SI Figure 1. Standard calibration curve for detection of d-DEHP in the spiked experiments. The equation of the calibration line is $Y = -0.41982 + 1.09325X$ 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 log₂ fold changes not equal to zero are considered differentially expressed (p<sub>adj</sub> ≤ 0.05). Contigs with log₂ fold changes not found to be statistically significant are plotted at zero. Log₂F 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, log₂F 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 β-oxidation pathway that were found in the metatranscriptome. All contigs with log_2 fold changes not equal to zero are considered differentially expressed (p_adj ≤ 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).