



**Figure 2 – figure supplement 2. Gene set enrichment analysis (GSEA) for the hypoxia and glycolysis gene sets in disturbed flow with siRNA targeted towards *HIF-1α* or control in HAECs.** HAECs were treated with control siRNA or siRNA targeted towards *HIF-1α* for 24 hours prior to 48 hours of DF, followed by 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 control siRNA sample.