Supporting Information

Farrerol Modulates Aorta Gene Expression Profile in Spontaneously Hypertensive Rats
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Figure 1S. Assessment of the degree of saturation in DEGs sequencing. A, B, C, and D present the relationships between the percentage of genes identified and total tag number in the libraries of Control-WKR, Control-SHR, Farrerol-SHR, and Verapamil-SHR, respectively.
Figure 2S. Distribution of total and distinct tags over different tag-abundance categories. (A) Distribution of total tags. Numbers within square brackets indicate the range of copy numbers for a specific category of tags. Numbers within parentheses represent the total tag copy number for all tags in that specific category. (B) Distribution of distinct tags. Numbers within square brackets indicate the range of copy numbers for a specific category of tags. Numbers within parentheses represent the total types of tags in that specific category.
Figure 3S. Histogram presentation of GO classification. The results are summarized in three main categories: biological process, cellular component, and molecular function. The right y-axis indicates the number of genes in a category. The left y-axis indicates the percentage of a specific category of genes in that main category.