



Figure 1 – figure supplement 1. Gene set enrichment analysis (GSEA) enrichment plots for the hypoxia and glycolysis gene sets in unidirectional vs disturbed flow in HAECs. HAECs were subjected to UF or DF for 24 hours before RNA isolation and total RNA sequencing (RNAseq). Genome-wide expression analysis of the RNAseq data was performed using gene set enrichment analysis (GSEA) software version 2.2.4 available from the Broad Institute (<http://www.broadinstitute.org/gsea/downloads.jsp>). The GSEA algorithm calculates an enrichment score reflecting the degree of overrepresentation at the top or bottom of the ranked list of the genes included in a gene set in a ranked list of all genes present in the RNAseq dataset. **(TOP)** A positive enrichment score (ES) indicates gene set enrichment at the top of the ranked list; a negative ES indicates gene set enrichment at the bottom of the ranked list. The final enrichment score for a set is the maximum deviation from zero encountered for that set. **(MIDDLE)** The location of the hypoxia or glycolytic genes in the ranked set of all genes. The “Rank Metric Score” is the signal-to-noise ratio for each gene used to position the gene in the ranked list. **(BOTTOM)** The distribution of the rank metric score across all genes present in the expression dataset. The gene set collection used was the h.all.v5.1.symbols.gmt [Hallmarks] gene sets database. The analysis demonstrates that known **(A)** hypoxia genes and **(B)** many glycolysis enzymes are positively enriched in the disturbed flow sample.