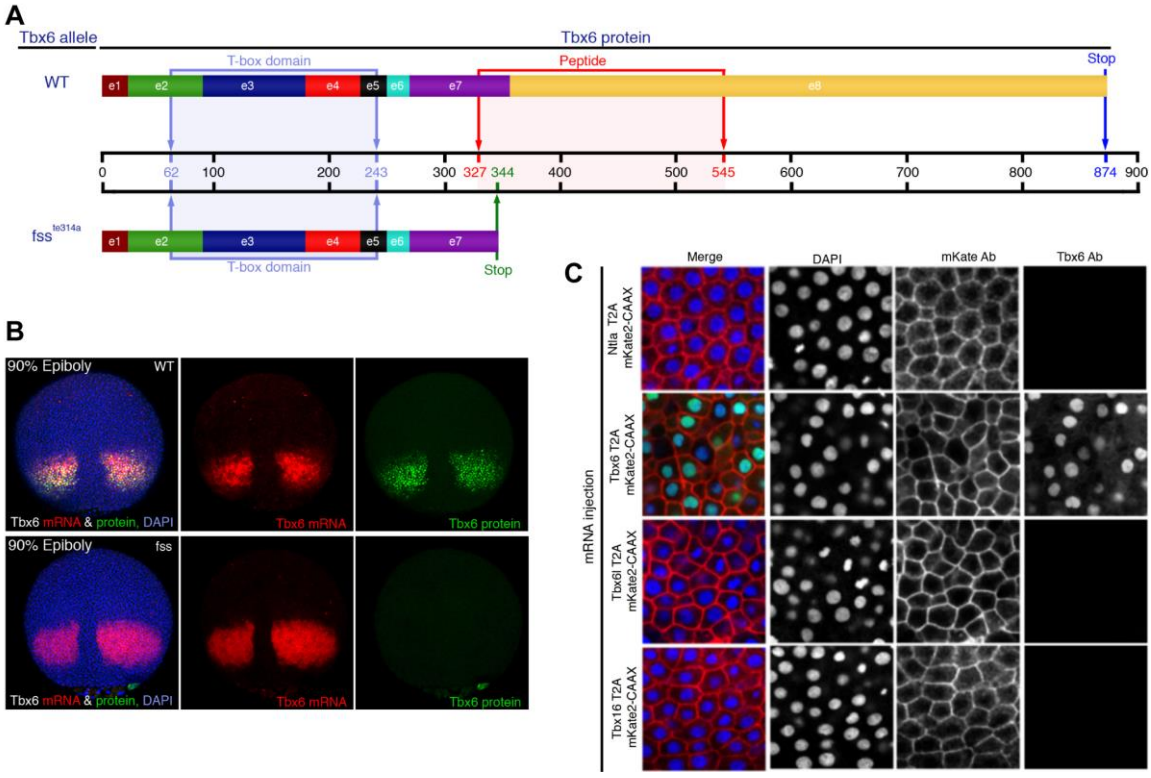

Figure S1. Tbx6 antibody-binding specificity. (A) Graphical representation of the full-length Tbx6 protein in wild-type embryos, and the truncated Tbx6 protein in *tbx6* mutants. All eight exons are depicted in different colors. The blue arrows represent the predicted T-box domain from amino acid 62 to 243. The sequence chosen to generate the Tbx6 antibody is highlighted in red, spanning the region from amino acid 327 to 545. (B) Representative example showing *tbx6* mRNA and protein expression patterns in wild type and in *tbx6* mutants at 90% epiboly. Immunolabeling using the Tbx6 antibody was followed by *in situ* hybridization using a *tbx6* probe and the Fast Red reaction (Roche) (C) Immunolabeling using Tbx6 (green) and tRFP (red fluorescent protein mKate2) antibodies. Animal poles of *tbx6* mutant embryos 4 hours post fertilization, injected at the 1-cell-stage with capped mRNAs (generated using the Tol2 kit and the mMessage kit, Ambion): *Ntla-T2A-mKate2CAAX*, *Tbx6-T2A-mKate2CAAX*, *Tbx6l-T2A-mKate2CAAX* or *Tbx16-T2A-mKate2CAAX*. The Tbx6 antibody only binds in embryos injected with *tbx6* mRNA. Embryos were imaged with a Zeiss LSM 780 and confocal *z*-stacks were flattened.

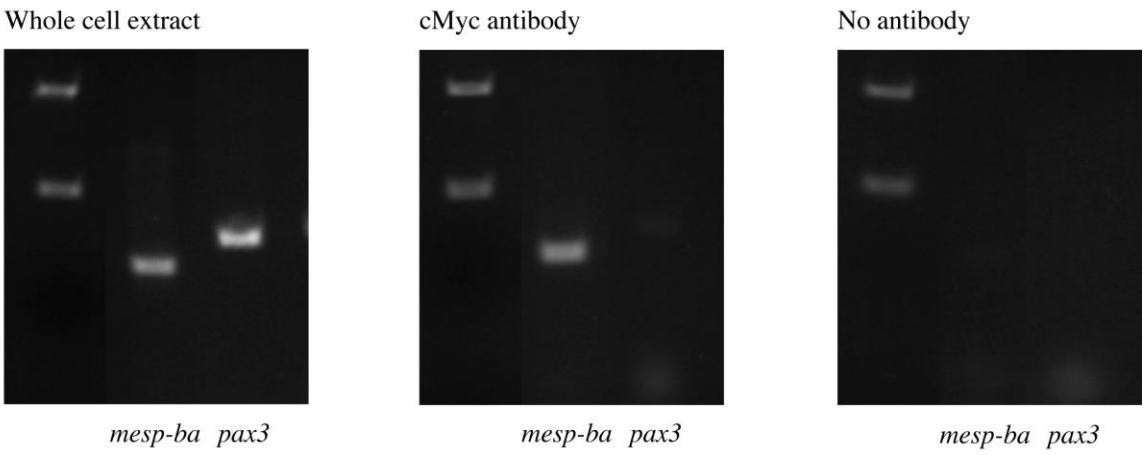

Figure S2. ChIP-PCR confirming Tbx6^{Myc} binding approximately 6700 bp upstream of the *mesp-ba* transcriptional start site (peak 16075430-16075735). *Tg(hsp70l:tbx6^{myc})* and wild-type embryos were heat-shocked, fixed and extracted as for ChIP-Seq. The extract was immunoprecipitated using the Myc epitope antibody (9B11, Cell Signaling Technology), as in Martins-Taylor et al. (2011). The DNA isolated by ChIP was amplified using the following primers: *mesp-ba* 5'-AATGGTAGTCAGGCAGAAGTG-3', 5'-CTGCAGCAAGTTGCCTTACAG-3'; *pax3* 5'-AGTAGTATCGCCCGGTCTTCTC-3', 5,-CCTGAGGGACAAAACATC-3'. Specificity of Tbx6^{Myc} binding was confirmed, as DNA upstream of the *pax3* gene is not pulled down using a Myc antibody, serving as a negative control, whereas a no-Myc-antibody control fails to immunoprecipitate DNA from upstream both of *mesp-ba* and *pax3*. Peak 16082055-16082560 was confirmed by Kawamura et al. (2008), using the following primers: 5'-CAACAAACACAAAAAGCACACGTT-3', 5'-GGTGAAAGGAGGATGGAGGTTTAT-3'.

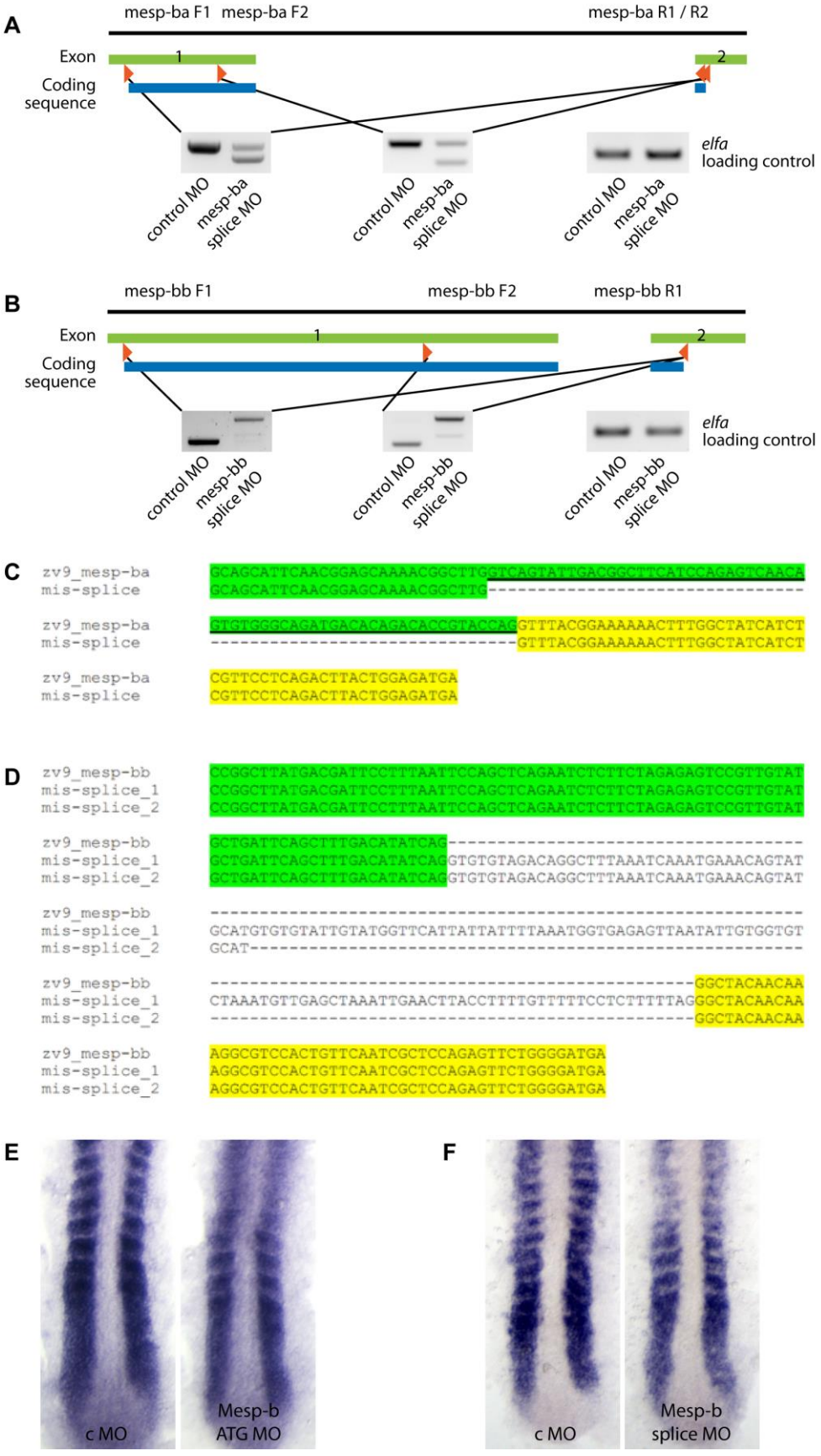

Figure S3. Mesp-b MO validation. (A,B) Mesp-ba (A) and Mesp-bb (B) splice morpholino transcript schematics and PCR primers are shown on top, the RT-PCR of

injected embryos is shown below. (C) Green highlight - 3' part of Zv9 *mesp-ba* exon 1; Yellow highlight - Zv9 *mesp-ba* exon 2 (until stop codon, excluding 3' UTR); Underlined - Sequence missing from *mesp-ba* mis-splice product. (D) Green highlight - 3' part of Zv9 *mesp-bb* exon 1; Yellow highlight - Zv9 *mesp-bb* exon 2 (until stop codon, excluding 3' UTR). Mis-splice_1 is the larger product, mis-splice_2 the smaller product shown in (B). (E,F) In situ hybridization for *meox1* mRNA in control and Mesp-b MO-treated embryos. Mesp-b ATG MOs and Mesp-b splice MOs cause similar reduction of *meox1* expression in maturing somites.

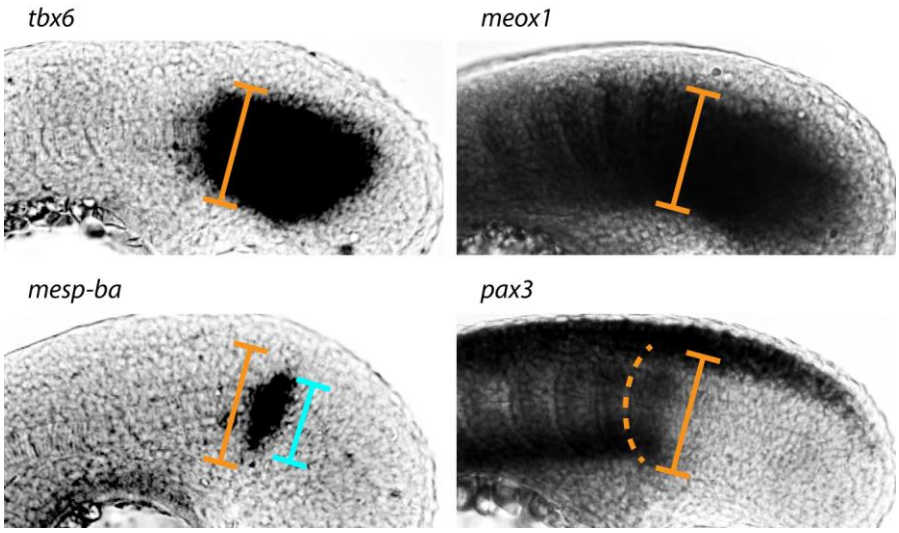

Figure S4. Expression of *tbx6, meox1, mesp-ba* and *pax3* mRNA. Expression of *tbx6*, *meox1* and *pax3* spans the entire dorsal-ventral extent of the paraxial mesoderm (orange brackets). *mesp-ba* mRNA is highly expressed in the central region (blue bracket) but not detectable in the peripheral portions of the presomitic paraxial mesoderm. Dashed line indicates most recently formed somite boundary.

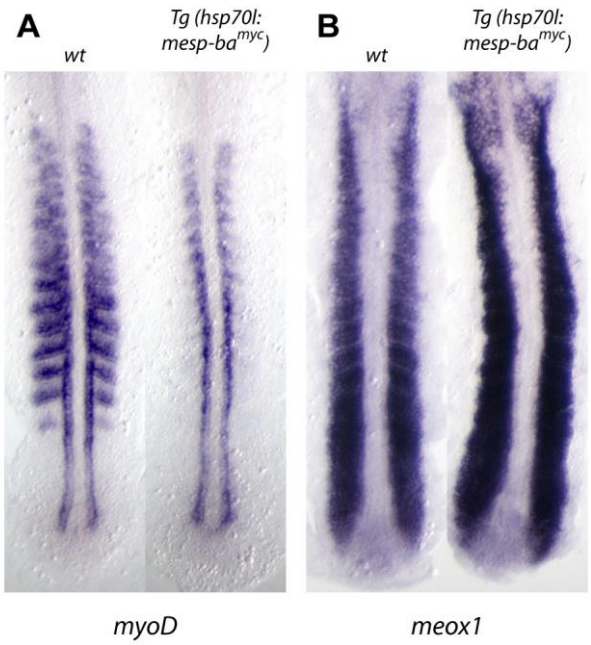

Figure S5. Ubiquitous Mesp-ba expression immediately changes *myoD* and *meox1* mRNA levels. *In situ* hybridization for *myoD* (C) and *meox1* (D) in wild-type (left side) and *Tg(hsp70l:mesp-ba^{myc})* embryos (right side) 15 minutes after the end of a 1-h heat shock. *myoD* is downregulated and *meox1* is upregulated in the lateral paraxial mesoderm.

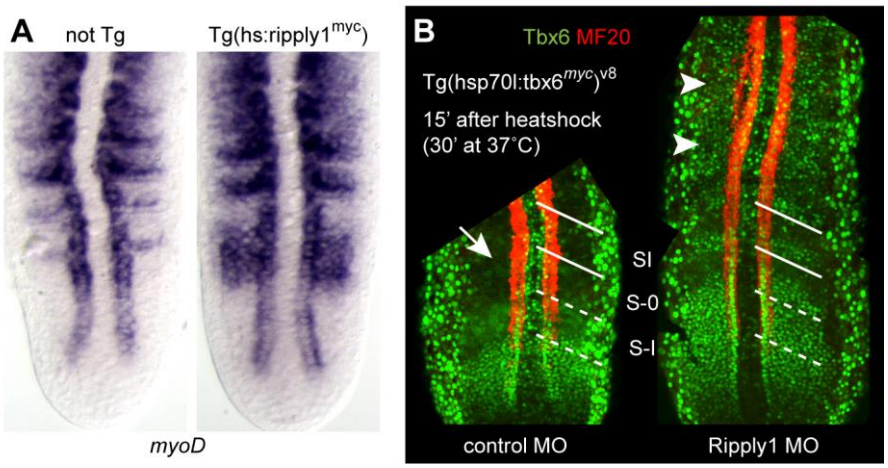

Figure S6. Ripply1 regulates Tbx6 function. (A) *In situ* hybridization for *myoD* in wild-type embryos and *Tg(hsp70l:ripply1^{myc})* siblings after a series of three heat shocks (30 minutes each, followed by 30-minute breaks). Ubiquitous expression of Ripply1 leads to an increase of *myoD* expression in the anterior presomitic mesoderm. (B) *Tg(hsp70l:tbx6^{myc})^{v8}* embryos, injected with control (left) or Ripply1 MOs (right); heat-shocked at the 10S stage for 30 minutes and fixed 15 minutes after the end of heatshock treatment. Immunolabeling shows expression of Tbx6 (green) and myosin heavy chain (MF20, red). Immediately after ubiquitous Tbx6^{Myc} expression, Tbx6 protein is cleared from the paraxial mesoderm in control but not in Ripply1 MO-treated embryos.

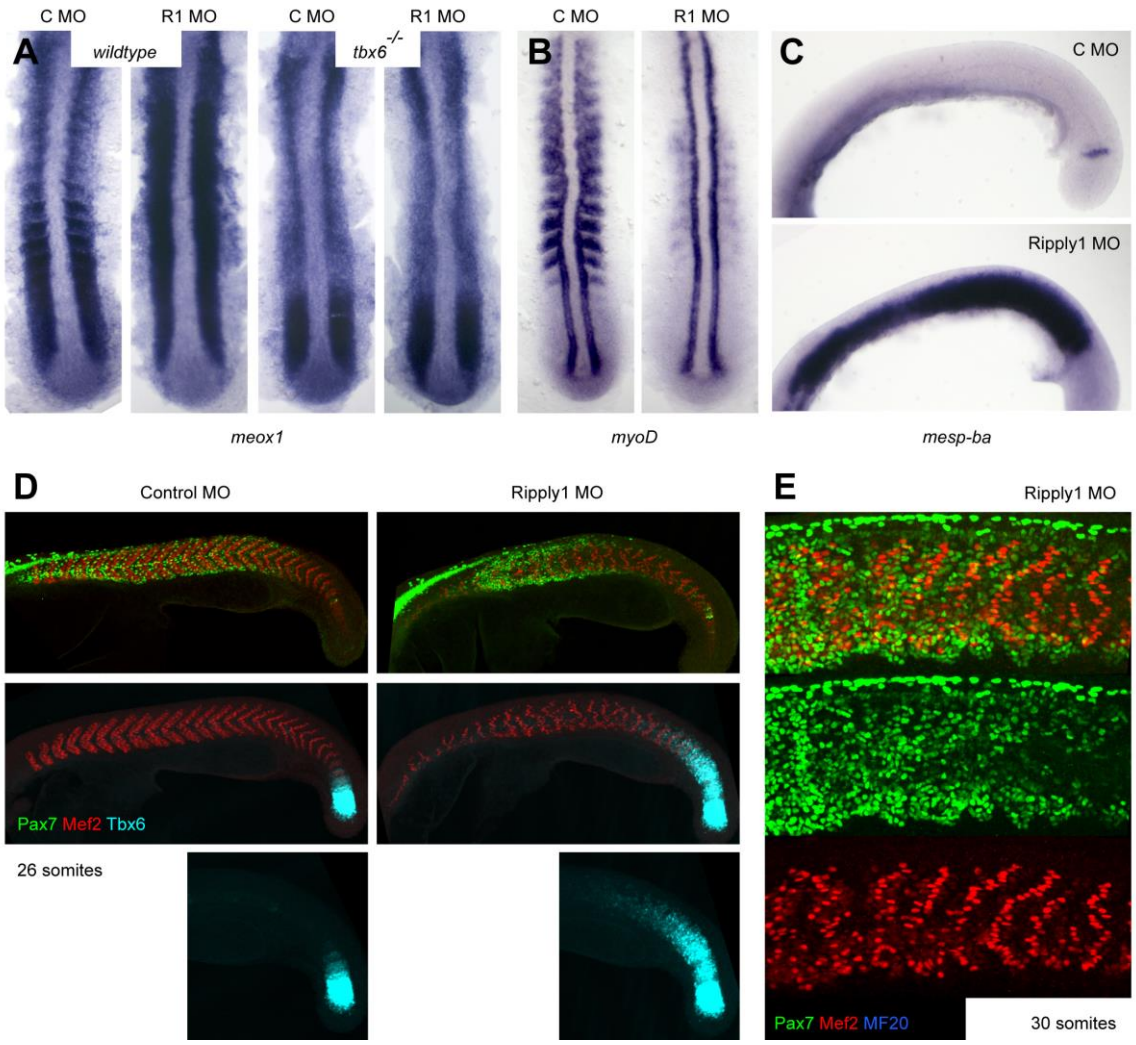

Figure S7. Knockdown of Ripply1 promotes dermomyotome development at the expense of primary fast myotome primary fast muscle formation but delays maturation. (A-C) *In situ* hybridization for *meox1* (A), *myoD* (B) and *mesp-ba* (C) in control MO and Ripply1 MO-injected embryos during segmentation. Note that Ripply1 MO treatment shows no effects in *tbx6* mutants. (D,E) Immunolabeling in Ripply1 MO- and control MO-treated embryos. (D) Comparison of Pax7 (green) and Tbx6 expression (cyan) in embryos at the 26S stage. Myonuclei are labeled with Mef2 (red). (E) Ripply1 morphant showing that the onset of Pax7 expression (green) spatially correlates with the appearance of the first primary fast myotome cells (Mef2, faint red). Slow fiber nuclei express Mef2 (bright) before the maturation of the dermomyotome.

Table S1. ChIP-Seq. Tables listing the positions of significant peaks identified in duplicate anti-Myc immunoprecipitation experiments from *Tg(hsp70l:tbx6^{myc})* embryos 1 h after heat shock treatment (see Fig. 1F), and corresponding gene positions.

Chromosome	Peak start	Peak stop	Peak size	Proximal gene
chr7	16074838	16075110	273	*mespba;mespaa*
chr7	**16075430**	**16075735**	306	*mespba;mespaa*
chr7	16077395	16077604	210	*mespba;mespaa*
chr7	**16082055**	**16082560**	506	*mespaa;mespba*
chr21	36933621	36934092	472	*mespbb;mespab*
chr21	36935687	36936177	491	*mespbb;mespab*
chr21	36936989	36937357	369	*mespbb;mespab*
chr21	36951345	36951918	574	*mespbb;mespab*
chr21	36952555	36952924	370	*mespbb;mespab*
chr21	36958013	36958556	544	*mespbb;mespab*
chr21	36960812	36961218	407	*mespbb;mespab*
chr25	11386856	11387147	292	*ripply1*
chr25	11386856	11387147	292	*ripply1*
chr25	11389407	11389883	477	*ripply1*
chr25	11393143	11393773	631	*ripply1*
chr25	11396259	11396835	577	*ripply1*
chr25	11398508	11398877	370	*ripply1*
chr25	11400599	11401158	560	*ripply1*

Gene name	Chromosome	Gene start	Gene stop	Strand
mespaa	chr7	16098653	16101163	1
mespba	chr7	16082277	16085567	1
mespab	chr25	11382068	11383326	-1
mespbb	chr25	11392554	11393558	-1
ripply1	chr21	36930713	36937075	-1

Table S2. Location of potential T-boxes within genomic regions represented in Figure 1F.

All Tboxes of >50% of the maximum possible score relative to the motif identified in this study are shown (see Materials and Methods). Whether each sequence is located under a ChIP-seq peak is indicated.

Chromosome	Region start	Region end	Tbox start	Tbox end	Tbox strand	% of max. score	Sequence	Under ChIP-seq peak
7	16069000	16104000	16070479	16070486	+	59.2	TCACACAC	
7	16069000	16104000	16070660	16070667	-	54.8	TCACAGCA	
7	16069000	16104000	16071406	16071413	-	54.8	TCACAGCA	
7	16069000	16104000	16071516	16071523	-	61.5	TCACACTA	
7	16069000	16104000	16071869	16071876	-	83.3	TCACACTT	
7	16069000	16104000	16072717	16072724	-	57.3	TGACACCA	
7	16069000	16104000	16074474	16074481	+	54.8	TCACAGCA	
7	16069000	16104000	16075011	16075018	+	100.0	TCACACCT	*
7	16069000	16104000	16075046	16075053	-	100.0	TCACACCT	*
7	16069000	16104000	16075312	16075319	-	100.0	TCACACCT	
7	16069000	16104000	16075592	16075599	+	61.5	TCACACTA	*
7	16069000	16104000	16077272	16077279	-	72.0	TCACATCT	
7	16069000	16104000	16077486	16077493	-	59.0	TCACACAA	*
7	16069000	16104000	16077497	16077504	+	100.0	TCACACCT	*
7	16069000	16104000	16077744	16077751	-	55.4	TCACATTT	
7	16069000	16104000	16078528	16078535	+	60.5	ACACACTT	
7	16069000	16104000	16078566	16078573	+	56.4	AGACACCT	
7	16069000	16104000	16078600	16078607	+	58.1	ACACACAT	
7	16069000	16104000	16078629	16078636	+	58.1	ACACACAT	
7	16069000	16104000	16079062	16079069	-	60.0	TCACAGTT	
7	16069000	16104000	16079666	16079673	+	83.3	TCACACTT	
7	16069000	16104000	16080777	16080784	+	55.4	TCACATTT	
7	16069000	16104000	16082207	16082214	+	100.0	TCACACCT	*
7	16069000	16104000	16082307	16082314	-	79.2	TGACACCT	*
7	16069000	16104000	16082310	16082317	+	55.2	TGTCACCT	*
7	16069000	16104000	16082740	16082747	+	52.6	TCTCAGCT	
7	16069000	16104000	16083275	16083282	+	55.3	ACACACCA	
7	16069000	16104000	16083386	16083393	-	60.1	TGACACAT	
7	16069000	16104000	16084350	16084357	-	58.1	ACACACAT	
7	16069000	16104000	16084624	16084631	+	55.4	TCACATTT	
7	16069000	16104000	16084808	16084815	-	79.2	TGACACCT	
7	16069000	16104000	16084871	16084878	+	77.2	ACACACCT	
7	16069000	16104000	16084924	16084931	-	60.5	ACACACTT	
7	16069000	16104000	16085135	16085142	+	51.3	TGACATCT	

7	16069000	16104000	16085366	16085373	+	78.1	TCACACCA	
7	16069000	16104000	16086360	16086367	-	76.7	TCACAGCT	
7	16069000	16104000	16088251	16088258	+	83.3	TCACACTT	
7	16069000	16104000	16089113	16089120	+	80.9	TCACACAT	
7	16069000	16104000	16089181	16089188	-	52.9	TCACATAT	
7	16069000	16104000	16089327	16089334	+	77.2	ACACACCT	
7	16069000	16104000	16089937	16089944	-	72.0	TCACATCT	
7	16069000	16104000	16090015	16090022	+	78.1	TCACACCA	
7	16069000	16104000	16090098	16090105	-	53.9	ACACAGCT	
7	16069000	16104000	16090220	16090227	+	58.1	ACACACAT	
7	16069000	16104000	16090266	16090273	-	80.9	TCACACAT	
7	16069000	16104000	16091463	16091470	+	58.1	ACACACAT	
7	16069000	16104000	16091896	16091903	+	80.9	TCACACAT	
7	16069000	16104000	16092292	16092299	+	80.9	TCACACAT	
7	16069000	16104000	16092376	16092383	-	83.3	TCACACTT	
7	16069000	16104000	16092567	16092574	+	52.9	TCACATAT	
7	16069000	16104000	16093663	16093670	+	100.0	TCACACCT	
7	16069000	16104000	16093721	16093728	+	51.3	TGACATCT	
7	16069000	16104000	16093753	16093760	+	57.3	TGACACCA	
7	16069000	16104000	16094026	16094033	-	78.3	TCACACCC	
7	16069000	16104000	16094395	16094402	+	55.3	ACACACCA	
7	16069000	16104000	16094402	16094409	-	55.4	TCACATTT	
7	16069000	16104000	16095140	16095147	-	53.9	ACACAGCT	
7	16069000	16104000	16095370	16095377	+	55.3	ACACACCA	
7	16069000	16104000	16095782	16095789	+	55.9	TGACAGCT	
7	16069000	16104000	16096636	16096643	+	60.5	ACACACTT	
7	16069000	16104000	16098455	16098462	-	80.9	TCACACAT	
7	16069000	16104000	16098493	16098500	+	100.0	TCACACCT	
7	16069000	16104000	16098980	16098987	+	54.1	TCTCACCA	
7	16069000	16104000	16099252	16099259	-	77.2	ACACACCT	
7	16069000	16104000	16099403	16099410	-	77.2	ACACACCT	
7	16069000	16104000	16099559	16099566	-	77.2	ACACACCT	
7	16069000	16104000	16099658	16099665	-	77.2	ACACACCT	
7	16069000	16104000	16100250	16100257	+	80.9	TCACACAT	
7	16069000	16104000	16101249	16101256	+	58.1	ACACACAT	
7	16069000	16104000	16101319	16101326	+	55.4	TCACATTT	
7	16069000	16104000	16102155	16102162	+	83.3	TCACACTT	
7	16069000	16104000	16102503	16102510	+	62.5	TGACACTT	
7	16069000	16104000	16102881	16102888	-	100.0	TCACACCT	
7	16069000	16104000	16103051	16103058	-	75.9	TCTCACCT	
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21	36929000	36964000	36929777	36929784	+	53.9	ACACAGCT	
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21	36929000	36964000	36931149	36931156	-	76.7	TCACAGCT	
21	36929000	36964000	36931207	36931214	+	76.7	TCACAGCT	
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21	36929000	36964000	36933942	36933949	+	61.7	TCACACTC	*
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21	36929000	36964000	36934098	36934105	+	59.2	TCACACAC	
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21	36929000	36964000	36939117	36939124	+	54.8	TCACAGCA	
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21	36929000	36964000	36945454	36945461	-	59.2	TCACACAC	
21	36929000	36964000	36945461	36945468	+	56.4	AGACACCT	
21	36929000	36964000	36946596	36946603	+	72.0	TCACATCT	
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21	36929000	36964000	36947552	36947559	-	77.2	ACACACCT	
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21	36929000	36964000	36947574	36947581	-	53.9	ACACAGCT	
21	36929000	36964000	36948050	36948057	+	61.5	TCACACTA	
21	36929000	36964000	36948126	36948133	+	50.2	TCACATCA	
21	36929000	36964000	36948548	36948555	+	61.5	TCACACTA	
21	36929000	36964000	36948712	36948719	-	61.5	TCACACTA	
21	36929000	36964000	36948837	36948844	+	61.7	TCACACTC	
21	36929000	36964000	36948971	36948978	-	77.2	ACACACCT	
21	36929000	36964000	36949300	36949307	+	58.1	ACACACAT	
21	36929000	36964000	36949320	36949327	+	59.2	TCACACAC	
21	36929000	36964000	36949760	36949767	-	55.5	ACACACCC	
21	36929000	36964000	36951248	36951255	+	61.7	TCACACTC	
21	36929000	36964000	36951646	36951653	+	100.0	TCACACCT	*
21	36929000	36964000	36952060	36952067	+	54.8	TCACAGCA	
21	36929000	36964000	36952725	36952732	-	77.2	ACACACCT	*
21	36929000	36964000	36952731	36952738	-	59.2	TCACACAC	*
21	36929000	36964000	36952736	36952743	+	57.3	TGACACCA	*
21	36929000	36964000	36952748	36952755	+	78.3	TCACACCC	*
21	36929000	36964000	36952762	36952769	+	60.5	ACACACTT	*
21	36929000	36964000	36952829	36952836	+	83.3	TCACACTT	*
21	36929000	36964000	36952921	36952928	-	52.9	TCACATAT	
21	36929000	36964000	36953072	36953079	-	77.2	ACACACCT	
21	36929000	36964000	36953184	36953191	-	56.4	AGACACCT	
21	36929000	36964000	36953906	36953913	+	77.2	ACACACCT	
21	36929000	36964000	36953949	36953956	-	58.1	ACACACAT	
21	36929000	36964000	36953951	36953958	-	59.2	TCACACAC	
21	36929000	36964000	36954424	36954431	+	51.3	TGACATCT	
21	36929000	36964000	36954474	36954481	+	55.9	TGACAGCT	
21	36929000	36964000	36954658	36954665	-	77.2	ACACACCT	
21	36929000	36964000	36956034	36956041	+	59.2	TCACACAC	
21	36929000	36964000	36956128	36956135	-	53.2	ACTCACCT	
21	36929000	36964000	36956161	36956168	+	60.5	ACACACTT	
21	36929000	36964000	36956187	36956194	+	56.4	AGACACCT	
21	36929000	36964000	36957174	36957181	+	52.9	TCACATAT	
21	36929000	36964000	36958185	36958192	-	83.3	TCACACTT	*
21	36929000	36964000	36958252	36958259	-	60.5	ACACACTT	*

21	36929000	36964000	36958278	36958285	-	57.3	TGACACCA	*
21	36929000	36964000	36958283	36958290	+	59.2	TCACACAC	*
21	36929000	36964000	36958289	36958296	+	77.2	ACACACCT	*
21	36929000	36964000	36960955	36960962	-	77.2	ACACACCT	
21	36929000	36964000	36961411	36961418	+	61.7	TCACACTC	
21	36929000	36964000	36961583	36961590	-	54.8	TCACAGCA	
21	36929000	36964000	36962019	36962026	-	80.9	TCACACAT	
21	36929000	36964000	36962880	36962887	-	60.5	ACACACTT	
21	36929000	36964000	36962890	36962897	-	58.1	ACACACAT	
21	36929000	36964000	36962959	36962966	+	52.6	TCTCAGCT	
21	36929000	36964000	36963846	36963853	+	61.7	TCACACTC	
21	36929000	36964000	36963954	36963961	-	61.7	TCACACTC	
25	11374000	11409000	11374093	11374100	-	59.0	TCACACAA	
25	11374000	11409000	11374140	11374147	+	62.5	TGACACTT	
25	11374000	11409000	11375064	11375071	-	59.3	TCTCACTT	
25	11374000	11409000	11375672	11375679	-	55.4	TCACATTT	
25	11374000	11409000	11375998	11376005	-	50.2	TCACATCA	
25	11374000	11409000	11378246	11378253	+	60.5	ACACACTT	
25	11374000	11409000	11378812	11378819	-	60.1	TGACACAT	
25	11374000	11409000	11379037	11379044	+	59.2	TCACACAC	
25	11374000	11409000	11379713	11379720	-	83.3	TCACACTT	
25	11374000	11409000	11379774	11379781	-	80.9	TCACACAT	
25	11374000	11409000	11380313	11380320	+	50.2	TCACATCA	
25	11374000	11409000	11380634	11380641	-	57.3	TGACACCA	
25	11374000	11409000	11380818	11380825	-	59.3	TCTCACTT	
25	11374000	11409000	11382630	11382637	-	55.4	TCACATTT	
25	11374000	11409000	11382846	11382853	-	72.0	TCACATCT	
25	11374000	11409000	11383368	11383375	-	100.0	TCACACCT	
25	11374000	11409000	11383457	11383464	+	50.2	TCACATCA	
25	11374000	11409000	11385436	11385443	-	83.3	TCACACTT	
25	11374000	11409000	11385805	11385812	-	59.0	TCACACAA	
25	11374000	11409000	11386512	11386519	-	60.5	ACACACTT	
25	11374000	11409000	11386528	11386535	-	62.5	TGACACTT	
25	11374000	11409000	11386649	11386656	+	60.0	TCACAGTT	
25	11374000	11409000	11386671	11386678	-	55.4	TCACATTT	
25	11374000	11409000	11386742	11386749	+	58.1	ACACACAT	
25	11374000	11409000	11387069	11387076	+	57.3	TGACACCA	*
25	11374000	11409000	11387985	11387992	-	79.2	TGACACCT	
25	11374000	11409000	11388062	11388069	+	52.9	TCACATAT	
25	11374000	11409000	11389022	11389029	-	58.1	ACACACAT	
25	11374000	11409000	11389642	11389649	+	79.2	TGACACCT	*
25	11374000	11409000	11389837	11389844	-	59.0	TCACACAA	*
25	11374000	11409000	11390563	11390570	+	60.1	TGACACAT	
25	11374000	11409000	11391722	11391729	-	55.0	TCACAGCC	

25	11374000	11409000	11391931	11391938	-	54.8	TCACAGCA	
25	11374000	11409000	11392669	11392676	+	54.1	TCTCACCA	
25	11374000	11409000	11392703	11392710	+	58.1	ACACACAT	
25	11374000	11409000	11392743	11392750	+	77.2	ACACACCT	
25	11374000	11409000	11393160	11393167	+	52.6	TCTCAGCT	*
25	11374000	11409000	11393507	11393514	-	100.0	TCACACCT	*
25	11374000	11409000	11393517	11393524	+	79.2	TGACACCT	*
25	11374000	11409000	11393635	11393642	-	80.9	TCACACAT	*
25	11374000	11409000	11394510	11394517	-	58.1	ACACACAT	
25	11374000	11409000	11395279	11395286	-	54.8	TCACAGCA	
25	11374000	11409000	11395641	11395648	+	54.8	TCACAGCA	
25	11374000	11409000	11395820	11395827	-	59.0	TCACACAA	
25	11374000	11409000	11396018	11396025	-	58.1	ACACACAT	
25	11374000	11409000	11396190	11396197	-	62.5	TGACACTT	
25	11374000	11409000	11396398	11396405	-	58.1	ACACACAT	*
25	11374000	11409000	11396538	11396545	-	55.3	ACACACCA	*
25	11374000	11409000	11396560	11396567	+	60.0	TCACAGTT	*
25	11374000	11409000	11396597	11396604	+	55.0	TCACAGCC	*
25	11374000	11409000	11396687	11396694	+	78.1	TCACACCA	*
25	11374000	11409000	11396742	11396749	+	59.0	TCACACAA	*
25	11374000	11409000	11396922	11396929	+	78.3	TCACACCC	
25	11374000	11409000	11397110	11397117	+	76.7	TCACAGCT	
25	11374000	11409000	11397612	11397619	-	61.5	TCACACTA	
25	11374000	11409000	11398176	11398183	+	60.5	ACACACTT	
25	11374000	11409000	11398539	11398546	-	58.1	ACACACAT	*
25	11374000	11409000	11398607	11398614	-	59.2	TCACACAC	*
25	11374000	11409000	11399755	11399762	-	54.3	TCTCACCC	
25	11374000	11409000	11400617	11400624	+	56.4	AGACACCT	*
25	11374000	11409000	11400705	11400712	+	54.3	TCTCACCC	*
25	11374000	11409000	11400798	11400805	+	55.0	TCACAGCC	*
25	11374000	11409000	11400979	11400986	-	61.7	TCACACTC	*
25	11374000	11409000	11401466	11401473	-	60.1	TGACACAT	
25	11374000	11409000	11401705	11401712	-	50.2	TCACATCA	
25	11374000	11409000	11401801	11401808	+	61.5	TCACACTA	
25	11374000	11409000	11402307	11402314	+	55.3	ACACACCA	
25	11374000	11409000	11402726	11402733	+	57.3	TGACACCA	
25	11374000	11409000	11402813	11402820	+	55.4	TCACATTT	
25	11374000	11409000	11403108	11403115	+	55.4	TCACATTT	
25	11374000	11409000	11403212	11403219	-	58.1	ACACACAT	
25	11374000	11409000	11403214	11403221	-	59.2	TCACACAC	
25	11374000	11409000	11404083	11404090	+	58.1	ACACACAT	
25	11374000	11409000	11404479	11404486	-	54.3	TCTCACCC	
25	11374000	11409000	11405325	11405332	+	55.5	ACACACCC	
25	11374000	11409000	11405362	11405369	+	61.5	TCACACTA	

25	11374000	11409000	11405827	11405834	-	100.0	TCACACCT	
25	11374000	11409000	11406440	11406447	-	55.4	TCACATTT	
25	11374000	11409000	11406938	11406945	-	57.3	TGACACCA	

Table S3. List of primers, antibodies and RNA probes

Morpholino sequences	
Ripply1	5'-CATCGTCACTGTGTTTTTCGTTTTG-3 (Kawamura et al., 2005)
Mesp-ba ATG	5'-TCGGTTCTTGCTTGAGGTTTGCATG-3' (Kawamura et al 2005)
Mesp-bb ATG	5'-CGTCCA TTCTGTGTGGTTGGAGA TT-3'
Mesp-ba splice	5'-TAACTTAACATACCTGGTACGGTGT-3'
Mesp-bb splice	5'-TTTAAAGCCTGTCTACACACCTGAT-3'
Standard control	5'-CCTCCTACCTCAGTTACAATTTATA-3'
p53 MO	5'-GCGCCATTGCTTTGCAAGAATTG-3' (Robu et al., 2007)

Primary antibodies	
Pax7, MF20, F59, cMyc	1:10, DSHB
Mef2	1:100, Santa Cruz
b-cat	1:1000, Sigma
Tbx6	1:250

Secondary antibodies	
Alexa-conjugated	1:800, Invitrogen

RNA probes	
meox	(Neyt et al., 2000)
mesp-ba	(Sawada et al., 2000)
mesp-bb	(Cutty et al., 2012)
myf5	(Coutelle et al., 2001)
myoD	(Weinberg et al., 1996)
pax3, pax7	(Seo et al., 1998)
ripply1, tbx6	(Kawahara et al., 2005)