Partial carotid ligation and flow pattern validation by high resolution ultrasound

All animal studies were performed with Male C57Bl/6 mice according to the approved IACUC protocol by Emory University. Mice (Jackson Laboratories) were partially ligated between 6 to 8 weeks of age as we recently described [1]. Briefly, three of four caudal branches of left common carotid artery (LCA) - left external carotid, internal carotid, and occipital artery - were ligated with 6-0 silk suture while the superior thyroid artery was left intact in anesthetized mice. Six hours post-surgery, each animal was examined by VEVO 770 High-resolution *in vivo* micro-imaging ultrasound system whether the ligation induced low and oscillatory shear stress in LCA with the contralateral RCA as a control [1].

Intimal RNA isolation from carotid arteries

Total RNA from intima were separately obtained from LCA and RCA at 12, 24 and 48 hr post-ligation as we described previously [1]. Briefly, LCA and RCA were quickly flushed (few seconds) with 150 μl of QIAzol lysis reagent (QIAGEN) using 29G insulin syringe into a microfuge tube. The eluate was then used for total intimal RNA isolation using miRNeasy mini kit (QIAGEN).

Microarray Procedures

Total intimal RNAs were obtained from LCA and RCA at 12hr and 48hr post-ligation. Intimal RNAs from three LCAs or RCAs were pooled to obtain ~30 ng total RNA. All RNA samples used for the microarray study passed a quality control test using Agilent BioAnalyze NanoChip. Each sample was linearly amplified by WT-Ovation RNA amplification system (NuGEN) and used for the microarray study using MouseWG-6 v2 Expression BeadChip array with 45,281 probes (Illumina) at the Emory Biomarker Service Center. After hybridization, BeadChips are scanned on the Illumina BeadArray Reader to determine the probe fluorescence intensity. The raw probe intensities were then normalized by the quantile normalization algorithm[2] using the GenomeStudio software from Illumina.

Microarray Data Analysis and Bioinformatics

The microarray data was statistically analyzed by Significance Analysis of Microarrays software (SAM) [3]. The differentially expressed genes between LCA and RCA were identified for those which showed more than 1.5 fold-changes at <10% false discovery rate. The lists of differentially expressed genes were interrogated for statistically significant overrepresented cellular functions and

disorders using DAVID analysis and Ingenuity Pathway (IPA) Analysis (Ingenuity Systems).

Quantitative real time PCR (qPCR) validation

Total RNA of each sample was reverse transcribed into cDNA using SuperScript III and random primers (Invitrogen) as we described [1]. Briefly, qPCR was performed on selected genes using Brilliant II SYBR Green QPCR Master Mix (Stratagene) with custom designed primers on a Real-Time PCR System (ABI StepOne Plus). Predesigned TaqMan Gene Expression Assay probes (Applied Biosystems) were also used for some selected genes. All qPCR results were normalized based on 18S RNA expression in each sample. Fold changes between LCA and RCA were determined using the $\Delta\Delta$Ct method [4].

Immunohistochemical staining

Paraffin section immunostaining **–** Mice were euthanized by CO_2 inhalation and then were pressure-perfused at 100 mmHg with normal saline followed by pressure fixation with a 10% formalin solution. LCA and RCA were collected *en block* with the trachea and esophagus. Paraffin sections (5 μm) were then microwaved for 20 min in citrate buffer (0.1 M, pH 6.0) for BMP4 and LMO4 staining or in Tris buffer (0.1 M, pH 9.0) for Angpt2 and Jam2 staining. Sections were blocked with 10% donkey serum for 1 hour at room temperature and incubated with primary antibodies specific to BMP4 (5 μg/ml, Biovision), Lmo4 (5 μg/ml, [5-7]), Jam2 (2 μg/ml, R&D System), and Angpt2 (0.4 μg/ml, Santa Cruz) overnight at 4°C in a humidified chamber [8]. To visualize primary antibodies, rhodamine-conjugated secondary antibodies (donkey anti-goat, anti-rat IgG, Jackson) were used for one hour at room temperature. Nuclei were counter stained with Hoechst #33258. All photographs were taken using a Zeiss epi-fluorescent microscope. Paraffin sections of human coronary arteries from patients undergoing heart transplants were obtained with the patients' consent according to the IRB protocol approved at Emory as described previously [8]. The same staining method used for mouse carotids as described above was used for Lmo4 staining.

En Face staining **-** Mice were euthanized by CO_2 inhalation and the aortas were pressure-perfused at 100 mmHg with normal saline followed by pressure fixation with a 10% formalin solution. The aortas were carefully dissected *in situ* and the aortic arches and thoracic aortas were dissected and stained with Lmo4 antibody [5-7], followed by rhodamine-conjugated secondary antibodies for 2 hours at room temperature. The aortas were then mounted on glass slides using Vectashield containing DAPI (Vector Laboratories). They were then opened and lesser curvature and the greater curvature of the arch were separated. *En face* images were obtained using a Zeiss LSM 510 META confocal microscope.

Ex vivo **tissue culture**

Mice were euthanized by CO_2 inhalation and then pressure-perfused with heparinized normal saline. Under sterile conditions, common carotid arteries were harvested and carefully cleaned of perivascular fat. Carotid artery rings (~3 mm) and incubated for 3 to 5 days at 37 °C and 5% CO2 in Dulbecco's Modified Eagle Medium (DMEM) supplemented with 100 U/mL of penicillin and 100 μg/mL of streptomycin and 10% of heat-inactivated fetal bovine serum.

Statistical analysis

Data are presented as mean±SEM. Paired Student's t-test was carried out for all qPCR results of each gene to compare LCA vs. RCA and $p<0.05$ (n=3-5) was considered statistically significant.

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Table S.1 The list of gene probes identified as significant expressed in microarray

12hr Down-regulated gene probes (LCA/RCA) (38)

Gene ID	Gene Name	Score(d)	Numerator(r)	Denominator(s+s0)	Fold Change	q-value(%)
ILMN_1232928	Timp3	25.53	347.03	13.59	0.61	0.00
ILMN_2604029	Klf2	15.76	204.23	12.96	0.30	0.00
ILMN_2686883	Gnaq	13.56	112.33	8.28	0.66	0.00
ILMN_2697304	Eln	12.97	664.84	51.24	0.56	0.00
ILMN_1235077	Capn2	12.97	113.98	8.79	0.55	0.00
ILMN_2595664	Dhh	12.33	467.52	37.91	0.50	0.00
ILMN_2672190	Id1	12.05	131.11	10.88	0.59	0.00
ILMN_2880906	Pdlim2	10.44	167.75	16.07	0.50	2.54
ILMN_2750053	Ptprj	10.43	459.92	44.08	0.53	2.54
ILMN_2424721	Pdgfa	9.84	183.84	18.68	0.54	4.78
ILMN_2634083	Cdkn1a	9.17	164.57	17.95	0.54	7.17
ILMN_2618408	Icam2	9.01	325.97	36.18	0.53	7.17
ILMN_2745876	BC020535	8.54	228.48	26.75	0.60	7.17
ILMN_1220170	Tek	8.09	271.04	33.50	0.64	7.17
ILMN_2498731	E030024M20Rik	8.01	200.79	25.05	0.48	7.17
ILMN_2950503	Dab2ip	7.94	82.96	10.45	0.66	7.17
ILMN_2999439	Klf4	7.57	162.86	21.52	0.48	7.17
ILMN_2675760	2310046K01Rik	7.52	181.95	24.20	0.46	7.17
ILMN_2976129	Tinagl	7.30	300.71	41.21	0.60	7.17
ILMN_2773211	Kras	7.16	51.76	7.23	0.54	7.17
ILMN_2608133	Rhpn2	7.14	358.28	50.18	0.48	7.17
ILMN_1216781	Rab11fip5	7.10	173.70	24.45	0.57	7.17
ILMN_2587084	C230009C22Rik	6.96	63.54	9.13	0.60	7.17
ILMN_2866267	F2rl1	6.88	128.94	18.75	0.56	7.17
ILMN_2789562	P4ha2	6.83	141.49	20.71	0.66	7.17
ILMN_1247916	Lims2	6.73	96.99	14.40	0.51	7.17
ILMN_1231445	Inmt	6.57	77.88	11.85	0.35	7.17
ILMN_2683586	Capn2	6.49	130.67	20.13	0.63	7.45
ILMN_2710274	Slc9a3r2	6.41	572.81	89.38	0.48	7.45
ILMN_1229745	Sertad4	6.39	163.24	25.54	0.62	7.45
ILMN_3140516	Rapgef1	6.32	103.56	16.39	0.58	7.45
ILMN_2641228	Hspa12b	6.28	300.72	47.88	0.46	7.45
ILMN_2738345	Lims2	5.76	81.77	14.20	0.65	9.70
ILMN_2699637	Lsr	5.74	113.06	19.69	0.51	9.70
ILMN_1243407	Klk10	5.73	931.40	162.41	0.31	9.70
ILMN_2689207	Col6a3	5.70	47.59	8.35	0.49	9.70
ILMN_2774056	Cmklr1	5.59	34.09	6.10	0.60	9.70
ILMN_1212703	Kras	5.57	181.54	32.58	0.50	9.70

12hr Up-regulated gene probes (LCA/RCA) (29)

Gene ID	Gene Name	Score(d)	Numerator(r)	Denominator(s+s0)	Fold Change	q-value(%)
ILMN_1235698	Bmp4	-17.05	-285.04	16.72	1.54	0.00
ILMN_2593496	Got2	-16.37	-103.56	6.33	1.68	0.00
ILMN_2909150	Ctgf	-13.70	-1531.93	111.85	4.81	0.00
ILMN_2932964	Ctps	-12.10	-190.35	15.73	2.03	0.00
ILMN_1239386	Galntl2	-12.01	-188.83	15.73	2.56	0.00
ILMN_2451036	LOC100047093	-11.79	-736.61	62.46	1.91	0.00
ILMN_1244612	Galntl2	-11.75	-547.54	46.58	1.82	0.00
ILMN_2694569	LOC631037	-9.82	-156.24	15.90	1.59	9.02
ILMN_1228475	Ulk1	-9.32	-176.19	18.91	1.64	9.02
ILMN_1236958	Gabarapl1	-9.29	-639.61	68.86	1.54	9.02
ILMN_2642403	Lmo4	-8.85	-133.04	15.03	1.82	9.02
ILMN_1231490	2410006H16Rik	-8.50	-66.77	7.86	2.17	9.37
ILMN_2596560	Phactr1	-8.46	-368.96	43.59	2.10	9.37
ILMN_1213034	2010312A17Rik	-8.34	-60.24	7.22	1.52	9.37
ILMN_2741621	Birc2	-8.12	-48.14	5.93	1.79	9.37
ILMN_2790373	Snn	-7.89	-86.61	10.98	1.63	9.56
ILMN_1258158	Aldh6a1	-7.63	-89.06	11.67	1.76	9.56
ILMN_2888552	Slc1a4	-7.48	-106.66	14.25	1.90	9.56
ILMN_2977558	Dapk2	-7.47	-145.95	19.53	4.43	9.56
ILMN_2909336	Gpm6a	-7.42	-248.37	33.47	2.23	9.56
ILMN_1238215	Ctgf	-7.21	-716.25	99.35	6.13	9.56
ILMN_2471996	AI317223	-7.12	-69.95	9.83	2.52	9.56
ILMN_1234487	Angpt2	-7.07	-58.39	8.26	1.97	9.56
ILMN_1216764	Ier3	-7.02	-447.96	63.85	1.65	9.56
ILMN_1252481	Fosl2	-6.95	-303.04	43.62	1.79	9.56
ILMN_1215136	Scn3b	-6.74	-45.96	6.82	1.73	9.56
ILMN_1223313	Fn3k	-6.64	-51.35	7.73	1.63	9.56
ILMN_2711966	Mrpl1	-6.62	-62.59	9.46	1.87	9.56
ILMN_1230596	E030033D05Rik	-6.34	-240.87	38.00	1.64	10.00

48hr Down-regulated gene probes (LCA/RCA) (338)

Gene ID	Gene Name	Score(d)	Numerator(r)	Denominator(s+s0)	Fold Change	q-value(%)
ILMN_2672190	Id1	48.65	122.48	2.52	0.45	0.00
ILMN_2588249	S3-12	31.40	73.58	2.34	0.38	0.00
ILMN_3113303	Atp2b2	29.64	181.01	6.11	0.32	0.00
ILMN_2619136	Pthlh	28.04	145.42	5.19	0.24	0.00
ILMN_2687547	Sdpr	22.68	568.94	25.08	0.52	2.91
ILMN_2765224	Bcam	22.64	569.06	25.13	0.23	2.91
ILMN_1237224	Kctd12	22.01	115.55	5.25	0.46	2.91
ILMN_3037580	Rbms2	20.05	96.76	4.83	0.48	3.26
ILMN_1228233	Gstm1	19.53	66.42	3.40	0.55	3.26
ILMN_1240938	AW212394	19.07	279.74	14.67	0.48	3.26
ILMN_2595664	Dhh	19.01	621.90	32.72	0.36	3.26
ILMN_2728539	Exdl2	17.83	30.51	1.71	0.65	3.26
ILMN_2630182	Syp	16.62	42.12	2.53	0.48	3.26
ILMN_1222685	1200016G03Rik	16.40	91.80	5.60	0.46	6.00
ILMN_1245307	Fbln2	16.40	53.34	3.25	0.62	6.00
ILMN_2628567	Phlda3	15.95	22.37	1.40	0.63	6.00
ILMN_1236168	C030034J23Rik	15.77	190.89	12.11	0.34	6.00
ILMN_2710159	MGC41689	15.70	278.76	17.75	0.35	6.00
ILMN_1253178	Aldh3a1	15.41	149.83	9.72	0.40	6.00
ILMN_2576994	C230096K16Rik	14.88	67.10	4.51	0.66	6.00
ILMN_2697304	Eln	14.82	934.16	63.02	0.57	6.00
ILMN_2904686	Cyb5r3	14.36	163.32	11.37	0.60	6.87
ILMN_1212935	Fzd4	14.35	37.25	2.60	0.66	6.87
ILMN_1258578	Ahnak	14.33	221.71	15.47	0.62	6.87
ILMN_2658804	Rras	13.77	78.66	5.71	0.59	6.87
ILMN_2441501	Clstn1	13.77	30.38	2.21	0.62	6.87
ILMN_2769567	F2rl1	13.13	125.14	9.53	0.60	6.87
ILMN_1238603	Pcolce2	13.11	71.99	5.49	0.48	6.87
ILMN_3066763	Arl4a	12.46	171.95	13.80	0.38	6.87
ILMN_2557319	D530030K12Rik	12.34	111.85	9.06	0.63	6.87
ILMN_2598103	Emp2	12.34	656.62	53.23	0.40	6.87
ILMN_2605539	Sgcd	12.12	47.08	3.88	0.52	6.87
ILMN_2772855	Plek2	12.07	45.53	3.77	0.50	6.87
ILMN_2736783	Kctd12	12.04	380.66	31.61	0.47	6.87
ILMN_2712873	Cyb5r3	12.00	101.47	8.46	0.61	6.87
ILMN_2625920	Aoc3	11.95	115.86	9.69	0.30	6.87
ILMN_3061923	Rbms2	11.63	89.70	7.71	0.59	6.87
ILMN_2691641	Gja5	11.56	678.83	58.73	0.58	6.87
ILMN_1240266	Ankrd25	11.24	195.29	17.38	0.52	6.87
ILMN_2765101	Nkx6-2	11.19	112.90	10.09	0.66	6.87
ILMN_2639809	Nucb1	11.10	78.22	7.05	0.63	6.87
ILMN_2710419	Plec1	11.04	286.97	26.01	0.62	6.87
ILMN_2798086	Fchsd2	10.98	145.35	13.23	0.60	6.87
ILMN_1220170	Tek	10.86	312.70	28.80	0.53	6.87
ILMN_1230039	Hyal2	10.81	202.21	18.71	0.43	6.87
ILMN_2745370	Sult1a1	10.74	185.57	17.27	0.38	6.87
ILMN_1257053	Trrp1	10.42	67.46	6.48	0.41	6.87
ILMN_2839886	Mxd4	10.39	59.76	5.75	0.54	6.87
ILMN_2908132	Gja5	10.30	997.06	96.77	0.62	6.87
ILMN_1220023	Snhg10	10.29	73.32	7.13	0.45	6.87
ILMN_3109360	Plec1	10.27	60.15	5.86	0.64	6.87

48hr Up-regulated gene probes (LCA/RCA)(250)

Gene ID	Gene Name	Score(d)	Numerator(r)	Denominator(s+s0)	Fold Change	q-value(%)
ILMN_2743013	Ncf4	-52.17	-92.58	1.77	3.20	0.00
ILMN_2939681	Lyzs	-39.30	-135.27	3.44	3.10	0.00
ILMN_2878071	Lyz	-24.78	-302.22	12.20	3.08	0.00
ILMN_2867147	Tyrobp	-24.36	-443.39	18.20	3.64	0.00
ILMN_2935386	6330548G22Rik	-22.59	-112.80	4.99	1.82	3.14
ILMN_1245129	Ifitm1	-21.94	-43.43	1.98	2.14	3.14
ILMN_2767918	Ifi30	-21.45	-28.37	1.32	1.61	3.14
ILMN_3120652	Smap2	-20.12	-224.65	11.17	1.56	3.14
ILMN_2511249	scl0002785.1_4	-20.10	-49.58	2.47	1.64	3.14
ILMN_1223257	Ccl4	-19.59	-42.79	2.18	2.41	3.14
ILMN_2718801	Fosl2	-18.65	-30.83	1.65	1.71	3.40
ILMN_3009860	Sell	-18.51	-58.24	3.15	2.82	3.40
ILMN_2712986	Chi3l3	-18.35	-191.36	10.43	6.37	3.40
ILMN_3127739	Sf3b4	-16.11	-82.72	5.13	1.75	7.51
ILMN_2737713	Edn1	-15.56	-444.25	28.56	2.86	7.51
ILMN_1252076	Lyz2	-15.32	-205.83	13.44	6.70	7.51
ILMN_2470131	6720475J19Rik	-14.90	-37.43	2.51	2.11	7.51
ILMN_2888834	Apob48r	-14.71	-126.35	8.59	4.83	7.51
ILMN_2920849	Pira4	-14.64	-46.79	3.20	2.38	7.51
ILMN_1240256	Slc9a3r1	-14.01	-130.32	9.30	1.92	7.51
ILMN_1251066	BC067047	-13.79	-42.11	3.05	1.90	7.51
ILMN_3117876	Chi3l3	-13.67	-211.31	15.45	5.78	7.51
ILMN_2714796	Coro1a	-13.61	-318.14	23.38	6.70	7.51
ILMN_1249242	Dnajc2	-13.27	-113.51	8.55	1.59	7.51
ILMN_1221354	9330156H06Rik	-13.19	-18.72	1.42	1.57	8.59
ILMN_1225192	Nfkbid	-12.91	-65.80	5.10	3.07	8.59
ILMN_2699531	Rgs10	-12.58	-71.58	5.69	1.52	8.59
ILMN_1217928	C230067O06Rik	-12.58	-77.27	6.14	1.80	8.59
ILMN_1217849	Laptm5	-12.52	-773.19	61.77	4.84	8.59
ILMN_3013874	EG434858	-12.45	-44.72	3.59	1.77	8.59
ILMN_2731760	Myo1f	-12.09	-64.59	5.34	2.76	8.59
ILMN_3089584	Cd74	-11.69	-301.56	25.80	3.80	8.59
ILMN_1221817	Cd74	-11.59	-223.38	19.28	3.42	8.59
ILMN_2652511	Hist1h2bj	-11.44	-125.50	10.97	1.62	8.59
ILMN_2571683	9830169E20Rik	-11.43	-166.80	14.59	2.12	8.59
ILMN_1259561	Prep	-11.40	-40.08	3.52	1.84	8.59
ILMN_2659151	Thbs1	-11.34	-387.28	34.15	3.36	8.59
ILMN_1248139	Gp49a	-11.16	-128.29	11.49	4.54	8.59
ILMN_1254513	4930553M18Rik	-11.12	-178.39	16.04	2.15	8.59
ILMN_2637165	2310001H17Rik	-11.09	-72.58	6.55	1.90	8.59
ILMN_2965903	Hdc	-11.02	-839.18	76.15	12.28	8.59
ILMN_1245109	3830430K15Rik	-10.94	-36.44	3.33	2.05	8.59
ILMN_2699923	Asprv1	-10.91	-29.92	2.74	1.84	8.59
ILMN_3160218	Amica1	-10.69	-240.98	22.54	7.73	8.59
ILMN_2712668	Pfkfb4	-10.49	-129.48	12.34	4.06	8.59
ILMN_2777491	Fhod1	-10.32	-116.98	11.34	1.91	8.59
ILMN_2565252	B130015M16Rik	-10.30	-77.99	7.57	1.73	8.59
ILMN_1244977	H2-DMb1	-10.21	-38.32	3.75	1.69	8.59
ILMN_2646630	Lrrc33	-10.03	-95.22	9.49	3.67	8.59
ILMN_2996904	Obfc2a	-9.99	-29.21	2.92	1.75	8.59
ILMN_2603689	Fmnl1	-9.82	-48.84	4.98	2.58	8.67

ILMN_2502860	Ern1	10.27	116.17	11.31	0.62	6.87
ILMN_3139103	Adam15	10.24	160.88	15.71	0.34	6.87
ILMN_1215859	Serpina1b	10.20	23.75	2.33	0.59	6.87
ILMN_1213456	Dhrs7	10.10	103.87	10.29	0.50	6.87
ILMN_2725493	2700078K21Rik	10.06	61.98	6.16	0.41	6.87
ILMN_2713835	Nos3	10.04	149.12	14.85	0.46	6.87
ILMN_1214275	Ddef2	9.65	43.46	4.50	0.66	7.51
ILMN_2596117	Kctd10	9.65	190.39	19.73	0.61	7.51
ILMN_2953751	Sec14l1	9.60	81.62	8.50	0.59	7.51
ILMN_2715195	Stxbp3a	9.43	52.44	5.56	0.63	7.51
ILMN_2801891	Cygb	9.41	49.01	5.21	0.43	7.51
ILMN_1236917	Tmem59	9.41	88.83	9.44	0.58	7.51
ILMN_1224018	Foxk1	9.19	58.55	6.37	0.46	7.51
ILMN_3022252	Arhgef15	9.15	171.08	18.69	0.60	7.51
ILMN_2646052	C4a	9.01	23.42	2.60	0.67	7.51
ILMN_1217742	Atp2b4	8.98	190.99	21.26	0.39	7.51
ILMN_1221146	Cytl1	8.98	765.84	85.29	0.41	7.51
ILMN_1230578	LOC100045421	8.97	34.39	3.83	0.50	7.51
ILMN_2710274	Slc9a3r2	8.86	728.41	82.22	0.32	8.11
ILMN_2630039	E130014J05Rik	8.77	58.00	6.61	0.58	8.11
ILMN_2738345	Lims2	8.64	162.65	18.82	0.40	8.11
ILMN_1253182	Hs3st1	8.64	64.10	7.42	0.66	8.11
ILMN_1245446	5730405I09Rik	8.63	47.55	5.51	0.63	8.11
ILMN_2970167	Wwp2	8.52	58.26	6.83	0.61	8.11
ILMN_2942674	Lims2	8.52	188.91	22.18	0.34	8.11
ILMN_1243080	Taf9b	8.51	61.14	7.19	0.62	8.11
ILMN_1243407	Klk10	8.48	840.82	99.17	0.10	8.11
ILMN_2416218	5530400B01Rik	8.45	84.43	10.00	0.40	8.11
ILMN_2511768	Ttc17	8.40	60.34	7.18	0.60	8.11
ILMN_2940642	St6galnac2	8.29	199.26	24.04	0.37	8.11
ILMN_2659879	Adcy6	8.22	66.22	8.06	0.54	8.11
ILMN_2744414	Nme3	8.21	50.86	6.20	0.58	8.11
ILMN_2778181	Plekha6	8.10	47.16	5.82	0.44	8.11
ILMN_1213850	Col4a3	8.00	394.35	49.30	0.22	8.11
ILMN_2638114	Ptn	7.99	18.90	2.36	0.62	8.11
ILMN_1225825	LOC100039175	7.99	104.11	13.03	0.49	8.11
ILMN_1248397	Smarcd3	7.98	41.30	5.18	0.56	8.11
ILMN_1239381	Klf3	7.96	295.85	37.19	0.35	8.11
ILMN_2633386	LOC100044190	7.91	163.23	20.63	0.53	8.11
ILMN_2669062	Pi16	7.87	839.18	106.64	0.27	8.11
ILMN_2479359	Tmod3	7.87	67.24	8.55	0.58	8.11
ILMN_2433213	Klf7	7.87	116.57	14.82	0.59	8.11
ILMN_1259554	Marveld1	7.86	253.40	32.24	0.48	8.11
ILMN_3094506	Arhgef15	7.78	171.53	22.04	0.54	8.11
ILMN_2755833	Lrrc3b	7.70	26.91	3.49	0.58	8.11
ILMN_2723024	BC004044	7.66	20.95	2.73	0.66	8.11
ILMN_1234318	Ubxd1	7.65	154.31	20.18	0.60	8.11
ILMN_2699637	Lsr	7.61	175.35	23.04	0.38	8.11
ILMN_2999439	Klf4	7.57	230.54	30.46	0.28	8.11
ILMN_1231439	Aatk	7.51	168.67	22.46	0.51	8.11
ILMN_2675760	2310046K01Rik	7.49	316.15	42.21	0.33	8.11
ILMN_2661422	Ramp2	7.48	563.57	75.38	0.44	8.11
ILMN_1248994	4933407C03Rik	7.38	107.64	14.59	0.47	8.11
ILMN_1260405	D330008E13Rik	7.36	35.13	4.77	0.65	8.11
ILMN_2675232	Klk8	7.29	118.36	16.23	0.43	8.11
ILMN_2608133	Rhpn2	7.29	599.12	82.24	0.26	8.11
ILMN_1248740	Sema3f	7.27	637.08	87.58	0.49	8.11
ILMN_2609025	Elmo1	7.21	59.82	8.30	0.66	8.11
ILMN_1230129	Adamts1	7.21	71.65	9.94	0.65	8.11
ILMN_1231802	Tbc1d9b	7.20	18.54	2.57	0.66	8.11
ILMN_2790842	Jam2	7.15	151.84	21.23	0.40	8.11
ILMN_1242787	4930557M22Rik	7.13	23.00	3.22	0.64	8.11
ILMN_1228031	Dusp8	7.13	323.32	45.34	0.27	8.11
ILMN_1224589	Tmem77	7.11	35.33	4.97	0.65	8.11
ILMN_2485594	B130005I07Rik	7.10	20.17	2.84	0.65	8.11
ILMN_1237264	Trspap1	7.10	37.17	5.23	0.59	8.11
ILMN_2678355	Amigo2	7.10	226.95	31.98	0.44	8.11
ILMN_1218934	Rdm1	7.05	64.87	9.20	0.54	8.11
ILMN_2777082	P4ha2	7.01	468.20	66.75	0.40	8.11
ILMN_2430542	Nos3	6.94	136.32	19.64	0.46	8.11
ILMN_3003864	Cgnl1	6.93	320.81	46.26	0.39	8.11
ILMN_2653215	Nagk	6.91	92.60	13.40	0.61	8.11
ILMN_2788593	Nos3	6.91	127.42	18.45	0.47	8.11
ILMN_2640248	Lama5	6.81	134.53	19.76	0.60	8.11
ILMN_2635631	Sema3f	6.80	413.55	60.82	0.49	8.11
ILMN_2876325	Fbxo34	6.79	47.47	6.99	0.55	8.11
ILMN_3111298	Mcfd2	6.78	128.32	18.92	0.62	8.11
ILMN_1241903	Klf4	6.76	62.46	9.24	0.37	8.11
ILMN_3132949	Fbln2	6.75	40.26	5.96	0.65	8.11
ILMN_2920759	Clip1	6.75	74.61	11.06	0.65	8.11
ILMN_1218949	Mterfd2	6.74	226.45	33.58	0.32	8.11
ILMN_2706730	Ptprr	6.73	75.38	11.21	0.38	8.11
ILMN_1230880	Myst4	6.72	38.24	5.69	0.60	8.11
ILMN_2461707	Rbms2	6.72	53.24	7.92	0.67	8.11
ILMN_2427021	Megf6	6.71	50.21	7.49	0.51	8.11
ILMN_1241892	Sod3	6.70	58.55	8.73	0.60	8.11
ILMN_3033533	Add1	6.69	143.80	21.48	0.63	8.11
ILMN_1254927	Ly6c1	6.67	420.23	62.98	0.31	8.11
ILMN_1248947	Mal	6.67	106.37	15.94	0.49	8.11
ILMN_1221264	Klf4	6.67	75.67	11.35	0.34	8.11
ILMN_2590034	Ltbp4	6.61	386.13	58.40	0.58	8.11
ILMN_2596346	Dcn	6.61	33.34	5.05	0.64	8.11
ILMN_2706853	Scamp1	6.61	349.47	52.90	0.65	8.11
ILMN_2599955	Btbd3	6.59	268.49	40.72	0.42	8.11
ILMN_2578183	E330020K23Rik	6.59	24.45	3.71	0.59	8.11
ILMN_2715558	Arhgap17	6.58	79.80	12.12	0.66	8.11
ILMN_1235230	Pdlim3	6.55	115.97	17.72	0.65	8.11
ILMN_2759079	Ppap2a	6.46	92.23	14.27	0.61	8.11
ILMN_2686244	Rassf4	-9.81	-74.07	7.55	3.21	8.67
ILMN_2609323	Lst1	-9.80	-71.92	7.34	2.85	8.67
ILMN_1226525	H2-Ab1	-9.24	-370.46	40.10	3.83	9.45
ILMN_3102376	Fcgr2b	-9.17	-23.48	2.56	1.70	9.45
ILMN_1258723	Bop1	-9.16	-36.00	3.93	1.76	9.45
ILMN_2766780	Lyzs	-9.15	-20.06	2.19	1.56	9.45
ILMN_2644587	Bzw2	-9.12	-35.95	3.94	1.57	9.45
ILMN_2669404	Lmnb2	-8.93	-294.56	33.00	1.89	9.45
ILMN_2416628	Pscd4	-8.87	-201.17	22.68	2.99	9.45
ILMN_2712151	1810033B17Rik	-8.85	-23.08	2.61	1.65	9.45
ILMN_1247377	Mpeg1	-8.79	-57.43	6.53	2.46	9.45
ILMN_2692960	Ero1lb	-8.73	-42.71	4.89	1.84	9.45
ILMN_1241302	Csf3r	-8.69	-33.12	3.81	2.03	9.45
ILMN_2606144	Cd300lf	-8.68	-221.92	25.56	7.18	9.45
ILMN_2685023	Hmha1	-8.65	-55.09	6.37	2.72	9.45
ILMN_1229530	Csk	-8.64	-97.86	11.32	1.53	9.45
ILMN_2820260	Wdr77	-8.59	-57.58	6.71	2.07	9.45
ILMN_2607880	Tkt	-8.53	-99.97	11.72	1.67	9.45
ILMN_2956092	Rassf4	-8.48	-79.40	9.36	3.33	9.45
ILMN_2909150	Ctgf	-8.48	-1891.21	223.12	6.00	9.45
ILMN_2687586	Cxcl16	-8.46	-282.89	33.45	2.20	9.45
ILMN_2924831	Gas7	-8.44	-56.56	6.70	2.08	9.45
ILMN_1238215	Ctgf	-8.37	-755.01	90.15	7.29	9.45
ILMN_2685393	Ccr5	-8.36	-69.17	8.27	3.39	9.45
ILMN_2607675	LOC641240	-8.35	-268.72	32.18	3.29	9.45
ILMN_2619861	Nipsnap1	-8.35	-48.60	5.82	1.54	9.45
ILMN_2673776	E2f2	-8.34	-69.27	8.31	1.89	9.45
ILMN_2910934	Cd52	-8.33	-214.32	25.72	5.07	9.45
ILMN_2694857	Gpatch3	-8.33	-23.57	2.83	1.53	9.45
ILMN_1256883	Rad51	-8.23	-43.04	5.23	2.15	9.45
ILMN_2559943	A230055O06Rik	-8.14	-56.18	6.90	1.59	9.45
ILMN_2629971	Fzr1	-8.03	-20.23	2.52	1.51	9.45
ILMN_1213364	LOC638892	-8.03	-112.73	14.04	1.68	9.45
ILMN_1223317	Lgals3	-8.01	-37.83	4.72	2.16	9.45
ILMN_2748875	Fcer1g	-8.00	-85.61	10.70	3.09	9.45
ILMN_1235392	LOC668183	-7.91	-76.35	9.65	2.58	9.45
ILMN_1239569	Lsg1	-7.89	-44.59	5.65	1.64	9.45
ILMN_1230157	Rnd3	-7.89	-113.47	14.38	2.15	9.45
ILMN_2787257	Coro1a	-7.86	-275.12	35.02	6.06	9.45
ILMN_2781030	Napsa	-7.80	-85.04	10.90	3.00	9.45
ILMN_1230440	1700041B20Rik	-7.79	-65.43	8.40	2.16	9.45
ILMN_1252804	Map4k1	-7.77	-26.02	3.35	1.66	9.45
ILMN_1236387	BC024537	-7.72	-178.09	23.07	1.76	9.45
ILMN_2887986	Cd300a	-7.72	-252.37	32.71	4.31	9.45
ILMN_1227434	Itgb7	-7.71	-42.06	5.45	2.10	9.45
ILMN_2749063	Dock10	-7.67	-63.52	8.28	2.52	9.45
ILMN_2460168	Wdr1	-7.65	-71.49	9.34	1.52	9.45
ILMN_1244123	Slc38a2	-7.54	-275.69	36.58	1.82	9.45
ILMN_1219712	Ctps	-7.50	-88.49	11.80	1.98	9.45
ILMN_1222471	Gmfg	-7.49	-64.19	8.57	2.23	9.45
ILMN_2816180	Lbh	-7.48	-169.34	22.65	2.13	9.45
ILMN_2769285	Sema6b	-7.42	-204.00	27.49	2.45	9.45
ILMN_2642403	Lmo4	-7.40	-105.47	14.25	1.70	9.45
ILMN_2657409	Rps18	-7.39	-48.59	6.58	1.79	9.45
ILMN_3113420	Ptpn6	-7.38	-71.35	9.66	2.87	9.45
ILMN_2665666	Pstpip1	-7.34	-40.93	5.58	2.26	9.45
ILMN_2747456	Ivns1abp	-7.33	-546.74	74.58	4.23	9.45
ILMN_2690603	Spp1	-7.32	-31.52	4.30	2.11	9.45
ILMN_1218123	Aif1	-7.28	-106.31	14.60	3.00	9.45
ILMN_2633062	9130422G05Rik	-7.25	-25.89	3.57	1.59	9.45
ILMN_2787785	Akna	-7.23	-33.42	4.62	1.75	9.45
ILMN_1224876	Znhit1	-7.22	-60.25	8.35	1.77	9.45
ILMN_2685392	Ccr5	-7.21	-59.36	8.23	2.87	9.45
ILMN_1255766	Sh3bp2	-7.20	-146.71	20.37	1.96	9.45
ILMN_2524817	Dnahc17	-7.14	-40.68	5.70	1.82	9.45
ILMN_1228657	Fcgr2b	-7.12	-25.28	3.55	1.77	9.45
ILMN_2628629	Cdh1	-7.03	-24.99	3.56	1.58	9.45
ILMN_2671984	Ptprc	-7.01	-60.84	8.67	2.59	9.45
ILMN_2619961	4933429F08Rik	-6.99	-22.30	3.19	1.61	9.45
ILMN_2663930	Slfn1	-6.95	-144.45	20.79	5.35	9.45
ILMN_2675223	Cd33	-6.91	-77.32	11.18	3.21	9.45
ILMN_1230287	4732429D16Rik	-6.87	-92.38	13.44	3.25	9.45
ILMN_2639925	Narg1	-6.80	-30.43	4.47	1.51	9.45
ILMN_2705628	Clec4d	-6.80	-91.72	13.48	3.50	9.45
ILMN_1226517	Ttll4	-6.76	-52.76	7.80	1.72	9.45
ILMN_2757428	Bloc1s2	-6.74	-51.08	7.58	1.56	9.45
ILMN_3158135	Sema6b	-6.71	-81.56	12.15	1.96	9.45
ILMN_1228320	Cfp	-6.69	-72.15	10.78	2.48	9.45
ILMN_2737302	Cxcl12	-6.67	-227.39	34.07	3.43	9.45
ILMN_1247626	As3mt	-6.67	-16.30	2.44	1.51	9.45
ILMN_1252335	Agpat6	-6.65	-360.09	54.13	1.53	9.45
ILMN_3008858	Ctsc	-6.64	-68.56	10.32	2.93	9.45
ILMN_2655024	Il17ra	-6.64	-184.59	27.80	3.69	9.45
ILMN_1236290	Ets1	-6.63	-57.83	8.72	2.29	9.45
ILMN_2891646	Hist1h2bm	-6.63	-115.02	17.35	1.62	9.45
ILMN_2689785	Cd68	-6.63	-43.77	6.61	2.10	9.45
ILMN_2631161	Fcgr4	-6.62	-194.07	29.32	7.08	9.45
ILMN_2544890	Pde4b	-6.58	-48.15	7.31	1.84	9.45
ILMN_2767057	3110082I17Rik	-6.57	-84.50	12.86	1.68	9.45
ILMN_1224353	Rcc2	-6.57	-88.50	13.48	1.72	9.45
ILMN_1239102	H2-Eb1	-6.56	-128.73	19.63	2.78	9.45
ILMN_3073899	Pira11	-6.51	-30.61	4.70	1.77	9.45
ILMN_2747060	Coro1a	-6.47	-67.65	10.46	2.86	9.45
ILMN_2913716	H2-Ab1	-6.47	-246.49	38.13	3.00	9.45
ILMN_2653132	Clec7a	-6.44	-34.16	5.30	2.01	9.45
ILMN_2842338	Tbc1d10c	-6.41	-45.49	7.10	2.03	9.45
ILMN_2887983	Cd300a	-6.34	-275.36	43.43	4.88	9.45
ILMN_1240566	Cep170	-6.33	-58.49	9.24	1.98	9.45

ILMN_1228245	Prickle1	6.46	27.93	4.32	0.64	8.11
ILMN_3137804	Pbx1	6.41	40.53	6.32	0.63	8.11
ILMN_2618408	Icam2	6.38	476.29	74.65	0.48	8.11
ILMN_1249888	Adcy6	6.36	80.57	12.66	0.42	8.11
ILMN_1215879	Pkhd1l1	6.36	31.44	4.94	0.60	8.11
ILMN_1218241	Slc9a3r2	6.35	33.07	5.20	0.55	8.11
ILMN_3049559	C4b	6.34	65.15	10.28	0.54	8.11
ILMN_1255416	Ly6a	6.30	685.75	108.79	0.53	8.11
ILMN_1257193	Ppm1a	6.30	47.33	7.51	0.64	8.11
ILMN_1241605	LOC383884	6.30	20.62	3.27	0.64	8.11
ILMN_2700166	Ccnd2	6.30	165.71	26.30	0.63	8.11
ILMN_1225657	2410095B20Rik	6.30	27.46	4.36	0.63	8.11
ILMN_2896843	Cd248	6.29	45.73	7.27	0.49	8.11
ILMN_2513922	Prdm16	6.27	25.09	4.00	0.63	8.11
ILMN_2614380	Map3k1	6.25	141.98	22.72	0.60	8.11
ILMN_1248895	Cachd1	6.21	24.29	3.91	0.60	8.11
ILMN_1260571	Spna2	6.18	81.47	13.18	0.65	8.11
ILMN_2640570	Pak4	6.12	267.69	43.75	0.42	8.11
ILMN_1243249	2810410A03Rik	6.08	242.39	39.89	0.51	8.11
ILMN_2733887	Mknk2	6.06	230.14	37.96	0.43	8.11
ILMN_1239673	LOC672215	6.04	41.20	6.82	0.53	8.11
ILMN_2963704	Sfxn3	6.01	410.52	68.36	0.66	8.11
ILMN_2513570	AW123240	5.99	48.15	8.04	0.64	8.11
ILMN_2670375	Itm2b	5.98	254.84	42.59	0.64	8.11
ILMN_1219447	Zmym3	5.97	77.53	12.98	0.57	8.11
ILMN_2761918	Mmrn2	5.96	506.28	84.98	0.54	8.11
ILMN_2789562	P4ha2	5.95	219.30	36.88	0.41	8.11
ILMN_2493521	Tnrc6c	5.94	52.82	8.89	0.62	8.11
ILMN_2728538	Exdl2	5.93	29.64	5.00	0.63	8.11
ILMN_2658407	Elmo1	5.91	52.73	8.92	0.62	8.11
ILMN_1223049	Tns1	5.89	137.96	23.43	0.49	8.11
ILMN_2855515	Pnpla6	5.86	69.34	11.82	0.62	8.11
ILMN_2913222	Efcab4a	5.84	136.41	23.35	0.50	8.11
ILMN_2577853	Rw1-pending	5.82	29.72	5.11	0.63	8.11
ILMN_1224866	Ptgs1	5.80	45.80	7.90	0.51	8.36
ILMN_2933431	Pps	5.78	25.83	4.47	0.62	8.36
ILMN_2750053	Ptprj	5.78	573.00	99.14	0.33	8.36
ILMN_2641228	Hspa12b	5.77	267.94	46.45	0.46	8.36
ILMN_2947526	Ecm1	5.76	102.54	17.79	0.55	8.36
ILMN_2757019	She	5.72	105.35	18.41	0.66	8.36
ILMN_2509327	Wipf3	5.71	25.26	4.42	0.60	8.36
ILMN_2633897	Pde6d	5.70	29.69	5.20	0.64	8.36
ILMN_2615035	Mgst3	5.70	156.45	27.43	0.56	8.36
ILMN_3126277	Palmd	5.70	375.82	65.94	0.58	8.36
ILMN_2743320	Myst4	5.66	35.97	6.35	0.63	8.36
ILMN_2592823	Cdc42ep5	5.65	46.78	8.28	0.60	8.36
ILMN_1241293	Cldn5	5.64	905.91	160.54	0.39	8.36
ILMN_2727687	Numb	5.64	40.69	7.21	0.63	8.36
ILMN_3111877	Rbms2	5.62	204.42	36.35	0.62	8.36
ILMN_2727309	LOC100044204	5.60	98.74	17.62	0.40	8.36
ILMN_3159275	Ahnak	5.60	146.55	26.17	0.62	8.36
ILMN_2877069	Tspo	5.60	108.53	19.38	0.60	8.36
ILMN_2678477	Gja5	5.60	81.70	14.60	0.44	8.36
ILMN_3052632	Epas1	5.59	1006.29	179.97	0.50	8.36
ILMN_2592881	Jam2	5.58	56.34	10.10	0.53	8.36
ILMN_3132223	C630004H02Rik	5.55	98.03	17.66	0.61	8.36
ILMN_2466164	Wfdc1	5.54	36.49	6.59	0.48	8.36
ILMN_3115796	Cd40	5.54	63.12	11.40	0.43	8.36
ILMN_2720083	Bace2	5.54	155.25	28.05	0.44	8.36
ILMN_2705128	Muted	5.53	212.07	38.32	0.65	8.36
ILMN_1220234	Serpina1e	5.52	64.66	11.71	0.37	8.36
ILMN_2599008	Kirrel3	5.51	37.01	6.71	0.53	8.36
ILMN_2588295	Rarres2	5.48	47.39	8.64	0.46	8.36
ILMN_2881681	Tnrc6c	5.47	157.45	28.76	0.47	8.36
ILMN_2865335	Krt80	5.46	205.30	37.58	0.47	8.36
ILMN_2432550	Trib2	5.46	148.79	27.26	0.36	8.36
ILMN_2756665	Cbr2	5.46	96.44	17.68	0.42	8.36
ILMN_2736379	Nfia	5.45	164.72	30.21	0.65	8.36
ILMN_2572849	C920007D24Rik	5.44	46.49	8.54	0.53	8.36
ILMN_1225988	Zdhhc3	5.44	49.76	9.15	0.44	8.36
ILMN_2862179	Ccl11	5.44	18.10	3.33	0.64	8.36
ILMN_1257077	Jag1	5.43	42.72	7.86	0.64	8.46
ILMN_2799596	AI662250	5.41	50.94	9.42	0.56	8.46
ILMN_3139693	Rab11fip5	5.41	113.90	21.07	0.65	8.46
ILMN_2991660	Mif4gd	5.40	29.68	5.50	0.65	8.46
ILMN_3079421	Pde6d	5.40	56.51	10.47	0.58	8.46
ILMN_2765032	Kcnn4	5.39	38.30	7.10	0.53	8.46
ILMN_2622089	5430432N15Rik	5.38	326.67	60.69	0.50	8.46
ILMN_2868457	Lrrc1	5.38	31.81	5.91	0.54	8.46
ILMN_2549903	6230401I02Rik	5.36	285.30	53.22	0.61	8.46
ILMN_2963700	Sfxn3	5.35	257.17	48.09	0.63	8.46
ILMN_1220360	Unc13b	5.33	210.62	39.49	0.47	8.46
ILMN_1258788	Snx27	5.32	62.41	11.73	0.60	8.46
ILMN_2913166	Serping1	5.31	121.92	22.96	0.48	8.46
ILMN_3129160	Epas1	5.30	179.95	33.95	0.51	8.46
ILMN_2803249	Inmt	5.30	31.55	5.96	0.48	8.46
ILMN_2618148	C330008K14Rik	5.29	42.60	8.05	0.53	8.46
ILMN_2495363	Wasf2	5.21	62.71	12.04	0.61	8.46
ILMN_2722864	Ncam1	5.14	58.40	11.37	0.42	8.46
ILMN_2872058	Ctsh	5.12	363.60	70.96	0.55	8.65
ILMN_2877029	Cytl1	5.11	779.95	152.71	0.42	8.65
ILMN_2745876	BC020535	5.07	257.63	50.83	0.42	8.65
ILMN_1225570	Serpina1d	5.07	32.89	6.49	0.48	8.65
ILMN_2627179	Ell3	5.07	27.22	5.37	0.65	8.65
ILMN_3163577	Scn3b	5.05	74.28	14.72	0.37	8.65
ILMN_2908133	Gja5	5.04	260.38	51.68	0.66	8.65
ILMN_3150811	Tsc22d3	5.03	175.46	34.88	0.53	8.65
ILMN_1242286	Ermp1	5.03	48.98	9.74	0.64	8.65
ILMN_1221736	Samhd1	-6.31	-108.70	17.22	2.13	9.45
ILMN_2634248	Syncrip	-6.31	-80.52	12.76	1.71	9.45
ILMN_2957167	4931417G12Rik	-6.30	-27.27	4.33	1.68	9.45
ILMN_2963974	Gemin4	-6.30	-34.03	5.40	1.63	9.45
ILMN_2742152	Gadd45a	-6.28	-138.42	22.03	4.87	9.45
ILMN_1219333	9830134K01Rik	-6.28	-25.26	4.02	1.61	9.45
ILMN_3157568	Bcl2l11	-6.28	-59.58	9.49	1.84	9.45
ILMN_2601155	Frzb	-6.28	-70.68	11.26	2.01	9.45
ILMN_2529254	LOC223653	-6.25	-26.41	4.23	1.64	9.45
ILMN_1249486	Mgl1	-6.21	-295.82	47.66	4.25	9.45
ILMN_2894211	8430408G22Rik	-6.18	-32.44	5.25	2.00	9.45
ILMN_2896805	Psmd12	-6.17	-62.78	10.17	1.57	9.45
ILMN_2906473	Gbl	-6.17	-88.64	14.36	1.53	9.45
ILMN_2821148	Serhl	-6.12	-96.50	15.77	2.29	9.45
ILMN_2685194	Lass6	-6.10	-44.65	7.32	2.43	9.45
ILMN_3139875	Acot1	-6.09	-46.77	7.67	1.79	9.45
ILMN_1254577	AI607873	-6.07	-63.12	10.39	2.81	9.45
ILMN_2526163	LOC380753	-6.07	-23.63	3.90	1.61	9.45
ILMN_2593496	Got2	-6.05	-127.90	21.14	1.62	9.45
ILMN_2618714	Pdgfb	-6.00	-192.47	32.06	3.27	9.45
ILMN_1255419	Zfpn1a1	-5.99	-32.61	5.44	2.04	9.45
ILMN_1259488	Mgea6	-5.93	-86.89	14.66	1.78	9.45
ILMN_2836137	E2f2	-5.89	-70.10	11.90	1.96	9.45
ILMN_2734729	H2-Aa	-5.89	-60.77	10.32	2.27	9.45
ILMN_2742592	Hist1h2be	-5.87	-169.99	28.97	1.74	9.45
ILMN_1254035	Myo10	-5.84	-31.72	5.43	2.00	9.45
ILMN_1256359	Smox	-5.82	-23.62	4.06	1.72	9.45
ILMN_1226606	Tmem132a	-5.81	-127.84	22.01	1.54	9.45
ILMN_1247832	Cd74	-5.80	-67.15	11.57	2.67	9.45
ILMN_2704919	Ube2t	-5.79	-19.63	3.39	1.64	9.45
ILMN_2494707	LOC381232	-5.73	-15.62	2.73	1.50	9.45
ILMN_2727663	Tgfbi	-5.69	-61.32	10.78	2.82	9.45
ILMN_2435584	scl0001978.1_6	-5.67	-196.97	34.71	1.83	9.45
ILMN_1214071	Ifitm1	-5.66	-211.63	37.41	4.60	9.45
ILMN_2552295	Vcam1	-5.65	-34.00	6.01	1.53	9.45
ILMN_2814974	Klra2	-5.64	-72.50	12.85	3.25	9.45
ILMN_2922899	Plcb2	-5.64	-21.05	3.73	1.57	9.45
ILMN_1247540	Vcan	-5.64	-21.42	3.80	1.62	9.45
ILMN_2810405	Myo1g	-5.64	-80.61	14.30	3.19	9.45
ILMN_2655336	Vcan	-5.61	-56.36	10.05	2.22	9.45
ILMN_1231012	Lcp2	-5.60	-24.11	4.31	1.74	9.45
ILMN_2915232	Cotl1	-5.58	-147.47	26.41	3.69	9.45
ILMN_1222059	Thbs1	-5.58	-1097.52	196.84	3.77	9.45
ILMN_2936380	Sgpl1	-5.56	-27.63	4.97	1.59	9.45
ILMN_2585233	Selpl	-5.56	-20.65	3.71	1.57	9.45
ILMN_1242661	Itgb2	-5.50	-38.79	7.06	1.89	9.45
ILMN_3072427	Il1rn	-5.49	-26.03	4.74	1.67	9.45
ILMN_2577664	Fcgr2b	-5.48	-38.40	7.00	2.12	9.45
ILMN_2715234	Rnmtl1	-5.45	-40.18	7.37	1.75	9.45
ILMN_3043669	Sla	-5.44	-29.67	5.45	1.77	9.45
ILMN_2957862	Noc4l	-5.42	-105.05	19.37	1.71	9.45
ILMN_1222803	Hspa9	-5.41	-121.18	22.38	1.65	9.45
ILMN_2547840	2200005K02Rik	-5.39	-96.34	17.86	2.08	9.45
ILMN_1227907	Gmfg	-5.39	-97.65	18.13	2.59	9.45
ILMN_1242457	Fpr2	-5.37	-102.16	19.04	4.03	9.45
ILMN_2752224	Mrps28	-5.35	-36.40	6.80	1.59	9.45
ILMN_2657478	Cd53	-5.33	-45.50	8.53	2.30	9.45
ILMN_1249498	Plek	-5.27	-34.74	6.59	1.95	9.45
ILMN_1251669	Evi2a	-5.26	-72.52	13.79	2.87	9.45
ILMN_1220418	Hcst	-5.25	-81.31	15.48	3.13	9.45
ILMN_2746501	Csf3r	-5.23	-31.19	5.97	1.93	9.45
ILMN_2859847	Pygl	-5.21	-26.85	5.15	1.71	9.45
ILMN_2666487	Ruvbl1	-5.21	-59.50	11.42	1.51	9.45
ILMN_2745425	Rcc1	-5.14	-123.41	24.01	2.70	9.45
ILMN_1248604	D030029G14Rik	-5.12	-26.35	5.14	1.62	9.45
ILMN_2485839	Tnfrsf1b	-5.12	-48.65	9.50	1.75	9.45
ILMN_3155245	Arhgap25	-5.10	-67.34	13.20	1.76	9.45
ILMN_2495068	scl000854.1_75	-5.09	-39.51	7.76	1.82	9.45
ILMN_2720634	Prmt5	-5.08	-67.20	13.22	1.84	9.45
ILMN_2653619	Ctage5	-5.03	-99.04	19.69	1.70	9.45
ILMN_2637714	Rasa3	-5.02	-154.22	30.73	1.96	9.45
ILMN_2595732	LOC100046232	-5.01	-234.04	46.69	3.20	9.45
ILMN_1215085	Fkbp10	-5.01	-89.20	17.81	1.72	9.45
ILMN_1220893	Zfp281	-5.00	-45.96	9.20	1.57	9.45
ILMN_2803674	S100a9	-4.99	-340.58	68.23	2.69	9.45
ILMN_1252673	Cugbp2	-4.96	-37.09	7.48	1.53	9.45
ILMN_2864309	OTTMUSG00000	-4.96	-24.97	5.04	1.62	9.45
ILMN_2702508	Ebna1bp2	-4.93	-143.36	29.08	1.56	9.45
ILMN_1213708	4732462B05Rik	-4.93	-58.66	11.90	1.57	9.45
ILMN_2539454	LOC100042952	-4.91	-81.08	16.52	1.57	9.45
ILMN_3074985	H2afz	-4.90	-228.29	46.57	1.56	9.45
ILMN_2620069	Rpo1-4	-4.86	-47.91	9.86	1.77	9.45
ILMN_2669441	Eftud2	-4.85	-142.99	29.51	1.68	9.45
ILMN_2918499	Abcb1b	-4.84	-26.61	5.49	1.62	9.45
ILMN_1220996	Ptpn6	-4.82	-137.80	28.58	3.74	9.92
ILMN_1245750	Prkcd	-4.81	-45.97	9.56	1.91	9.92
ILMN_2686044	Eif5a	-4.81	-950.62	197.72	1.59	9.92
ILMN_1254630	Ptpre	-4.80	-26.34	5.48	1.66	9.92
ILMN_2833243	C330023M02Rik	-4.80	-23.80	4.96	1.64	9.92
ILMN_1226785	Homer1	-4.79	-32.30	6.74	1.86	9.92
ILMN_2712066	Pgd	-4.76	-210.62	44.29	1.61	9.92
ILMN_1250947	Txndc5	-4.73	-245.15	51.78	1.96	9.92
ILMN_2837779	Trpv2	-4.72	-19.06	4.03	1.61	9.92
ILMN_2685668	Nek6	-4.72	-25.91	5.49	1.67	9.92
ILMN_2820893	Selplg	-4.71	-82.36	17.48	3.13	9.92
ILMN_1237948	Tes	-4.71	-39.06	8.29	2.09	9.92
ILMN_2593143	Dock10	-4.71	-19.73	4.19	1.59	9.92
ILMN_3154691	Sirpb1	-4.70	-37.49	7.97	2.11	9.92

ILMN_1238936	D130063P19Rik	5.02	29.32	5.84	0.61	8.65
ILMN_3112526	Ldb2	5.02	75.50	15.04	0.49	8.65
ILMN_1233340	Pkp4	5.00	332.80	66.59	0.64	8.65
ILMN_2454786	Tpcn1	4.99	92.71	18.58	0.52	8.65
ILMN_3163020	Klc1	4.98	54.81	11.01	0.66	8.65
ILMN_1232123	Traf3ip2	4.97	33.68	6.77	0.60	8.65
ILMN_1231520	Trpv4	4.97	66.51	13.39	0.51	8.65
ILMN_2449620	5830427D02Rik	4.96	23.51	4.74	0.61	8.65
ILMN_2740628	Ndrg3	4.95	28.58	5.78	0.58	8.65
ILMN_2931918	4432416J03Rik	4.95	29.33	5.93	0.56	8.65
ILMN_2834370	Cutc	4.94	67.50	13.65	0.63	8.65
ILMN_2610442	Wscd1	4.91	90.57	18.44	0.56	8.65
ILMN_2663211	Stbd1	4.88	61.45	12.58	0.58	8.65
ILMN_2688236	Atp2a3	4.87	1787.36	366.78	0.63	8.65
ILMN_1212703	Kras	4.87	110.37	22.66	0.63	8.65
ILMN_2870522	Plekha6	4.86	249.03	51.28	0.20	8.65
ILMN_2790839	Jam2	4.85	246.15	50.75	0.40	8.65
ILMN_2621038	Hoxa7	4.84	33.50	6.92	0.64	8.65
ILMN_2745367	Myo1c	4.84	54.10	11.18	0.64	8.65
ILMN_1253304	Stmn2	4.81	137.74	28.63	0.27	9.10
ILMN_2473692	1110059G02Rik	4.81	31.28	6.51	0.64	9.10
ILMN_2923607	Phlda3	4.80	107.05	22.30	0.54	9.10
ILMN_1238331	Rom1	4.79	154.73	32.29	0.46	9.10
ILMN_1250469	Bcl9l	4.78	650.33	136.03	0.46	9.10
ILMN_2507400	9330180L10Rik	4.77	53.34	11.19	0.62	9.10
ILMN_3161897	Dync1li2	4.76	80.60	16.93	0.62	9.10
ILMN_2686087	Cutc	4.74	50.46	10.64	0.55	9.10
ILMN_1229828	Adamts10	4.72	32.02	6.79	0.57	9.10
ILMN_2700408	Mgll	4.71	45.83	9.72	0.46	9.10
ILMN_2624451	4933407C03Rik	4.71	193.57	41.08	0.45	9.10
ILMN_2474515	9430020K01Rik	4.68	42.93	9.17	0.66	9.10
ILMN_1259753	Sp4	4.67	31.44	6.73	0.59	9.10
ILMN_2727481	Palmd	4.66	261.30	56.11	0.57	9.10
ILMN_2597769	Igf2	4.65	190.26	40.93	0.29	9.10
ILMN_2697760	Nkx2-3	4.65	63.00	13.56	0.58	9.10
ILMN_2622354	Arfl4	4.65	30.19	6.50	0.57	9.10
ILMN_2838317	Pqlc3	4.63	32.01	6.91	0.55	9.10
ILMN_2604029	Klf2	4.62	118.69	25.69	0.27	9.10
ILMN_1246346	B230107H12Rik	4.62	37.68	8.16	0.63	9.10
ILMN_1222365	2610200O14Rik	4.61	34.86	7.56	0.62	9.10
ILMN_1251524	Them4	4.58	27.08	5.91	0.66	9.10
ILMN_2993109	Ddit4	4.58	343.37	75.01	0.63	9.10
ILMN_2646166	Ndrl	4.57	110.74	24.23	0.64	9.10
ILMN_2729153	Nos3	4.56	129.94	28.49	0.45	9.45
ILMN_1237671	Setmar	4.56	43.57	9.56	0.50	9.45
ILMN_2634689	Itgb4	4.55	122.74	26.97	0.40	9.45
ILMN_1217061	Casp9	4.54	95.47	21.03	0.64	9.45
ILMN_2833781	Pwwp2b	4.54	76.92	16.96	0.52	9.45
ILMN_2857957	Mgll	4.53	41.95	9.26	0.48	9.45
ILMN_1232928	Timp3	4.52	366.95	81.19	0.55	9.45
ILMN_2622500	Zbtb7c	4.52	209.94	46.49	0.19	9.45
ILMN_1249637	Peg13	4.51	25.91	5.75	0.64	9.45
ILMN_2765047	Chrd	4.50	62.48	13.88	0.37	9.45
ILMN_1217606	1500005K14Rik	4.50	75.17	16.71	0.39	9.45
ILMN_2683095	Ap1g2	4.48	89.31	19.91	0.67	9.45
ILMN_2498731	E030024M20Rik	4.48	198.90	44.37	0.33	9.45
ILMN_1232295	Sort1	4.47	75.52	16.89	0.66	9.45
ILMN_2614889	B3gnt8	4.46	250.68	56.27	0.28	9.45
ILMN_2602185	9/9/2009	4.44	141.84	31.92	0.50	9.45
ILMN_2661299	Pmp22	4.44	20.82	4.68	0.66	9.45
ILMN_2504268	Gcap26	4.40	113.00	25.68	0.24	9.45
ILMN_2620233	Fmo5	4.38	28.06	6.41	0.57	9.45
ILMN_2876579	Ubxd1	4.37	94.21	21.57	0.57	9.45
ILMN_3144575	Itgb4	4.36	182.41	41.81	0.43	9.45
ILMN_2755424	Bcorl1	4.36	50.23	11.52	0.60	9.45
ILMN_2880906	Pdlim2	4.36	201.44	46.22	0.29	9.45
ILMN_2798993	Nr1d2	4.35	76.58	17.59	0.66	9.45
ILMN_2702547	4930519N16Rik	4.34	48.97	11.29	0.40	9.45
ILMN_2759563	2410008K03Rik	4.34	54.93	12.66	0.54	9.45
ILMN_2583163	D430023I21Rik	4.33	34.78	8.03	0.62	9.45
ILMN_2674367	Agrn	4.31	206.43	47.88	0.49	9.45
ILMN_3138157	Arl6ip2	4.30	34.42	8.00	0.55	9.92
ILMN_2615557	Dab2ip	4.30	277.58	64.54	0.62	9.92
ILMN_1238479	Mgst3	4.30	40.69	9.47	0.66	9.92
ILMN_1228942	Cd59a	4.28	193.36	45.16	0.45	9.92
ILMN_2846812	Sp100	4.28	85.94	20.08	0.57	9.92
ILMN_2664224	Ephx1	4.28	122.70	28.70	0.51	9.92
ILMN_2419858	E230020D15Rik	4.27	33.59	7.87	0.61	9.92
ILMN_2416876	Gm967	4.26	77.39	18.17	0.44	9.92
ILMN_2913089	Brd9	4.25	55.60	13.08	0.65	9.92
ILMN_2741464	Fgd5	4.23	74.06	17.50	0.50	9.92
ILMN_2702997	Thap7	4.23	58.84	13.92	0.42	9.92
ILMN_1242571	Pkn3	4.21	369.99	87.85	0.54	9.92
ILMN_1227126	Ppp2r3a	4.21	20.51	4.88	0.65	9.92
ILMN_2790188	4921533L14Rik	4.20	143.07	34.07	0.41	9.92
ILMN_2742627	Six2	4.19	54.10	12.91	0.57	9.92
ILMN_1256136	Nme7	4.19	34.40	8.22	0.56	9.92
ILMN_1222004	Rbbp9	4.17	32.90	7.89	0.55	9.92
ILMN_2418725	Zdhhc3	4.17	35.63	8.54	0.54	9.92
ILMN_2706268	Scara3	4.17	84.36	20.24	0.48	9.92
ILMN_1225835	Mfap5	4.17	206.03	49.44	0.33	9.92

ILMN_2633275	Golt1b	-4.70	-20.69	4.41	1.52	9.92
ILMN_1257019	BC037034	-4.69	-178.07	37.97	1.66	9.92
ILMN_2507890	Ddx27	-4.66	-59.63	12.79	1.79	9.92

Table S2. Common mechanosensitive genes between 12hr and 48hr

Up-regulated (LCA/RCA)	Down-regulated (LCA/RCA)
Ctgf	2310046K01Rik
Ctps	BC020535
Fosl2	Dab2ip
Got2	Dhh
Lmo4	E030024M20Rik
	Eln
	F2rl1
	Icam2
	Id1
	Inmt
	Klf2
	Klf4
	Klk10
	Kras
	Lims2
	Lsr
	P4ha2
	Pdlim2
	Ptprj
	Rab11fip5
	Rhpn2
	Slc9a3r2
	Tek
	Timp3

Table S3. Taqman qPCR probes

Assay Type	Gene Name	Assay ID
Angpt2,mCG1200	angiopoietin 2	Mm00545822_m1
Bcam,mCG4887	basal cell adhesion molecule	Mm00522338_m1
Bmp4,mCG4634	bone morphogenetic protein 4	Mm00432087_m1
Cd300a,mCG13614	CD300A antigen	Mm00468054_m1
Col4a3,mCG118161	collagen, type IV, alpha 3	Mm00483656_m1
Ctgf,mCG6745	connective tissue growth factor	Mm01192931_g1
Cxcl12,mCG133006	chemokine (C-X-C motif) ligand 12	Mm00445553_m1
Cxcl16,mCG21161	chemokine (C-X-C motif) ligand 16	Mm00469712_m1
Dhh	desert hedgehog	Mm03053542_s1
Dusp8,mCG130915	dual specificity phosphatase 8	Mm00456230_m1
Emp2,mCG123874	epithelial membrane protein 2	Mm00801709_m1
Epas1,mCG20417	endothelial PAS domain protein 1	Mm00438717_m1
Hdc,mCG2100	histidine decarboxylase	Mm00456104_m1
Icam1,mCG14043	intercellular adhesion molecule 1	Mm00516023_m1
Igf2,mCG11082	insulin-like growth factor 2	Mm00439565_g1
Jam2,mCG129050	junction adhesion molecule 2	Mm00470197_m1
Klf2,mCG18931	Kruppel-like factor 2 (lung)	Mm00500486_g1
Klk10,mCG22144	kallikrein related-peptidase 10	Mm00505112_m1
Lat2,mCG16701	linker for activation of T cells family, member 2	Mm00499104_m1
Mif, mCG3124	macrophage migration inhibitory factor,macrophage migration inhibitory factor-like	Mm01611157_gH
Nos3,mCG16477	nitric oxide synthase 3, endothelial cell	Mm00435204_m1
Pprc1,mCG10300	peroxisome proliferative activated receptor, gamma, coactivator-related 1	Mm00521078_m1
Pthlh,mCG7104	parathyroid hormone-like peptide	Mm00436057_m1
Ramp2,mCG20228	receptor (calcitonin) activity modifying protein 2	Mm00490256_g1
Rhpn2,mCG113678	rhophilin, Rho GTPase binding protein 2	Mm00518451_m1
Tgfb1,mCG7649	transforming growth factor, beta 1	Mm03024053_m1
Tyrobp,mCG22805	TYRO protein tyrosine kinase binding protein	Mm00449152_m1
Vcam1,mCG19764	vascular cell adhesion molecule 1	Mm01320970_m1

Table S4. SYBR Green qPCR probes

Gene Symble	Gene ID	Gene Name	Forward primer 5'-3'	Reverse primer 5'-3'
Ankrd25	NM_145611.4	Mus musculus KN motif and ankyrin repeat domains 2	CCAGGTCCTGCATGTGCCCG	TCCAGGTCCAGGCGGTAGCC
Arhgef15	NM_177566.3	Mus musculus Rho guanine nucleotide exchange factor (GEF) 15	GGCCCAGCAGGTTCCTGACC	ACCTGGGGTGGGGAAGGCTC
Ctps	NM_016748.2	Mus musculus cytidine 5'-triphosphate synthase	TCCCTGGGGTGCCAGGACTC	ATGGCGAGGGCAACCACAGC
Cyb5r3	NM_029787.2	Mus musculus cytochrome b5 reductase 3	GTGCGTGAGGCCACCGTCTC	GGTGATGGCCGGTGTGGAGC
ICAM2	NM_010494.1	Mus musculus intercellular adhesion molecule 2	CACGGTGTCCCCTGTGCAGC	CGTGGCTGTGGCCTCTTGGG
KLF4	NM_010637.3	Mus musculus Kruppel-like factor 4 (gut	GCAGGTGCCCCGACTAACCG	CTGCACCAGCTCCGCCACTC
Lims2	NM_144862.3	Mus musculus LIM and senescent cell antigen like domains 2	ACGCCAACTGGCATCCTGGC	TTGTGGCAAGGCCGGCAGAG
Lmo4	NM_010723.3	Mus musculus LIM domain only 4 (Lmo4)	GCCGGCTCCCTCTCCTGGAA	GGACGTGCCAATGTCGCCCA
Mfap5	NM_015776.2	Mus musculus microfibrillar associated protein 5	GGCCACCGGCAGACAGATCG	CCGCGTTGACCACTGACCCC
Pak4	NM_027470.3	Mus musculus p21 protein (Cdc42/Rac)-activated kinase 4	CCAGGAGGACCCCAGGAGGC	GTGGTCCGTGTCAGCCCGTG
Plec1	NM_201394.2	Mus musculus plectin 1 (Plec1), transcript variant 11	TCAGAGCCTCCGAGGGCAAGA	GGTTGTGGCCATCACGGAGGTC
Plek2	NM_013738.3	Mus musculus pleckstrin 2 (Plek2)	ACGGCGTGCTCAAGGAAGGC	CCTTGGGCGGGGTTACTCGC
Ptprj	NM_008982.5	Mus musculus protein tyrosine phosphatase, receptor type, J	TGCCCCACAGTCCCCTTCCC	CTTCCTCCCCACCCCCACCC
Rab11fip5	NM_001003955.2	Mus musculus RAB11 family interacting protein 5 (class I)	AGTGGGATCCTGGCCCCTGC	TCTCCCTGGGGCTCTGTCGC
Sgcd	NM_011891.4	Mus musculus sarcoglycan, delta (dystrophin-associated glycoprotein)	CTGCGTCTGCGCCAATGGGA	TGCTGCCGGCAATTGTCCACT
Slc9a3r2	NM_023055.2	Mus musculus solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2	GGGCGAGACGCATCACCAGG	AGTGCAGGTCAGTTGCCGCC
Tek	NM_013690.2	Mus musculus endothelial-specific receptor tyrosine kinase	ACTTGCCGCATGCTCAGCCC	TCGGGCCCCCACTTCTGAGC
Timp3	NM_011595.2	Mus musculus tissue inhibitor of metalloproteinase 3	GCTGGAGCCTTGGGCACTGG	AGGGCCCCTCCTTCACCAGC

Table S5. Overrepresented Gene Ontology categories regulated by flow-disturbance in mouse carotid endothelium

12hr post-ligation	*No. of Genes*	*48hr post-ligation*	*No. of Genes*
Diseases and Disorders		**Diseases and Disorders**	
Developmental Disorder	10	Immunological Disease	40
Cancer	9	Inflammatory Response	75
Immunological Disease	4	Connective Tissue Disorders	22
Cardiovascular Disease	6	Inflammatory Disease	36
Respiratory Disease	4	Skeletal and Muscular Disorders	34
Molecular and Cellular Functions		**Molecular and Cellular Functions**	
Cellular Growth and Proliferation	12	Cellular Movement	70
Cellular Development	20	Cell-To-Cell Signaling and Interaction	76
Cell Morphology	12	Antigen Presentation	30
Cellular Function and Maintenance	6	Cellular Function and Maintenance	44
Cell Cycle	4	Cellular Growth and Proliferation	73

Table S6. Comparison of flow-sensitive genes found in vivo mouse carotid endothelium to cultured HUVEC

Gene Symbol	Gene Name	Carotid 48hr (LCA/RCA) microarray	Carotid 48hr (LCA/RCA) qPCR	HUVEC 24hr (OS/LS) microarray	Congruency
Downregulated (LCA/RCA)					
KLK10	kallikrein related-peptidase 10	0.10	0.01	ND	N
Col4a3	collagen, type IV, alpha 3	0.22	0.11	ND	N
Bcam	basal cell adhesion molecule	0.23	0.10	0.81	Y
Pthlh	parathyroid hormone-like peptide	0.24	0.08	0.06	Y
Rhpn2	rhophilin, Rho GTPase binding protein 2	0.26	0.12	1.52	N
KLF2	kruppel-like factor 2	0.27	0.06	0.37	Y
Dusp8	dual specificity phosphatase 8	0.27	0.12	0.70	Y
KLF4	kruppel-like factor 4	0.28	0.06	0.12	Y
IGF2	insulin-like growth factor 2	0.29	0.15	0.78	Y
Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2	0.32	0.11	0.22	Y
Ptprj	protein tyrosine phosphatase, receptor type, J	0.33	0.13	ND	N
Mfap5	microfibrillar associated protein 5	0.33	0.13	0.94	N
Dhh	desert hedgehog	0.36	0.11	0.16	Y
Emp2	epithelial membrane protein 2	0.40	0.22	1.09	N
Lims2	LIM and senescent cell antigen like domains 2	0.40	0.09	0.45	Y
Jam2	junction adhesion molecule 2	0.40	0.17	0.45	Y
Pak4	p21 (CDKN1A)-activated kinase 4	0.42	0.36	0.78	Y
Ramp2	receptor (calcitonin) activity modifying protein 2	0.44	0.16	0.33	Y
NOS3	nitric oxide synthase 3	0.46	0.28	0.25	Y
ICAM2	intercellular adhesion molecule 2	0.48	0.19	1.04	N
Plek2	pleckstrin 2	0.50	0.24	0.52	Y
Epas1	endothelial PAS domain protein 1	0.50	0.20	0.59	Y
Ankrd25	ankyrin repeat domain 25	0.52	0.22	ND	N
Sgcd	sarcoglycan, delta	0.52	0.16	0.97	N
Tek	endothelial-specific receptor tyrosine kinase	0.53	0.23	0.30	Y
Timp3	tissue inhibitor of metalloproteinase 3	0.55	0.30	1.26	N
Arhgef15	Rho guanine nucleotide exchange factor (GEF) 15	0.60	0.29	1.12	N
Cyb5r3	cytochrome b5 reductase 3	0.61	0.40	0.71	Y
Plec1	plectin 1	0.62	0.36	0.50	Y
Rab11fip5	RAB11 family interacting protein 5 (class I) (Rab11fip5), transcript variant 1	0.65	0.56	0.73	Y
Upregulated (LCA/RCA)					
Angpt2	angiopoietin 2	8.44	7.81	4.53	Y
Ctgf	connective tissue growth factor	6.00	22.88	3.87	Y
Cd300a	CD300A antigen	4.31	11.36	ND	N

Tyrobp	TYRO protein tyrosine kinase binding protein	3.64	37.05	ND	N
Cxcl12	chemokine (C-X-C motif) ligand 12	3.43	4.33	1.14	N
Cxcl16	chemokine (C-X-C motif) ligand 16	2.20	1.74	0.56	N
Ctps	cytidine 5'-triphosphate synthase 2	1.98	1.64	1.63	Y
Lmo4	LIM domain only 4	1.70	1.87	1.18	N
VCAM1	vascular cell adhesion molecule 1	1.53	1.90	0.87	N
BMP4	Bone morphogenetic protein 4	1.37	1.25	4.57	Y
					23/42

Table S7. Comparison of gene expressions between different microarray studies

Gene Symbol	Gene Name	Mouse Carotid 48hr (LCA/RCA) microarray	HUVEC 24hr (OS/LS) microarray	HUVEC 24hr (RF/HSS) microarray	Pig Aorta (DF/UF) microarray	Category *
Downregulated (LCA/RCA)						
KLK10	kallikrein related-peptidase 10	0.10	ND	ND	NA	**-**
Col4a3	collagen, type IV, alpha 3	0.22	ND	ND	NA	**-**
Bcam	basal cell adhesion molecule	0.23	0.81	1.60	NA	**b**
Pthlh	parathyroid hormone-like peptide	0.24	0.06	0.23	NA	**b,c**
Rhpn2	rhophilin, Rho GTPase binding protein 2	0.26	1.52	1.56	NA	**-**
KLF2	kruppel-like factor 2	0.27	0.37	0.69	NA	**b,c**
Dusp8	dual specificity phosphatase 8	0.27	0.70	0.57	NA	**b,c**
KLF4	kruppel-like factor 4	0.28	0.12	0.45	0.59	**a,b,c**
IGF2	insulin-like growth factor 2	0.29	0.78	0.63	2.18	**b,c**
Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2	0.32	0.22	0.63	NA	**b,c**
Ptprj	protein tyrosine phosphatase, receptor type, J	0.33	ND	0.98	NA	**-**
Mfap5	microfibrillar associated protein 5	0.33	0.94	ND	NA	**-**
Dhh	desert hedgehog	0.36	0.16	1.37	NA	**b**
Emp2	epithelial membrane protein 2	0.40	1.09	0.76	NA	**c**
Lims2	LIM and senescent cell antigen like domains 2	0.40	0.45	0.45	NA	**b,c**
Jam2	junction adhesion molecule 2	0.40	0.45	0.59	NA	**b,c**
Pak4	p21 (CDKN1A)-activated kinase 4	0.42	0.78	1.12	NA	**b**
Ramp2	receptor (calcitonin) activity modifying protein 2	0.44	0.33	0.73	NA	**b,c**
NOS3	nitric oxide synthase 3	0.46	0.25	0.44	0.78	**b,c**
ICAM2	intercellular adhesion molecule 2	0.48	1.04	0.75	NA	**c,**
Plek2	pleckstrin 2	0.50	0.52	0.53	NA	**b,c**
Epas1	endothelial PAS domain protein 1	0.50	0.59	0.71	NA	**b,c**
Ankrd25	ankyrin repeat domain 25	0.52	ND	0.58	NA	**c**
Sgcd	sarcoglycan, delta	0.52	0.97	ND	NA	**-**
Tek	endothelial-specific receptor tyrosine kinase	0.53	0.30	0.36	NA	**b,c**
Timp3	tissue inhibitor of metalloproteinase 3	0.55	1.26	ND	NA	**-**
Arhgef15	Rho guanine nucleotide exchange factor (GEF) 15	0.60	1.12	0.82	NA	**-**
Cyb5r3	cytochrome b5 reductase 3	0.61	0.71	1.75	NA	**b**

Plec1	plectin 1	0.62	0.50	1.69	NA	**b**
Rab11fip5	RAB11 family interacting protein 5 (class I) (Rab11fip5), transcript variant 1	0.65	0.73	0.70	NA	**b,c**
Upregulated (LCA/RCA)						
Angpt2	angiopoietin 2	8.44	4.53	1.69	0.61	**b,c**
Ctgf	connective tissue growth factor	6.00	3.87	0.79	1.59	**b**
Cd300a	CD300A antigen	4.31	ND	2.02	NA	**c**
Tyrobp	TYRO protein tyrosine kinase binding protein	3.64	ND	2.04	NA	**c**
Cxcl12	chemokine (C-X-C motif) ligand 12	3.43	1.14	0.65	NA	**-**
Cxcl16	chemokine (C-X-C motif) ligand 16	2.20	0.56	1.84	NA	**c**
Ctps	cytidine 5'-triphosphate synthase 2	1.98	1.63	1.06	NA	**b**
Lmo4	LIM domain only 4	1.70	1.18	0.97	NA	**-**
VCAM1	vascular cell adhesion molecule 1	1.53	0.87	ND	NA	**-**
BMP4	Bone morphogenetic protein 4	1.37	4.57	0.91	NA	**b**

***** **a** : gene expression is consistent between mouse and pig (2)

b : gene expression is consistent between mouse and HUVEC (OS/LS) (23)

c : gene expression is consistent between mouse and HUVEC (RF/HF) (21)

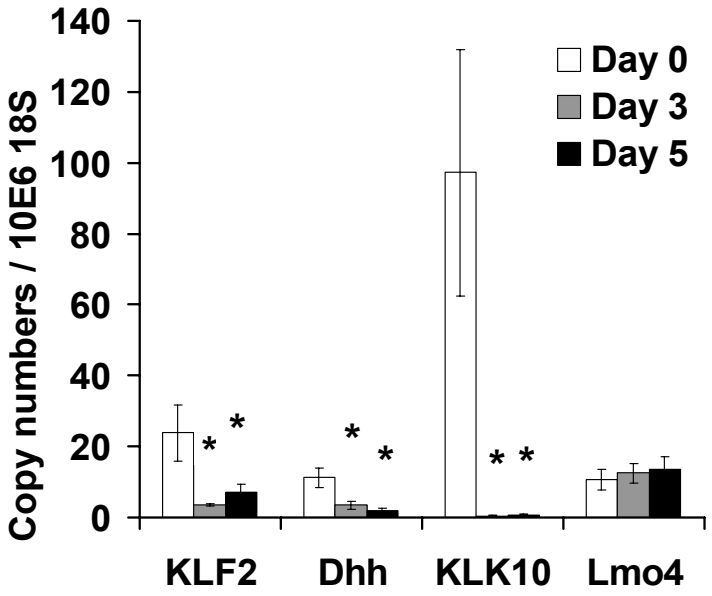

Fig. S1 Endothelial expression of *KLF2, Dhh, and KLK10, but not Lmo4*, decreased during *ex vivo* tissue culture. Mouse carotid rings were incubated *ex vivo* in a growth medium. Intimal RNAs were collected after 0, 3, and 5 days during culture. qPCR analyses were carried out to examine the mRNA levels of *KLF2, Dhh, KLK10 and Lmo4.* mRNA copy numbers were normalized against 18S and were shown as mean± SEM (n=3), * $p<0.05$ (vs. Day 0).

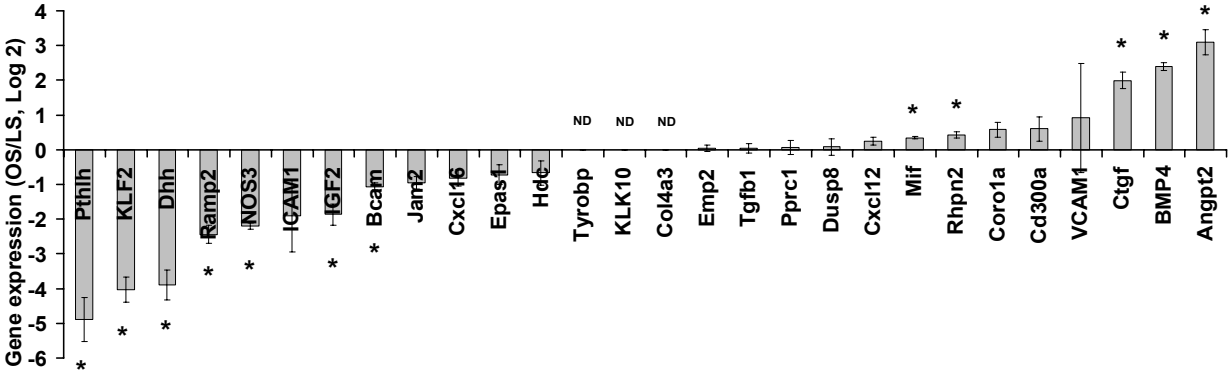

Fig. S2 Validation of shear-sensitive mRNAs in HUVEC by qPCR. Total RNAs were collected from HUVECs exposed to OS or LS for 24hr. qPCR analysis was then performed using SYBR green with custom design primers. mRNA copy numbers were normalized against 18S and are shown as mean± SEM (n=4). p*< 0.05 (OS vs, LS). ND is not detectable in qPCR.

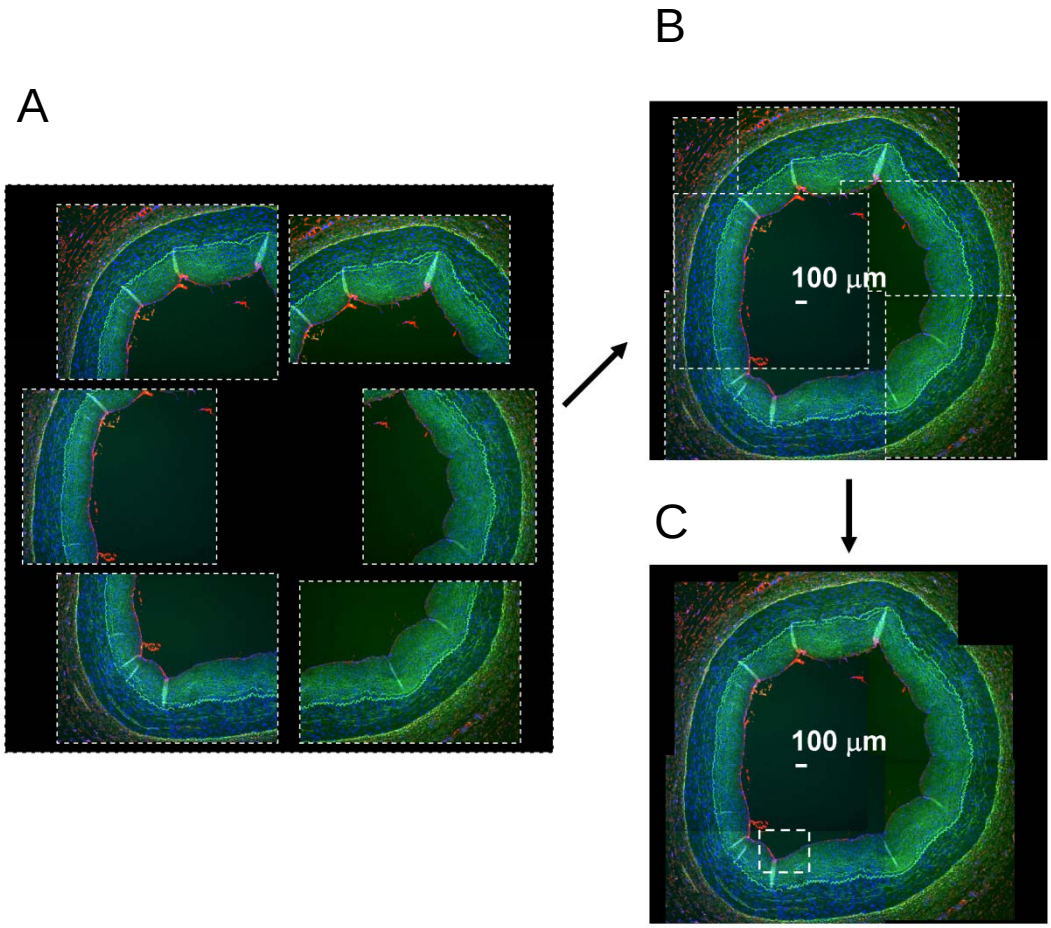

Fig. S3. The raw images of the composite figure shown in Fig 4B. Paraffin sections of human left anterior descending coronary artery were stained for Lmo4 protein expression. A) Fluorescence photomicroscopic images were taken from six different but overlapping regions of the stained section. B) The six images were then overlapped together to make a composite image in order to show an overall staining pattern of the entire coronary artery section. C) White dashed lines indicate the edges of each image. C. White dashed lines were removed for a cleaner view and the final picture is shown in Figure 4B.