**Supplementary Figure 1.** **Clustergram visualization of the expression of XMEs in colorectal tumor and normal mucosa tissues with dietary factors among patients with colorectal cancer.**

Hierarchical clustering was performed using the Scipy library in Python with cosine distance and average linkage. Patients are represented as rows, with green boxes representing the consumption of red meat, processed meat, raw vegetables or cooked vegetables greater than once weekly, and white boxes representing consumption less than or equal to once weekly. Columns represented individual XME gene expression. Phase I enzymes are represented by blue boxes, and Phase II enzymes are represented by yellow boxes. Colorectal tumor tissue is indicated by blue boxes, and normal mucosa tissue by purple boxes. Red cells in the matrix represent positive relative expression values.

Abbreviations: GSTM1, glutathione S-transferase mu 1; GSTA1, glutathione S-transferase alpha 1; UGT1A8, UDP glucuronosyltransferase family 1 member A8; UGT1A10, UDP glucuronosyltransferase family 1 member A10; CYP3A4, cytochrome P450 family 3 subfamily A member 4; CYP2C9, cytochrome P450 family 2 subfamily C member 9; GSTP1, glutathione S-transferase pi 1; CYP2W1, cytochrome P450 family 2 subfamily W member.

**Supplementary Figure 1.**

