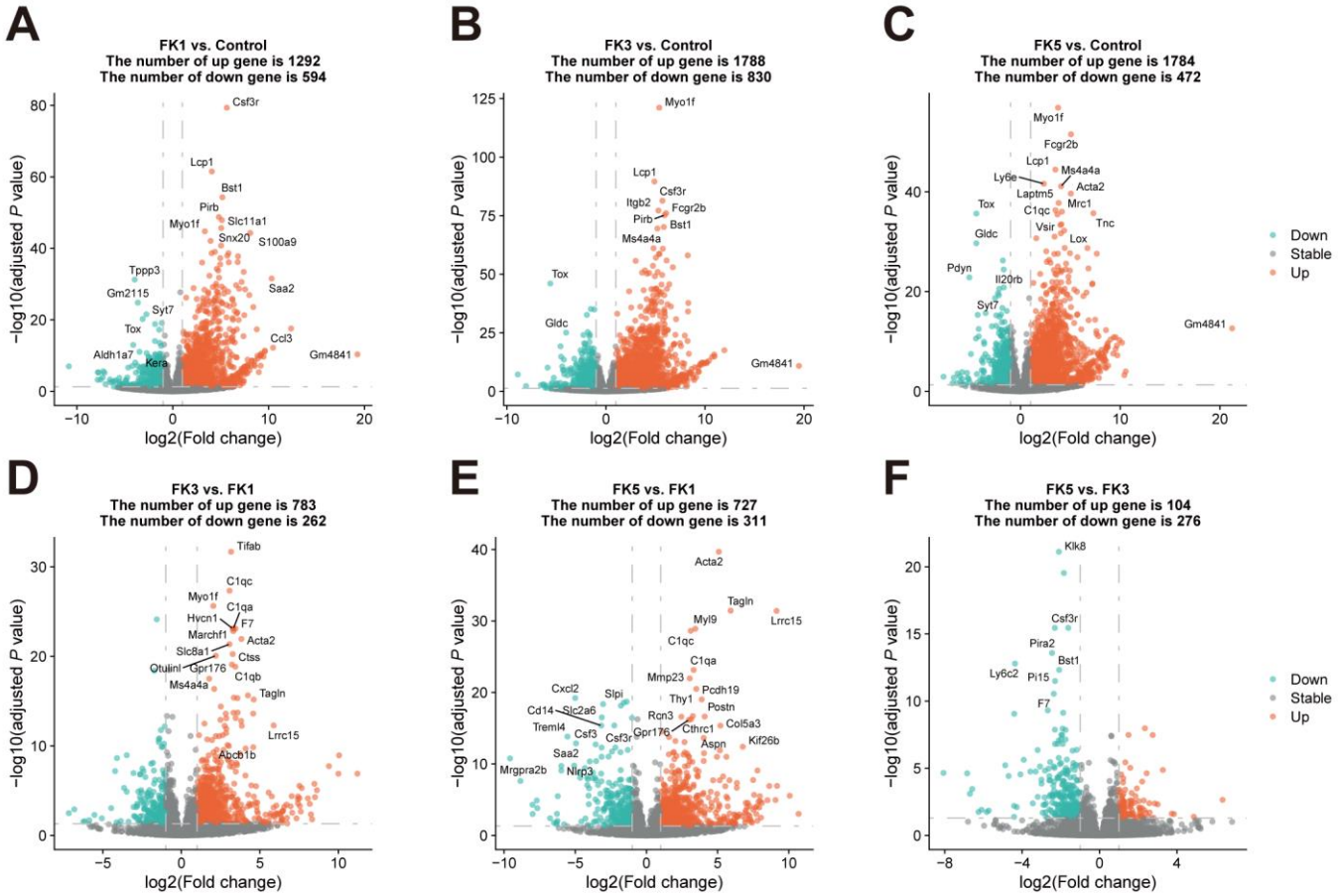

Figure S1. Volcano plots of pairwise comparison groups highlighting the differentially expressed genes. (A) FK1 vs. Control. (B) FK3 vs. Control. (C) FK5 vs. Control. (D) FK3 vs. FK1. (E) FK5 vs. FK1. (F) FK5 vs. FK3. The dashed horizontal grey line indicated statistical significance threshold (Benjamini–Hochberg (BH) adjusted $P < 0.05$). Two vertical grey lines showed the threshold of fold change (FC) ($\log_2$FC > 1 or < −1). The red dots represented upregulated DEGs ($\log_2$FC > 1), and the blue dots represented the downregulated ones ($\log_2$FC < −1) with BH-adjusted $P < 0.05$.

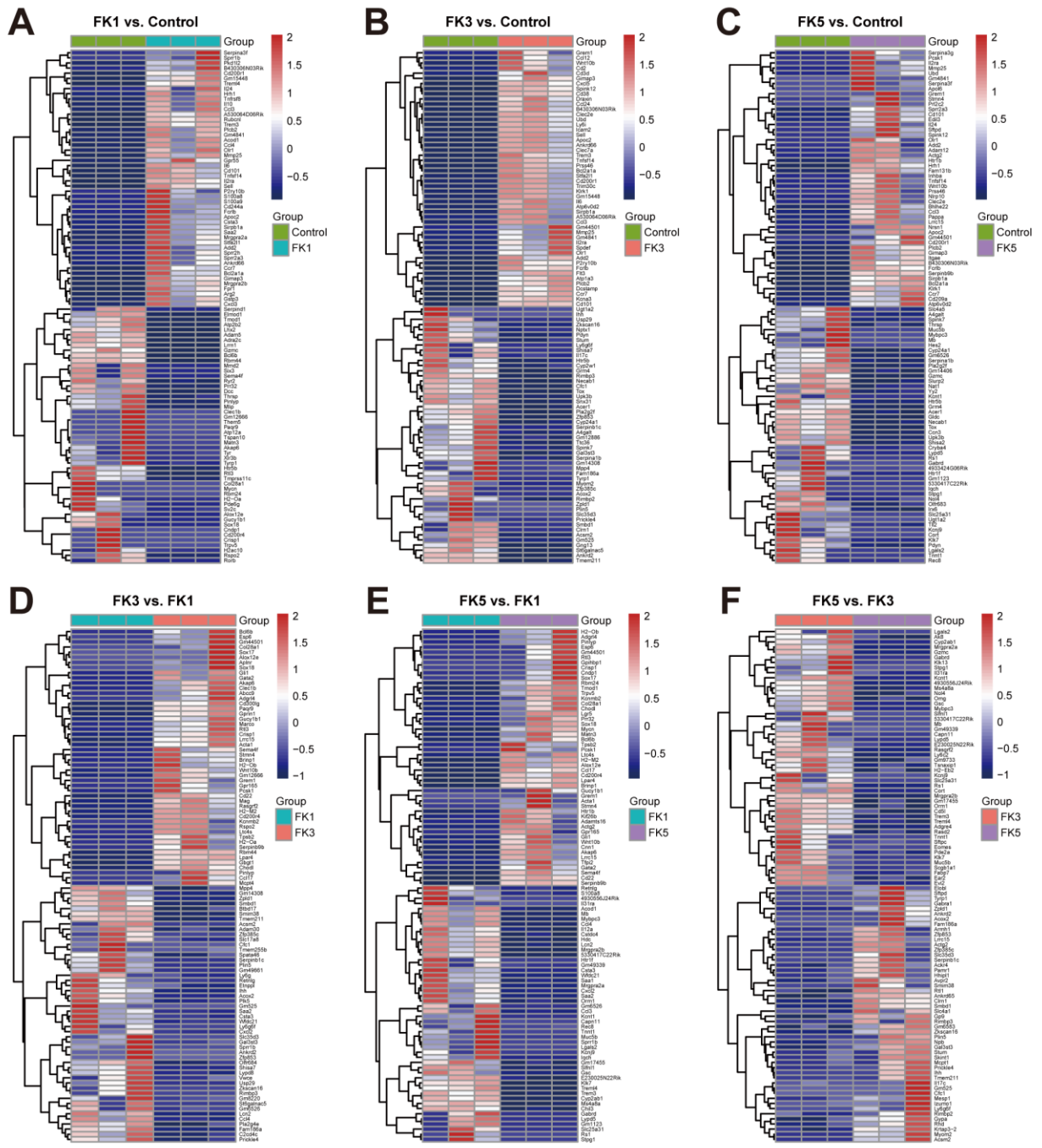

Figure S2. Heatmaps showing the top 100 differentially expressed genes between pairwise comparison groups. (A) FK1 vs. Control. (B) FK3 vs. Control. (C) FK5 vs. Control. (D) FK3 vs. FK1. (E) FK5 vs. FK1. (F) FK5 vs. FK3.

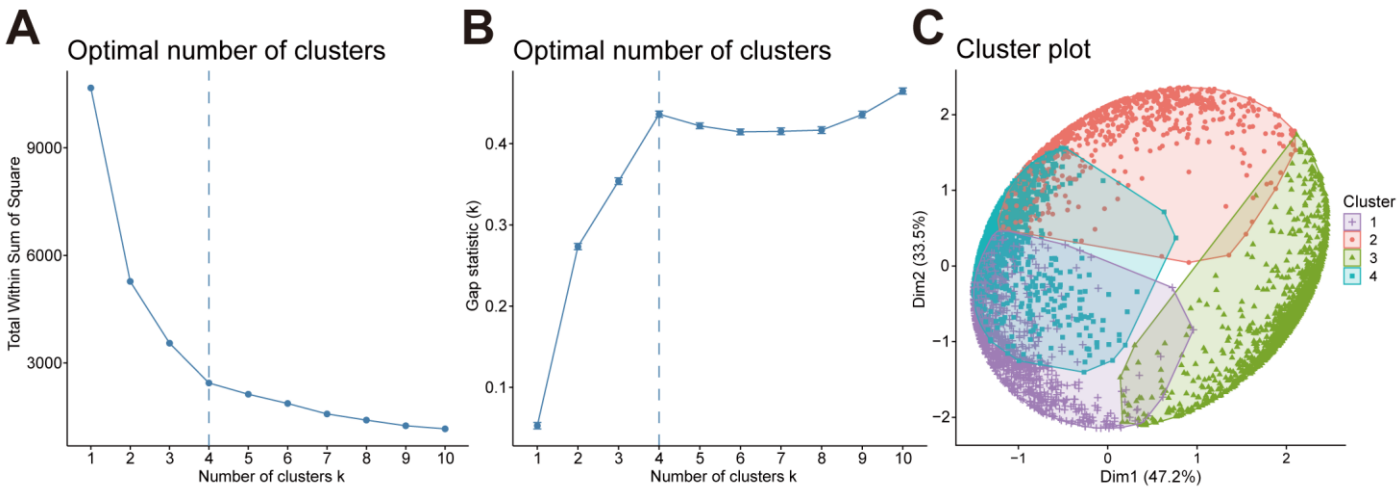

Figure S3. Determination of the optimal number of clusters for fuzzy k-means method using all differentially expressed genes. (A) Elbow-plot of the total within sum of squares between groups. The increasing number of clusters were used to determine the optimal number of clusters for fuzzy k-means. The optimal number of clusters (k = 4) was indicated by the blue dashed line. (B) Line plot showing the change in within-cluster dispersion of applying the "gap statistic" method for estimating the optimal number of clusters. The blue dashed line indicated the optimal number of clusters (k = 4). (C) Cluster plot displaying the distribution of all DEGs using the optimal number of clusters.

Supplementary Material

Table S1 The sequences of primers for qPCR.

Table S2 DEGs identified in this study.

Table S3 Common DEGs among three different FK comparison groups.