Table S1. Primers used for isolation and cloning of *Tbx20*, and the generation of *Tbx20*-EGFP transgenic constructs

Primer description	Primer sequence
X. laevis Tbx20 exon1/forward (for BAC screen probe)	5′-CCA CTG TCA CAG CTC GAA CAT AGA-3′
X. laevis Tbx20 exon1/reverse (for BAC screen probe)	5′-CCT TGG GTG TCC CAC TTG ACA TTA-3′
Tbx20 5′ deletions (–1969)/forward	5′-CGC CGA ATT CAT GAC ACT TAC CAG ATA TG-3′
Tbx20 5′ deletions (–1483)/forward	5′-CGC CGA ATT CTG TAT TTA GCG CAC CTA-3′
Tbx20 5′ deletions (–944)/forward	5′-CGC CGA ATT CCC GTG AGG GGC AGT CAA-3′
Tbx20 5′ deletions (–334)/forward	5′-CGC CGA ATT CCT GCC CTA TTT GAT CAG C-3′
Tbx20 5′ deletions 3′ end/reverse	5′-CGG TGG ATC CAC TTC CAT-3′
Tbx20 (–251)/forward 5′ end	5′-CTT CTC TTA TGT CAC GTG TGC-3′
Tbx20 (–81)/forward 5′ end	5′-GTG ACG CTG CAG GGC TCC-3′
Tbx20 (–251/–81)/reverse 3′ end	5′-CCG GTG GAT CCA CTT CCA TG-3′
Tbx20 elimination of 334 bp element/forward	5′-CCG AAT TCT CAT AAA GCA GCT TATG-3′
Tbx20 elimination of 334 bp element/reverse	5′-GTG GAT CCG ATA TTT TAA TAA ATA AAC-3′

Table S2. PCR primers used in 5′ RLM-RACE

Primer description	Primer sequence
X. tropicalis Tbx20-specific 5′ primer	5′-AGC AGC TTA TGG TAG GGT TTC T-3′
X. tropicalis Tbx20 5′ RLM-RACE inner	5′-CTT TCA GCA TTC ACA CGC TTC A-3′
X. tropicalis Tbx20 5′ RLM-RACE outer	5′-TGT ACT CAT TCC CGA CAG CGT-3′
X. tropicalis Tbx20-specific 5′ primer (2)	5′-ACT GTC AGA GCT CCA ACC TAG ACT-3′
X. tropicalis Tbx20 5′ RLM-RACE inner (2)	5′-AGA GGG TGT GTA TTC CAT GCT GGA-3′
X. tropicalis Tbx20 5′ RLM-RACE outer (2)	5′-TGC TCT CCT GTG TCT CTT TGT CCA-3′

Table S3. ChIP primer sequences

ChIP primer	Primer sequence
Xnr6 inner/forward	5′-GGT AGA TGA AAG GCT GAC AGG TGT G-3′
Xnr6 inner/reverse	5′-GGC TGT TGA AAA CTG AAA TGA AGC-3′
SMAD1 sites/forward	5′-TTT CTC TCG GAG CCC AGT GA-3′
SMAD1 sites/reverse	5′-GCT GAT AAG TGT CTG GGA GG-3′
Non-canonical SMAD1 site/forward	5′-ATA GGA TCT GTG TGG CCA TG-3′
Non-canonical SMAD1 site/reverse	5′-CTG ACA GTG GCC AGG AGA TT-3′

Table S4. Dissociation constants (K_d), standard deviation and nucleotide sequence for each oligonucleotide analyzed in fluorescence polarization studies

Oligonucleotide	K_d (mM)	Standard deviation	Oligonucleotide sequence
xVent	7.829	0.7465	AGAGAGAATGTTTAGCATAACAATAGC
SRF site	13.59	0.6407	AGCTTCTTTACACAGGATGTCCATATTAGGACATCTGCGTCAGCAA
Oligo 21	6.535	0.2181	CTATTTGATCAGCAAACGAGATGGATTACA
Oligo 20	8.512	0.3635	ACGAGATGGATTACAGATGAGCATCCTTAG
Oligo 19*	3.758	0.2244	GATGAGCATCCTTAGATTACTCTAAAAGCC
Oligo 18	9.539	0.4817	ATTACTCCTAAAAGCCCCGCCCTTCTCTTAT
Oligo 17	5.631	0.4146	CCGCCCTTCTCTTATGTCACGTGTGCTTTT
Oligo 16*	2.848	0.08203	GTCACGTGTGCTTTTTTTTAGTAAGTCTTT
Oligo 15	8.428	0.1427	TTTTAGTAAGTCTTTTTCTCTCGGAGCCCA
Oligo 14	9.473	0.7696	TTCTCTCGGAGCCCAGTGAGAAAAAGAAGT
Oligo 13*	3.56	0.19	GTGAGAAAAAGAAGTAGCTCGGCTGATCCT
Oligo 12	9.128	1.409	AGCTCGGCTGATCCTATCTGGCCCTGCTCC
Oligo 11	6.382	0.6181	ATCTGGCCCTGCTCCATCCCTGCTGCCCTT
Oligo 10	5.97	0.598	ATCCCTGCTGCCCTTCATTCATTGCCTGTG
Oligo 9*	2.836	0.3847	CATTCATTGCCTGTGCTCCAGCCGCCACCT
Oligo 8*	2.078	0.2239	CTCCAGCCGCCACCTCCCAGACACTTATCA
Oligo 7	5.566	0.4806	CCCAGACACTTATCAGCTGTATCAGGCAGA
Oligo 6*	2.402	0.1846	GCTGTATCAGGCAGATGTGACGCTGCAGGG
Oligo 5	7.201	0.5312	TGTGACGCTGCAGGGCTCCAATTGGCCAGG
Oligo 4	8.436	0.3279	CTCCAATTGGCCAGGAGAGAGATAGGATCT
Oligo 3	10.03	0.4913	AGAGAGATAGGATCTGTGTGGCCATGAAAT
Oligo 2*	3.106	0.1021	GTGTGGCCATGAAATTAAGGAAGCAGAGGC
Oligo 1	14.03	1.1	TAAGGAAGCAGAGGCTGAGAATGGGAACAG

*Oligonucleotides bound by SMAD1.