Table S1. Genotype of newborn progeny obtained from *Bicc1*$^{+/-}$ intercrosses

	+/+	+/–	–/–	Missing*
n	70	134	34	(34)
%	26	49	12.5	(12.5)

*Number of Bicc1$^{-/-}$ mutants estimated by a Mendelian distribution to have died in utero.

Table S2. Altered gene expression patterns of *Xnr1* and *Pitx2c* in xBicC MO1/2 morphant *Xenopus* tadpoles

		***Xnr1* expression pattern**					
Injection	*n*	l	r	bi	absent	*P*-value	Significance
Uninjected	152	150	0	2	0	0.634	ns
DsRed	17	17	0	0	0		
Co-MO	66	65	0	1	0		
xBicC MO1/2 2 pmol	61	55	0	4	2	0.0401	ns†
xBicC MO1/2 4 pmol	99	45	1	7	46	$<10^{-3}$	***†

		***Pitx2c* expression pattern**					
Injection	*n*	l	r	bi	absent	*P*-value	Significance
Uninjected	187	186	0	0	1	0.7369	ns
DsRed	21	21	0	0	0		
Co-MO	81	76	0	4	1	$<10^{-3}$	***
xBicC MO1/2 4 pmol	84	54	3	3	24		

Embryos were injected into the dorsal marginal zone at the four-cell stage with mRNA encoding the lineage tracer DsRed, a control morpholino oligonucleotide (Co-MO), or a mixture of two morpholino oligonucleotides targeting *xBicC* (xBicC MO1/2) at the indicated amounts per embryo. Embryos were cultured to stage 22 for examination of *Xnr1* transcription (number of experiments, *n*=7) or stage 34 for in situ hybridization with a *Pitx2c* specific probe (*n*=6). Statistical significance was calculated by comparison of control and treated groups using Pearson's chi-square test in Statistica (StatSoft, Hamburg, Germany). ns, not significant; ***, very highly significant; †, Bonferroni-corrected.