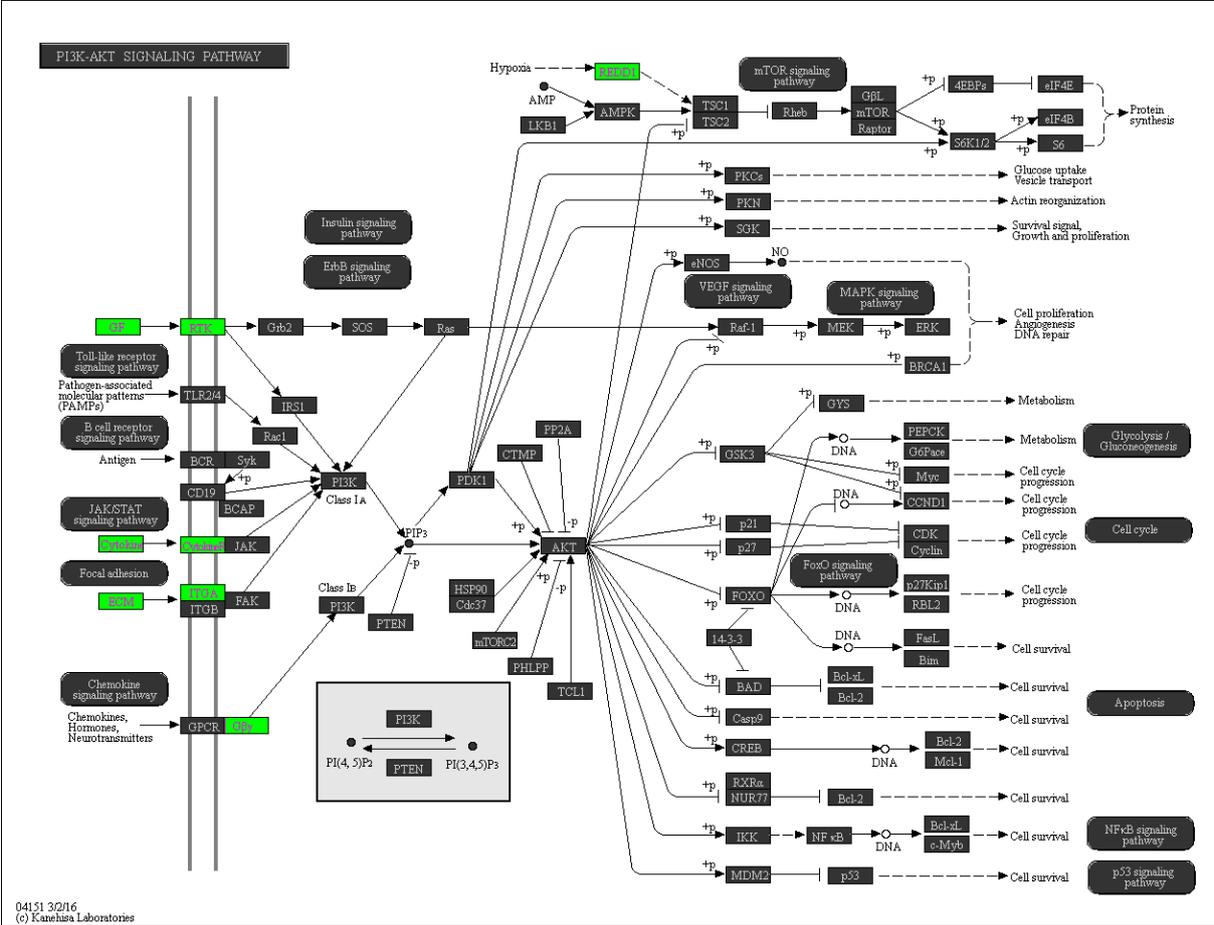




**Figure S2.** KEGG pathway enrichment analysis on the PI3K-AKT signaling pathway. The microarray-detected transcriptome profiles of human upper tract urothelial carcinoma and adjacent normal tissues were compared and mapped by using a Partek Genomics software for pathway analysis. The up-regulated genes are highlighted in green boxes.



**Figure S3.** KEGG pathway enrichment analysis on the NOTCH signaling pathway. The microarray-detected transcriptome profiles of human upper tract urothelial carcinoma and adjacent normal tissues were compared and mapped by using a Partek Genomics software for pathway analysis. The up-regulated genes are highlighted in green boxes.

