

-2921 ACATGTTGCT ATTTGCAATACTTTGCAT **TGACC**AAAAGGACCCTAAACTGTGTGGGAAAAAGC **TGACC**
 TCACAAGCGACCT ACTCTGTA CCGCATCCTA TAACACTCTCACAATGACAGATGTATAGAG G G
 GTTCTGTTGGTAGTTTCTGGGCTAATGGGAGACAGAGCTCAGACA GAAAGGAATGAAGGGAATGG
 AAGGGAATGGGGCATGAAGTAGCTTTTGTAT **GGCTGG**GGGC GGTT **CTGCC**TCTTGTGTATGGTG
 GTGGCACCT**TGACTCC**ATCCATCAA CACGTG CAT**TGCGTCA** GAGTACACACACACTGAGATCT
 GACTGTGGTCTGAGTGTTTGCAATTCCTGT CTTATCA AAATCAGTAACCTACTTCTTGTCTTCTGT
 ATAGTTATGA **TGATGTAAT**CGCCACAAGAAGCTGAGTG **GGGTGG** TCCATGGGACTTAACACTTTC
 TGTGAGTCTAAAA TTATCT CAGAAAGTTTTTATACAAGCATAAAGAAATTAAGATTCCCCTCTAGA
-2403 GAGATGGCTCAGCAAGTTAAGAGCATTGGCTGCTTTCAGAGGACATAGGTTCTATTCCAGTACC
 TAGCTGAGTGGCTCACACCAAGGTAACCCAGCCCCAGTGCAGATGCCCTCTTCTGGTCTCAG
 TAGGCAACAGCAGCTCATATGTAGACACACACACACACACA CACACACACACATAGAAATATTTTTAA
 TTATCCTTTTTCTTACATATACTTAAGGAATACAACATGACATTTTGTATACCTACACACAATGAAAT
 TGTGACGATAGT**TAACTCA**GCATCTCTACTCTTTGGGGGGCACTCTAAAGTCTTACTATGGGCTGTT
 AGCAATTGGATGAGACAGTCCAGAGCGAGCACGGTCCACTCTGAG GGTGTA CAAGCTTTTACCT
 TTAATATTCTACATAG**AGATAG**AAACCTCTGACTTCAATGGCTGCTTCCCTGTGGCACACATTGCC
 AGGTCTGTGG**TGACACA**ATGTGGCCGTTTTGAATACGGCAGCCTCTGAGTTGAGAGCTCCTCCTT
 CAGATCTCACAGAGGACAAT CTATCA CAACAGCCTGACTAGCCAGGCCAGAGAGACAACGTTAAC
-1800 TATGACAGCTGGGAACCTTTCTAGATGTGGA CCGCAGCCTCCT GCAGCTGCTCGTCTTCTGGATGGC
 CAGCGGAAGACCTGTTGTTCCCAAGACACTCATCAGAGGCAATGTCTTAAAGC CGTCCAGATT
 CAGGGGTGCCTGGGTAGTTGTAATGTCTTTTTAATATTTTAAAAATTTCTTCTTATATTCTGCTTG
 TGTGCATACAGAGAGAGAGAGAGGTTTTTTTT TCTTTTTGTTTTGTTTTGTT TTTTGTATTAGTTT
 GTTGCTTT**TTAGGAAAT**TTCAAATAAGAAATGTGTGTGTGATGAATTTTTTGTAGATATGGCTATAC
 TACATGGCTCAGGTTGGCTTTGGCTTTGAACTCTTCCACTTCTGCTTCTGAGTCCAAGGTTGCAGA
 CATATATCACTGTTTCTGTCTAAGCTCTATACTCAAGGAGTCCAATG**TGACC**GTTGGATATAAAGTA
 CGTAGGGCAATGGTCTGCTCCGCGGAGATTTACTCTCCGTTTACACACCCATTAGCCTATTTACAC
 A**CCCACC**CATGTCTTCATTTCCAGGCTTGGAGAAGAGTCTCCTTAAATGTCAAGGGCATGGGATCC
-1195 TTTCAAAGGACTTCTTAAGGTGGCAGAT**GGTCA**GCTGTGGTGGATCAGAGGAGTGAGTAGAGGGAA
 CCTATGGTGACAAGACCGATCCCAGGGCC **GGCTGGG**AATTGTTCTTCTGCTAGAT **CTGCC**A
 ATCCGTGCCTCTGCTGCATCAGAGCCAGCAGT**TGTTTCA** GCACTGAAGGCAT **CTGCC**ACAGA GA
 TTAGTAA TGAAGACCGATGTCAAAAAGGACTAT CCGTCCCCAAA**TGATAG**ACCATTTCAGTAAATA
 CGGAACGAAAATCGATTAATAACATTTACTCCA AAACAAATTAATATTTTGTCTTGTGCATAACTGT
 AATA ATTCTCT GTATCT TAAATATCCTTGAATAAT TTAATTTTTCAAAGGATTTTTGTCTATAAA
 ATAGAGATATGCTGGGCTTTTTAATTACATTTTGTAGTTGCCATACAAAATAATGGACTTCGTTGTG
 TAGCTCA GTGGTAGGGCACTTGAAGACTCTTC**TGAGTAA****CCCACC**CACACCCT**CCCAAG**ACAC
 ACACATCACCT**CCCAAG**ACATACACATACAAACACATACACACATACACATACCCACATACACAC
-602 ACAAAACCATATACATAC AGATAC CCATACACACAAACCACTCACATACACATACCCACA
 TATACACACAAACCATACACATACCCATACCCACATACATACACATACACAC CACACACACATG
 TATTTTCATCAAATGTTGTTAATCCTCACATTCCTGCTACCCCTGGTCCCTCTTCTGCTCTGGTGTG
 CAGTTAGTTTCTCTCCCAAACCTTTTCCCTTATTCACTCAAGCACACATGGATGCACACATCACACA
 CAAATAAATATACAAATAAATAAATAAATAAGTACTGTTGGAGAAATAAG**TCTAGTGG**CCATGTGGG
 AATCAACAGTACAAATA**GGGTGG**ACAAGCAAAGCCTGGAAGACAGCGGTGCAGGCCAGGTGACAG
 ATGATGCAAAGATGCTGGCTTAAGGTGACTAGCAGCTTAATCCCTTCCCAAACCTG**TGACC**GTGAC
 GACCTGCATGGGAAATGGGCCTCACAGGGATGACAGCTAAGAATCTCCA**GGTGGG**AGGGTTGTTCTG
 TATTATCC**GGGCAAGCTGACC**CAGTTGTAAGGACT**TTAATAGAT**GTGATGGGAG**GGTCA**GA
 ↗**TSS+1**
G **TG**AGGCAAGATGTGAGCACAACTGGAGCAAGGGTGACTCGATGCCAGGAAGAGAGCAGCCAA

Supplementary Figure 1. Transcription factor binding sites in -2921 nt upstream of KCNE2 TSSs (red font and underlined). The predominant start site T is bold and marked with an arrow. All numbering are based on this site (+1). The potential TATA box is in blue font and underlined. Transcription factor binding sites that were identified using Transcription Element Search Software (TESS) and MatInspector are highlighted. Green box, ERE and ½ EREs; grey box, AP-1; magenta box, Sp1; yellow box, GATA; olive box, C/EBP α ; orange box, C/EBP β and blue box, NKX2.5. The mismatches in TATA box and in full ERE are shown in lowercase letters.