

Figure S1. GO analysis of DeMRGs between prostate cancer and normal prostate tissue. (A) The first three graphs (from top to bottom are BP, MF and CC in sequence.) show GO analysis of all significantly upregulated DeMRGs (a total of 54 genes) in three datasets. (B) The last three graphs (from top to bottom are BP, MF and CC in sequence.) show GO analysis of all significantly downregulated DeMRGs (a total of 63 genes). GO, Gene Ontology; DeMRGs, differentially expressed mitochondrial genes; BP, Biological Process; MF, Molecular Function; CC, Cellular Component.

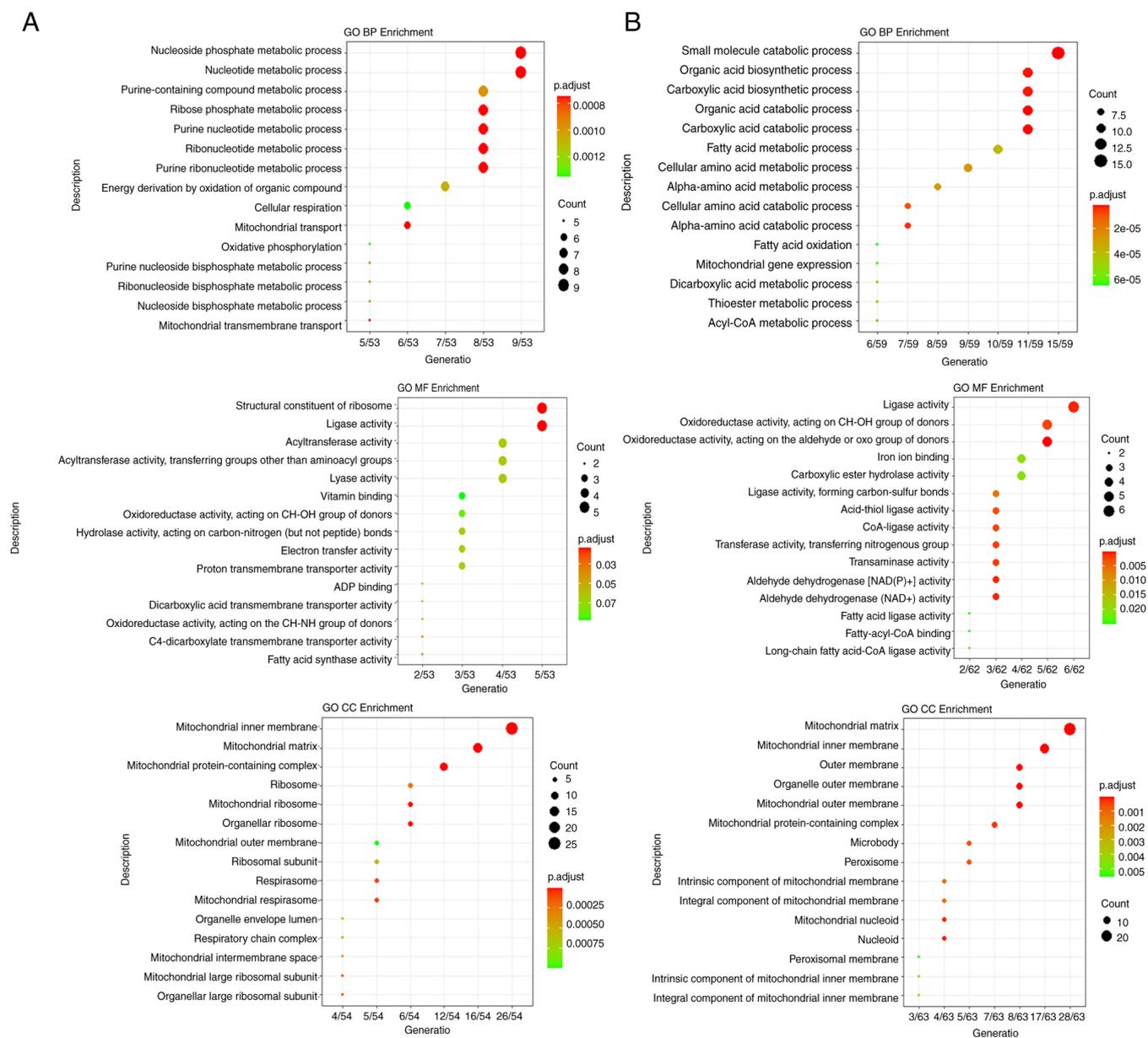


Figure S2. GSEA between core differential mitochondrial mRNAs in prostate cancer and normal prostate tissue. Single gene (MRPL12, MCCC2, FASN, PDK4, GATM and ACACB) GSEA. GSEA, Gene Set Enrichment Analysis; ACACB, acetyl-CoA carboxylase β ; PDK4, pyruvate dehydrogenase kinase 4; GATM, glycine amidinotransferase; MCCC2, methylcrotonyl-CoA carboxylase subunit 2; MRPL12, mitochondrial ribosomal protein L12; FASN, fatty acid synthase.

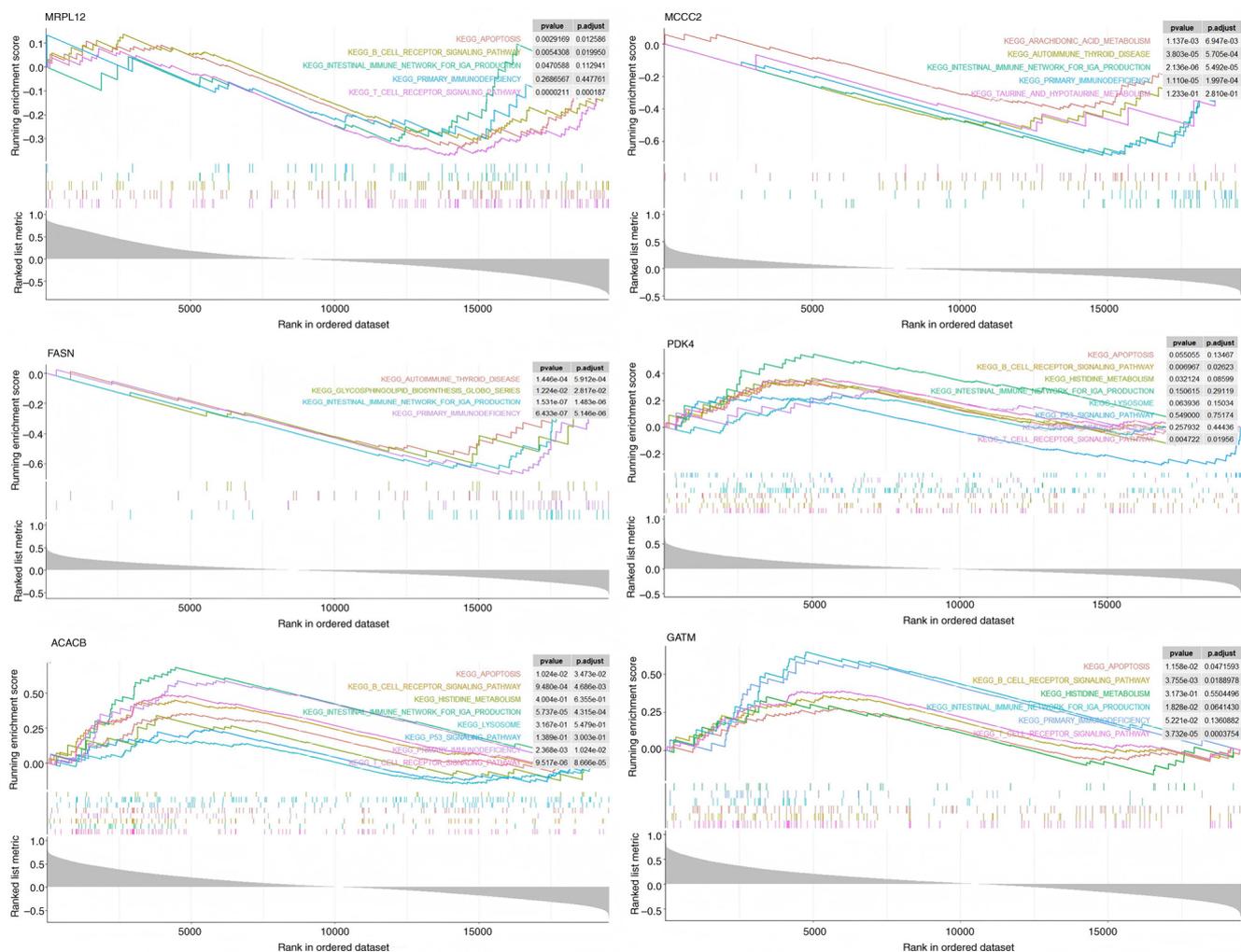


Figure S3. Mitochondrial respiratory chain genes most relevant to the four hub genes (MRPL12, PDK4, ACACB and GATM) were selected to generate correlation linear regression scatter plots. (A) Correlation analysis between mitochondrial respiratory chain genes and MRPL12. (B) Correlation analysis between mitochondrial respiratory chain genes and PDK4. (C) Correlation analysis between mitochondrial respiratory chain genes and ABACB. (D) Correlation analysis between mitochondrial respiratory chain genes and GATM. TCGA, The Cancer Genome Atlas; PRAD, prostate adenocarcinoma; ACACB, acetyl-CoA carboxylase β ; PDK4, pyruvate dehydrogenase kinase 4; GATM, glycine amidinotransferase; MCCC2, methylcrotonyl-CoA carboxylase subunit 2; MRPL12, mitochondrial ribosomal protein L12; FASN, fatty acid synthase.

