MS PG-00034-2020R2: Identification of a peripheral blood gene signature predicting aortic valve calcification. D. MacGrogan et al.

Supplemental Tables are available at:

SUPPLEMENTARY TABLES CONTENT:

Supplementary Table S1. Characteristics of fetuses and patients in the RNA-seq study.

Supplementary Table S2 (9 sheets). Differential expression analysis for relevant pairwise comparisons. RNA-seq-derived, raw count expression values for conditions E22wk (embryo week 22, n=2), E13wk (embryo week 13, n=3), E9wk (embryo week 9, n=4), E (embryo, E22wk+E13wk+E9wk), cBAV (n=15), cTAV (n=16), D (disease, cTAV+cBAV), A (adult, cTAV+cBAV+CTL) and CTL (Control, 16 replicate samples). Data were processed with a pipeline that used ComBat to correct for batch effects, TMM for normalization and limma for differential expression testing. Only genes with an expression value of at least 1 count per million (CPM) in at least 10 samples were considered for testing. Nine pairwise comparisons were performed, and results are presented in different sheets. For each contrast and each gene, the following values are presented: Ensembl gene ID, HGNC symbol, average expression value for the conditions compared in the contrast, log fold change, p-value, Benjamini-Hochberg (B-H) adjusted p-value and gene description. Differential expression was considered significant if associated to B-H adjusted p_value < 0.05.

Supplementary Table S3. Number of differentially expressed genes for each contrast of interest and for the ANOVA test across all conditions.

Supplementary Table S4 (6 sheets). Functional annotation of metaclusters. Six gene metaclusters defined as described in Figure 2 were annotated with IPA. Complete Canonical Pathway enrichment results for each metacluster are presented in separate spreadsheets (MC1 to MC6). For each pathway, the following information is provided: statistical significance of enrichment, corrected for multiple testing with the B-H method (-log(B-H p-value)); fraction of pathway genes that are included in the metacluster (Ratio); enrichment value (Enrichment); and names of pathway genes that are included in the metacluster (Molecules). Canonical pathways

with -log(B-H p-value) > 1.3 were considered as significantly enriched, and selected for display in Figure 3.

Supplementary Table S5. Differentially expressed genes detected after comparing PESA subclinical disease individuals (PESA-SD, n=59) with PESA no calcification individuals (PESA-CTL, n=396). The following values are presented: Ensembl gene ID, HGNC symbol, average expression value for the conditions compared in the contrast, log fold change, p-value, B-H adjusted p-value.

Supplementary Table S6. Gene markers of subclinical CAVD.

Supplementary Table S7. Characteristics of CAVD patients in the qRT-PCR study.

Supplementary Table S8. *P* values of single genes.

Supplementary Table S9. Linear relationship between level of gene expression and the amount of CAC -AV

Supplementary Table S10. Expression changes of genes in valves used for comparison to the PESA study.

Supplementary Table S11. Confusion matrix for the predictions of the gene signature presented in Figure 4A.

Supplementary Table S12. References for TaqMan Assays.