

A Sequence of *D. melanogaster* DC enhancer

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1      GAGGAACAAA GAGCAGTCAG CATTATATA CTTTGTGATT
41     ACGGACGGAC AGTCCCAAAA AGCATTCTGT GCCAAGCACT
81     TAACGCCAAA AGTGAACAAA ACAACACTTG CTCTATTAAC
121    AGCCACACT   GTCTGAAGC  AGTCGGCTA ACGGAAACA
161    AGAATATCCT  ACGTGTGGCT AATTTGCGGT TAAGGAAGGC
201    CCCATGATAT  ATAAAGCCAA AAAATAAAGC AAAACCGCAG
241    CAGTTCATTC  AAATTTTGTG TGGCCAAAAC AAATATTAAG
281    ATAAAAGTCA  GTGGGGACTA TAATTTGAGT TATTTCAAATG
321    CAATAAATCC  GCGGAACCAA ACGAGTTGCT AATTTACGT
361    TAGAGCCCT   TTAATTTCAC GCTGCCATTT GTGGCTTCCG
401    TTTCGTATAA  GTTTGGGTCG ATGATTTTTA GAATTTGCAT
441    TTTC AATTTG  AATATAAAAA ACCGCGCTG  CAGGTTTGCA
481    GCTTTTAAAG  TGATCCGCAA TCTCATTCCT AGTCAGTCGA
521    AAAAAGGTAA  GATAGAGAAA  AGAACAGAAA TGACTACAAA
561    ATTAAGTACC  GAATTTTGTG CCATCGTAAT AGTTTTTCGC
601    CATTTCCCTT  TCACGGGTTT AACTGTTAAT TATGTAATTA
641    AATGTAAAGT  CGTGGAACTC GCGTPTTTTT CTGTATCAAT
681    ATACACATAT  TTCCGGCGCA AATGCTATTT TTAGAGCAT
721    TTCATGTAAT  TATTGAGACT AATAGGAAGA CAGATCTTGT
761    TTGGGTGCAG  GGAAAGTCA  ACTTAATCGC TCAATTTGAG
801    ATCGCCTGGT  CCCTTGAGAT TCGACTGTAA TTGAAATTTT
841    TGCTTTTGAT  CGGAGCCAGA CTTCAGACGG GGC AAAACAAA
881    AAGACTTTGT  TGGTGGTAGG GTAGGATCGT AAAAAGAACT
921    CAGAACAGAA  CCAGAATAAA AATTCGGATA AGGATGTGA
961    GCCTGTAGTC  GTACAAAAAA AGATAATTCT GTCTGCAGGT
1001  AAAAAAAAAA  GGCAGATATA GTTGGCAGCT GTATAAACT
1041  AATGCACTTG  CAGTCCAATC TAATCGTTTG CCAAATGTCA
1081  AACGAGTTTC  ATTCATCCGG CGATACCCCT TCCTTTAAAT
1121  CTTCCTTTTC  CCTTTTTTTA AAGTAAACTG TGAGTCAGCT
1161  CATTCATGGA  GAACCGTGAC GATAAGTCCG CCTCTTTATT
1201  TTCGATATGA  CAAACACGCG TGAATAGCGT CAAACGTTTT
1241  TAGAGCTCTT  ATCGTCATGG TTTAATTAAA AGGTTATTCT
1281  TGTAGGCAGG  ATAACATTGC GGCCGAAAGG ATGCAATTGA
1321  ATFTGCTGTA  TTGGGGTAAT TATTCAGTGC CTTATCTTAA
1361  AGACTTTCTG  ACCTTCCCAT CCAAACGAAA AACCGAAAGT
1401  CGACCGCAA  GATC
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Red indicates putative dTCF sites.

GATA sites are underlined.

B dTCF sites in *D. mel* DCE compared to consensus

dTCF site 1: GCTTTGATCGGA

dTCF site 2: TCGTTGACATTT

dTCF site 3: ACGTTGACGCTA

consensus: CCTTTGATCTT

Red bases match the consensus.

Core bases are underlined.

C Bases mutated in the DCE-T123 reporter construct

dTCF site 1 (845-847): GCTTTGATCGGA
GCA

dTCF site 2 (1076-1079): TCGTTGACATTT
TA--

dTCF site 3 (1230-1231): ACGTTGACGCTA
TC

Red indicates altered bases.

Core bases are underlined.