

TABLE S1. FAP siRNA sequences

siRNA Name	Sense Strand (5'→3')	Antisense Strand (5'→3')
siFAP-1	CCUCGAGUGACUACUAAUUUTT	AAAUAGUAGUCACUCGAGGTT
siFAP-2	GCAAGUGGGAGGCCAUUAUATT	UAUAAUGGCCUCCCACUUGCTT
siFAP-3	CUGCAGUGGAAAUUUAAGAAATT	UUUCUAAAAUUUCCACUGCAGTT

TABLE S2. Top 30 DEGs with the lowest padj in the serum-stimulated group (SiFBS vs NcFBS)

Gene Name	log2FC (SiFBS vs NcFBS)	P Value	padj
Poglut3	-1.27	4.13E-106	5.90E-102
Ccnd3	-1.58	2.35E-84	1.68E-80
Ctdsp1	-1.27	1.02E-78	4.85E-75
Ccdc47	-1.47	9.30E-66	3.32E-62
Sel1l	-1.00	6.53E-57	1.86E-53
Fap	-2.23	1.14E-46	2.71E-43
Atad1	-1.19	1.74E-43	3.56E-40
Efemp1	1.59	6.60E-39	1.18E-35
Cnpy4	-1.22	1.19E-37	1.89E-34
ENSRNOG00000064136	-1.41	2.38E-36	3.40E-33
Rnf26	-1.04	3.01E-31	3.07E-28
Ckb	1.08	7.05E-28	5.92E-25
ENSRNOG00000078092	1.52	4.29E-25	3.22E-22
Cth	-1.03	2.20E-24	1.50E-21
Net1	-1.08	4.74E-22	2.60E-19
Tlcd3a	-1.17	3.34E-20	1.49E-17
Rps17l2	-1.07	1.71E-19	6.42E-17
Gbp1	1.86	5.96E-19	2.03E-16
Fras1	1.88	4.23E-18	1.28E-15
Mmp11	-1.01	1.06E-17	3.10E-15
Adh1c	1.02	3.63E-17	9.77E-15
Ripor3	1.82	2.23E-16	5.22E-14
Ak4	-1.04	2.83E-16	6.42E-14
Fyco1	-1.08	3.81E-16	8.37E-14
Myh1	1.88	5.26E-16	1.12E-13
ENSRNOG00000086174	1.14	6.81E-16	1.41E-13
Pclaf	-1.43	2.95E-15	5.54E-13
Ttc9	1.16	3.11E-15	5.77E-13
Pappa2	1.06	1.27E-14	2.18E-12
Oasl	1.14	4.94E-13	6.92E-11

padj, adjusted p value; DEGs, differentially expressed genes.

TABLE S3. Top 30 DEGs with the lowest padj in the no-serum-stimulated group (SiNs vs NcNs)

Gene Name	log2FC (SiNs vs NcNs)	P Value	padj
Fap	-2.15	9.05E-138	1.22E-133
Ccdc47	-1.04	5.97E-75	4.04E-71
Poglut3	-0.87	3.04E-71	1.37E-67
Psen2	-1.09	5.88E-66	1.99E-62
Ccnd3	-1.29	1.35E-59	3.66E-56
Ctdsp1	-0.92	1.81E-56	4.08E-53
ENSRNOG00000064136	-1.05	3.66E-41	7.08E-38
Reck	-0.68	7.44E-39	1.26E-35
Efemp1	1.28	4.75E-36	7.15E-33
Adamts8	0.64	9.23E-32	1.25E-28
Grem1	0.51	3.58E-31	4.41E-28
Vldlr	-0.59	7.26E-31	8.19E-28
Nqo1	0.83	1.75E-30	1.82E-27
Sel1l	-0.61	1.03E-26	9.94E-24
Sema3d	0.82	2.75E-26	2.48E-23
Ephx1	0.69	7.14E-26	6.04E-23
Mmp11	-0.83	1.69E-24	1.34E-21
Tfric	-0.6	2.48E-24	1.86E-21
Cnpy4	-0.79	3.70E-24	2.64E-21
Atad1	-0.79	7.40E-24	5.01E-21
Fyco1	-0.87	8.73E-22	5.62E-19
Ass1	0.8	6.24E-20	3.84E-17
Gucy1a1	0.81	3.70E-19	2.18E-16
Idh2	-0.57	2.76E-18	1.56E-15
Gys1	-0.49	1.01E-17	5.47E-15
Olr1	0.43	5.68E-17	2.96E-14
Adamts15	0.65	9.96E-17	4.92E-14
Serping1	0.55	1.02E-16	4.92E-14
Lvrn	-0.63	1.39E-16	6.34E-14
Pgk1	-0.53	1.41E-16	6.34E-14

padj, adjusted p value; DEGs, differentially expressed genes.

TABLE S4. GO Functional Enrichment in the serum-stimulated group (SiFBS vs NcFBS)

Category	Description	GeneRatio	BackgroundRatio	pvalue	padj	Up	Down
BP	G-protein-coupled receptor signaling pathway	11/57	223/4053	0.000213	0.030885	11	0
MF	signaling receptor activity	11/88	226/6752	0.000153	0.008180	11	0
MF	molecular transducer activity	11/88	226/6752	0.000153	0.008180	11	0
MF	G-protein-coupled receptor activity	9/88	172/6752	0.000372	0.013263	9	0
MF	transmembrane signaling receptor activity	9/88	211/6752	0.001610	0.043067	9	0

GeneRatio, the ratio of DEGs annotated to the term to total DEGs; BackgroundRatio, the ratio of all genes annotated to the term to total background genes; padj, adjusted p value. Up, number of upregulated genes; Down, number of downregulated genes.

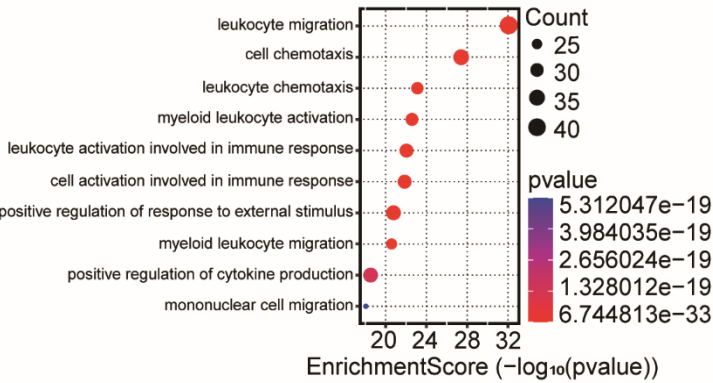
TABLE S5. GO Functional Enrichment in the no-serum-stimulated group (SiNs vs NcNs)

Category	Description	GeneRatio	BackgroundRatio	pvalue	padj	Up	Down
BP	cell adhesion	5/34	88/4056	0.000727	0.033421	2	3

GeneRatio, the ratio of DEGs annotated to the term to total DEGs; BackgroundRatio, the ratio of all genes annotated to the term to total background genes; padj, adjusted p value. Up, number of upregulated genes; Down, number of downregulated genes.

A

Biological Process (Commonly Upregulated Genes)



B

Cellular Component (Commonly Upregulated Genes)

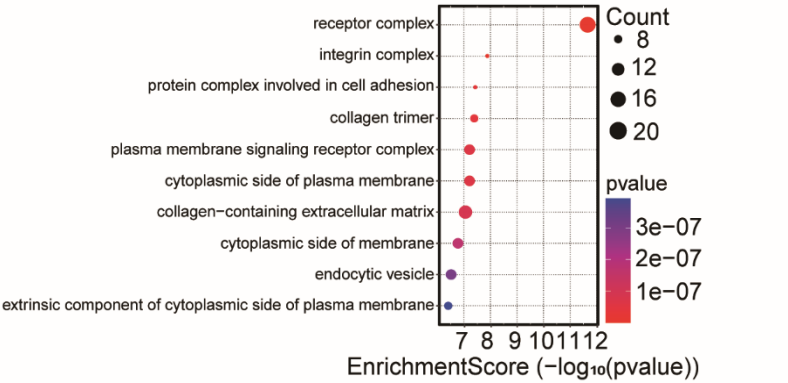
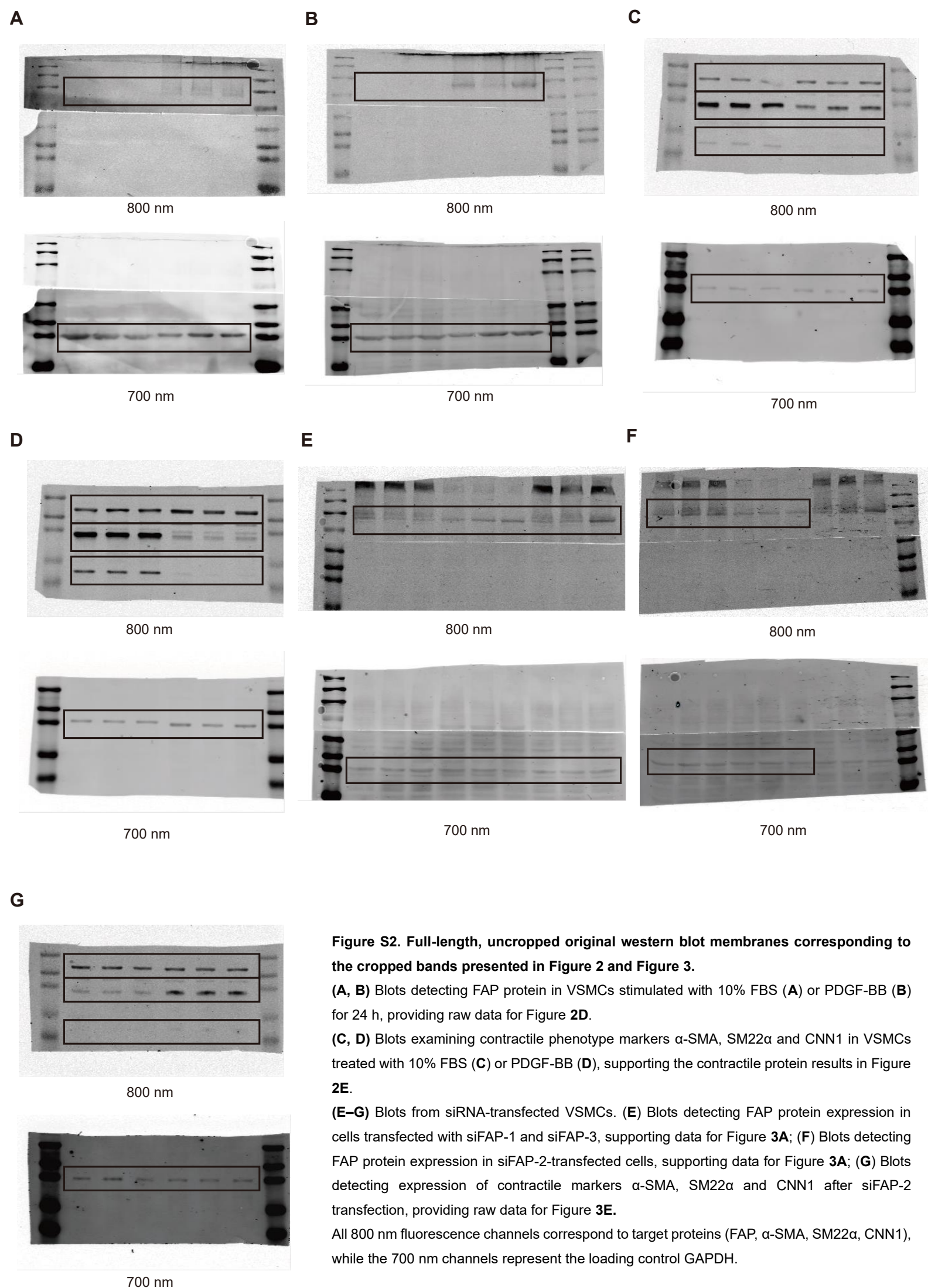


Figure S1. GO enrichment analysis of commonly upregulated genes from GEO datasets

(A) Biological Process (BP) enrichment analysis of the 256 commonly upregulated genes. **(B)** Cellular Component (CC) enrichment analysis of the 256 commonly upregulated genes. Only significantly enriched GO terms are displayed.



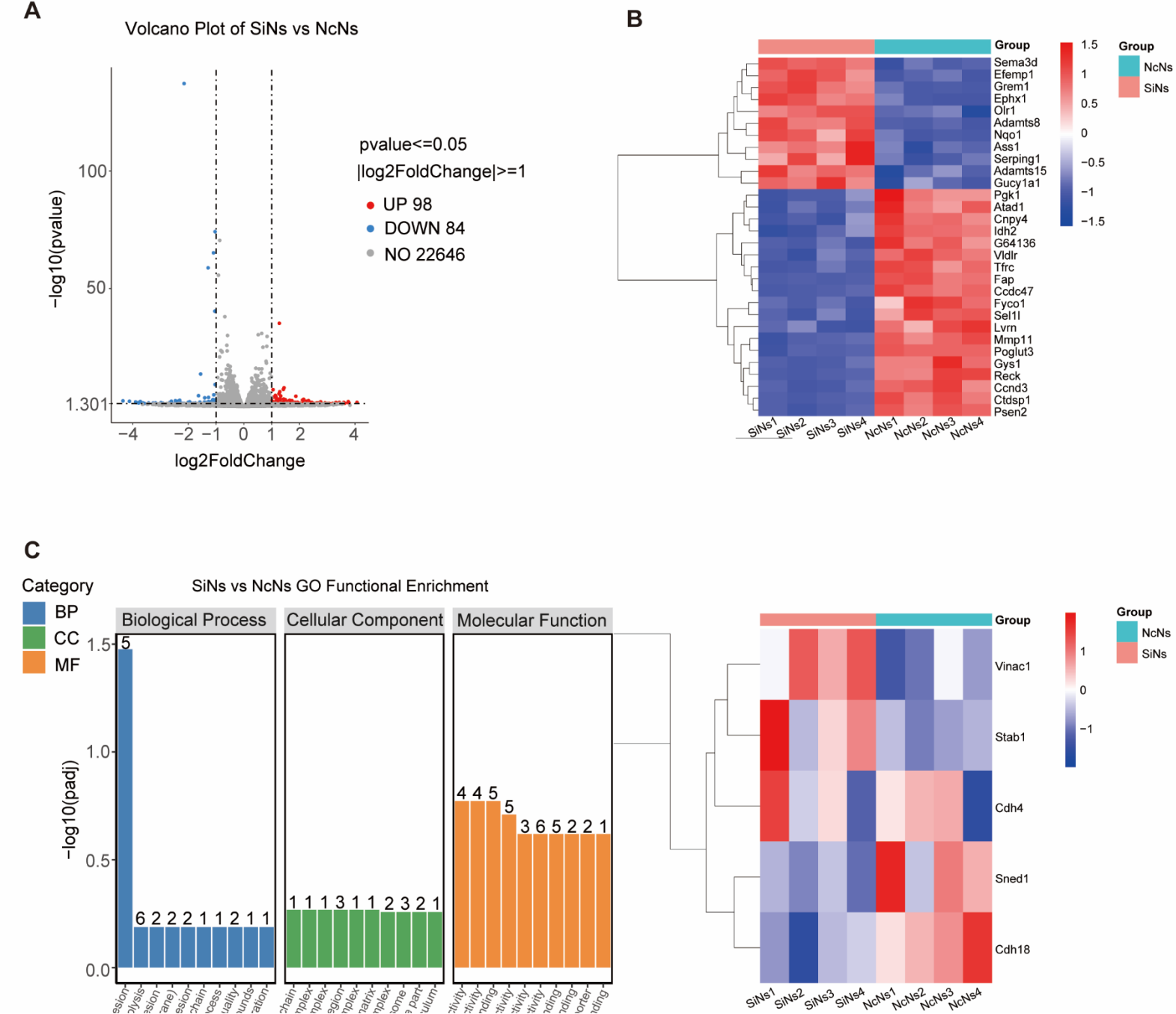


Figure S3. Transcriptomic analysis of FAP-deficient VSMCs under non-stimulated conditions

(A) Volcano plot showing differentially expressed genes (DEGs) between the SiNs and NcNs groups. **(B)** Heatmap of the top 30 DEGs ranked by adjusted P value (padj) in the SiNs versus NcNs comparison. **(C)** GO enrichment analysis of DEGs identified in the SiNs versus NcNs comparison.