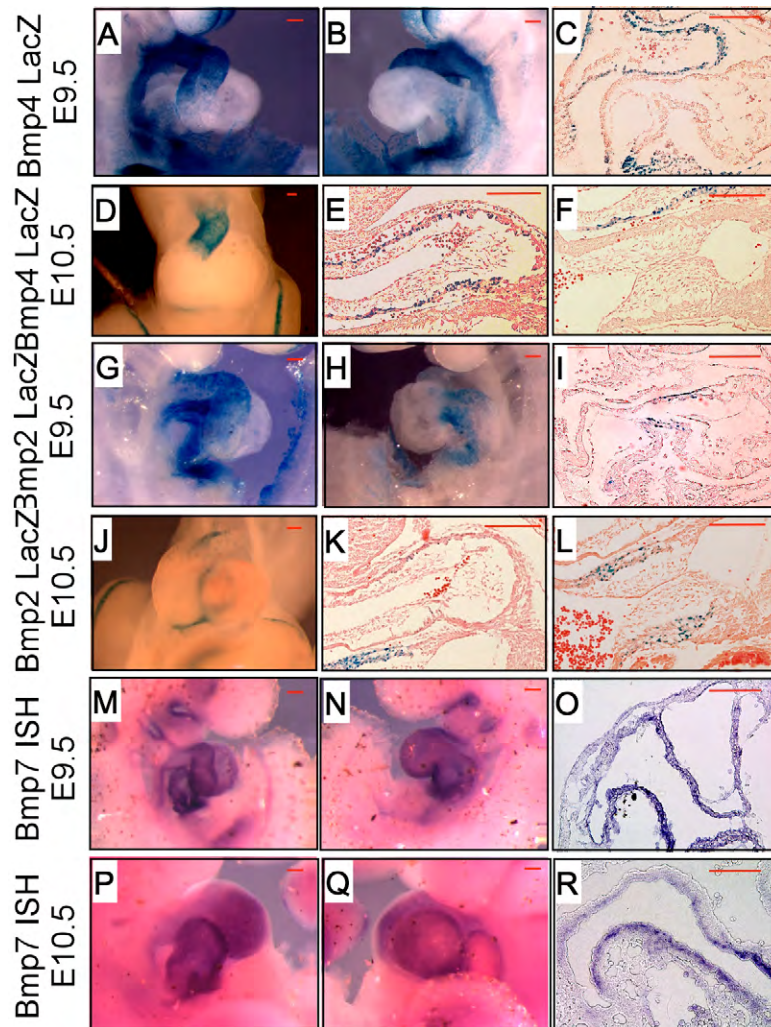


**Fig. S1. Targeting scheme for the inactivation of *Bmp7*.** (A) Targeting strategy for *Bmp7* ablation. (B) Southern blot analysis of the *Bmp7* flox allele. (C) qRT-PCR analysis of *Bmp7* in wild-type and knockout samples. (D) Quantification of *Bmp7* mRNA level.



**Fig. S2. Expression of *Bmp2/4/7* in the heart at E9.5 and E10.5.** (A-F) *Bmp4* is expressed in SHF, OFT, inflow tract and right ventricle at E9.5. Sections reveal that *Bmp4* is exclusively expressed in myocardium and not in endocardium or cushion mesenchyme of the OFT. (G-L) *Bmp2* is expressed in the OFT and AV cushion in E9.5 and E10.5 embryos. Its expression in the OFT is limited. (M-R) *In situ* hybridization shows that *Bmp7* is broadly expressed throughout the entire heart tube. At E10.5, *Bmp4* expression is restricted to the myocardium of the OFT; *Bmp7* expression is similar to that at E9.5. Scale bars: 100  $\mu$ m.

**Table S1. Oligonucleotides used for gene amplification, ChIP-PCR and qRT-PCR**

Primer	Sense (5'-3')	Antisense (5'-3')
Vegfa-promoter	AGGGTACCAGGGGACAGAGCCACA	ACCTCGAGCACGATTTAAGAGGGG
Vegfa-3'UTR	GT <u>ACTAGT</u> GCCAGGCTGCAGGAAGGAGCCTCCCTC AGGGTTT	GG <u>ACGCGT</u> TTTGAGATCAGAATTCAATTCTTTAAT ACAAA
s1-mut	CTGGCCTACCTACCTTCTGAGGTTTAGGGTAGGT TTGAATCACC	GGTGATTCAAACCTACCCTAA <u>ACCT</u> CAGAAAGGTA GGTAGGCCAG
SBE1-mut	CAGGAGGAACAAGGGCCTCTGA <u>ATTCCC</u> AGCTGTC TCTCCTTCAG	GAAGGAGAGACAGCTGGGA <u>ATTC</u> AGAGGCCCTTG TTCTC
SBE2-mut	CTCCTTCAGGGCTCTGC <u>CTCG</u> AGACACAGTGCATA CGTGG	CCACGTATGCACTGTGT <u>CTCG</u> AGGCAGAGCCCTGA AGGAG
SBE3-mut	CGTGA <u>ACTTGGGCGAGCCGAA</u> ATTCGTGAGGGA GGACGCGTGTG	CACACGCGTCTCCCTCACGAA <u>ATTC</u> GGCTCGCC CAAGTTCACG
3'UTR-mut	GGAGACTCTTCGAGGACTCGAGCGGGTCCGGAGG GCGAGACTCCGG	GGAGACTCTTCGAGGACTCGAGCGGGTCCGGAGG GCGAGACTCCGG
Site1-ChIP	TGGGAGGACAGAGTACACCCCTGA	CAGAGGCCCTTGTTCTCCTGA
Site2-ChIP	GGCACCTGGCTCAGTTCCC	TGCGTGTTGACCTCGGAAGC
Site3-ChIP	CCCCTTTCCAAGACCCGTGCC	ACCCCTGGCTTTCTCCCCCA
Id1	CCGCTCAGCACCTGAACGG	CCCCTGGGAACCGAGAGCA
Id2	TCCAGGACGCCGCTGACCA	CAACGTGTTCTCTGGTCAAATGGC
Slug	GCACTGTGATGCCAGTCTA	CAGTGAGGGCAAGAGAAAGG
Snai1	AAACCCACTCGGATGTGAAG	GAAGGAGTCTGGCAGTGAG

Underlines indicate restriction sites in Vegfa primers and mutation sites in other primers