

Supplementary Figure legend

Supplementary Figure 1. mRNA expression of PDH genes in prostate tissues and prostate cancer. RNA-seq data from normal tissues are from the database GTEx (Genotype-Tissue Expression), and data are expressed as RPKM (reads per kilobase per million mapped reads). RNA-seq data from tumors are from database TCGA (The Cancer Genome Atlas), and data are expressed as FPKM (fragments per kilobase of exon per million reads). All data are from <https://www.proteinatlas.org/>.

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