

Supplementary Materials: Integrative Analysis of Metabolomic, Proteomic and Genomic Data to Reveal Functional Pathways and Candidate Genes for Drip Loss in Pigs

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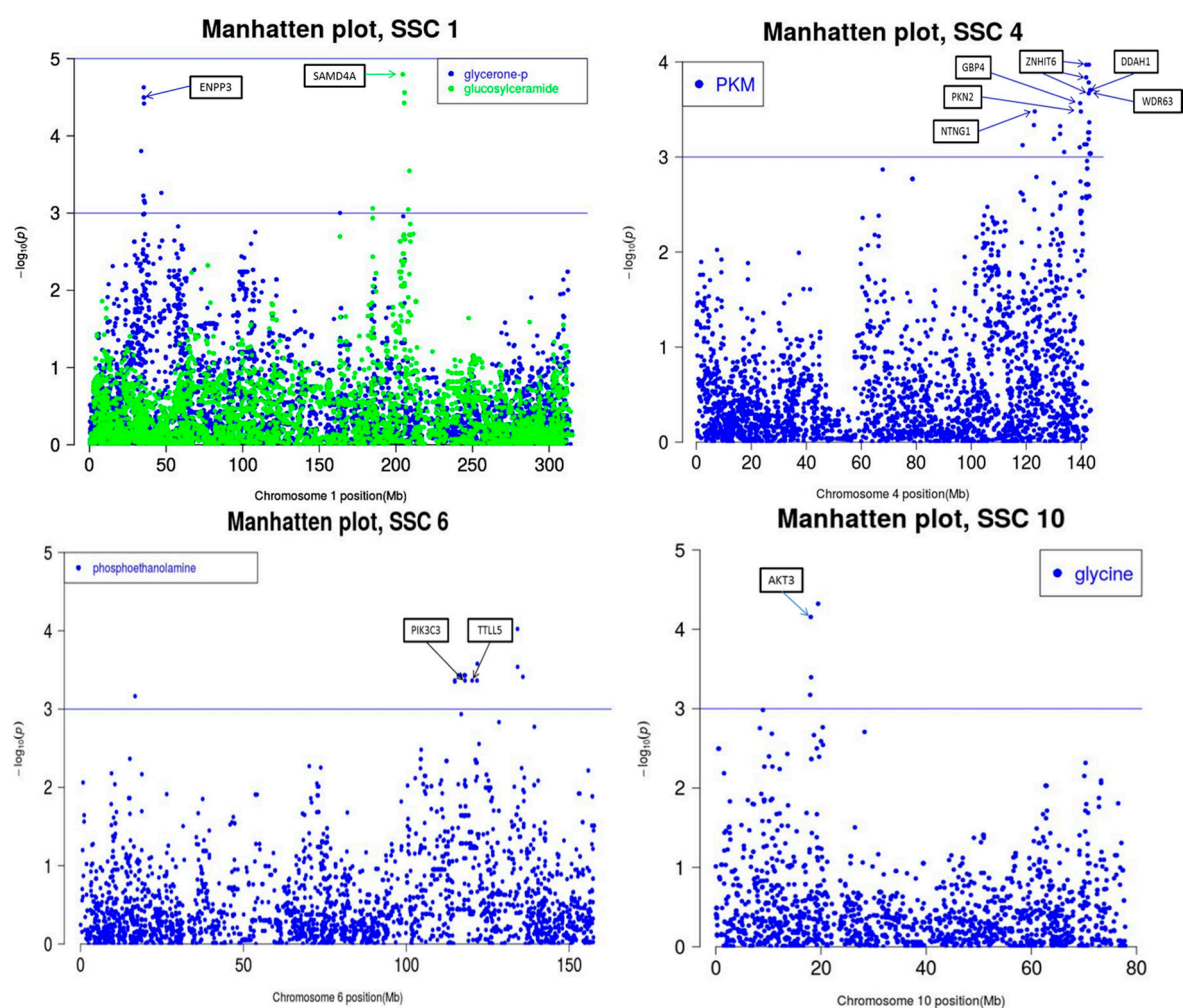


Figure S1. Cont.

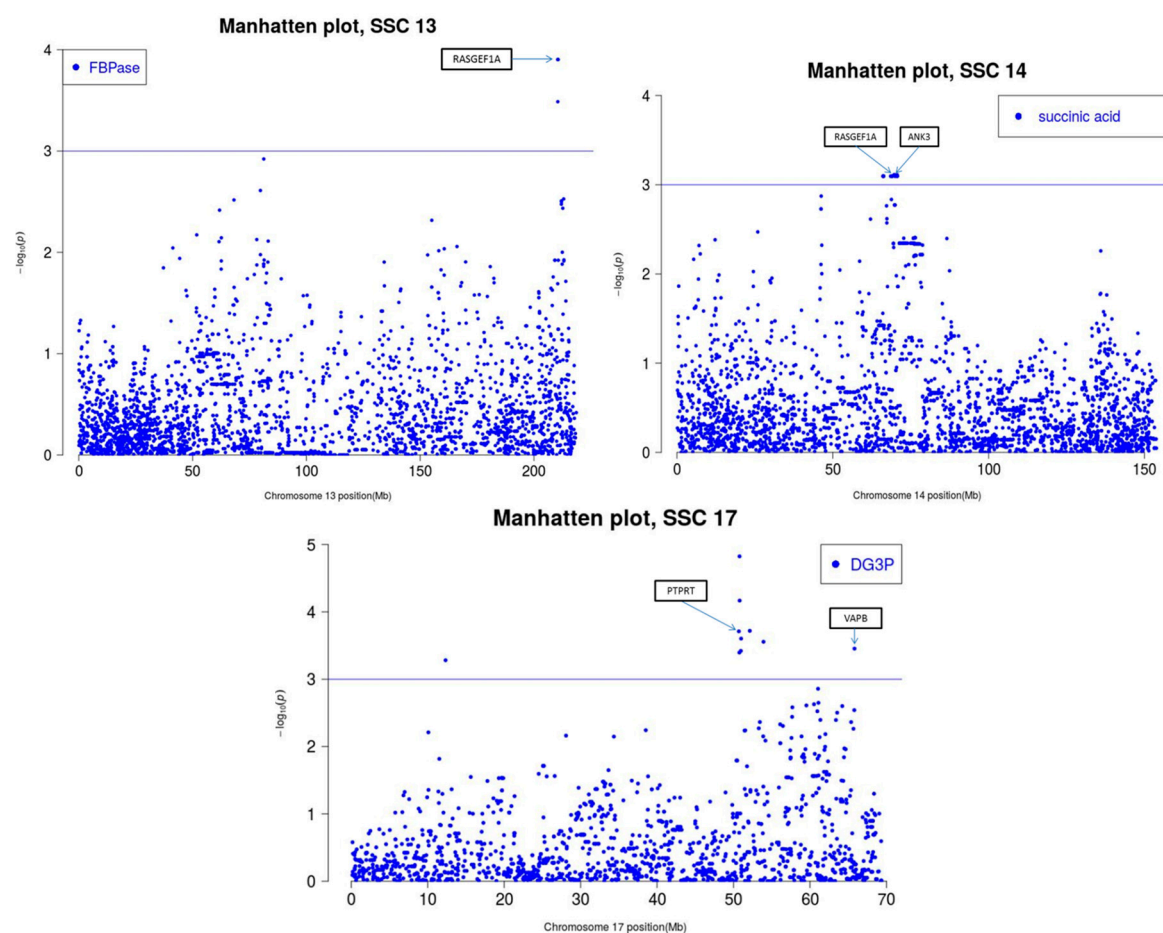


Figure S1. Chromosome-wide Manhattan plots of *sus scrofa* chromosomes (SSC) 1, 4, 6, 10, 13, 14 and 17. Glycerone-p = dihydroxyacetone phosphate; DG3P = D-glycerate-3-phosphate; PKM = pyruvate kinase (muscle); FBPase = fructose-1,6-bisphosphatase 2; the declaration of gene symbols (in black lettering) can be obtained from Ensembl or <http://www.ncbi.nlm.nih.gov/genegenes>.

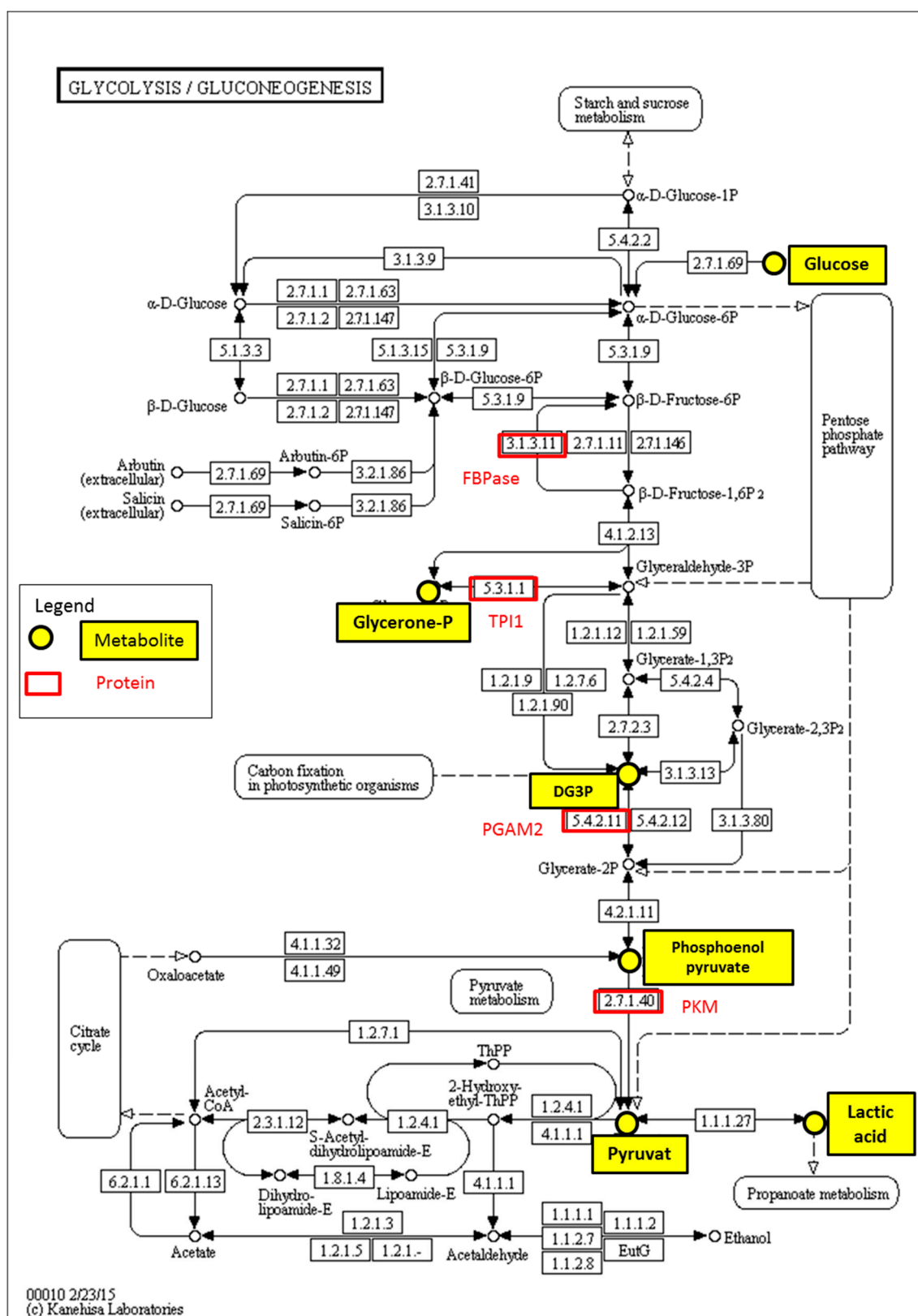
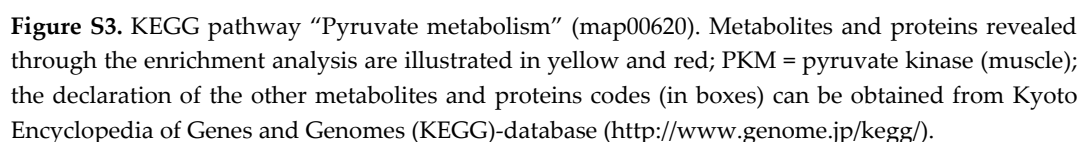


Figure S2. KEGG pathway "Glycolysis/Gluconeogenesis" (map00010). Metabolites and proteins revealed through the enrichment analysis are illustrated in yellow and red; Glycerone-p = dihydroxyacetone phosphate; PGAM2 = phosphoglycerate mutase 2 (muscle); PKM = pyruvate kinase (muscle); FBPase = fructose-1,6-bisphosphatase 2; TPI1 = triosephosphate isomerase 1; DG3P = D-glycerate-3-phosphate; The declaration of the other metabolites and proteins codes (in boxes) can be obtained from Kyoto Encyclopedia of Genes and Genomes (KEGG)-database (<http://www.genome.jp/kegg/>).



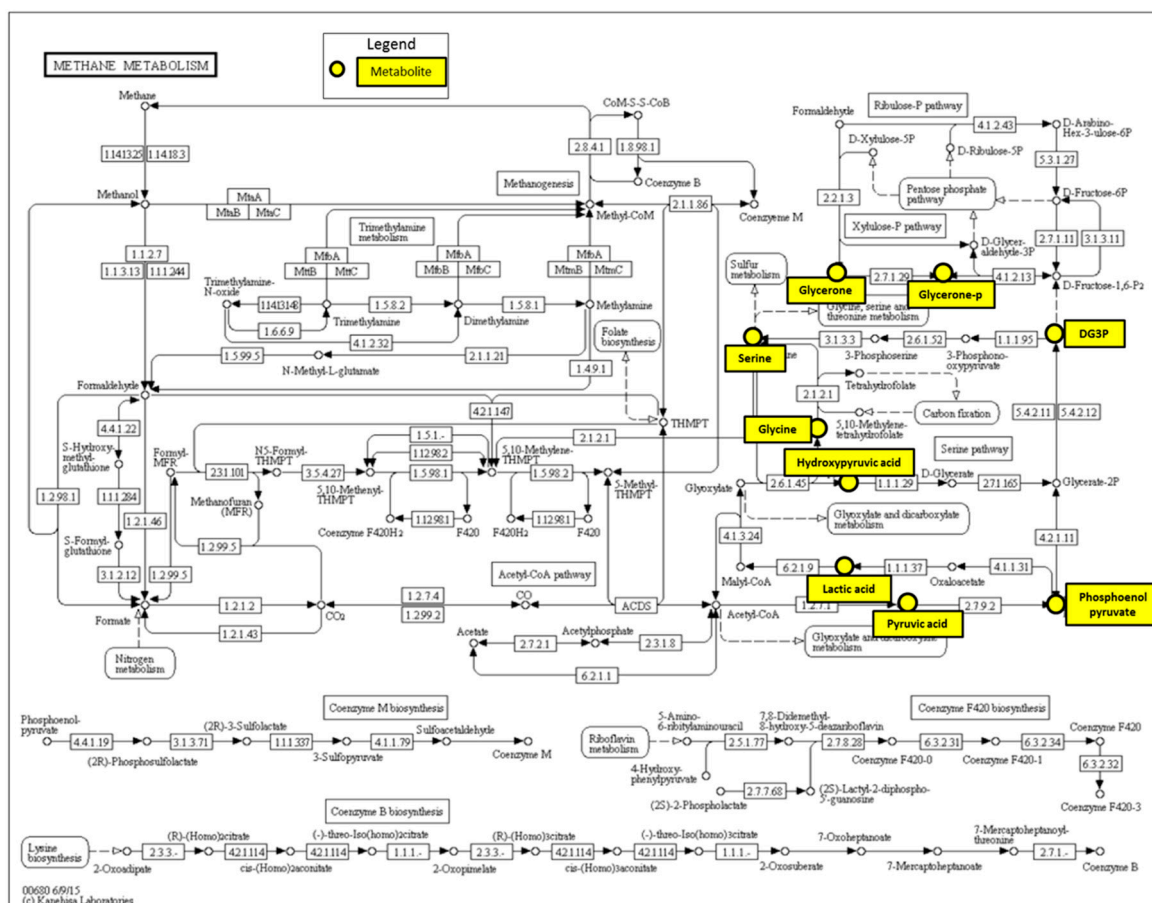


Figure S4. KEGG pathway "Methane metabolism" (map00680). Metabolites and proteins revealed through the enrichment analysis are illustrated in yellow and red; Glycerone-p = dihydroxyacetone phosphate; DG3P = D-glycerate-3-phosphate. The declaration of the other metabolites and proteins codes (in boxes) can be obtained from Kyoto Encyclopedia of Genes and Genomes (KEGG)-database (<http://www.genome.jp/kegg/>).

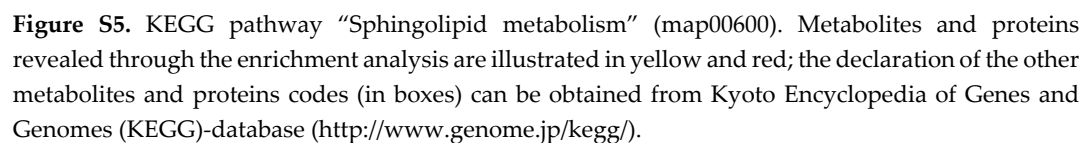


Figure S5. KEGG pathway “Sphingolipid metabolism” (map00600). Metabolites and proteins revealed through the enrichment analysis are illustrated in yellow and red; the declaration of the other metabolites and proteins codes (in boxes) can be obtained from Kyoto Encyclopedia of Genes and Genomes (KEGG)-database (<http://www.genome.jp/kegg/>).