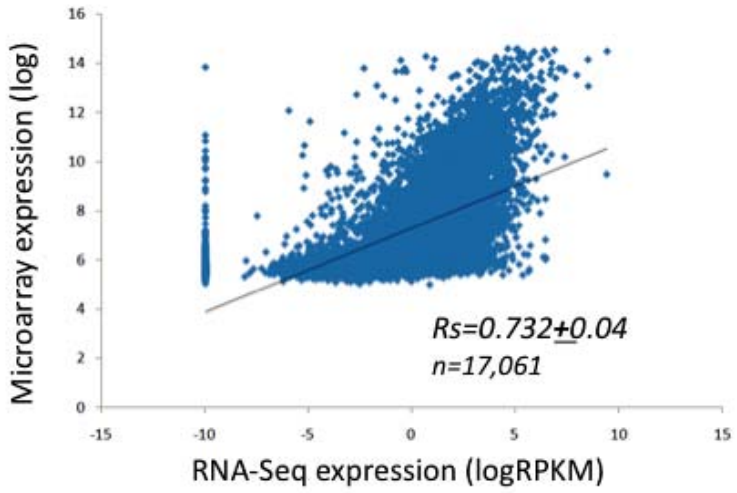
Supplementary Figure 1. Comparison of WT-RNA-seq and microarray gene expression.

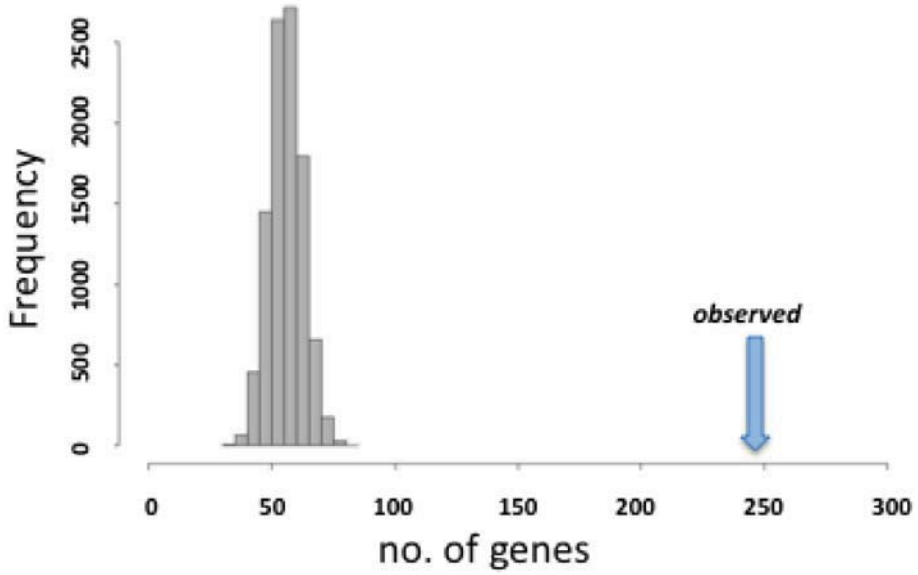
(A) The expression correlation between the two platforms in a representative sample. The average Spearman's rank (Rs) across multiple samples= 0.732 ±0.04.

(B) In the RNA-seq expression analysis, we identified 356 genes as differentially expressed genes in the 5-group comparison (single-factor ANOVA). Using the same analysis, 78% of these genes showed significant expression changes (raw $P < 0.05$) with the same direction (tumor vs. normal) on a microarray dataset of 83 samples. If the same number of genes were randomly chosen, only 17% would be expected ($P<1\times10^{-4}$). The figure was generated based on 10,000 random samples; blue arrow indicates the observed number.

(A)

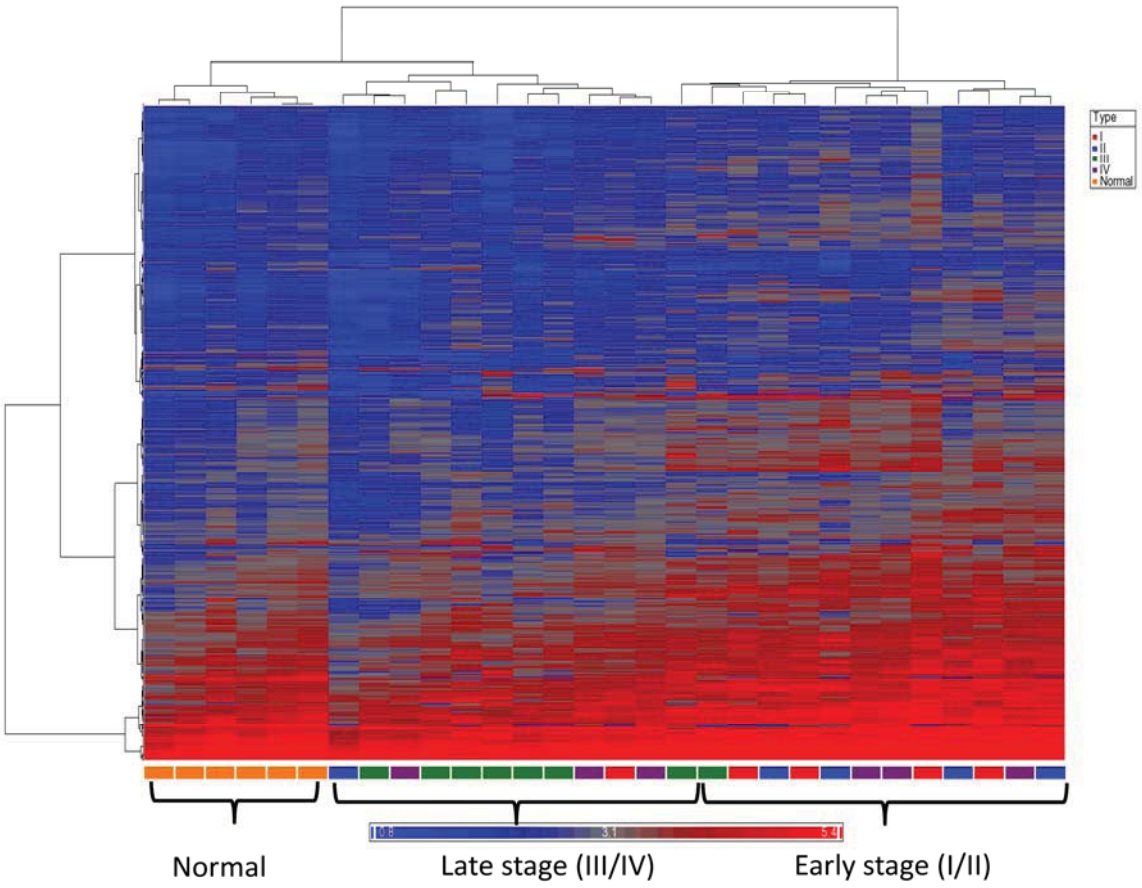


(B)



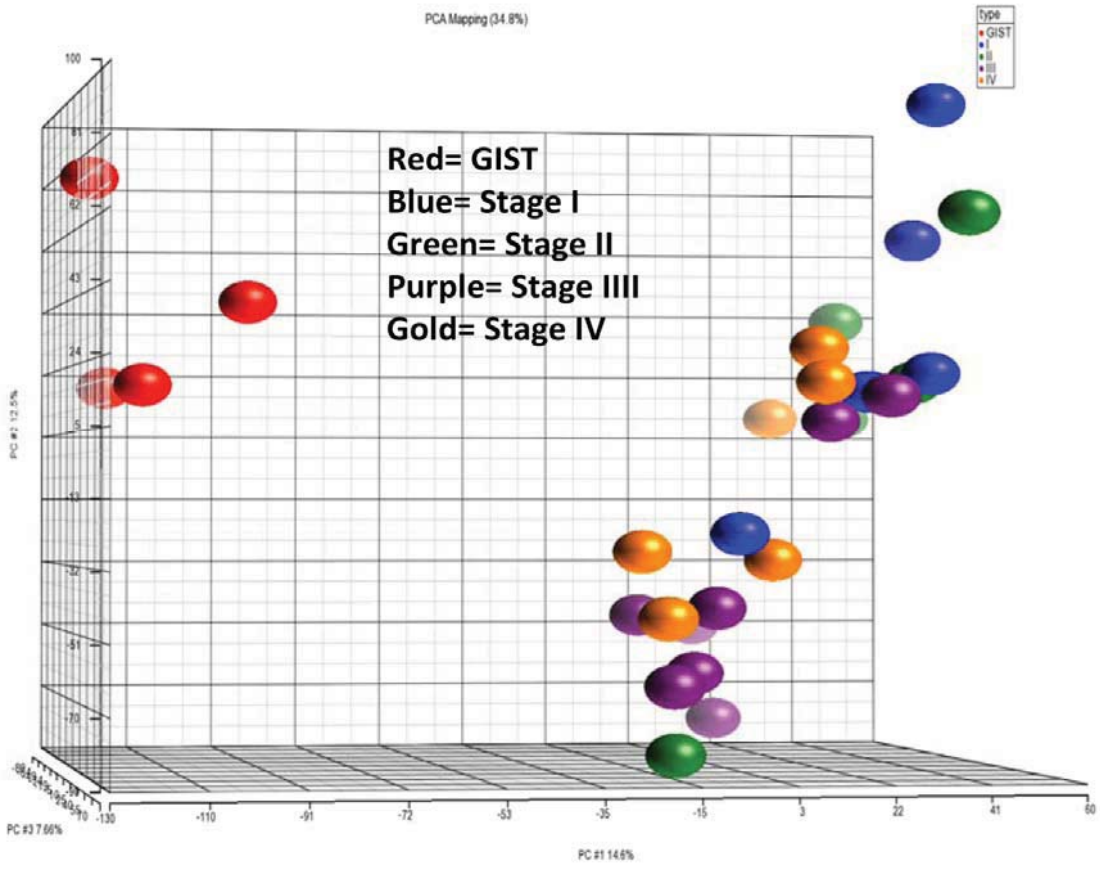
Supplementary Figure 2. The unsupervised clustering pattern of all the gastric samples.

The unsupervised analysis was based on 5000 genes with the highest expression level (median expression across 30 samples). Normal samples are shown in gold; gastric tumor samples of stages I-IV are in red, blue, green and purple, respectively.

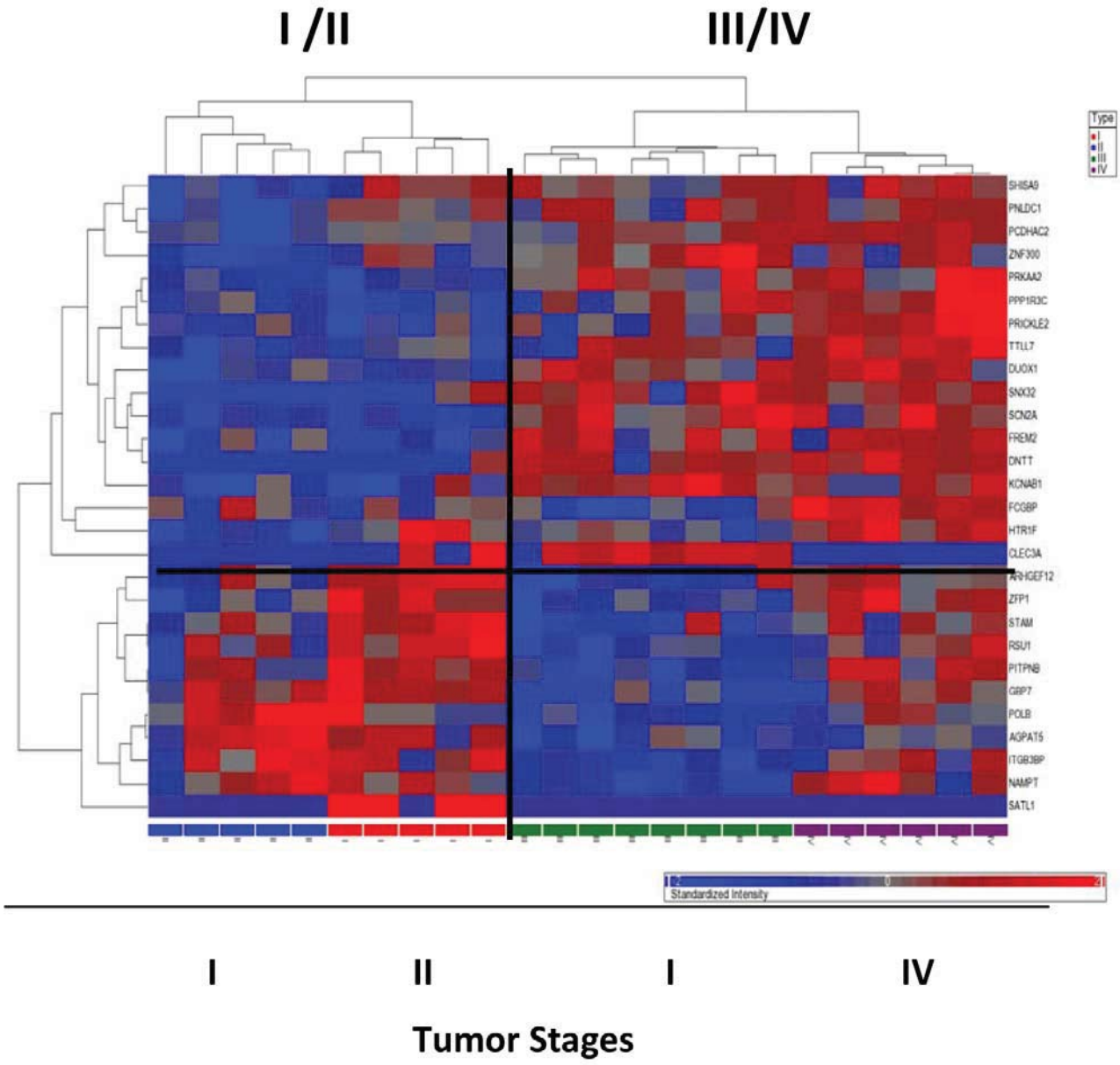


Supplementary Figure 3. Principal component analysis of different sample groups based on transcriptome-wide gene expression data.

We used principal component analysis on the expression of 18,890 coding genes to validate the type of tumor samples. Gastric intestinal stromal tumor (GIST) samples are shown in red; gastric tumor samples of stages I-IV are in blue, green, purple and gold, respectively. Image generated with Partek® Genomics Suite™ v 6.5.

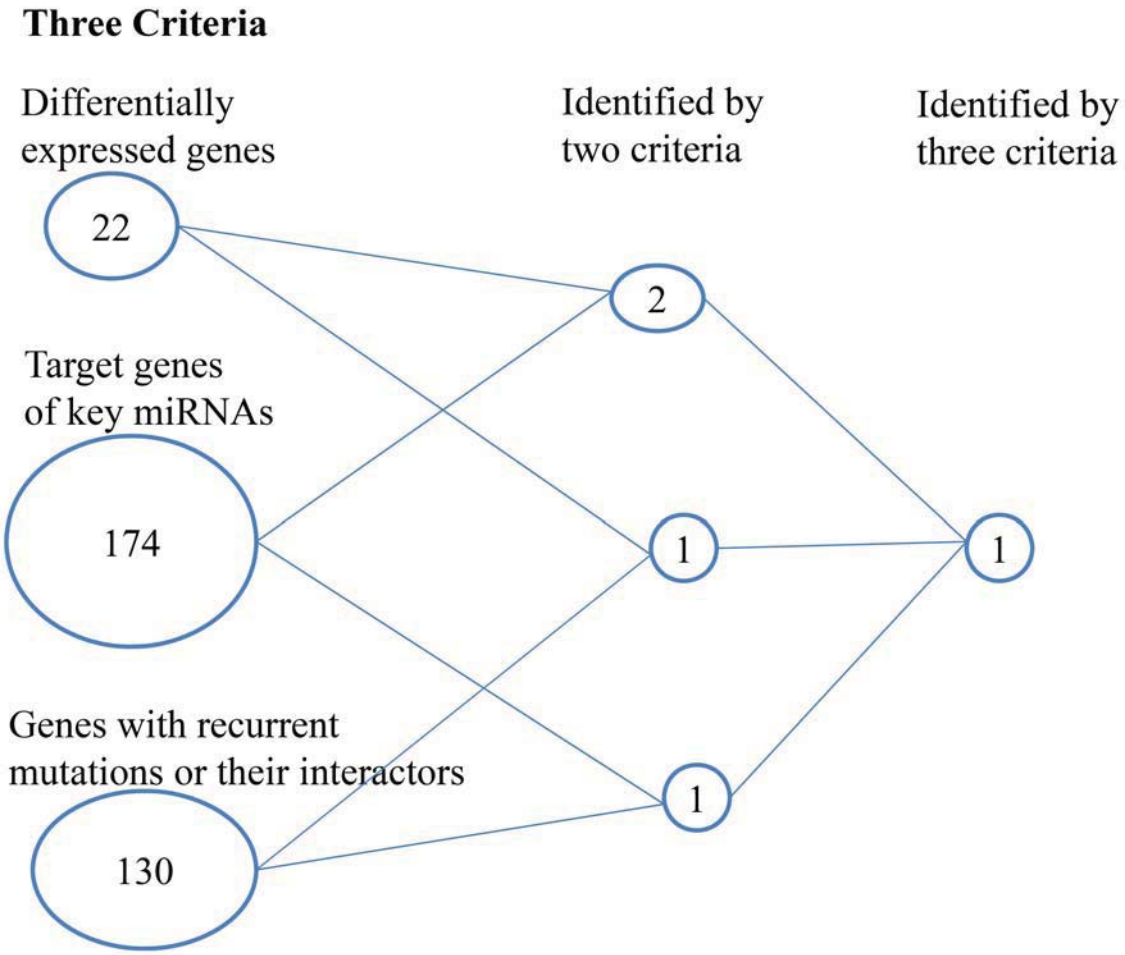


Supplementary Figure 4. Identified 28 genes with significant stage-specific expression change based on the expression data of 24 tumor samples (raw $P < 7\times10^{-4}$).



Supplementary Figure 5. The integrative analysis of three types of transcriptional aberrations related to gastric cancer.

We used three selection criteria to select key genes for detailed studies. (i) Differentially expressed genes that were identified in both 5-group and 4-stage differential expression analysis; (ii) Target genes of six key differentially expressed miRNAs, the target genes predicted by TargetScan with a significant expression anti-correlation ($Rs < -0.4$, $P < 0.05$); (iii) Genes with recurrent somatic mutations or their interacting partner (IPA annotation). Only two genes were identified by two criteria; and PRKAA2 is the only gene identified by the three criteria simultaneously, thereby being selected for detailed studied.



Supplementary Figure 6. The unique expression pattern of *PRKAA2* (AMPK-α-2) among AMPK subunits.