

Supplementary Materials

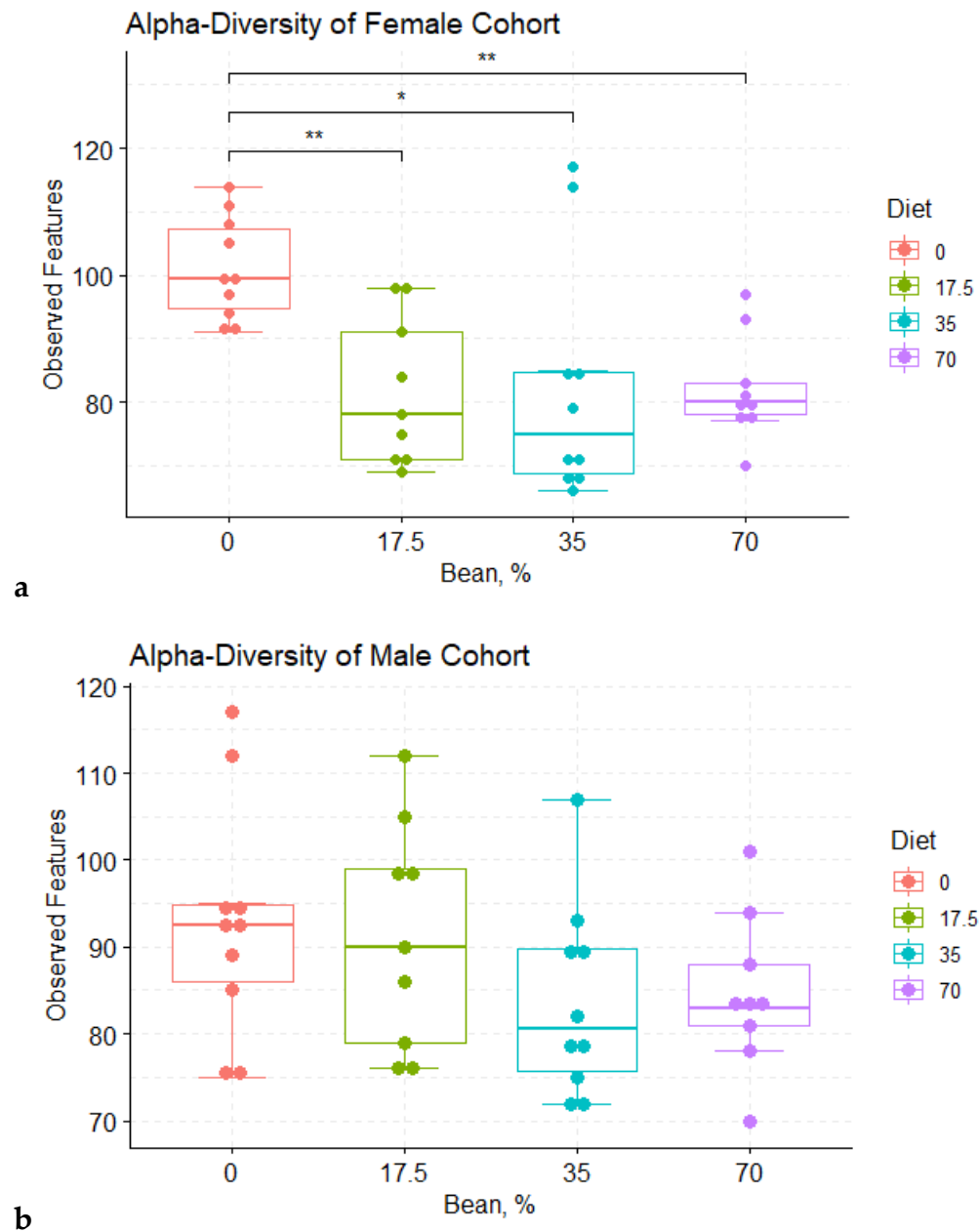


Figure S1. (a) Observed features of α -diversity of the female cohort. Statistically significant differences were determined by the Kruskal-Wallis test (p -value = 0.006) with * q -value < 0.05; ** q -value < 0.01; **(b)** Observed features of α -diversity of the male cohort. Statistically significant differences were tested with the Kruskal-Wallis method (p -value = 0.265).

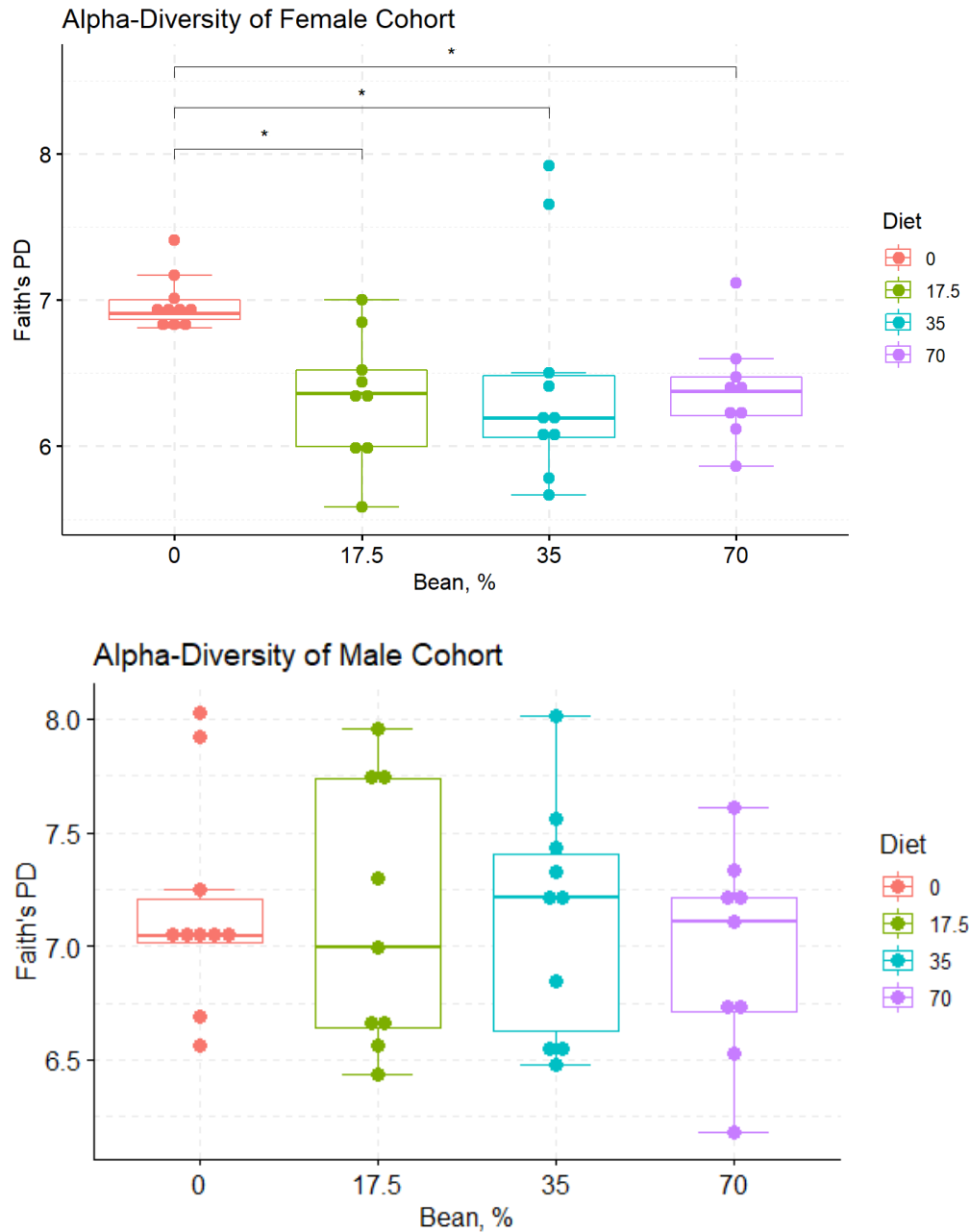


Figure S2. (a) Faith's phylogenetic α -diversity of the female cohort. Statistically significant differences were determined by the Kruskal-Wallis test (p -value = 0.008) with * q -value < 0.05; ** q -value < 0.01; **(b)** Faith's phylogenetic α -diversity of the male cohort. Statistically significant differences were tested with the Kruskal-Wallis method (p -value = 0.941).

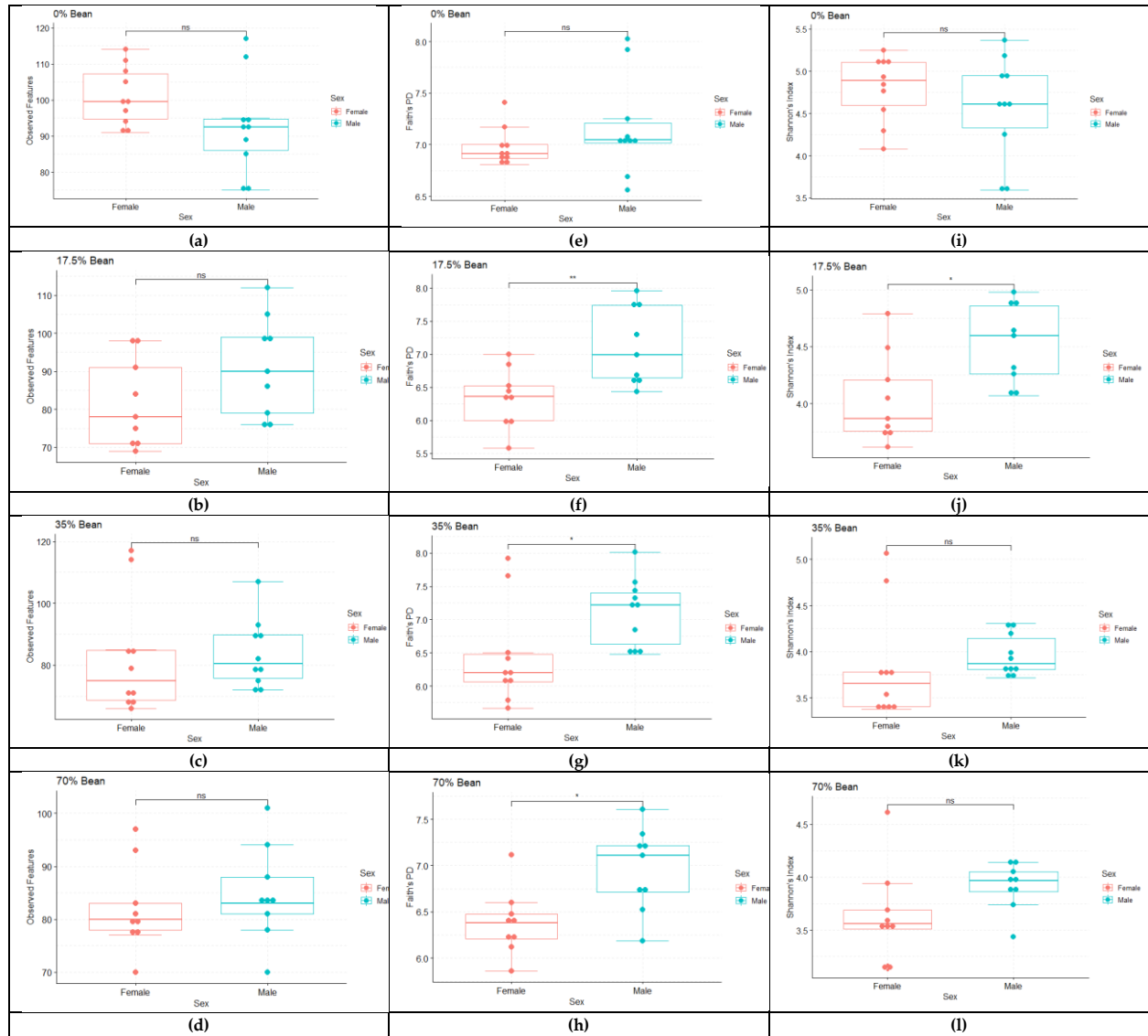


Figure S3. Sex-pairwise comparison of α -diversity. Statistically significant differences were determined by the Wilcoxon signed-rank tests with * p -value < 0.05 ; ** p -value < 0.01 ; (a–d) Observed α -diversity features; (e–h) Faith's phylogenetic α -diversity; (i–l) Shannon's indices of α diversity.

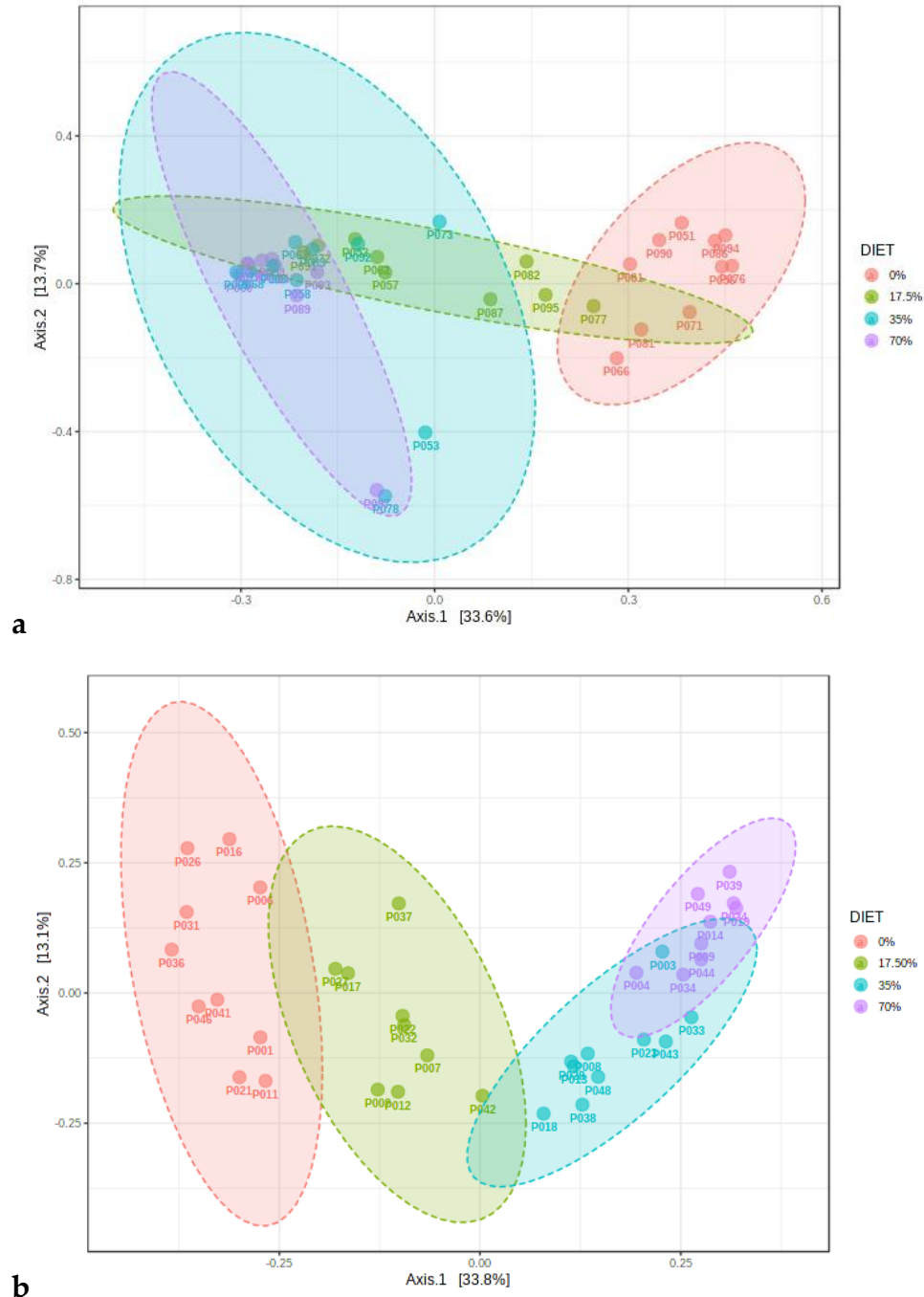


Figure S4. Jaccard indices were used to explain β -diversity across the diet groups. Differences between the samples were tested by the permutational multivariate analysis of variance (PERMANOVA); samples are colored and grouped by their corresponding diet group into ellipses representing 95% confidence intervals. **(a)** in the female cohort, pseudo- F -value = 7.251; p -value < 0.001. All diet groups statistically differed from one another; **(b)** in the male cohort, pseudo- F -value = 8.85; p -value < 0.001. All diet groups statistically differed from one another.

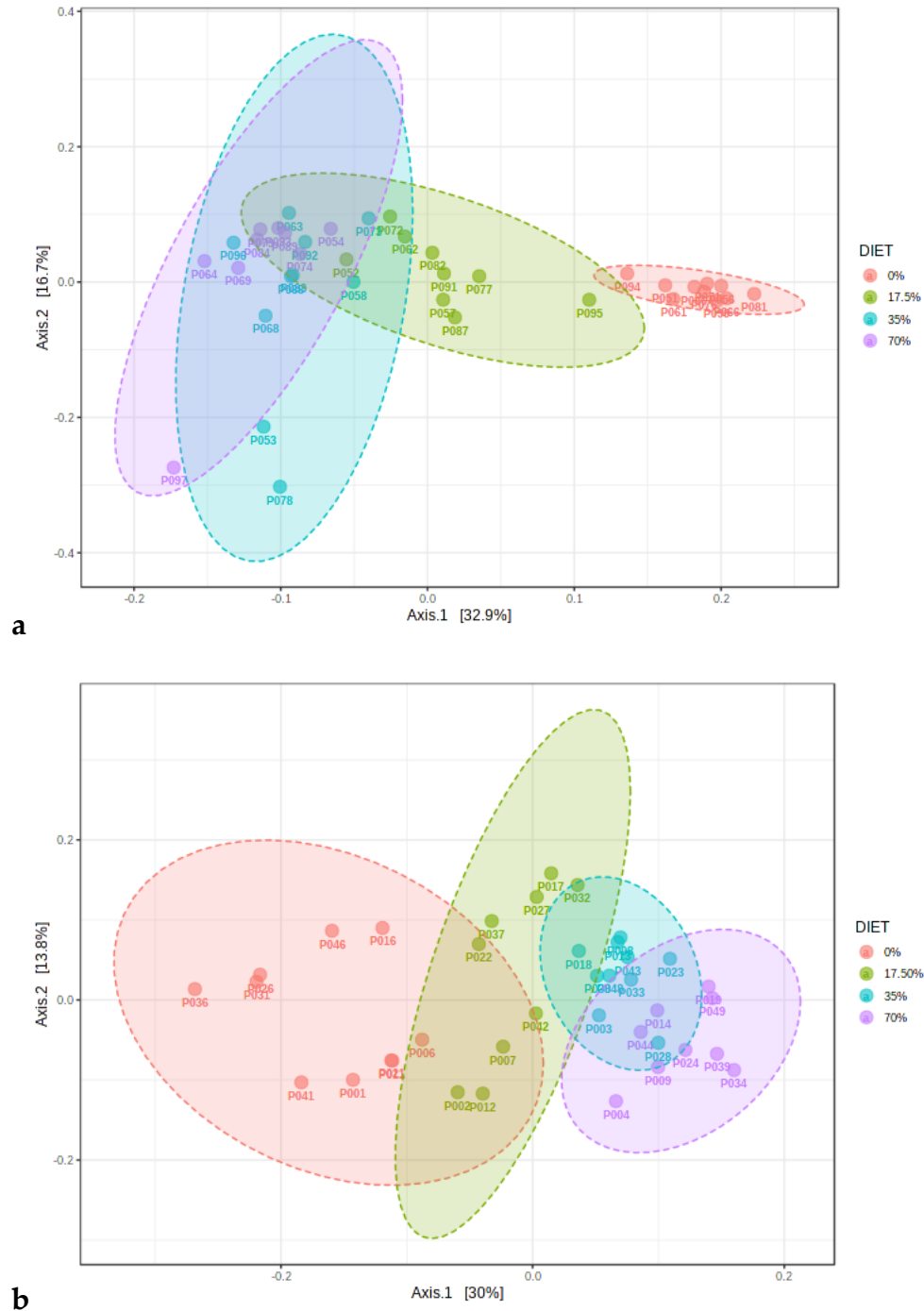


Figure S5. Phylogenetic Unweighted UniFrac distances were used to explain β -diversity across diet groups. Differences between the samples were tested by the permutational multivariate analysis of variance (PERMANOVA): samples are colored and grouped by their corresponding diet group into ellipses representing 95% confidence intervals. **(a)** in the female cohort, pseudo- F -value = 7.236; p -value < 0.001. All diet groups differed from one another, except for 35% vs 70% groups; **(b)** in the male cohort, pseudo- F -value = 7.192; p -value < 0.001. All diet groups differed from one another.

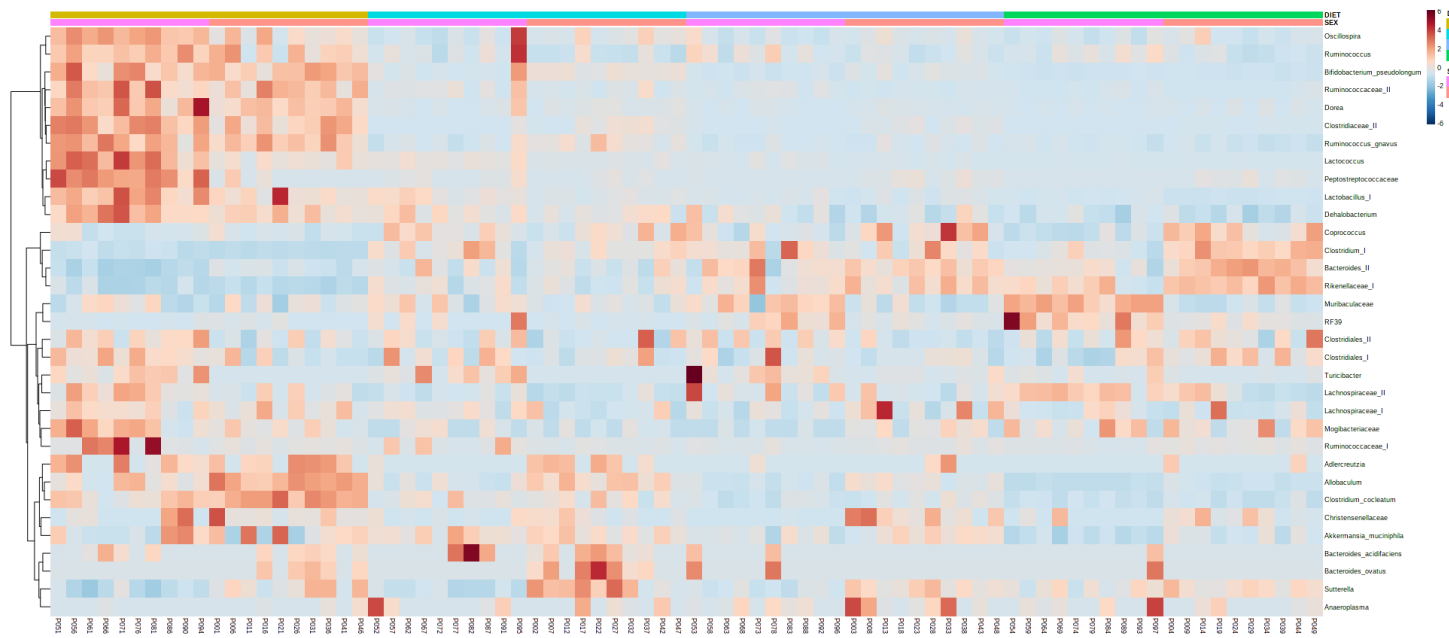
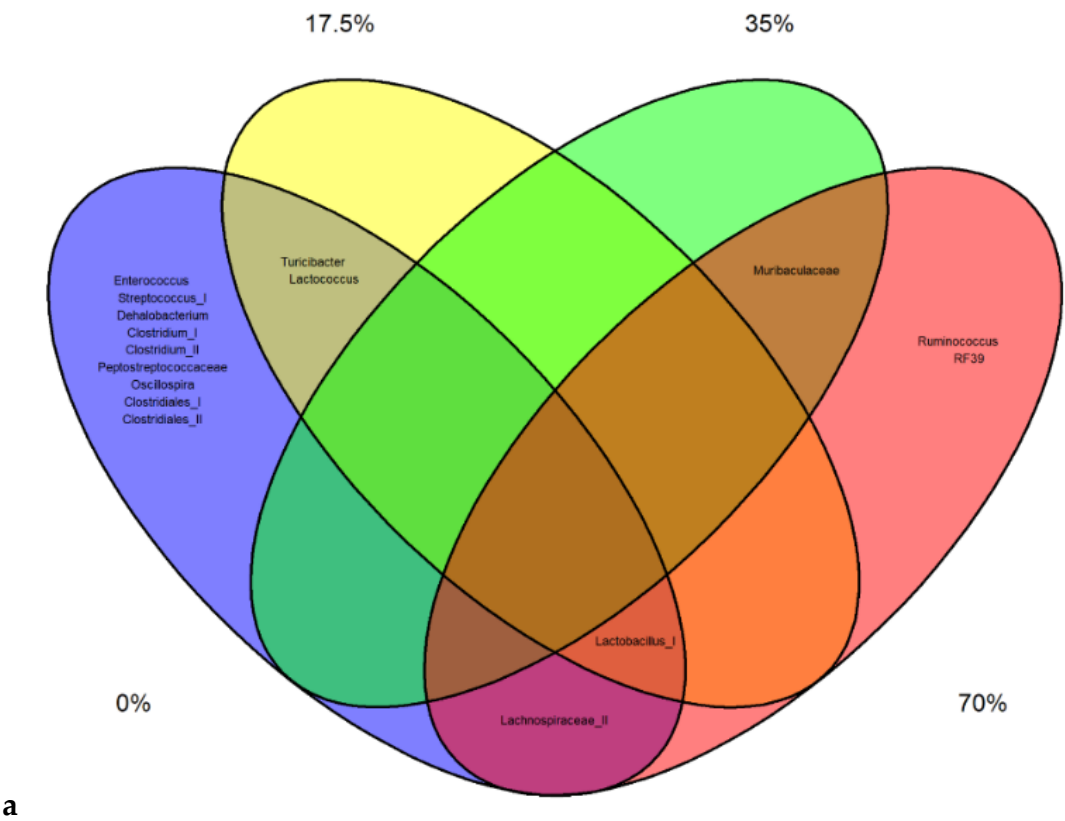
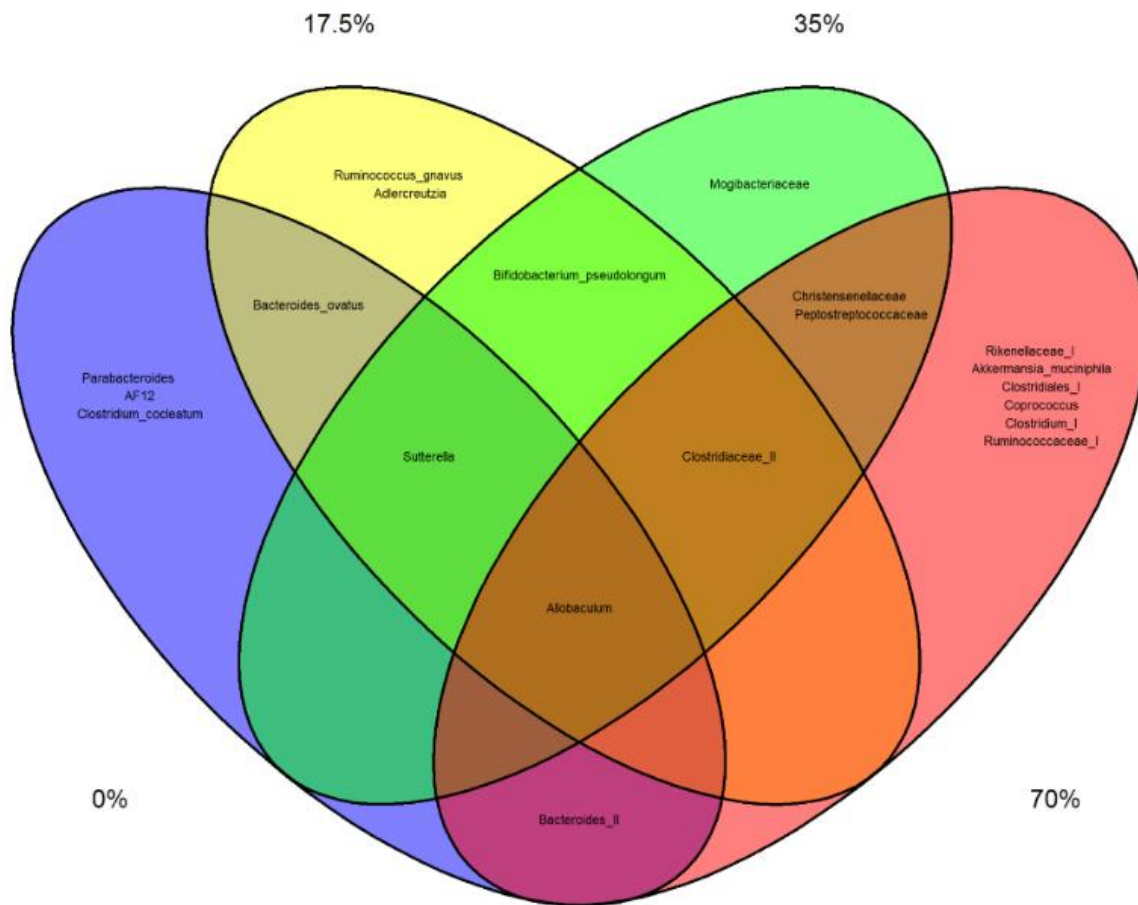


Figure S6. Heatmap representing hierarchical clustering analysis results at the feature level. Clusters were organized by the diet group factor using Ward’s algorithm and Minkowski’s distance measure.

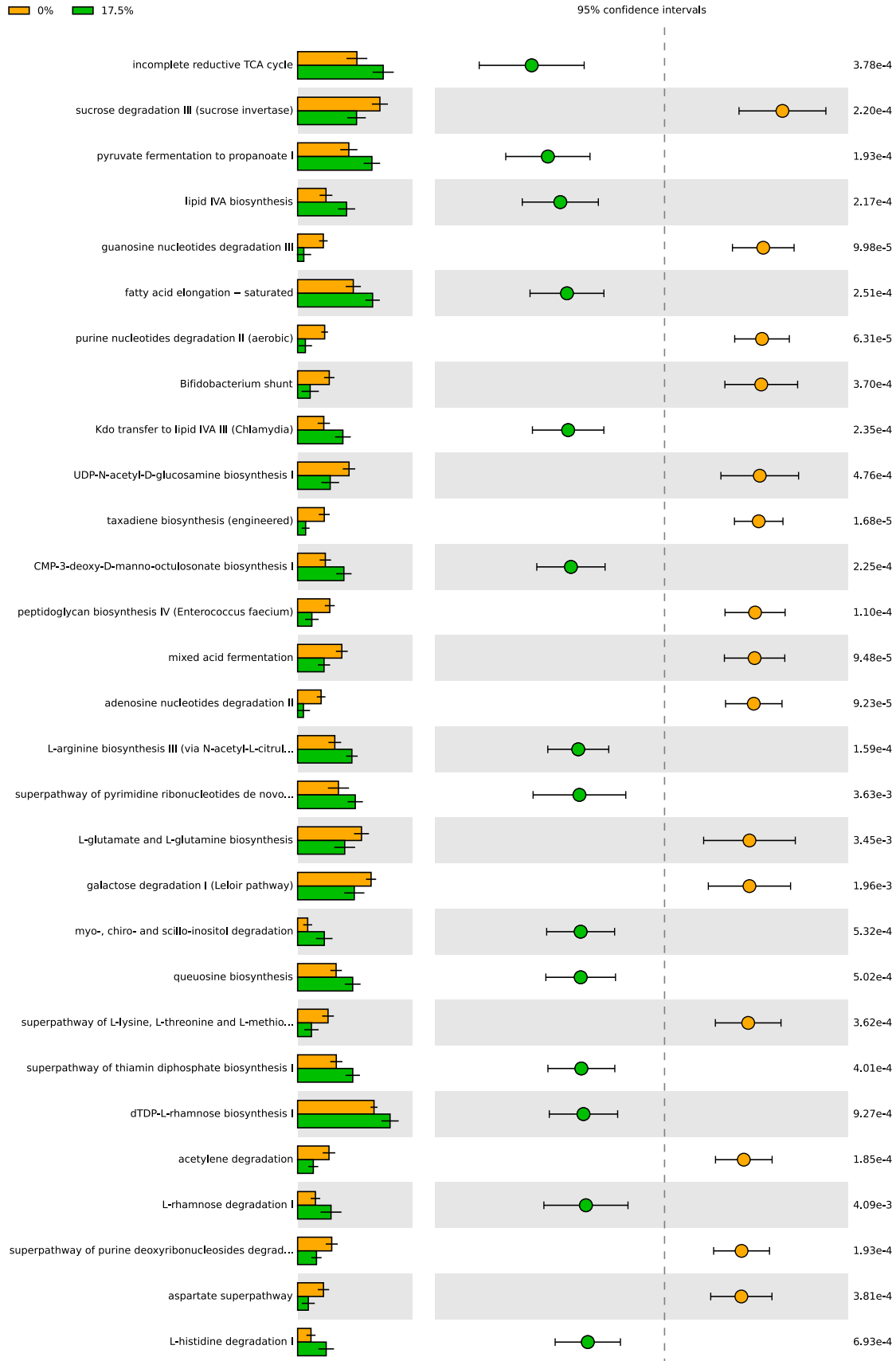


a

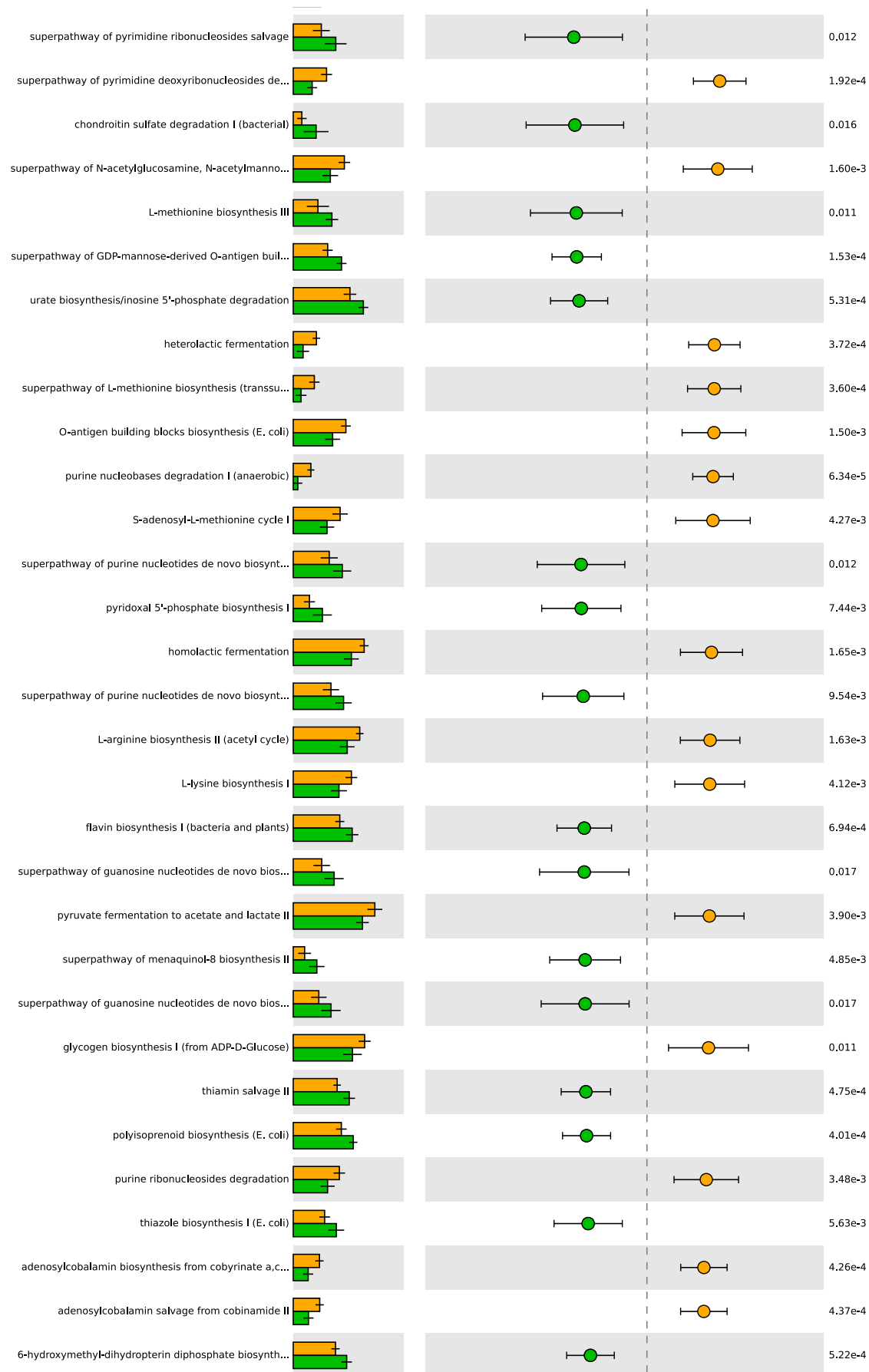


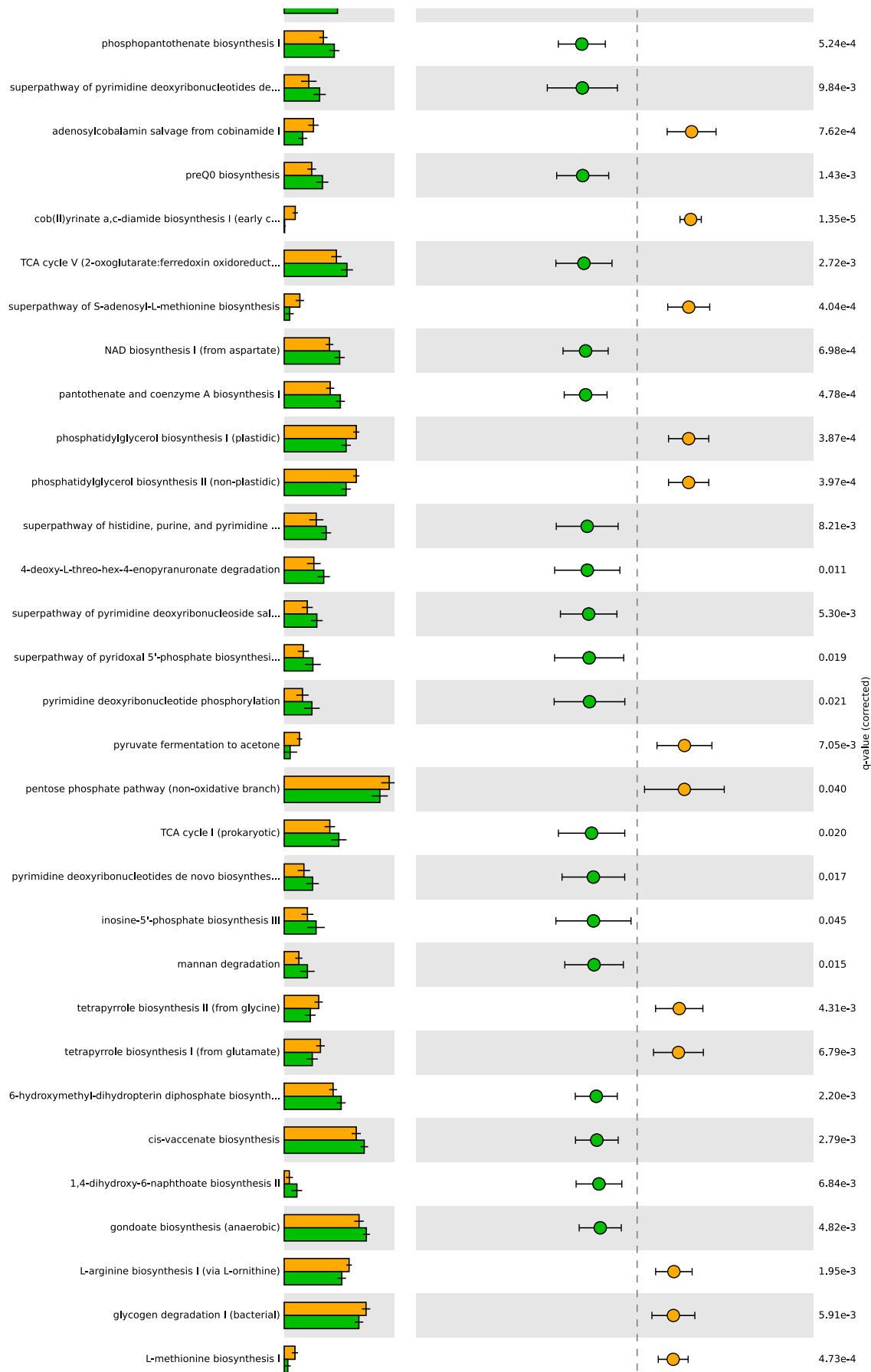
b

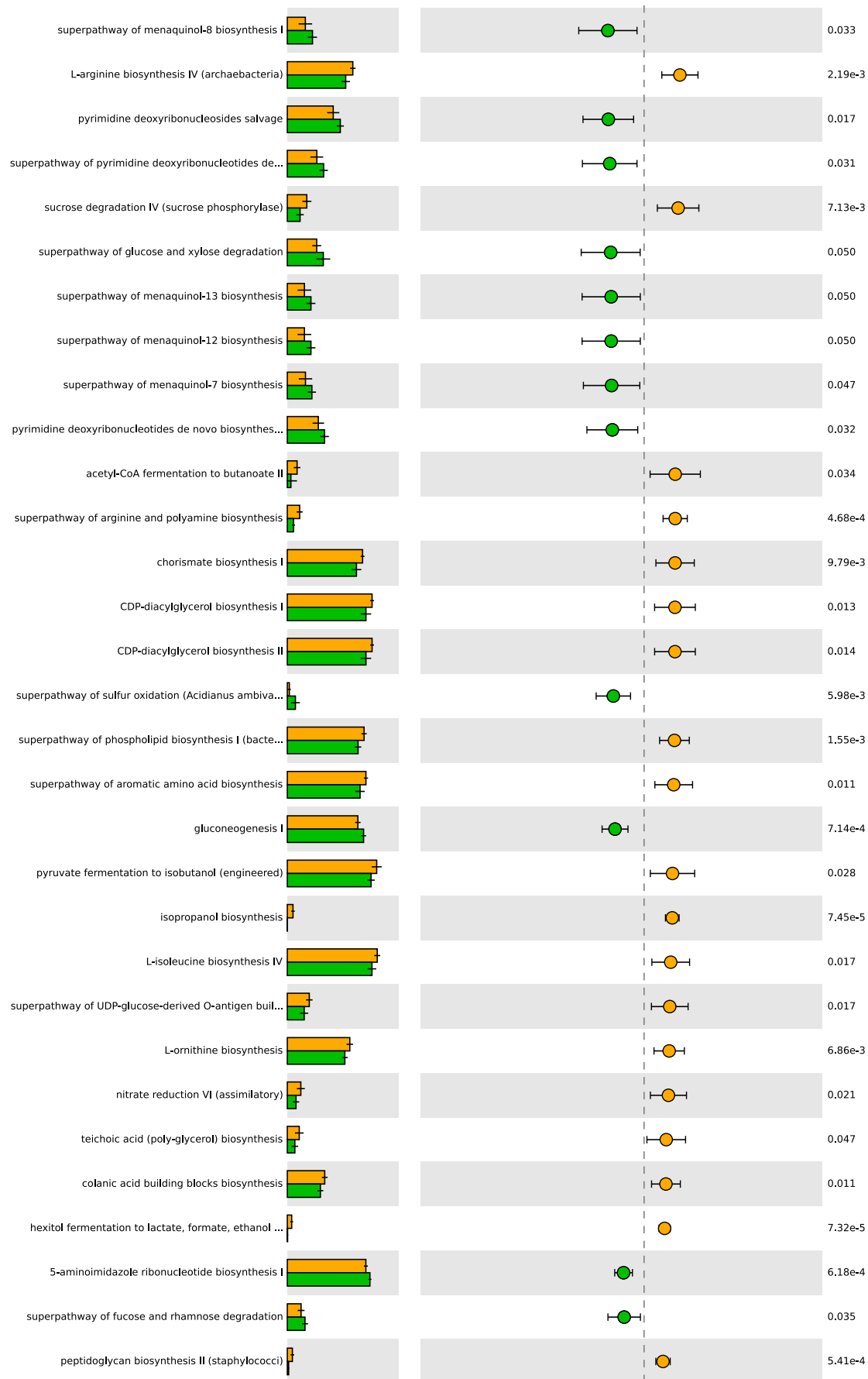
Figure S7. Bacterial sex-dependent biomarkers of the **(a)** female and **(b)** male cohorts in each diet group according to the pairwise linear discriminant analysis (LDA) of effect size (LEfSe) at the feature level. All represented bacteria were statistically significant (LDA score > |2.0|, FDR-adjusted p -value < 0.05).

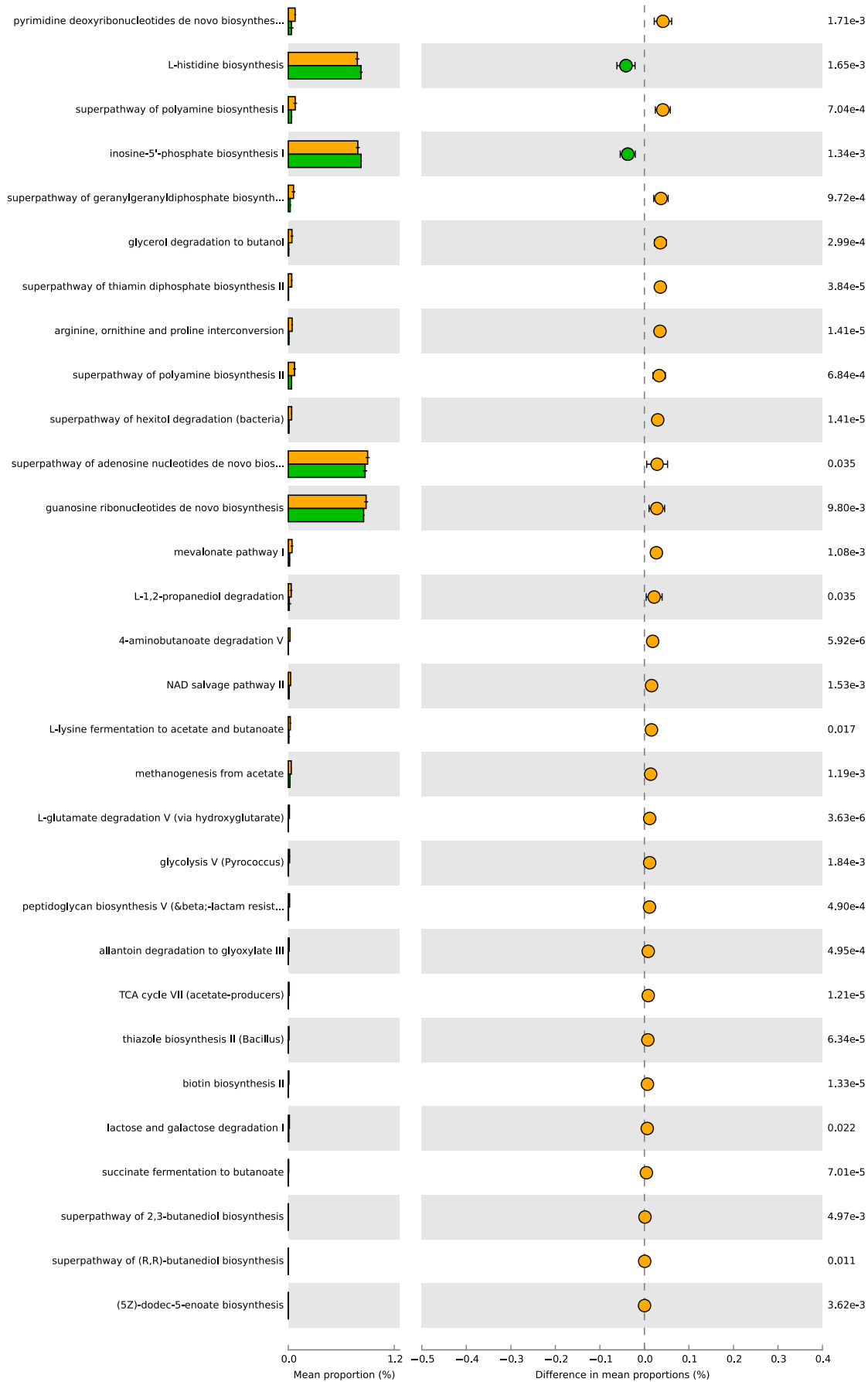


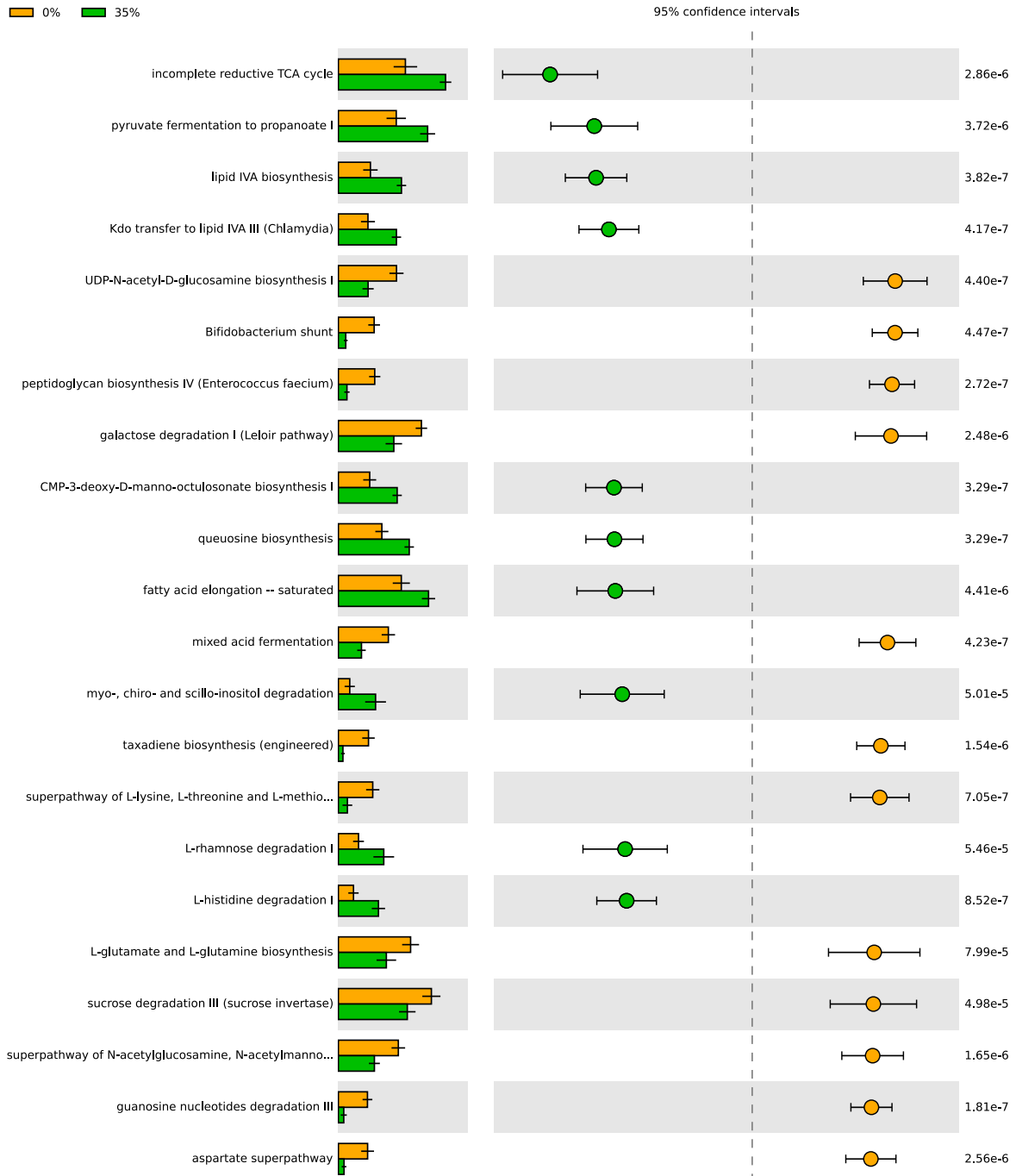
a.



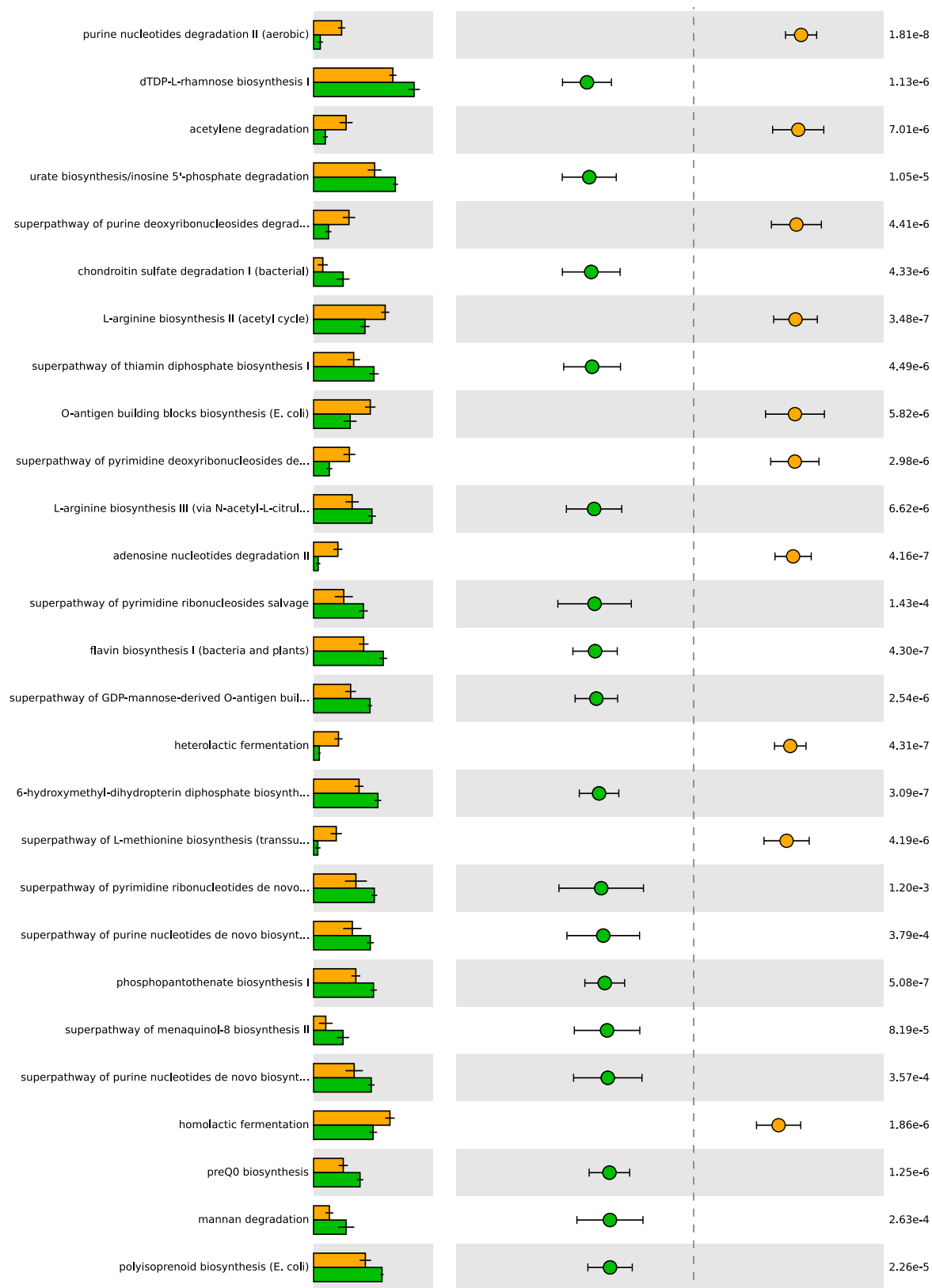


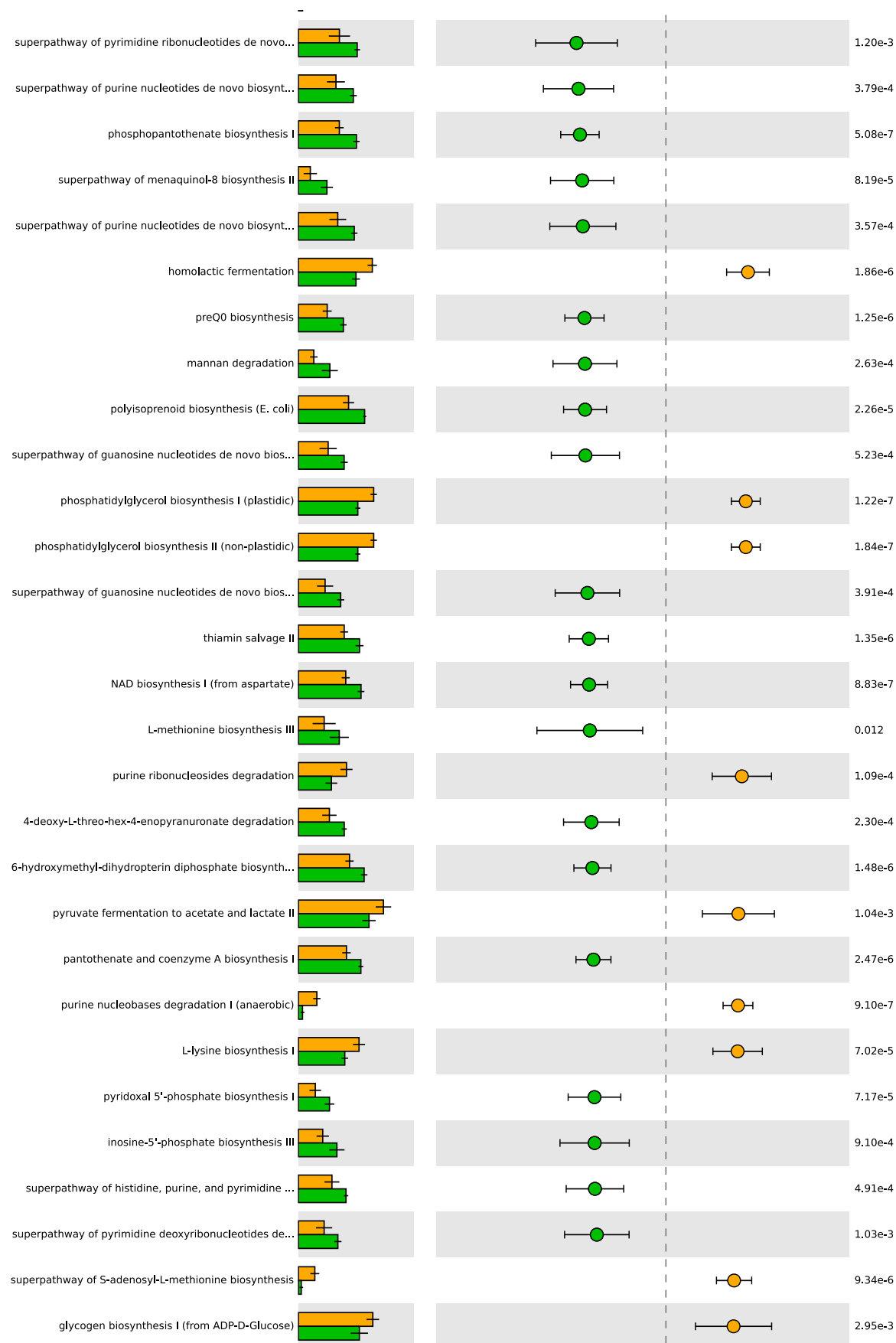


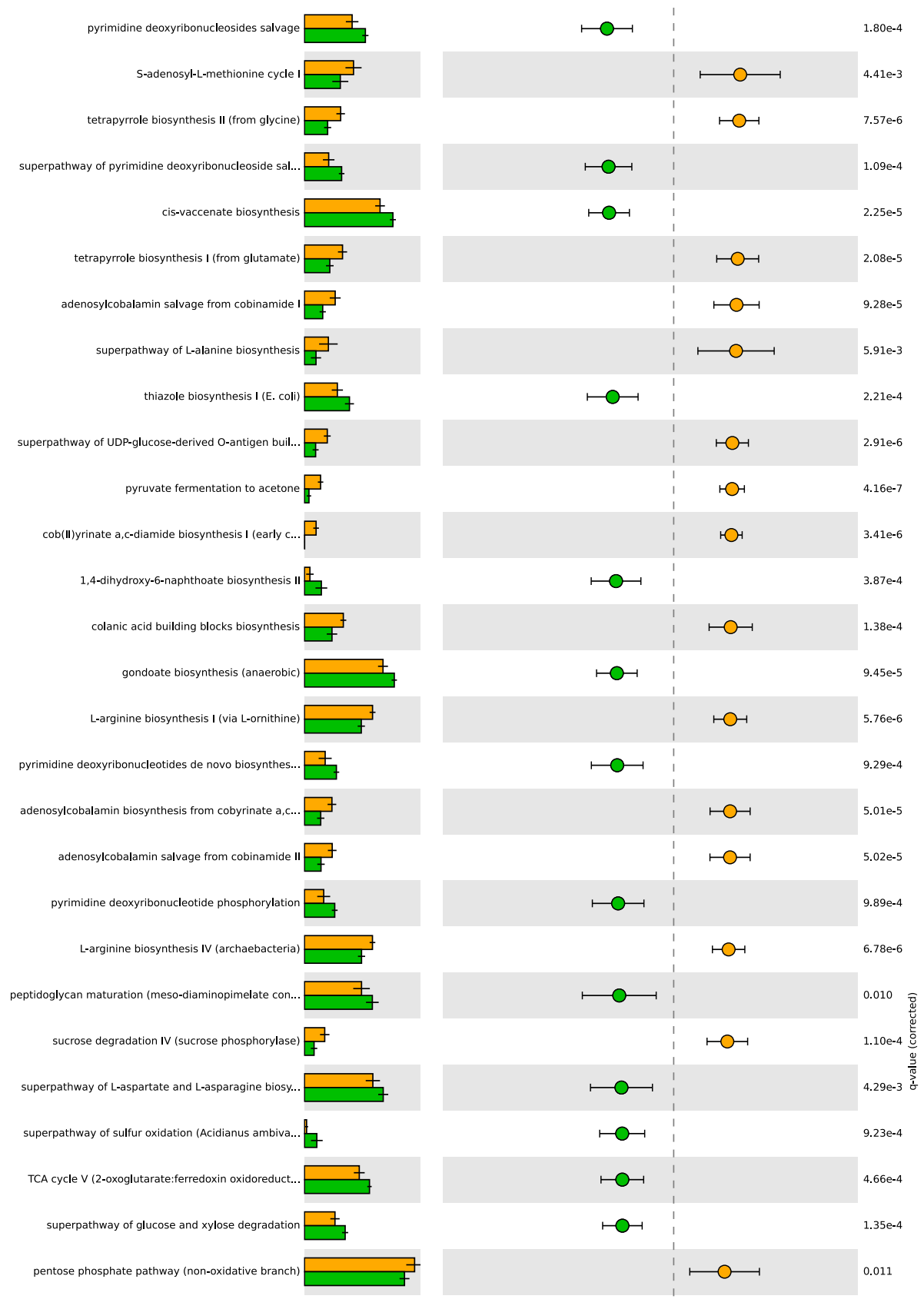


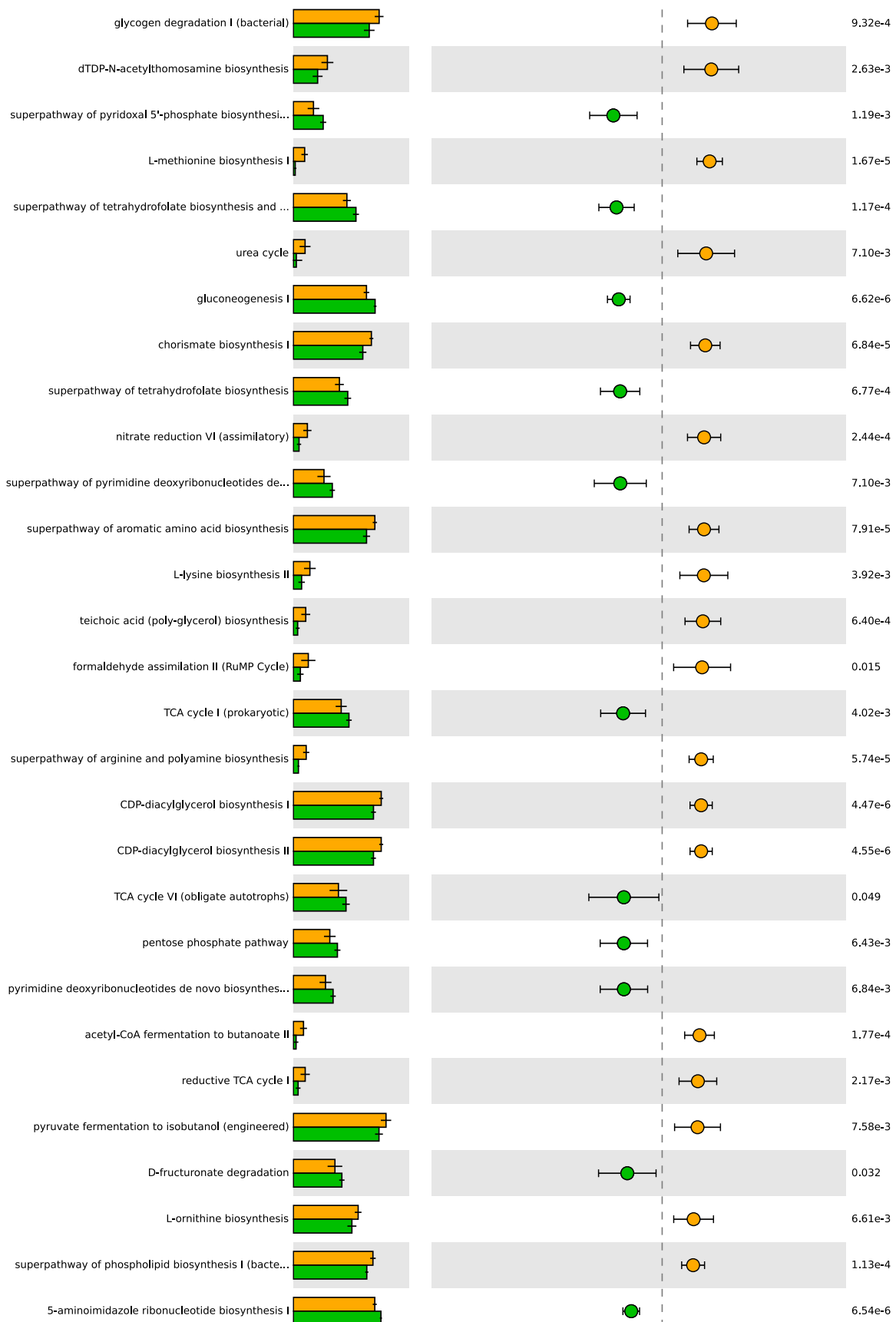


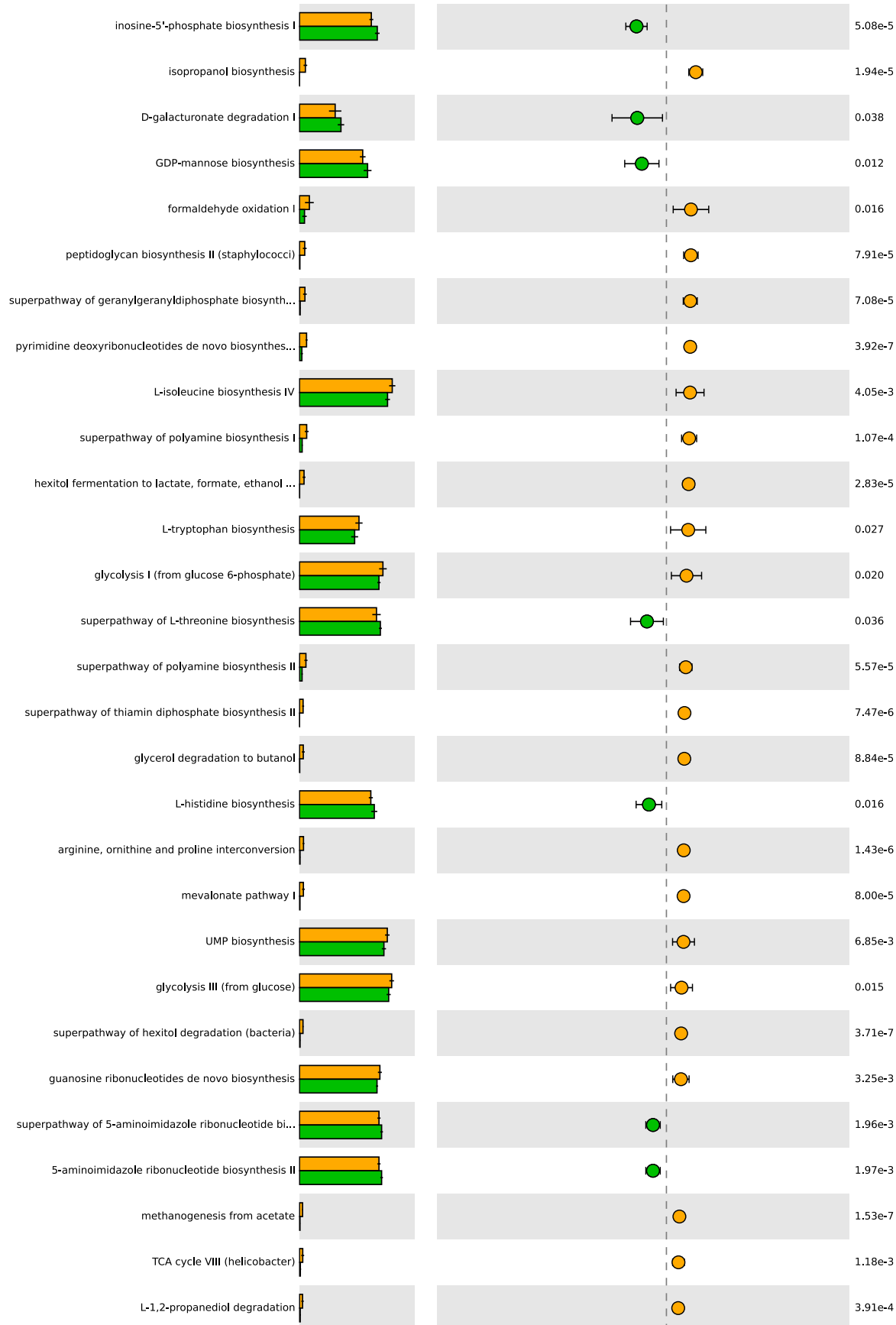
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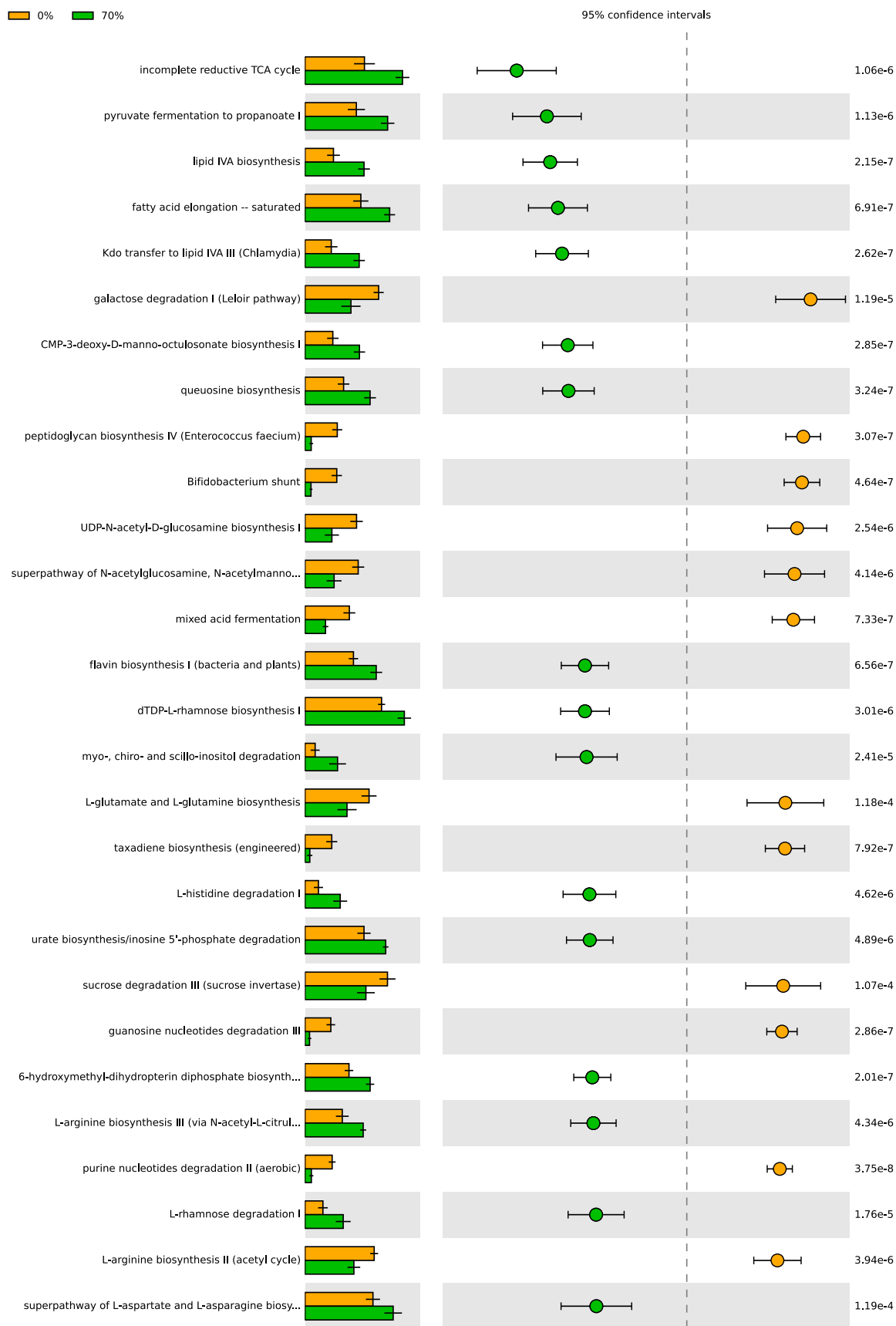




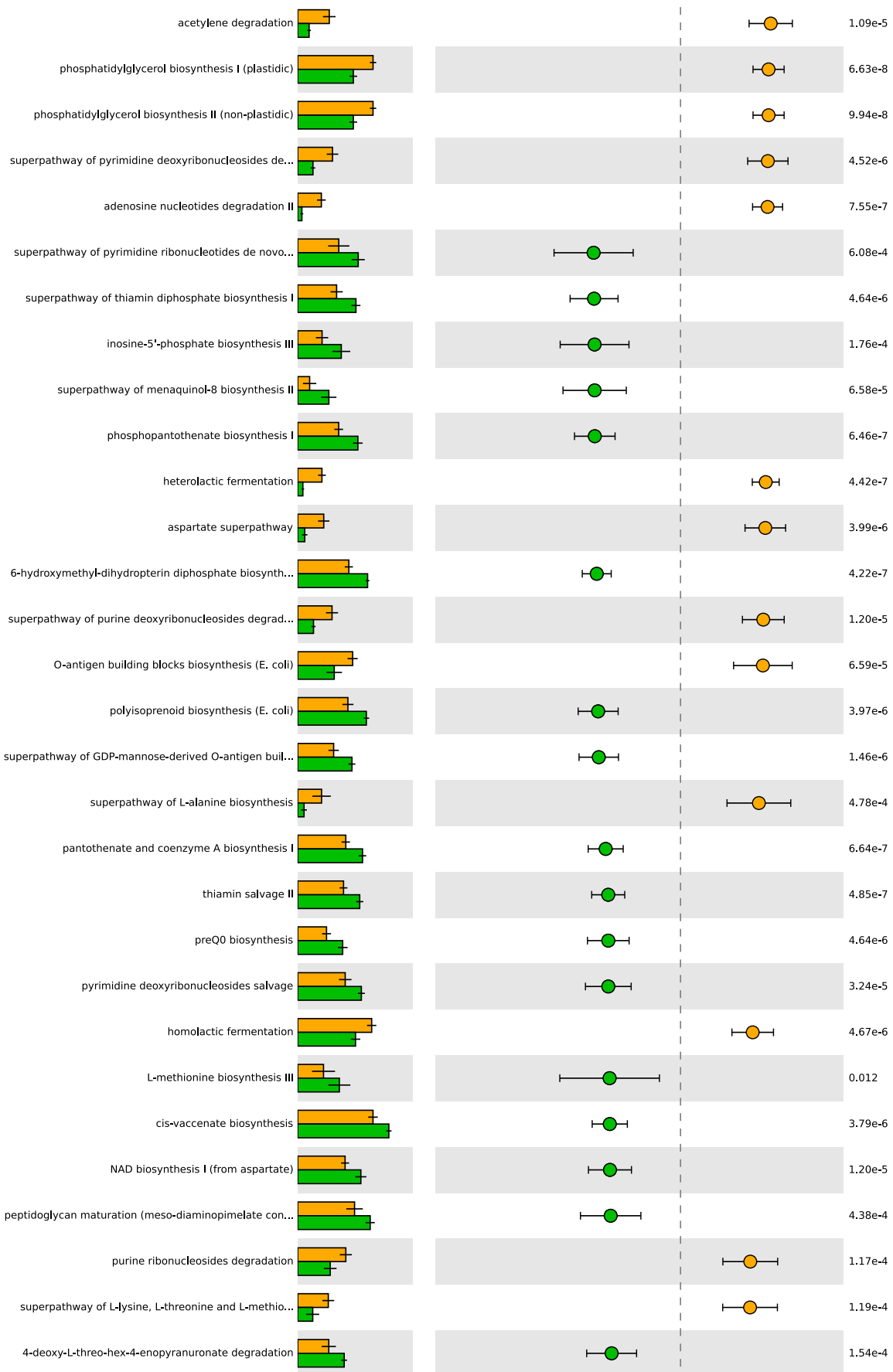




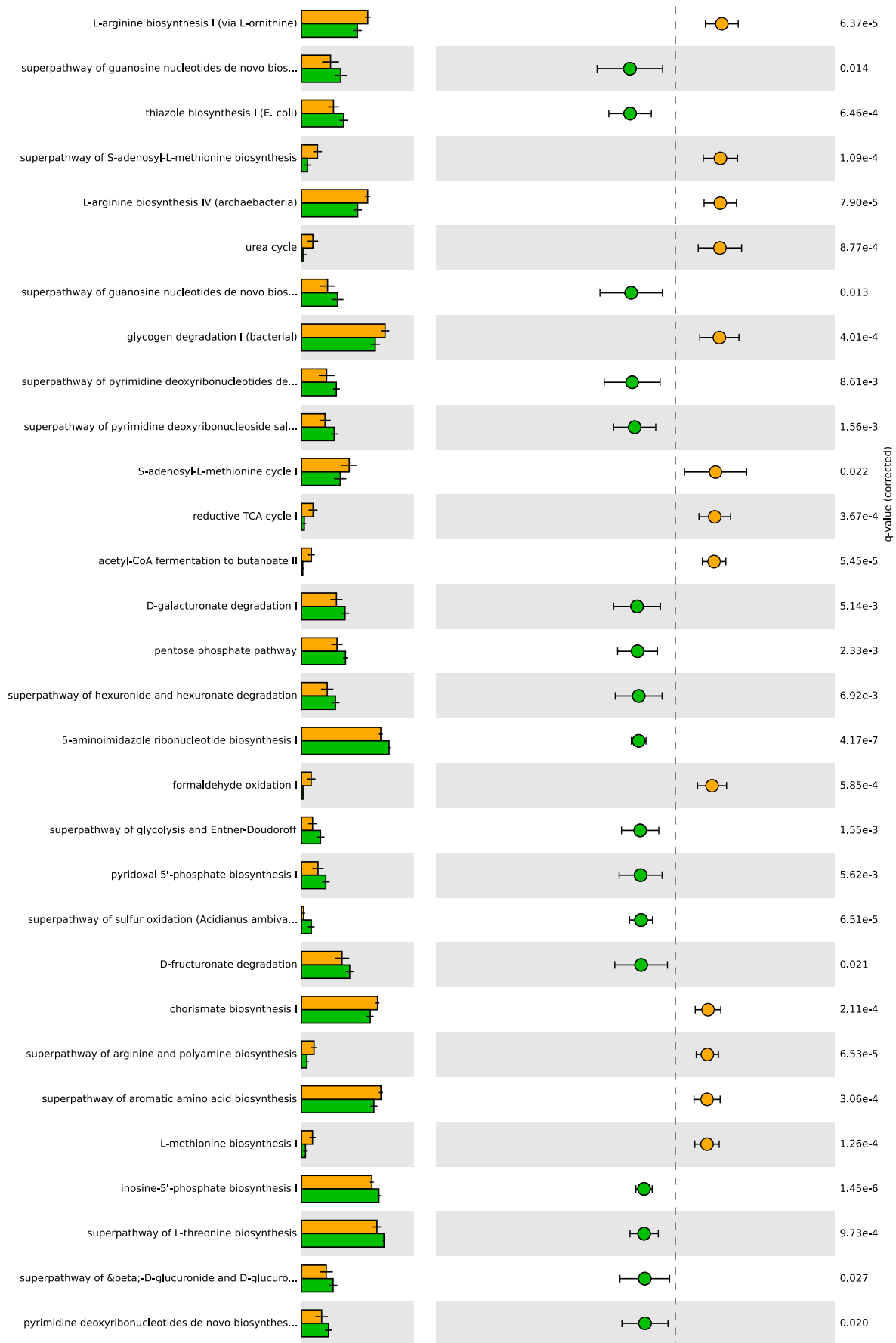


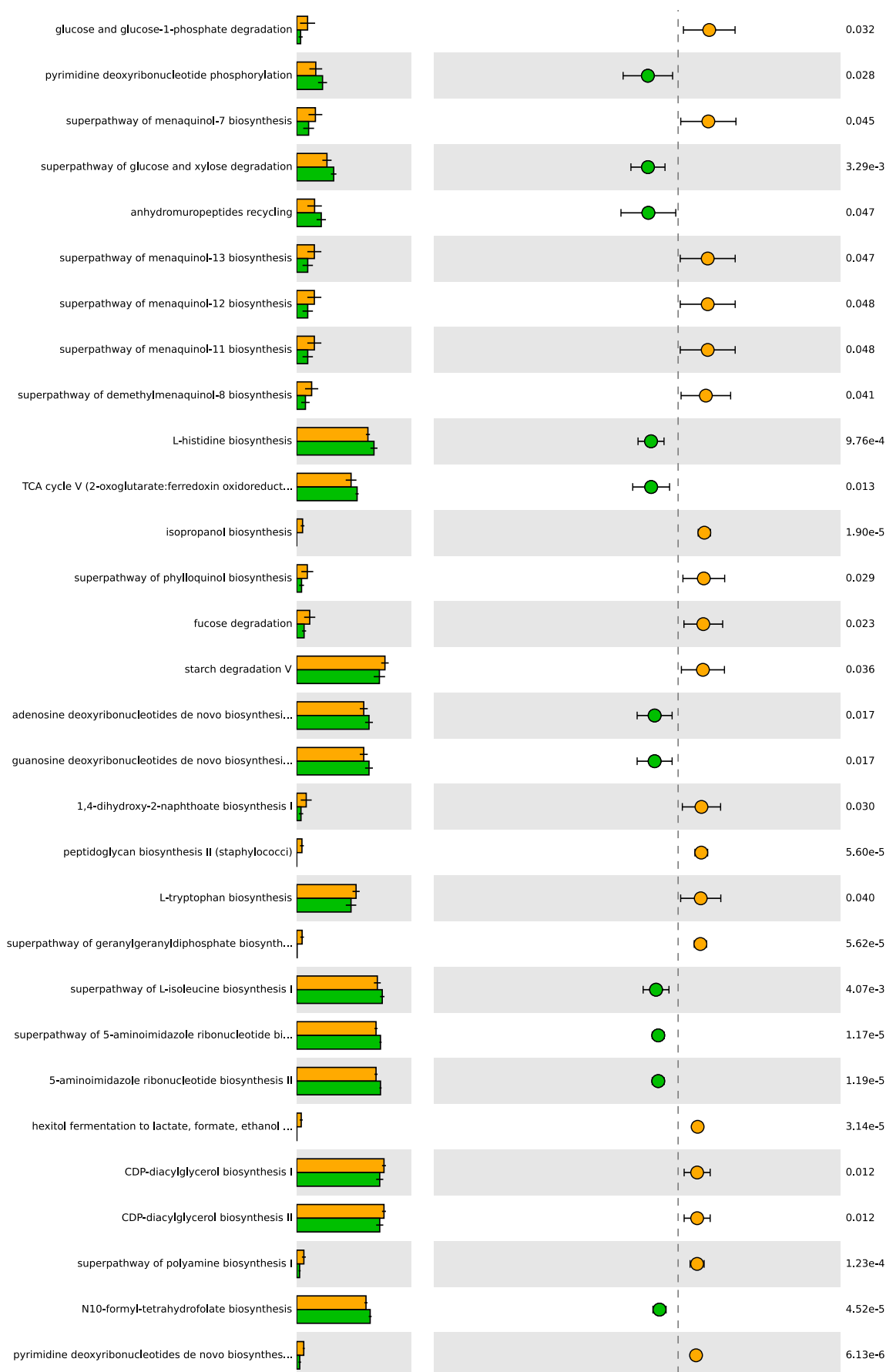


C.









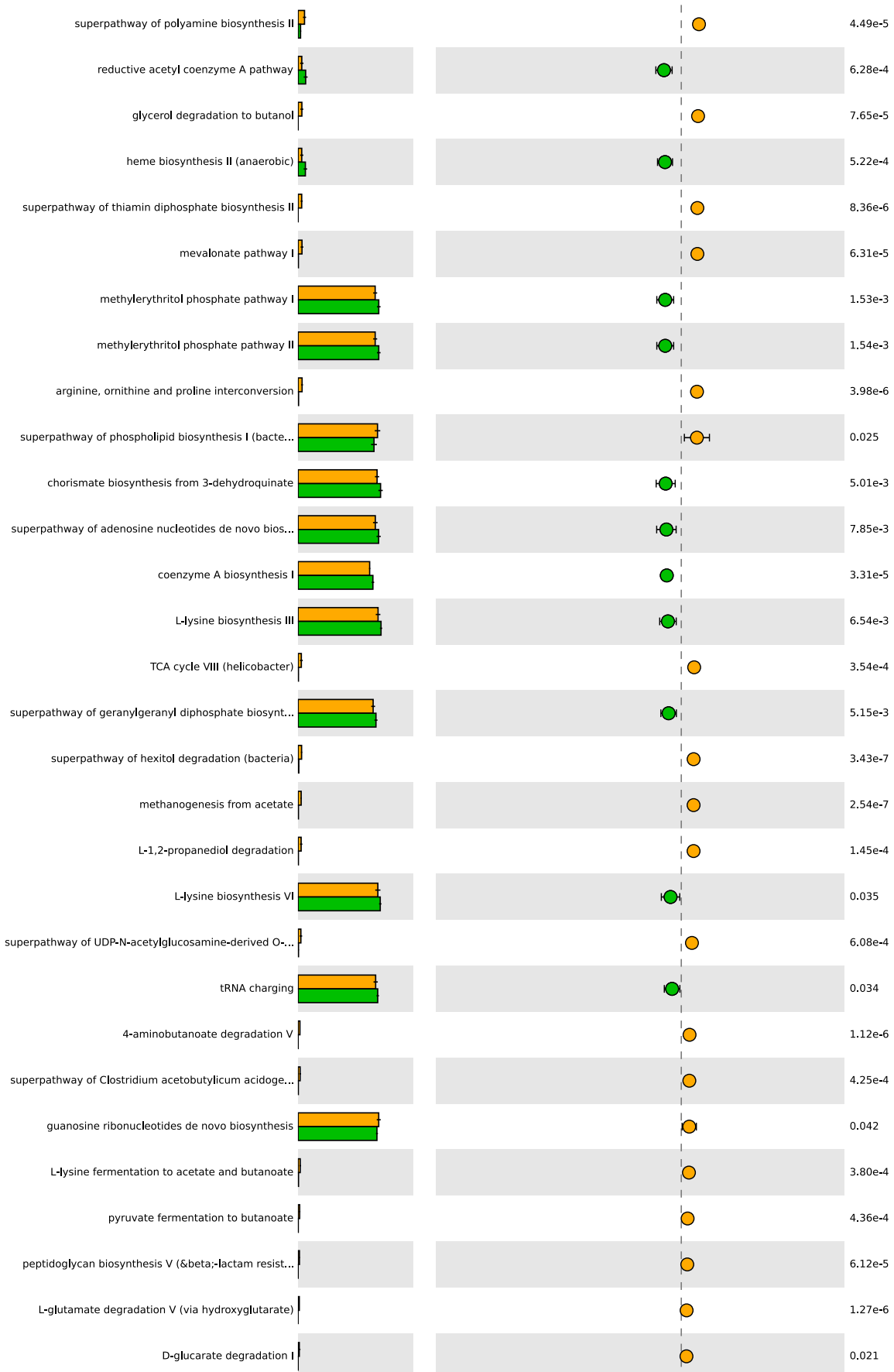
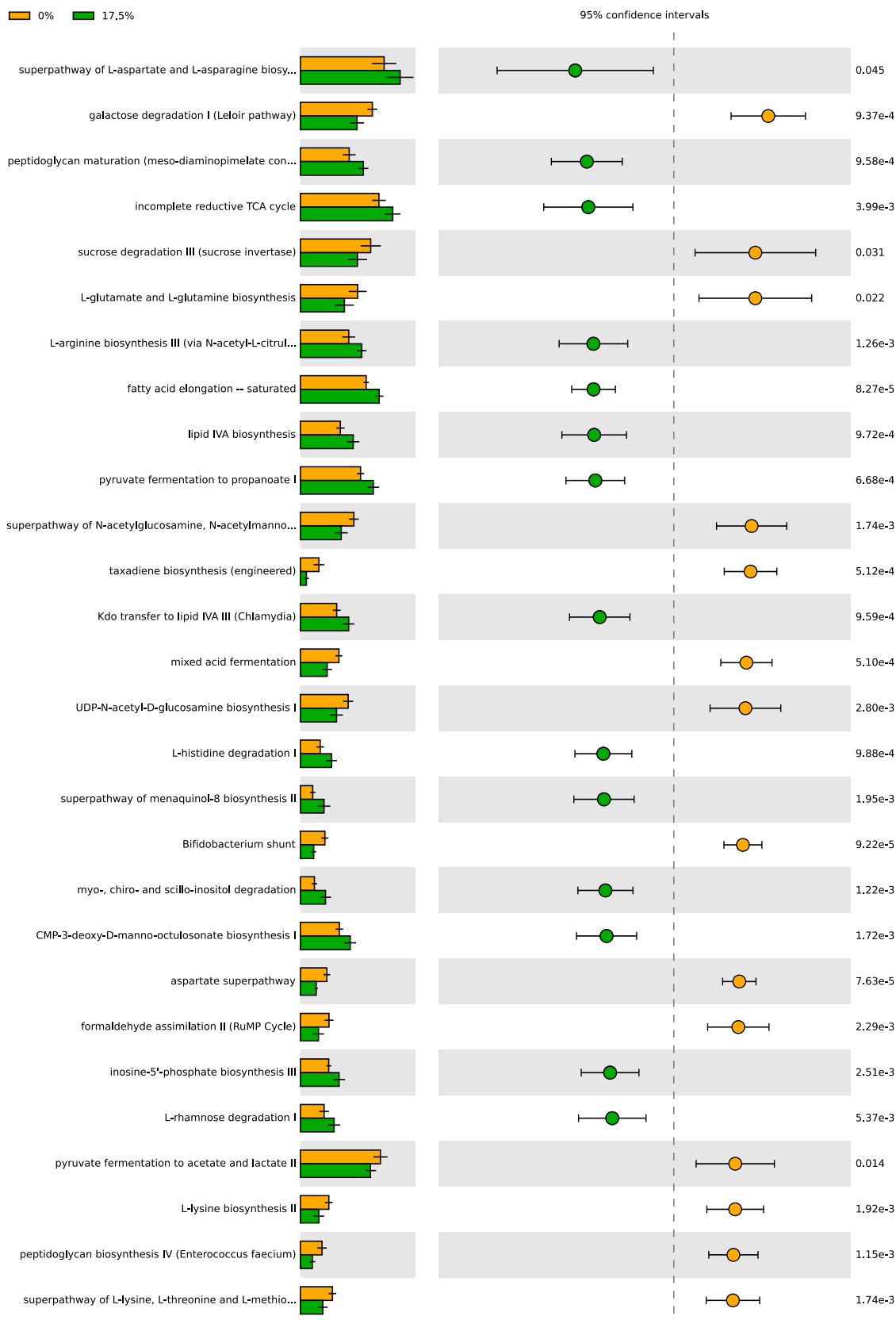
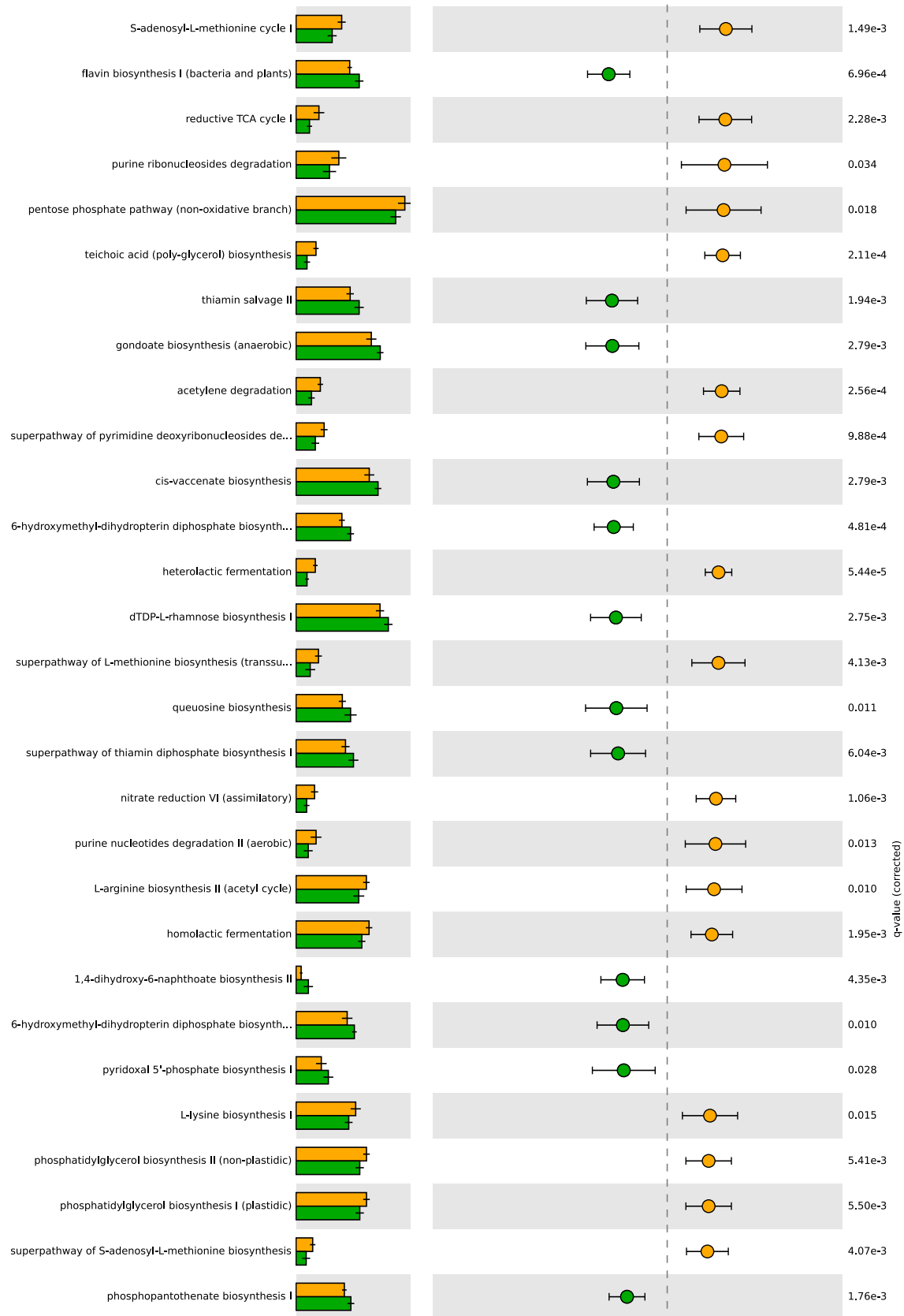




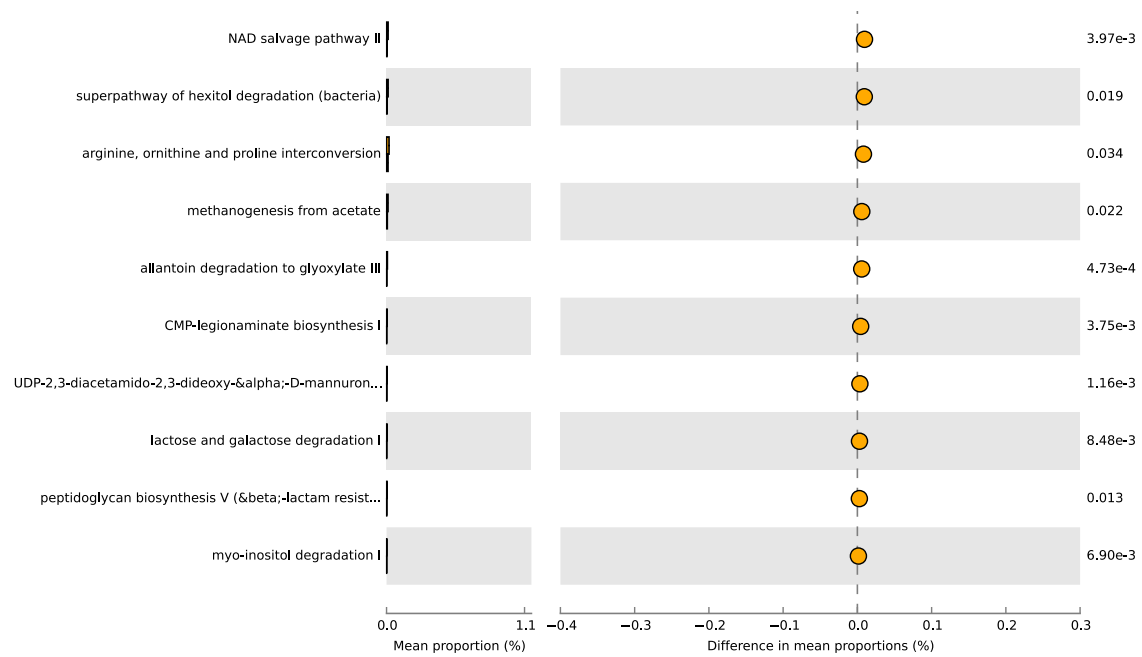
Figure S8. PICRUSt2 results indicating differential predicted functional pathways between the bean-free and the bean-containing diet groups in the female cohort: **(a)** 152 pathways in 0% vs 17.5% bean; **(b)** 183 pathways in 0% vs 35% bean; **(c)** 198 pathways in the 0% vs 70% bean. The bean-free diet (0%) is indicated in beige, while the bean-based diet samples (17.5%; 35%, and 70%)—in green. Extended error bar plot indicating the mean proportion of pathways assigned to each group, difference between them, and corrected *p*-value (*q*-value) of each.

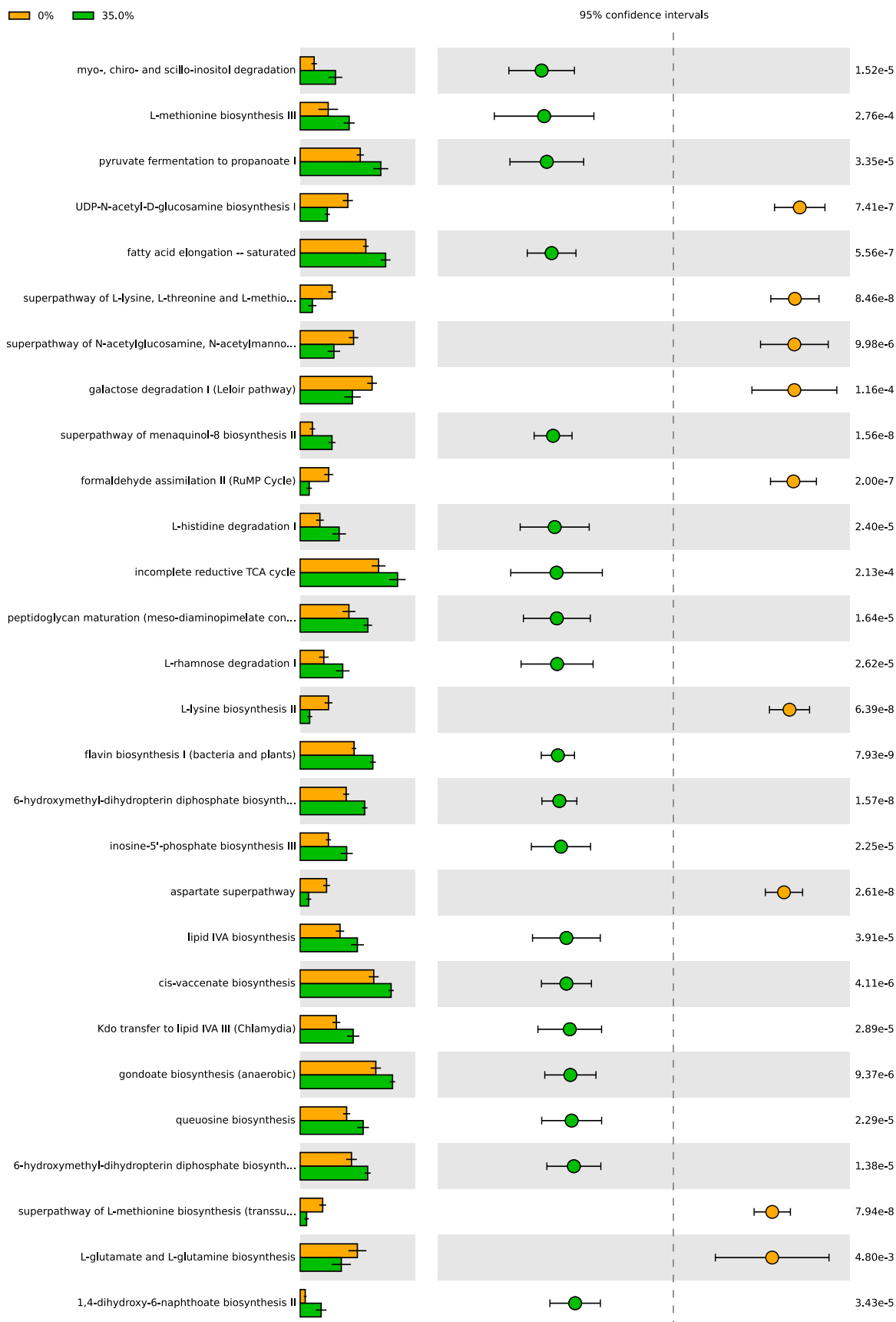


a.

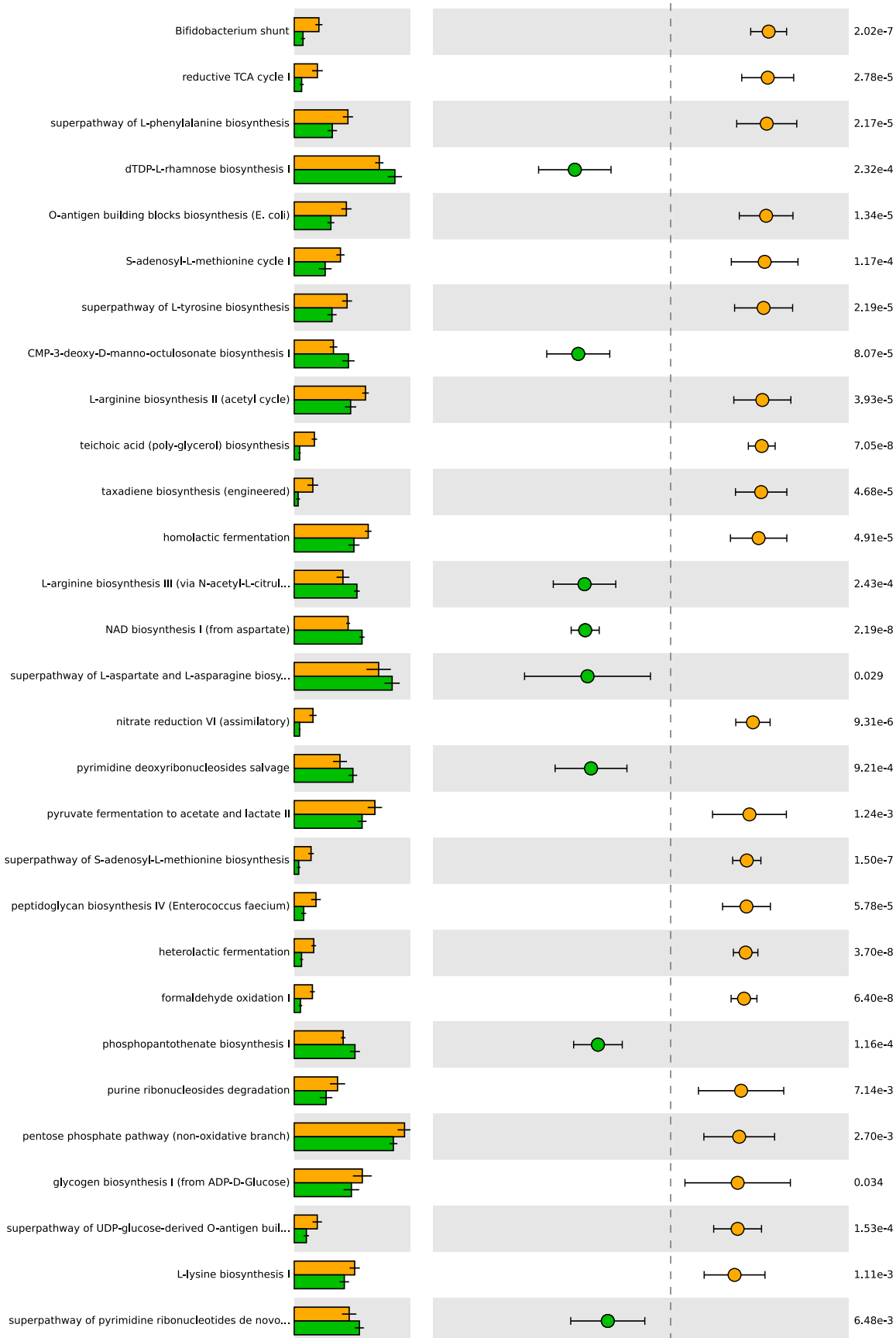


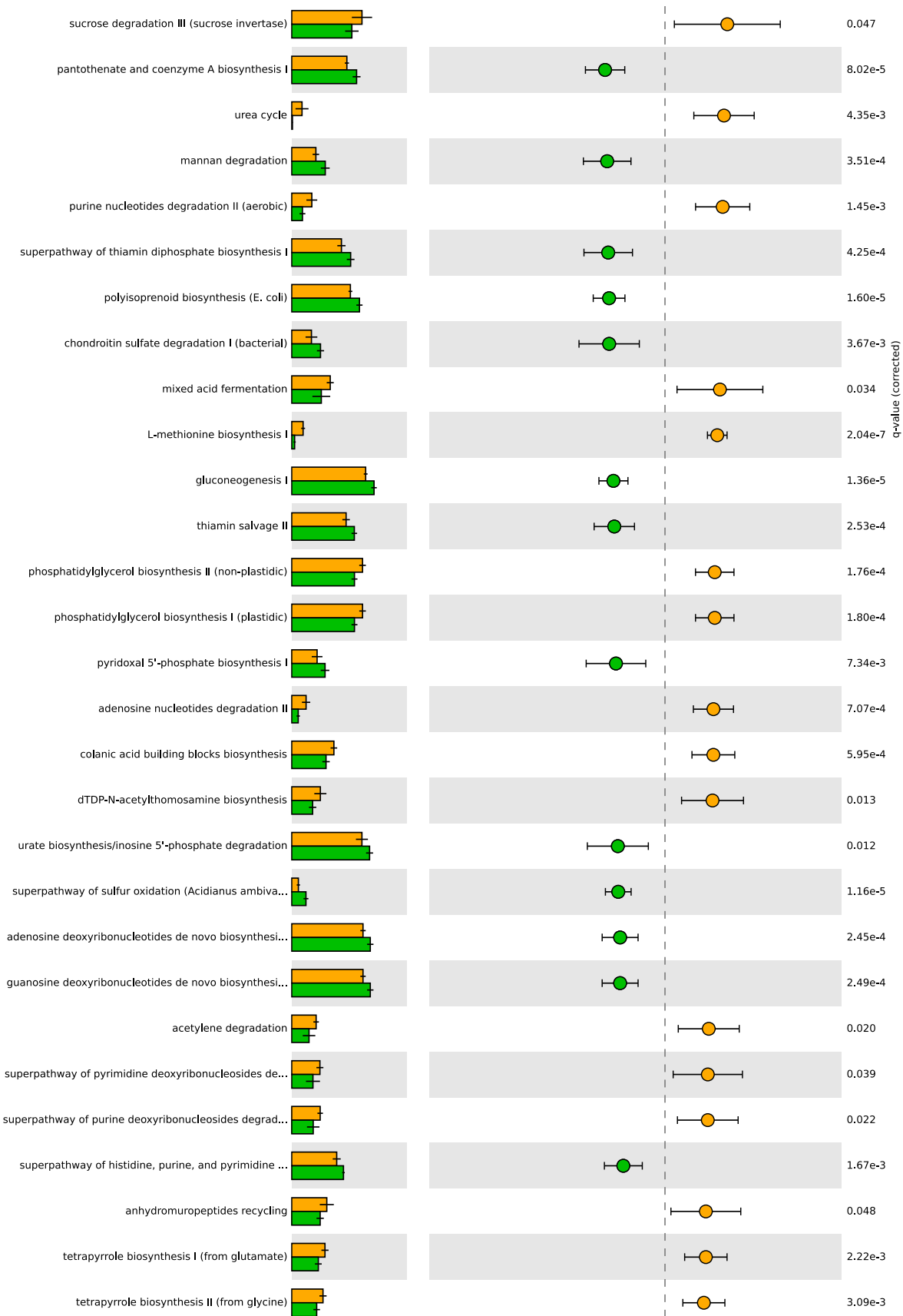


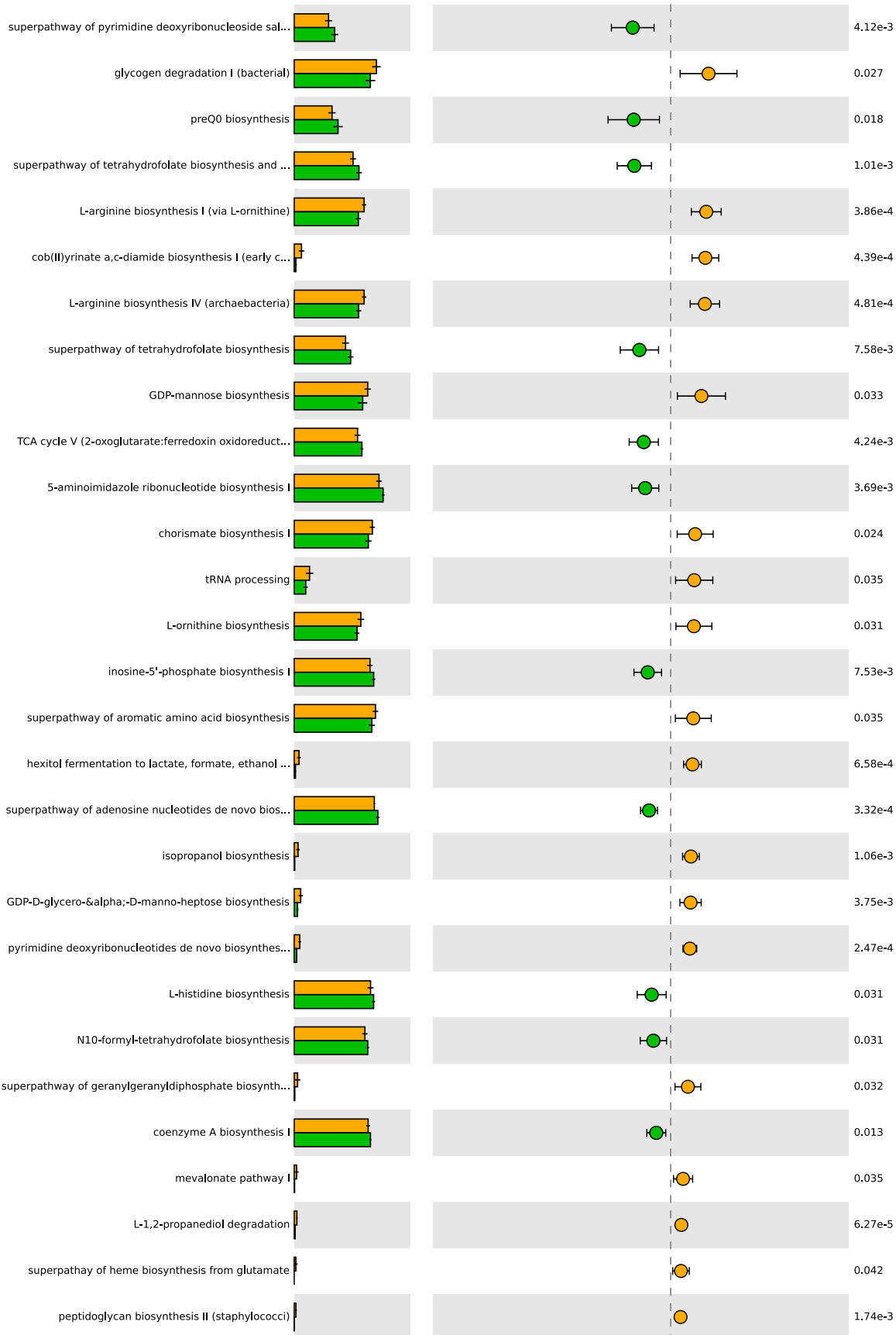


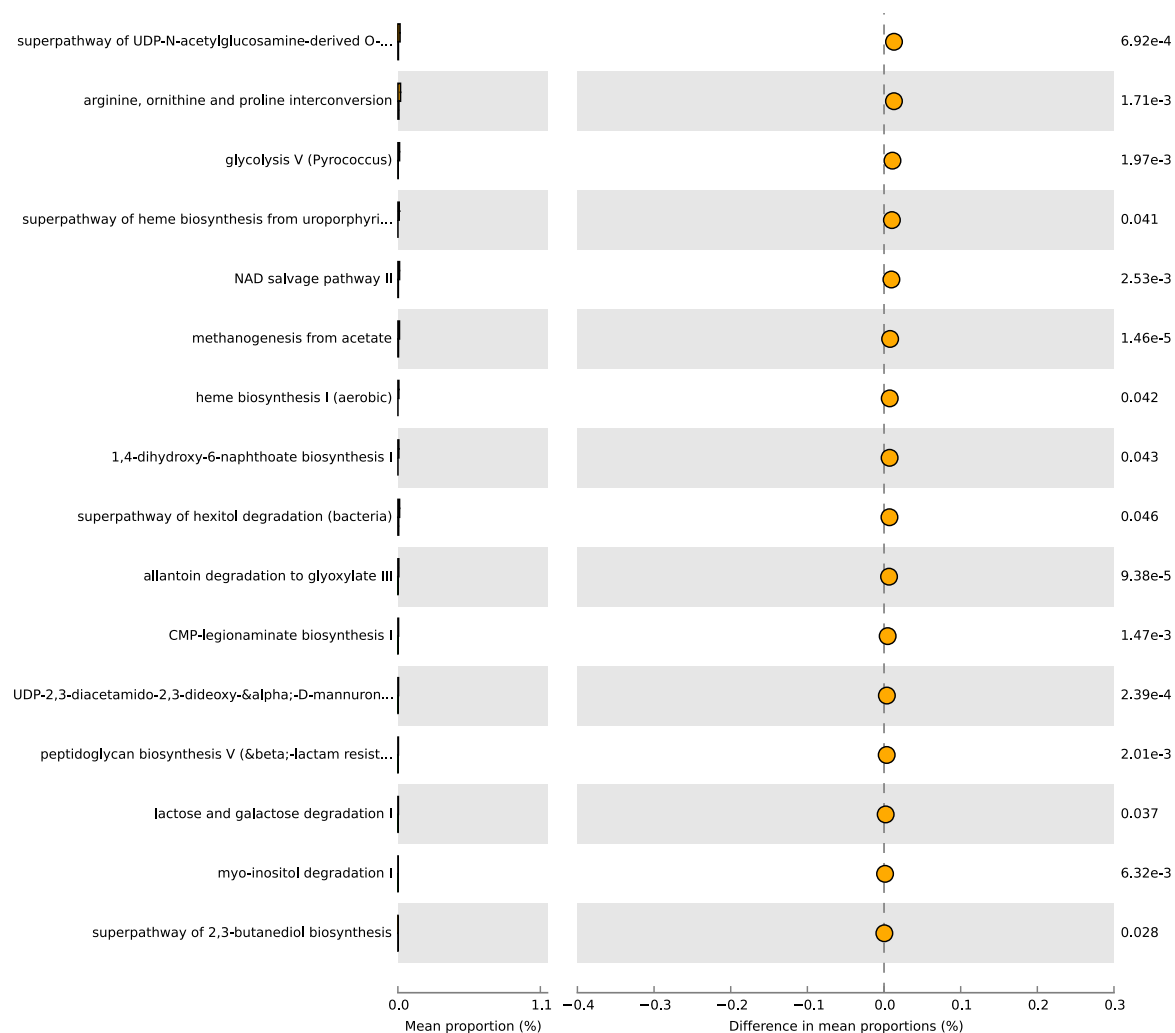


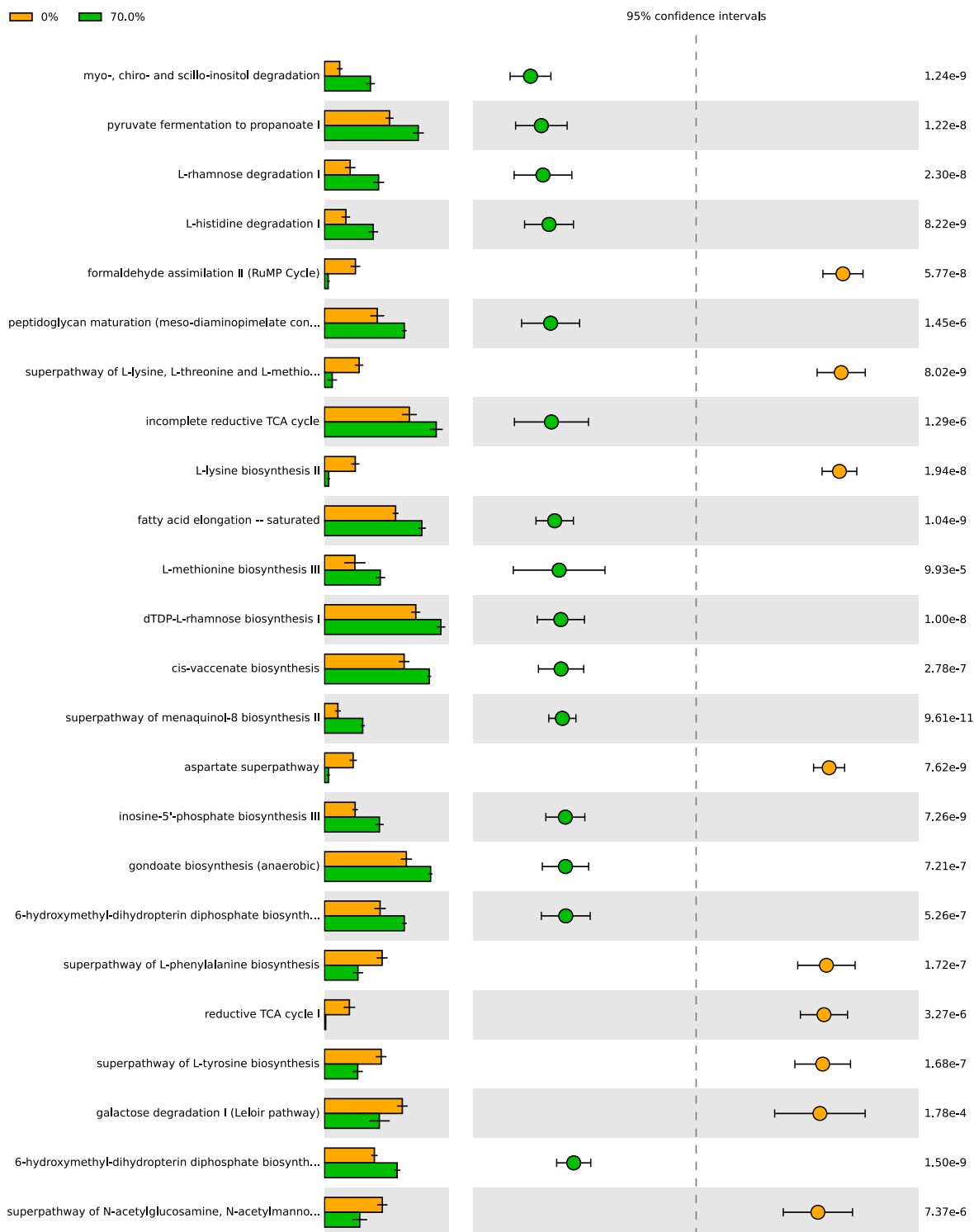
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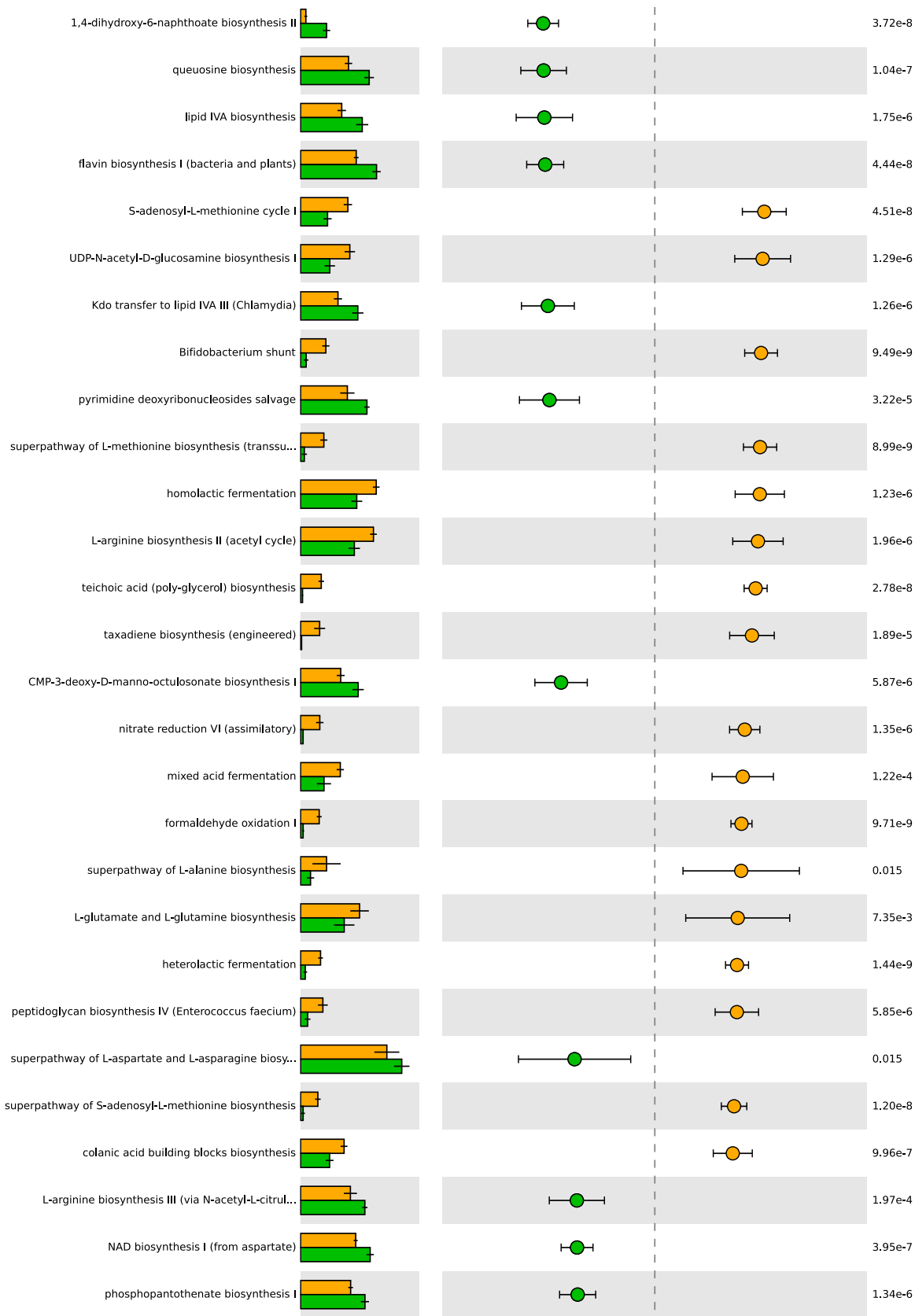


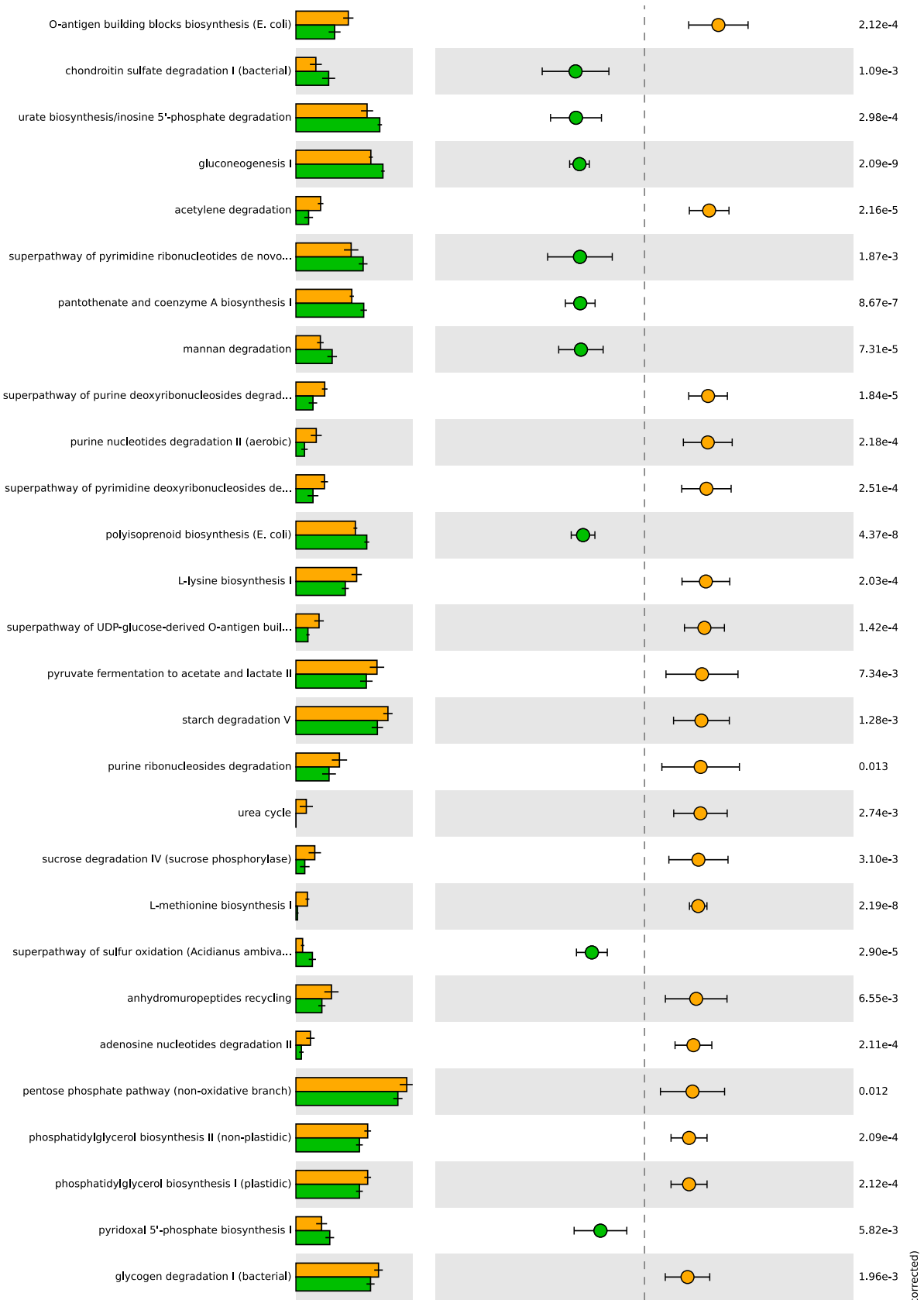




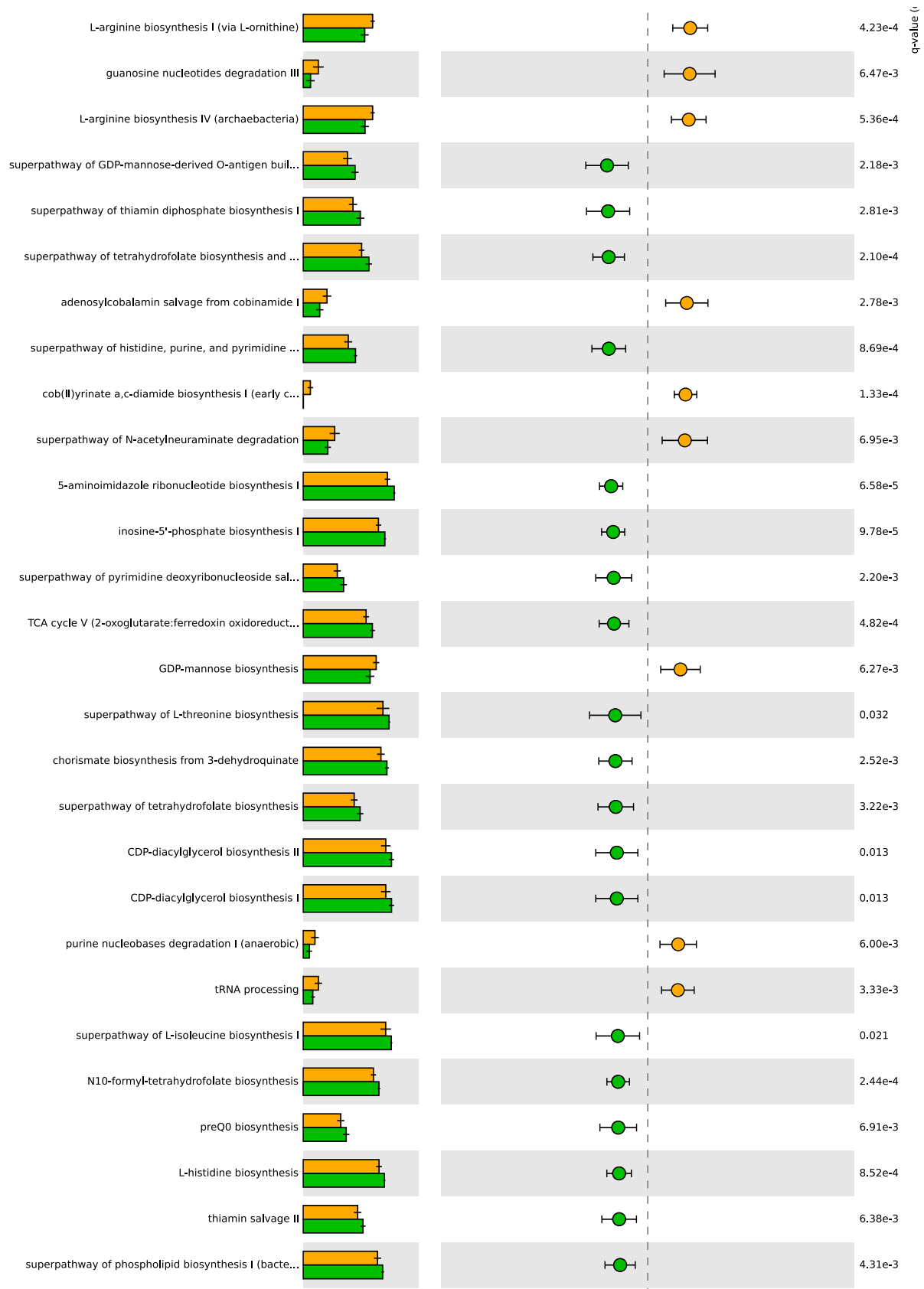


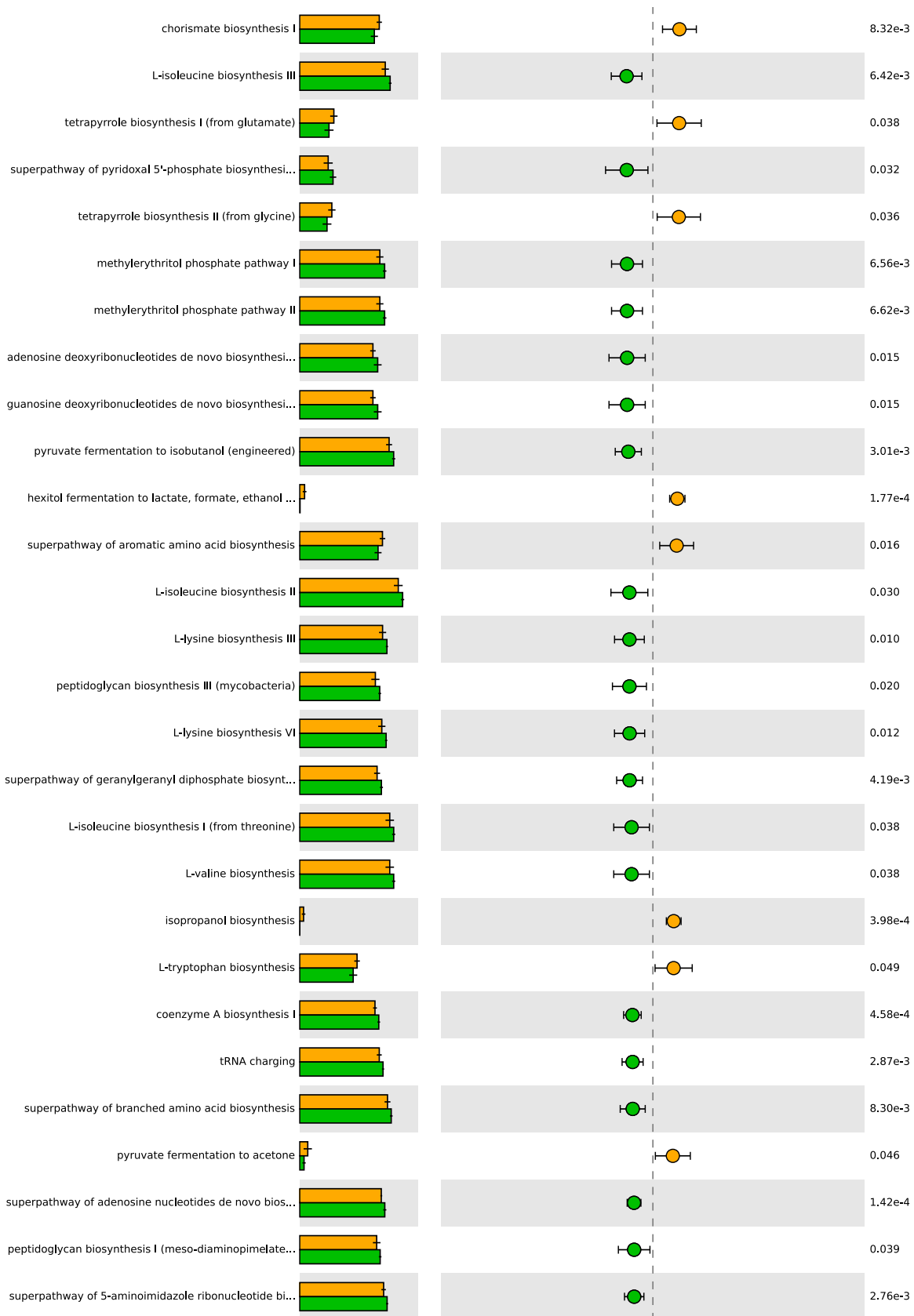
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(corrected)





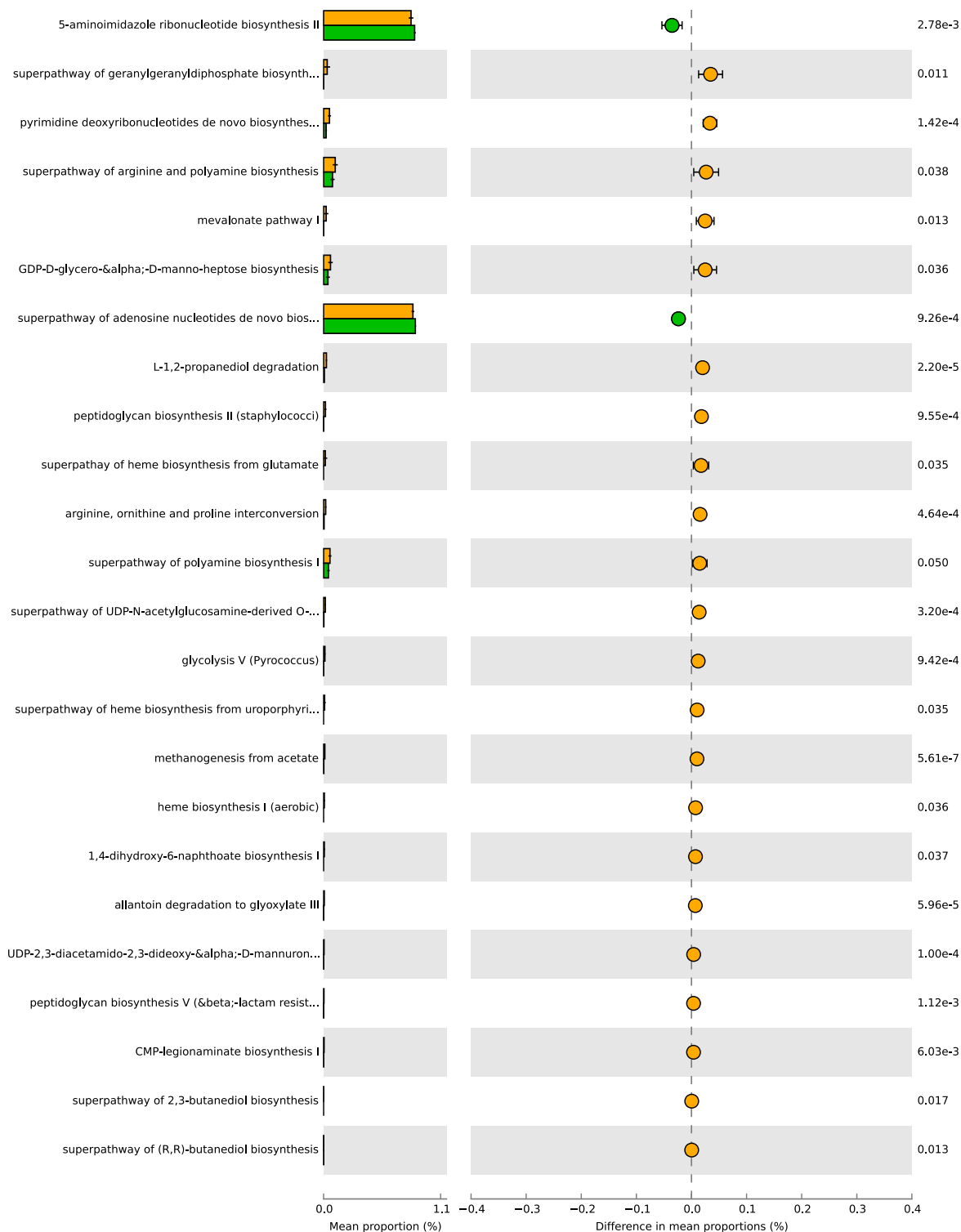


Figure S9. PICRUSt2 results indicating differential predicted functional pathways between the bean-free and the bean-containing diet groups in the male cohort: **(a)** 95 pathways in 0% vs 17.5% bean; **(b)** 131 pathways in 0% vs 35% bean; **(c)** 160 pathways in the 0% vs 70% bean. The bean-free diet (0%) is indicated in beige, while the bean-based diet samples (17.5%; 35%, and 70%)—in green. Extended error bar

plot indicating the mean proportion of pathways assigned to each group, difference between them, and corrected p -value (q -value) of each.