**Dataset S1. RPKM data, differential expression testing, and gene location and annotation information from RNA-Seq analysis of cultures grown in the presence of glucose and G-type aromatics.**

**Figure S1. HPLC-UV analysis of extracellular compounds found in the media of cultures grown on glucose plus G-diketone at timepoints 0 hours and 75.5 hours and comparison to standards**.

**Figure S2. Mass spectra of extracellular compounds identified in the media of cultures grown on glucose plus G-diketone at timepoint 75.5 hours analyzed via GC-MS and comparison to GP-1 and threo-GD standards.** We have also included the published spectrum for GP-2 from Mitchell (2014) (1) for reference to our proposed identification of GP-2.

**Figure S3. Number of genes that significantly differ in transcript abundance during growth in the presence of glucose alone compared to glucose plus each indicated aromatic substrate.** Genes with a q-value < 0.01 are considered significant. Panel A displays counts of genes with increased transcript abundance compared to the glucose control, while Panel B displays counts of genes with decreased transcript abundance.

**Figure S4. Genomic neighborhoods of** *N. aromaticivorans* **genes associated with β-O-4 linked aromatic dimer degradation.** Shown are position and genes linked to transcripts with increased abundance when cells were grown in the presence of G-diketone and glucose compared to glucose alone.

Figure S5. Reaction velocity vs. substrate concentration used to calculate Km and kcat values for LigL, LigN, and LigD on GGE, G-diketone, and GD.

**Figure S6. Growth of individual 12444ΔLigLNDOdeletion strains on glucose and glucose plus G-diketone compared to that of the 12444ΔSacBparent strain.**