

**Table S3. Proteomics Analysis of Lipid Raft Proteins in Endothelial Cells with Flow Treatment.**

A.

Classification	OS up	OS down	PS up	PS down	Opposite
Binding	29	17	27	22	0
Catalytic	28	13	27	16	0
Enzyme Regulator	5	4	4	7	3
Ion Channel	2	2	0	2	0
Motor	1	0	1	0	0
Receptor	13	7	4	9	1
Structural Molecular	11	1	10	3	0
Transcription Regulator	2	0	1	0	0
Translocation Regulator	3	0	3	0	0
Transporter	8	7	3	7	0

B.

Function	GI number	Protein name	Fold		P <sub>peptides</sub>
			OS	PS	
Receptor	Gi 31438	Integrin $\alpha$ 5	1.828	0.609	0.05

HUVECs were treated with OS ( $0.5 \pm 4$  dyn/cm<sup>2</sup>) or PS ( $12 \pm 4$  dyn/cm<sup>2</sup>) for 2 hr, and purified lipid raft proteins were analyzed by iTRAQ-LC-MS/MS. Proteins with significant change were sorted into functional groups by use of Panther (<http://www.pantherdb.org>). Up, upregulated; down, downregulated; opposite, regulated in opposite fashion.