

Supplemental Figure 1. Integrative omics; TMWAS of Se supplement. Transcriptome and high-resolution metabolome (HRM) data were collected for liver from C57BL/6 mice exposed to an adequate intake and supplemental Se in drinking water for 16 weeks. The supplemental Se provided approximately 4-fold Se compared to the controls. Changes in transcription were determined using Gene-Set Enrichment, and the enriched gene sets were used to test for correlated metabolites. Extensive network structures were observed with a correlation threshold of 0.7 (top left). By using greater stringency ($r > 0.8$), two central subnetworks (A and B) were observed. Examination at $r > 0.9$ showed that the two central subnetworks were associated with the transcript for the reversible glucose transporter (*Glut2*) and transcripts for proteins involved in fatty acid metabolism (*Acaa1b*, *Cpt2*). Each of these transcripts correlated with multiple types of lipids, including acylcarnitines, acyl-CoAs and sterols. Collectively, the results show that data-driven integration of omics data provides a way to map complex network structures associated with variation in exposure to Se. Data from [23].

