

File S2

New Insights into *Dehalococcoides mccartyi* Metabolism from a Reconstructed Metabolic Network-Based Systems-Level Analysis of *D. mccartyi* Transcriptomes

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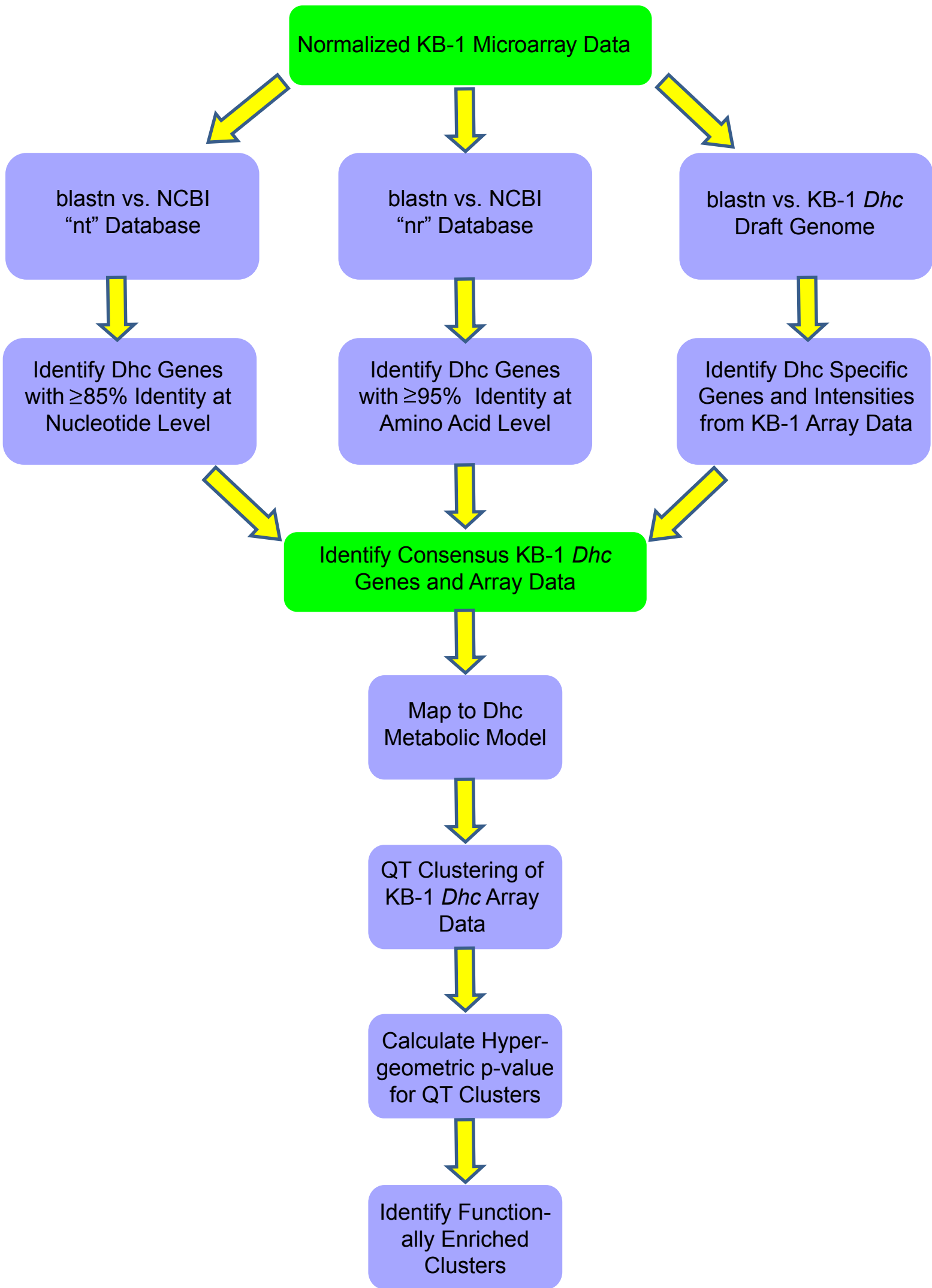


Figure S1. Workflow for Analyzing Pre-Processed KB-1 Microarray Data

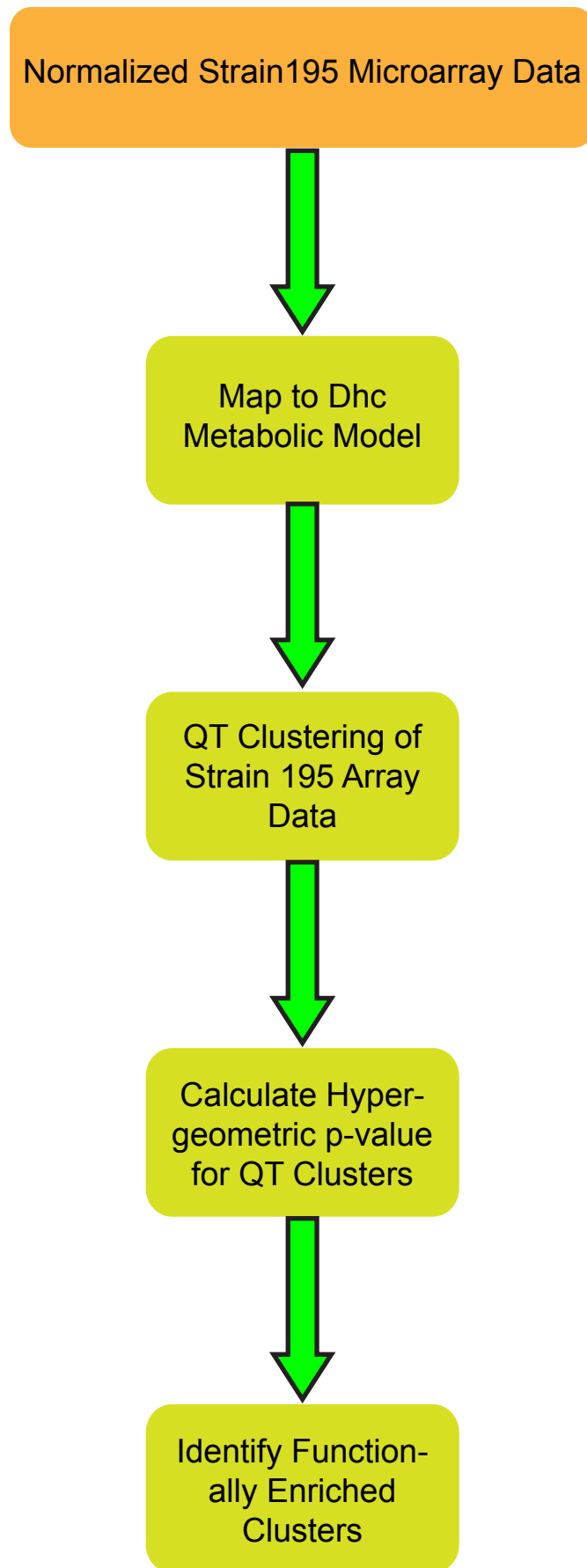


Figure S2. Workflow for Analyzing Pre-Processed Strain 195 Microarray Data

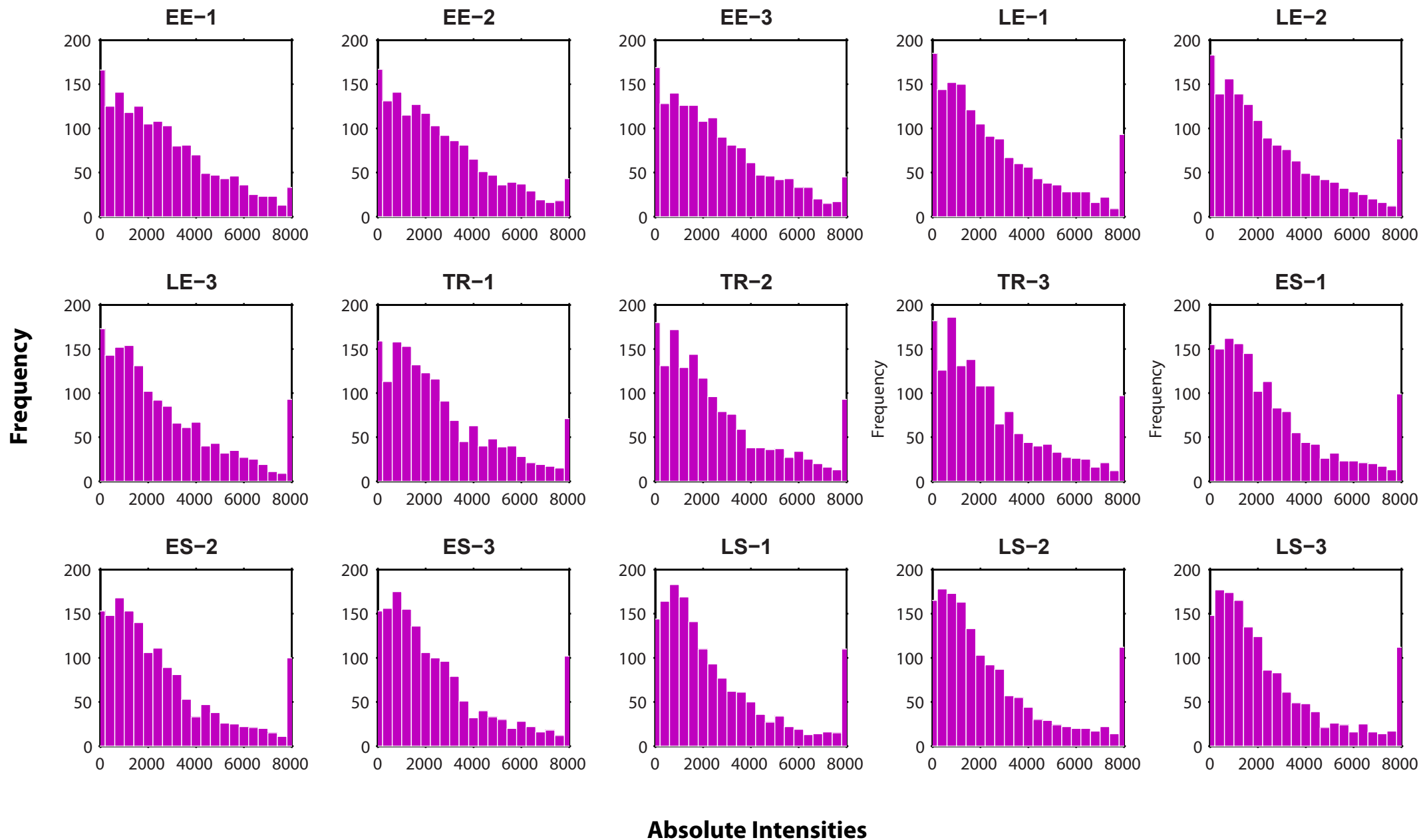


Figure S3. Distribution of Strain 195 Gene Expression Intensities for 27 Samples

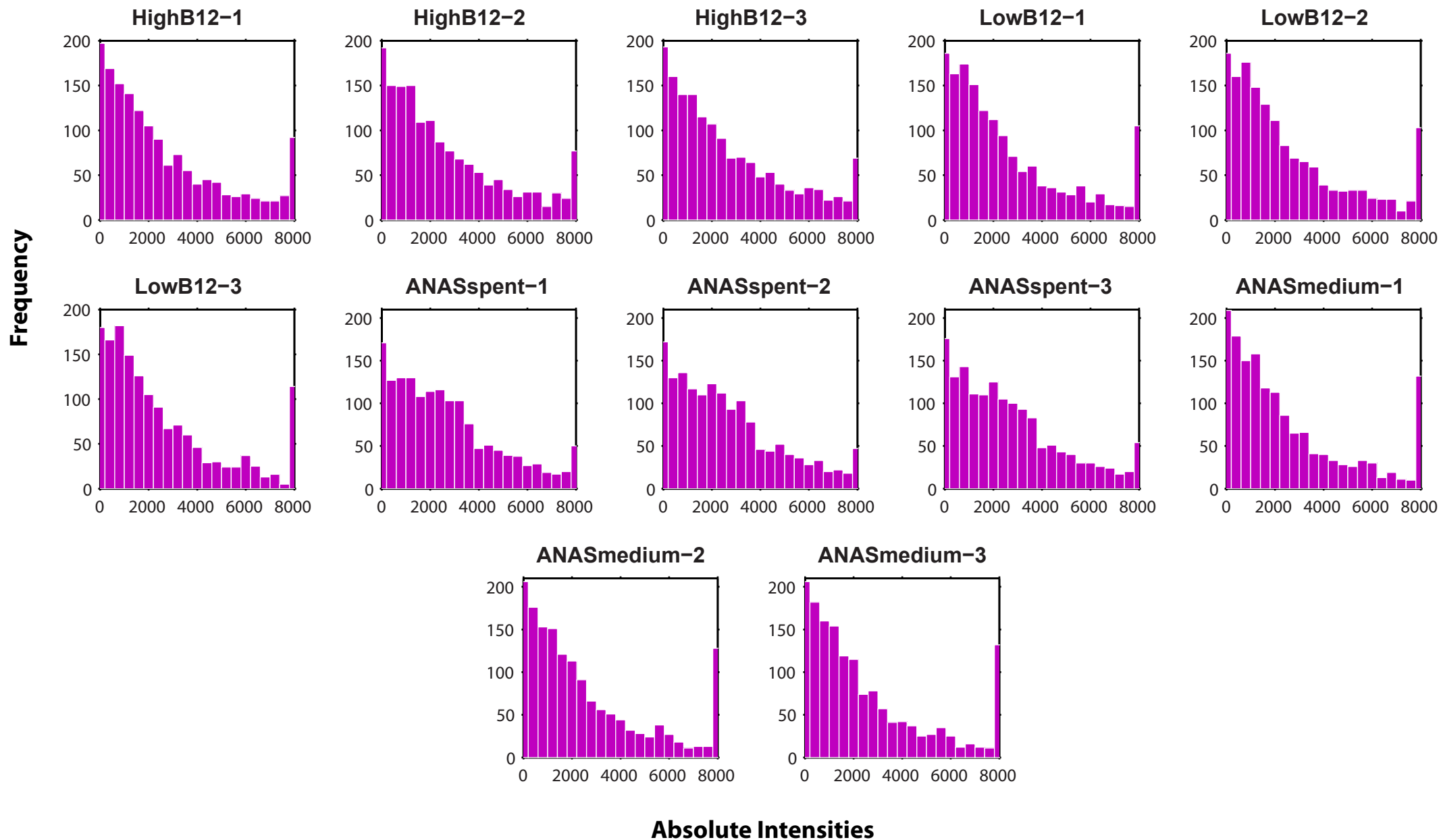


Figure S3. Distribution of Strain 195 Gene Expression Intensities for 27 Samples (continued from previous page)

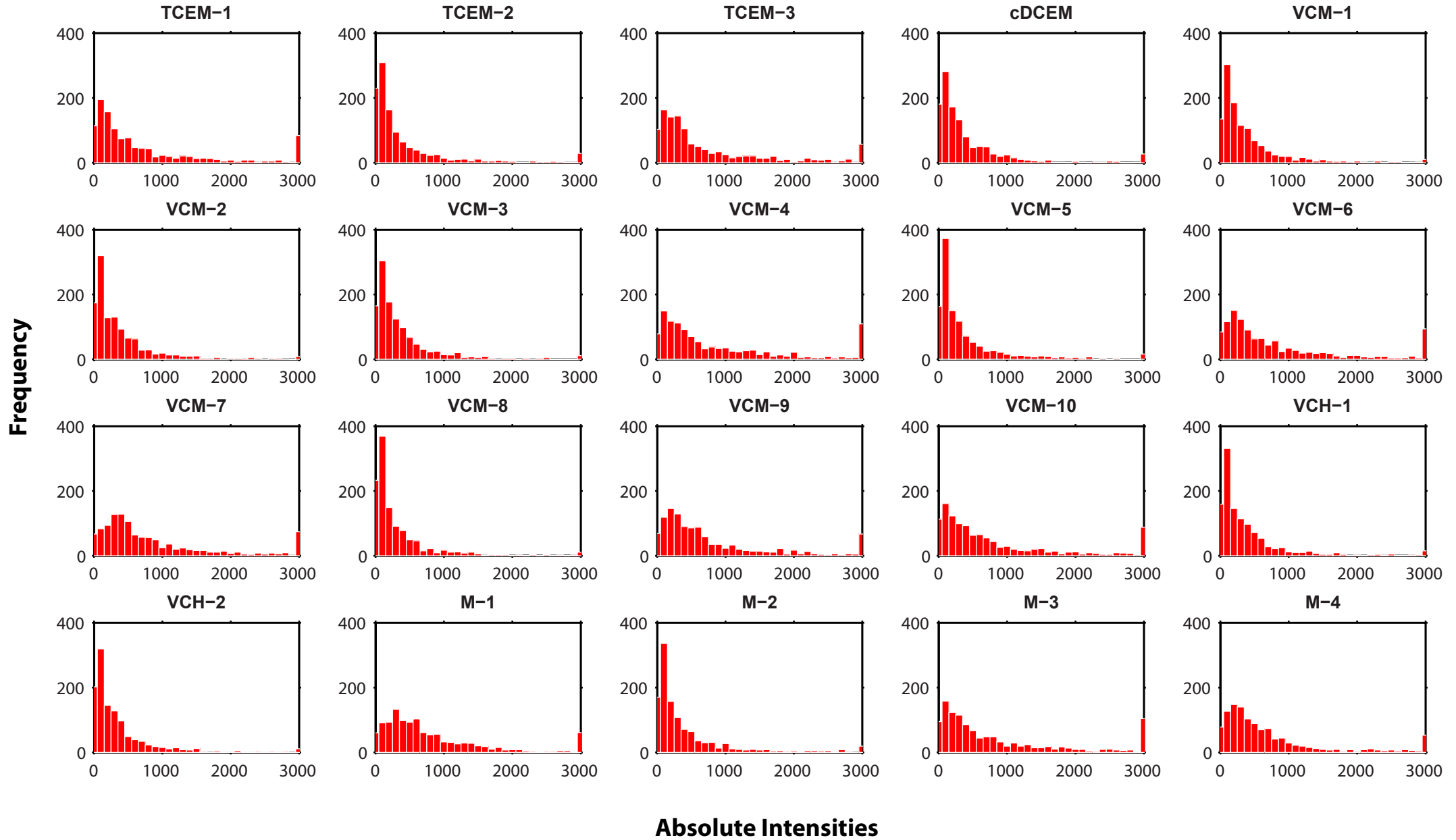


Figure S4. Distribution of KB-1 *Dhc* Gene Expression Intensities for 33 Samples

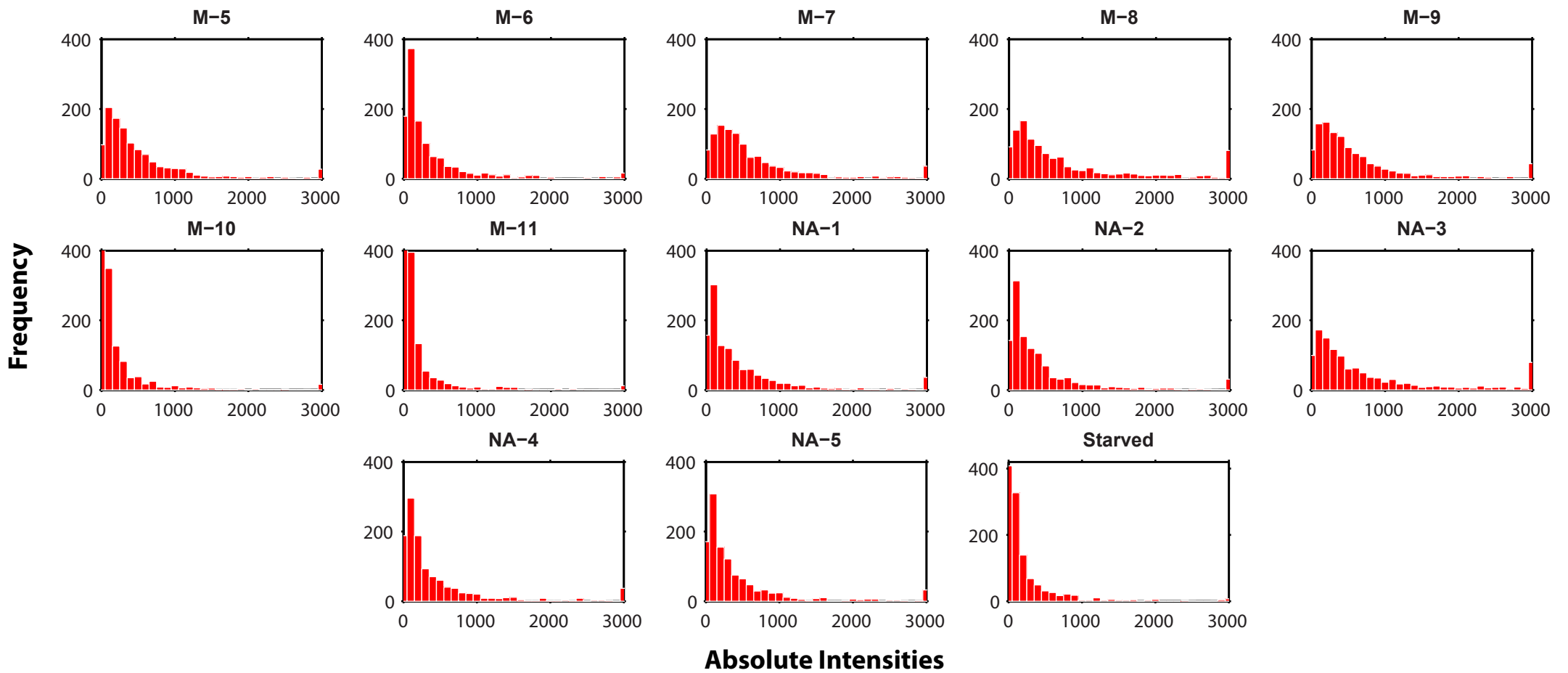


Figure S4. Distribution of KB-1 *Dhc* Gene Expression Intensities for 33 Samples (continued from previous page)