

Supplementary Figures

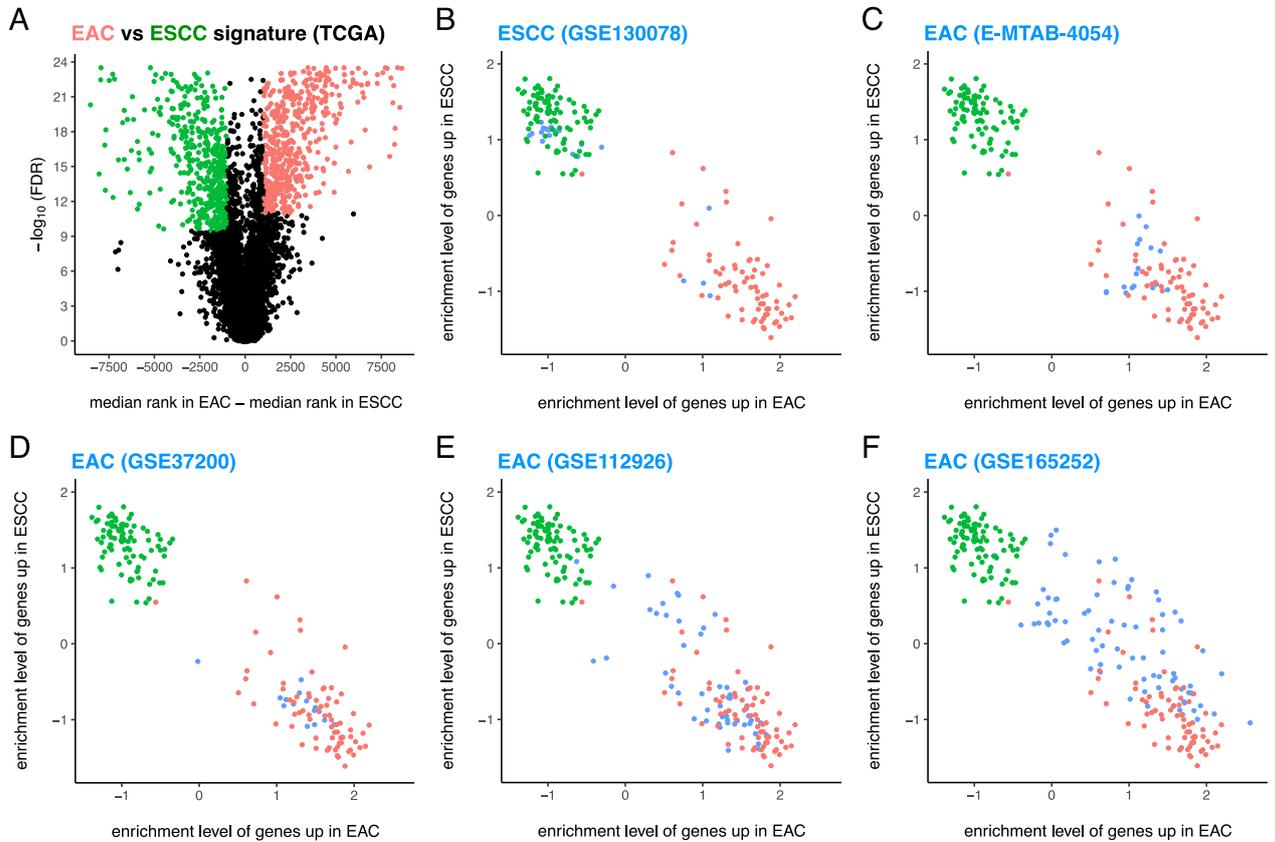


Figure S1. Construction and validation of gene expression signatures of esophageal adenocarcinoma (EAC) and esophageal squamous cell carcinoma (ESCC). (A) Gene expression signatures of EAC (consisting of 500 EAC^{hi} genes in red) and ESCC (consisting of 500 ESCC^{hi} genes in green) constructed from the Cancer Genome Atlas. Validation of these gene expression signatures in (B) a dataset of ESCC and (C-F) 4 datasets of EAC: red = EAC cases from TCGA, green = ESCC cases from TCGA, blue = test samples (various types of samples from datasets other than TCGA).

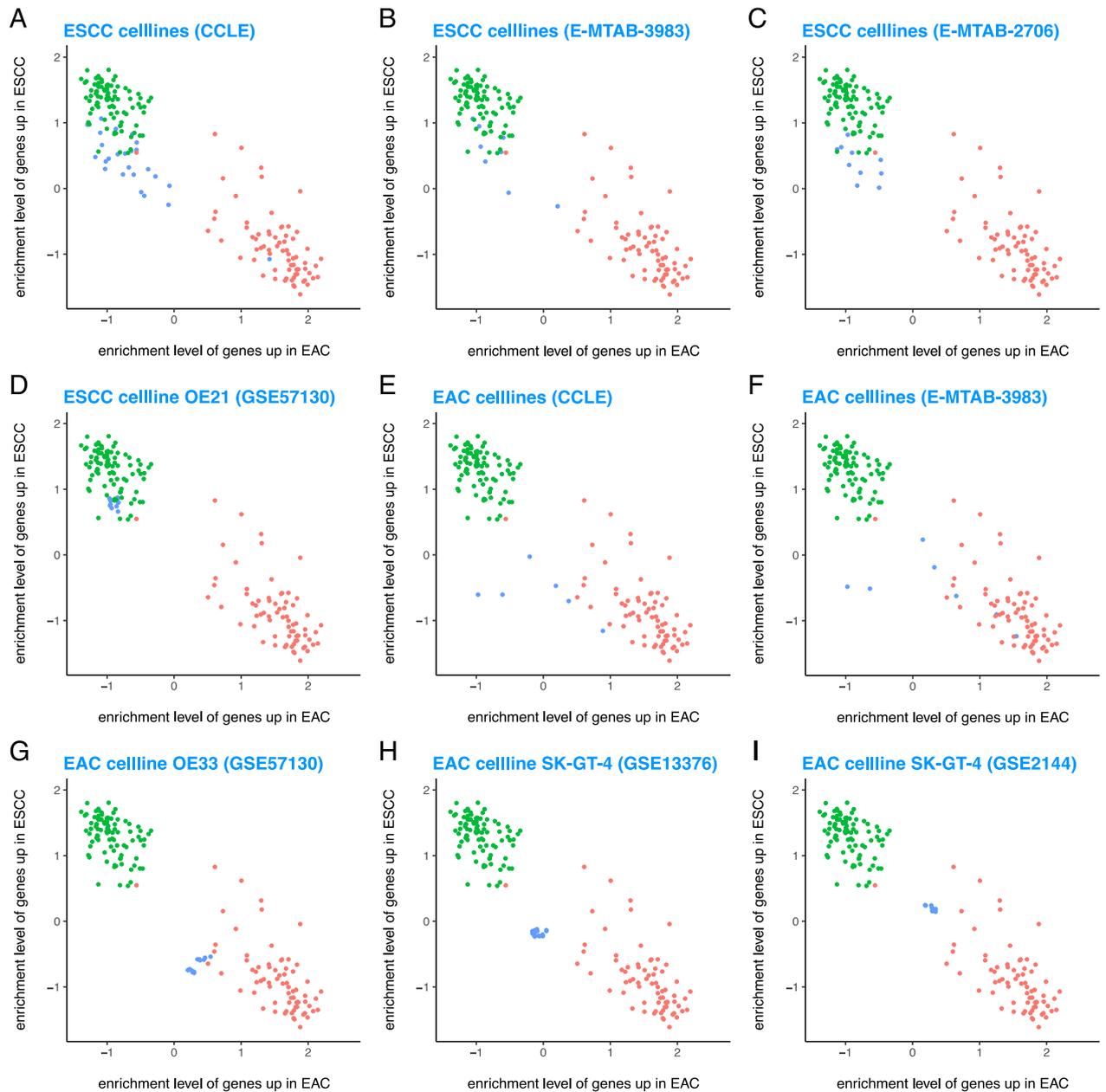


Figure S2. ESCC cell-lines are quite similar to primary ESCC tumors, but EAC cell-lines (although EAC-like) are considerably different from primary EAC tumors. Enrichment level of 500 EAC^{hi} and 500 ESCC^{hi} genes shows that (A-D) ESCC cell-lines cluster with primary ESCC tumors, but (E-I) EAC cell-lines often cluster near primary EAC tumors. red = EAC cases from TCGA, green = ESCC cases from TCGA, blue = test samples (various types of samples from datasets other than TCGA).

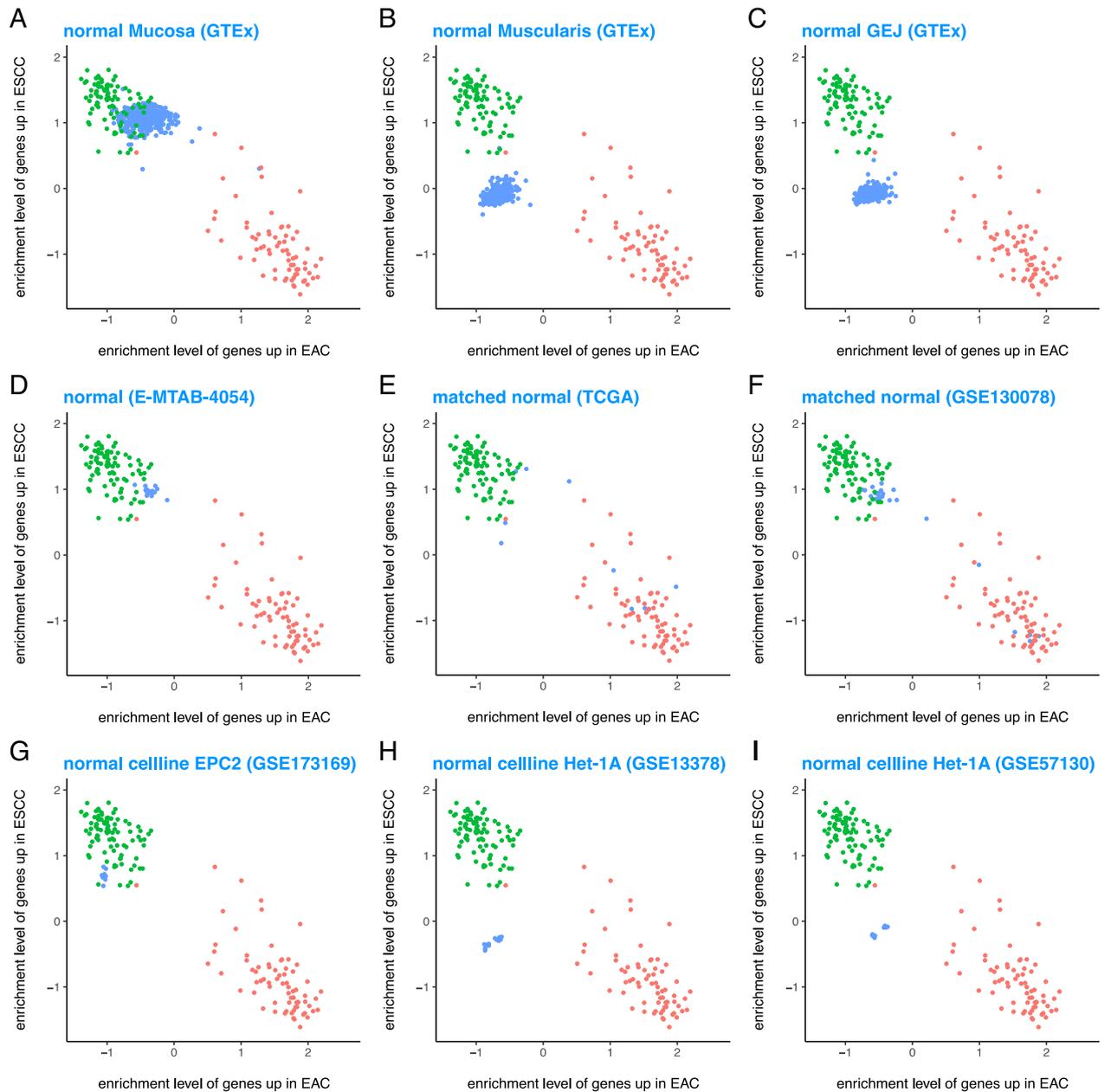


Figure S3. Normal esophageal cell-lines are quite similar to tissues derived from various parts of the normal esophagus. Enrichment levels of 500 EAC^{hi} and 500 ESCC^{hi} genes show that (A) normal esophagus mucosa is ESCC-like, (B) normal esophagus muscularis and (C) normal gastro-esophageal junction are neither EAC-like nor ESCC-like, (D) normal squamous esophagus is ESCC-like similar to normal esophagus mucosa, (E,F) matched normal esophagus from esophageal cancer patients are all over the place, (G) normal esophageal cell-line EPC2 is similar to normal esophagus mucosa (ESCC-like), (H,I) normal esophageal cell-line Het-1A is similar to normal esophagus muscularis and normal gastro-esophageal junction (neither EAC-like nor ESCC-like). red = EAC cases from TCGA, green = ESCC cases from TCGA, blue = test samples (various types of samples from datasets other than TCGA).

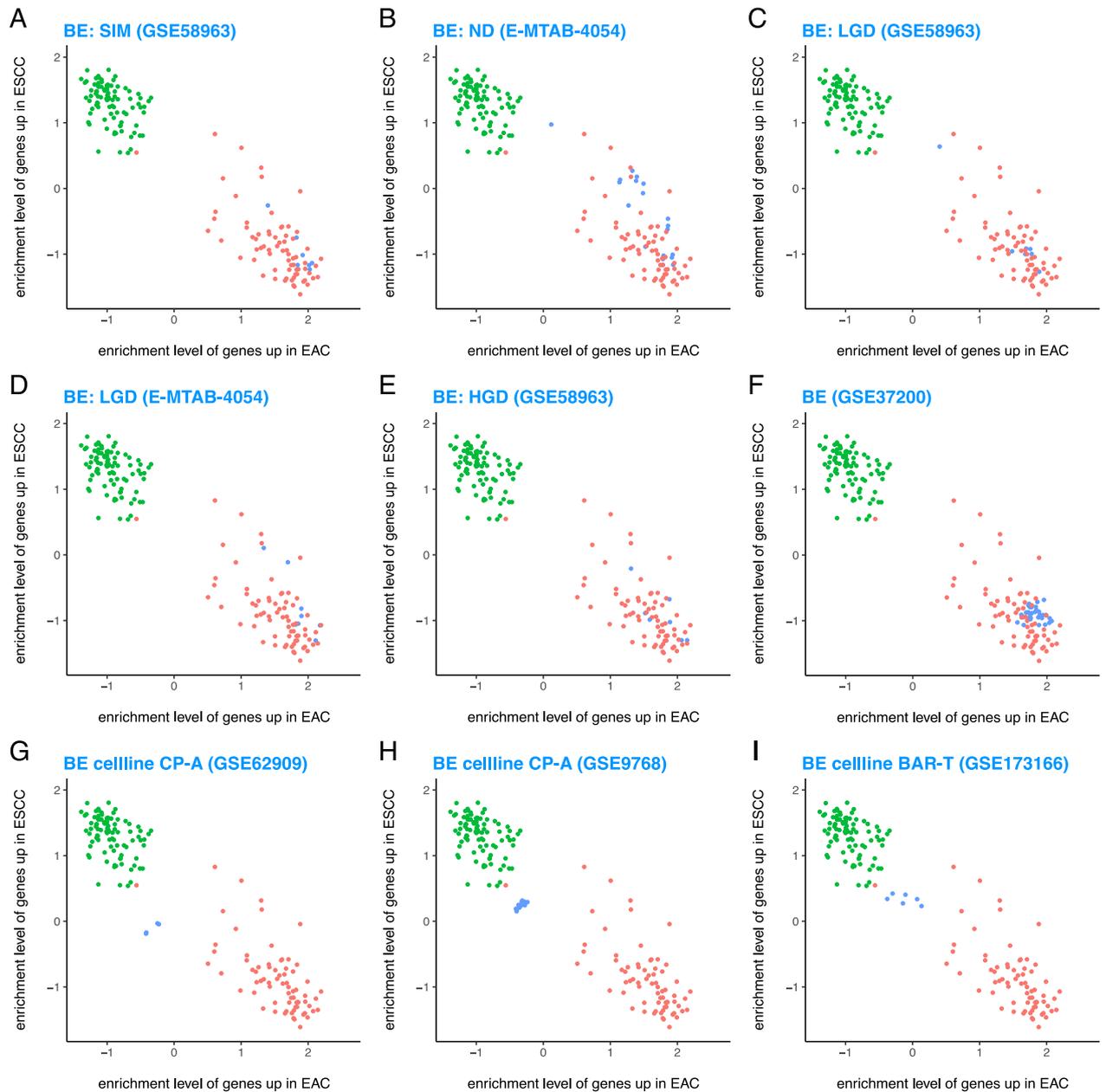


Figure S4. Barrett's Esophagus (BE) cell-lines were ESCC-like and extremely different from EAC-like primary BE tissues. Enrichment levels of 500 EAC^{hi} and 500 ESCC^{hi} genes show that (A-F) primary BE tissues are EAC-like at all stages (SIM = specialized intestinal metaplasia, ND = non-dysplastic, LGD = low grade dysplasia, HGD = high grade dysplasia), (G-I) BE cell-lines (CP-A, BAR-T) are surprisingly ESCC-like, and extremely different from primary BE tissues. red = EAC cases from TCGA, green = ESCC cases from TCGA, blue = test samples (various types of samples from datasets other than TCGA).

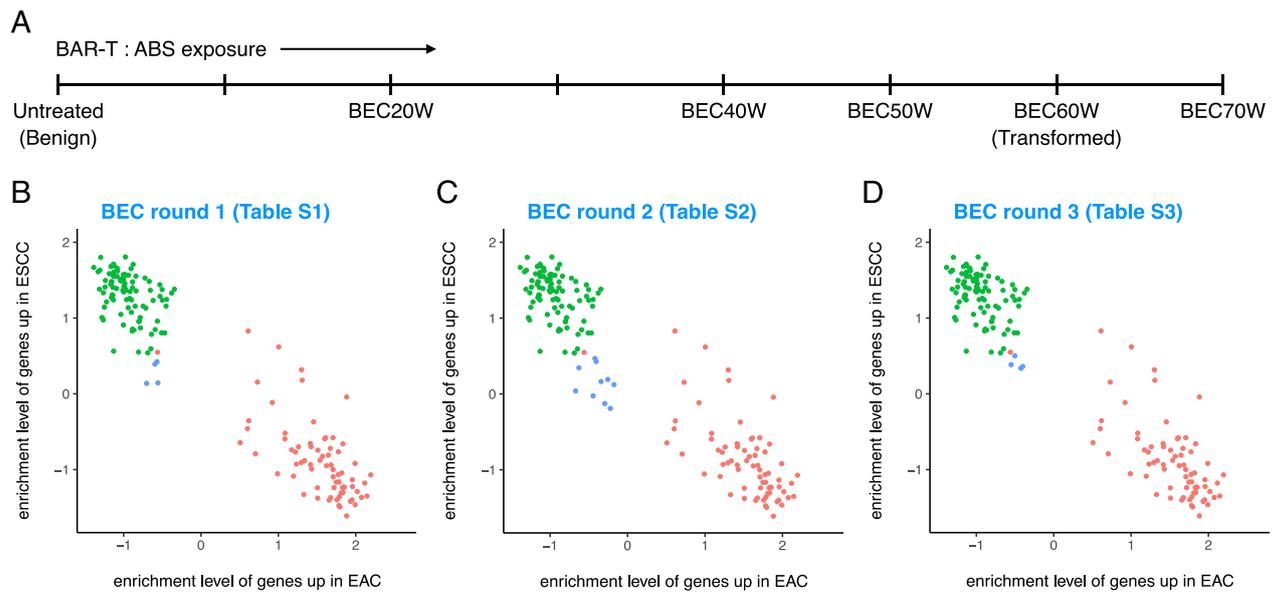


Figure S5. ABS exposure was not sufficient to induce EAC-like GEP in the BE cell line BAR-T and it remained ESCC-like even after malignant transformation. **(A)** Outline of the various time points at which BAR-T samples were collected from a previously established in-vitro model of BE carcinogenesis. Several untreated BAR-T samples were also included in the analysis. **(B-D)** Enrichment levels of 500 EAC^{hi} and 500 ESCC^{hi} genes showed that BAR-T samples remain ESCC-like despite ABS exposure and do not become EAC-like even after malignant transformation. red = EAC cases from TCGA, green = ESCC cases from TCGA, blue = test samples (various types of samples from datasets other than TCGA).