Table S3 A. Identification and quantification statistics of the effect of Angiotensin II on the VSMC proteome

Duration of AngII-treatment	NS[1]	NP[2]	NQ[3]	k	Scan variance (σ^2_{SP})	Peptide variance (σ^2_{PQ})	Protein variance (σ^2_{QA})	Scan outliers (%)	Peptide outliers (%)	Protein abundance changes
2h	165226	30249	5633	1372.32	0.0390	0.0472	0.0008	2.93	3.01	40
4h				1035.99	0.0429	0.0352	0.0024	2.66	3.03	64
6h				1040.51	0.0331	0.0278	0.0020	2.56	3.08	65
8h				1581.01	0.0358	0.0400	0.0025	2.69	3.16	66
10h				1179.71	0.0378	0.0393	0.0012	2.60	3.29	76

[1] Number of scans quantified; [2] Number of peptides quantified; [3] Number of proteins quantified. All the identified proteins were quantified. Scan and peptide outliers were detected at 1%FDR, whereas protein outliers (i.e., abundance changes) were detected at 5% FDR.