Figure S1: Identification and validation of hub genes.
(a) Common genes were visualized by heatmap.
(b) A total of 54 DEFRGs were obtained.
(c) PPI network of DEFRGs.
(d) Screening hub genes of 10 algorithms with R package “UpSetR”.
(e) Cluster dendrogram for 38 samples and OA trait.
(f) Soft-threshold power for WGCNA. The red line in the left panel indicates R2 =0.85.
(g) Clustering dendrogram for modules.
(h) Correlation between OA trait and modules.
(i) Two genes were obtained by WGCNA and PPI analyses.
(j) The differential expression and diagnostic effectiveness of SLC3A2 were further validated with another GEO dataset GSE169077.