



**Fig. S2. Dendrogram of genes identified by Ingenuity Pathway Analysis in the 2 HSP patient clusters.** HSP-normal samples are labelled in black and HSP-inflamed samples are labelled in red. The log<sub>10</sub> normalized counts were transformed into row z-scores for each gene and depicted in a colour scale with blue as the minimum value and red as the maximum value. The samples and genes are clustered using hierarchical clustering of the Euclidean distance with average linkage.