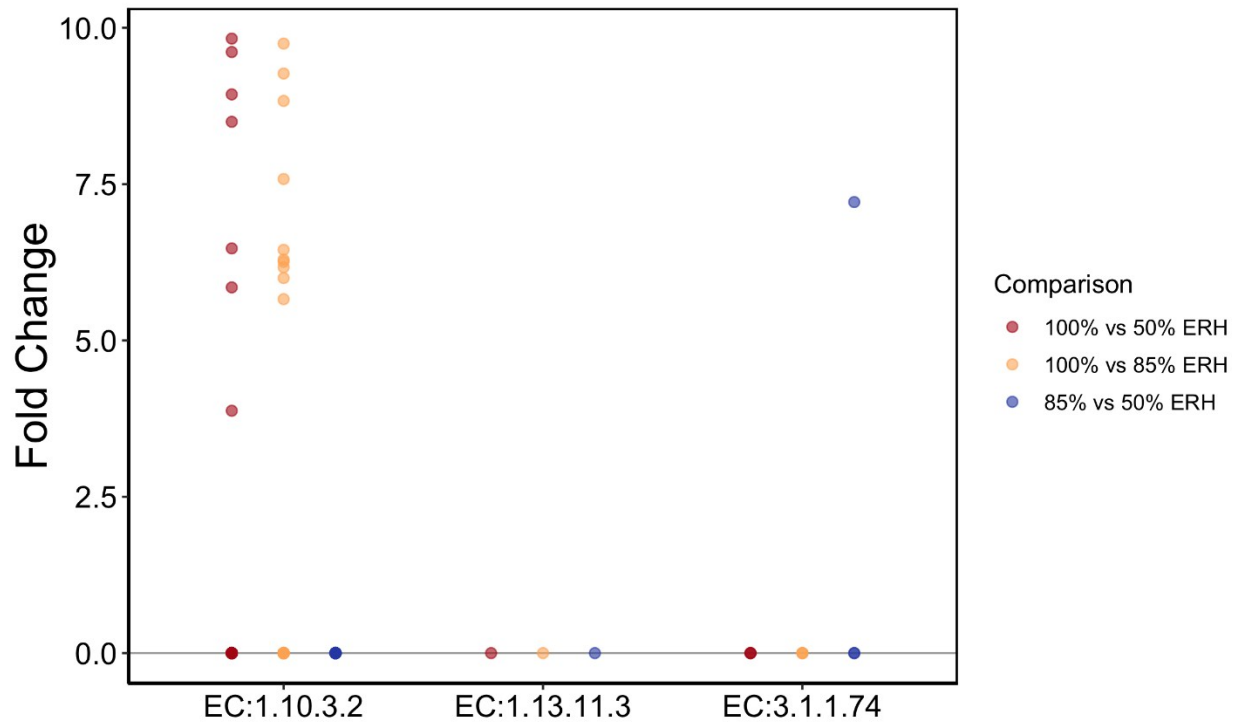
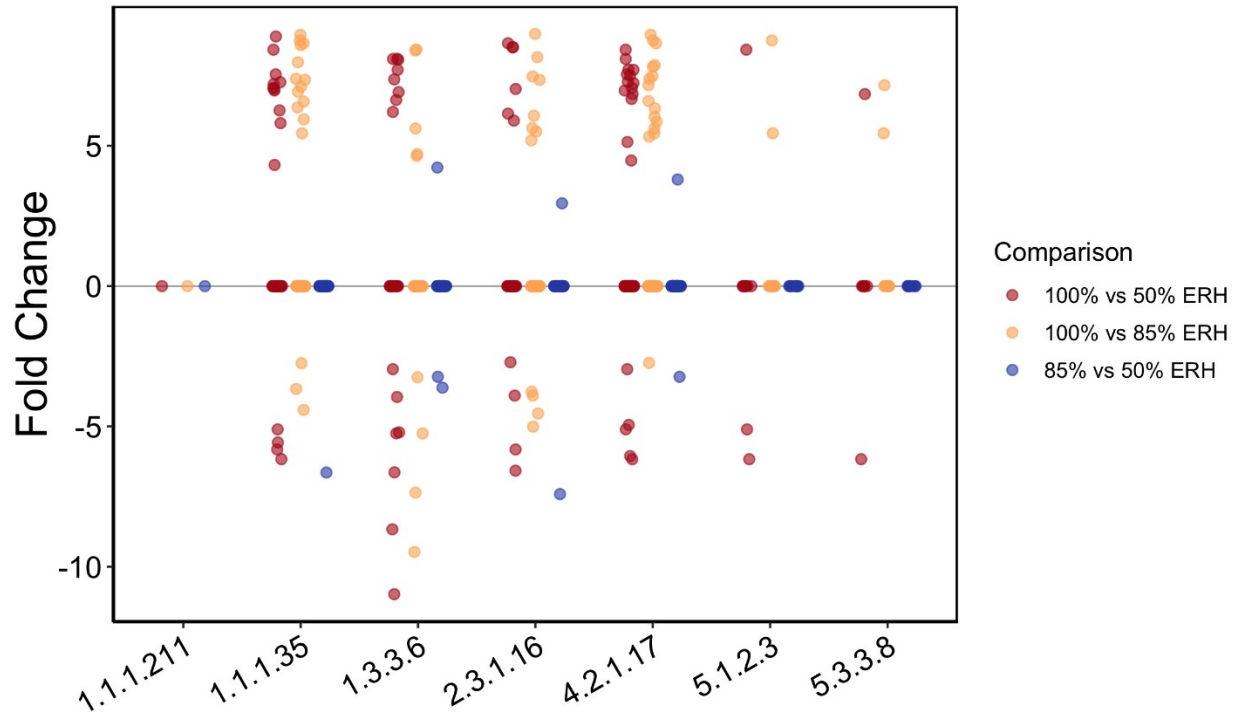


**SI Figure 1.** Standard calibration curve for detection of d-DEHP in the spiked experiments. The equation of the calibration line is  $Y = -0.41982 + 1.09325 * X$  and  $R^2 = 0.9971$ . The response ratio is generated using the ratio of the of d-DEHP peak area to the benzyl benzoate internal standard peak area.



**SI Figure 2.** Differential expression of genes with known phthalate degradation potential. All contigs with  $\log_2$  fold changes not equal to zero are considered differentially expressed ( $p_{\text{adj}} \leq 0.05$ ). Contigs with  $\log_2$  fold changes not found to be statistically significant are plotted at zero.  $\log_2$ F changes greater than zero indicate that contigs at 100% ERH are more highly expressed than at 50% ERH (100% vs 50% ERH in red) or 85% ERH (100% vs 85% ERH in orange). Similarly,  $\log_2$ F changes greater than zero indicate that contigs at 85% ERH are more highly expressed than at 50% ERH (85% vs 50% in blue). EC:1.10.3.2 is the enzyme commission number for laccase, EC:1.13.11.3 is for E10 3,4-protocatechuate deoxygenase, and EC:3.1.1.74 is for cutinase.



**SI Figure 3.** Differential expression for genes in the  $\beta$ -oxidation pathway that were found in the metatranscriptome. All contigs with  $\log_2$  fold changes not equal to zero are considered differentially expressed ( $p_{\text{adj}} \leq 0.05$ ). Contigs with  $\log_2$  fold changes not found to be statistically significant are plotted at zero.  $\log_2$ F changes greater than zero indicate that contigs at 100% ERH are more highly expressed than at 50% ERH (100% vs 50% ERH in red) or 85% ERH (100% vs 85% ERH in orange). Similarly,  $\log_2$ F changes greater than zero indicate that contigs at 85% ERH are more highly expressed than at 50% ERH (85% vs 50% in blue).