Supplementary Table 7. Logistic regression analysis to assess independent associations of gene mutation status with the presence of *F nucleatum animalis* in colorectal cancer tissues.

Mutation status mutated vs non-mutated	**Univariate OR (95% CI)**	**FDR p-value***	**Multivariable OR (95% CI)#**	**FDR p-value***
KRAS	1.27 (0.77-2.09, p-val = 0.34)	0.38	1.32 (0.78-2.21, p-val = 0.30)	0.67
TP53	0.49 (0.33-0.72, p-val = 0.00029)	0.0013	0.71 (0.46-1.1, p-val = 0.089)	0.33
POLE	3.21 (1.1-7.93, p-val = 0.02)	0.042	4.03 (1.16-12.27, p-val = 0.011)	0.085
ERBB2	1.74 (0.51-4.55, p-val = 0.31)	0.38	1.063 (0.29-3.0, p-val = 0.916)	0.94
ERBB3	7.56 (3.16-16.77, p-val = 1.55e-6)	1.40e-5	3.76 (1.44-9.19, p-val = 0.0047)	0.043
APC	0.64 (0.43-0.94, p-val = 0.023)	0.042	0.90 (0.59-1.39, p-val = 0.64)	0.94
BRAF	2.34 (1.14-4.49, p-val = 0.014)	0.042	1.03 (0.45-2.23, p-val = 0.94)	0.94
PIK3CA	1.44 (0.87-2.29, p-val = 0.14)	0.21	1.19 (0.71-1.94, p-val = 0.49)	0.89
SMAD4	1.07 (0.55-1.91, p-val = 0.83)	0.83	1.09 (0.55-1.97, p-val = 0.79)	0.94

In the regression analysis, *F nucleatum* was used as a binary outcome variable (negative = 0 vs positive = 1) and gene mutation status as the predictor variable.
logistic regression model adjusted for sex, age at diagnosis, tumour site, MSI and hypermutation status,
**p*-values were adjusted for multiple testing using the Benjamini-Hochberg method.
OR = Odds Ratio, CI = Confidence Interval, FDR = False Discovery Rate