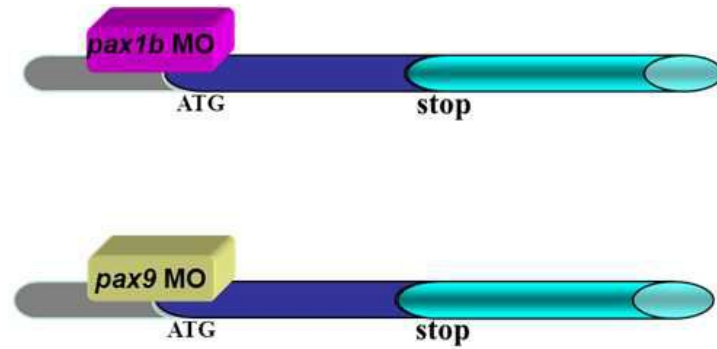**Supporting Information**

Figure S1. Schematic diagram of *pax1b* and zebrafish *pax9* translation blockers. The three-dimensional cubes represent two independent MOs and are not to scale.

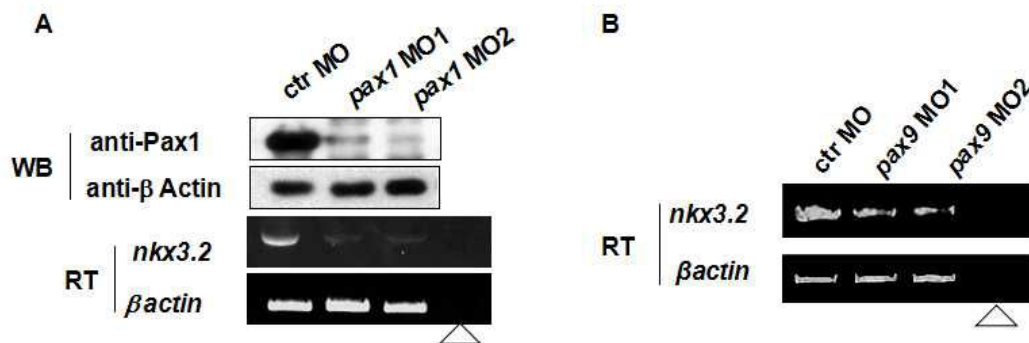**Figure S2. *pax1b* and zebrafish *pax9* morpholino efficiency.** (A) Western blot and RT-PCR analysis demonstrated that *pax1b* morpholino disrupted the production of PAX1 and its target *nkx3.2* cDNA, respectively. (B) zebrafish *pax9* morpholino reduced the production of its target *nkx3.2* cDNA assessed by RT-PCR. The triangles indicate the negative control, using TE buffer without template.
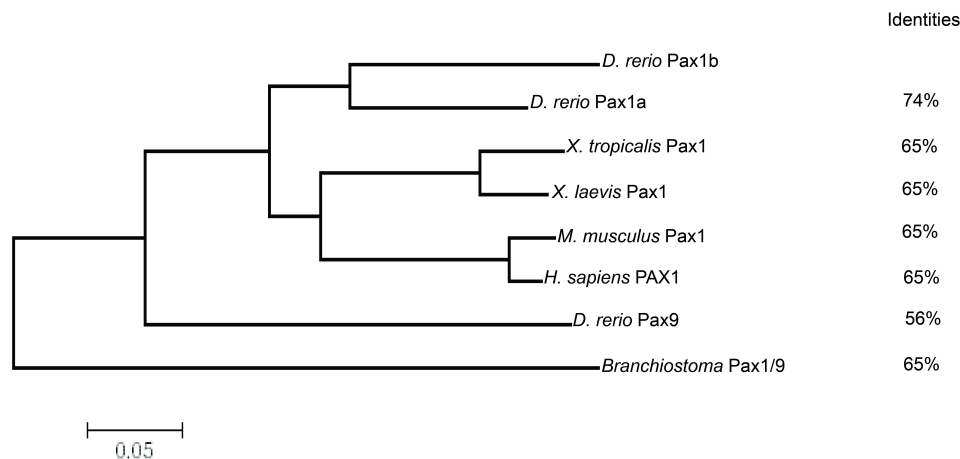
D. rerio Pax1b

D. rerio Pax1a　74%

X. tropicalis Pax1　65%

X. laevis Pax1　65%

M. musculus Pax1　65%

H. sapiens PAX1　65%

D. rerio Pax9　56%

Branchiostoma Pax1/9　65%

0.05

Figure S3. Phylogenetic analysis of Pax1a, Pax1b and Pax9 proteins from following species: *Danio rerio, Xenopus tropicalis, Xenopus laevis, Mus musculus, Homo sapiens, Branchiostoma belcheri.*

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                              10        20        30        40        50        60        70        80
Danio Pax1a           1   MLSCFAEQTYGEVNQLGGCVFVNGRPLPNAIRLRIVELAQLGIRPCDISRQLFVSHGCVSKILARYNETGSILPGAIGGSKPR
Danio Pax1b           1   ---MQMDQTYGEVNQLGGCVFVNGRPLPNAIRLRIVELAQLGIRPCDISRQLFVSHGCVSKILARYNETGSILPGAIGGSKPR
Danio Pax9            1   ------MEPAFGEVNQLGGCVFVNGRPLPNAIRLRIVELAQLGIRPCDISRQLFVSHGCVSKILARYNETGSILPGAIGGSKPR
Branchiostoma Pax1/9  1   ---MMNMEQTFGEVNQLGGCVFVNGRPLPNAIRLRIVELAQLGIRPCDISRQLFVSHGCVSKILARYNETGSILPGAIGGSKPR

                              90        100       110       120       130       140       150       160
Danio Pax1a          83   VTTPVVVKIRLYKQSDPGIFAWEIRDRLLADGVCDKANVPSVSSISRILRNKIGNLSQPNFYENG-KQAPEQSSISYNHIY
Danio Pax1b          80   VTTPVVVKSIRLYKQGDPGIFAWEIRDRLLADGVCDKANVPSVSSISRILRNKIGNLSQPSQYDS--KTSPHQ--ISYNPVY
Danio Pax9          78   VTTPVVVKFIRTYKQRDPGIFAWEIRDRLLADGVCDKFNVPSVSSISRILRNKIGNLSQQNQYESSKQASHQPQPTIPYNH
Branchiostoma Pax1/9 81  VTTPIVVKILFYKTLDPGIFAWEIRDRLLADGVCDKANVPSVSSISRILRNKIGNTIQLPDSFYGHPVKPEQHRPLYNPIY

                              170       180       190       200       210       220       230       240
Danio Pax1a         164  FYSYPNAMPSGTKMSSPPGVPVTGGHVSISRGWPSFHIVSNILGIFRAFMDPTATASAEGYAPKMEDW-GVNRATFQS---
Danio Pax1b         158  FYSYPNTMSPIGSKLGSPP-----AVSVSLSRAWPSFHIVSNILGIFRAFMDPAAIAGSESYQPKMEDWTGVNRFSFPSV--
Danio Pax9         160  LYSYPTPIAAFGTKVPTPPGMPTLPGHMAMFRIWPSFHSVIDILGIFRSTTEQQISDNPSFPSAKLEEWRAINRSNFSPANS
Branchiostoma Pax1/9 163 TYFVGPPAFAFGAFGVPNQS-----QIFMHMRAWPSFHIVSDILGFFRFGVPINANEQTGPVSGAISNESARYQTQMGEG--

                              250       260       270       280       290       300       310       320
Danio Pax1a         241  HGVNLTDKSS-IDADLKYPQPSS----TLSSYVFA--CAYSPSNQYGVYGGPAGGYVSPGHHWQAQGTSLTHP----GGGV
Danio Pax1b         232  HGVNGIDKPP-LESDLKYTQASS----NLSGYVFA---CAYSATNQYGYGG-HGNYG----HWQSQSAGLSHP----NTGT
Danio Pax9         241  PLVMNGVDKPH-LEPEAKYNQTPNG-LPTVNSYVFAPSIHHYHPPTQVSFVYGYSGTTS-----AYVTGPTWQPP---SGSAL
Branchiostoma Pax1/9 238 YGINFMNQMQGQTEHVKYPDVSQSSLPAVSSFVFAP--YPGPPPPQTMAYMPYHQSPT-----TVGPTTGWQQPRFP-SAGA

                              330       340       350       360       370       380
Danio Pax1a         311  AMHPSD----THSSMPFKHAVRDGD---RKPPSPLSKQQHEALSGIHGLSISTSSS
Danio Pax1b         297  MIQSPN----LHSALSFKNTSREAV---ERK-SPLSKHQHEGLSPVHGLSDS
Danio Pax9         313  SPHSCD----ISSPLPFKSMS-------------ATR------DSVHSLVASAL
Branchiostoma Pax1/9 312 FVTTSEGGISIPAFLFFKPVTAAQTGLEDTKPHNSTSKVGPPTSDIPSASSS
```
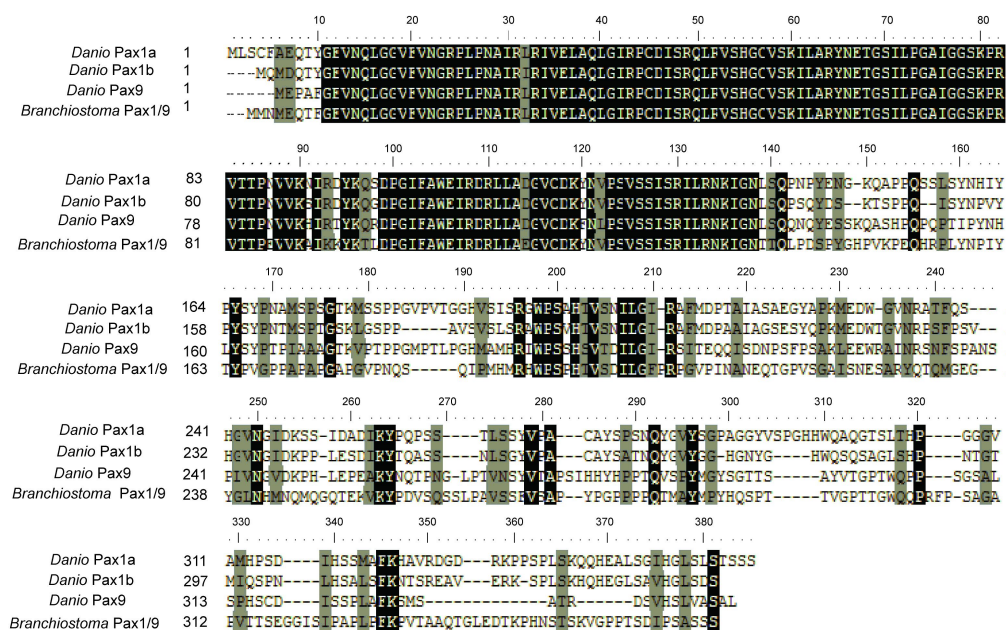
Figure S4. Amino acid sequence alignment done with DNAssist software. Black boxes represent identical amino acid residues, and gray boxes represent conserved amino acid residues.

Supplemental Table 1. Primer sequences used in RT-PCR.

Primer Name	Primer Sequences	Fragment Length
nkx3.2 forward	atggctgtgcgcagtaactc	738
nkx3.2 reverse	tcactggtttccagagcaggc	
aggrecan forward	gggggtccagaggagcaagc	519
aggrecan reverse	ttagagttgtttctccaatgc	
col2a1a forward	ccattaggaccaccgggtgc	156
col2a1a reverse	aaatcctgacctggtgttgg	
actin forward	atggatgatgaaattgccgcac	475
actin reverse	accatcaccagagtccatcacc	