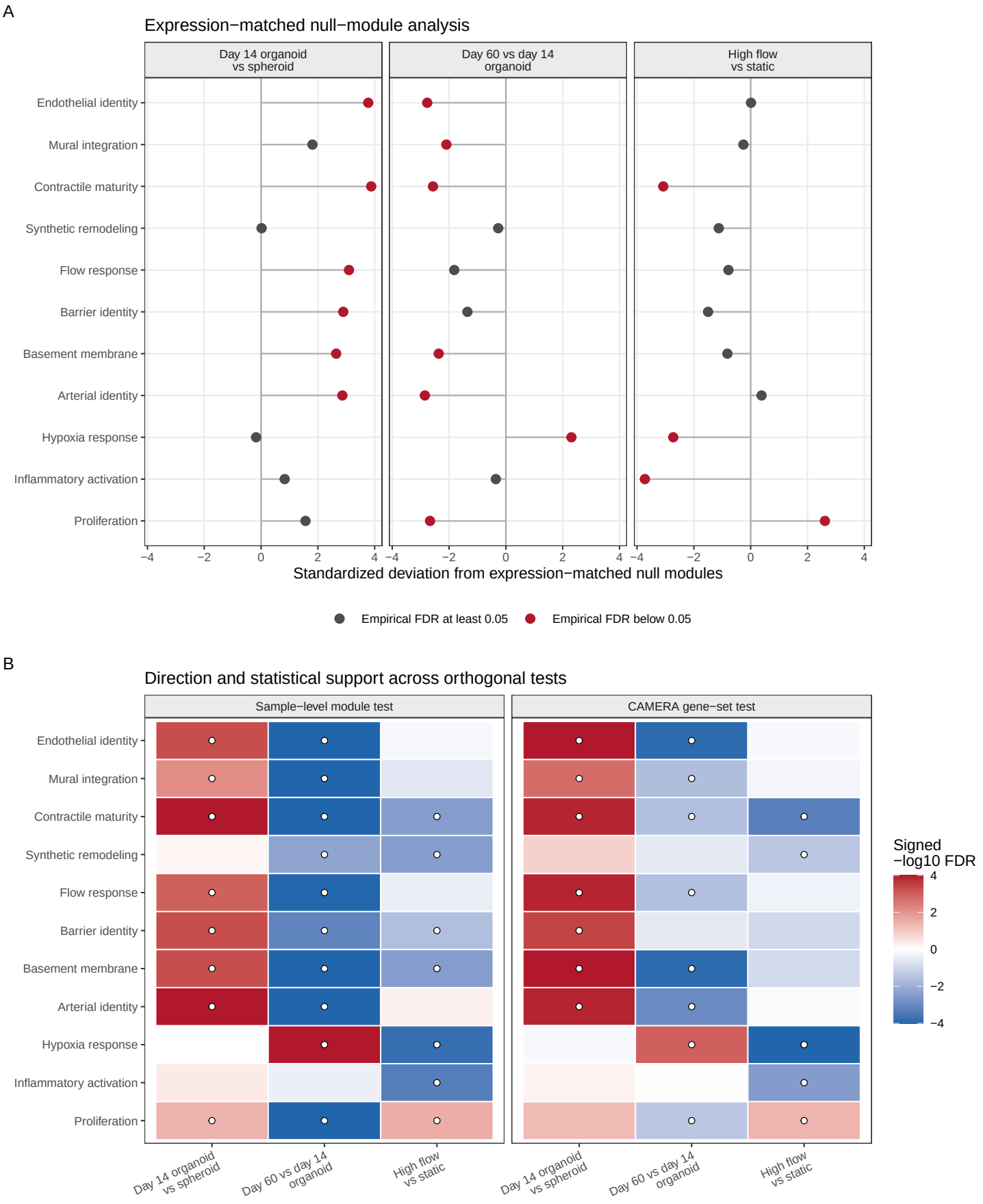


Supplementary Figure S1. Robustness of bulk RNA-sequencing module analyses. (A) For each of the three primary comparisons, the standardized deviation of each observed module effect from the null distribution generated by 2,000 expression-matched random modules is shown. The null modules matched each target module in size and mean-expression-bin composition. Red points indicate empirical FDR < 0.05. (B) Effect direction and statistical support from sample-level module tests and CAMERA competitive gene-set tests. Colors indicate signed -log10 FDR (absolute values capped at 4); red indicates a higher module score in the first condition and blue a lower score. White circles indicate FDR < 0.05.