Figure S1

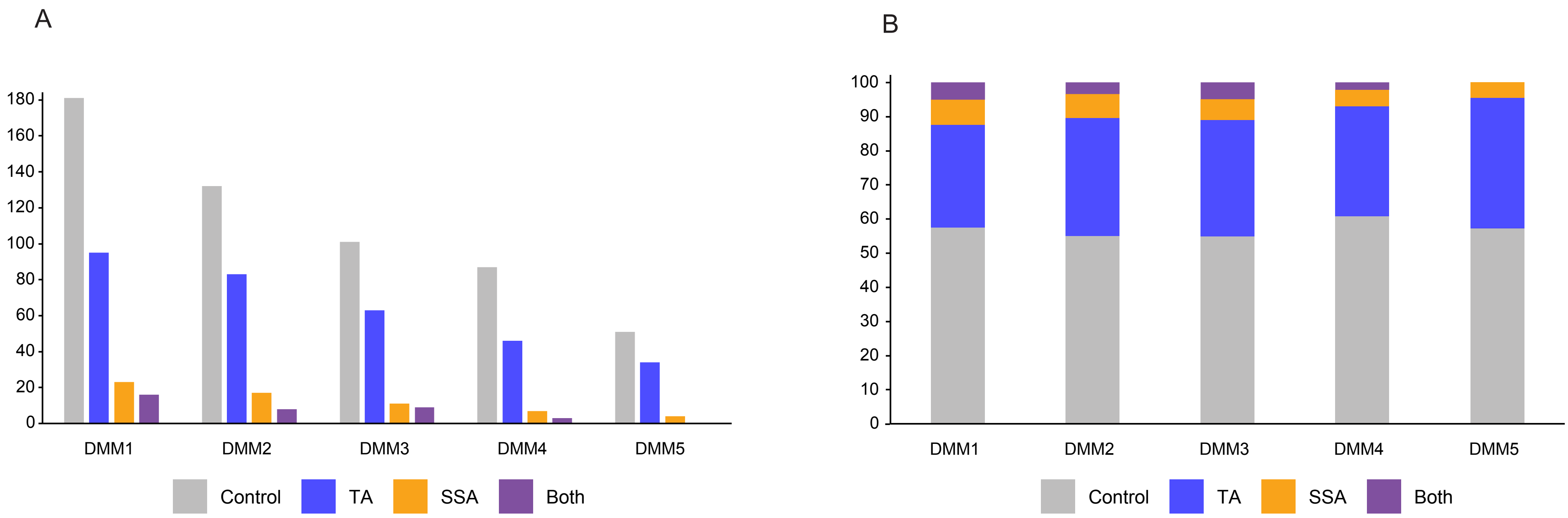

Figure S1: Prevalence of adenoma subtypes amongst varying DMM subgroups, Related to Figure 2. Barplot of the (A) counts and (B) proportions of subjects without adenomas (grey), with TA only (blue), with SSA only (orange) and with both TA & SSA (purple), stratified by the 5 DMM subgroups.

Figure S2

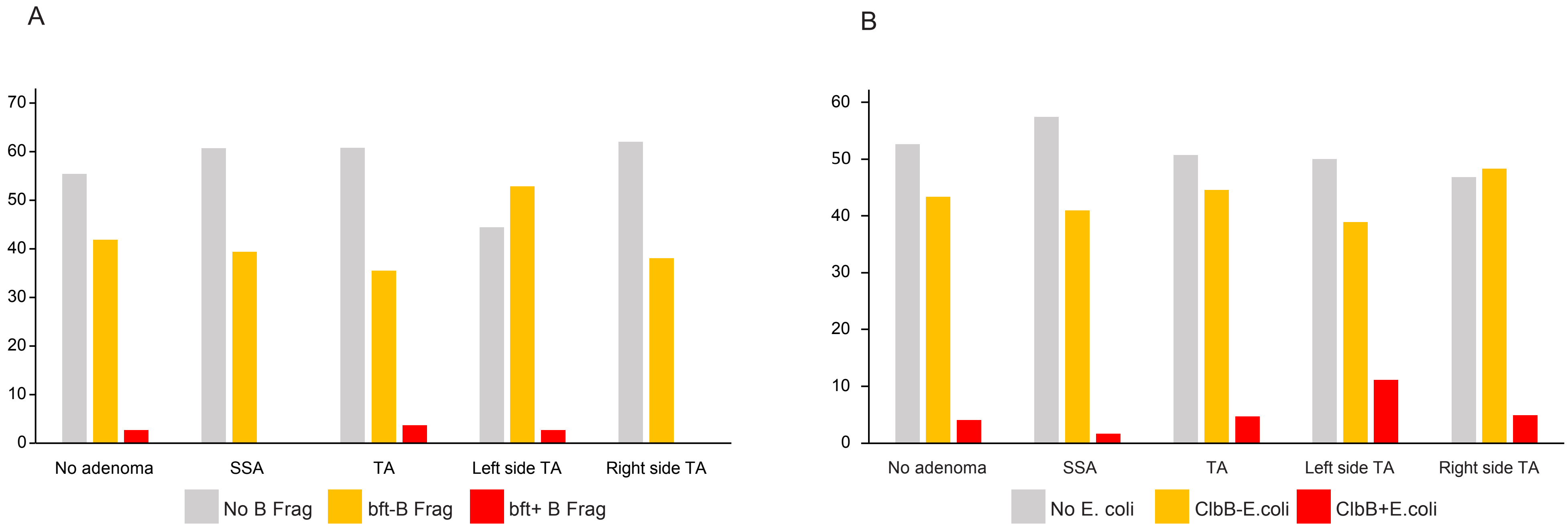

Figure S2: Specific CRC-associated strains prevalence in GIDER, Related to Figure 3. Barplots depicting the proportions of subjects (%) with either bft+ *B. fragilis* (A: red) or ClbB+ *E. coli* (B: red) stratified by adenoma morphology (no adenoma, sessile adenoma only, tubular adenoma only, SSA & TA, left-sided TA, and right-sided TA).

Figure S3

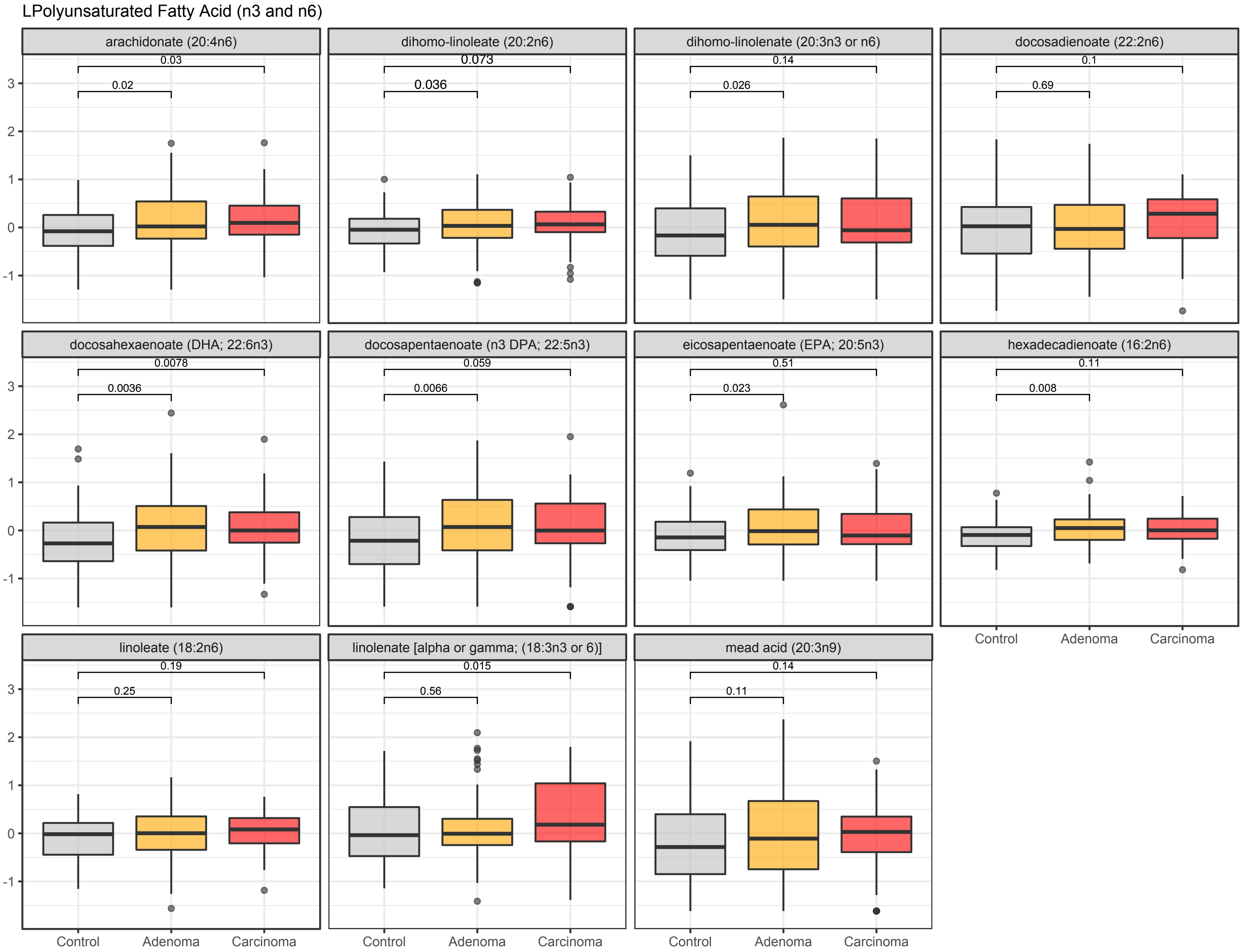

Figure S3: External validation of predicted microbial metabolites associated tubular adenomas, Related to Figure 4. Boxplots of specific polyunsaturated fatty acids (PUFA) abundances stratified by the subjects' presence of colonic lesions (ie. control - grey, adenoma - yellow, carcinoma - red), with demonstration of significant uptrend of both n3 and n6 PUFAs with increasing stage of adenoma-carcinoma carcinogenesis in an external reference cohort [S1].

References

S1. Kim, M., Vogtmann, E., Ahlquist, D.A., Devens, M.E., Kisiel, J.B., Taylor, W.R., White, B.A., Hale, V.L., Sung, J., Chia, N., et al. (2020). Fecal Metabolomic Signatures in Colorectal Adenoma Patients Are Associated with Gut Microbiota and Early Events of Colorectal Cancer Pathogenesis. MBio 11. 10.1128/mBio.03186-19.