

Supplementary Information

Table S1. Vectors used in this study.

Name	Vector	Inserted Fragment Name	Inserted Fragment Size (bp)
pE2.2	pEGFP-1	–	2166
pL2.2	pGL3-Basic	F2166	2166
pL1.8	pGL3-Basic	F1886	1886
pL1.3	pGL3-Basic	F1320	1320
pL0.8	pGL3-Basic	F870	870
pL0.5	pGL3-Basic	F589	589
pL0.4	pGL3-Basic	F460	460
pL0.3	pGL3-Basic	F357	357
pL0.2	pGL3-Basic	F200	200
pL0.4A	pGL3-Basic	F427	427
pL0.4B	pGL3-Basic	F376	376
pL0.4-0.3	pGL3-Basic	F128	128
pL0.4-0.1	pGL3-Basic	F285	285
pEC1-LHX8	pEGFP-C1	<i>LHX8</i>	888
pEGFP-C1	pEGFP-C1	–	–

Table S2. Primers used in this study.

Name	Sequences	Accession Number	Size (bp)
B2.2	F: TAGCAAAATAGGCTGTCCCC R: CCCAAGCTTCCATCTTGAAAGACTTGTTTCAGCAA ^a	KF114861.1	2166
B1.8	F: CCGCTCGAGTGAAGTCACTAGAGATAATGCCAGA R: CCCAAGCTTCCATCTTGAAAGACTTGTTTCAGCAA	KF114861.1	1886
B1.3	F: CCGCTCGAGCCTCACAACAACTGTGAGATAAAA R: CCCAAGCTTCCATCTTGAAAGACTTGTTTCAGCAA	KF114861.1	1320
B0.8	F: CCGCTCGAGCAACTTGGTTGCACATTAATATCAC R: CCCAAGCTTCCATCTTGAAAGACTTGTTTCAGCAA	KF114861.1	870
B0.5	F: CCGCTCGAGATCAGAGAATCCATGATTTGGTCTG R: CCCAAGCTTCCATCTTGAAAGACTTGTTTCAGCAA	KF114861.1	589
B0.4	F: CCGCTCGAGGTGGGATGGGATCAGGA R: CCCAAGCTTCCATCTTGAAAGACTTGTTTCAGCAA	KF114861.1	460
B0.3	F: CCGCTCGAGTGGATAAGGTAAGGGAGTAGGTC R: CCCAAGCTTCCATCTTGAAAGACTTGTTTCAGCAA	KF114861.1	357
B0.2	F: CCGCTCGAGCAATTTAGAAGACCTCCTTTGGATC R: CCCAAGCTTCCATCTTGAAAGACTTGTTTCAGCAA	KF114861.1	200
B0.4A	F: CCGCTCGAGTAAGGGCTGATTAAGAGACCACCT R: CCCAAGCTTCCATCTTGAAAGACTTGTTTCAGCAA	KF114861.1	427
B0.4B	F: CCGCTCGAGGGCTGCTTCTTTACATCCTAGTG R: CCCAAGCTTCCATCTTGAAAGACTTGTTTCAGCAA	KF114861.1	376
B0.4-0.3	F: CCGCTCGAGGTGGGATGGGATCAGGA R: CCCAAGCTTGACCTACTCCCTTACCTTATCCACT	KF114861.1	128
B0.4-0.1	F: CCGCTCGAGGTGGGATGGGATCAGGA R: CCCAAGCTTGATCCAAAGGAGGTCTTCTAAATTG	KF114861.1	285

Table S2. Cont.

Name	Sequences	Accession Number	Size (bp)
<i>GAPDH</i>	F: ACCTGCCGCCTGGAGAAACC R: GACCATGAGGTCCACCACCCTG	NM_001206359.1	252
<i>BMP15</i>	F: TGGTCCTCCTCAGCATCATTAG R: TAGGTGAAGTTGATGGCGATAAA	NM_001005155.1	428
<i>FOXO1</i>	F: CCTACTTCAAGGATAAGGGCGA R: GGTGGGTACACCATAGAATGCA	NM_214014.2	466
<i>LHX8</i>	F: CTGTGCTGGCATGTTCGGT R: GGGCACCTTCAACACTTATTCC	NM_001166315.2	361
<i>LHX8 CDS</i>	F: CCGCTCGAGCCATGGCCTCGGGCTCCGTCT R: CGCGGATCCTTAGGTATGACTTATTGGCAGTTG	NM_001166315.2	888
<i>NOBOX</i>	F: CAGCCCCAGTTTCCATACCT R: CCAAAGCCTGAGCATACGG	NM_001195116.1	319
<i>PITX1</i>	F: CAACGCACGCACTTCACAAG R: GAGTTAAGCGAGGAGCCAGTGA	NM_001244370.1	491

^a AAGCTT, CTCGAG, GGATCC refer to restriction enzyme sites of HindIII, XhoI and BamHI.