

Figure S1. PCA of normalized expression. Plot of the two first principal component axes, based on PCA of the normalized expression of all probes. Black text indicates patients with cervical cancer stage II; red text indicates patients with cervical cancer stage III; green text indicates patients with cervical cancer stage IV; blue text indicates patients with unknown cervical cancer stage; pink text indicates controls; turquoise text indicates patients with cervical intraepithelial neoplasia stage 1. PCA, principal component analysis.

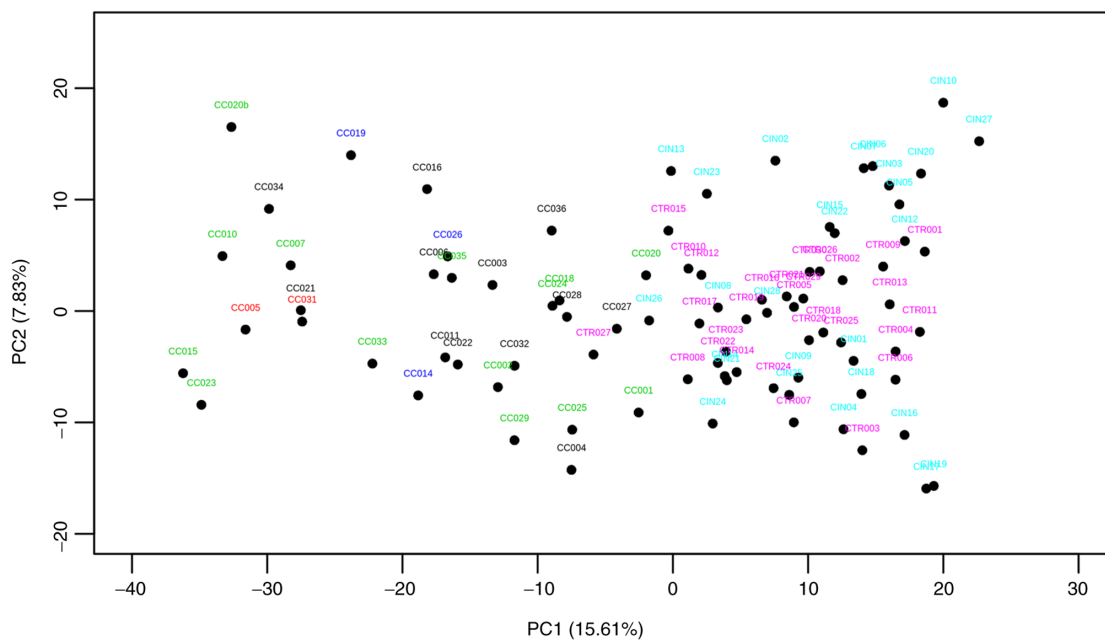


Figure S2. Heatmap of sample-sample distances. The Euclidean distances were computed from log<sub>2</sub>-transformed normalized expression data between each sample and hierarchical clustering was performed on the distances (dendrogram). The names of the samples and the scale for the distance are on the right of the heatmap.

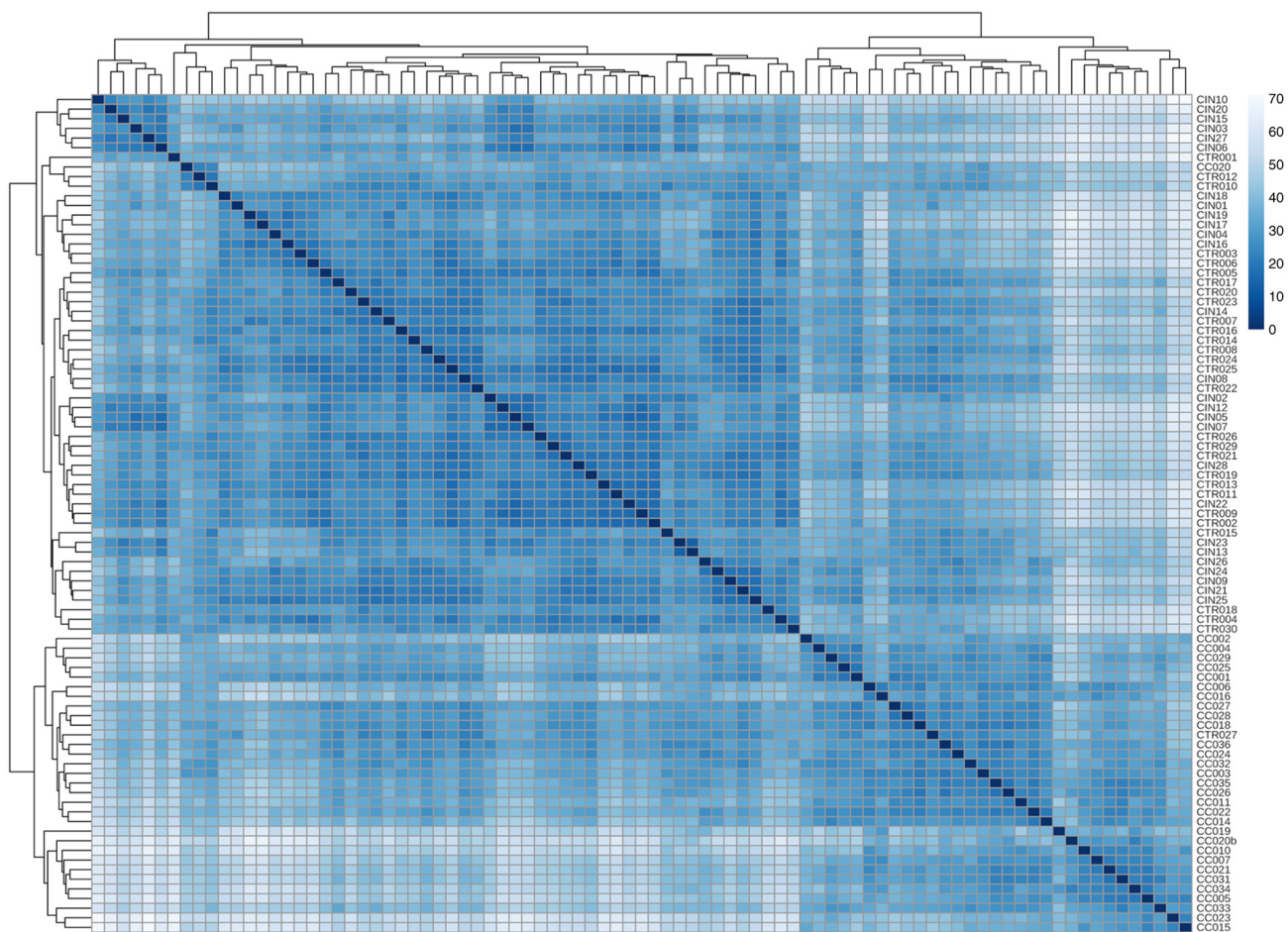


Figure S3. Dot plots of log<sub>2</sub>-transformed normalized expression of the genes exhibiting the lowest log<sub>2</sub>FC and the strongest P-values for the CC versus CTR or for the CC versus CIN1 comparisons. Differentially expressed genes were identified from log<sub>2</sub>-transformed normalized expression values using the Linear Models for Microarray Data and a moderated t-test. (A) Expression levels of the *CD27* gene. (B) Expression levels of the *STMN3* gene. (C) Expression levels of the *RPL38* gene. (D) Expression levels of the *RPL36* gene. (E) Expression levels of the *TRA* gene. CC, cervical cancer; CIN1, cervical intraepithelial neoplasia; CTR, control; FC, fold change.

