Fig. S1 Example of spectral data and results from animals in three hibernation stages for the plasma compound glycerol (Metabolon, Inc.). (A) GC-MS chromatogram from one arousing animal showing retention time vs. relative peak abundance (total ion scan). (B) GC-MS electron-impact (EI) ionization spectrum from the 6.09 minute retention time compared to the bistrimethyl-silyl-triflouroacetamide (BSTFA)-derivatized glycerol standard from the Metabolon database, shown in (C). (D) Expansion and overlay of the 205 anion quantitation peak at 6.09 retention time from animals in LT (black), Ar (blue) and IBA (green) hibernation stages. Note: integrated peak area values in the inset table are shown at original ion count scale and therefore differ from the median-scaled values in the supplementary tables.

Fig. S2 Box plots for all identified thirteen-lined ground squirrel plasma metabolites identified in this study. Triangle, mean standardized quantity; bold horizontal line, median quantity; colored region, center 50th percentile; outside horizontal lines, 100th percentile; circles represent outliers; hibernation stages indicated below along x-axis are as delineated in Fig. 1; y-axis, standardized abundance.

Table S1 The median-scaled imputed minimum data from Metabolon, Inc. for each identified compound, all squirrels. First column, Martin lab animal number; first row, identified metabolites sorted by name.

Table S2 ANOVA and Tukey statistical results for plasma metabolites.