

cagct**AAGGAGAAAGCAAAACAAAACAAT**gataaaaacgtttaaaatccaaggacaaaaaccggagtctg
gtctcaaaatccgcgccgttcagtgtctcactcggtagctcactcggctcagggcccggcctggccggagcaacgcggg
ggacacccccgattccgctggggagcgcagcccacagctccccctcgcagggcggccaaggaccctcaaggcggggg
cccacactgaagcctgggaacgcgcagacagaaaccctctcctcaagcagtttctgctcgtcggatgagaggcgc
ccaattgaagcagaatgatcctcatctactaatatccagcgtggccacaaagcactggccatttacgccaccactttaa
caaagatatttggttattcccgggaagcaagagcacttttgcattggctgagctcggggcggaggcgcagcctcggcccagc
ctcccggcctgagctgcccgcactcggcattcggcccctcctggccagcgtccagccgcccgggggttcaggctcagtt
ccggccggcaacagacagacgggactcacgccctcctgctcgcgcgtccctgaagcatcagaggggaaaacagc
gtggctctgggctcgggtgctggggctgtgatgtcctcggaaagtcaactccagccccagatccccgcgtgtctgggagat
gggaggggtcagggacaccaggtttgttcaggtggggcaactcagtgacggaccctcccgtgagaccccttccatc
ctcccagctctggggccagtgctgtgttctcggccgggggtgggggggggggggaagaccttgggggagggcgtgt
tagcgggggtggccactgaaaaaccctgagctcggggggcgggttggctcgggga**tccgggacagcctccggg**
aggcagtcgatcccactcagcgcctccgcccgtcggattctcctcggtagggggaaagggggcggggagcaga
gg**TGTC**cctctgacggcggcagaagagagg**CAGACAGACTgaCAGAC**acgt**AGAC**caacagtgcggcccca
gggttcgtccc**CAGACT**cgtcgtcattgttggcgactggggctcagcgcagcgaagccc**atgtgtcggaggca**
gtgggaaggcgcggggctgggaggccgcggcgggaggaggagcagccccggcaggtcaggtgaaacccccacct
gtccctcagccccctcctctaaagacctgtccgtgccggggaaccccaccgaattgaaagtggttccactttgtaact
ccgcaagttggtgcaaagcagcattcaccttctcctcaaccatctcctcctctgttactccccacccacctctg
ccctccccgctctcggttccctcctcctccctccctccacctcctccccgcgtccgctggtacccccaaaaaatgggg
gtgggggtgtccaaggagggggggaaatgcttgggtctcgtctcgtcctcctcctctctttagacacataaaatcctg

acaagtgaac **T**(+1)taa

Deletion control: aaggagaaagcaaaacaaaaacaat (-1590/-1566)

Deletion1 : **GACAGACTgaCAGAC**acgt**AGAC**ca (-538/-514)

Deletion2: **AGAC**acgt**AGAC** (-527/-516)

Mutation control:gg**tg**tccc (-570/-563)

gg**ct**gtccc

Mutation1: ga**CAGAC**acgt**AGAC** (-530/-516)

ga**GCTTCT**cg**CTTC**

Mutation2: g**CAGACAGACTgaCAGAC**acgt**AGAC** (-541/-516)

g**TGCCTTGACTgaGCTTCT**cg**CTTC**

Mutation3: g**CAGACAGACTgaCAGAC**acgt**AGAC**caacagtgcggccccagggttcgtccc**CAGAC** (-541/-484)

g**TGCCTTGACTgaGCTTCT**cg**CTTC**caacagtgcggccccagggttcgtccc**TCTGCT**

SUPPLEMENTARY FIG. S4. NKX2-1 promoter and putative SMAD binding elements (SBEs). This region contains 1599 bp, from -1595 to +4 relative to the transcription start site of NKX2-1. Bold: transcription start site. Red letters for mutated nucleotide residues. Putative SBEs, including a consensus sequence [C]AGAC in capitals.