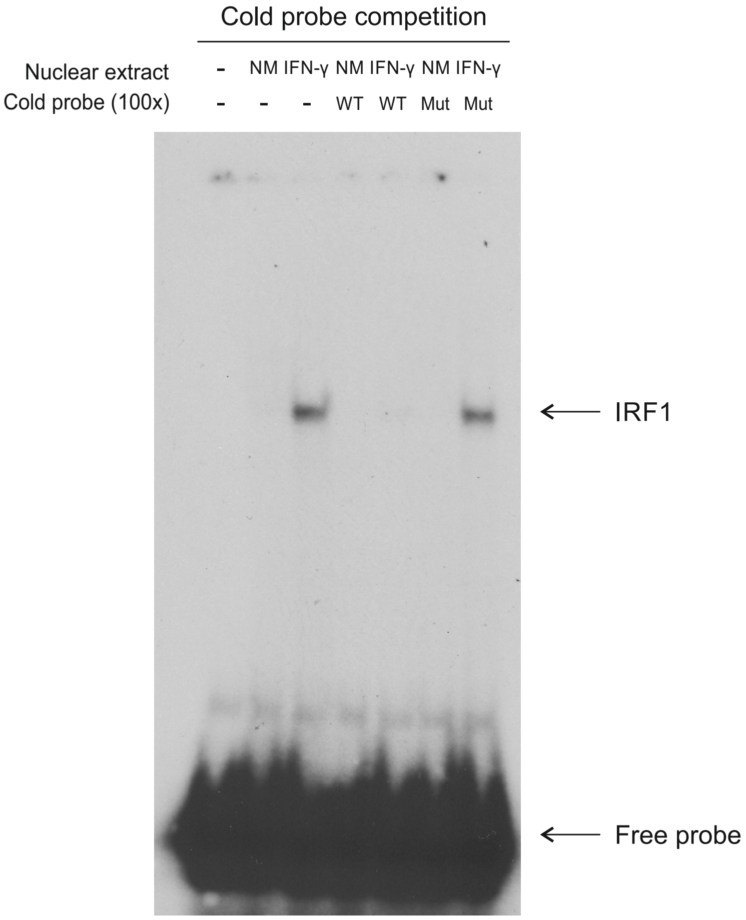
Appendix

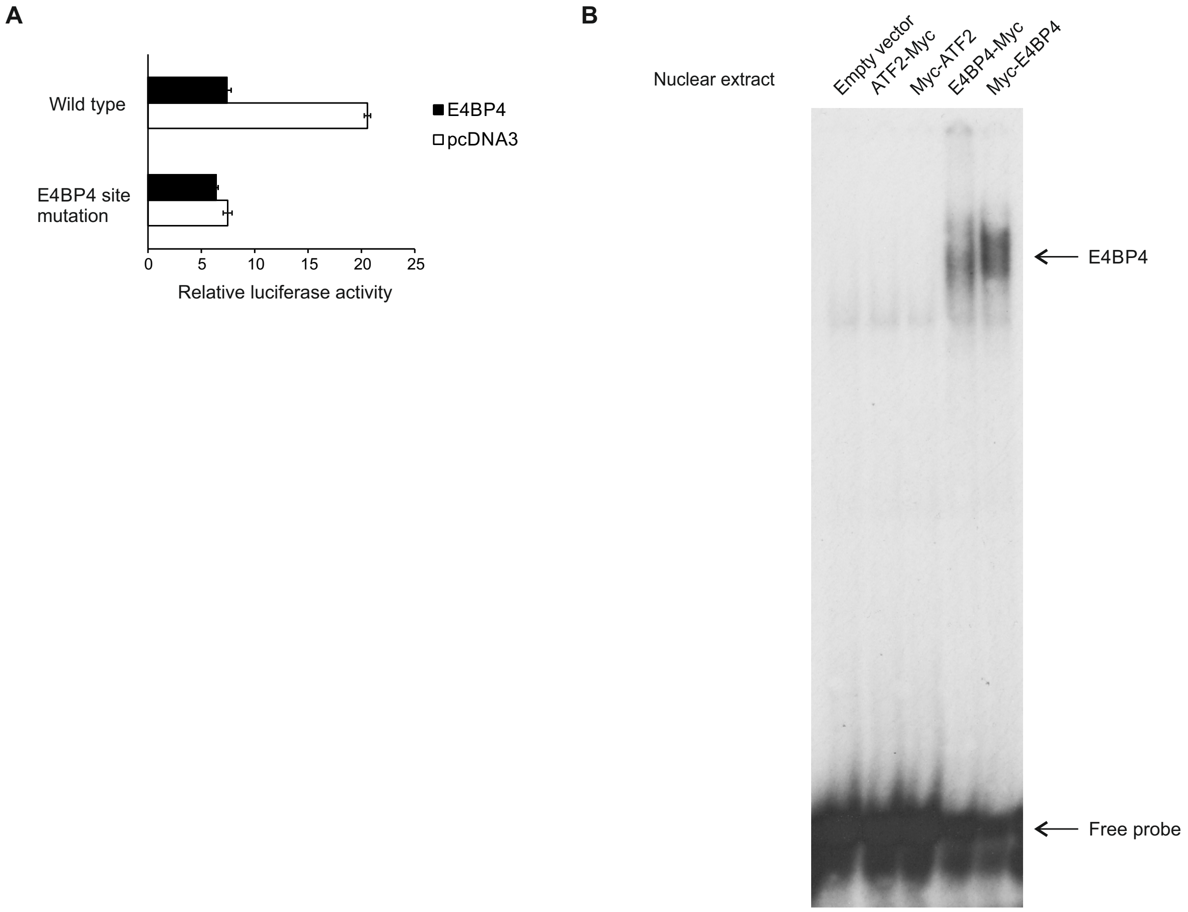
Appendix figures

Appendix tables



Appendix Figure S1. Specific binding of IRF1 to the IRF1 binding site in the upstream MICA promoter.

EMSA showing specific binding of IRF1 to the upstream promoter site. Nuclear extracts from untreated (NM) or interferon-γ treated (IFN-γ) primary human arterial endothelial cells were pre-incubated with excess unlabeled probe containing the wild-type upstream promoter IRF1 site (WT) or the mutant site used in the reporter assay (Mut), before addition of the ^{32}P-labeled probe containing the wild-type upstream promoter IRF1 site. The binding of IRF1 induced by interferon-γ was competed off by the wild-type, but not the mutant cold probe. This demonstrates that specific binding of IRF1 to the upstream promoter site is induced by interferon-γ.



Appendix Figure S2. E4BP4 represses the upstream MICA promoter.

A. Reporter assays of upstream promoter activity showing repression of the upstream promoter by E4BP4. E4BP4 overexpression in HeLa cells causes significant downregulation of wild-type upstream promoter activity, whereas mutation of the E4BP4 binding site within the upstream promoter abolishes this response to E4BP4. Error bars represent standard deviations of 3 replicates.

B. EMSA showing binding of E4BP4 to the upstream promoter. Nuclear extracts from 293T cells transfected with the constructs indicated were incubated with ^{32}P-labeled probes containing the upstream promoter E4BP4 site. The E4BP4 site binds to both N- and C-terminal myc-tagged E4BP4, but not to control ATF2 transcription factor.

Appendix Table S1. Summary of isogenic BAC cell lines

BAC name	Clones screened	Clones verified
53kb-WT	56	2
53kb-UPdel	56	2
53kb-SPdel	34	2
53kb-Ter	46	4
53kb-UP-Dox	35	5
53kb-SP-Dox	36	5
161kb-WT	32	2
161kb-UPdel	32	3
161kb-SPdel	32	2
161kb-Ter	32	3
Total (success rate)	391	30 (8%)

Appendix Table S2. Primer sequences.

Primer ID	Sequence
CO196	AATATTGGATCCATGGCCCCGACGTCGCCACCC
CO211	AATTAAAGCTTAAGTACTTAAGAGAAACTGAGGAGGAAGAG
CO213	AATTAAAGCTTAGGCAATTCTCTTAGTAGAAAGAGG
CO219	AATTAAAGCTTCGAAGCTGGTCCCTGCTTTAGGC
CO230	AGTCCTCGCGACAAGTTTAATTAATAAGTTTCCGCGGCGCCTTCTC
CO233	AATTATCGCGACAAGTATGCATCTAAGTTCCGGGCCCCAGTTTC
CO315	ATAAATTGTGTGGCATATGAATTCTC
CO400	AATTAAAGCTTTCTGCCCGGAGCCTGCAGAC
CO440	AATTAAGCTTCCAAGCGTGGCCCCGCCC
CO441	AATTAAGCTTCGCTCGTGATTGGCCCTAAGTT
CO455	GACGCAAATGGGCGGTAGGCG
CO606	CCAGGACCTGCAGGCTCACGA
CO631	TCCATGACAACTTTGGTATCGTGG
CO632	CACCACCCTGTTGCTGTAGCC
CO717	AATTAAGCTTAAATTAGGATCCTCACTGAAGTGG
CO744	AATTAAGCTTAGAGCAGACGGGGTTGGAGG
CO745	AATTAAGCTTACAGAAAAGTGTAGGCTAGGGATC
CO1074	AATTAAGCTTCCCTCTCTCAGACTTTAGGC
CO1075	AATTAGATCTAAATTAGGATCCTCACTGAAGTGG
CO1099	TTCCGGACCCTGCAGTGGCG
CO1109	GGGTCATCCTGAGGTCCTTTCCG
CO1111	TCTTCCTGCTTCTGGCTGGCAT
CO1163	AATTACTCGAGCGGCGCCCTCAGTGGAACCAG
CO1169	AATTAAGCTTCCGGACCCTGCAGTGGCG
CO1176	AATTACGCGTCACTGTGGTAGTGGAGATGTGG
CO1408	AATTAGATCTATCCCAGTCCTCGCAGTGAATTC
CO1409	AATTAGATCTAGGAGAATCGCTTAAACCTTGGAG
CO1410	AATTAGATCTATCCTGGAATACGTGGGCGGC
CO1612	AATTAGATCTCAGCCTGGGCAACAAGAGGGA
CO1613	AATTAGATCTCCGCCCTGGGTTATGTAAGCG
CO1641	AATTAGATCTTTCGGGGGCGGAGCGGAG
CO1642	AATTAGATCTAAACTCCGTCGCAAAAACTTTCGG
CO1743	AATTAGGATCCGCCATGGGGCTGGGCCCGGTCT
CO1780	AATTAGGATCCTTCCGGACCCTGCAGTGGCG
CO1831	GAATGCCGAAGAGGAAGGCCAG
CO1832	GGCAAGGGCAGGAAGATGACTC
CO1892	GATCTGGTACCATGGCATCAATGCAGAAGCTGATCTCAGAGGAGGACCTGCTTGGATCCGAATTCC
CO1893	TCGAGGAATTCGGATCCAAGCAGGTCCTCCTCTGAGATCAGCTTCTGCATTGATGCCATGGTACCA
CO2296	GATCCGAATTCCTCGAGGAACAAAAACTCATCTCAGAAGAGGATCTGTGAG
CO2297	TCGACTCACAGATCCTCTTCTGAGATGAGTTTTTGTTCCTCGAGGAATTCG
CO2354	AATTACTCGAGGGCGCCCTCAGTGGAGCCAG
CO2405	AATTAGGATCCAAATTCAAGTTACATGTGAATTCTGC
CO2406	AATTACTCGAGACTTCCTGAGGGCTGTGACTGG
CO2407	AATTAGGATCCGCCATGAAATTCAAGTTACATGTGAATTCTG
CO2408	AATTACTCGAGTCAACTTCCTGAGGGCTGTGACT
CO2409	AATTAGGATCCCAGCTGAGAAAAATGCAGACCGT
CO2410	AATTACTCGAGCCCAGAGTCTGAAGCAGAGATTG
CO2411	AATTAGGATCCGCCATGCAGCTGAGAAAAATGCAGACC
CO2412	AATTACTCGAGTTACCCAGAGTCTGAAGCAGAGAT
CO2486	GCCCCGCCCTGGGTTGGATCCGCGACCGCGCTGGGC
CO2487	GCCCAGCGCGGTCGCGGATCCAACCCAGGGCGGGGC
CO2717	CTATGCCCCAGTAAGCTAGG
CO2718	GCCTTCCATAGACATCCTGA
CO2871	CATGATGAGTCTCTTCTCGAGGC
CO2872	ATCCTGACGCCAGGTCAGTATGA
CO2974	ACTGAAAGCTTGGGTCGAAAGGCCCGGAGATGAG
CO3036	ACTGAGCGGCCGCATCGATTCCCCAGCATGCCTGCTATTGTC
CO3050	ACAGGCAGAAATGCAGGGCAAAGCCCCAGGGACAGTGGGCAGAAGATGTCGGCCTGGTGATGATGGCGGGATCG
CO3051	GCAGAATTGGAGGGAGAGGAGAGCCCCTGGCCAGCGTCGGTACCTGTTCTTCAGAAGAACTCGTCAAGAAGGCG
CO3150	ACTGAGCTAGCTAGGTCCCTCGACTATAGGGTC
CO3151	ACTGACCTGCAGGTATTTGAAGCTGAAGAAGTTATCACT
CO3154	ACTGACCTGCAGGCTCCCTCCCGTGCTCTGTCATT
CO3156	ACTGACCCGGGATATCGCGGCCGCCTGGCCGTCGA
CO3162	ACTGACTCGAGGAAGTTCCTATTCTCTAGAAAGTATAGGAACTTCTCTAGAAAAGGCGCCTGGGAATTC
CO3163	ACTGAAAGCTTTACCGTTCGTATAGCATACATTATACGAAGTTATACCAATATGGGATCGGCCATTGA
CO3164	ACTGAGGATCCATAACTTCGTATAGTATACATTATACGAAGTTATCCCCAGCTGGTTCTTTCCGCC
CO3169	ACTGAGGATCCATGCCCACGCTACTGCGGGTTT
CO3170	ACTGAGCTAGCCTCAGTTAGCCTCCCCCATCTCC
CO3173	ACTGAAAGCTTGCGGCCGCGAAGTTCCTATTCTCTAGAAAGTATAGGAACTTCGCCACCATGGGGAAAAAGCCTGAACTCACCGCGAC
CO3174	ACTGAGGATCCTTCCTTTGCCCTCGGACGAGTG
CO3175	CGATCCGCGGAGATCTGGTACCCTCGAGC
CO3176	CCGGGCTCGAGGGTACCAGATCTCCGCGGAT
CO3411	ACTGAAGATCTGCGCAGTTTCCTACTCACCCGG
CO3446	ACTGAAGATCTATAACTTCGTATAGCATACATTATACGAACGGTAGCCACCATGGGGAAAAAGCCTG
CO3447	ACTGACTCGAGGAAGTTCCTATACTTTCTAGAGAATAGGAACTTCTCCCCAGCATGCCTGCTATTGTC
CO3449	ACTGAGATATCCACTGCTTGAGCCGCTGAGAGG
CO3450	ACTGAGATATCAAAGTTTTTGCGACGGAGTTTTCCC
CO3451	ACTGAGATATCTTCCGGACCCTGCAGTGGCG
CO3469	ACTGAGATATCAGTAGCTGAGAGTACAGCTCCAA
CO3494	GTGGTCGCGATGCCGGGAGGGCAGGCAGGGCCCTGGCCGTGCTTATGAAGGGCCTGGTGATGATGGCGGGATCG
CO3495	AGCCAGAAGCAGAAAGACCGGGCCCAGCCCCATGGCCCCGACGTCGCCACTCAGAAGAACTCGTCAAGAAGGCG
CO3496	CGGGGGCGGAGCGGAGCCCCGCCCTGGGTTATGTAAGCGACCGCGCTGGGGGCCTGGTGATGATGGCGGGATCG
CO3497	CCCCATGCACTCACGAGCACAGAGGCGACTTCCCTCTCTCAGACTTTAGGTCAGAAGAACTCGTCAAGAAGGCG
CO3506	GTTTCTTGCTGAGGTACACTTGGACGGACAGCCCTTCCTGCG
CO3507	CGCAGGAAGGGCTGTCCGTCCAAGTGTACCTCAGCAAGAAAC

CO3525	GAAGGGCTGTCCGTCCAAG
CO3526	TTCTGCTTCTGGCTGGCAT
CO3540	ACTGACCTGCAGGTCAGGTCCTGAATATCTTTGTTAATTT
CO3541	ACTGACTCGAGGCGGCCGCGAATATATGAATGATTGGTGTACCTG
CO3611	CTGGGCCGTTTCTCTTTCTTTTCCG
CO3612	CGGAAAAGAAAGAGAAACGGCCCAG
CO3615	CTGGGCCGTTTCTGTCGACTTTCCG
CO3616	CGGAAAGTCGACAGAAACGGCCCAG
CO3621	CGCGCTGGGCCGTTTCTGTCGACTTTCCGGACCCTGCAGT
CO3622	ACTGCAGGGTCCGGAAAGTCGACAGAAACGGCCCAGCGCG
CO3705	AGAGGGAAGTCGCCTCTGTGCT
CO3706	TGGCATCTTCCCTTTTGCACC
CO3707	CCAGGGTCATCCTGAGGTCCTTT
CO3708	CTGGTCTCTCTGTCCCATGTCTTATT
CO3740	CCAATCCGTGCATTGGTTACAAGT
CO3741	GGCTGCCTGGAGTACTGCATCA
CO3744	TTGCCATCAATGACCCCTTCA
CO3745	CGCCCCACTTGATTTTGGA
CO3746	GTAACCCGTTGAACCCCATT
CO3747	CCATCCAATCGGTAGTAGCG
CO3812	ACTGAGGTACCAAGTTTAAACAAGAGCTCACGGGGAGAGCCCC
CO3813	ACTGACTCGAGCTCACTGACTCCGTCCTGGAGT
CO3814	ACTGAGCGGCCGCGAGCTCACGGGGAGAGCCCC
CO3815	ACTGACCGCGGAAGTTTAAACAACTCACTGACTCCGTCCTGGAGT
CO4080	GAAGGGCTGACCATCCAGA
CO4210	GCTGATGGCGATGAATGAACACT
CO4211	TGCGTTTGCTGGCTTTGATGAAA
CO4311	ACTGAGGTACCTATCATGCCTCTTTGCACCATTCTA
CO4312	ACTGAGGTACCATTCATCCCACATAACTGAAATTTTATAC
CO4313	ACTGAGGTACCCAAGCCCTTACCTCCACGGTGT
CO4314	ACTGAGGTACCGGACCTGTGTCAGGAGAGCTAG
CO4420	CACGGAGGAAGTCCTGGAGGGAGGGTAGACACCGTGGAGGTAAGGGCTTGGGCCTGGTGATGATGGCGGGATCG
CO4421	CTAGTGAGAGACTGGGAGGGAGATGGACCTAGCTCTCCTGACACAGGTCCTCAGAAGAACTCGTCAAGAAGGCG
CO4475	ACTGAGGATCCGCCACCATGTCTAGGCTGGACA
CO4476	ACTGACTCGAGTTACCCGGGGAGCATGTCAAGG
CO5217	TACCTGTCGTTTCTGGCAAGCGT
CO5218	TCTGGCTGTTTCTAGCCCACGC
CO5219	TTTCCGGACCGAGTTGTGCCAG
CO5220	TTCCCGACCCTGTAGTGGTACC
CO5221	GACACTTCCTGAGGTCCTCTACT
CO5222	AGAAGTTTTCTGAGCTCCTTCCAG
CO5223	AAGCTCACTGGCATGGCCTTCC
CO5224	TGAGGTCCACCACCCTGTTGCT
CO5418	ACTGAGGATCCACTGTCTATGCCTGGGAAAGGGT
CO5419	ACTGAGCGGCCGCATAACTTCGTATAATGTATACTATACGAAGTTATCAAGAAAGCGAGCTTCTAGCTTATC
CO5420	CGTAAGCGGGGCACATTTCATTACCTCTTTCTCCGCACCCGACATAGATAACTGTCTATGCCTGGGAAAGGGT
CO5421	TCACTTAACATACTGACCTCCAGTTCCATCCATGTTGCTGCTAGTTATTAGCGGCCGCATAACTTCGTATAATG
CO5468	TCGACGAATCCATGTGGGAGTTTATTCTTGACACAGATATTTATGATATAATAACTGAGTAAGCTTAACATAAGGAGGAAAAACA
CO5469	TATGTTTTTCCTCCTTATGTTAAGCTTACTCAGTTATTATATCATAAATATCTGTGTCAAGAATAAACTCCCACATGGATTCG
CO5470	ACTGAGGATCCATATGTTACGCAGCAGCAACGATGTT
CO5471	ACTGAGCTAGCTTAGGTGGCGGTACTTGGGTCG
CO5489	CCGATGCAAGTGTGTCGCTGTCGACGGTGACCCTATAGTCGAGGGACCTACGAATCCATGTGGGAGTTTATTCTT
CO5490	TGGCTGATCGCCCAAGGAATGGTGTCATATTGAGAGCTCAGTGTTGGTCTTTAGGTGGCGGTACTTGGGTCG
CO5943	CACCGAGCGAAGACCGCTATAAGTC
CO5944	AAACGACTTATAGCGGTCTTCGCTC
CO6334	CACCGGTCGCAAAAACTTTCGGGGG
CO6335	AAACCCCCCGAAAGTTTTTGCGACC
CO6336	CACCGTCCGTCGCAAAAACTTTCGG
CO6337	AAACCCGAAAGTTTTTGCGACGGAC
CO6338	CACCGGTTATGTAAGCGACCGCGCT
CO6339	AAACAGCGCGGTCGCTTACATAACC
CO6340	CACCGGGCGCCTAAAGTCTGAGAGA
CO6341	AAACTCTCTCAGACTTTAGGCGCCC
CO6351	TGGGAGAATAGCCACGCGTT
CO6357	CCCATTAAACCGGCTCTCACTG
CO6358	CCGGCCGCCCCATTAAAC
CO6359	CACCGCAACTGTCTCCTGCGTTGCT
CO6360	AAACAGCAACGCAGGAGACAGTTGC
CO6392	CTCCCTCAGCACTTGCCTTATAC
CO6395	CCGGGCAGCAAAATTCAAAACACA
CO6696	GCCCTGGGTTATGTAAGCGA
CO6699	TCCAACCCCGTCTGCTCTA
CO8273	CACCGGCCCCCGAAAGTTTTTGCGA
CO8274	AAACTCGCAAAAACTTTCGGGGGCC
CO8287	CACCGCCAGAAAATGGGGAGCACGC
CO8288	AAACGCGTGCTCCCCATTTTCTGGC
CO8293	CACCGGAAGCGTGGGATCTGGAATC
CO8294	AAACGATTCCAGATCCCACGCTTCC
CO8295	CACCGTGGCCTCTGACTTACTTGGA
CO8296	AAACTCCAAGTAAGTCAGAGGCCAC
CO8299	ACTGAGACGTCGAGGAGAATCCTGGCCCAATGGTGAGCAAGGGCGAGGA
CO8300	ACTGATTACTTGTACAGCTCGTCCATGCCG

Appendix Table S3. Details of plasmid construction.

Plasmid information				Cloning details[1]						
Plasmid type	Plasmid name	Plasmid ID	Source	Vector ID	Vector enzymes	Mutagenesis primers	Insert	Insert enzymes	Insert2	Insert2 enzymes
Reporter assay	MICA-ST-P-28bp	POC155	-	POC147	SmaI/NcoI	NA[2]	POC347-CO230/196	NruI/NcoI	NA	NA
Reporter assay	MICA-ST-P-85bp	POC159	-	POC147	SmaI/NcoI	NA	POC347-CO233/196	NruI/NcoI	NA	NA
Reporter assay	MICA-ST-P-100bp	POC278	-	POC147	HindIII/NcoI	NA	POC347-CO441/196	HindIII/NcoI	NA	NA
Reporter assay	MICA-ST-P-124bp	POC277	-	POC147	HindIII/NcoI	NA	POC347-CO440/196	HindIII/NcoI	NA	NA
Reporter assay	MICA-ST-P-232bp	POC149	-	POC147	HindIII/NcoI	NA	POC347-CO219/196	HindIII/NcoI	NA	NA
Reporter assay	MICA-ST-P-877bp	POC150	-	POC147	HindIII/NcoI	NA	POC347-CO211/196	HindIII/NcoI	NA	NA
Reporter assay	MICA-ST-P-1643bp	POC151	-	POC147	HindIII/NcoI	NA	POC347-CO213/196	HindIII/NcoI	NA	NA
Reporter assay	MICA-ST-P-2233bp	POC385	-	POC147	HindIII/NcoI	NA	POC347-CO745/196	HindIII/NcoI	NA	NA
Reporter assay	MICA-ST-P-2779bp	POC383	-	POC147	HindIII/NcoI	NA	POC347-CO744/196	HindIII/NcoI	NA	NA
Reporter assay	MICA-ST-P-3755bp	POC347	-	POC147	HindIII/NcoI	NA	Human genomic DNA-CO717/196	HindIII/NcoI	NA	NA
Reporter assay	MICA-ST-P-3755bp-WT	POC1315	-	POC147	HindIII/NcoI	NA	BAC-BLB53-CO717/196	HindIII/NcoI	NA	NA
Reporter assay	MICA-ST-P-3755bp-SPdel	POC1316	-	POC147	HindIII/NcoI	NA	BAC-BLB55-CO717/196	HindIII/NcoI	NA	NA
Reporter assay	MICA-ST-P-3755bp-UPdel	POC1317	-	POC147	HindIII/NcoI	NA	BAC-BLB58-CO717/196	HindIII/NcoI	NA	NA
Reporter assay	MICA-UT-P-39bp	POC918	-	POC147	BglII/HindIII	NA	POC1284-CO1613/1074	BglII/HindIII	NA	NA
Reporter assay	MICA-UT-P-61bp	POC1286	-	POC147	BglII/HindIII	NA	POC1284-CO1641/1074	BglII/HindIII	NA	NA
Reporter assay	MICA-UT-P-78bp	POC1287	-	POC147	BglII/HindIII	NA	POC1284-CO1642/1074	BglII/HindIII	NA	NA
Reporter assay	MICA-UT-P-99bp	POC917	-	POC147	BglII/HindIII	NA	POC1284-CO1612/1074	BglII/HindIII	NA	NA
Reporter assay	MICA-UT-P-162bp	POC916	-	POC147	BglII/HindIII	NA	POC1284-CO1409/1074	BglII/HindIII	NA	NA
Reporter assay	MICA-UT-P-403bp	POC915	-	POC147	BglII/HindIII	NA	POC1284-CO1408/1074	BglII/HindIII	NA	NA
Reporter assay	MICA-UT-P-702bp	POC914	-	POC147	BglII/HindIII	NA	POC1284-CO1410/1074	BglII/HindIII	NA	NA
Reporter assay	MICA-UT-P-861bp	POC913	-	POC147	BglII/HindIII	NA	POC1284-CO1075/1074	BglII/HindIII	NA	NA
Reporter assay	MICA-UT-P-3167bp	POC1284	-	POC147	MluI/HindIII	NA	Human genomic DNA-CO1176/1074	MluI/HindIII	NA	NA
Reporter assay	MICA-UT-P-78bp-ISREmut	POC1311	-	POC1287	NA	CO3621/3622	NA	NA	NA	NA
Reporter assay	MICA-UT-P-702bp	POC1338	-	POC1342	HindIII/NcoI	NA	POC914	HindIII/NcoI	NA	NA
Reporter assay	MICA-UT-P-702bp-E4BP4m	POC1339	-	POC1338	NA	CO2486/2487	NA	NA	NA	NA
CRISPR	PX458-C40	POC1331	-	POC1329	BbsI	NA	Oligos CO6334/6335 annealed	NA	NA	NA
CRISPR	PX458-C41	POC1332	-	POC1329	BbsI	NA	Oligos CO6336/6337 annealed	NA	NA	NA
CRISPR	PX458-C42	POC1333	-	POC1329	BbsI	NA	Oligos CO6338/6339 annealed	NA	NA	NA
CRISPR	PX458-C43	POC1334	-	POC1329	BbsI	NA	Oligos CO6340/6341 annealed	NA	NA	NA
CRISPR	PX458-C50	POC1335	-	POC1329	BbsI	NA	Oligos CO6357/6358 annealed	NA	NA	NA
CRISPR	PX458-C52	POC1336	-	POC1329	BbsI	NA	Oligos CO6359/6360 annealed	NA	NA	NA
CRISPR	PX458-C14	POC1330	-	POC1329	BbsI	NA	Oligos CO5943/5944 annealed	NA	NA	NA
SAM	UniSamG-MICAUT	POC1407	-	POC1406	BbsI	NA	Oligos CO8273/8274 annealed	NA	NA	NA
SAM	UniSamG-MICAST	POC1408	-	POC1406	BbsI	NA	Oligos CO8287/8288 annealed	NA	NA	NA
SAM	UniSamG-CD43	POC1409	-	POC1406	BbsI	NA	Oligos CO8293/8294 annealed	NA	NA	NA
SAM	UniSamG-CD36	POC1410	-	POC1406	BbsI	NA	Oligos CO8295/8296 annealed	NA	NA	NA
Overexpression	MICA-ST-myc	POC1289	-	POC992	BamHI/XhoI	NA	HT29 cDNA-CO1743/2354	BamHI/XhoI	NA	NA
Overexpression	MICA-UT-myc	POC1290	-	POC992	BamHI/XhoI	NA	HT29 cDNA-CO1780/2354	BamHI/XhoI	NA	NA
Overexpression	pcDNA3-Cmyc	POC992	-	POC167	BamHI/XhoI	NA	Oligos CO2296/2297 annealed	NA	NA	NA
Overexpression	MICA-UT	POC1285	-	POC366	XhoI/HindIII	NA	HT29 cDNA-CO1169/1163	XhoI/HindIII	NA	NA
Overexpression	E4BP4	POC987	-	POC167	BamHI/XhoI	NA	PBMC cDNA-CO2411/2412	BamHI/XhoI	NA	NA
Overexpression	pcDNA3-Nmyc	POC931	-	POC167	BamHI/XhoI	NA	Oligos CO1892/1893 annealed	NA	NA	NA
Overexpression	Myc-E4BP4	POC990	-	POC931	BamHI/XhoI	NA	PBMC cDNA-CO2409/2412	BamHI/XhoI	NA	NA
Overexpression	E4BP4-Myc	POC991	-	POC992	BamHI/XhoI	NA	PBMC cDNA-CO2410/2411	BamHI/XhoI	NA	NA
Overexpression	Myc-ATF2	POC1340	-	POC931	BamHI/XhoI	NA	PBMC cDNA-CO2405/2408	BamHI/XhoI	NA	NA
Overexpression	ATF2-Myc	POC1341	-	POC992	BamHI/XhoI	NA	PBMC cDNA-CO2406/2407	BamHI/XhoI	NA	NA
BAC landing site	pBS-Landing	POC1314	-	POC1313	KpnI/XhoI	NA	POC1312	KpnI/XhoI	NA	NA
Lentivirus	pHR-SIN-rtTA3	POC1325	-	POC567	BamHI/XhoI	NA	POC1324-CO4475/4476	BamHI/XhoI	NA	NA
BAC modification	-	POC1309	-	POC1292	NA	CO3506/3507	NA	NA	NA	NA
BAC modification	-	POC1308	-	POC1306	EcoRV/BamHI	NA	BAC-CH501-248L24-CO3411/3450	EcoRV/BamHI	NA	NA
BAC modification	-	POC1307	-	POC1305	EcoRV/EcoRI	NA	BAC-CH501-248L24-CO213/3469	EcoRV/EcoRI	NA	NA
BAC modification	-	POC1323	-	POC1308	EcoRV/CIP	NA	POC1319	XhoI/EcoRI/Klenow	NA	NA
BAC modification	-	POC1322	-	POC1307	EcoRV/CIP	NA	POC1319	XhoI/EcoRI/Klenow	NA	NA
BAC modification	-	POC1321	-	POC1318	KpnI/CIP	NA	POC1320-CO4311/4312	KpnI	NA	NA
BAC modification	-	POC1328	-	POC1135	SalI/NheI	NA	POC1327-CO5470/5471	NdeI/NheI	Oligos CO5468/5469 annealed	NA
BAC modification	-	POC1304	-	POC1301	BglII/XhoI	NA	POC1303-CO3446/3447	BglII/XhoI	NA	NA
BAC modification	-	POC1310	-	POC1304	SbfI/NotI	NA	BAC-CH501-248L24-CO3540/3541	SbfI/NotI	NA	NA
Intermediate	-	POC1406	-	POC1405	AatII/BsrGI	NA	POC1288-CO8299/8300	AatII/BsrGI	NA	NA
Intermediate	-	POC1326	-	POC167	BamHI/NotI	NA	POC1337-CO5418/5419	BamHI/NotI	NA	NA
Intermediate	-	POC1303	-	POC1299	BamHI/Eco53KI	NA	POC1300-CO455/3036	BamHI	NA	NA
Intermediate	-	POC1301	-	POC1297	ClaI/XmaI	NA	Oligos CO3175/3176 annealed	NA	NA	NA
Intermediate	-	POC1297	-	POC1294	SbfI/XmaI	NA	BAC-CH501-181B23-CO3154/3156	SbfI/XmaI	NA	NA
Intermediate	-	POC1294	-	POC1295	SbfI/NheI	NA	BAC-CH501-181B23-CO3150/3151	SbfI/NheI	NA	NA
Intermediate	-	POC1295	-	POC1135	NotI/T4 DNA polymerase	NA	NA	NA	NA	NA
Intermediate	-	POC1299	-	POC1032	HindIII/BamHI	NA	POC1293-CO3173/3174	HindIII/BamHI	NA	NA
Intermediate	-	POC1300	-	POC167	BamHI/XbaI	NA	POC1296-CO3169/3170	BamHI/NheI	NA	NA
Intermediate	-	POC1312	-	POC1302	KpnI/XhoI	NA	Chicken genomic DNA-CO3812/3813	KpnI/XhoI	NA	NA
Intermediate	-	POC1302	-	POC1298	HindIII/XhoI	NA	POC1291-CO3162/2974	HindIII/XhoI	NA	NA
Intermediate	-	POC1298	-	POC1032	HindIII/BamHI	NA	POC1027-CO3163/3164	HindIII/BamHI	NA	NA
Intermediate	-	POC1313	-	POC1302	NotI/SacII	NA	Chicken genomic DNA-CO3814/3815	NotI/SacII	NA	NA
Intermediate	-	POC1292	-	POC1135	SmaI/CIP	NA	BAC-CH501-248L24-CO2871/2872	None	NA	NA
Intermediate	-	POC1306	-	POC1135	EcoRI/SmaI	NA	BAC-CH501-248L24-CO3451/315	EcoRI	NA	NA
Intermediate	-	POC1305	-	POC1135	PstI/SmaI	NA	BAC-CH501-248L24-CO3449/400	PstI	NA	NA
Intermediate	-	POC1318	-	POC1308	SacII/EcoRI	NA	BAC-CH501-248L24-CO3411/4313	SacII/KpnI	BAC-CH501-248L24-CO4314/315	KpnI/EcoRI
Source	pTREtight	POC1319	Clontech							
Source	pIRES1neo	POC1027	Clontech							
Source	pEGFP-N1	POC1288	Clontech							
Source	pBluescript II-KS+	POC1032	Stratagene							
Source	pTRIPZ	POC1324	Dharmacon							
Source	pACYC-cpn10/cpn60	POC1327	Agilent							
Source	pcDNA 3.1/myc-His(-) C	POC366	Invitrogen							
Source	pcDNA3	POC167	Invitrogen							
Source	pFUSE-hIgG1-Fc1	POC1337	Invivogen							
Source	pGL3B	POC147	Promega							
Source	pGL4.23	POC1342	Promega							
Source	pSV2hph	POC1293	ATCC							
Source	pPGK.NeoR	POC1291	ATCC							
Source	pHR-SIN-BX-IRES-Emerald	POC567	Dr Xiaoning Xu							
Source	bd5-7	POC1320	Prof Nicholas Proudfoot							
Source	PX458	POC1329	Addgene							
Source	pHSV-TK	POC1296	Dr Ben Davis							
Source	pSG80A	POC1135	Dr Ben Davis							
Source	UniSam	POC1405	Addgene							

1. Plasmids were constructed by either PCR-based site-directed mutagenesis followed by DpnI digestion, or standard restriction enzyme-based cloning. For site-directed mutagenesis, the primers used are listed under "Mutagenesis primers". For standard cloning, the source of the insert is listed under "Insert", which could be either a PCR product, a plasmid or double strand DNA resulting from annealing two oligonucleotides. The restriction enzymes used to digest the insert are listed under "Insert enzymes", and the vector name and enzymes used to digest the vector under "Vector ID" and "Vector enzymes". Some of the plasmids were constructed by three-way ligation, for which details of the second insert are listed under "Insert2" and "Insert2 enzymes".

2. NA, Not applicable

Appendix Table S4. Details of BAC construction.

			Step 1: MICA tagging[1]		Step 2: MICA tagging		Step 3: Promoter modification		Step 4: Promoter modification		Step 5: Truncation, concatenation or retrofitting		Step 6: Truncation, concatenation and/or retrofitting	
BAC name	BAC ID	Parent BAC vector	Recombineering construct	Selection[2]	Recombineering construct	Selection	Recombineering construct	Selection	Recombineering construct	Selection	Recombineering construct	Selection	Recombineering construct	Selection
53kb-WT	BLB53	CH501-248L24	Rpslneo-CO3050/3051	Chl+Kan+Tet	POC1309-NcoI/XhoI	Chl+Str+Tet	NA[3]	NA	NA	NA	POC1304-SbfI	Chl+Amp	NA	NA
53kb-UPdel	BLB58	CH501-248L24	Rpslneo-CO3050/3051	Chl+Kan+Tet	POC1309-NcoI/XhoI	Chl+Str+Tet	Rpslneo-CO3496/3497	Chl+Kan+Tet	POC1308-BamHI/SalI	Chl+Str+Tet	POC1304-SbfI	Chl+Amp	NA	NA
53kb-SPdel	BLB55	CH501-248L24	Rpslneo-CO3050/3051	Chl+Kan+Tet	POC1309-NcoI/XhoI	Chl+Str+Tet	Rpslneo-CO3494/3495	Chl+Kan+Tet	POC1307-PstI/EcoRI	Chl+Str+Tet	POC1304-SbfI	Chl+Amp	NA	NA
53kb-UP-Dox	BLC46	CH501-248L24	Rpslneo-CO3050/3051	Chl+Kan+Tet	POC1309-NcoI/XhoI	Chl+Str+Tet	Rpslneo-CO3496/3497	Chl+Kan+Tet	POC1323-BamHI/SalI	Chl+Str+Tet	POC1304-SbfI	Chl+Amp	NA	NA
53kb-SP-Dox	BLC45	CH501-248L24	Rpslneo-CO3050/3051	Chl+Kan+Tet	POC1309-NcoI/XhoI	Chl+Str+Tet	Rpslneo-CO3494/3495	Chl+Kan+Tet	POC1322-NdeI/PstI	Chl+Str+Tet	POC1304-SbfI	Chl+Amp	NA	NA
53kb-Ter	BLC50	CH501-248L24	Rpslneo-CO3050/3051	Chl+Kan+Tet	POC1309-NcoI/XhoI	Chl+Str+Tet	Rpslneo-CO4420/4421	Chl+Kan+Tet	POC1321-BamHI/SalI	Chl+Str+Tet	POC1304-SbfI	Chl+Amp	NA	NA
161kb-WT	BLD33	CH501-248L24	Rpslneo-CO3050/3051	Chl+Kan+Tet	POC1309-NcoI/XhoI	Chl+Str+Tet	NA	NA	NA	NA	POC1310-SbfI	Chl+Amp+Tet	BLD24-BspEI	Chl+Zeo+Amp
161kb-UPdel	BLD35	CH501-248L24	Rpslneo-CO3050/3051	Chl+Kan+Tet	POC1309-NcoI/XhoI	Chl+Str+Tet	Rpslneo-CO3496/3497	Chl+Kan+Tet	POC1308-BamHI/SalI	Chl+Str+Tet	POC1310-SbfI	Chl+Amp+Tet	BLD24-BspEI	Chl+Zeo+Amp
161kb-SPdel	BLD34	CH501-248L24	Rpslneo-CO3050/3051	Chl+Kan+Tet	POC1309-NcoI/XhoI	Chl+Str+Tet	Rpslneo-CO3494/3495	Chl+Kan+Tet	POC1307-PstI/EcoRI	Chl+Str+Tet	POC1310-SbfI	Chl+Amp+Tet	BLD24-BspEI	Chl+Zeo+Amp
161kb-Ter	BLD36	CH501-248L24	Rpslneo-CO3050/3051	Chl+Kan+Tet	POC1309-NcoI/XhoI	Chl+Str+Tet	Rpslneo-CO4420/4421	Chl+Kan+Tet	POC1321-BamHI/SalI	Chl+Str+Tet	POC1310-SbfI	Chl+Amp+Tet	BLD24-BspEI	Chl+Zeo+Amp
181B23Z1G1	BLD24	CH501-181B23	NA	NA	NA	NA	NA	NA	NA	NA	POC1326-CO5420/5421	Chl+Zeo+Tet	POC1328-CO5489/5490	Chl+Zeo+Gen

1. BAC modifications were carried out by homologous recombination-based recombineering using linear DNA fragments listed under "Recombineering construct" followed by selection with the antibiotics listed under "Selection". Modification steps that included tetracycline selection were carried out at 30˚C to retain the pRed-E/T recombineering plasmid to facilitate subsequent recombineering steps. Modification steps without tetracycline selection were carried out at 37˚C to remove the recombineering plasmid.

2. Amp, Ampicillin 50 µg/ml; Chl, Chloramphenicol 12.5 µg/ml; Gen, Gentamicin 2 µg/ml; Kan, Kanamycin 15 µg/ml; Str, Streptomycin 50 µg/ml; Tet, Tetracycline 3 µg/ml; Zeo, Zeocin 25 µg/ml.

3. NA, not applicable

Appendix Table S5. Coordinates of promoter pairs

Species	Series	Gene	Strand	Upstream promoter[1]	Downstream promoter[1]
Human	Macrophage response to LPS	CRYBG1	+	chr6:106959693-106959893	chr6:106960041-106960241
Human	Macrophage response to LPS	MAD2L2	-	chr1:11751501-11751701	chr1:11741076-11741276
Human	Epithelial to mesenchymal	RTKN	-	chr2:74668917-74669117	chr2:74667577-74667777
Human	Epithelial to mesenchymal	PNKD	+	chr2:219135145-219135345	chr2:219187779-219187979
Human	Lymphatic EC response to VEGFC	MAGED2	+	chrX:49344444-49344644	chrX:49364723-49364923
Human	Lymphatic EC response to VEGFC	PLD3	+	chr19:40854503-40854703	chr19:40871670-40871870
Human	MCF7 response to HRG	ASAH1	-	chr8:17942369-17942569	chr8:17941514-17941714
Human	MCF7 response to HRG	YARS	-	chr1:33283653-33283853	chr1:33282858-33283058
Mouse	Tracheal to ciliated epithelium	Lama3	+	chr18:12492379-12492579	chr18:12662607-12662807
Mouse	Tracheal to ciliated epithelium	Ptpre	+	chr7:142729406-142729606	chr7:142797221-142797421
Mouse	BMM activation IL13	Ciita	+	chr16:10480064-10480264	chr16:10489737-10489937
Mouse	BMM activation IL13	Sdf4	+	chr4:155366882-155367082	chr4:155367249-155367449
Mouse	MSC to adipocyte	Cast	-	chr13:74945971-74946171	chr13:74907980-74908180
Mouse	MSC to adipocyte	Ppig	+	chr2:69560766-69560966	chr2:69561220-69561420
Mouse	MSC to osteocyte	Ak1	+	chr2:32483844-32484044	chr2:32484901-32485101
Mouse	MSC to osteocyte	Pde4a	+	chr9:20970092-20970292	chr9:20985930-20986130

1. Coordinates for tandem promoter pairs for which expression is plotted in Figure 7