**Figure 5. Correlation between metabolite abundance and microbial function**. **A**. Principal component analysis (PCA) scoreplots of vaginal metabolome as detected by GC-MS (left) or NMR (right). ­Each point represents a single sample from a single women colored according to their microbiota subtype. Positions of points display dissimilarities in the metabolome, with points furthest from one another being most dissimilar. **B**. Correlations between metabolite abundance and positions of samples on compositional biplots built from SEED subsys4 aggregated metatranscriptomic data. Correlations were scaled by the first and second component of the biplots, and metabolites plotted according to ­their scaled position. Only metabolites that differed significantly between BV and health are shown. GHB: gamma-hydroxybutyrate, 2HG: 2-hydroxyglutarate, 2HIC: 2-hydroxyisocaproate, PhLa: phenyllactate, Tyr: tyramine, Cad: cadaverine, Pip: pipecolate, Gluc: glucose, Malt: maltose, Fruc: fructose, U: unknown, TMA: trimethylamine, Lact: lactate, Acet: acetate, Form: formate, 2HV: 2-hydroxyisovalerate, Chol: choline, Succ: succinate.