SUPPLEMENTAL MATERIAL

Data S1.

Supplemental Methods

Immunofluorescence

For immunofluorescent staining, transfected HUVECs and HBVSMCs were fixed in paraformaldehyde. After permeabilization in 0.2% Triton X-100 and blocking, the cells were incubated with primary antibodies against β-catenin (1:250, ab32572, Abcam) overnight at 4°C and then incubated with an Alexa Fluor 488-conjugated goat antibody against rabbit (1:200, ab150077, Abcam) at room temperature for 1 h. Finally, the cells were counterstained with 4,6-diamidino-2-phenylindole and imaged using an EVOS™ FL Auto 2 Imaging System (Invitrogen).

Western blotting

Whole-cell lysates were prepared using RIPA buffer. Equal amounts of total protein (20 μg) from cell lysates were loaded on a 10% SDS/PAGE gel, transferred to a PVDF membrane (Millipore), and detected using a BOX F3 Gel Documentation System (Syngene). The primary antibodies used were as follows: FZD10 (1:1000, NBP2-23659SS, Novus), MYOC (1:500, MAB3446, R&D), β-catenin (1:4000, ab32572, Abcam), JNK (1:1000, 9252S, CST) and p-JNK (1:1000, Thr183/Tyr185, 81E11, CST). β-actin (1:2000, P30002M, Abmart) was used as the

loading control. The secondary antibodies used were goat anti-rabbit (1:3000, M21002, Abmart) and goat anti-mouse (1:3000, M21001, Abmart) IgG-HRP.

Wound healing assay

Wound healing assays were performed with an Ibidi Culture-Insert (Ibidi). Briefly, transfected cells were seeded into the wells to obtain a confluent layer. After appropriate cell attachment, the Culture-Insert was gently removed using sterile tweezers. Then, the well was filled with serum-free medium to exclude the effect of cell proliferation. The percentage of the reduced area was measured at 48 h post-transfection with NIH ImageJ software.

Tube formation assay

Ibidi μ-Slide Angiogenesis (Ibidi) was used to perform tube formation assays with HUVECs and HBVSMCs. Briefly, 48 h after transfection, cells were seeded on Matrigel (BD Inc., San Jose, CA, US) in the wells of the Slides. After the formation of tube structures, the number of meshes was measured and quantified.

Proliferation assay

Briefly, cells (1×10^4 cells/well) were seeded in 96-well plates with 100 μL of medium per well. Cell Counting Kit-8 solution (Dojindo Laboratories, Kumamoto, Japan) was added to the cell culture medium to a final concentration of 5 μL/100 μL and incubated for an additional 3 h

at 37°C. The absorbance at 450 nm was measured using a microplate reader (Molecular Devices).

Table S1. Primers used for RT-qPCR.

Primers for genes	Sequence
FZD10-F	TATCGGGCTCTTCTCTGTGC
FZD10-R	GACTGGGCAGGGATCTCATA
MYOC-F	ATCTCAGGAGTGGAGAGGGA
MYOC-R	CTGGCTGATGAGGTCATACTC
AXIN2-F	AGTGTGAGGTCCACGGAAAC
AXIN2-R	CTGGTGCAAAGACATAGCCA
TCF-1-F	AGGAGATGAGAGCCAAGGTCA
TCF-1-R	AGCCTGGGTATAGCTGCATGT
GAPDH-F	AATGACCCCTTCATTGAC
GAPDH-R	TCCACGACGTACTCAGCGC

Table S2. Differential expression profile.

Ensembl ID	Gene symbol	FPKM (LFR)	FPKM (HFR)	FC	P value
ENSG00000198812.3	LRRC10	0.036	0.006	6.338	7.41E-06
ENSG00000120833.9	SOCS2	16.421	7.754	2.118	1.46E-05
ENSG00000223516.1	AFF2-IT1	0.288	0.040	7.196	4.89E-05
ENSG00000183888.4	C1orf64	2.004	0.933	2.149	5.19E-05
ENSG00000204950.2	LRRC10B	4.075	1.551	2.628	6.55E-05
ENSG00000167034.9	NKX3-1	1.892	0.767	2.467	7.85E-05
ENSG00000111432.4	FZD10	1.935	0.726	2.667	0.000112
ENSG00000133665.8	DYDC2	0.473	0.157	3.010	0.000124
ENSG00000244040.1	IL12A-AS1	0.147	0.060	2.446	0.00014
ENSG00000185022.7	MAFF	42.090	19.994	2.105	0.000164
ENSG00000108342.8	CSF3	9.461	1.070	8.842	0.000169
ENSG00000172602.5	RND1	23.382	9.117	2.565	0.000211
ENSG00000034971.10	MYOC	0.329	0.067	4.895	0.000237
ENSG00000197826.7	C4orf22	0.416	0.049	8.434	0.000252
ENSG00000231274.4	SBK3	0.136	0.014	9.535	0.000347
ENSG00000171124.8	FUT3	0.064	0.011	5.928	0.000403
ENSG00000180616.4	SSTR2	9.698	4.829	2.008	0.000489
ENSG00000228002.2	DHX9P1	0.049	0.014	3.424	0.000525
ENSG00000268654.1	MIMT1	0.420	0.141	2.987	0.000711
ENSG00000130164.7	LDLR	45.012	21.491	2.094	0.000761
ENSG00000199218.1	RN7SKP184	1.105	0.400	2.762	0.000798
ENSG00000137699.12	TRIM29	0.633	0.216	2.934	0.00086
ENSG00000213612.3	FAM220CP	0.867	0.377	2.300	0.000889
ENSG00000100078.3	PLA2G3	0.060	0.014	4.181	0.001184
ENSG00000142973.8	CYP4B1	0.514	0.095	5.405	0.001186
ENSG00000244112.2	RN7SL508P	1.858	0.501	3.710	0.001364
ENSG00000235631.1	RNF148	1.429	0.700	2.042	0.001417
ENSG00000164736.5	SOX17	9.911	4.394	2.256	0.001599
ENSG00000147869.4	CER1	0.122	0.037	3.274	0.001648
ENSG00000228670.4	NANOGP2	0.471	0.184	2.565	0.001669
ENSG00000115602.12	IL1RL1	11.498	3.403	3.379	0.001871
ENSG00000101187.11	SLCO4A1	6.244	2.778	2.248	0.001963
ENSG00000134398.8	ERN2	0.099	0.027	3.664	0.00215
ENSG00000271723.1	MROH7-TTC4	0.873	0.414	2.108	0.002176
ENSG00000232354.3	VIPR1-AS1	0.494	0.238	2.075	0.002255

ENSG00000007908.11	SELE	53.814	19.319	2.786	0.002313
ENSG00000117595.6	IRF6	2.576	1.140	2.259	0.002518
ENSG00000116176.6	TPSG1	0.162	0.065	2.491	0.002607
ENSG00000057593.9	F7	0.462	0.205	2.256	0.002872
ENSG00000171873.6	ADRA1D	0.593	0.296	2.000	0.003027
ENSG00000229268.1	PES1P2	0.185	0.084	2.209	0.003077
ENSG00000165269.8	AQP7	0.315	0.132	2.385	0.003103
ENSG00000198535.5	C2CD4A	0.895	0.144	6.200	0.003158
ENSG00000137225.8	CAPN11	0.112	0.271	0.413	0.003262
ENSG00000257482.3	ZNF727	0.663	0.310	2.139	0.003354
ENSG00000158055.11	GRHL3	0.853	0.393	2.171	0.003587
ENSG00000164142.11	FAM160A1	0.939	0.349	2.687	0.003625
ENSG00000175592.4	FOSL1	17.211	7.112	2.420	0.003666
ENSG00000104369.4	JPH1	3.205	1.446	2.216	0.00376
ENSG00000177182.6	CLVS1	2.702	1.325	2.039	0.003943
ENSG00000154864.7	PIEZO2	4.403	8.821	0.499	0.004084
ENSG00000146674.10	IGFBP3	75.574	36.226	2.086	0.004172
ENSG00000130037.3	KCNA5	7.247	3.254	2.227	0.004236
ENSG00000267206.1	LCN6	1.904	0.926	2.056	0.004536
ENSG00000234373.1	SNX18P7	0.766	0.175	4.377	0.004598
ENSG00000127530.2	OR7C1	0.168	0.066	2.562	0.00464
ENSG00000174567.7	GOLT1A	0.269	0.081	3.299	0.004671
ENSG00000241890.1	RPL13P4	0.283	0.088	3.224	0.00474
ENSG00000180440.3	SERTM1	2.006	0.753	2.664	0.004994
ENSG00000181577.11	C6orf223	0.422	0.205	2.061	0.00529
ENSG00000149735.2	GPHA2	0.346	0.155	2.235	0.005382
ENSG00000086544.2	ITPKC	16.885	7.662	2.204	0.005402
ENSG00000206199.5	ANKUB1	0.528	1.083	0.487	0.005797
ENSG00000086717.14	PPEF1	0.781	0.382	2.043	0.005863
ENSG00000125144.9	MT1G	59.161	28.311	2.090	0.005964
ENSG00000149305.2	HTR3B	0.863	0.301	2.871	0.00632
ENSG00000256977.6	LIMS3	1.790	0.522	3.428	0.006417
ENSG00000205177.5	C11orf91	3.039	1.170	2.598	0.006421
ENSG00000272636.1	DOC2B	6.229	3.054	2.040	0.006435
ENSG00000224551.1	HMGB3P21	0.174	0.476	0.364	0.006437
ENSG00000172987.8	HPSE2	0.704	0.290	2.427	0.006449
ENSG00000136244.7	IL6	129.305	40.561	3.188	0.006634
ENSG00000137251.11	TINAG	0.084	0.022	3.772	0.006641
ENSG00000171056.6	SOX7	8.044	3.779	2.128	0.006691

ENSG00000172995.12	ARPP21	33.612	16.146	2.082	0.006779
ENSG00000156427.7	FGF18	2.521	1.061	2.375	0.006899
ENSG00000124249.5	KCNK15	1.340	0.617	2.171	0.007017
ENSG00000205502.3	C2CD4B	17.177	5.054	3.399	0.007036
ENSG00000160963.9	COL26A1	2.743	1.311	2.093	0.007248
ENSG00000257302.1	FAHD2P1	0.372	0.115	3.231	0.007249
ENSG00000256391.1	SDIM1	0.554	0.206	2.681	0.007385
ENSG00000174482.6	LINGO2	2.772	1.319	2.101	0.00746
ENSG00000237990.2	CNTN4-AS1	0.250	0.108	2.320	0.007565
ENSG00000187479.4	C11orf96	219.261	100.593	2.180	0.007604
ENSG00000226627.1	SHANK2-AS1	0.614	0.300	2.046	0.007605
ENSG00000229417.1	NPM1P25	0.446	0.958	0.466	0.007795
ENSG00000121446.13	RGSL1	0.013	0.004	3.027	0.007928
ENSG00000141433.8	ADCYAP1	3.499	0.871	4.018	0.008021
ENSG00000053438.7	NNAT	25.518	10.636	2.399	0.008035
ENSG00000258392.1	RPA2P1	0.261	0.117	2.226	0.008127
ENSG00000264315.1	HNRNPA1P11	1.133	0.342	3.312	0.008148
ENSG00000254244.1	PAICSP4	1.582	0.682	2.319	0.008468
ENSG00000183729.3	NPBWR1	0.122	0.042	2.886	0.008484
ENSG00000237665.1	GRM7-AS2	0.975	0.243	4.015	0.008604
ENSG00000229975.1	LIPT1P1	0.804	0.354	2.269	0.008689
ENSG00000143333.6	RGS16	28.924	13.181	2.194	0.008781
ENSG00000121742.11	GJB6	7.545	3.026	2.493	0.009014
ENSG00000136883.8	KIF12	0.479	0.187	2.558	0.00905
ENSG00000255277.2	ABCC6P2	0.234	0.111	2.096	0.009177
ENSG00000140968.6	IRF8	11.845	25.039	0.473	0.009297
ENSG00000176697.14	BDNF	2.186	0.871	2.508	0.009474
ENSG00000145040.3	UCN2	1.194	0.524	2.276	0.009507
ENSG00000224683.1	RPL36AP29	0.550	0.178	3.092	0.009523
ENSG00000183036.6	PCP4	9.836	4.837	2.033	0.009578
ENSG00000132510.6	KDM6B	65.547	32.118	2.041	0.009782
ENSG00000130368.4	MAS1	0.762	0.278	2.742	0.009861
ENSG00000188817.3	SNTN	0.082	0.035	2.347	0.009937
ENSG00000120280.5	CXorf21	2.545	5.396	0.472	0.009988
ENSG00000188282.8	RUFY4	0.288	0.678	0.425	0.010029
ENSG00000168334.8	XIRP1	1.756	0.561	3.128	0.010062
ENSG00000266274.1	RN7SL138P	8.730	21.470	0.407	0.010375
ENSG00000103196.7	CRISPLD2	76.349	36.091	2.115	0.010533
ENSG00000213450.4	VDAC1P7	0.182	0.062	2.927	0.010617

ENSG00000167772.7	ANGPTL4	16.794	8.347	2.012	0.010703
ENSG00000226981.2	ABHD17AP6	0.404	0.103	3.926	0.01083
ENSG00000171643.9	S100Z	0.178	0.495	0.360	0.010835
ENSG00000143627.13	PKLR	0.079	0.029	2.704	0.011001
ENSG00000264668.1	ZFP41	0.519	0.241	2.158	0.011084
ENSG00000103154.5	NECAB2	10.238	4.693	2.182	0.011159
ENSG00000179639.6	FCER1A	1.410	2.904	0.486	0.011223
ENSG00000110680.8	CALCA	0.480	0.149	3.215	0.011261
ENSG00000157502.8	MUM1L1	0.924	0.440	2.100	0.011372
ENSG00000136997.10	MYC	54.727	26.951	2.031	0.011519
ENSG00000188522.10	FAM83G	2.543	1.141	2.228	0.011593
ENSG00000261429.2	DPPA2P4	0.421	0.135	3.119	0.011595
ENSG00000129451.7	KLK10	0.211	0.065	3.239	0.01165
ENSG00000010319.2	SEMA3G	13.011	6.071	2.143	0.011757
ENSG00000229001.1	ACTBP14	0.111	0.052	2.136	0.011815
ENSG00000198576.2	ARC	23.119	7.884	2.932	0.011908
ENSG00000101204.11	CHRNA4	2.483	1.186	2.093	0.011911
ENSG00000183186.6	C2CD4C	3.168	1.370	2.312	0.01208
ENSG00000172818.5	OVOL1	0.175	0.059	2.959	0.012181
ENSG00000235280.2	MCF2L-AS1	0.306	0.135	2.268	0.012291
ENSG00000149380.7	P4HA3	0.993	2.229	0.446	0.012513
ENSG00000244752.2	CRYBB2	0.185	0.091	2.025	0.01252
ENSG00000178394.3	HTR1A	2.163	0.906	2.388	0.01261
ENSG00000095752.2	IL11	1.019	0.373	2.732	0.012832
ENSG00000116544.7	DLGAP3	18.073	8.741	2.068	0.013064
ENSG00000181418.7	DDN	25.821	11.666	2.213	0.013537
ENSG00000137825.6	ITPKA	8.021	3.359	2.388	0.013837
ENSG00000139865.12	TTC6	0.261	0.105	2.481	0.013882
ENSG00000184908.13	CLCNKB	0.151	0.063	2.395	0.013972
ENSG00000138316.6	ADAMTS14	0.742	1.821	0.407	0.014085
ENSG00000111247.10	RAD51AP1	1.131	2.484	0.455	0.014337
ENSG00000233123.1	LINC01007	1.620	0.329	4.930	0.014378
ENSG00000128342.4	LIF	32.215	11.834	2.722	0.014481
ENSG00000124664.6	SPDEF	0.227	0.099	2.289	0.014839
ENSG00000271108.1	KATNBL1P5	0.203	0.645	0.315	0.015181
ENSG00000143228.8	NUF2	0.494	1.236	0.400	0.0154
ENSG00000149654.5	CDH22	4.936	2.270	2.175	0.015578
ENSG00000188959.9	C9orf152	0.115	0.049	2.370	0.016061
ENSG00000225101.3	OR52K3P	0.391	0.881	0.443	0.01636

ENSG00000177508.11	IRX3	2.102	0.927	2.268	0.016441
ENSG00000105509.6	HAS1	3.376	1.368	2.468	0.016618
ENSG00000184601.6	C14orf180	0.416	0.196	2.119	0.016819
ENSG00000144550.8	CPNE9	1.875	0.851	2.202	0.016827
ENSG00000166823.5	MESP1	1.135	0.555	2.045	0.017257
ENSG00000226510.1	UPK1A-AS1	0.135	0.057	2.360	0.017289
ENSG00000144119.3	C1QL2	1.780	0.721	2.468	0.017418
ENSG00000118017.3	A4GNT	0.045	0.124	0.359	0.017737
ENSG00000251449.2	MTND1P19	2.828	0.902	3.135	0.017775
ENSG00000143340.6	FAM163A	0.309	0.093	3.327	0.017798
ENSG00000071282.7	LMCD1	67.751	30.796	2.200	0.017922
ENSG00000123219.8	CENPK	1.367	2.982	0.458	0.018003
ENSG00000189181.3	OR14I1	0.709	0.251	2.829	0.018163
ENSG00000263878.1	DLGAP1-AS4	2.446	1.070	2.286	0.018291
ENSG00000134551.8	PRH2	0.325	0.659	0.493	0.018548
ENSG00000239794.2	RN7SL653P	1.805	0.863	2.092	0.01859
ENSG00000105492.11	SIGLEC6	0.144	0.402	0.358	0.018599
ENSG00000089558.4	KCNH4	0.737	0.331	2.229	0.018821
ENSG00000168634.4	WFDC13	0.086	0.034	2.552	0.018962
ENSG00000173714.7	WFIKKN2	1.109	0.369	3.004	0.018964
ENSG00000105383.10	CD33	3.986	8.132	0.490	0.019101
ENSG00000241295.1	ZBTB20-AS2	0.534	1.524	0.350	0.019237
ENSG00000205358.3	MT1H	8.658	3.946	2.194	0.019397
ENSG00000126583.6	PRKCG	7.575	3.316	2.284	0.019407
ENSG00000265264.1	TIMM10B	0.357	0.128	2.795	0.019473
ENSG00000255734.1	HNRNPABP1	0.066	0.199	0.331	0.019511
ENSG00000220868.2	MRPL35P1	0.341	0.156	2.192	0.019618
ENSG00000175793.10	SFN	0.784	0.342	2.292	0.019672
ENSG00000198153.7	ZNF849P	0.063	0.024	2.593	0.019934
ENSG00000197901.7	SLC22A6	4.578	1.076	4.256	0.019936
ENSG00000171954.8	CYP4F22	0.025	0.074	0.345	0.020205
ENSG00000233642.1	GPR158-AS1	0.100	0.049	2.029	0.020424
ENSG00000101280.6	ANGPT4	1.011	0.502	2.014	0.020446
ENSG00000183856.6	IQGAP3	0.352	0.866	0.407	0.020525
ENSG00000235489.3	DBF4P1	0.141	0.055	2.555	0.020528
ENSG00000162510.5	MATN1	0.234	0.109	2.139	0.020957
ENSG00000230539.1	AOAH-IT1	0.239	0.529	0.451	0.021147
ENSG00000256193.1	LINC00507	2.060	0.721	2.858	0.021506
ENSG00000196946.5	ZNF705A	0.052	0.011	4.818	0.021808

ENSG00000184185.5	KCNJ12	1.818	0.802	2.266	0.021884
ENSG00000120093.7	HOXB3	0.341	0.784	0.434	0.021909
ENSG00000151117.4	TMEM86A	3.267	6.651	0.491	0.02197
ENSG00000227766.1	HCG4P5	0.915	2.096	0.437	0.022002
ENSG00000268849.1	SIGLEC22P	0.564	1.187	0.475	0.022127
ENSG00000123338.8	NCKAP1L	12.876	26.771	0.481	0.0224
ENSG00000187094.7	CCK	38.377	17.314	2.217	0.022716
ENSG00000152430.13	BOLL	0.102	0.223	0.460	0.022842
ENSG00000225781.1	OR6V1	0.208	0.518	0.402	0.022859
ENSG00000229570.2	GAPDHP58	0.206	0.074	2.776	0.022971
ENSG00000147571.3	CRH	0.750	0.301	2.493	0.022987
ENSG00000249206.2	GCNT1P2	0.256	0.109	2.362	0.023202
ENSG00000188985.5	DHFRP1	0.092	0.035	2.618	0.023241
ENSG00000237575.4	PYY2	0.154	0.337	0.457	0.023647
ENSG00000182048.7	TRPC2	0.124	0.286	0.434	0.023745
ENSG00000258956.2	COX4I1P1	0.382	0.164	2.338	0.02391
ENSG00000161640.11	SIGLEC11	0.788	1.637	0.482	0.024011
ENSG00000232901.1	CYCSP10	0.667	1.406	0.474	0.024067
ENSG00000132671.4	SSTR4	0.268	0.121	2.217	0.024373
ENSG00000184060.6	ADAP2	13.831	28.044	0.493	0.024495
ENSG00000221890.2	NPTXR	31.510	13.989	2.253	0.024516
ENSG00000106236.3	NPTX2	17.779	5.529	3.215	0.025088
ENSG00000100122.5	CRYBB1	0.879	1.986	0.443	0.025235
ENSG00000230453.5	ANKRD18B	1.349	0.525	2.570	0.025815
ENSG00000089169.10	RPH3A	19.873	8.988	2.211	0.025923
ENSG00000240014.2	RN7SL254P	1.003	0.464	2.163	0.026169
ENSG00000095970.12	TREM2	18.718	41.030	0.456	0.026339
ENSG00000242285.1	RPL6P8	0.082	0.221	0.370	0.02634
ENSG00000158488.11	CD1E	0.330	0.674	0.490	0.026659
ENSG00000138413.9	IDH1	16.933	41.071	0.412	0.026738
ENSG00000253974.1	NRG1-IT1	0.821	0.378	2.173	0.026848
ENSG00000243547.1	HNRNPKP4	0.048	0.021	2.322	0.027674
ENSG00000156970.8	BUB1B	0.706	1.780	0.397	0.027833
ENSG00000225079.2	FTH1P22	0.287	0.586	0.489	0.027941
ENSG00000080986.8	NDC80	0.758	1.637	0.463	0.028307
ENSG00000268598.1	VN1R80P	0.694	1.436	0.483	0.028491
ENSG00000122223.8	CD244	0.642	1.381	0.465	0.028492
ENSG00000169218.9	RSPO1	0.069	0.021	3.327	0.028715
ENSG00000159173.14	TNNI1	0.082	0.023	3.606	0.028744

ENSG00000205002.3	AARD	0.178	0.076	2.349	0.028754
ENSG00000102239.4	BRS3	0.036	0.012	3.005	0.028845
ENSG00000172938.3	MRGPRD	0.166	0.069	2.420	0.02889
ENSG00000233261.1	LINC00264	0.116	0.285	0.407	0.029358
ENSG00000152213.3	ARL11	0.662	1.324	0.500	0.029478
ENSG00000235129.1	FABP7P2	0.366	0.144	2.547	0.029613
ENSG00000144481.12	TRPM8	0.263	0.554	0.475	0.02981
ENSG00000138160.4	KIF11	0.705	1.469	0.480	0.029926
ENSG00000154975.9	CA10	7.075	3.355	2.109	0.030006
ENSG00000197616.7	MYH6	0.042	0.007	5.903	0.03013
ENSG00000232417.5	CT45A3	0.737	0.259	2.850	0.030538
ENSG00000006116.3	CACNG3	5.267	2.605	2.022	0.030579
ENSG00000231784.4	DBIL5P	0.984	0.481	2.045	0.030714
ENSG00000171551.7	ECEL1	0.264	0.112	2.350	0.030833
ENSG00000271956.1	DLX6-AS2	0.156	0.055	2.840	0.030847
ENSG00000174946.5	GPR171	2.984	1.466	2.036	0.031234
ENSG00000211956.2	IGHV4-34	0.406	3.321	0.122	0.0319
ENSG00000256316.1	HIST1H3F	4.580	13.161	0.348	0.031967
ENSG00000135426.10	TESPA1	9.804	4.885	2.007	0.031982
ENSG00000211666.2	IGLV2-14	2.394	17.935	0.133	0.032099
ENSG00000143632.10	ACTA1	1.716	0.525	3.268	0.032209
ENSG00000185482.3	STAC3	1.305	2.831	0.461	0.03234
ENSG00000178999.8	AURKB	0.541	1.346	0.402	0.03305
ENSG00000174576.4	NPAS4	20.761	5.020	4.136	0.033282
ENSG00000222004.3	C7orf71	0.109	0.229	0.474	0.033308
ENSG00000074966.6	TXK	0.865	1.896	0.457	0.033352
ENSG00000235076.2	GAPDHP52	0.129	0.274	0.472	0.033909
ENSG00000184408.5	KCND2	4.132	2.022	2.043	0.033992
ENSG00000179363.6	TMEM31	0.156	0.076	2.060	0.034254
ENSG00000134115.8	CNTN6	1.514	0.700	2.163	0.034266
ENSG00000237152.2	DLEU7-AS1	0.272	0.561	0.485	0.034298
ENSG00000223414.2	LINC00473	3.683	1.719	2.142	0.034442
ENSG00000101825.7	MXRA5	4.520	10.106	0.447	0.034526
ENSG00000153303.12	FRMD1	0.169	0.079	2.134	0.034726
ENSG00000138778.7	CENPE	0.649	1.351	0.480	0.034749
ENSG00000119283.11	TRIM67	0.636	0.261	2.438	0.034901
ENSG00000105549.6	THEG	0.100	0.042	2.373	0.035013
ENSG00000240183.2	RN7SL297P	0.776	1.724	0.450	0.03507
ENSG00000024526.12	DEPDC1	0.188	0.506	0.371	0.035105

ENSG00000079841.14	RIMS1	18.421	8.261	2.230	0.035436
ENSG00000171320.10	ESCO2	0.314	0.919	0.342	0.035437
ENSG00000134595.6	SOX3	0.066	0.026	2.575	0.036208
ENSG00000166863.7	TAC3	2.912	1.451	2.007	0.036323
ENSG00000227477.1	STK4-AS1	0.088	0.178	0.495	0.036348
ENSG00000183742.8	MACC1	0.632	1.329	0.475	0.036704
ENSG00000110148.5	CCKBR	2.651	1.319	2.009	0.036785
ENSG00000172724.7	CCL19	37.792	18.598	2.032	0.037114
ENSG00000134690.6	CDCA8	0.348	0.696	0.499	0.037148
ENSG00000101057.11	MYBL2	0.328	1.144	0.287	0.037604
ENSG00000003137.4	CYP26B1	11.011	5.314	2.072	0.037625
ENSG00000182611.3	HIST1H2AJ	2.379	8.581	0.277	0.037841
ENSG00000175879.7	HOXD8	0.131	0.382	0.342	0.037977
ENSG00000145386.5	CCNA2	0.605	1.394	0.434	0.038007
ENSG00000167613.11	LAIR1	21.365	43.614	0.490	0.038351
ENSG00000163331.6	DAPL1	2.548	1.117	2.281	0.038393
ENSG00000178462.7	TUBAL3	0.056	0.026	2.176	0.038525
ENSG00000204291.6	COL15A1	9.049	19.180	0.472	0.038643
ENSG00000101292.6	PROKR2	0.365	0.174	2.093	0.038752
ENSG00000158402.14	CDC25C	0.173	0.356	0.486	0.03892
ENSG00000110975.4	SYT10	0.378	0.181	2.094	0.039013
ENSG00000206014.5	OR7E161P	0.091	0.036	2.508	0.039249
ENSG00000179046.4	TRIML2	0.094	0.044	2.124	0.039313
ENSG00000027644.4	INSRR	1.075	0.528	2.037	0.039349
ENSG00000130035.2	GALNT8	2.436	1.134	2.149	0.039719
ENSG00000218698.1	ST13P16	0.165	0.079	2.105	0.040044
ENSG00000211663.2	IGLV3-19	1.086	6.359	0.171	0.040235
ENSG00000186185.9	KIF18B	0.271	0.647	0.418	0.040503
ENSG00000168078.5	PBK	0.188	0.768	0.245	0.040639
ENSG00000182156.5	ENPP7	0.046	0.109	0.428	0.040649
ENSG00000066279.12	ASPM	0.291	0.889	0.327	0.041036
ENSG00000230316.2	FEZF1-AS1	0.100	0.043	2.327	0.041518
ENSG00000166183.11	ASPG	0.251	0.121	2.082	0.041539
ENSG00000148677.6	ANKRD1	2.217	0.835	2.655	0.041548
ENSG00000147432.2	CHRNB3	0.413	0.171	2.409	0.041559
ENSG00000236062.1	GSTM5P1	0.222	0.099	2.254	0.041574
ENSG00000182572.2	HIST1H3I	4.752	14.066	0.338	0.042085
ENSG00000211821.2	TRDV2	0.191	0.522	0.365	0.042159
ENSG00000142945.8	KIF2C	0.632	1.278	0.494	0.042269

ENSG00000196183.4	RPS2P4	0.111	0.044	2.556	0.042341
ENSG00000197153.3	HIST1H3J	1.570	5.006	0.314	0.042527
ENSG00000188778.3	ADRB3	0.152	0.074	2.065	0.04265
ENSG00000121933.13	ADORA3	10.490	23.524	0.446	0.042746
ENSG00000211788.2	TRAV13-1	0.265	0.661	0.402	0.042902
ENSG00000175325.2	PROP1	0.091	0.035	2.587	0.043057
ENSG00000196747.3	HIST1H2AI	5.424	15.676	0.346	0.043415
ENSG00000137077.3	CCL21	5.297	2.603	2.035	0.043434
ENSG00000240048.1	DDX50P2	0.046	0.020	2.284	0.043601
ENSG00000164794.4	KCNV1	3.123	1.524	2.050	0.043622
ENSG00000213423.4	RBMX2P2	0.056	0.153	0.364	0.043692
ENSG00000089199.5	CHGB	23.824	11.731	2.031	0.043791
ENSG00000196132.7	MYT1	1.346	0.591	2.277	0.043805
ENSG00000118193.7	KIF14	0.173	0.451	0.384	0.043869
ENSG00000243137.3	PSG4	0.264	0.129	2.042	0.043903
ENSG00000163395.12	IGFN1	2.534	0.997	2.541	0.044013
ENSG00000148773.8	MKI67	0.722	2.334	0.310	0.044175
ENSG00000132821.7	VSTM2L	14.679	7.060	2.079	0.044221
ENSG00000134762.12	DSC3	0.301	0.134	2.252	0.044448
ENSG00000198558.2	HIST1H4L	4.528	10.743	0.421	0.044712
ENSG00000258548.1	LINC00645	0.111	0.052	2.120	0.044796
ENSG00000135625.6	EGR4	7.491	2.233	3.355	0.044845
ENSG00000159166.9	LAD1	0.096	0.221	0.436	0.044938
ENSG00000240541.2	TM4SF1-AS1	0.234	0.115	2.031	0.044952
ENSG00000118640.6	VAMP8	18.034	40.739	0.443	0.045152
ENSG00000258555.2	SPECC1L -ADORA2A	0.308	0.145	2.121	0.045191
ENSG00000215475.3	SIAH3	0.750	0.347	2.160	0.045421
ENSG00000169777.5	TAS2R1	0.085	0.041	2.091	0.045447
ENSG00000211940.2	IGHV3-9	0.432	3.591	0.120	0.045465
ENSG00000232144.1	PSAT1P2	0.064	0.160	0.397	0.045582
ENSG00000234611.1	OR2AT2P	0.082	0.038	2.170	0.045695
ENSG00000250305.4	KIAA1456	10.051	4.379	2.295	0.045773
ENSG00000198829.5	SUCNR1	0.568	2.760	0.206	0.046493
ENSG00000109193.6	SULT1E1	0.052	0.267	0.196	0.046551
ENSG00000010327.6	STAB1	38.073	83.408	0.456	0.046582
ENSG00000242076.1	IGKV1-33	1.408	8.014	0.176	0.04668
ENSG00000203747.5	FCGR3A	29.148	59.196	0.492	0.046691
ENSG00000174083.13	PIK3R6	0.767	1.644	0.467	0.046905

ENSG00000157456.3	CCNB2	0.747	1.738	0.430	0.047054
ENSG00000090889.10	KIF4A	0.348	0.749	0.465	0.047117
ENSG00000231211.2	RPL17P49	0.601	0.242	2.480	0.047247
ENSG00000004809.9	SLC22A16	0.147	0.379	0.389	0.047269
ENSG00000255833.1	TIFAB	0.092	0.264	0.349	0.047368
ENSG00000174600.9	CMKLR1	10.782	21.840	0.494	0.047391
ENSG00000007968.6	E2F2	0.201	0.429	0.469	0.04743
ENSG00000077009.9	NMRK2	0.163	0.066	2.480	0.047639
ENSG00000258477.1	PPIAP6	0.198	0.399	0.496	0.047861
ENSG00000237697.2	LINC00312	4.808	2.322	2.070	0.047967
ENSG00000239577.2	RN7SL388P	0.377	0.873	0.432	0.048326
ENSG00000111206.8	FOXM1	1.075	2.322	0.463	0.04834
ENSG00000122859.4	NEUROG3	0.063	0.031	2.050	0.048365
ENSG00000189430.8	NCR1	0.239	0.496	0.481	0.048619
ENSG00000130701.3	RBBP8NL	0.057	0.019	2.971	0.048691
ENSG00000198374.3	HIST1H2AL	3.302	9.059	0.365	0.048731
ENSG00000126787.8	DLGAP5	0.282	1.026	0.275	0.048794
ENSG00000100721.6	TCL1A	0.149	0.373	0.401	0.049107
ENSG00000134757.4	DSG3	0.040	0.009	4.308	0.04915
ENSG00000197459.2	HIST1H2BH	5.450	14.621	0.373	0.049397
ENSG00000197629.5	MPEG1	13.408	29.311	0.457	0.049451
ENSG00000215498.4	FAM230B	0.057	0.021	2.649	0.049883

FPKM Indicates fragments per kilobase of exon per million fragments mapped; LFR, low flow rate; HFR, high flow rate; FC, fold change.

Table S3. GO and KEGG analysis enriched by upregulated genes in low flow rate bAVMs.

GeneSet	Description	P value
GO:0042127	regulation of cell proliferation	7.37E-05
GO:0050727	regulation of inflammatory response	7.72E-05
GO:0007267	cell-cell signaling	8.05E-05
GO:0032103	positive regulation of response to external stimulus	1.41E-04
GO:0061888	regulation of astrocyte activation	1.49E-04
GO:0033993	response to lipid	1.59E-04
GO:0050729	positive regulation of inflammatory response	1.63E-04
GO:0032101	regulation of response to external stimulus	1.76E-04
GO:0002675	positive regulation of acute inflammatory response	1.93E-04
GO:0038031	non-canonical Wnt signaling pathway via JNK cascade	2.22E-04
GO:0008285	negative regulation of cell proliferation	2.41E-04
GO:0009914	hormone transport	2.51E-04
GO:0038030	non-canonical Wnt signaling pathway via MAPK cascade	3.11E-04
GO:2000381	negative regulation of mesoderm development	4.13E-04
GO:0002673	regulation of acute inflammatory response	4.55E-04
GO:1901700	response to oxygen-containing compound	7.80E-04
GO:0043030	regulation of macrophage activation	9.74E-04
GO:0032722	positive regulation of chemokine production	0.001032
GO:0008283	cell proliferation	0.00125
GO:0010469	regulation of signaling receptor activity	0.001306
GO:0046879	hormone secretion	0.001341
GO:0046677	response to antibiotic	0.001431
GO:0048143	astrocyte activation	0.001522
GO:1903978	regulation of microglial cell activation	0.001522
GO:0042074	cell migration involved in gastrulation	0.001522
GO:0007188	adenylate cyclase-modulating G protein-coupled receptor signaling pathway	0.001535
GO:0046887	positive regulation of hormone secretion	0.001611
GO:0042542	response to hydrogen peroxide	0.001705
GO:0006954	inflammatory response	0.001775
GO:0007189	adenylate cyclase-activating G protein-coupled receptor signaling pathway	0.001903
GO:2000380	regulation of mesoderm development	0.001962
GO:0043491	protein kinase B signaling	0.002099
GO:0010647	positive regulation of cell communication	0.002304
GO:1902533	positive regulation of intracellular signal transduction	0.002304
GO:0008284	positive regulation of cell proliferation	0.002369

GO:0023056	positive regulation of signaling	0.002384
GO:0023019	signal transduction involved in regulation of gene expression	0.00272
GO:0051384	response to glucocorticoid	0.002723
GO:0030072	peptide hormone secretion	0.002753
GO:0032642	regulation of chemokine production	0.002788
GO:0007187	G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	0.002899
GO:1900120	regulation of receptor binding	0.002999
GO:0043567	regulation of insulin-like growth factor receptor signaling pathway	0.002999
GO:0002526	acute inflammatory response	0.003067
GO:0045597	positive regulation of cell differentiation	0.003124
GO:0003018	vascular process in circulatory system	0.003139
GO:0009636	response to toxic substance	0.003216
GO:1903532	positive regulation of secretion by cell	0.003415
GO:0051897	positive regulation of protein kinase B signaling	0.003439
GO:0032602	chemokine production	0.003626
GO:0042116	macrophage activation	0.003626
GO:0014068	positive regulation of phosphatidylinositol 3-kinase signaling	0.003626
GO:0046883	regulation of hormone secretion	0.003779
GO:0010817	regulation of hormone levels	0.003867
GO:0002793	positive regulation of peptide secretion	0.003901
GO:0150077	regulation of neuroinflammatory response	0.003912
GO:0031960	response to corticosteroid	0.00401
GO:0051240	positive regulation of multicellular organismal process	0.004233
GO:0001934	positive regulation of protein phosphorylation	0.004496
GO:0007369	gastrulation	0.004835
GO:0042493	response to drug	0.004895
GO:0051047	positive regulation of secretion	0.004959
GO:0032958	inositol phosphate biosynthetic process	0.005305
GO:0048710	regulation of astrocyte differentiation	0.005305
GO:0019933	cAMP-mediated signaling	0.005339
GO:0044093	positive regulation of molecular function	0.005686
GO:0031347	regulation of defense response	0.005728
GO:0080134	regulation of response to stress	0.005846
GO:0090277	positive regulation of peptide hormone secretion	0.005898
GO:0007202	activation of phospholipase C activity	0.006074
GO:0042327	positive regulation of phosphorylation	0.006182

GO:0060251	regulation of glial cell proliferation	0.006477
GO:0001774	microglial cell activation	0.006477
GO:0002269	leukocyte activation involved in inflammatory response	0.006477
GO:0048333	mesodermal cell differentiation	0.006477
GO:0021782	glial cell development	0.006619
GO:0019932	second-messenger-mediated signaling	0.006743
GO:0009967	positive regulation of signal transduction	0.006881
GO:0043114	regulation of vascular permeability	0.006891
GO:0007218	neuropeptide signaling pathway	0.007192
GO:0014002	astrocyte development	0.007317
GO:0035567	non-canonical Wnt signaling pathway	0.00739
GO:0048009	insulin-like growth factor receptor signaling pathway	0.007755
GO:0009719	response to endogenous stimulus	0.007833
GO:0071396	cellular response to lipid	0.008143
GO:0032956	regulation of actin cytoskeleton organization	0.008165
GO:0060416	response to growth hormone	0.008205
GO:0051345	positive regulation of hydrolase activity	0.008231
GO:0090276	regulation of peptide hormone secretion	0.008392
GO:0030073	insulin secretion	0.008533
GO:0023061	signal release	0.008599
GO:0016055	Wnt signaling pathway	0.008599
GO:0051896	regulation of protein kinase B signaling	0.008676
GO:0019935	cyclic-nucleotide-mediated signaling	0.008821
GO:0198738	cell-cell signaling by Wnt	0.008865
GO:0014013	regulation of gliogenesis	0.009086
GO:0002791	regulation of peptide secretion	0.00923
GO:0061061	muscle structure development	0.009435
GO:0010562	positive regulation of phosphorus metabolic process	0.009603
GO:0045937	positive regulation of phosphate metabolic process	0.009603
GO:0061900	glial cell activation	0.009622
GO:0001704	formation of primary germ layer	0.009776
GO:0014066	regulation of phosphatidylinositol 3-kinase signaling	0.009776
GO:0051247	positive regulation of protein metabolic process	0.00981
GO:0000302	response to reactive oxygen species	0.009878
GO:0014014	negative regulation of gliogenesis	0.010622
GO:0007186	G protein-coupled receptor signaling pathway	0.010641
GO:0014009	glial cell proliferation	0.011139
GO:0032880	regulation of protein localization	0.011502
GO:0010863	positive regulation of phospholipase C activity	0.011667

GO:0042551	neuron maturation	0.011667
GO:0009725	response to hormone	0.011949
GO:0051094	positive regulation of developmental process	0.012115
GO:0042325	regulation of phosphorylation	0.012309
GO:0019220	regulation of phosphate metabolic process	0.012449
GO:0007498	mesoderm development	0.012564
GO:0051174	regulation of phosphorus metabolic process	0.012566
GO:0097305	response to alcohol	0.012595
GO:0002437	inflammatory response to antigenic stimulus	0.012755
GO:0032355	response to estradiol	0.013114
GO:1900274	regulation of phospholipase C activity	0.013315
GO:0009790	embryo development	0.01337
GO:0032970	regulation of actin filament-based process	0.013409
GO:0006952	defense response	0.013445
GO:0044703	multi-organism reproductive process	0.01387
GO:0034260	negative regulation of GTPase activity	0.013885
GO:2000026	regulation of multicellular organismal development	0.013948
GO:0050921	positive regulation of chemotaxis	0.014257
GO:0045944	positive regulation of transcription by RNA polymerase II	0.01449
GO:0051962	positive regulation of nervous system development	0.014613
GO:0045860	positive regulation of protein kinase activity	0.014742
GO:0001503	ossification	0.014773
GO:0009991	response to extracellular stimulus	0.015002
GO:0010720	positive regulation of cell development	0.015002
GO:0150076	neuroinflammatory response	0.015058
GO:0032270	positive regulation of cellular protein metabolic process	0.015156
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	0.015904
GO:0050714	positive regulation of protein secretion	0.016177
GO:0001706	endoderm formation	0.016271
GO:0031401	positive regulation of protein modification process	0.016332
GO:0014065	phosphatidylinositol 3-kinase signaling	0.016389
GO:0043085	positive regulation of catalytic activity	0.016987
GO:0051091	positive regulation of DNA-binding transcription factor activity	0.0175
GO:0048545	response to steroid hormone	0.017599
GO:0001932	regulation of protein phosphorylation	0.017665
GO:0035051	cardiocyte differentiation	0.017683
GO:0008277	regulation of G protein-coupled receptor signaling	0.01869

	pathway	
GO:0002865	negative regulation of acute inflammatory response to antigenic stimulus	0.019354
GO:0071651	positive regulation of chemokine (C-C motif) ligand 5 production	0.019354
GO:0090118	receptor-mediated endocytosis involved in cholesterol transport	0.019354
GO:0031547	brain-derived neurotrophic factor receptor signaling pathway	0.019354
GO:0080184	response to phenylpropanoid	0.019354
GO:0003307	regulation of Wnt signaling pathway involved in heart development	0.019354
GO:1904352	positive regulation of protein catabolic process in the vacuole	0.019354
GO:0030263	apoptotic chromosome condensation	0.019354
GO:0010641	positive regulation of platelet-derived growth factor receptor signaling pathway	0.019354
GO:0060664	epithelial cell proliferation involved in salivary gland morphogenesis	0.019354
GO:2000660	negative regulation of interleukin-1-mediated signaling pathway	0.019354
GO:1900223	positive regulation of amyloid-beta clearance	0.019354
GO:1900145	regulation of nodal signaling pathway involved in determination of left/right asymmetry	0.019354
GO:1900175	regulation of nodal signaling pathway involved in determination of lateral mesoderm left/right asymmetry	0.019354
GO:0038169	somatostatin receptor signaling pathway	0.019354
GO:0038170	somatostatin signaling pathway	0.019354
GO:0071557	histone H3-K27 demethylation	0.019354
GO:0043410	positive regulation of MAPK cascade	0.019444
GO:0042063	gliogenesis	0.019851
GO:0009306	protein secretion	0.020076
GO:0051960	regulation of nervous system development	0.020487
GO:0033674	positive regulation of kinase activity	0.02056
GO:0070555	response to interleukin-1	0.020799
GO:1903530	regulation of secretion by cell	0.020818
GO:0030029	actin filament-based process	0.020961
GO:1905114	cell surface receptor signaling pathway involved in cell-cell signaling	0.021383
GO:0010518	positive regulation of phospholipase activity	0.021524

GO:0046173	polyol biosynthetic process	0.021524
GO:1902531	regulation of intracellular signal transduction	0.022305
GO:1901701	cellular response to oxygen-containing compound	0.022926
GO:0071385	cellular response to glucocorticoid stimulus	0.022933
GO:0010986	positive regulation of lipoprotein particle clearance	0.02318
GO:0060696	regulation of phospholipid catabolic process	0.02318
GO:0043569	negative regulation of insulin-like growth factor receptor signaling pathway	0.02318
GO:0060770	negative regulation of epithelial cell proliferation involved in prostate gland development	0.02318
GO:0001957	intramembranous ossification	0.02318
GO:0036072	direct ossification	0.02318
GO:1904587	response to glycoprotein	0.02318
GO:0098914	membrane repolarization during atrial cardiac muscle cell action potential	0.02318
GO:2000553	positive regulation of T-helper 2 cell cytokine production	0.02318
GO:0003160	endocardium morphogenesis	0.02318
GO:0150079	negative regulation of neuroinflammatory response	0.02318
GO:0009996	negative regulation of cell fate specification	0.02318
GO:0048598	embryonic morphogenesis	0.023629
GO:0051093	negative regulation of developmental process	0.023916
GO:0045685	regulation of glial cell differentiation	0.025116
GO:0031349	positive regulation of defense response	0.025388
GO:0048015	phosphatidylinositol-mediated signaling	0.025394
GO:0043408	regulation of MAPK cascade	0.025551
GO:0002790	peptide secretion	0.02565
GO:0071384	cellular response to corticosteroid stimulus	0.025862
GO:0061371	determination of heart left/right asymmetry	0.025862
GO:0034097	response to cytokine	0.026275
GO:0014823	response to activity	0.026617
GO:0048017	inositol lipid-mediated signaling	0.026622
GO:0003348	cardiac endothelial cell differentiation	0.026992
GO:0060956	endocardial cell differentiation	0.026992
GO:1903997	positive regulation of non-membrane spanning protein tyrosine kinase activity	0.026992
GO:0015793	glycerol transport	0.026992
GO:0042661	regulation of mesodermal cell fate specification	0.026992
GO:1905770	regulation of mesodermal cell differentiation	0.026992
GO:1905902	regulation of mesoderm formation	0.026992
GO:0060372	regulation of atrial cardiac muscle cell membrane	0.026992

	repolarization	
GO:0086028	bundle of His cell to Purkinje myocyte signaling	0.026992
GO:0086043	bundle of His cell action potential	0.026992
GO:2000542	negative regulation of gastrulation	0.026992
GO:0071694	maintenance of protein location in extracellular region	0.026992
GO:0035766	cell chemotaxis to fibroblast growth factor	0.026992
GO:0035768	endothelial cell chemotaxis to fibroblast growth factor	0.026992
GO:1904847	regulation of cell chemotaxis to fibroblast growth factor	0.026992
GO:2000544	regulation of endothelial cell chemotaxis to fibroblast growth factor	0.026992
GO:0009249	protein lipoylation	0.026992
GO:0099004	calmodulin dependent kinase signaling pathway	0.026992
GO:2000659	regulation of interleukin-1-mediated signaling pathway	0.026992
GO:0002826	negative regulation of T-helper 1 type immune response	0.026992
GO:0038107	nodal signaling pathway involved in determination of left/right asymmetry	0.026992
GO:1900094	regulation of transcription from RNA polymerase II promoter involved in determination of left/right symmetry	0.026992
GO:1900164	nodal signaling pathway involved in determination of lateral mesoderm left/right asymmetry	0.026992
GO:0045162	clustering of voltage-gated sodium channels	0.026992
GO:0001826	inner cell mass cell differentiation	0.026992
GO:0051965	positive regulation of synapse assembly	0.027381
GO:0050708	regulation of protein secretion	0.027456
GO:0051050	positive regulation of transport	0.02789
GO:0001707	mesoderm formation	0.028153
GO:0045893	positive regulation of transcription, DNA-templated	0.02934
GO:0060193	positive regulation of lipase activity	0.029725
GO:0048332	mesoderm morphogenesis	0.029725
GO:0043647	inositol phosphate metabolic process	0.029725
GO:0045595	regulation of cell differentiation	0.029888
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GO:0050769	positive regulation of neurogenesis	0.030126
GO:0050796	regulation of insulin secretion	0.030493
GO:0048708	astrocyte differentiation	0.030523
GO:0010517	regulation of phospholipase activity	0.030523
GO:0060350	endochondral bone morphogenesis	0.030523
GO:0007417	central nervous system development	0.030618
GO:0061476	response to anticoagulant	0.030789
GO:0070444	oligodendrocyte progenitor proliferation	0.030789

GO:0070445	regulation of oligodendrocyte progenitor proliferation	0.030789
GO:1903995	regulation of non-membrane spanning protein tyrosine kinase activity	0.030789
GO:0071692	protein localization to extracellular region	0.030789
GO:0001781	neutrophil apoptotic process	0.030789
GO:0034638	phosphatidylcholine catabolic process	0.030789
GO:1905906	regulation of amyloid fibril formation	0.030789
GO:2000288	positive regulation of myoblast proliferation	0.030789
GO:0070327	thyroid hormone transport	0.030789
GO:1900107	regulation of nodal signaling pathway	0.030789
GO:1905165	regulation of lysosomal protein catabolic process	0.030789
GO:0003140	determination of left/right asymmetry in lateral mesoderm	0.030789
GO:0001714	endodermal cell fate specification	0.030789
GO:0032024	positive regulation of insulin secretion	0.03133
GO:0043507	positive regulation of JUN kinase activity	0.032146
GO:0031328	positive regulation of cellular biosynthetic process	0.032269
GO:0007422	peripheral nervous system development	0.033802
GO:0007492	endoderm development	0.033802
GO:0048262	determination of dorsal/ventral asymmetry	0.034571
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GO:0048617	embryonic foregut morphogenesis	0.034571
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GO:0060124	positive regulation of growth hormone secretion	0.034571
GO:0071649	regulation of chemokine (C-C motif) ligand 5 production	0.034571
GO:0051901	positive regulation of mitochondrial depolarization	0.034571
GO:0086015	SA node cell action potential	0.034571
GO:0086018	SA node cell to atrial cardiac muscle cell signaling	0.034571
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GO:0051347	positive regulation of transferase activity	0.034886
GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	0.035124
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GO:2000551	regulation of T-helper 2 cell cytokine production	0.038339
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GO:0007028	cytoplasm organization	0.038339
GO:0032966	negative regulation of collagen biosynthetic process	0.038339
GO:0006928	movement of cell or subcellular component	0.038402
GO:0032755	positive regulation of interleukin-6 production	0.038964
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GO:0002237	response to molecule of bacterial origin	0.039825
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GO:1903508	positive regulation of nucleic acid-templated transcription	0.041338
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GO:0002862	negative regulation of inflammatory response to antigenic stimulus	0.042092
GO:1904181	positive regulation of membrane depolarization	0.042092
GO:0040015	negative regulation of multicellular organism growth	0.042092
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GO:0015791	polyol transport	0.042092
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	positive regulation of nucleobase-containing compound	

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GO:0002830	positive regulation of type 2 immune response	0.056962
GO:0007039	protein catabolic process in the vacuole	0.056962
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KEGG: hsa05143	African trypanosomiasis - Homo sapiens (human)	0.008511
KEGG: hsa04080	neuroactive ligand-receptor interaction - Homo sapiens	0.023739

	(human)	
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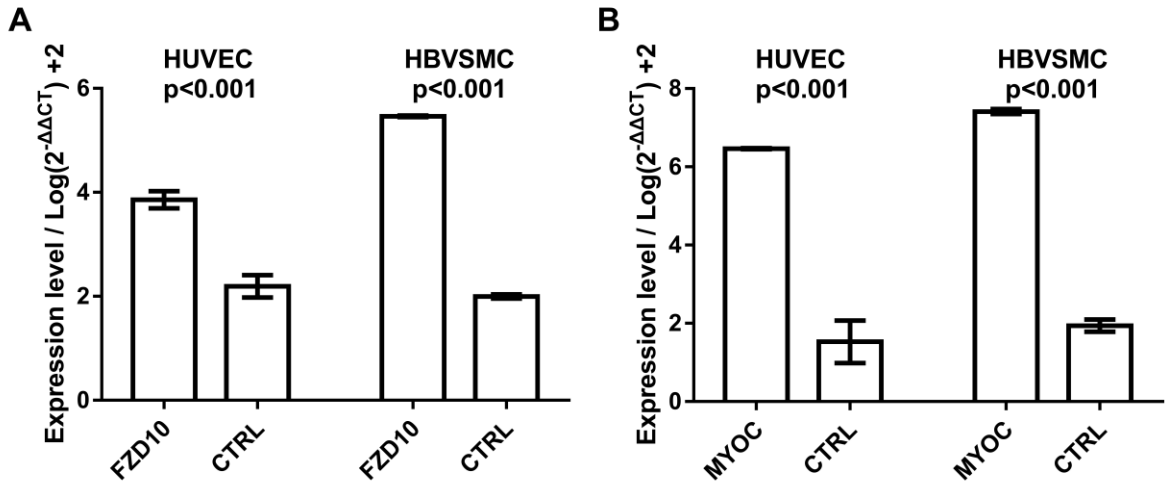

Figure S1. Expression level of FZD10 (A) and MYOC (B) in HUVECs and HBVSMCs after transfection.