

## SUPPLEMENTAL INFORMATION

### Supplementary Tables

**Table S1. Summary of the proteomic results comparing MET versus CTR, METCC versus MET, CTRCC versus CTR.** Proteomic data were analysed by Perseus software (version 1.5.5.3, [www.biochem.mpg.de/mann/tools](http://www.biochem.mpg.de/mann/tools)). Proteins were considered differentially expressed if they were present only in one condition or showed significant t-test difference (Student's T-test  $p$  value  $\leq 0.05$ ). In each comparison the terms increased or decreased refer to proteins up- or down-regulated in CTR, respectively.

**Table S2. Proteins differentially expressed the comparison MET vs CTR.** Proteins were considered differentially expressed if they were present only in one condition or showed statistically significant difference (Student's T-test  $p$  value  $\leq 0.05$ ).

**Table S3. Proteins differentially expressed the comparison CTRCC vs CTR.** Proteins were considered differentially expressed if they were present only in one condition or showed statistically significant difference (Student's T-test  $p$  value  $\leq 0.05$ ).

**Table S4. Proteins differentially expressed the comparison METCC vs CTR.** Proteins were considered differentially expressed if they were present only in one condition or showed statistically significant difference (Student's T-test  $p$  value  $\leq 0.05$ ).

**Supplementary Figure S1** (related to Fig. 3) Hierarchical clustering heatmap from One-way ANOVA analysis of the entire set of metabolites differentially expressed.

