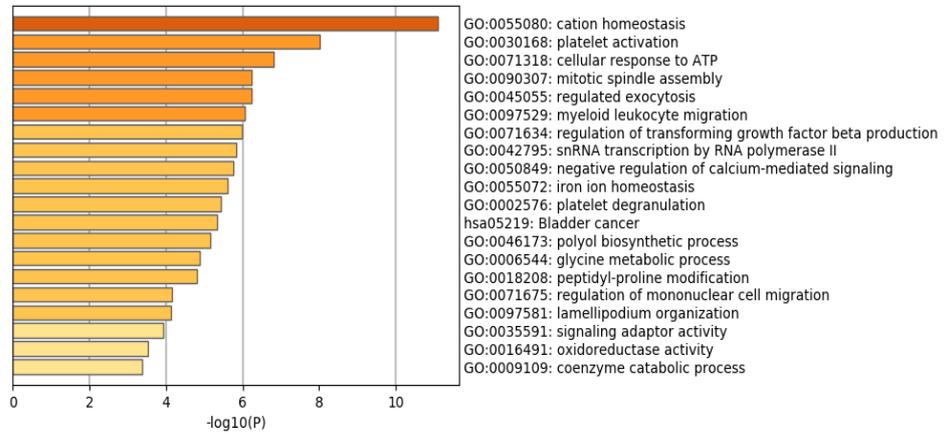
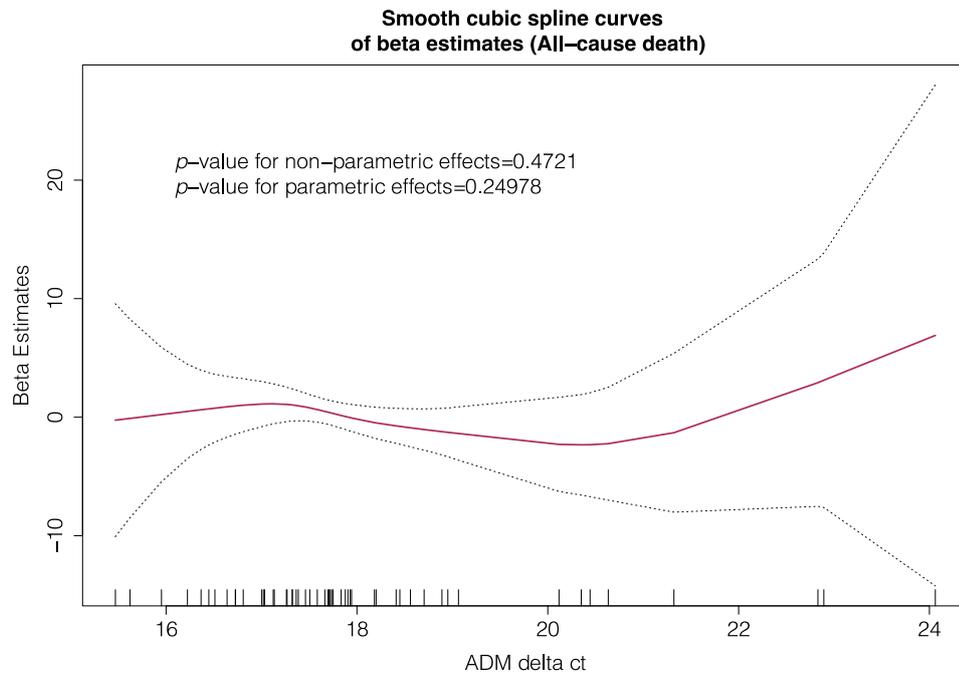


Figure S1: Enriched gene ontology (GO) analysis of differential expression genes observed in the transcriptome analyses of blood samples in cohort #1. Analysis was carried out by Metascape. The x-axis denotes  $-\log_{10}(P)$  values based on the cumulative hypergeometric distributions. The colors denote the relative value of  $-\log_{10}(P)$ : darker colors indicate a greater value of  $-\log_{10}(P)$ .



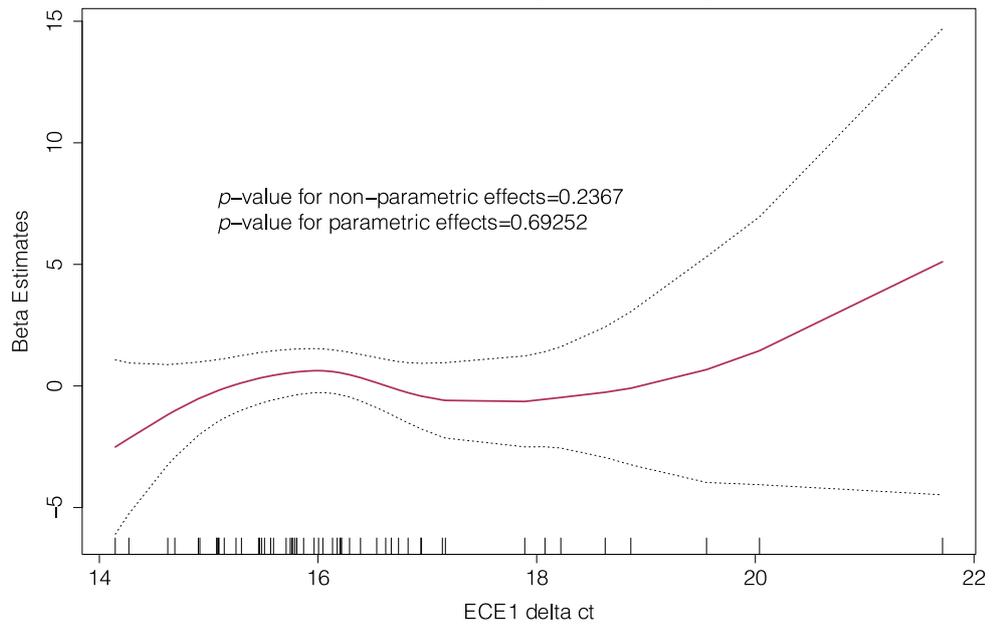
Supplementary Figure S2: Smooth spline estimates of all-cause death according to gene expression of *ADM* (A), *ECE1* (B), *FTMT* (C), *SIRT7* (D), *SMIM20* (E) and *TFRC* (F).  $\Delta$ ct: change in gene expression cycle threshold. Ct levels are inversely proportional to the amount of target nucleic acid in the sample (i.e., the lower the Ct level the greater the amount of target nucleic acid in the sample). Plots show the beta estimates of the outcome.

(A)



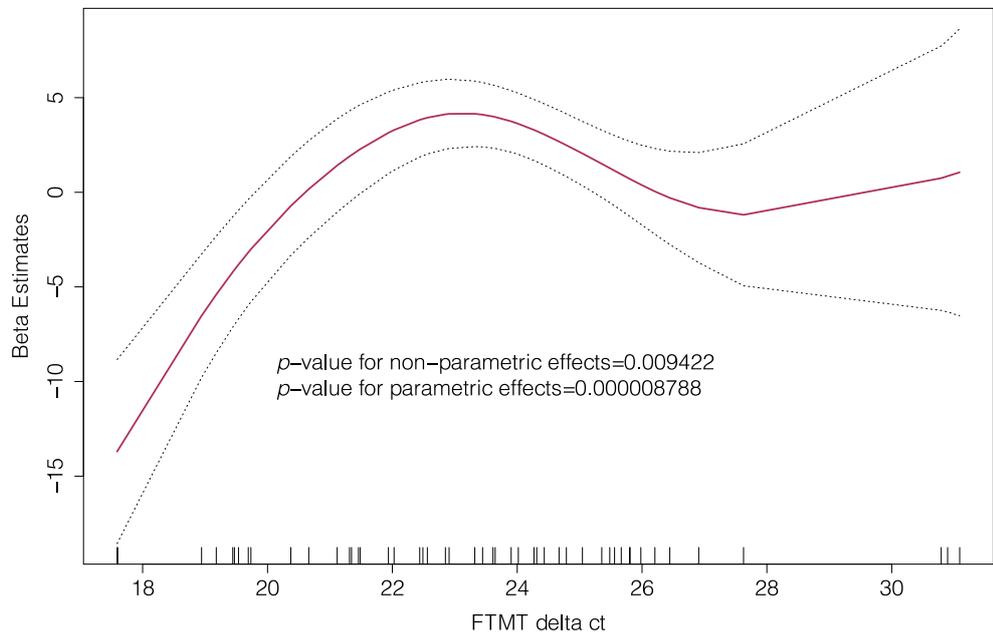
(B)

**Smooth cubic spline curves  
of beta estimates (All-cause death)**



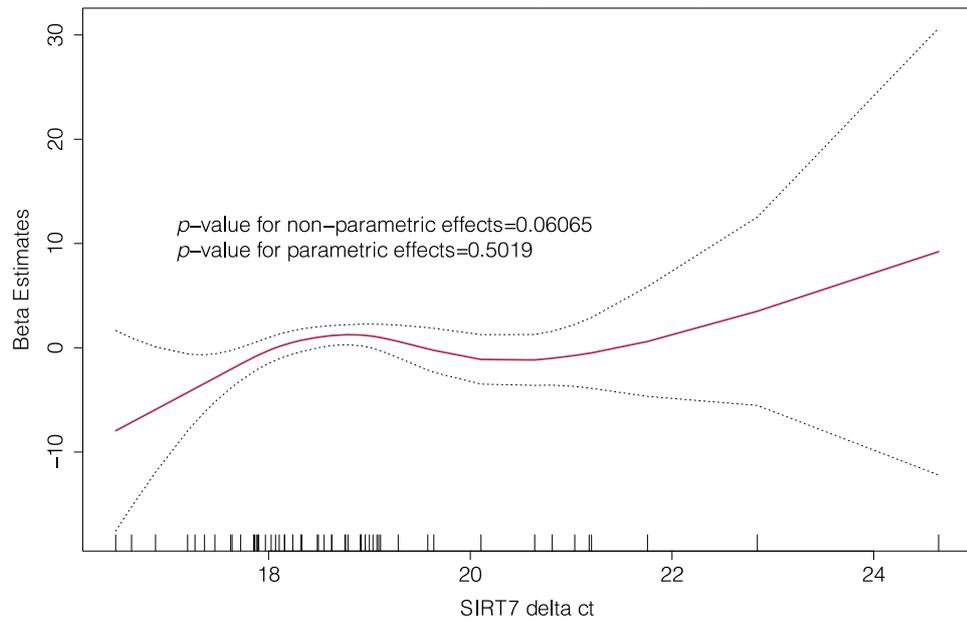
(C)

**Smooth cubic spline curves  
of beta estimates (All-cause death)**



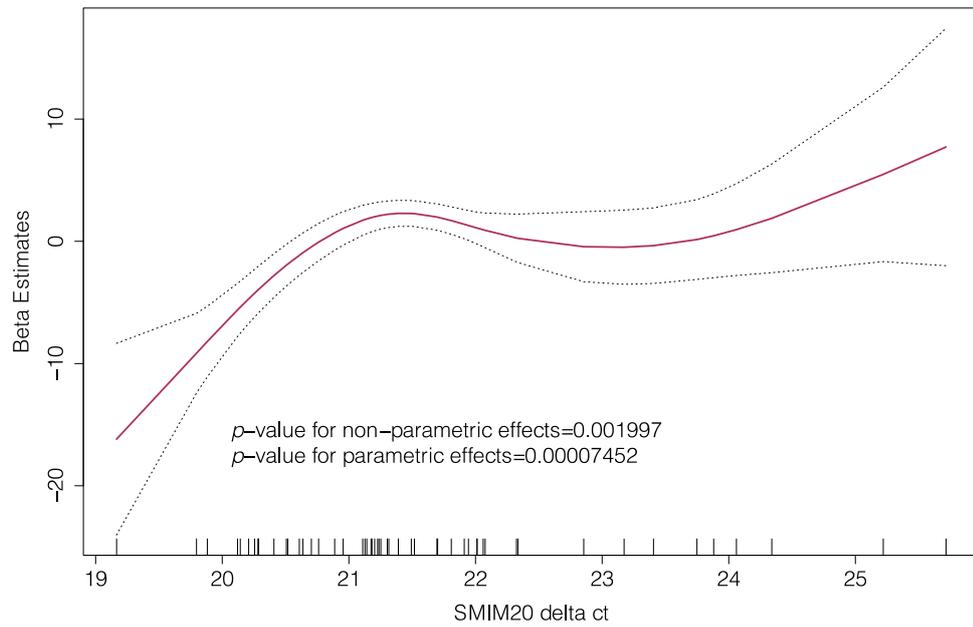
(D)

**Smooth cubic spline curves  
of beta estimates (All-cause death)**

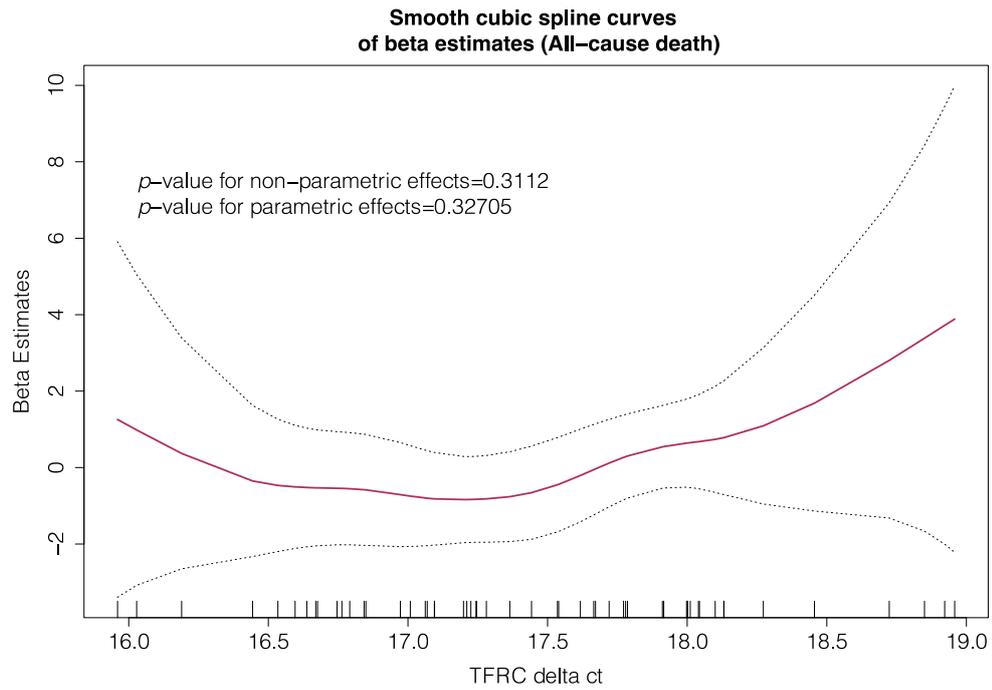


(E)

**Smooth cubic spline curves  
of beta estimates (All-cause death)**

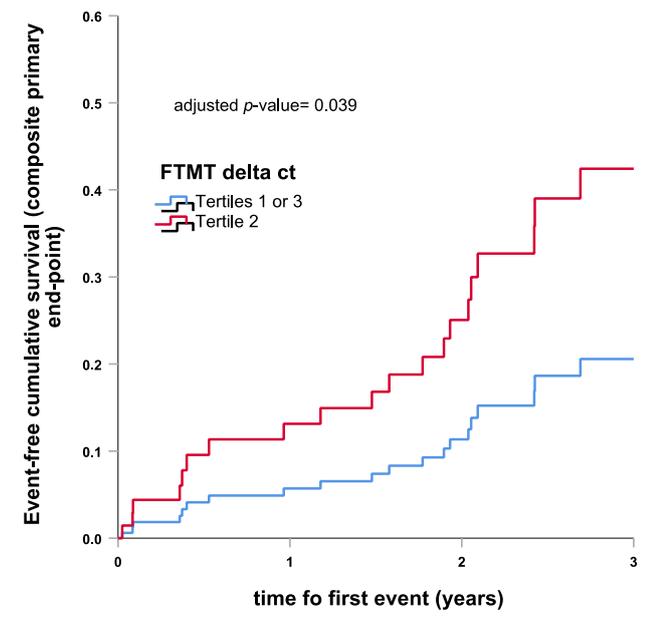


(F)

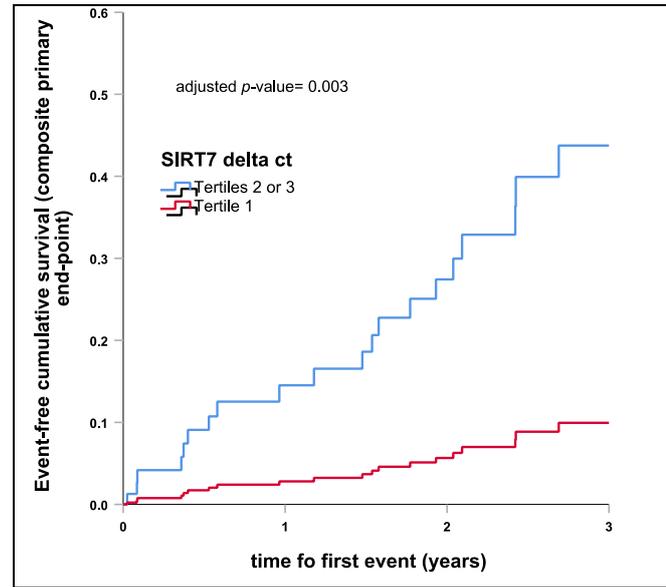


Supplementary Figure S3: Adjusted survival curves of significant associations between gene expression and primary composite endpoint (all-cause death or HF hospitalization).  $\Delta$ ct express change in gene expression cycle threshold.

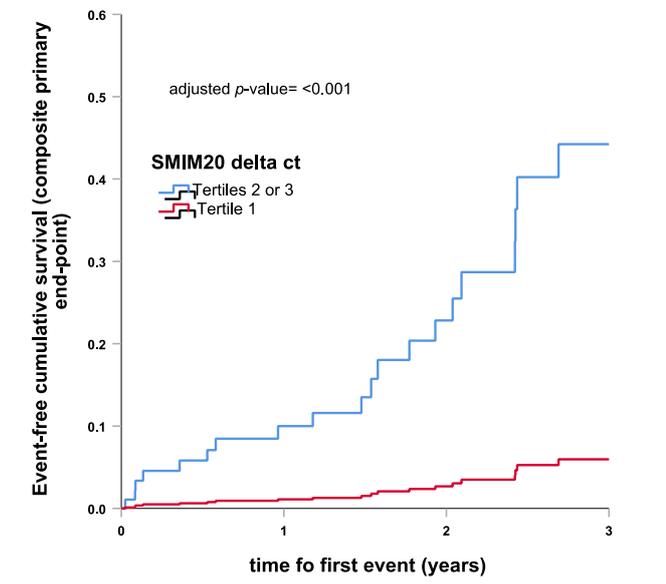
Panel A: FTMT mid-range expression (tertile 2 of  $\Delta$ ct) compared to high expression (lower tertile of  $\Delta$ ct –tertile 1) or low expression (higher  $\Delta$ ct –tertile 3) of FTMT.



Panel B: SIRT7 mid-range expression (tertile 2 of  $\Delta$ ct) or low expression (higher  $\Delta$ ct –tertile 3) compared to high expression (lower tertile of  $\Delta$ ct –tertile 1) of SIRT7.

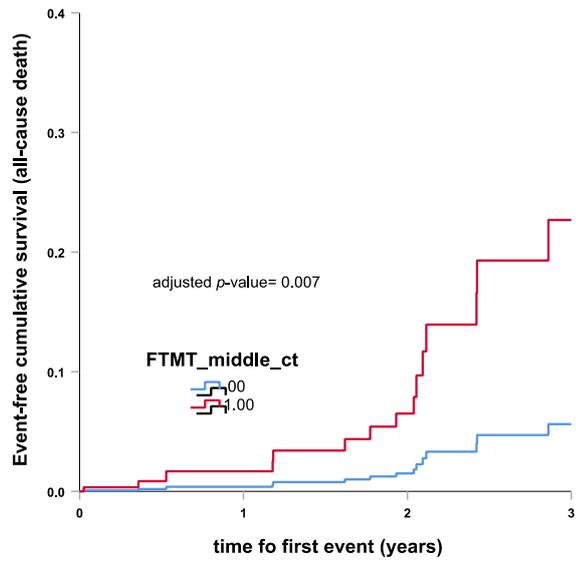


Panel C: SMIM20 mid-range expression (tertile 2 of  $\Delta$ ct) or low expression (higher  $\Delta$ ct –tertile 3) compared to high expression (lower tertile of  $\Delta$ ct –tertile 1) of SMIM20.

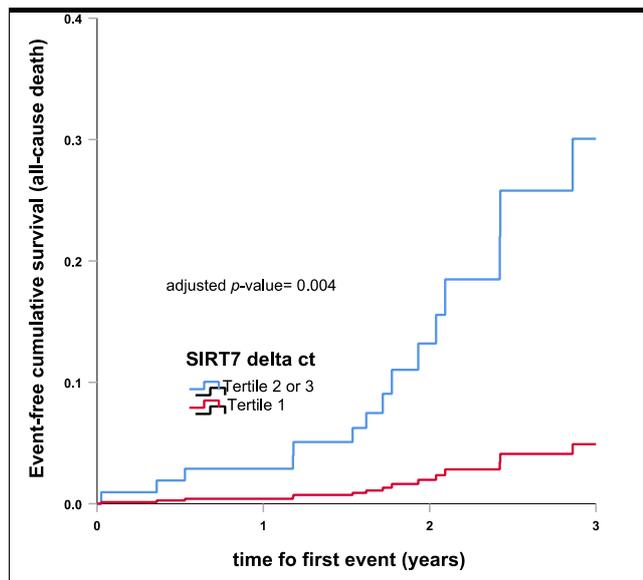


Supplementary Figure S4. Adjusted survival curves of significant associations between gene expression and all-cause death.  $\Delta$ ct: change in cycle threshold gene expression

Panel A: FTMT mid-range expression (tertile 2 of  $\Delta$ ct) compared to high expression (lower tertile of  $\Delta$ ct –tertile 1) or low expression (higher  $\Delta$ ct –tertile 3) of FTMT.



Panel B: SIRT7 mid-range expression (tertile 2 of  $\Delta$ ct) or low expression (higher  $\Delta$ ct –tertile 3) compared to high expression (lower tertile of  $\Delta$ ct –tertile 1) of SIRT7.



Panel C: SMIM20 mid-range expression (tertile 2 of  $\Delta$ ct) or low expression (higher  $\Delta$ ct –tertile 3) compared to high expression (lower tertile of  $\Delta$ ct –tertile 1) of SMIM20.

