Supplementary Figure Legends:

Supplementary Figure 1. Representative EI fragmentation mass spectra for key metabolites. GC/MS EI fragmentation patterns for sarcosine (A) and 2-hydroxyglutarate (B). In panels A and B, representative experimental samples are shown at the top, while authentic standards are shown at the bottom. Ions at 147 and 73 m/z displayed within the authentic standard for sarcosine (panel A, bottom) are related to the TMS derivative and are ignored in compound identification matches since they are ubiquitously detected on molecules with multiple TMS derivatization sites and are not ions specific to sarcosine.

Supplementary Figure 2. Canonical pathways affected in tumor tissue. Metabolites that were altered in tumor tissue *vs.* normal mucosa were analyzed by IPA and significantly affected canonical pathways are shown. Blue bars represent the -log p-value (left axis) and the threshold represents a p-value which equals 0.05. Yellow boxes represent the percent of molecules altered as compared to all the metabolites in a given pathway (i.e. ratio) (right axis).