**Supporting Information**

**S1:** Selected common subsystems and their related genes based on the fluxes trends (increase or decrease from normal to cancer) during cancer progression (XLSX)

**S2:** Common genes between lung and prostate co-expression networks in normal and cancer cells (XLSX)

**S3:** Common normal and cancer state-specific genes and their gene expression alteration values (XLSX)

**S4:** Information including a script for applying E-Flux algorithm to the human metabolic model, biomass compositions, medium compositions, inferred expression and flux alteration for 19 selected genes, and references of gene expression data (DOCX)

**S5:** Sub-networks and number of interactions for normal and cancer networks of prostate and lung (XLSX)

**S6:** Biological process GO analysis of state-specific genes (XLSX)

**S7:** Expression alteration of the state-specific genes that are selected for lung and prostate networks (XLSX)

**S8:** Normal and cancer metabolic models as MATLAB structure files (RAR)

**S9:** FBA and FVA results related to normal and cancer metabolic models (RAR)