significant altered in the TCGA-COAD-READ cohort.

**Supplementary Table 6.**

Association between protein expression profiles and *Fusobacteriales* relative abundance in the TCGA-COAD-READ patients was assessed by Spearman correlation. Correlation coefficient R, corresponding 95% confidence intervals, unadjusted- and FDR-corrected P-values are reported for each protein that was found to be statistically significant altered in the TCGA-COAD-READ cohort.

**Supplementary Table 7.**

Un-adjusted and adjusted Cox regression models for patients of the TCGA-COAD-READ cohort. Cox regression models were fitted with an interaction term between *Fusobacteriales* (high vs. low, using the 75th percentile relative abundance as cut-off) and mesenchymal status.

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(mesenchymal vs. non-mesenchymal). Adjusted model 1 and 2 were fitted including precision variables. Model 1 used as adjustment covariates key clinical-pathological characteristics, namely age (continuous), stage (categorical, I to IV), tumour location (categorical, colon vs. rectum) and sex (categorical, male vs. female). Model 2 used as adjustment covariates a more extensive set (i.e. super-set) of clinico-pathological characteristics additionally including history of colon polyps (categorical, yes vs. no) and history of other malignancy as comorbidities.

Supplementary Table 8.

Detailed statistical output (coefficients and P-values) of logistic models 1 (Fusobacteriales~gene/signature) and 2 (Fusobacteriales~gene/signature:molecular subtype) fitted for a set of hypothesis-driven gene/signature profiles in patients of the TCGA-COAD-READ cohort presented in Fig. 6A. Table include all genes/signatures tested (regardless of statistical significance) reported in ascending order of interaction P-values from model 2 determined in the TCGA-COAD-READ cohort (discovery cohort). For completeness, detailed statistical output is also reported for the Taxonomy cohort.

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