

## Supplements

**Table S1**

### 275 Gene List

Gene	Accession number	Position	Target sequence
ABCA1	NM_013454.3	6866-6965	CTCCTTGTCTCTCTAGCCAGGATATTCAGCATCCTCTCCCAGAGCAAAAAGCGACTCCACATAGAAGACTACTCTGTCTCTCAGACAACACTTGACCAA
ACAT1	NM_144784.3	1331-1430	TGCTGATTGAGAAGCTGTAGACAACCTGTTTTAGGAGACAGTTCCATGTGACCGGCTGAAGTAAATGTGACTCCCTGGGCCAGGTTATATTCAGCATAA
ACE	NM_009598.1	326-425	AGATCCTGCTTGAGAAAAGCACGGAGGTATCCAATCACACCCTGAAATATGGCACCCGGGCCAAGACATTTGATGTGAGCAACTTTCAAACCTCTTCCAT
ACTA2	NM_007392.2	46-145	GGAACCCTGAGACGCTGCTCCAGCTATGTGTGAAGAGGAAGACAGCACAGCCCTGGTGTGCGACAATGGCTCTGGGCTCTGTAAGGCCGGCTTCGCTGGT
ACTB	NM_007393.1	816-915	CAGGTCATCACTATTGGCAACGAGCGGTTCCGATGCCCTGAGGCTCTTTCCAGCCTTCTTCTTGGGTATGGAATCCTGTGGCATCCATGAAACTACAT
ACTN4	NM_021895.2	270-369	CAGCCTGGTGCAACTCTCATCTTCGGAAGGCTGGCCTCAGATCGAGAATATCGATGAGGACTTCAGGGATGGGCTCAAACCTTATGCTTCTGTTGGAGGT
ACVRL1	NM_009612.2	2986-3085	AGAGAAGTGAAGTGTAGGCGAGGCTTAAGAAGGGTAAAGCAGGGTTCAGGCAAGAGACAAGGTCAGCCTCATCTTGGGAAGACCTGGCCTAGAAACTAT
EMR1	NM_010130.1	996-1095	TGATGAGTGCACCCAAGATCCATTACAATGTGGACTGAATTCTGTCTGCACCAATGTACCAGGCTCCTACATCTGTGGCTGCCTCCCTGACTTTCAAATG
ADIPOQ	NM_009605.4	781-880	GACCACAATGGACTCTATGCAGATAACGTCAACGACTCTACATTTACTGGCTTTCTTCTCTACCATGATACCAACTGACTGCAACTACCCATAGCCCATA
AGER	NM_007425.2	362-461	CAACTACCGAGTCCGAGTCTACCAGATTCTGGGAA GCCAGAAATTGTGGATCCTGCCTCTGAACTCACAGC CAGTGTCCCTAATAAGGTGGGGACATGT
AGT	NM_007428.3	882-981	CACTTCCAAGGAACGATGAGAGGTTTCTCTCAGCTG CCTGGAGTCCATGAATTCTGGGTGGACAACAGCATC TCGGTGTCTGTGCCCATGATCTCCGGCA
AGTR1A	NM_177322.3	1668-1767	AAGGACAAGTCAGGAGCTGGATGGATTTGTGGGTT TAAAACGGTTTGCTGGCAGACACGCAATCGCAGCG GTCTCCTTTTGATTTCCACACATAGGTATG
AGTR2	NM_007429.4	986-1085	TTCTGACCTTCTTGGATGCTCTGACCTGGATGGGTA TCATTAATAGCTGTGAAGTTATAGCAGTCATTGACC TGGCACTTCTTTTGCCATCCTCCTGGG
ANGPT2	NM_007426.3	2021-2120	GAAGAATGTTCCGTGGGAGTTCAGCAGTAAATAACT GGAAAACAGAACACTTAGATGGTGCAGATAAATCTT GGGACCACATTCCTCTAAGCACGGTTTC
APLN	NM_013912.3	2627-2726	TATTCAGGAGGGCATTCTTTTTCTCCTAGGGCCAAT CTTGTCCCTGTGCCACAGATTGCACGTGTAGGGA GGTGAGTGCTTGATCCCAAATTGGTTCT
APOB	NM_009693.2	6331-6430	CCAGACTATTTGGAGAGAAATCGAAGAGGAATGATA AGTCTACTGGAAGCCATGCGAGGGGAATTGCAACG CCTCAGTGTTGATCAGTTTGTGAGGAAAT

APOE	NM_009696. 2	11-110	CGGAAGGAGCTGACTGGCCAATCACAATTGCGAAG ATGAAGGCTCTGTGGGCCGTGCTGTTGGTCACATT GCTGACAGGATGCCTAGCCGAGGGAGAGCC
AQP1	NM_007472. 1	2256- 2355	ACACTCGTCTCCGTTCCCTAGCAGACTGTACCCA CTTAACAGATAAGGGCACTGAGGACCCATATGCTCA ACTGTATCATATTGGATCAAGCTTAGCA
AR	NM_013476. 3	2216- 2315	CATGGGTTGGCGGTCCTTCACTAATGTCAACTCCAG GATGCTCTACTTTGCACCTGACTTGGTTTTCAATGA GTACCGCATGCACAAGTCTCGGATGTAC
ARG1	NM_007482. 3	627-726	GTACATTGGCTTGGCGAGACGTAGACCCTGGGGAAC ACTATATAATAAAAACTCTGGGAATTAAGTATTTCTC CATGACTGAAGTAGACAAGCTGGGGATT
B2M	NM_009735. 3	178-277	CTGAACTGCTACGTAACACAGTTCACCCGCCTCAC ATTGAAATCCAAATGCTGAAGAACGGGAAAAAATT CCTAAAGTAGAGATGTCAGATATGCTCT
B4GAT1	NM_175383. 2	1147- 1246	AGGAAAGGTGCCACATTTGACGAACGCTTTCGGC AGTATGGTTTTCAATCGAATCAGCCAGGCTTGTGAGC TGCACGTGGCAGGGTTAATTTTGAAGTG
BAX	NM_007527. 3	736-835	CATAAATTATGACATTTTCTGGGATGAATGGGGGA AGGGGAAAGGCATTTTTCTTACTTTTGTAAATTATTGG GAGGGGTGGGAATGGTGGCCTGGGGAG
BGLAP	NM_007541. 2	252-351	GTGAGCTTAACCCTGCTTGTGACGAGCTATCAGACC AGTATGGCTTGAAGACCGCCTACAAACGCATCTATG GTATCACTATTTAGGACCTGTGCTGCCC
BSG	NM_009768. 2	971- 1070	AGCACTGAAGCCAATGGCAAGTATGTGGTGGTATC CACGCCTGAGAAGTCACAGCTGACCATCAGCAACCT TGACGTAATGTTGACCCTGGCACCTACG
C5AR1	NM_007577. 3	596-695	CATTGCTCCTCACCATTCCATCCTTCGTGTACCGGG AGGCATATAAGGACTTCTACTCAGAGCACACTGTAT GTGGTATTA ACTATGGTGGGGGTAGCTT
CASP3	NM_009810. 2	631-730	GAGGCTGACTTCTGTATGCTTACTCTACAGCACCT GGTACTATTCTGGAGAAATTCAAAGGACGGGTGCG TGGTTCATCCAGTCCCTTTGCAGCATGC
CAV1	NM_007616. 3	1921- 2020	AACCCAAACTGAGGAATTTACCTGTGTACCTGAGT CTCCAGAAAGCTGCCTGCCTGGGACACCCAAAAGC CTTTTACTTCCCAGCTCACATTACAGCTC
CAV2	NM_016900. 4	361-460	CTACACACTCCTTTGACAAAGTGTGGATCTGCAGCC ATGCTCTCTTTGAAATCAGCAAATATGTGATGTACAA GTTCTGACCGTATTTCTGGCCATCCC
CCL11	NM_011330. 3	431-530	CAACCTCCTCTTTGACACTAACCCAGAGCCTAAGA ACTGCTTGATTCTTCTCTTTCTAAGACGTGCTCTG AGGGAATATCAGCACCAGTCGCCAAG
CCL12	NM_011331. 1	1-100	TTTCGAAGTCTTTGACCTCAACATGAAGATTTCCACA CTTCTATGCCTCCTGCTCATAGCTACCACCATCAGT CCTCAGGTATTGGCTGGACCAGATGCG
CCL19	NM_011888. 2	466-565	CTTCTGCCAAGAACAAGGCAACAGCACCAGAAGG AGCCCTGTGTCTTGAGTAAAGAGATGTGAATCACTC TGGCCCAGGAAACCAAGGACCAGAAGAGA
CCL2	NM_011333. 3	416-515	TCTTCAGCACCTTTGAATGTGAAGTTGACCCGTA TCTGAAGCTAATGCATCCACTACCTTTTCCACAACCA CCTCAAGCACTTCTGTAGGAGTGACCA
CCL20	NM_016960. 1	121-220	GCAGCAAGCAACTACGACTGTTGCCTCTCGTACATA CAGACGCCTCTTCTTCCAGAGCTATTGTGGGTTTC ACAAGACAGATGGCCGATGAAGCTTGTG
CCL22	NM_009137. 2	1097- 1196	CCAAGAATCAACTTCCACCCCTTCAACCATGC TAGGGTCTTTTACTTTCTCTGCCCCACACCTTTGACT

			CCTTGCCTGTGTAGCTGATAGTCGAAG
CCL26	NM_0010134 12.2	141-240	CAGCTATAAGTTCACCGACAAGAGCTGCACCAAGTGA CGGTGTGATATTCTTTACAAAAACAGGTAAGCAATT CTGTGTCCAGCCAGGGGCCAAATGGGTG
CCL3	NM_011337. 1	61-160	TCTGTCACCTGCTCAACATCATGAAGGTCTCCACCA CTGCCCTTGCTGTTCTTCTCTGTACCATGACACTCTG CAACCAAGTCTTCTCAGCGCCATATGG
CCL5	NM_013653. 1	166-265	CCTCGTGCCACGTCAAGGAGTATTTCTACACCAGC AGCAAGTGCTCCAATCTTGACAGTCGTGTTTGTCACT CGAAGGAACCGCCAAGTGTGTGCCAACCC
CCL7	NM_013654. 2	216-315	ACAGAAGGATCACCAGTAGTCGGTGTCCCTGGGAA GCTGTTATCTTCAAGACAAAGAAGGGCATGGAAGTC TGTGCTGAAGCCCATCAGAAGTGGGTCTGA
CCL9	NM_011338. 2	1126- 1225	ATGGCAACCCAGGTACATTCAACTAGGATGAAATAA ATTCTGCCTTAGCCCAGTAGTATGTCTGTGTTTGTAA GGACCCAGCTGATTTTCCCACCACCCC
CCR1	NM_009912. 4	1527- 1626	CTTCTGATT CAGACCATAGGTGTCAACCAAGGAAGG TCTAAGAAGAGAATGAGGAGACAGTATATAGCTCTC CAAGACTGATACTGACAGTTCTTACAGT
CCR2	NM_009915. 2	2966- 3065	ATGAACTAACATAGACAGCTCAGGATTAACAGGGAC TTGTGTTTTGTGGTCTGTGGGCTTATCCAAGCATGG TGATTTAGACTCTAAGGTCCGTCTGGAT
CD163	NM_053094. 2	3226- 3325	TCACGGCACTCTTGGTTTGTGGAGCCATTCTATTGG TCCTCCTCATTGTCTTCTCCTGTGGACTCTGAAGC GACGACAGATT CAGCGACTTACAGTTTC
CD36	NM_007643. 3	1521- 1620	GGGACCATTGGTGATGAAAAAGCAGAAATGTTCAA ACACAAGTGACTGGGAAAATCAAGCTCCTTGGCATG GTAGAGATGGCCTTACTTGGGATTGGAG
CD38	NM_007646. 4	1491- 1590	TATTCACATGGTAAACCTGAGGTCATAGGGTCATTA TAGGGAAGGTGCTGTGTGGGAACTACCCACGTGCC CTGTGCTTTAATCTTTAACTCAACACATC
CD4	NM_013488. 2	951- 1050	AAGAGGTGTCCGTACAAAAGTCCACCAAAGACCTCA AGCTCCAGCTGAAGGAAACGCTCCCCTCACCCTCA AGATACCCAGGTCTCGCTTCAGTTTGC
CD68	NM_009853. 1	637-736	AGCCCGAGTACAGTCTACCTGGACTACATGGCGGT GGAATACAATGTGTCCTTCCACAGGCAGCACAGTG GACATTCATGGCGCAGAATTCATCTCTTC
CD80	NM_009855. 2	211-310	TGGCTTTCCCATCATGTTCTCAAAGCATCTGAAG CTATGGCTTGCAATTGTCAGTTGATGCAGGATACAC CACTCCTCAAGTTTCCATGTCCAAGGCT
CD86	NM_019388. 3	252-351	CAAAACATAAGCCTGAGTGAGCTGGTAGTATTTTGG CAGGACCAGCAAAAGTTGGTTCTGTACGAGCACTAT TTGGGCACAGAGAACTTGATAGTGTGA
CD8A	NM_0010811 10.2	356-455	CCACCTTCGTTGTCTATATGGCTTCATCCCACAACAA GATAACGTGGGACGAGAAGCTGAATTCGTGAAAC TGTTTTCTGCCATGAGGGACACGAATAA
CDH1	NM_009864. 2	1611- 1710	TCGAAGTGCCCGAAGACTTTGGTGTGGGTGTCAGGAA ATCACATCTTATACCGCTCGAGAGCCGGACACGTTT ATGGATCAGAAGATCACGTATCGGATTTG
CDH5	NM_009868. 3	1616- 1715	CAGCAACTTCACCCTCATAAACAACCATGACAACAC CGCCAACATCACGGTCAAGTATGGGCAGTTTAATCG GGAGCATGCCAAGTTCCACTACCTGCC
CDKN1A	NM_007669. 4	1671- 1770	AATACCGTGGGTGTCAAAGCACTTAGTGGGTCTGAC TCCAGCCCCAACATCCCTGTTTCTGTAACATCCTG GTCTGGACTGTCTACCCTTAGCCCGCAC
CIDEB	NM_009894.	180-279	ATCCACTGTGAGCTCGGAGTTAAGCCGTAGGGTCT

	3		GGAACTCAGCTCCTCCACCTCAGCGACCCTTCCGTG TCTGTGATCATAAGCGGACAGTCCGGAAA
CIDEC	NM_178373. 3	1516- 1615	GTAACCTAAAAGCTCATAGATTCACCAAGCTGGACT TGGGTGAAACCGCGGCTTAGCCTCTCATTGCCTGAA TGGACACAGTTCCTGTTCTCCTGGGAAA
CMA1	NM_010780. 2	861-960	GAGGGAGAATTAAGTCTGGAGCTTTTGCCAGCCTGT GAGGAAATCTGGAAGTGAATAGTGCAGGTTTTGT GTGCCATGCGATCTGGCCTGTCTGTAGTT
COL1A1	NM_007742. 3	216-315	CAATGGTGAGACGTGGAACCCGAGGTATGCTTGA TCTGTATCTGCCACAATGGCACGGCTGTGTGCGATG ACGTGCAATGCAATGAAGAACTGGACTGT
COL1A2	NM_007743. 2	4026- 4125	GCTGTGCTTCTGCAGGGTTCCAACGATGTTGAACTT GTTGCTGAGGGCAACAGCAGGTTACCTACTCTGTC CTAGTCGATGGCTGCTCCAAAAAGACAA
COL3A1	NM_009930. 1	4371- 4470	CAAGACAGTCTTTGAATATCAAACACGCAAGGCAAT GAGACTACCCATCATAGATATCGCACCTATGACAT TGGGGTCTGATCAAGAATTTGGTGTG
COL4A1	NM_009931. 2	6111- 6210	CATGGTGTCTGATAATGAGCCCTGTGCCTGGCGCTT CTTGCTTCTGCTCTGCGTGGAGTATTTTCAGGGTTT GCAACACTAACCACAGACTGAATGACTG
COL4A2	NM_009932. 3	5601- 5700	TTGTGGCAAACCTCCTGCCTCAGCTTCCCAGATGCT GGGATTATGGGCATGCGCCACCACACCAGCTTGG TGCTTACTCTTAACTTATTACCTCAGATG
CPM	NM_027468. 1	1245- 1344	TATCCAATCCTTCGTGCCCGATGATTCCGCTGTACA AATTCATGCCAAGCCACTCGGCTGCCACAAAGCCTA GTCTGGGCGTGTTCATGACTCTTTT
CRP	NM_007768. 4	164-263	TTGTATTTCCCAAGGAGTCAGATACTTCTATGTGTC TCTGGAAGCAGAGTCAAAGAAGCCACTGAACACCTT TACTGTGTGTCTCCATTTCTACTGTC
CSF1	NM_0011135 30.1	834-933	TCCAGCTGCTGGAGAAGATCAAGAAGTCTTTAATG AAACAAAGAATCTCCTTAAAAGGACTGGAACATTT TTACCAAGAAGTGAACAACAGCTTTGC
CSF2	NM_009969. 4	733-832	CTGAATCCAGCTTCTCAGACTGCTGCTTTTGTGCCT GCGTAATGAGCCAGGAACTTGGAAATTTCTGCCTTAA AGGGACCAAGAGATGTGGCACAGCCACA
CTGF	NM_010217. 2	2241- 2340	GGCTCAGGGTAAGGTCCGATTCCTACCAGGAAGTG CTTGCTGCTTCTTTGATTATGACTGGTTTGGGGTGG GGGGCAGTTTATTTGTTGAGAGTGTGACC
CTSG	NM_007800. 1	786-885	CTATGGAAGCAACAATGGTAACCCTCCAGCTGTATT CACCAAAATCCAGAGCTTCATGCCCTGGATCAAAG AACAATGAGACGCTTTGCACCAAGATAT
CTSK	NM_007802. 4	1201- 1300	GCGCTCCTGAGAGGGACGCAGCGATGCTAACTAAG ATTGTTTCATTTCTCCTCTCGTTGGTGTCTCCAGTGA CAACTTACTTCCCTTCTCTGCCCAG
CTSS	NM_021281. 2	741-840	AGACGCTTCTATCCCTACAAAGCCACGGATGAAAA GTGTCATAACTCAAAAAATCGAGCTGCCACGTG TTCAAGGTACATTCAGCTCCCGTTTGGT
CX3CL1	NM_009142. 3	126-225	CGTTCCTCCATTTGTGTAATCTGCTGCCGGGTGAGC ACCTCGGCATGACGAAATGCGAAATCATGTGCGAC AAGATGACCTCACGAATCCCAGTGGCTTT
CX3CR1	NM_009987. 3	2697- 2796	TCCTGTGTTGGTTGTGATAACCATTTCAGAAGTCTCT CCCAGCCTGTTGCTCACGGCGGCATGTCTGATATCT CCTTGGCAGTCTGTATGTTTGTGTCGA
CXCL1	NM_008176. 1	561-660	TGCTAGTAGAAGGGTGTGTCGAAAAGAAGTGCA GAGAGATAGAGTTTAGTATTATGTTTTGTATGTATTA GGGTGAGGACATGTGTGGGAGGCTGTGT

CXCL10	NM_021274.1	116-215	AGGACGGTCCGCTGCAACTGCATCCATATCGATGAC GGGCCAGTGAGAATGAGGGCCATAGGGAAGCTTGA AATCATCCCTGCGAGCCTATCCTGCCAC
CXCL11	NM_019494.1	346-445	TTAAGGCGTCAAACATGTGACATCCTGGGAACGTC TGACTGTGAGCCCTCAATAAGAACTCTGTGCCAGG AACCTGACCCTCTGCTGTCTTGGAACAT
CXCL12	NM_021704.3	260-359	CTGAAAATCCTCAACTCCAACTGTGCCCTTCAG ATTGTTGCACGGCTGAAGAACAACAACAGACAAGT GTGCATTGACCCGAAATTAAGTGGATCC
CXCL2	NM_009140.2	766-865	GGTGGGGGTGGGGACAAATAGATGCAGTCGGATG GCTTTCATGGAAGGAGTGTGCATGTTACATCATTT TTTTGTAAGCACCGAGGAGAGTAGAACAGC
CXCL5	NM_009141.2	566-665	CCCAGTGAAGATAAGAAGAAAGGGCTGATTCTCTCC ACCCACGGATTTTCTTTATGAACTCCCTGCTTTGATG AGAAAAGGGAAACCATTGTCCCTGAAG
CXCL9	NM_008599.2	41-140	TAGAACTCAGCTCTGCCATGAAGTCCGCTGTTCTTT TCCTCTGGGCATCATCTTCTGGAGCAGTGTGGAG TTCGAGGAACCCTAGTGATAAGGAATGC
CYBB	NM_007807.2	1536-1635	ACAGAAGACTCTGTATGGACGGCCCAACTGGGATA ACGAGTTCAAGACCATTGCAAGTGAACACCCTAACA CCACAATAGGCGTTTTCTGTGTGGCCCT
DCN	NM_001190451.1	1320-1419	CCAAACACCTTCAGATGTGTCTATGTGCGTTCTGCC ATTCAACTTGAAACTACAAGTAACCCTCAGACGGC CTAATTCTTATAATCTGGAAAAACACCC
DPP4	NM_001159543.1	1304-1403	AAGAGGGGATCACTATTTATGTGATGTGGTGTGGG CTACAGAAGAAAGAATTTCACTACAGTGGCTCAGGA GGATTCAGAACTATTCCGTGATGGCTATC
EDNRA	NM_010332.2	1915-2014	CGCATGTCATTTCCAACACTTGAAAATTAGAGCTGG GAGAAAGGAGATGATGGTTCAAAGAAGCCACCTAG CTGCCGCTTTGCATGAACACAGAGTTTG
EDNRB	NM_001136061.2	973-1072	ACAGTGCTGAGTCTTTGTGCTCTAAGTATTGACAGA TATCGAGCTGTTGCTTCTGGAGTCGAATTAAGGA ATTGGGGTTCCAAAATGGACAGCAGTAG
EGFR	NM_207655.2	1336-1435	TGCTACAAACATCAAACACTTCAAATACTGCACTGC CATCAGCGGGGACCTTCACATCCTGCCAGTGGCCTT TAAGGGGATTCTTTCACGCGCACTCCT
ELANE	NM_015779.2	492-591	AGGTTGGGCACAAACAGACCATCACCCAGTGTGCT ACAAGAGCTCAATGTGACAGTGGTGACTAACATGTG CCGCCGTCTGTGAACGTATGCACTCTGG
ESM1	NM_023612.3	1006-1105	GAACTTGAGATGGCCTTGCTGTGATGAGTAATCCA ATCAAAGCTGAAGGACCGACCGGTGGTTTCATTGAC CTGGGTGCACATTCTTATTGTGATACAG
ETS1	NM_001038642.1	741-840	GAAAGAGGATGTGAAACCATATCAGGTTAATGGAG CCAACCCTACCTACCCAGAATCCTGTTACACCTCGG ATTACTTCATCAGCTACGGTATCGAGCAT
F3	NM_010171.3	1171-1270	AGAGAGGCTGCCTTCATGGCCTGTTACTCCAGCTAA CGCTTTGATTCAAACACTAGCATTTGTCACGTTAGG ACGAACTGAAACGGTACAAACTGGTTAA
FASN	NM_007988.3	6561-6660	TTCTCCTCTGTAAGCTGCGGGCGTGGTAATGCTGGC CAAATAACTACGGCTTCGCCAACTCTACCATGGAG CGTATATGTGAACAGCGCAGGCACGATG
FAIM3	NM_026976.2	191-290	ATGCCCACTCCCTCAACTACACGTAAGGATGTATCT GTGTCGGCAGATGGCCAAACCTGGGATATGCTCCA CTGTGGTGTCCAACACCTTTGTCAAGAAG
FGA	NM_010196.3	1376-1475	TGGCGATGCCACCGAGTTAGACATATCCCACAGTTT TAGCGGCAGTCTCGACGAACTCTCTGAAAGGCATCC

			TGACCTTTCTGGGTTTTTTGACAACCAC
FGF2	NM_008006.2	288-387	CTCTACTGCAAGAACGGCGGCTTCTTCTGCGCATC CATCCCACGGCCGCGTGGATGGCGTCCGCGAGAA GAGCGACCCACACGTCAAACATAACTCC
FGF9	NM_013518.3	1071-1170	ATTAGCAGTGCCGTCACCTCAGCTCCACTGTTGCCA AACTTTGTCGCATGCATATGAATGATGGAAGCTTGG ATGAGGACTTGCCAATTTGCTCTGCACT
FGG	NM_133862.1	1106-1205	ACGCAGGCCACCTCAATGGAGTTTATCACCAAGGTG GTACTIONTCAAATCATCTACTACTAATGGTTTCGA CGACGGCATTATTTGGGCGACCTGGAA
FN1	NM_010233.1	2628-2727	TCCAGACCCTACCGTGGACCAGGTTGATGATACTTC CATTGTTGTTGCGTGGAGTAGACCCAGGCACCTAT CACAGGGTATAGAATTGTCTATTACCT
FOXC1	NM_008592.2	2161-2260	CCCTGCCAGTCAGTCTCTGTACCGCACGTCCGGGG CTTTCGTCTATGACTGTAGCAAATTTGACCCTATT CCGGCACTCTTAGAGCCAAATGGAATGG
GAPDH	NM_001001303.1	891-990	AGTTTGTCTCCTGCGACTTCAACAGCAAACCTCCACT CTTCCACCTTCGATGCCGGGGCTGGCATTGCTCTCA ATGACAACCTTTGTCAAGCTCATTTCCTG
GCG	NM_008100.3	311-410	GCCCAAGATTTTGTGCAGTGGTTGATGAACACCAAG AGGAACCGGAACAACATTGCCAAACGTGATGATGAA TTTGAGAGGCATGCTGAAGGGACCTTA
GCGR	NM_008101.2	1311-1410	GCACCCTGCGCTCCACCAAGCTTTTTTTGACCTGT TCCTCAGCTCCTCCAGGGTCTGCTGGTGGCTGTT TCTACTGTTTCTCAACAAGGAGGTGCA
GIPR	NM_001080815.1	469-568	TGATGGCCAGTGGGGATCTTGAGAGACCACACTC AGTGTGAGAATCCAGAGAAGAATGGGGCTTTTCAG GACCAGACGCTGATCCTGGAGCGCCTGCAG
GLP1R	NM_021332.2	408-507	AGAGAACTTTCTGAGGAACAGCTCCTGTCCCTGT ACATTATCTACACAGTGGGGTACGCACTTTCTTTCT CGCCTTGGTCATCGCTTCAGCCATCCT
GLP2R	NM_175681.3	1109-1208	TGTTATTCCCTGGATTTTGTCCGAGCAAGCCTGGA GAATACAGGGTGTGGGCAGTAAATGAGAATAAGA AAATCTGGTGGATCATCAGAGGACCCATT
GMFG	NM_001039192.1	643-742	TATCTGCAAAATCTGAGCCTCTTTGTTGGTGCCGCC GGACAGTCCCTACAGTTCCAACCTTTGGCCGGGAGG GGCGGACGTTTCCAGCGAAACCAAGCTG
GREM1	NM_011824.4	1086-1185	GAGGGCTGCATTAGACTCGGAACTGTTCACTGCTC GCCCTATGCTCCCATAGCCCATCCCTTTCTTTGCTCT CCCTGACATCTCAGTCGTAGCCCATGTT
GUSB	NM_010368.1	1736-1835	AATACGTGGTCCGAGAGCTCATCTGGAATTTGCGCG ACTTCATGACGAACCAGTCAACGCTGAGAGTAATCG GAAACAAGAAGGGGATCTTCACTCGCCA
GZMB	NM_013542.2	1021-1120	TTCTGCCACCATGCTGTGACAACCAACTGACATCT TCCTATGGAAGTTTGCCTCTCCACAAAAGAAGTAG AATGTTTGCATTGGAGCTGGGCATGCTC
KIM-1	NM_134248.2	116-215	CATGTACTTACTCAACATATCGTGGAAATCACAACGA CATGTTGGGGCCGAGGGCAATGCCCATCTTCTGCTT GTCAAATAACACTTATTTGGACCAATGG
HIF1A	NM_010431.2	1295-1394	ACCATGATATGTTTACTAAAGGACAAGTCACCACAG GACAGTACAGGATGCTTGCCAAAAGAGGTGGATAT GTCTGGGTTGAAACTCAAGCAACTGTCAT
HMOX1	NM_010442.2	611-710	CTGGGGAGGGCCTGGCTTTTTTTACCTTCCCGAACA TCGACAGCCCCACCAAGTTCAAACAGCTCTATCGTG CTCGAATGAACACTCTGGAGATGACACC
HPRT	NM_013556.	31-130	TGCTGAGGCGGCGAGGGAGAGCGTTGGGCTTACCT

	2		CACTGCTTTCCGGAGCGGTAGCACCTCCTCCGCCG GCTTCCTCCTCAGACCGCTTTTTGCCGCGA
HSPG2	NM_008305. 3	6163- 6262	CACGCATTCAGGTGGTCGTCCTCTCAGCTTCGGGTG CCAACCTCAGTGCCAGTCAGGATAGAATCCTCGTCGC CATCCGTGACTGAAGGACAGACGCTTGA
ICAM1	NM_010493. 2	2196- 2295	CACATGGGTCGAGGGTTTTCTCTACTGGTCAGGATG CTTTTCTCATAAGGGTTCGACTTTTTTACCAGTCACA TAAACACTATGTGGACTGGCAGTGGTTC
IFNG	NM_008337. 1	96-195	CTAGCTCTGAGACAATGAACGCTACACACTGCATCT TGGCTTTGCAGCTCTTCTCATGGCTGTTTCTGGCT GTTACTGCCACGGCACAGTCATTGAAAG
IGF1R	NM_010513. 2	3391- 3490	CGTATGAGAACTTCATGCATCTGATCATTGCTCTGC CGTTGCCATCCTGCTGATCGTTGGGGGGCTGGTT ATCATGCTGTATGTCTTCCATAGAAAGAG
IGFBP3	NM_008343. 2	1646- 1745	ATGTTCTAGGGCACTCTGGGAGCCCATAAGGACAA GGATAAGGACCTTTCTTTGTGAGGCATCTTCTTGAT GACTTGGCCCAGCAGAAAGCCCCAAGTGG
IL10	NM_010548. 1	986- 1085	GGGCCCTTTGCTATGGTGTCTTTCAATTGCTCTCA TCCCTGAGTTCAGAGCTCCTAAGAGAGTTGTGAAGA AACTCATGGGTCTTGGGAAGAGAAACCA
IL-11	NM_008350. 2	286-385	GCGCTGGGACATTGGGATCTTTCAGCTTCCTGGT GTGCTGACAAGGCTTCGAGTAGACTTGATGTCCTAC CTCCGGCATGTACAATGGCTGCGCCGTGC
IL12A	NM_008351. 1	356-455	TCATGAAGACATCACACGGGACCAAACCAGCACATT GAAGACCTGTTTACCACTGGAACCTACACAAGAACGA GAGTTGCCTGGCTACTAGAGAGACTTCT
IL12B	NM_008352. 1	1046- 1145	TCGTAGAGAAGACATCTACCGAAGTCCAATGCAAAG GCGGGAATGTCTGCGTGCAAGCTCAGGATCGCTAT TACAATTCCTCGTGCAGCAAGTGGGCATG
IL13	NM_008355. 2	426-525	AGCTACACAAAGCAACTGTTTCGCCACGGCCCCTTC TAATGAGGAGAGACCATCCCTGGGCATCTCAGCTGT GACTCATTTTTCTTTCTCACATCAGAC
IL17A	NM_010552. 3	206-305	ACCTCAAAGTCTTTAACTCCCTTGGCGCAAAAGTGA GCTCCAGAAGGCCCTCAGACTACCTCAACCGTTCCA CGTCACCCTGGACTCTCCACCGCAATGA
IL18	NM_008360. 1	271-370	ACTTTGGCCGACTTCACTGTACAACCGCAGTAATAC GGAATATAAATGACCAAGTTCTCTTCGTTGACAAAA GACAGCCTGTGTTGAGGATATGACTGA
IL1A	NM_010554. 4	226-325	ACCTCTGAAACGTCAAAGATGTCCAACCTTCACCTTC AAGGAGAGCCGGGTGACAGTATCAGCAACGTCAAG CAACGGGAAGATTCTGAAGAAGAGACGGC
IL1B	NM_008361. 3	1121- 1220	GTTGATTCAAGGGGACATTAGGCAGCACTCTCTAGA ACAGAACCTAGCTGTCAACGTGTGGGGGATGAATT GGTCATAGCCCGCACTGAGGTCTTTTATT
IL1R1	NM_0011233 82.1	821-920	CTTCTTCGGAGTAAAAGATAAACTGTTGGTGAGGAA TGTGGCTGAAGAGCACAGAGGGGACTATATATGCC GTATGTCCTATACGTTCCGGGGGAAGCAA
IL1RN	NM_031167. 5	225-324	CAACCAGCTCATTGCTGGGTACTTACAAGGACCAAA TATCAAACCTAGAAGAAAAGATAGACATGGTGCCTAT TGACCTTCATAGTGTGTTCTTGGGCATC
IL2	NM_008366. 2	486-585	GCAACTGTGGTGGACTTTCTGAGGAGATGGATAGC CTTCTGTCAAAGCATCATCTCAACAAGCCCTCAATA ACTATGTACCTCCTGCTTACAACACATAA
IL22	NM_016971. 1	478-577	AGAAGAATGTCAGAAGGCTGAAGGAGACAGTGA AAGCTTGGAGAGAGTGGAGAGATCAAGGCGATTGG GAACTGGACCTGCTGTTTATGTCTCTGAG

IL2RA	NM_008367.2	326-425	AAGGAATTGGTCTATATGCGTTGCTTAGGAACTCC TGGAGCAGCAACTGCCAGTGCACCAGCAACTCCCA TGACAAATCGAGAAAGCAAGTTACAGCTC
IL2RB	NM_008368.3	2366-2465	TTATTTTATGTGTTCTTGGGCGATGCTGGTCTATGTA AGGGGTGGGGGCGCGGGGTTGATTGAAGTGAGGG CTCCTTCTATGTTGCTTTGGGGACCTTGT
IL3	NM_010556.4	156-255	TGCAGCTCTATTGTCAAGGAGATTATAGGGAAGCTC CCAGAACCTGAACTCAAACCTGATGATGAAGGACCC TCTCTGAGGAATAAGAGCTTTCGGAGAG
IL33	NM_133775.1	1012-1111	ATGACTTACGGCGTTGGTAAAGAACTGAAGGAGA TTCAGCCTTGCTCTTTCCTTTTCTCTGCCTTGAGTCC TGTATGAAATCACACTCACGGACTTCAG
IL4	NM_021283.1	346-445	TGCTTGAAGAAGAACTCTAGTGTTCATGGAGCTG CAGAGACTCTTTCGGGCTTTCGATGCCTGGATTCA TCGATAAGCTGCACCATGAATGAGTCCA
IL6	NM_031168.1	41-140	CTCTCTGCAAGAGACTTCCATCCAGTTGCCTTCTTG GGACTGATGCTGGTGACAACCACGGCCTTCCCTACT TCACAAGTCCGGAGAGGAGACTTCACAG
IL7	NM_008371.2	1056-1155	AAACATTCATTGGTGAACCACTGGGGGAGTGGAAC TGTCTGTTTTAGACTGGAGATACTGGAGGGCTCAC GGTGATGGATAATGCTCTTGAAAACAAGA
INSR	NM_010568.2	1083-1182	CACTGTCATCAATGGGCAGTTTGTGGAACGGTGCT GGACACACAGTCATTGTCAGAAAGTTTGCCCAACCA TCTGTAAGTCACATGGCTGCACAGCTGAA
IRS1	NM_010570.4	2136-2235	CCACTTCAGACTGTCTTCCCAGGGCGCTCTAGTG CTTCCGTGTCCGTTTCGCCTAGCGATGGCGGTTTCA TCTCTTCTGATGAGTATGGTTCTAGTCC
IRS2	NM_001081212.1	3877-3976	GGCACTGGAGCTTTGCCCTCTGCCAGCACCTATGCA AGCATCGACTTCCCTGTCCCATCACTTGAAGGAAGCC ACAGTCGTGAAAGAGTGAAGCGCTACCA
ITGA1	NM_001033228.3	2551-2650	ATTGAAGTCTAAAGAAGACTCAGTTTACGAGGCTGA TCTGCAGTACCGTGTCAACCCTTGATTGCTGAGGCA GATATCACGGAGCTTTTTTTCTGGAAC
ITGA3	NM_013565.2	1066-1165	AAGGACTGGGATTTATCTGAATATAGCTACAGGGGC TCAGAGGAGCAAGGAAACCTTTATATTGGGTACACG GTGCAGGTAGGCAACGCCATCCTACATC
ITGA4	NM_010576.3	6601-6700	AATTTGTTGAGACCACTGGTCACTTGGACAGTCCCT TACTTCAACAGGGTGGAGCTTTGATCTTCAGGCTAC TGGCCTTAGTCATCTGACAAGACTTAGA
ITGA5	NM_001314041.1	2623-2722	CCTCAGCAAGAACCTGAACAACCTCACAAAGCAACGT GGTCTCCTTCCCACTCTCGGTGGAGGCTCAAGCCCA GGTCTCCCTTAATGGTGTCTCCAAGCCT
ITGAM	NM_001082960.1	3026-3125	ATCCCTGTTTCAAGTCAACAATGTGACCGTATGGGAT CATCCCCAGGTCATCTTCTCCCAGAACCTCTCAAGT GCCTGTCACACTGAGCAGAAATCCCCC
ITGAX	NM_021334.2	328-427	GGGCCTGTCCCTTGCTGCTGCCACCAACCCTTCTTG GCTGTTGGCTTGTGGTCTACTGTGCACCACACATG CAGAGAGAATATATACTTGACAGGGCTC
ITGB1	NM_010578.1	1856-1955	CTGTGATAGGTCTAATGGCTTAATTTGTGGAGGCAA TGCGGTGTGCAGGTGTCGTGTTTGTGAATGCTATCC CAATTACACTGGCAGTGCATGTGACTGT
ITGB2	NM_008404.4	2543-2642	GCTCGGTTTCTTCCGCCATTATATCAAGTCTGCCA GGGTTTCCAGGGACTTGTCTTCCGACCTGCACAATC TTGCCGCAGAGCCCTAAGAATTGTCCCG
KCP	NM_001029985.4	595-694	GCCGGCCAGGCTGTGAATATGAAGGGCAGCTTAC CAGGAAGGGTCTAGTTTCTTGCCAGTTCCAACCCA



			TGCCTCCAGTGCTCTTGCCTGAGGAGCCT
NEPH1	NM_0011709 85.1	1247- 1346	CTTGATTGAAGACGCCCATGAGAGTCGCTATGAGAC AAACGTTGACTATTCCTTCTTCACGGAGCCTGTGTC TTGTGAGGTTTATAACAAAGTCGGGAGC
NEPH2	NM_0011909 14.1	113-212	TCCGAGTGGGCACATTGCTAAGGATCCCGGCTTCC CGAGGCGACTGAAAACAAGCATTTGGTTTCGGCTG CCTGCAGATACCCGGAGACACAACGAGACC
KITL	NM_013598. 1	281-380	CTGCGGGAATCCTGTGACTGATAATGTAAAAGACAT TACAAAAGTGGTGGCAAATCTTCAAATGACTATAT GATAACCCTCAACTATGTGCGCCGGGATG
KLF2	NM_008452. 2	106-205	ACCCGAGGCGGGCGGCACGGATGAGGACCTAAAC AACGTGTTGGACTTCATCCTCTCCATGGGATTGGAC GGTCTGGGCGCCGAAAATCCTCCCGAGCCC
KLF4	NM_010637. 3	2398- 2497	GACTGGAAGTTTGTGGATATCAGGGTATACACTAAA TCAGTGAGCTTGGGGGGAGGGAAGACCAGGATTCC CTTGAATTGTGTTTCGATGATGCAATACA
KRT18	NM_010664. 1	10-109	GAACTCCTGTTCTGGTCTCTCGCTTCGCTCTCCTCTC CAGACAAGATGAGCTTCACAACTCGCTCCACCACCT TCTCCACCAACTACCGGTCCCTGGGCT
KRT8	NM_031170. 2	1490- 1589	CGCACCACCAAGGCTGTGGTTGTGAAGAAGATTGA AACCCGAGATGGGAAGCTGGTGTCCGAGTCTTCTG ATGTCGTGTCCAAGTGAATGGCCACTGAAG
LAMB1	NM_008482. 2	1971- 2070	GAGTCATTGTGGTGGAAAGGCAGTACATTGAGGAC CGCATTCTTCTGGACAGGACCTGGGTTTCGTCCG GGTGCCTGAAGGGGCTTATTTGGAGTTTTT
LAMC1	NM_010683. 2	1046- 1145	GTTCTCAAGTCTTACTATTACGCAATCTCAGACTTTG CTGTGGGCGGCAGGTGTAATGTAACGGACATGCC AGCGAGTGTGTAAGAACGAGTTTGACA
NGAL	NM_008491. 1	191-290	GCAGGCAATGCGGTCCAGAAAAAACAGAAGGCAG CTTTACGATGTACAGCACCATCTATGAGCTACAAGA GAACAATAGCTACAATGTCACCTCCATCC
LEP	NM_008493. 3	1116- 1215	CCTATTGATGGGTCTGCCAAGGCAAACCTAATTTT TGAGTGACTGGAAGGAAGGTTGGGATCTTCCAAAC AAGAGTCTATGCAGGTAGCGCTCAAGCTT
LEPR	NM_010704. 2	3187- 3286	TGTTCTGGGCACAAGGACTGAATTTCCAAAAGGTC ACTGTTTAAGTATTTTAACCCAGATATCTAAGGTTGC AGTTTAGATGCCACAGTACTTACAGAT
LEPR	NM_146146. 2	3999- 4098	TCACAAGATAATGGAGAATAAGATGTGTGACTTAAC TGTGTAATCTCATCCAAGAAGCCTCAAGGTTCCATT CCAGTAGAGCCTGTCATGTATAATGTGT
LGALS3	NM_0011459 53.1	1006- 1105	CATCCATTTAATAAAGTCTCATGCTGAGAGATACCC ATCGCTTTGGGGGTTTTTATGATACTGGATGTCAA TCTTAGGACTGCTCGTGACTGCTAGGCA
LIF	NM_008501. 2	3436- 3535	ACATCTTTCACCTGGAAGCATTGACTTCCACCGAGC ATAGTAGGTAGTGTGTCTGGACCAGAGAAAAAGGG ATGGGGCATTGTCAGTTTATCCAGAGAG
LOXL2	NM_033325. 2	3701- 3800	TTCCACTTGGCGCTCTGGTCTTCCAAACTCCCACCA CAATAACCCATTGAGTTCTGTTCTCTAAAAGCGCTCT AGGGCTTCTGGACCCAAAGTTCTAAGT
LPL	NM_008509. 1	2806- 2905	CCATGCTGTAACCAAGTCTGGCCTAGAATAAATA TGTATTTGAGGCTGGCCTGAACTCTCAACCATCCT GCCTTAGCTTCTGTGTCCTGGGAGCTT
LY6C1	NM_010741. 3	52-151	AACCCTTCTGAGGATGGACACTTCTCACACTACA AAGTCCTGTGTGCTCATTCTTCTGTGGCCCTACTG TGTGCAGAAAGAGCTCAGGGACTGCAGT
MEF2C	NM_0011705	4342-	TTCTACTACTAAAGGTATCAATGGAACATGAAGACG

	37.1	4441	AGTATTTAGGCAGAAGCAAAACAGGAAACCATCCTT ACAAACATGCTTACCTGCACATCTGTTT
MMP12	NM_008605. 3	593-692	AAGGTGGTACACTAGCCCATGCTTTTTATCCTGGAC CTGGTATTCAAGGAGATGCACATTTTGATGAGGCAG AAACGTGGACTAAAAGTTTTCAAGGCAC
MMP13	NM_008607. 1	191-290	ACAGTGACCTCCACAGTTGACAGGCTCCGAGAAAT GCAATCTTTCTTTGGCTTAGAGGTGACTGGCAAAT TGATGATCCCACCTTAGACATCATGAGAA
MMP14	NM_008608. 3	555-654	AGTTTGGGACTGAGATCAAGGCCAATGTTTCGGAGG AAGCGCTATGCCATTCAGGGCCTCAAGTGGCAGCA TAATGAGATCACTTTCTGCATTCAGAATTA
MMP1A	NM_032006. 3	955- 1054	ACATTCGGGTAAATAGATTCATGCCAGAACCTGAGC TCAATTTAATAGGTATTCTCTGGCCAAATCTTCCAGT TAAACTTGACGCTGCTTATGAAGCTAG
MMP2	NM_008610. 2	2377- 2476	AGTTAACAGCCTTCTCCTTCACCTGGTGACTTCAG ATTTAAGAGGGTGGCTTCTTTTTGTGCCAAAGAAA GGTGCTGACTGTACCCTCCCGGGTGCTG
MMP3	NM_010809. 1	1576- 1675	TCTTTGTGAAAGGAAGTGCTTTGTTTCAGCATGTGCT ATGGCAGAACCAAACAGGAGCTATGGATGACACCA GTCAACGTCAAGTTGTCAAAGGATGTTCA
MMP7	NM_010810. 4	351-450	CACCTACAGAATTGTATCCTATACTTCAGACTTACCT CGGATCGTAGTGGATCAAATCGTGAAAAAAGCTCTC AGAATGTGGAGTATGCAGATCCCCTG
MMP8	NM_008611. 4	2286- 2385	GGAGGGCTGTATCTATAAATCTATTTGCCAATAAGT TCCAGGCAGAGGCAGGTAGGAGGGGTTTAAAAAA AAGGACCATTCTTTCTCAAGCACATTCC
MMP9	NM_013599. 2	1571- 1670	CCTCTACAGAGTCTTTGAGTCCGGCAGACAATCCTT GCAATGTGGATGTTTTTGATGCTATTGCTGAGATCC AGGGCGCTCTGCATTTCTTCAAGGACGG
MPO	XM_0065324 04.1	1389- 1488	CAGTACCGATCTTACAACGACTCAGTAGACCCTCGA ATCGCCAATGTCTTACCAACGCTTCCGTTATGGC CACACCCTCATCCAACCCTTCATGTTCC
MRC1	NM_008625. 1	3993- 4092	GTTCCGAAATGTTGAAGGGAAGTGGCTTTGGTTGAA CGACAATCCTGTCTCCTTTGTCAACTGGAAAACAGG CGATCCCTCTGGTGAACGGAATGATTGT
MSR1	NM_0011133 26.1	556-655	GATTTTCGTAGTCCAGGAACATGGGAATTCCTGGA TGCAATCTCCAAGTCTTGCAGAGTCTGAATATGAC ACTGCTTGATGTTCAACTCCATACAGAA
MTOR	NM_020009. 2	2433- 2532	CATGGAGCCTATCCTGAAGGCTTTAATTTTGAAACT GAAAGATCCAGACCCTGACCCAAACCCGGGCGTGA TCAATAACGTGTTGGCCACTATAGGAGAA
NFE2L2	NM_010902. 3	1666- 1765	CCAAGGAGCAATTCAATGAAGCTCAGCTCGCATTGA TCCGAGATATACGCAGGAGAGGTAAGAATAAAGTC GCCGCCAGAACTGTAGGAAAAGGAAGCT
NFKB1	NM_008689. 2	2126- 2225	GTCTTACACTTAGCCATCATCCACCTCCACGCTCAG CTTGTGAGGGATCTGCTGGAAGTCACATCTGGTTTG ATCTCTGATGACATCATCAACATGAGAA
NGF	NM_0011126 98.1	631-730	CAAGGAGGTGACAGTGCTGGCCGAGGTGAACATTA ACAACAGTGTATTCAGACAGTACTTTTTTGAGACCA AGTGCCGAGCCTCCAATCCTGTTGAGAGT
NID1	NM_010917. 2	735-834	AAAGCCAAGTACCTGCTGTGGTTGGTTTCAGCAAAG GTCTAGTAGGATTTCTATGGAAGAGCAACGGAGCCT ATAACATATTTGCCAATGACAGAGAATC
NID2	NM_008695. 2	2587- 2686	GGCCCTAATTCTGTGTGTGTCAACTTGGTGGGAAGC TACAGGTGTGAATGCCGCAGTGGCTATGAATTTGCA GATGACCAGCACACTTGTATCTTGATCG

NLRP3	NM_145827.3	509-608	ACGTGTACATCACATTCTCTATGGTATGCCAGGAG GACAGCCTTGAAGAAGAGTGGATGGGTTTGCTGGG ATATCTCTCCCGCATCTCCATTTGTA AAA
NOS2	NM_010927.3	3716-3815	CCCCCTCCTCCACCCTACCAAGTAGTATTGTACTAT TGTGGACTACTAAATCTCTCTCCTCTCCTCCCTCCCC TCTCTCCCTTTCTCCCTTCTTCTCC
NOS3	NM_008713.4	3614-3713	ATACCTGGTTCCTGACAGTCTTCTCCCTCCAGTT CCCGAAAGAGGGATTGTGTCACTTCGTTTCGGTTG ACCAAGGCTAGCCACCCTCTCTGAAGAAT
NOX1	NM_172203.1	476-575	CTCCAAACATGACAGTGATGTATGCAGCATTTACCA GTATTGCTGGCCTTACTGGAGTGATTGCCACTGTAG CTTTGGTTCTCATGGTAACGTCAGCTAT
NOX3	NM_198958.2	1241-1340	CAGATGTATTTCACTACCCCGTGAGCGTGTGCATTG CAACGGGAATTGGAGTCACTCCCTTCGCCTCTCTTC TGAAGTCTGTGTGGTATAAGTGTGTGA
NOX4	NM_015760.4	501-600	TCCAGAAAGCTTCTCTTCAACAACCATTCTGGTCT GACGGGTGTCTGCATGGTGGTGGTATTGTTCTCAT GGTTACAGCTTCTACCTACGCAATAAGA
NPHS1	NM_019459.2	382-481	TGGAAGGAGACAGTGCTAAAGGTGAGTTCCACCTG CTTATTGAAGCCTGTGACCTCAGCGATGATGCGGAG TACGAGTGCCAAGTCGGCCGCTCCGAGTT
NPHS2	NM_130456.3	551-650	GGTTGATCTCCGTCTCCAGACCTTGGAAATACCTTT CCATGAGGTGGTAACCAAGATATGTTTATAATGGA GATAGACGCTGTCTGCTACTACCGCATG
NPNT	NM_001029836.1	2651-2750	ATGGTGACCTGTCATCTATGCTATGACTTAAACCAG CAGCAAGAAAAGTGGCAAAGGTGTGCGGCTTGGGG TAGTGTGATGATGGCTTTGTTTCTGTGTC
OLR1	NM_138648.1	1491-1590	TGCCTCCTGTTGCTGCATGAAAGACAGGATGTAGAA ATCCTCCTCAAGTGCAGGCAGAGGGCTCAAAGGCA AAGCTCGTCCGAGAAATAACATGCAAAGA
OSM	NM_001013365.2	580-679	CACGGTCCACTACAACACCAGATGTCTTTAATACCA AGATAGGCAGCTGTGGCTTTCTCTGGGGATAACCATC GCTTCATGGGCTCAGTGGGGAGGGTCTT
PCSK9	NM_153565.2	2789-2888	CAGGAAGATCATAATGGACAGAGATCCTTGGAGGT TCAAAGACCAAGTACCAGACTGGAAAATTGAGTCTG AAAGCCACAAGGACAGTCAACTCACAGCC
PDGFA	NM_008808.3	806-905	TGTGCGTGCGGTGTGACATTCTGAACATACTATGT ATGGTGCTTCATTGCCAATGTGCGTGCAGTCTTTGT TCTCCTCCGTGAAAAGTGTGTCCGAGG
PDGFB	NM_011057.3	2326-2425	AGCAAGGTTGTAATGGGATGTATATTGCACATGATG CACTGCGTGTGGAGACTGCTGTTACACCCTAAATA TGCCAACCTGCCTATTATGACGTTCTG
PDGFC	NM_019971.2	1166-1265	GTTGTCACTATATCTGGTAATGGGAGCATCCACAGC CCGAAGTTTCTCATAACATACCCAAGAAATATGGTG CTGGTGTGGAGATTAGTTGCAGTAGATG
PDGFD	NM_027924.2	157-256	ACGCGATCCCTAGGTCGCTGAGCCCAAATGCAACG GCTCGTTTTAGTCTCCATTCTCCTGTGCGGCAACTTT AGCTGCTATCCGGACACTTTTGCGACTC
PDGFRB	NM_008809.1	1186-1285	CTCAAGGACAACCGTACCTTGGGTGACTCCGGCGC TGCGCAGTTAGTTTTGTCTACTCGCAACATGTCTGA GACCCGGTACGTGTCAGAACTGATCCTGG
PECAM1	NM_008816.2	1101-1200	ACACCTGCAAAGTGGAAATCAAACCGTATCTCCAAAG CCAGTAGCATCATGGTCAACATAACAGAGCTGTTTC CCAAGCCGAAGTTAGAGTTCTCCTCCAG
PLA2G5	NM_001122954.1	1541-1640	AGCCCTGGCTTCTGGCAGCTGTATGGTCTTTTAAAC CTTTGGATAGTCCGAATCTCTCTGGCTCTCCTCAA

			ATATAAAACAAGGCTCCTTCCAGGAGTA
PLAT	NM_008872.1	646-745	CCCTGGTGCTATGTCTTTAAGGCAGGGAAGTATACC ACGGAGTTCTGTAGCACACCAGCTTGCCTAAGGG AAAAAGCGAGGACTGCTATGTTGGGAAAG
PLAU	NM_008873.2	1951-2050	CAAGTCTAGGTATTTCCCTAACTCCAGACTGTGATG CGGGGCCATTTGGTCTTCCATGTGATGCTCCACGTG AATGTATCATTCCCGGGCGTGACCCGTG
PLAUR	NM_011113.3	1086-1185	TTCTTTGGACCTCAGTTTTTCCATGAACCAGAAGAG AATTGGAACAAGGGCTGCGGGCAGCAGGGGCCTCT TAGTTGAGATAATATTGTTGCTGTTATTA
PLIN2	NM_007408.3	197-296	TGCCCTTGGTGAGCTCTACCTACGACCTTGTGTCCT CCGCTTATGTCAGTACAAAGGATCAGTACCCGTATT TGAGATCCGTGTGTGAGATGGCCGAGAA
PLIN4	XM_006524705.2	2217-2316	GATACTAGCCAGAGAGTGCTGACAGGCACAAAGGA CAATGTATATGCTGGGGTCACTGGTGCAGTAAATGT GGCAAAGGTACCATCCAGGGCGGCTTGG
PLIN5	NM_001077348.1	1584-1683	CCCCTGGTGGTCATGTGACAGCACTCACGCAGGCT AGGGCTTCTGTTCCCTTCCCTGCCCTGGATGATTTT GAGGTCTAAGTGGACCTCAGCAGGTCACT
PODX1	NM_013723.3	2801-2900	GATCTAACCTACCAGGCATTATTATTATCCACAGG AAGCTCAGGGACTTTTCAAGTTGCTGAGAGCTTGGG TTGGTGTGCTGTGGTGTGTTGTGTGTGT
PPARA	NM_011144.2	1346-1445	GGACTTGAACGACCAAGTCACCTTGCTAAAGTACGG TGTGTATGAAGCCATCTTCACGATGCTGTCCTCCTT GATGAACAAAGACGGGATGCTGATCGCG
PPARG	NM_011146.1	1061-1160	ACCAAGTGACTCTGCTCAAGTATGGTGTCCATGAGA TCATCTACACGATGCTGGCCTCCCTGATGAATAAAG ATGGAGTCCCTCATCTCAGAGGGCCAAGG
PPIA	NM_008907.1	391-490	CCAAGACTGAATGGCTGGATGGCAAGCATGTGGTC TTTGGGAAGGTGAAAGAAGGCATGAACATTGTGGA AGCCATGGAGCGTTTTGGGTCCAGGAATGG
PRF1	NM_011073.2	1351-1450	ACAGCTACTGATGCCTACCTAAAGGTCTTCTTTGGT GGCCAGGAGTTCAGGACCGGTGTCGTGTGGAACAA TAACAATCCCCGGTGGACTGACAAGATGG
PROCR	NM_011171.1	306-405	GCCTGCAGATCTATCTGACCCAGTTCGAAAGCCTGG TGAAGCTGGTATATCGCGAGCGCAAGGAGAACGTG TTCTTTCTCTCACTGTTAGCTGCTCCCT
PRTN3	NM_011178.2	641-740	GCAATGGCATTCTTCATGGAGTGGACTCCTTCGTGA TCCGCGAATGCGCCTCCCTCCAGTTCCTGATTTCT TCGCCCGGGTGTCCATGTATGTGGACTG
PTGIR	NM_008967.3	1732-1831	GGTTCTATGGCTCTCAAGAAGGATTCTCTCAAATA ACCAGGGCCTGGGCAGGCTGCTCTGGCCCCTGGGC TCCTCCATCCATCTCTGTCTAAATATT
PTGIS	NM_008968.3	1065-1164	CACGGTCTGGCAAGCAGAGCAGCCTGTTTCACAGA TGACCACACTCCCACAGAAGATTCTAGACAGCATGC CTGTGCTAGACAGTGTGCTCAATGAGACA
PTGS2	NM_011198.3	676-775	CCATCAGTTTTTCAAGACAGATCATAAGCGAGGACC TGGGTTACCCGAGGACTGGGCCATGGAGTGGACT TAAATCACATTTATGGTGAAACTCTGGAC
RASGRP3	NM_001166493.1	941-1040	CATGGCTGTCTGGAGAATAACCCGACATTGGAGAG ATCTATTGCTTTATTTAATGGAATCTCTAAGTGGGTC CAGTTGATGGTTCTTAGCAAACCAAGTG
REN1	NM_031192.3	26-125	GAACCAGATGGACAGAAGGAGGATGCCTCTCTGGG CACTCTTGTTGCTCTGGAGTCTTGCACCTTCAGTC TCCAACACGCACCGCTACCTTTGAACGA
REN2	NM_031193.3	18-117	CTTTCATGGTCCCACAGGCCCTGGGGTAATAAATCA

	2		GAGCAGAGCCTGTGATACATGGTGTGTATAAAAAGA AGGCTCAGGGGGTCTGGGCTACACAGCTC
RETNLB	NM_023881. 3	530-629	GGCCTCTGCCCCGCTGCTGCCGAATGGTTTAAAGAAT GAGGAGGTTGAGAAACCAATTTCAAATGATGAGCA TAATGAAACCACGGTCTCGACCAGGAAAC
RPS18	NM_011296. 2	421-520	CAGCACACCAAGACCACTGGCCGCAGGGGCCGAAC TGTGGGTGTATCCAAGAAGAAATGAGTCTCTGGGC CTTTGCTGTTAATAAATAGTTTATATACCT
S100A8	NM_013650. 2	281-380	ATAAAAGTGGGTGTGGCATCTCACAAAGACAGCCA CAAGGAGTAGCAGAGCTTCTGGCCTAGGGCTGGGT CCCTGGATATGTCTACAGAATAAAGTCATC
S100A9	NM_009114. 2	358-457	AAAGGCTGTGGGAAGTAATTAAGAGGTCAGCCATG TGACAGCTGCCCAACCAAGTCTAAAGGGAATGGCTT ACTCAATGGCCTTTGTTCTGGGAAATGAT
S1PR1	NM_007901. 4	851-950	CTGCCCAGTGGTTTCTGCGGGAAGGGAGTATGTTT GTGGCTCTCTGTCATCAGTCTTCAGCCTCCTTGCC ATCGCCATTGAGCGCTACATCACCATGCT
SAA1	NM_009117. 3	352-451	GGCAAAGACCCCAATTACTACAGACCTCCTGGACTG CCTGACAAATACTGAGCGTCCTCCTATTAGCTCAGT AGTTTGTGCTGGGGGCCTGAGGGTGGGG
SAA2	NM_011314. 2	342-441	ACATGGCCGCAGTGGCAAAGACCCCAATTACTACA GACCTCCTGGACTGCCTGCCAAATACTGAGAGTCCT CCTATTAGTTCAGAAGGCTGTGTTGGGGT
SAA3	NM_011315. 3	253-352	TAAAGTCATCAGCGATGCCAGAGAGGCTGTTTCAGA AGTTCACGGGACATGGAGCAGAGGACTCAAGAGCT GACCAGTTTGCCAATGAGTGGGGCCGGAGT
SAA4	NM_011316. 3	1625- 1724	CGAAACAAAAGTCTGCTTTCCGCTCTAGAAGGGAAG CAAGACACAACATCACTGAGCGGGAGTAAATGAATT GGTCCCTCATAAAGCAAAGGCATTCTT
SCARB1	NM_016741. 1	671-770	CCTTGGCGCTGGTCACCATGGGCCAGCGTGCTTTTA TGAACCGCACAGTTGGTGAGATCCTGTGGGGCTAT GACGATCCCTTCGTGCATTTTCTCAACAC
SELE	NM_011345. 2	2576- 2675	TCAGTGGCTGCCGAAGTATTCTTGAACATTGTGTTT TGTGTCTGGCACTGAAGCCAGCATGAGATCCATCA TTCTTATGTCAGCTCAAGGGTCAAAGG
SELP	NM_011347. 1	1571- 1670	TGGATTGTTCTCATGTCCACGGAGAGTTTGGTGTG GCTCTATCTGTCACTTCTCCTGCAATGAGGACTTTG AGCTACTGGGATCTGAAAATGTGGAATG
SERPIND 1	NM_008223. 3	766-865	TCGAAAGCTGACCCATCGTCTATTGAGGAGGAATTT TGGGTACACACTTCGGTCAGTTAATGGCCTTTATAT TCAGAAGCAGTTTCCCATACGGGAGGAC
SERPINE 1	NM_008871. 2	1823- 1922	AGGGGCAACGGATAGACAGATCAAATGGTGGCCCA ATAGCGAGCCTTCTCCCTGCTCCCTCCCTTGACACA GCTTGCTTATGTTATTTAGAGTGTAGGT
SH2D1A	NM_011364. 3	251-350	TTGTATCAAGGTTACATCTACACATATCGAGTGTCC CAGACAGAAACAGGTTCTTGGAGTGCCGAGACAGC ACCTGGAGTACATAAAAGATTTTTCCGGA
SLC27A4	NM_011989. 4	2981- 3080	TAGCCCCTTTTCGCTTAGCCCTTGGGATAAGCCCTTA GCCAGTCTCTTTTCAAAGCTCTGCCTTCTATAAC TCCTTAGGAGAGACTCCCACCAGATCT
SMPDL3 A	NM_020561. 2	1067- 1166	TGTTTTGTGGCACCTGCTGTTACACCAAGTAAAGGAG TTTTACAAAAGGAGACCAACAATCCCGGTGTCCGCC TATTTAGTACAAGCCTGGTGATTACAC
SNAI1	NM_011427. 2	911- 1010	TCACTGCCAGGACTCCTTCCAGCCTTGGTCCGGGG ACCTGTGGCGTCCATGTCTGGACCTGGTTCTGCTT GGCTCTTTGGTGGCCTTTGCCGCAGGTG

SNAI2	NM_011415.2	816-915	AGACCCACTCTGATGTAAAGAAATACCAAGTGCAAAA ACTGCTCCAAAACCTTCTCCAGAATGTCGCTTCTGC ATAAACATGAGGAGTCTGGCTGCTGTGT
SOX17	NM_011441.4	2151-2250	ACTGAGCTCCTAGGGGAGGTGGACCGCACGGAATT CGAACAGTATCTGCCCTTTGTGTATAAGCCCGAGAT GGGTCTTCCCTACCAGGGACACGACTGCG
SOX7	NM_011446.1	2486-2585	TAGAAACCTAAAACGTCTGTCCACAAAAGTGTTGGG GTGTGCTGATTTCTAGAGCAGAGCTGTAGCATACTC TTATCTACAGATGCAAAAGATGACTCTC
SPP1	NM_009263.3	421-520	TGAATCTGACGAATCTCACCATTTCGGATGAGTCTGA TGAGACCGTCACTGCTAGTACACAAGCAGACACTTT CACTCCAATCGTCCCTACAGTCGATGTC
SPRY1	NM_011896.2	1611-1710	GAGCAGCGAGGGCCTGTGTGCTGCATCCGCTCTCC AGCTGCTTCCGTGAAGATATACGCATGCCCGGATTT GGCCGAGAGTTGTTTGGGGTCTGGTACTG
SYK	NM_011518.2	3971-4070	TGATAGGGAGGCACTATGCTTAGAGCATGGTTAGG AAGTATTTAGAAGCTATTGGTGTGTCTTGGAAATTGT GTTAGTAGGTCAACCGTCTGTGGAGGGA
SYNPO	NM_177340.2	1099-1198	CGCCCACTAAGGTGTATAGTGAAGTACATCTCACAC TAGCCAAGCCTGCATCCGTGGTCAACAGGACCGCC AGGCCTTTTGGGATCCAGTCGCCAGGGAC
TAGLN	NM_011526.2	421-520	GTTGACCTCTATGAAGGTAAGGATATGGCAGCAGT GCAGAGGACTCTAATGGCTTTGGGCAGTTTGGCTG TGACCAAAAACGATGGAAACTACCGTGGAG
TBP	NM_013684.3	71-170	GTGGCGGGTATCTGCTGGCGGTTTGGCTAGGTTTC TGCGGTCGCGTCATTTTCTCCGCAGTGCCACGATC ACTATTTTATGGTGTGTGAAGATAACCCA
TFRC	NM_011638.3	1931-2030	CTGAACCAGTTCAAACAGATATCAGGGATATGGGT CTAAGTCTACAGTGGCTGTATTCCGCTCGTGGAGAC TACTTCCGTGCTACTTCTAGACTAACAA
TGFB1	NM_011577.1	1471-1570	GGAGTTGTACGGCAGTGGCTGAACCAAGGAGACGG AATACAGGGCTTTTCGATTCAGCGCTCACTGCTCTTG TGACAGCAAAGATAACAAACTCCACGTGG
TGFB2	NM_009367.1	1686-1785	CCCAAAGCCAGAGTGGCCGAGCAGCGGATTGAACT GTATCAGATCCTTAAATCCAAAGACTTAACATCTCCC ACCCAGCGCTACATCGATAGCAAGGTTG
TGFB3	NM_009368.2	2411-2510	TCATGTAATTAGTTTCTGGGCCAGCACTAGCTATC TCAGGTCCCTTAGAGATGCTGGACTCAAAGCAGA GGTCAGAATTGGTTCTCTCATGTATTCCC
TGFBI	NM_009369.4	1296-1395	TCTGTGTTCAAAGATGGTGTCCCTCGCATCGACGCC CAGATGAAGACTTTGCTTCTGAACCACATGGTCAA GAACAGTTGGCCTCCAAGTATCTGTACT
TGFBR2	NM_009371.2	476-575	TGTGCAAGTTTTGCGATGTGAGACTGTCCAATTGCG ACAACCAGAAGTCTGTCATGAGCAACTGCAGCATCA CGCCATCTGTGAGAAGCCGCATGAAGT
THBD	NM_009378.3	2846-2945	CCTTTGACATGACAATAGGACATTGCTATCTTGAG ACATACTGGGCCACATTCATAGCTTTCCAAGGATGT ATGTGGTCCTGCCTCAACATATCAGAGC
THPO	XM_011245868.1	647-746	ATCCCTGTTCTGCTGCCTGCTGTGGACTTTAGCCTG GGAGAATGGAAAACCCAGACGGAACAGAGCAAGGC ACAGGACATTCTAGGGGCAGTGTCCCTTC
THY1	NM_009382.3	426-525	ACTTTTGTGAGCTTCAAGTCTCGGGCGCGAATCCCA TGAGCTCCAATAAAAGTATCAGTGTGTATAGAGACA AGCTGGTCAAGTGTGGCGGCATAAGCCT
TIMP1	NM_011593.2	437-536	AAGCCTCTGTGGATATGCCACAAGTCCCAGAACCG CAGTGAAGAGTTTCTCATCACGGGCCGCTAAGGA

			ACGGAAATTTGCACATCAGTGCCTGCAGC
TIMP2	NM_011594.3	656-755	TTGCAGGAAAGGCAGAAGGAGATGGCAAGATGCAC ATTACCCTCTGTGACTTCATTGTGCCCTGGGACACG CTTAGCATCACCCAGAAGAAGAGCCTGAA
TLR2	NM_011905.2	256-355	GCAGGCGGTCACTGGCAGGAGATGTGTCCGCAATC ATAGTTTCTGATGGTGAAGGTTGGACGGCAGTCTCT GCGACCTAGAAGTGGAAAAGATGTGCTTC
TLR4	NM_021297.2	2511-2610	AACGGCAACTTGGACCTGAGGAGAACAAACTCTG GGGCCTAAACCCAGTCTGTTTGCAATTAATAAATGC TACAGCTCACCTGGGGCTCTGCTATGGAC
TNF	NM_013693.1	1136-1235	TTCCTGAGTTCTGCAAAGGGAGAGTGGTCAGGTTG CCTCTGTCTCAGAATGAGGCTGGATAAGATCTCAGG CCTTCCTACCTTCAGACCTTCCAGACTC
TNFRSF1A	NM_011609.2	616-715	CTCCTTGCCAAGCTGACAAGGACACGGTGTGTGGC TGTAAGGAGAACCAGTTCCAACGCTACCTGAGTGA GACACACTTCCAGTGCCTGGACTGCAGCCC
TNFRSF1B	NM_011610.3	3271-3370	GTGTGTGTCCATGTTTGCATGTATGTGTGTGCCAGT GTGTGGAGGCCAGAGGTTGGCTTTGGGTGTGTTT ATCACTCTCAGTTACTGAGGCAGGGCTCT
TNPO1	NM_001048267.1	2161-2260	GCATGCAGGATAAAAATGCCCGAGGTTCCGGCAGAGT TCTTTTGCATTGCTAGGTGACCTGACTAAAGCGTGC TTCCAGCATGTAAAGCCTTGTATAGCTGA
TPSAB1	NM_031187.4	664-763	GGCTGGGGTAACATCGACAATGGTGTAAACCTGCC GCCACCATTTCTTTGAAGGAGGTGCAAGTTCCCAT TATAGAAAACCACCTTTGTGACTTGAAGT
TPSB2	NM_010781.3	503-602	TGATAATGACGAGCCTCTCCACCTCCTTATCCTCT GAAGCAAGTGAAGGTTCCCATTTGTGAAAACAGCC TGTGTGACCGGAAGTACCACACTGGCCTC
TYROBP	NM_011662.2	131-230	CCCAGAGTGACACTTCCCAAGATGCGACTGTTCTT CCGTGAGCCCTGGTGTACTGGCTGGGATTGTTCTG GGTGACTTGGTGTGACTCTGCTGATTGC
UCP2	NM_011671.4	951-1050	TGTGCTGAGCTGGTGACCTATGACCTCATCAAAGAT ACTCTCCTGAAAGCCAACCTCATGACAGATGACCTC CCTTGCCACTTCACTTCTGCCTTCGGGG
UTS2	NM_011910.2	81-180	GAATCCACTGCTGTCCCTTCCCGTCACGGACACTGG TGAGAGGACTCTTCAGCTTCCAGTGCTTGAGGAAGA CGCTCTTCGGGCTCTGGAGGAGCTGGAG
VCAM1	NM_011693.2	1441-1540	GGTTTTGAGGATGAACACTCTTACCTGTGCGCTGTG ACCTGTCTGCAAAGGACACTGGAAAAGAGAACCCA GGTGGAGGTCTACTCATTCCCTGAAGATC
VEGFA	NM_001025250.3	3016-3115	TCTCTCTCTCCAGATCGGTGACAGTCACTAGCTTG TCTGAGAAGATATTTAATTTTGCTAACACTCAGCTC TGCCCTCCCTTGTCACCACACATT
VIM	NM_011701.4	35-134	CAGCGCTCCTACGATTCACAGCCACCGCGCCCTCAT TCCCTGTTGCAGTTTTTCCAGCCGAGCAAGCCAG CCCACCTTCGAAGCCATGTCTACCAGGT
VIPR1	NM_011703.4	2481-2580	CCTCCATCTTTATAGCGATAATGGCTTCTAATCCAAA CTGGTGTGAGCGGGCTCTTCTCAGAGCTGCACCAG GCTTGTATGACAATAAACATTGGCTCTA





**Supplementary Table 3. p-values from all comparisons in Figure 4D.**

Gene name	LDLr <sup>-/-</sup> mice								ApoE <sup>-/-</sup> mice							
	Vehicle, WD vs. Semaglutide, WD, 4µg/kg		Vehicle, WD vs. Semaglutide, WD, 12µg/kg		Vehicle, WD vs. Semaglutide, WD, 60µg/kg		Vehicle, WD vs. Vehicle, Chow		Vehicle, WD vs. Semaglutide, WD, 4µg/kg		Vehicle, WD vs. Semaglutide, WD, 12µg/kg		Vehicle, WD vs. Semaglutide, WD, 60µg/kg		Vehicle, WD vs. Vehicle, Chow	
	p-value	BH Corrected p-value	p-value	BH Corrected p-value	p-value	BH Corrected p-value	p-value	BH Corrected p-value	p-value	BH Corrected p-value	p-value	BH Corrected p-value	p-value	BH Corrected p-value	p-value	BH Corrected p-value
<i>Abca1</i>	<0.0001	0.0005	<0.0001	0.0002	0.0004	0.0015	<0.0001	<0.0001	0.2608	0.7789	0.5127	0.6387	0.9588	0.9813	<0.0001	0.0002
<i>Ccl2</i>	0.0002	0.0011	0.0006	0.0020	<0.0001	0.0002	<0.0001	<0.0001	0.9318	0.9704	0.0121	0.0674	0.0024	0.0500	0.0022	0.0080
<i>Cd163</i>	0.0927	0.1620	0.3743	0.4567	0.0111	0.0246	0.4918	0.6030	0.1093	0.7645	0.0085	0.0586	0.0161	0.1252	0.0275	0.0645
<i>Il1rn</i>	<0.0001	0.0003	<0.0001	<0.0001	<0.0001	0.0001	<0.0001	<0.0001	0.7413	0.9226	0.0012	0.0232	0.0995	0.3336	<0.0001	<0.0001
<i>Il6</i>	0.0030	0.0091	0.0024	0.0062	0.0240	0.0473	<0.0001	<0.0001	0.1615	0.7645	0.0026	0.0331	0.0419	0.1863	0.1669	0.2636
<i>Mmp13</i>	0.0002	0.0013	<0.0001	<0.0001	0.0029	0.0083	0.0005	0.0011	0.0211	0.7222	0.0242	0.0995	0.0045	0.0661	0.0005	0.0024
<i>Mmp3</i>	0.1161	0.1913	0.0445	0.0788	0.0076	0.0186	<0.0001	0.0001	0.1812	0.7645	0.4223	0.5790	0.1853	0.4299	0.0077	0.0233
<i>Ptgis</i>	0.0006	0.0025	<0.0001	<0.0001	0.0006	0.0021	<0.0001	<0.0001	0.8226	0.9405	0.0006	0.0181	0.0015	0.0500	<0.0001	<0.0001
<i>Sele</i>	0.0031	0.0093	0.0035	0.0084	0.0021	0.0064	<0.0001	<0.0001	0.4404	0.8566	0.0011	0.0232	0.0306	0.1747	<0.0001	0.0002
<i>Spp1 (Opn)</i>	<0.0001	0.0003	<0.0001	<0.0001	<0.0001	0.0002	<0.0001	<0.0001	0.1349	0.7645	0.0086	0.0586	0.1100	0.3523	<0.0001	0.0001
<i>Vcam1</i>	<0.0001	0.0006	<0.0001	<0.0001	0.0001	0.0004	<0.0001	<0.0001	0.2080	0.7645	0.1999	0.3632	0.5642	0.7932	<0.0001	<0.0001

BH = Benjamini-Hochberg

**Supplementary Table 4. p-values from all comparisons in Figures 5B & C**

Gene name	Vehicle, WD vs. Semaglutide, WD, 4µg/kg		Vehicle, WD vs. Semaglutide, WD, 12µg/kg		Vehicle, WD vs. Semaglutide, WD, 60µg/kg		Vehicle, WD vs. Vehicle, Chow	
	p-value	BH Corrected p-value	p-value	BH Corrected p-value	p-value	BH Corrected p-value	p-value	BH Corrected p-value
<i>Agtr1a</i>	0.0276	0.1147	0.0134	0.0473	<0.0001	0.0003	0.0029	0.0081
<i>Casp3</i>	0.0011	0.0155	0.0002	0.0025	0.0002	0.0028	0.0134	0.0289
<i>Cx3cr1</i>	0.0047	0.0404	0.0003	0.0025	0.0109	0.0588	<0.0001	0.0002
<i>Hmox1</i>	0.0615	0.1777	0.0668	0.1483	0.0422	0.1561	<0.0001	<0.0001
<i>SI00A8</i>	<0.0001	0.0001	0.0001	0.0022	0.0001	0.0025	0.0008	0.0030
<i>SI00A9</i>	<0.0001	0.0001	0.0001	0.0013	<0.0001	0.0017	0.0005	0.0021
<i>Timp1</i>	0.0036	0.0318	0.0002	0.0025	0.0061	0.0402	0.0001	0.0005
<i>Ace</i>	0.0026	0.0279	0.0002	0.0025	0.0021	0.0223	0.0003	0.0013
<i>Col1a1</i>	0.1829	0.3505	0.0024	0.0127	0.1471	0.3014	0.0025	0.0073
<i>Col3a1</i>	0.1948	0.3564	0.0018	0.0115	0.2020	0.3665	0.0004	0.0019
<i>Col1a2</i>	0.1233	0.2748	0.0022	0.0124	0.3270	0.4928	0.0027	0.0077
<i>Col4a2</i>	0.3702	0.5622	0.3073	0.4375	0.8863	0.9414	0.0300	0.0549
<i>Tlr2</i>	0.0003	0.0058	0.0128	0.0462	0.0053	0.0385	<0.0001	<0.0001
<i>Vegfa</i>	0.0239	0.1044	0.0001	0.0021	0.0048	0.0385	0.0077	0.0183
<i>Col4a1</i>	0.4608	0.6285	0.1083	0.2000	0.4406	0.5942	0.0037	0.0099

BH = Benjamini-Hochberg