Cell, Volume *135*

Supplemental Data

Combinatorial Regulation of Endothelial Gene Expression by Ets and Forkhead Transcription Factors

Sarah De Val, Neil C. Chi, Stryder M. Meadows, Simon Minovitsky, Joshua P. Anderson, Ian S. Harris, Melissa L. Ehlers, Pooja Agarwal, Axel Visel, Shan-Mei Xu, Len A. Pennacchio, Inna Dubchak, Paul A. Krieg, Didier Y.R. Stainier, and Brian L. Black

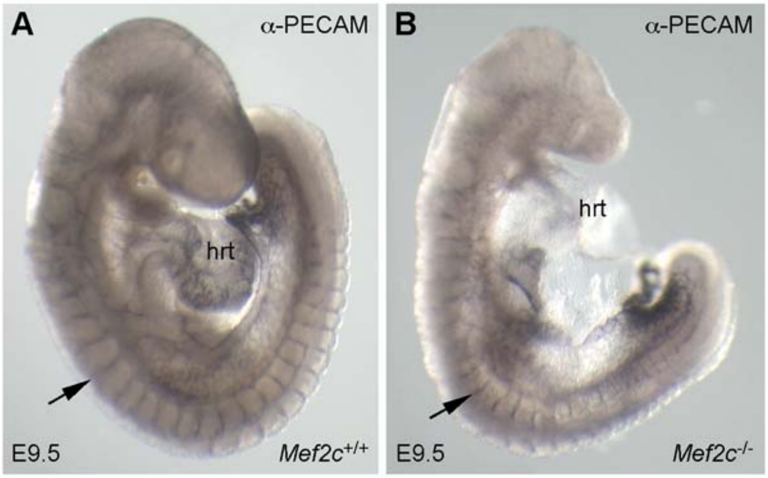

Figure S1. *Mef2c*-null embryos display aberrant vascular development. (A) *Mef2c*$^{+/+}$ and (B) *Mef2c*$^{-/-}$ embryos were collected at 9.5 days post-coitum, fixed in 4% paraformaldeyde overnight, and stained with anti-PECAM antibody as previously described (De Val *et al*., *Dev Biol*. 275, 2004). Consistent with previous reports (Lin *et al*., *Development* 125, 1998), PECAM staining was detected in the *Mef2c* null embryo but was less extensive than in the wild-type control, indicating that vascular development was defective, but not abolished, in the absence of MEF2C. Arrows mark PECAM expression in intersomitic vessels. hrt, heart.

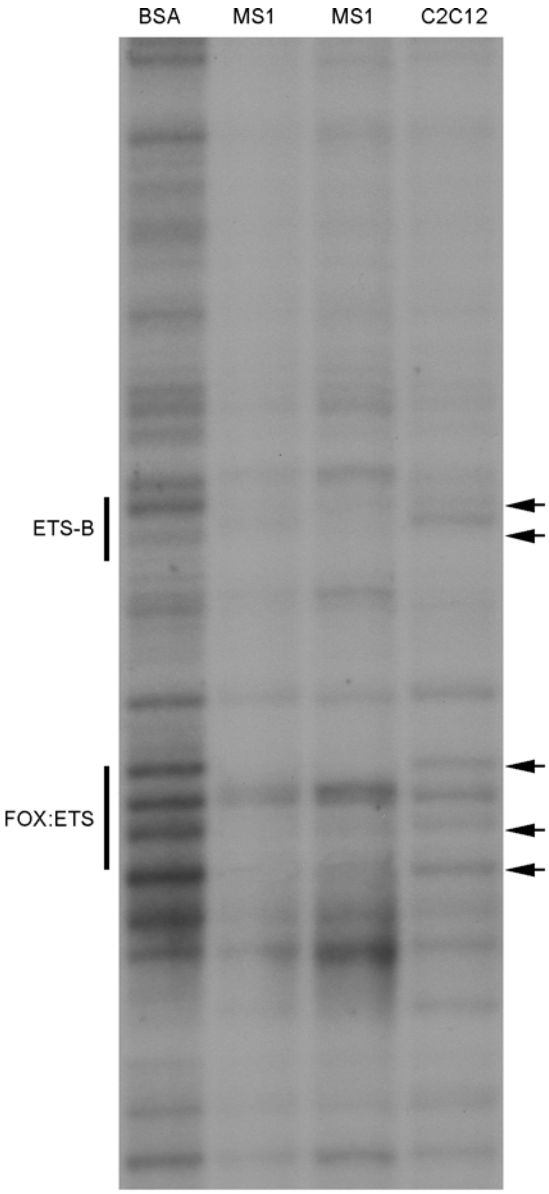

Figure S2. DNase I footprinting analysis identified regions of *Mef2c* F10-44 protected by binding activities present in extracts of the MS-1 endothelial cell line but not in extracts from the C2C12 myoblast cell line. The two protected regions correspond to the FOX:ETS motif and ETS-B site within *Mef2c* F10-44. Arrows indicate regions of protection, which can be seen as the loss of cleaved bands in the presence of MS-1 cell extract compared to BSA or C2C12 cell extracts. DNAse I footprinting was performed as described by Kucharczuk and Goldhamer, *Methods in Cell Biology* 52, 1997. The F10-44 probe was labeled by filling in recessed 3′ ends with Klenow fragment and radiolabeled dCTP. Probes were purified using micro bio-spin P-30 Tris chromatography columns (BioRad). Cell extracts were prepared as described by Francis *et al*., *Mol Endocrinol*. 20, 2006.

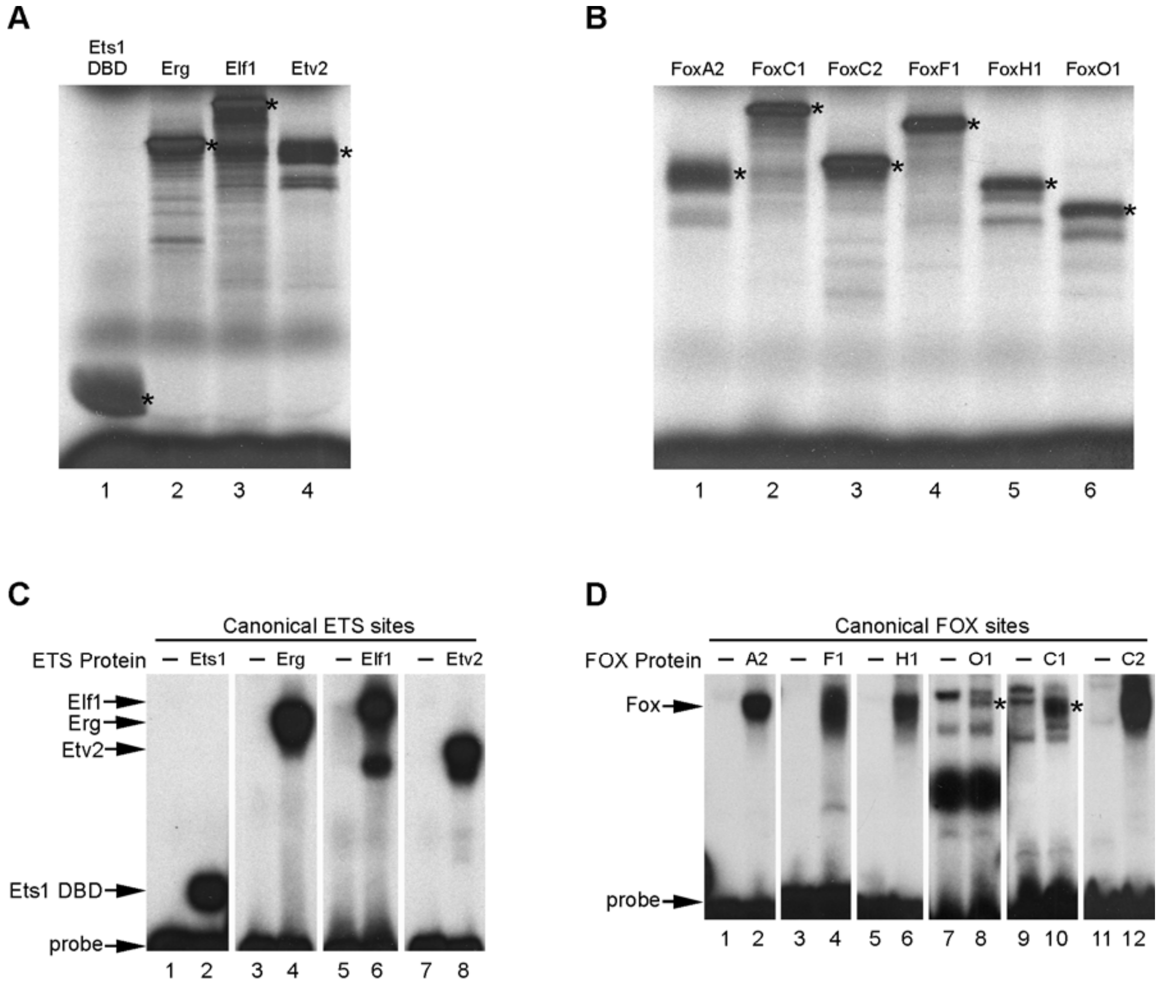

Figure S3. Ets and Forkhead proteins used in these studies were efficiently synthesized *in vitro* and bound efficiently to canonical, control sequences. (A-B) Ets (A) and Forkhead (B) proteins used in these studies were efficiently synthesized in coupled transcription-translation reactions *in vitro*. Proteins were labeled using [^{35}S]-Methionine.
(C) EMSA demonstrating that all four Ets proteins used in the EMSA shown in Figs. 2B and 2F bound to their canonical binding sites (lanes 2, 4, 6, and 8). In each case, the protein was made alongside the radiolabeled protein seen in (A) and was the same batch of protein used for the EMSAs shown in Fig. 2. The canonical sites used in these assays are shown in Supplemental Material, Table S4.
(D) EMSA demonstrating that the six Forkhead proteins used in the EMSA shown in Figs. 2C and 2F bound to their consensus sites (lanes 2, 4, 6, 8, 10, and 12). In each case, the protein was made alongside the radiolabeled protein shown in (B) and was the same batch of protein used for the EMSAs shown in Fig. 2. The canonical sites used in these assays are shown in Supplemental Material, Table S4.

```
MOUSE       CAAAGCATGTTTACTAGTTCAACATGGTCAAAATATACCTAAGTTAAAGGTCAAAGAAT
HUMAN       AAAAACATGTTTACTAGTTCAACAAAGCCAAA-TGTACCTAAGGGAAAGGTCAAAGGAT
OPPOSUM     AAAAACATGTTTACTAGCTCAACCAAGTCAAAATGTACTTAAGGTAAAGGTCAGAGAAT
CHICKEN     AAAAACATGTTTACTAGTTCTGTGCTGCTAAAATGTTCATAAGGTAAAGGTCAAAGAAT
             *** ************ **      *  *** * * * ****  ******** ** **

MOUSE       CCTACATTCCCTGCTGAGCTAA--CTCAGGAAGCACATTTGTCTACGCTTTCCTGTCAT
HUMAN       ACTTCATTCCCTGCTGAGCAAATGCTCAGGAAGCACATTTGTCTACATTTTCCTGTCAT
OPPOSUM     GCTTCATTCCCTGCTGAGCAAATGGTCAGGAAGCACATTTGTCTGCA-TTTCCTGTCAT
CHICKEN     ATTTCTTTCCCTGCTGAGCAAATGGTCAGGAAGCACATTTGTCTGCA-TTTCCTGTCAT
              * * ************* **   ******************* *  ***********

MOUSE       AACAGGAAGAGAGTAACTTCTTCCTTCCCACAGTGGCTTCAGTTTTAGCTCCCAACTCC
HUMAN       AACAGGAAGAGTGTAACTTCTTCCTTTCCACAATAGCCTAGGTTTTACCTCCTAACTCC
OPPOSUM     AACAGGAAGAATGTAACTTCTTCCTTTCCACAATGGCTTAAGTTCTACCTCCTAACTAC
CHICKEN     AACAGGAAGAGTGTAACTTCTTCCTCTCCACAATGGCTTCAGTTCTACCTCCCACCTCC
            **********  *************  ***** * ** *  *** ** **** * ** *

MOUSE       AATATTTT-----------CTCCCTCAGGGCCTTCCAAATCAATCCTTGCAAGACAGAA
HUMAN       AATATTTT-----------CTCCCCCAGGGCCTTCCAAATCAATCCTTGCAAGACAGA-
OPPOSUM     AGCTTTTTTTTTTTTTTCCCTCCCTCAGGGCCTTCCAAATCAATCCTTGTAAGACAGAA
CHICKEN     AGATCTTT-----------CTCCCTTAGGGCTTTCCAAACCAGTCCTTGCAAGACAGTA
            *    ***           *****  ***** ******* ** ****** *******
```

Figure S4. Extended conservation of the region surrounding the *Mef2c* F10-44 enhancer. ClustalW analysis (Thompson *et al*., *Nucleic Acids Res*. 22, 1994) was used to compare the sequence of the region surrounding *Mef2c* F10-44 enhancer (red) from mouse, human, opossum, and chicken. Asterisks denote nucleotides that have been perfectly conserved among all four species. No significant conservation within F10E was detected beyond the region shown.

GENE NAME	NO. OF HITS	FOX:ETS MOTIF	LOCATION	ANOTHER GENE WITHIN 10KB OF MOTIF
ANGPT1	0			
ANGPT2	0			
CALCRL	1	TGATGTAACAGGAAGCT	CHR2:188,138,544-188,138,560	N
CD34	1	TCCCCTAACAGGAAAGT	CHR1:204,452,173-204,452,189	N
CDH5	1	AACAATAACAGGAAACC	CHR16:64,957,955-64,957,971	N
CTGF	0			
CTNNB1	0			
CYR61	0			
DSCR1	0			
EDG1	0			
EDG3	0			
EDN1	0			
EFEMP1	0			
EFNA1	0			
EFNB2	0			
ENG	1	CAAGAAAACAGGAAGTG	CHR9:127,686,977-127,686,993	N
EPHB4	0			
ESM1	2	AGAGAAAACAGGAATTA AACAGAAACAGGAAATA	CHR5:54,302,791-54,302,807 CHR5:54,302,814-54,302,830	N N
F2R	0			
F2RL1	0			
F2RL3	0			
FLT1	0			
FOXC1	1	TGGCACAACAGGAAAGC	CHR6:1,564,936-1,564,952	Y
FOXC2	0			
GATA2	0			
GJA1	1	CAGAACAACAGGAAAGG	CHR6:121,801,453-121,801,469	N
GJA7	0			
ICAM1	0			
ICAM2	0			
IGFBP1	0			
IGFBP2	0			
IGFBP3	0			
IGFBP4	1	AGGGAAAACAGGAAGGA	CHR17:35,855,300-35,855,316	N
IGFBP5	0			
IGFBP6	0			
ITGA5	0			
ITGB3	0			
KDR	3	AACAACAACAGGAAGTG TGTCATAACAGGAAGAA CAGGAAAACAGGAACTC	CHR4:55,814,306-55,814,322 CHR4:55,828,453-55,828,469 CHR4:55,828,525-55,828,541	N N N
KLF2	0			
KLF4	0			
LAMA4	1	TAAAATAACAGGAAACC	CHR6:112,643,014-112,643,030	N N

LMO2	0			
MCAM	0			
MEF2C	1	GGAGGAAACAGGAAAGA	CHR5:88,155,425-88,155,441	N
MFNG	0			
MMRN1	1	TACAGAAACAGGAAACC	CHR4:91,173,120-91,173,136	N
NFATC3	0			
NFATC4	0			
NOS3	0			
NOTCH4	1	AGAATAAACAGGAAAGG	CHR6:32,299,043-32,299,059	N
NR4A2	0			
NRP1	1	TCTGTAAACAGGAAAGA	CHR10:33,631,344-33,631,360	N
PDGFRB	1	AAGCACAACAGGAAATG	CHR5:149,497,296-149,497,312	N
PECAM1	0			
PODXL	0			
PPP1R16B	2	GGACAAAACAGGAAGCT GAAGCAAACAGGAAGCA	CHR20:36,874,399-36,874,415 CHR20:36,937,666-36,937,682	N N
PROCR	0			
PTN	0			
RHOJ	0			
ROBO4	0			
SELE	0			
SERPINE1	0			
SPARCL1	0			
TAL1	1	CACAATAACAGGATGTG	CHR1:47,389,774-47,389,790	N
THBS1	0			
TIE1	0			
VCAM1	0			
VHL	0			
VWF	0			

Table S1A: Endothelial gene set used in computational scan.

GENE NAME	NO. OF HITS	FOX:ETS MOTIF	LOCATION	ANOTHER GENE WITHIN 10KB OF MOTIF
AATF	0			
ABCG2	0			
ACTB	0			
ACTN4	0			
ADAR	0			
AFG3L2	0			
AGPAT1	0			
AHSA1	0			
AKR1A1	0			
ALDOA	0			
ALDOC	0			
ANAPC5	0			
ANP32B	0			
ANXA2	0			
ANXA6	0			
AP2M1	0			
APLP2	0			
APOBEC3C	0			
ARF1	0			
ARF4	0			
ARF5	0			
ARHGAP1	0			
ARHGDIA	0			
ARHGEF18	0			
ARL2	0			
ARMET	0			
ARPC2	0			
ARPC3	0			
ARPC4	0			
ATP5A1	0			
ATP5G1	0			
ATP5G3	0			
ATP5H	0			
ATP5I	0			
ATP5J2	0			
ATP5O	0			
BAT1	0			
BLOC1S1	0			
BRMS1	0			
BTBD2	0			
BTF3	0			
BUD31	0			
C14ORF2	0			
C21ORF33	0			
C9ORF16	0			
CALM1	0			
CALM2	0			
CANX	0			
CAPNS1	0			
CAPZB	0			
CCBP2	0			
CCT3	0			
CCT7	0			
CDC2L2	0			
CENPB	0			

CFL1	0			
CGB7	0			
CHD4	0			
CHIT1	0			
CIZ1	0			
CKAP1	0			
CLSTN1	0			
CLTA	0			
CNTN1	0			
COBRA1	0			
COMMD4	0			
COPS6	0			
COX4I1	0			
COX5A	0			
COX5B	0			
COX6A1	0			
COX7A2L	0			
COX7C	0			
CPNE1	0			
CPNE6	0			
CREB3	0			
CSK	1	GCAGAAAACAGGAAGCC	CHR15:72,856,902-72,856,918	N
CSNK1E	0			
CSNK2B	0			
CSTB	0			
CTBP1	0			
CXYORF3	0			
CYC1	0			
DAD1	0			
DAP	0			
DAZAP2	0			
DDOST	0			
DIAPH1	1	ACCACAAACAGGAAATG	CHR5:140,918,168-140,918,184	N
DKK4	0			
DNPEP	0			
DRAP1	0			
DULLARD	0			
DUOXA1	0			
DYNLL1	0			
EIF3S2	0			
EIF3S4	0			
EIF3S5	0			
EIF3S8	0			
EIF4A2	0			
EIF4G2	0			
ENTPD6	0			
ERP29	0			
EXTL3	0			
FAU	0			
FBXO7	0			
FCER2	0			
FEZ1	0			
FOLR1	0			
FTH1	0			
GABARAP	0			
GABARAPL2	0			
GANAB	0			
GAS1	0			
GDI1	0			
GDI2	0			
GGTLA1	0			

GM2A	0			
GNAI2	1	CAGAAAAACAGGAAGGG	CHR3:50,267,523-50,267,539	N
GNAS	0			
GNB2	0			
GPAA1	0			
GPI	0			
GRIK5	0			
GRM4	0			
GSK3A	0			
GUK1	0			
H2AFY	0			
H3F3A	0			
H6PD	0			
HADHA	0			
HADHB	0			
HAX1	0			
HIST1H2BC	0			
HLA-C	0			
HNRPD	0			
HNRPH1	0			
HPCAL1	0			
HSBP1	0			
HSP90AB1	0			
HYOU1	0			
IDH3B	0			
IER2	0			
IFITM1	0			
ILK	0			
IMPDH2	0			
JTB	0			
KDELR1	0			
KIF1C	0			
KIFC3	0			
LASP1	0			
LDHA	0			
LDHB	0			
LYPLA2	0			
MAP4	0			
MAPK8IP1	0			
MC2R	0			
MCM3AP	0			
MDH1	0			
MEA1	0			
MFN2	0			
MLF2				
MRLC2	0			
MRPL23	0			
MRPL9	0			
MRPS12	0			
MSN	0			
MTX1	0			
MVK	0			
MYL6	0			
NDUFA1	0			
NDUFA2	0			
NDUFA7	0			
NDUFB7	0			
NDUFC1	0			
NDUFS5	0			
NONO	0			
NUDT3	0			

NXF1	0			
ODC1	0			
PABPC1	0			
PABPN1	0			
PAK4	0			
PAX8	0			
PCGF2	0			
PDAP1	0			
PFDN1	1	CTGCACAACAGGAAAAG	CHR5:139,653,654-139,653,670	N
PFDN5	0			
PGD	0			
PGK1	0			
PHF1	0			
PHGDH	1			
PITPNM1	0			
PKM2	0			
PLSCR3	0			
POLR2F	0			
PPP1R11	0			
PPP2CB	0			
PPP2R1A	0			
PRDX1	0			
PRKAG1	0			
PRPF8	0			
PRPH	0			
PSMB1	0			
PSMB2	0			
PSMB4	0			
PSMB7	0			
PSMD11	0			
PSMD8	0			
PTBP1	0			
PTDSS1	0			
PTTG1IP	0			
RAB1A	0			
RAB8A	0			
RABAC1	0			
RAD23A	0			
RAD9A	0			
RAN	0			
RBM8A	0			
RBPMS	0			
RERE	1	GTTTATAACAGGAAGTG	CHR1:8,817,287-8,817,303	N
RNPS1	0			
RPA2	0			
RPL10	0			
RPL10A	0			
RPL11	0			
RPL13	0			
RPL13A	0			
RPL14	0			
RPL15	0			
RPL17	0			
RPL18	0			
RPL19	0			
RPL27	0			
RPL29	0			
RPL3	0			
RPL32	0			
RPL34	0			
RPL35	0			

RPL36AL	0			
RPL37	0			
RPL38	0			
RPL5	0			
RPL8	0			
RPLP1	0			
RPLP2	0			
RPN1	0			
RPS10	0			
RPS11	0			
RPS13	0			
RPS14	0			
RPS15	0			
RPS16	0			
RPS18	0			
RPS19	0			
RPS2	0			
RPS24	0			
RPS25	0			
RPS27A	0			
RPS5	0			
RPS6KB2	0			
RPS9	0			
RRBP1	0			
RUVBL2	0			
SAFB	0			
SAP18	0			
SCAMP3	0			
SDHA	0			
SEC61B	0			
SEC61G	0			
SFRS9	0			
SGSH	0			
SIAHBP1	0			
SLC25A1	0			
SLC25A11	0			
SLC25A3	0			
SLC6A7	0			
SLC6A8	0			
SLC9A3R2	0			
SNRP70	0			
SNRPA	0			
SNRPB	0			
SNRPG	0			
SNX3	0			
SPAG7	0			
SRM	0			
SRRM1	0			
SSR2	0			
SSTR5	0			
STARD7	0			
STK19	0			
STK24	0			
SUMO2	0			
SUMO3	0			
SYNGR2	0			
TADA3L	0			
TAGLN	0			
TALDO1	0			
TAPBP	0			
TCEB2	0			

TCOF1	0			
TEGT	0			
TERF2IP	0			
TETRAN	0			
TEX261	0			
TKT	0			
TLN1	0			
TMED2	0			
TMEM4	0			
TMSB10	0			
TPMT	0			
TRAP1	0			
TSFM	0			
TSTA3	0			
TTC1	0			
TUBB4	0			
TUBGCP2	0			
TUT1	0			
UBE1	0			
UBE2D2	0			
UBE2I	0			
UBE2M	0			
UQCR	0			
UQCRC1	0			
UQCRFS1	0			
UQCRH	0			
USP11	0			
VIL2	0			
WDR1	0			
YARS	0			
YWHAH	0			
YWHAQ	0			
YWHAZ	0			
ZFPL1	0			
ZNF384	0			
ZNF91	0			

Table S1B: Housekeeping gene set used in computational scan.

GENE NAME	NO. OF HITS	FOX:ETS MOTIF	LOCATION	ANOTHER GENE WITHIN 10KB OF MOTIF
ALDOA	0			
ATP2A1	0			
ATP2A1	0			
ATP2A2	0			
CA3	0			
CACNA1S	0			
CACNG1	0			
CASQ1	0			
CFL2	0			
CKM	0			
CMYA5	0			
COX6A2	0			
CPT1B	0			
DES	0			
DUSP13	0			
DYSF	0			
DYSFIP1	0			
EEF1A2	0			
ENO3	0			
FLNC	0			
GAA	0			
GANAB	0			
HFE2	0			
KCNA7	0			
LMCD1	0			
MUSTN1	0			
MYBPC1	0			
MYBPC2	0			
MYBPH	0			
MYF5	0			
MYF6	0			
MYH1	0			
MYH2	0			
MYH4	0			
MYL1	0			
MYL6B	0			
MYLK2	0			
MYLPF	0			
MYO18B	0			
MYOG	0			
MYOM2	0			
MYOT	0			
MYOZ1	0			
MYOZ2	0			
NEB	0			
PDK4	0			
PFKM	0			
PGAM2	0			
PHKA1	0			
PRKAA2	0			
PRRX1	0			
PVALB	0			
PYGM	0			
PYGM	0			
RYR1	0			

SGCA	0			
SGCG	0			
SIX1	0			
SMPX	0			
SMYD1	0			
SRL	0			
TCAP	0			
TMOD4	0			
TNNC1	0			
TNNC2	0			
TNNI1	0			
TNNI2	0			
TNNT3	0			
TPM2	0			
TPM3	0			
TRDN	0			
TTN	0			
UGP2	0			
UNC45B	0			
ZNF185	0			

Table S1C: Skeletal muscle gene set used in computational scan.

Gene name	FOX:ETS motif (human sequence)	Location (human 2004 assembly)	Bind in EMSA	Conservation	Endothelial specific enhancer	Endothelial/ Express/Tg
FLT4	TAGGAAAACAGGAAGTG	chr5:179983112-179983128	yes	Human: Xenopus	Yes	4/4/7
FOXP1	AGTCCAAACAGGAAAGG	chr3:71576377-71576393	yes	Human: Fugu	Yes	4/3/6
NRP1	TCTGTAAACAGGAAAGA	chr10:33631344-33631360	yes	Human: chicken	Yes	7/7/7
ECE1	TAGCTAAACAGGAAGGG	chr1:21351860-21351876	yes	Human: opposum	Yes	5/5/8
PDGFRB	AAGCACAACAGGAAATG	chr5:149497296-149497312	yes	Human: opposum	Yes	4/4/7
FGFR2	GAGAAAAACAGGATATT	chr10:123346296-123346312	Yes	Human: chicken	No	0/1/6
NR4A3	TGATAAAACAGGAAAAC	chr9:99656354-99656364	Yes	Human: chicken	No	0/5/8
EFNB1	CAGCCAAACAGGAAGAT	chr23:67854018-67854034	Yes	Human: chicken	No	0/3/5
WNT2B	TTCTGAAACAGGAAAAC	chr1:112765333-112765349	Yes	Human: chicken	ND	
STAT5B	AATACAAACAGGAAGCA	chr17:37678267-37678283	Yes	Human: Xenopus	ND	
ESM1	AACAGAAACAGGAAATA	chr5:54302814-54302830	No	Human: chicken	ND	
FOXO1A	GTGAAAAACAGGAATTT	chr13:40036590-40036606	No	Human: chicken	ND	
RAC1	CAGAGAAACAGGAAATG	chr7:6187392-6187408	No	Human: chicken	ND	

Table S2. Putative enhancers identified in genome-wide scan for FOX:ETS motifs.

Primer name	**Primer sequence**
mef2c-F10 (+)	catctccttttcccggggtttcc
mef2c-F10(-)	ccttctcccgggcccatctctgt
mef2c-F10 •44 (+)	gttactgttagctcagcagggaat
mef2c-F10 •44 (-)	gctaacagtaacttcttccttcccac
mef2c-F10 44bp (+)	tcgagcaggaagcacatttgtctacgctttcctgtcataacaggaagaga
mef2c-F10 44bp (-)	agcttctcttcctgttatgacaggaaagcgtagacaaatgtgcttcctgc
mef2c-F10 mutFOX:ETS (+)	tgtcata**t**c**ta**gaagagagtaact
mef2c-F10 mutFOX:ETS (-)	agttactctcttc**ta**g**a**tatgaca
VE-CADHERIN 377bp (+)	aggagggttactagtgatgctgca
VE-CADHERIN 377bp (-)	agggctgagcactagtggagctctgtgg
VE-CADHERIN 3.5kb (+)	agtgccctgggaactagtaagagggagt
VE-CADHERIN 3.5kb (-)	ttccactagtctgcctgtccgtccagg
VE-CADHERIN 3.5kb mutFOX:ETS (+)	aagg**c**ac**c**ata**tg**agg**c**aaccatcccaggg
VE-CADHERIN 3.5kb mutFOX:ETS (-)	ggttgcct**ca**tat**g**gt**g**cctttgtgagggc
Flk1 enhancer (+)	acaagaaatgtcagtgggcc
Flk1 enhancer (-)	gggattgactttgccccagt
NOTCH4 enhancer (+)	cacactcccgggcaggtcccttgtc
NOTCH4 enhancer (-)	ggctcaatgctcggcctttccgg
Tie2 promoter (+)	tgtcagggtacccaaatgcaccccagag
Tie2 promoter (-)	tccacactcgagcatgagtccctgggaa
Mef2c ChIP PCR (+)	tattggagttgggagctaaa
Mef2c ChIP PCR (-)	ctacattccctgctgagcta
Ve-cadherin ChIP PCR (+)	caccgcagggcctgcctat
Ve-cadherin ChIP PCR (-)	tgtcagccgaccgtctttgga
Flk1 ChIP PCR (+)	aagaccttgaagttggcaac
Flk1 ChIP PCR (-)	gggattgactttgccccagt
Tal1 ChIP PCR (+)	ccagctcctacttaagctct
Tal1 ChIP PCR (-)	ctgctatcggcacagcagt
Notch4 ChIP PCR (+)	caggccttccattcatagct
Notch4 ChIP PCR (-)	ttaggtgtctcagccattca
Tie2 ChIP PCR (+)	caagccctgctgataccaagt
Tie2 ChIP PCR (-)	caaggagaaacaccacagaa
FLT4 putative enhancer (+)	acaggacccgggatagtgaggcaga
FLT4 putative enhancer (-)	aggagacccgggccattactgccat
PDGFRß putative enhancer (+)	agtcaaaagcttccacgtcccaagcct
PDGFRß putative enhancer (-)	gagagcaagcttcaccccattcagt
ECE1 putative enhancer (+)	cataatcccgggcaaaaacacgcga
ECE1 putative enhancer (-)	tgactgacccgggccagacatcacc
NRP1 putative enhancer (+)	tcaggacccgggtcatgggcatgcat
NRP1 putative enhancer (-)	agatttcccgggttcatactggct
FOXP1 putative enhancer (+)	ctctccaagcttctcaacagtcat
FOXP1 putative enhancer (-)	ctccagaagcttttgctattgctgtt
FGFR2 putative enhancer (+)	cctccaaagcttagacccatctcttcg
FGFR2 putative enhancer (-)	aggaccaagcttctgcgtttggagt
NR4A3 putative enhancer (+)	attttgcccgggttatgctattgtt
NR4A3 putative enhancer (-)	gatagtcccgggctcactttatgatt
EFNB1 putative enhancer (+)	ctagaacccgggtcttctgtcttcaa
EFNB1 putative enhancer (-)	gagagtcccgggcttgaaatccca
Foxc1a morpholino	cctgcatgactgctctccaaaacgg
Foxc1b morpholino	gcatcgtacccctttcttcggtaca
Flk1 qPCR (+)	ggagttcttggcttcaagaa
Flk1 qPCR (-)	ctgtcaaagatggttctgg
Pecam qPCR (+)	atgagtgtgacgtgttctgtg

Pecam qPCR (-)	gacagccatgcaatgtctatg

Table S3: Oligonucleotide primers for cloning, mutagenesis, morpholino knockdown, qPCR, and ChIP.

Oligo name	**Oligo sequence**
Mef2c-F10-44 FOX-NC (+)	ggaagttactctcttcctgttatgacaggaaagcgtagaca
Mef2c-F10-44 mut FOX-NC (+)	ggaagttactctcttc**ta**g**a**tatgacaggaaagcgtagaca
Mef2c-F10 FOX:ETS (+)	aagttactctcttcctgttatgacagg
Mef2c-F10-44 ETS-A (+)	ggagttactctcttcctgttatgaca
Mef2c-F10-44 mutETSA (+)	ggagttactctcttc**ta**g**a**tatgaca
Flk1 FOX:ETS (+)	ggctgcccattcttcctgttatgacagagcttgtgaa
Flk1 mutFOX:ETS (+)	ggctgcccattcttcc**acggcc**gacagagcttgtgaa
Tal1 FOX:ETS (+)	ggcgaacggatcacatcctgttattgtgtggaaagaaagaa
Tal1 mutFOX:ETS (+)	ggcgaacggatcacatcctg**agc**t**c**gtgtggaaagaaagaa
CDH5 FOX:ETS (+)	ggcctcgggatggtttcctgttattgttcctttgtgagctg
CDH5 mutFOX:ETS (+)	ggcctcgggatggtttcctg**agctc**gttcctttgtgagctg
NOTCH4 FOX:ETS (+)	ggccctacccccctttcctgtttattctctggcctc
NOTCH4 mutFOX:ETS (+)	ggccctacccccctttcc**acca**tattctctggcctc
Tek FOX:ETS (+)	ggtgcaaaggaaacaggaaaaaggaactt
Tek mutFOX:ETS (+)	ggtgcaaaggaa**tcta**gaaaaaggaactt
FoxC1/2 control site (+)	ggggaggagcagcctgtttgttttgccagatctgtgc
FoxF1/FoxA2 control site (+)	ggcttgcacgtaattgtttstttacgagcgt
FoxH1 control site (+)	gggattagaagatgtggattgcgtccgg
FoxO1 control site (+)	gggacgttttaggttgtttattcct
Ets1/ER71 control site (+)	ggaaccaagcttgagtaccggaagagtacaccg
Erg control site (+)	gggagagtgcaccggaagtcagttaa
Elf1 control site (+)	taaacccggaagtgtagtacatctggatcg

Table S4: Sense strand sequence of oligonucleotide probes used in EMSA. For the mutant FOX:ETS oligonucleotides for *Mef2c*, *Flk1*, *Tal1*, *CDH5*, *NOTCH4*, and *Tek*, the mutations were confirmed experimentally to disrupt binding in EMSA by FoxC2, Etv2, and the Ets1 DNA binding domain.