

Metabolomic Analysis of Liver and Skeletal Muscle Tissues in C57BL/6J and DBA/2J Mice
Exposed to 2,3,7,8-Tetrachlorodibenzo-*p*-Dioxin

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Figure S1. Variance explained (%) of PCA models generated from the tissue sample sets. The accumulative eigenvalues of the first two components were 97.29%, 93.62%, 75.02% and 79.44% for C6 liver (A), C6 skeletal muscle (B), D2 liver (C) and D2 skeletal muscle (D), respectively.

Figure S2. Classifications of C6 liver (A), C6 skeletal muscle (B), D2 liver (C) and D2 skeletal muscle (D) in SVM models were performed using RBF kernel (C6: n=8 in control group, n=7 in TCDD group; D2: n=5 in control group, n=7 in TCDD group).

Figure S3. Grid parameter search for regression. The color bars denote the accuracy of the classification performance of SVM models and the parameters C and γ could be checked back from the corresponding area. The wide range from 10^{-10} to 10^{10} for either C or γ was selected. The grid search computational results for the raw data sets from C6 liver (A), C6 skeletal muscle (B), D2 liver (C) and D2 skeletal muscle (D), respectively. The results varied with the kernel parameter γ from large to small along the direction of the arrow.

Figure S4. Z-score plots of C6 skeletal muscle sample sets for 15 metabolites (red: control; green: TCDD exposure. z-score range: -5 to 20).

Figure S5. Z-score plots of D2 liver sample sets and D2 skeletal muscle sample sets (red: control; green: TCDD exposure. z-score range: -5 to 20 for D2 liver; z-score range: -10 to 8 for D2 skeletal muscle).

Figure S1.

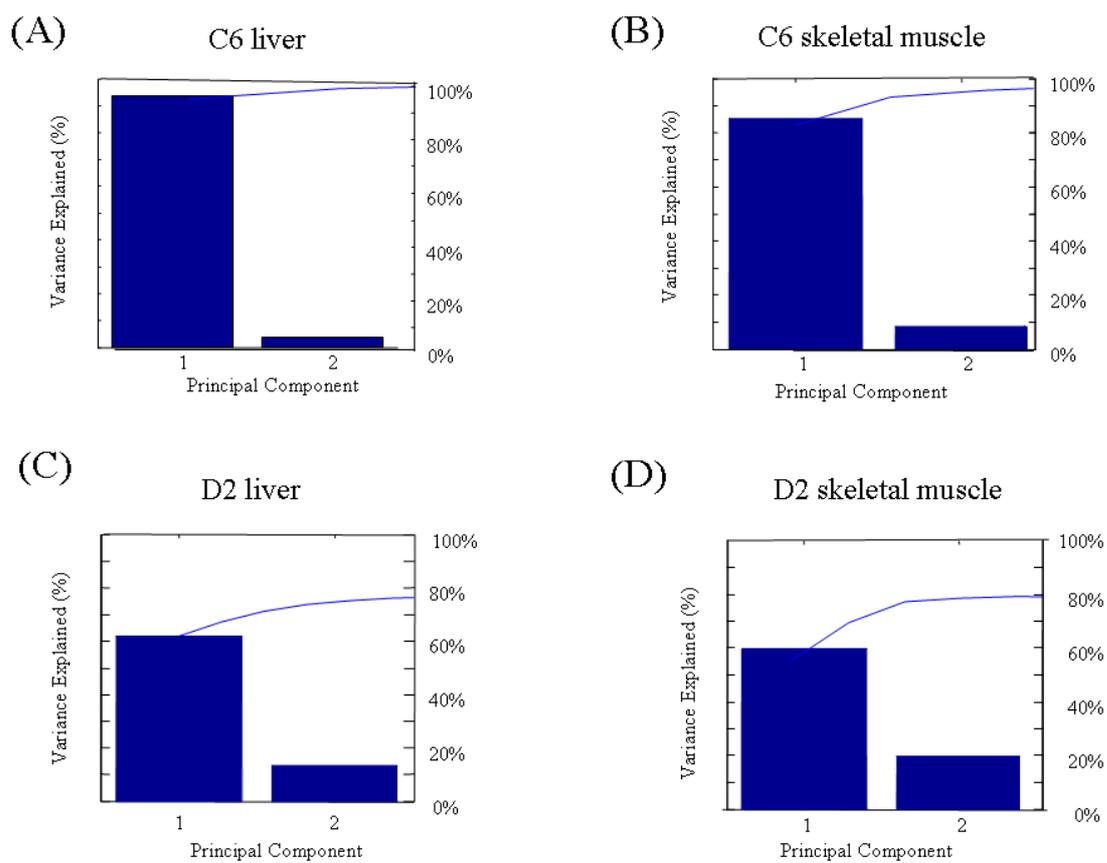


Figure S2.

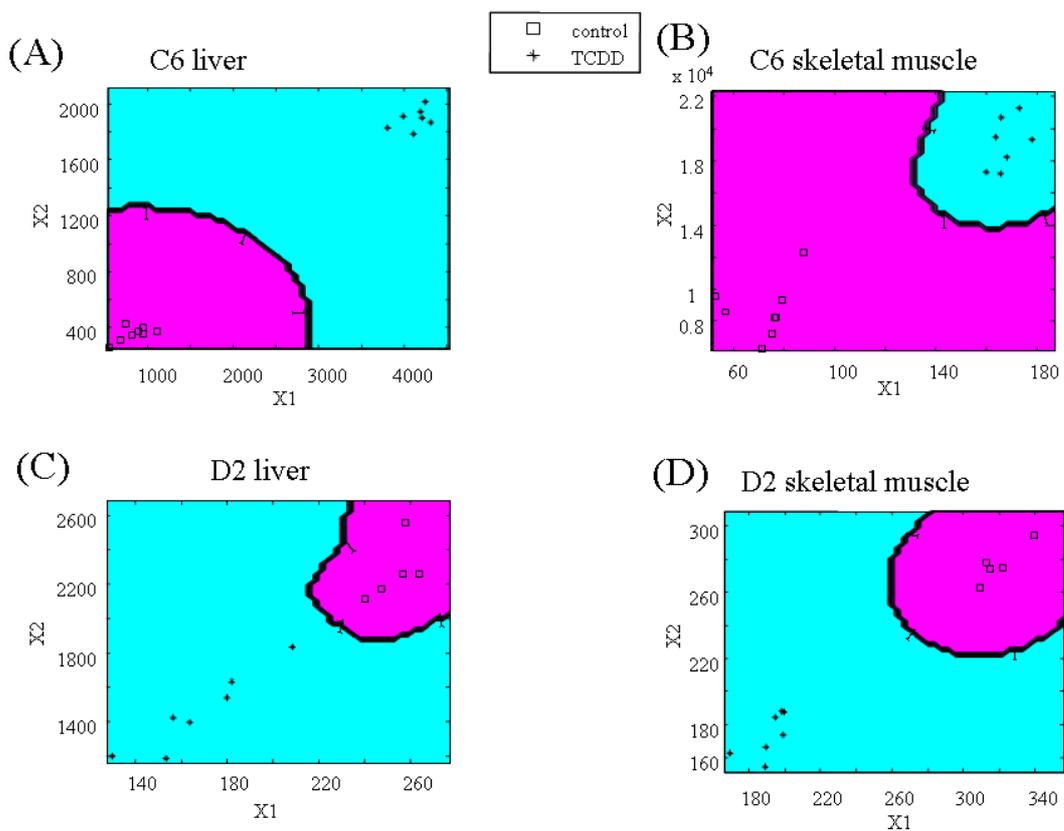


Figure S3.

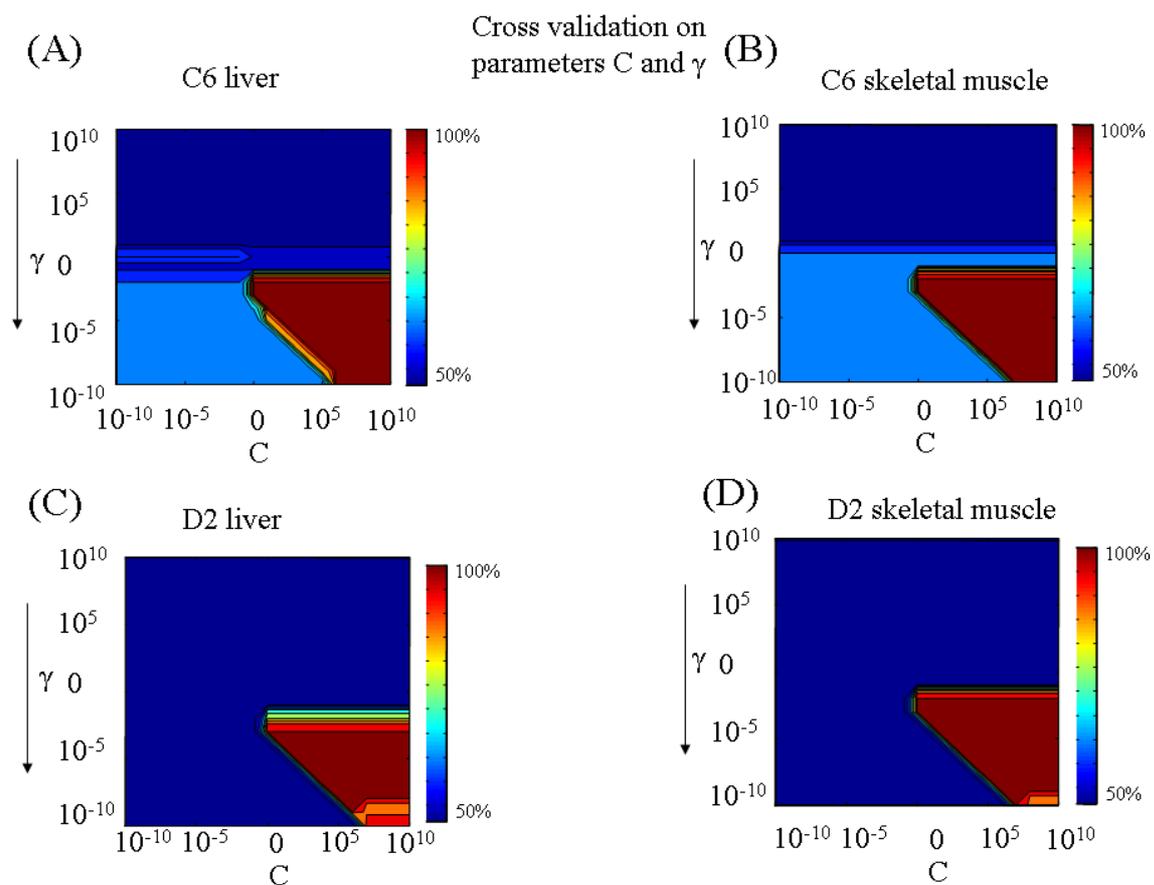


Figure S4.

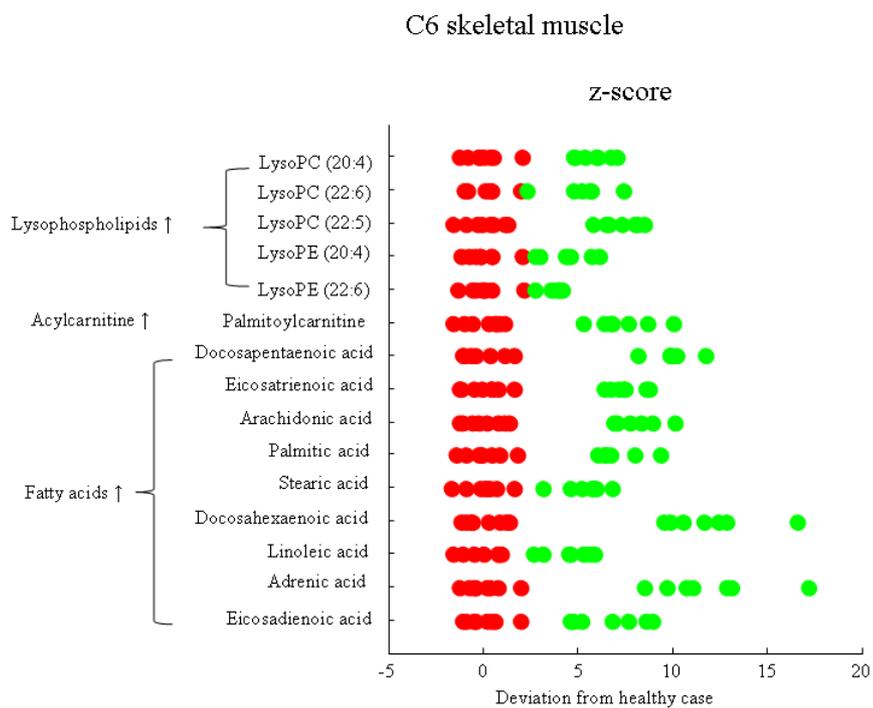


Figure S5.

