

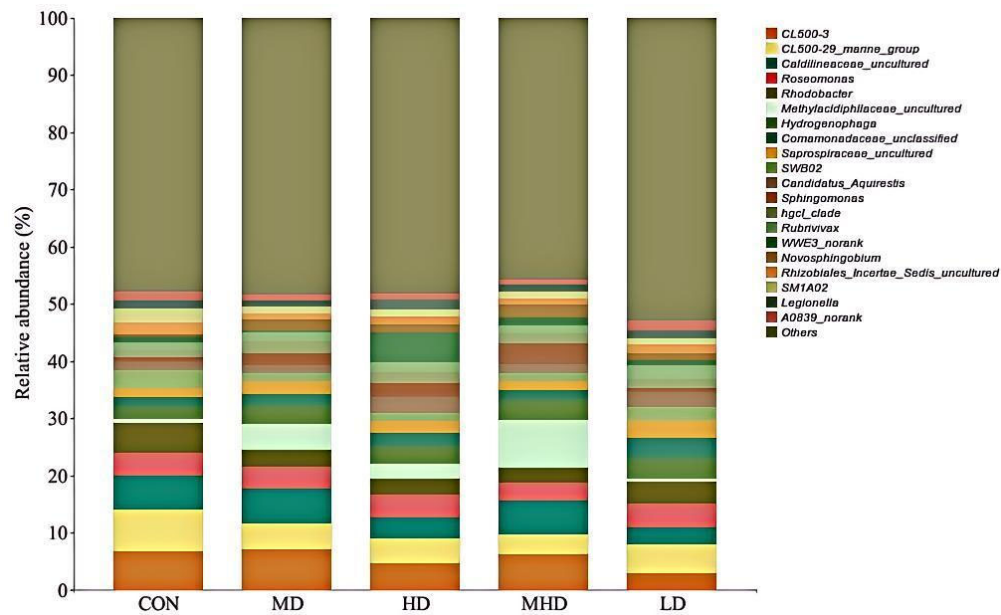


Figure S1. Genus-level bacterial community composition among *Bellamya* stocking-density treatments. Bars show treatment-level mean relative abundances of the 20 most abundant genus-level taxa in the normalized OTU table; all remaining taxa were grouped as “Others”.

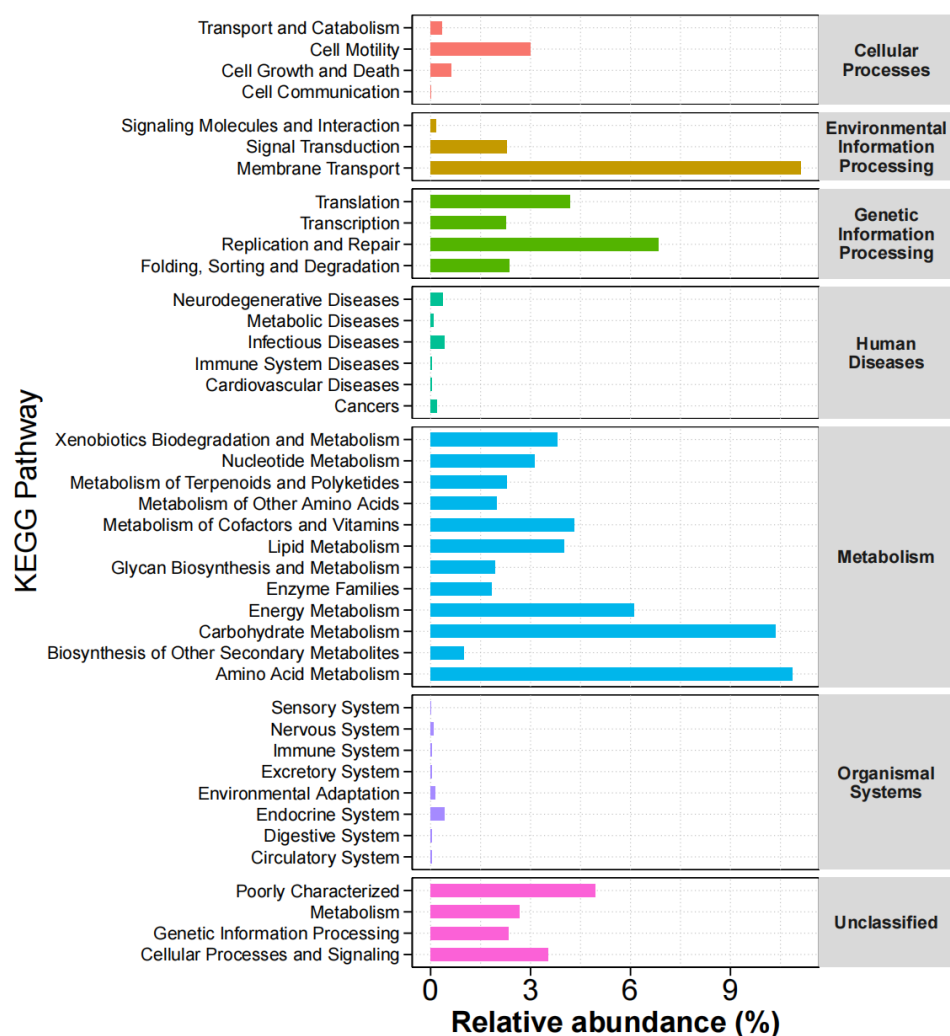


Figure S2. PICRUSt2-predicted KEGG Level 2 functional composition. Bars show the mean within-sample relative abundance of predicted functional categories across the 15 samples. These values are 16S-based predictions and do not represent direct measurements of genes, transcription, enzyme activity or pathway flux.

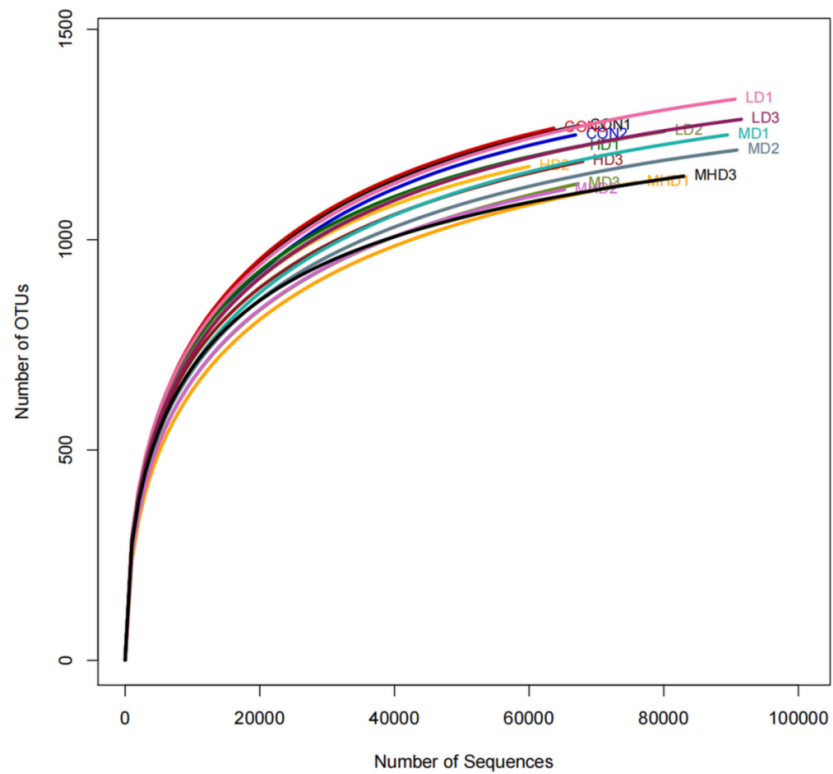


Figure S3. Rarefaction curves for bacterial OTUs clustered at 97% sequence similarity. Each curve represents one sample; the x-axis indicates sequencing depth and the y-axis observed OTUs. Curves approaching a plateau indicate adequate sequencing coverage.

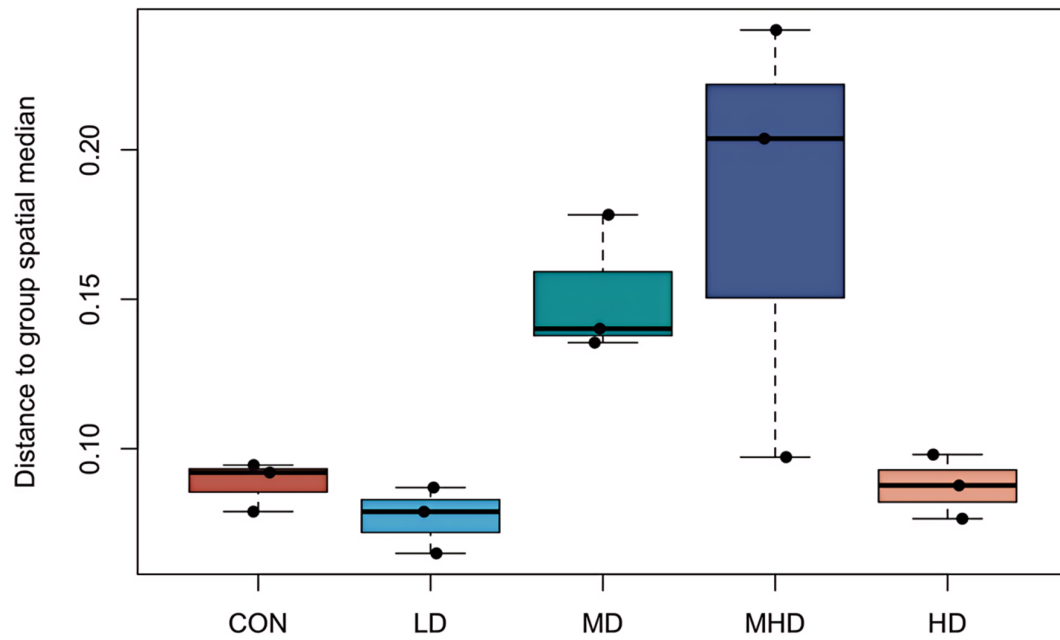


Figure S4. Multivariate dispersion of bacterial communities based on Bray–Curtis dissimilarity. Boxplots show sample distances to the treatment-group spatial median ($n = 3$ per treatment), calculated using `betadisper` (type = “median”); larger values indicate greater within-group dispersion. PERMDISP: $F_{4,10} = 4.99$, $P = 0.001$ (999 permutations).

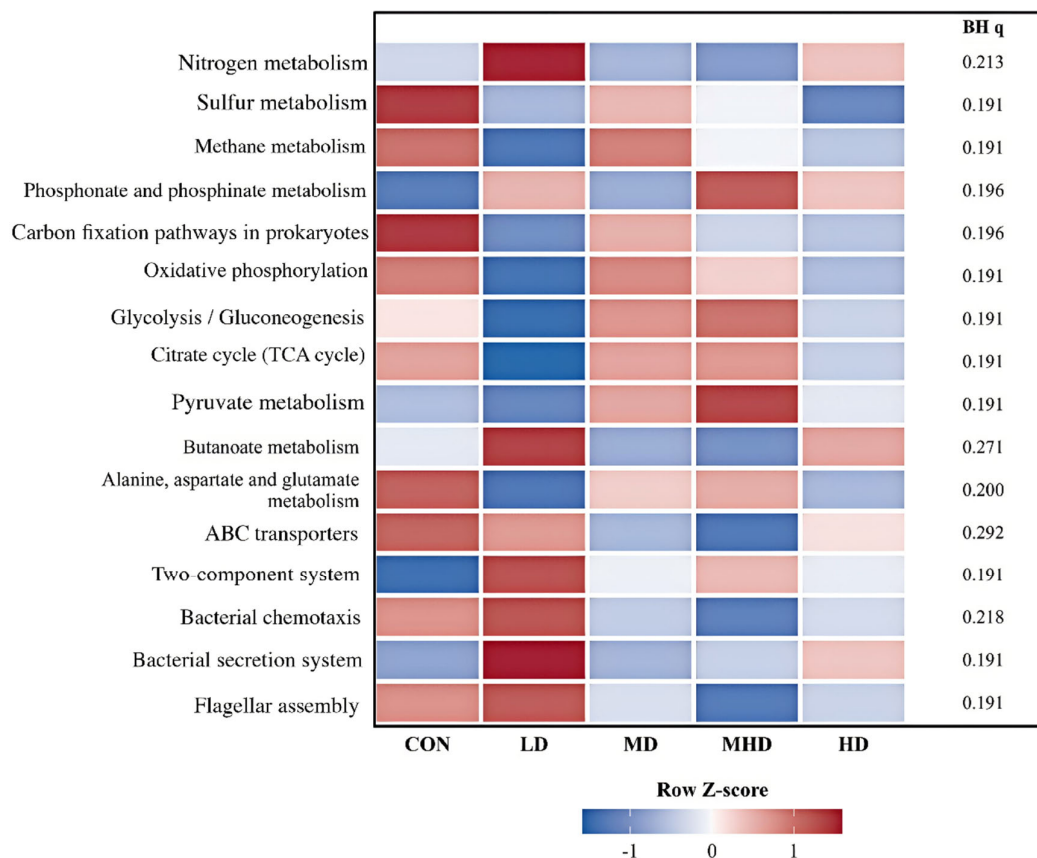


Figure S5. PICRUSt2-predicted KEGG Level 3 functional trends among *Bellamya* stocking-density treatments. Pathway abundances were converted to within-sample relative abundances, treatment means were calculated, and rows were standardized as Z-scores. The right-hand values are Benjamini–Hochberg-adjusted q values calculated across all 306 testable pathways. No pathway remained significant after FDR correction (all $q \geq 0.05$); the heatmap is therefore descriptive and does not demonstrate pathway activation or inhibition.