Transcriptomic Redox Dysregulation in a Rat Model of Metabolic Syndrome-Associated Kidney Injury

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Supplementary Figure and Table

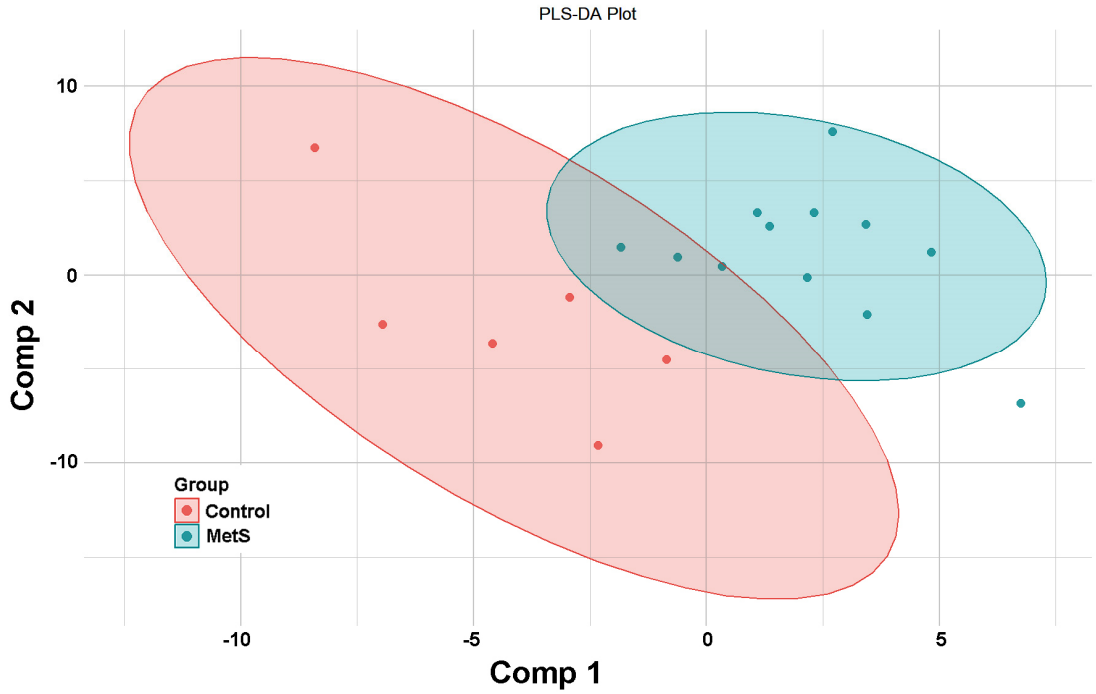


Figure S1. Partial least squares-discriminant analysis (PLS-DA). Cross-validated PLS-DA score plot comparing redox gene expression profiles between the control group (red dots, n = 6) and the

metabolic syndrome (MetS) group (green dots, n = 12), showing clear separation based on multivariate gene expression patterns. The analysis was performed using R software (version 4.3.3, The R Project for Statistical Computing). PLS-DA was conducted using the "pls" package (version 2.8-5), which includes functions for Partial Least Squares Regression (PLSR) and Principal Component Regression. The PLSR function was applied to construct models based on ΔCt-transformed gene expression data. Model performance was evaluated by extracting component scores and loadings using the "scores" function. Colored ellipses represent 95% confidence intervals. Components (comp) 1 and 2 accounted for 11.1% and 14.0% of the total variance, respectively.

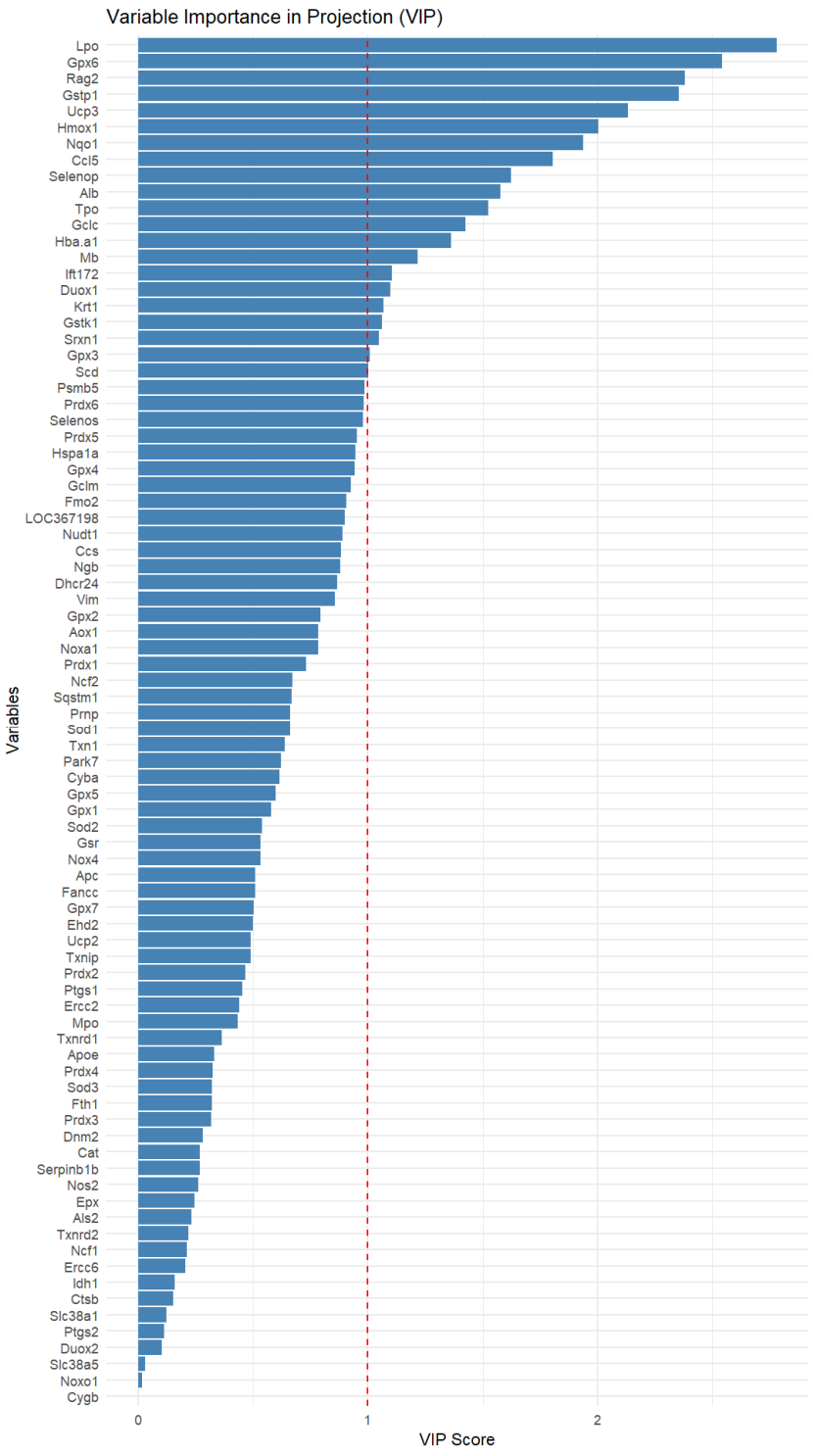


Figure S2. Variable Importance in Projection (VIP) Score Plot. VIP scores were derived from the PLS-DA model shown in Figure S1. To identify key variables contributing to group separation, VIP values were calculated using the VIP function. Genes with a VIP score greater than 1.0 were considered significant discriminators between control and MetS groups. Notably, CCL5 exhibited

a VIP score of 1.8062, ranking among the top contributors, thereby supporting its biological relevance in the context of metabolic syndrome.

Table S1. List of VIP scores from PLS-DA model for six downregulated genes. The six downregulated genes are listed from high to low VIP scores. This highlights CCL5's potential role in transcriptomic shifts associated with metabolic syndrome. Given its controversial roles in some diseases and metabolic dysfunction, CCL5 was selected for downstream validation by qPCR.

Gene	VIP Score
Gpx6	2.5409
Rag2	2.3807
NQO1	1.9373
CCL5	1.8062
SEPP1	1.6224
Gclc	1.4268