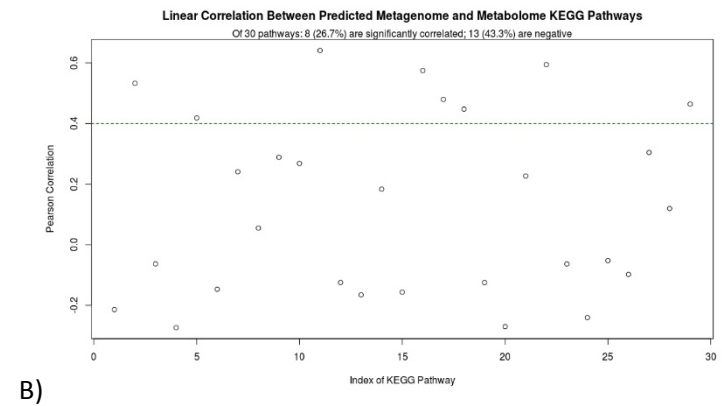
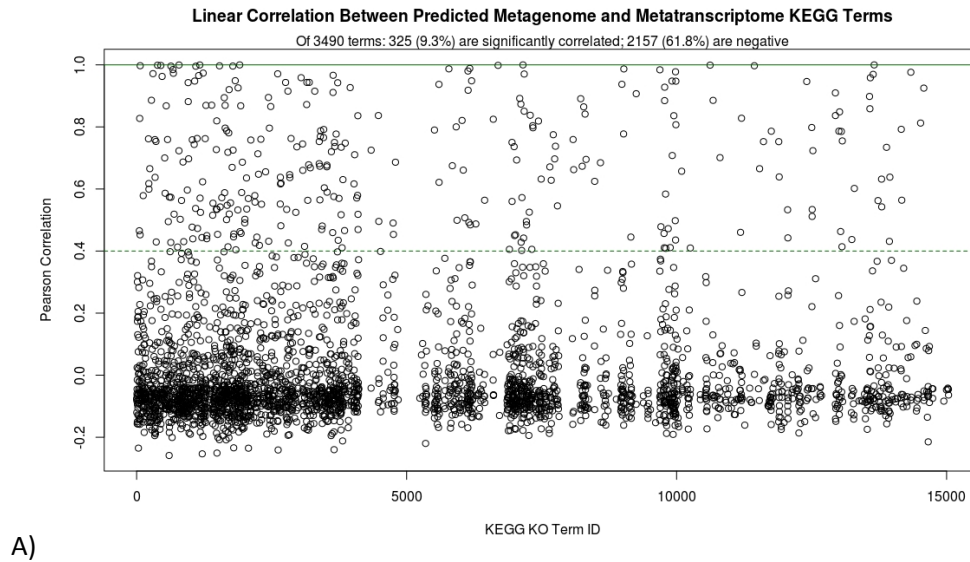


**Figure 1 Correlation of KEGG terms between levels.** (A) Correlation between KEGG terms assigned to the predicted metagenome and those assigned to the metatranscriptome. The solid black line represents a correlation of 1.0, or perfect Pearson correlation. (B) Correlation between KEGG pathway terms assigned to the predicted metagenome and the metabolome. The dashed green lines in each figure represent a correlation of 0.4; anything above this line is significantly correlated.



**Figure 2 Differential abundance/expression in HIV infection.** (A) Significance, as measured by the raw p-value of a Wilcoxon test, for each KEGG term as calculated for the predicted metagenome, or 16S, on the X-axis and the metatranscriptome on the Y-axis. (B) Significance, as measured by the raw p-value of a Wilcoxon test, for each KEGG pathway term as calculated for the predicted metagenome, or 16S, on the X-axis and the metabolome on the Y-axis. For both figures, KEGG terms represented by green dots are considered over-abundance/expressed on both biologic levels in HIV infection, terms represented by red dots are considered under-abundance/expressed on both biologic levels in HIV infection, and terms represented by gray dots are over-abundant/expressed according to one level and the opposite direction by the other level. The dashed lines represent a nominally significant difference.

