Figure S1. Modules in irradiated esophageal squamous cell carcinoma cells. (A) Turquoise, (B) magenta and (C) brown modules. All the genes expression in modules was showed in heatmap, and the average gene expression level was showed in graph, and the hub-genes were showed in network. RA, samples with final radiation dose in Gy.
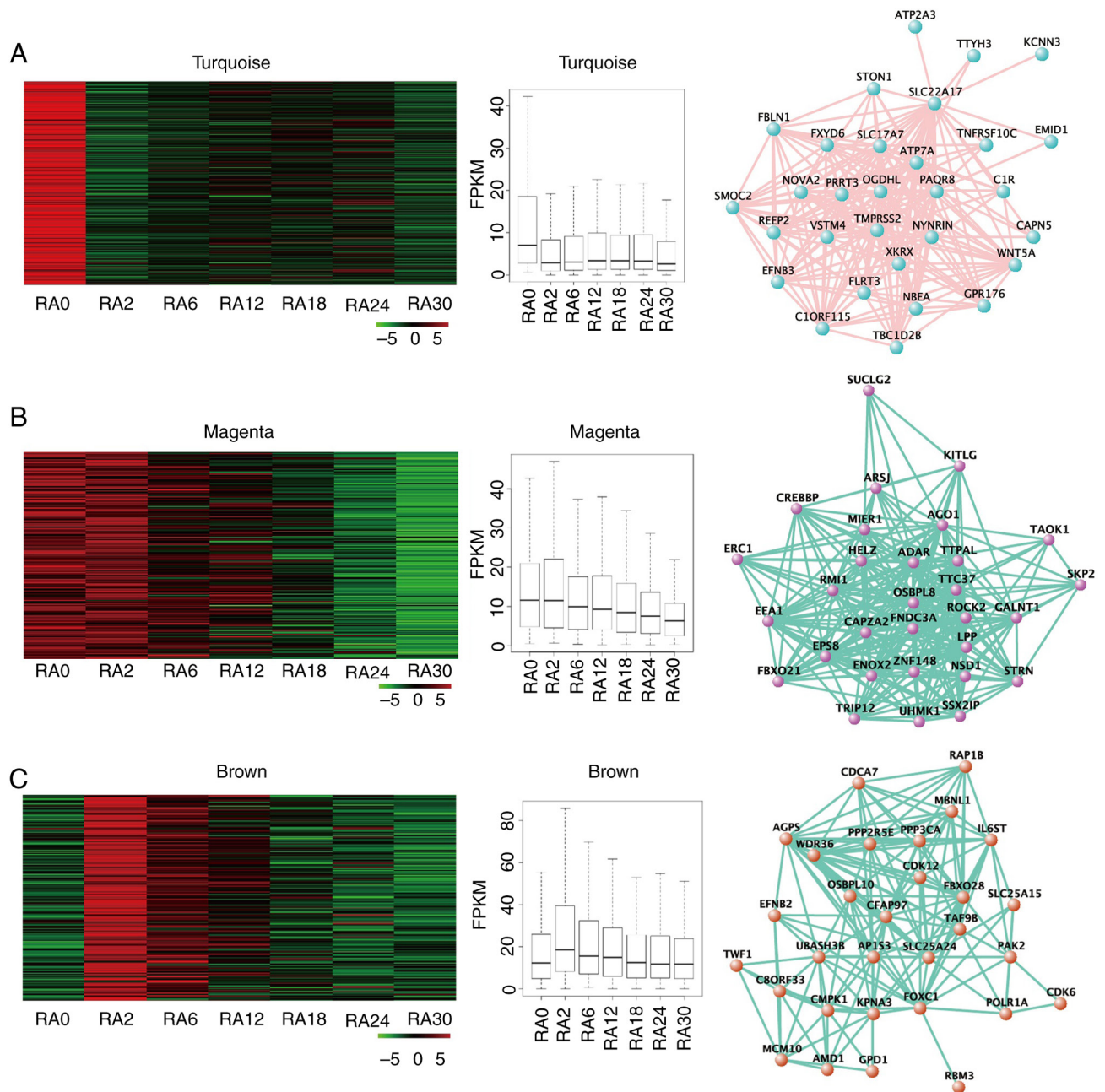
Figure S2. Gene expression statistics. (A) Replicate sequencing showing high repeatability of expression level (r=0.96). (B) Expression distribution after depth normalization revealed similar medians for all cells analyzed. (C) Expression data of discrete genes suggested a correlation of increased expression with decreased discrete degree; count ratio ≤2 for inclusion. (D) RSD of gene expression assayed by duplicate sequencing appearing highly linear (r=0.98). RSD, relative standard deviation.
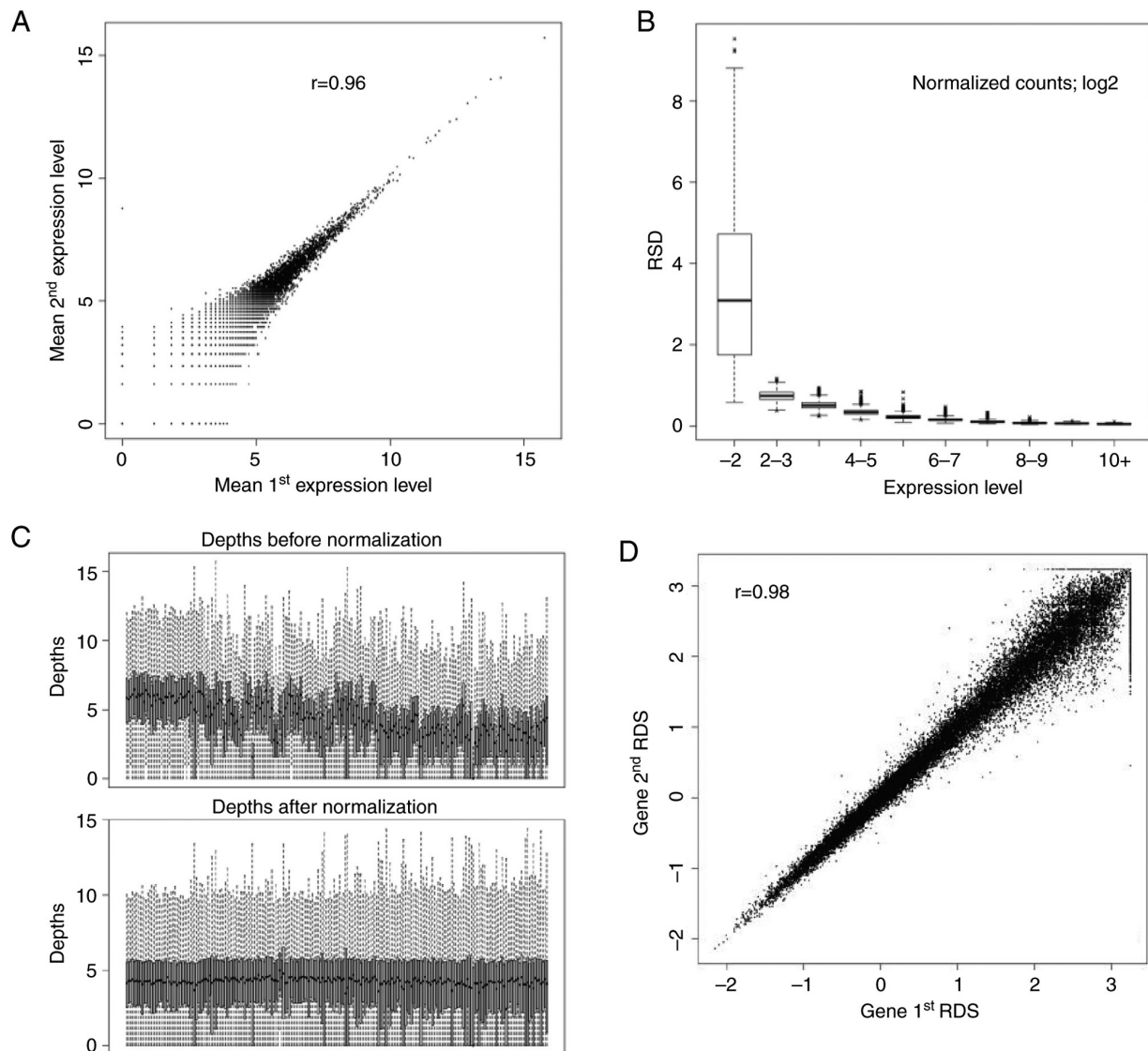
Figure S3. Principal Components Analysis (PCA) of single cell data. PCA data including (A) all expressed gene data and (B) differentially expressed gene data for clustering groups. PCA, principal component analysis; RA, samples with final radiation dose in Gy; sc, single radioresistant cell.
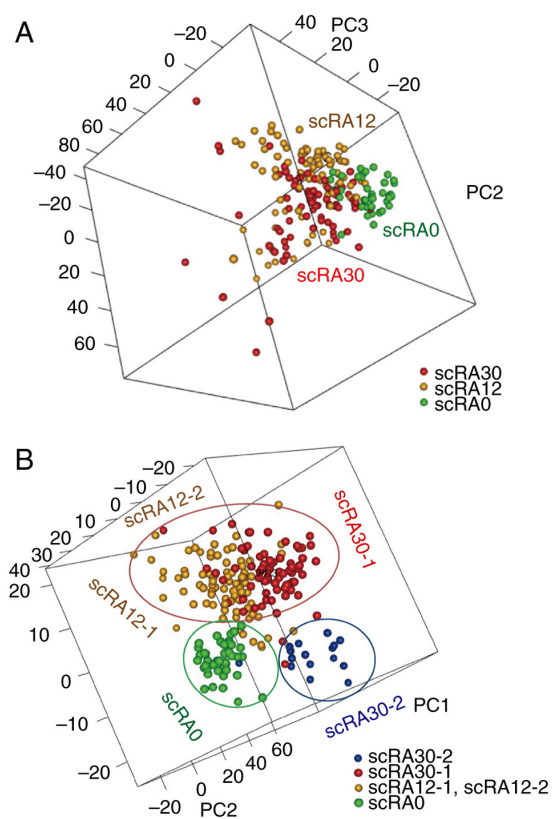
Figure S4. Radioresistance modules of single cell RNA-seq. Hub-gene networks of (A) scRed and (B) scBrown.
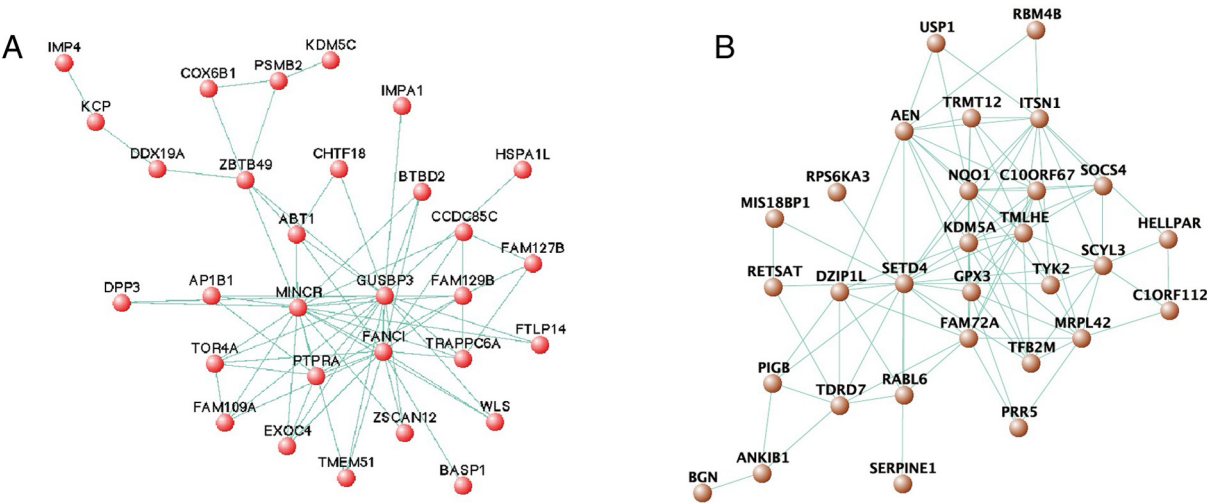
Figure S5. Radioresistance genes in bulk cancer cells, patient tissues and single-cell RNA-seq. Venn diagrams for genes in (A) 'cyan' (bulk) and scYellow, (B) 'cyan' (bulk) and scBlue, (C) scYellow and the radioresistant ESCC sample, and (D) scBlue and the radioresistant ESCC sample; genes associated with radioresistance in red; potential radioresistant genes in blue. ESCC, esophageal squamous cell carcinoma; sc, single cell.