**Cells**

We used de-identified primary human lymphatic endothelial cells (HLECs) for experiments. HLEC-1 were from Lonza (CC-2812) and were used for RNA-seq analysis with shGATA2. HLEC-2 (Lonza, CC-2516) were used for RNA-seq analysis with miR-126 sponge. HLECs were grown on firbonectin-coated plates or glass slide and were maintained in EBM2 media from Lonza. All experiments were conducted using passage 5-6 cells. HLECs were treated as potential biohazards and were handled according to institutional biosafety regulations.

**Knockdown of GATA2**

shGATA2 (TTAACAGGCCACTGACCATGAAGAAGGAA) was cloned into a pLV plasmid. Cyagen Bioscience (Santa Clara, CA, USA) generated the lentiviral particles using LentiPAC 293 cells. HLECs were seeded at 50-60% confluence on fribronectin-coated plates. The following day cells are infected with equal amounts of pLV control or shGATA2 virus according to manufacturer protocol for 4-6 hrs in Opti-MEM medium and then changed to regular EBM2 media. After 3 days cells were harvested with Trizol (Invitrogen, Carlsbad, CA, USA) for RNA-seq study.

**Knockdown of miR-126**

pSFFV plasmid (miR-126 sponge) to sequester miR-126 were reported previously (Gentner et al. 2009). Cyagen Bioscience (Santa Clara, CA, USA) generated the lentiviral particles using LentiPAC 293 cells. HLECs were seeded at 50-60% confluence on fribronectin-coated plates or glass slide. The following day cells are infected with equal amounts of pSFFV control or miR-126 sponge virus for 4-6 hrs according to manufacturer protocol using EBM2 medium and then changed to fresh medium. After 3 days cells were harvested for RNA-seq study.

**RNA-seq analysis**

Total RNA was purified from HLECs infected with shGATA2 or control shRNA expressing lentivirus particles. RNA was subjected to ribosomal RNA depletion followed by Truseq stranded total RNA library preparation according to the manufacturer’s instruction (Illumina). RNA from miR-126-sponge treated HLEC-2 were processed using NEB Ultra II directional RNA Library kit for Illumina. The resulting RNA-seq libraries were analyzed on the Illumina HiSeq sequencing platform. The obtained sequencing reads were mapped with the bowtie2 algorithm using the RefSeq annotations (hg19 genome build) (1). We utilized the RNA-seq analysis work flow within the Partek Genomics Suite (Partek Incorporated) for quantitation and statistical analysis (ANOVA) of the transcriptome data. We identified those transcripts that exhibited statistically significant differential expression in the shGata2 samples compared to the shControl samples. We rank ordered the two lists based on the expression level and magnitude of change. Using these rank-ordered list, we performed gene ontology (GO) analysis for enriched biological terms (2). The genes commonly regulated by GATA2 and miR-126 were analyzed using the functional annotation platform of DAVID (3, 4).

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