

Supplementary Files 2

for

lncRNA *TUG1* as a ceRNA promotes PM exposure-induced airway hyper-reactivity

Bin Li ^a, Nannan Huang ^a, Shengnan Wei ^a, Jie Xv ^a, Qingtao Meng ^b, Xiaobo Li ^{a*},

Rui Chen ^{b, c, *}

^a Key Laboratory of Environmental Medicine Engineering, Ministry of Education, School of Public Health, Southeast University, Nanjing, 210009, P.R. China

^b Department of Toxicology and Sanitary chemistry, School of Public Health, Capital Medical University, Beijing 100069, P.R. China

^c Institute for Chemical Carcinogenesis, Guangzhou Medical University, Guangzhou, 511436, P.R. China

* Corresponding to: Key Laboratory of Environmental Medicine Engineering, Ministry of Education, School of Public Health, Southeast University, Dingjiaqiao 87, Nanjing, 210009, China. E-mail address: 101011116@seu.edu.cn (X. Li);

or

Department of Toxicology and Sanitary chemistry, School of Public Health, Capital Medical University, Xitoutiao 10, Beijing, 100069, China. E-mail address: 101011816@seu.edu.cn (R. Chen).

Sequence alignment between *TUG1-miR-222-3p-CELF1* (hsa) and *Tug1-mir-222-3p-Celf1* (mmu) network were exhibited as follow utilizing the EMBL-EBI search and sequence analysis tools (**Madeira, et al., 2019**) (<https://www.ebi.ac.uk/Tools/msa/mafft/>). Binding sequences among *TUG1-miR-222-3p-CELF1* (hsa) or *Tug1-mir-222-3p-Celf1* (mmu) network was marked yellow.

Sequence Alignment 1

Homo sapiens microRNA hsa-miR-222-3p (miR-222-3p), microRNA

Sequence ID: MIMAT0000279

Length: 21 bp

Mus musculus microRNA mmu-miR-222-3p (mir-222-3p), microRNA

Sequence ID: MIMAT0000670

Length: 21 bp

miR-222-3p sequence has 100% homology with mir-222-3p (3' – 5'):

1-21

miR-222-3p UGGGUCAUCGGUCUACAUCGA

mir-222-3p UGGGUCAUCGGUCUACAUCGA

Sequence Alignment 2

Homo sapiens taurine up-regulated 1 (TUG1), transcript variant 1, long non-coding RNA

Sequence ID: NR_110492.1

Length: 7598 bp

Mus musculus taurine upregulated gene 1 (Tug1), transcript variant a, long non-coding RNA

Sequence ID: NR_002321.2

Length: 4731 bp

TUG1 sequence has 59.1% homology with Tug1 (5' – 3'):

1-80

TUG1 TCCTGCTTTCCTGACCCTCTCCGCCATTTAAAGAAACAGTACCGGGGGCGGGCCGAGCGACGCAGCCGGGACGGTAGCTG

Tug1 -----

81-160

TUG1 CGGTGCGGACCGGAGGAGCCATCTTGTCGTGCGCCGGGAGTCAGGCCCTAAATCGAAGAAGCCCTGGCGGCCCTCC

Tug1 -----

161-240

TUG1 CCCCCTCCCGGTCTGGTAGGGCGAAGGAACGGGCGTGCGGTCGATCGAGCGATCGGTTGGCGGCTCTTCTCCTGCTCT

Tug1 -----

241-320

TUG1 GGCATCCAGCTCTTGGGGCGCAGGCCCGGCCGCCGGCGCGCCCGGTGGCCGTTGGCGCTCGCGCCGCGTCTTTCTT

Tug1 -----AGGCCCGGCCGCCGGCGCGCCCGGTGGCCGTTGGCGCTCGCGCCGCGTCTTTCTT

321-400

TUG1 CTCGTACGCAGAAGCTCGGGCGGCGGCCTATGCGTTTGCATTTCGACGAGGAGTCGTCCGGGTGGTCGGCGGCGGGCA

Tug1 CTC-----

401-480

TUG1 GCTGCTCCGCCCCGCTCCGGGGGAGGCGGCGGCGCAGCGGCCGCGGGATTGGAGCGCCGGGGAGGCGGGGTGGCCG

Tug1 -----

481-560

TUG1 GGGCCGGCTTGGAGGCCTGGCGCCACCCTTCGGGGCCTGCAAGGACCCAGTTGGGGGGCAGGAGGGGCCGGAGGATGG

Tug1 -----

561-640

TUG1 TTGGTTGTGGGATTCTACTTTGCCTTTTCCTCCTTATGCCGCTTAGTGAGGGGCGGGAGCTCTGGCGGCAGCCCCGGG

Tug1 -----

641-720

TUG1 GTGGGAGACGAGCTCCGGAGTCGGAAGAGCTGGGTTTTCTTCCGGGCCTAGCCACCAGTTGGCGGAGTGACCTTAGCCG

Tug1 -----

721-800

TUG1 AGTCACTCTGTAATTTGTCTGCGCCTCAGTTTCCTCCTCTGCCTATCAATGTGTGTGGGTTGAAATCGCTTTGTAAACT

Tug1 -----

801-880

TUG1 ATAAAGCGTGGGTGTACGTAAAGGATGGTTATTGTTTATAATTTTTTTGAGTTGTAAGAAAACCTTAGCAGTTCCCAAT

Tug1 -----

881-960

TUG1 CCTTGGGTTTTGAACCTGGGAACCTTGATTGGAGTTGGGGATCCCAAACTTCCTGAAATTGTGGGAATGTGCGGTTTG

Tug1 -----

961-1040

TUG1 GGGGAATGATGGGAATTTGTGGGAATGTGCGTTTTAGGGGAATGATGATCCATCGCTAGCAAGTTTTCCAAGGGGCTGT

Tug1 -----

1041-1120

TUG1 GACCCAGAAGAGTTAAGAATCACAATTTCTTCATGCTACAGAGAGGAAACTGAGGCCTAGATGTCATTTGGGACCCTTCA

Tug1 -----

1121-1200

TUG1 CAACCATTTTGAAGCCCTGTTTGTGAGTCCCTGGGATATGTGAGCTGTTTCTATGCATAATGGATATTCGGGGTTAACAACA

Tug1 -----

1201-1280

TUG1 GTCCCCTGCTGGCTTCTATTCTGAATCCTTTTCTTTTACCATGGGGTGCCTGAAGGGTGGCTGATGCATATGGTACAAT

Tug1 -----

1281-1360

TUG1 GGCACCCAGTGTAAGCAGCTACAATTAGGAGTGGATGTGTTCTGTAGCATCCTATTTAAATAAGCCTATTTTATCCTTT
Tug1 -----

1361-1440

TUG1 GGCCCGTCAACTCTGTTATCTGCTGCTTGTACTGGTGCCTGTACTTTTCTGACTCTCATTGACCATATCCACGACCATG
Tug1 -----

1441-1520

TUG1 GTTGTCATCCATTACTTGATCCTACTTTACATGTCTAGGCTGTGTGGTTGGTGGTGAATAGGCTTCTTTTTACATGGTGC
Tug1 -----

1521-1600

TUG1 TGCCAGCCCAGCTAATTAATGGTGCACGTGGACTTTTAGCAAGCGGGCTCACTGGAAGAGACTGAACCTGGCATGGAATT
Tug1 -----

1601-1680

TUG1 CCTGAAGATGTTGGGGTTTTTTCTTTCTTAATCGAAAGTTAACATTGTCTGAAAAGTTTTGTTAGAACTACTGCGGAA
Tug1 -----

1681-1760

TUG1 CCTCAAAATCAGTAGATTGGAAGTGATTCAAAGCTAAACTTTTTCTTGGCCCTCCTTGTTCTAATTGCTTGCAAGT
Tug1 -----

1761-1840

TUG1 GTAATACTAGGATGTCCAAGATGCCAGTTTTTGCTTCTTTGTTAGTTGTCAGCTGCTTTTATCAAATTCAGGCCATTAT
Tug1 -----

1841-1920

TUG1 CCAACAAACTATAAAAAATGTTGAACAATTGGATTCAAACATTTTCGTTTTGTGGAGTGGTGCTACCAAGTGGTAC
Tug1 -----

1921-2000

TUG1 AGCCCTAAGCAAGTGAACACAAACACATTTAAGTGTATTTTGCTGATTAGATGTTAGCCAGTTATGCTATTTTCATTCAA
Tug1 -----

2001-2080

TUG1 ATGTCTGAAAAAATCAATTGACTATTCCTTTTCCTAAAGGGCAGAGACAGATAATCTCACTCCAGAGAAATGAC---T
Tug1 -----GGCCAGAGACAAATGGTTTCCTTTCAAGAGAAATGACTGTT

2081-2160

TUG1 TGGAGAAAAAAGTGTGGTCTTTTTGCTCTTTTGTAATTAATCCGGATGTACCTCAAAGAC---TTAAGACTGTGG
Tug1 TTGAAGAAAACTCTGTTGGTC--TTAGCTCTTTGTAATTAATCTGGATGTACCTCAAAGACTCTTTAAGACTGTGG

2161-2240

TUG1 TGATAAGATGCTTTCCTCAGCAGAAAGGAGGGAAA-AAAAACAACCTGGAACCTC-AAAGCTTGAAATCTGTGGCAAAAACA
Tug1 TGTAAAAGGCTTTCCTCTGGAGAAGGAGAAAAATAAAATCAACTGGAACCTAAAAGCTTGAAATCCATGACAAAACA

2241-2320

TUG1 TGAGATGTCCAGGATTGGAGGTTGAAAAGATTTCACTACAGTGTTCGCAATAGTTGGAGCAGAT--AACTTTCAGTGTA
Tug1 C-AGATGTCCAGGATTGGAGGTTCATAAAGT-----ACATGCAGTAGTTGGAGTGGATTCCATTTTCAGTGTA

2321-2400

TUG1 GCCACAGCCATGGACTCCAGATTTCCAGATTTTCAAGACCTGGACCTGGAACCCGAAAGAGCTTGTCACGATGCGGCAGG
Tug1 GCTGCCACCATGGACTCCAGGCTCCAGATTTTCAAGAACTGGACCTGTGACCCAGAAGAGCTTGTC AAGATATGACAGG

2401-2480

TUG1 AACACTGGAGGTAGATTTTTTTTTATTTTTGAATTTTGGGACTGTTGACCTTGCTGTGAGAAAAGAGACA-ACGACTGAG
Tug1 AACTCTGGAGGTGGACGTTTT---GTATTCAATTTTGGAACTGTTGATCTTGCCGTGAGAAAAGAGAGACACGACTCAC

2481-2560

TUG1 CAAGCACTACCACCAGCACTGTTACTGGGAATTAGAAGACCTGAGTTTCTGTCCAGACCCTCAGTGCAAACCTGAGGATGC
Tug1 CAAGCACTGCCACCAGCACTGTCACTGGAACTTGAAGATCCAAGTTTCTGTCCAGAACCTCAGTGCAAACCTGACAACAC

2561-2640

TUG1 TCCATCCAAAGTGAATTATGATAGCAGACTCCTTGAAAGCAGGGTCTTGTGTTAGTGCATCTTGGCCACATACACCACA
Tug1 TCCATCCAAAGTGAACCTACGTC-----CCGTGCCTCCTGATTGCTGAATGTTACCTGGACCTGCCA--

2641-2720

TUG1 ACATATCAAGATGCATTTATTAGGAAGGAGGAGTTAGAGAGCAGGCTATCAGAATAACCACTCACCTACAGACCTGGTA
Tug1 ----ATGACCTTCCTTCTGCTA-----CTCCATCAGCCTACAGACCTGGTA

2721-2800

TUG1 CCTGGATTTTTGCCCGAGATGATTCTTACCACCTTACTACTGACGAAGACACCCATTCCAGTGGACCACTGTGACCCAGG
Tug1 CTGGATTTTTGTCCATGGTGATTCTTACCACCTTACTACTGAAGAAGACA-CCATTCCAGTGGACCACTGTGACCCAAG

2801-2880

TUG1 AGGCATTCAGCCATCATGATGTGGCCTTTACCTCCACTCCTGTCTTGTCTACCCAGATTCAGCACAGCCCTTTATAGTG
Tug1 AAGCATTCAGCCATCATGATGTGGCCTTTACCTCCACTCCTGTCTTGTCTACTCTGCCAGATTCAGCACAGCCCTTTATAGTG

2881-2960

TUG1 AAGTC-AGAGTCTCAAGCCAAATAGCTAAAGCTGTTTTATCACAACAAAGGCCAGTTTGTTCATGAGTGTGCATTTTC
Tug1 CAGTCAAGAGTCTTCAAGCCAAATAACTGAAGCTATTTTATCACAACAAAGGCCAGGTTTATCCATAAATGTACAGTTC

2961-3040

TUG1 ATTTCTTCAGTTAAAGCCTTCAGAGACACACAATAAATTTGGACCAGGGGATT-----TTTTAGTTATTAATGCTCT
Tug1 ATTTCTGCAGTT-TATTCTTCAGAGACACATAGTAAATTTGGACCAGGGGATTTGTTTTGTTTATATTGTCAACACTGT

3041-3120

TUG1 CTGAAGAAAAGGCAACATCTTTTTGAGAGCAGCATTGGACCACACCCCAATCTCAAATGATTGAAA-TTCATGAAC-AT
Tug1 CTGAAGAAAAGGCA-----TCTCTGAGAACAGCATTGGACCCTACTCCACAATCTCAAATGATTGAAGTTTCATAAACTGC

3121-3200

TUG1 CTAGGATCCCGTGAAGGTCACCTGGACCC---TGTTTTTCTACTTCAAATCCTGTAGTAGCCTACTGAATGAGAAAAC--
Tug1 CTAGGATCCTGTCAAGGCCACTGGACTCTTGTCTTTTCCTACTTCAAAATCTGTAGCTGTCTACTAAATGACAAAGCAG

3201-3280

TUG1 ATATTCTGACCCATTGGGATCAAATCAAAGGCACAGTGAACCTCATAGCATCTTCTTTGGAATTACTCAGGAACCAGA
Tug1 ATATTCTGACCCATTGGGATCAAACCAAGGCATTTGAATTCTCATAGTATCATCTTCGG-GTTACTCAGGAACCAA

3281-3360

TUG1 ACTTTTTACACAAATGTAAGAAATTCTACCAAGGAGTCCCTTACCTAACAGCATCTCACAAGGCTGC-ACCAGATTCCA
Tug1 ACTTTTACACCAATTTAAGAAATTCTACTGAGGAATCCCTTTACCTAAC--CATCTCACAAGGCTCAACCAGATTCTC

3361-3440

TUG1 GAAAAGGCTTCTCTTGATACATCAAGGTAGAACCTCTATGCATTTTGTGACCGACTTATTCTTAGATCATTGGTTTTCCA
Tug1 GAAAAGGC--CTCTTGATATATCAAGATAGAACCTACATGCATTTTGTGAACAACCT-----ATCACTGATTTTCCA

3441-3520

TUG1 AAGGCTTTGTGGCCATGAAGCCCTTTGAGTGAAAACCTGTGCAGAAGCCAGAGTAAAAGTGAAGCTGCTCTGGATGAAGT
Tug1 AAGGCTTTGTGCTCTTGAAGTCTTTGAAGGAAAGCTGTGTGGAAGTCCAGAGT-AAAGTGAAGCTGCTCTGGATGAAGT

3521-3600

TUG1 AGTGAAGCAAGAGTAGGGCCTGAATCCTGTACAACCTATCTCCTTTACCACCGTGGTGACACCTAAGGGGACTTCCTT
Tug1 AGTGAAGTGGGAGTTGAGGTCTACAACCTGCCACAACCTATCTCCTTTACCACCATGGTGATGCCAAAAGGGACTTCCTT

3601-3680

TUG1 ACAACACCTTGAACCTTCCGAACACAGTTTGAAAACCACTGCCCCAGACAGCAATATGTTTGACCTGAATGGCATTCCA
Tug1 AAAGCTTTCAGAAAATCCTG-----CTTGAAACCACTACCCTAGA---CAACATGTTTGACCTGGATGGCAT----

3681-3760

TUG1 ATCTTTTCTGTACCTCCACTCAGCACAGTTCATGTTTCAGTAGATGCTGAACATTCTTAGAAAATACTGTGTGTGAACCTTAG
Tug1 -----TCTCTTCAAAACAATTCATATTCAGTTGATGCTCAACATGTTTGGAGATGC-----

3761-3840

TUG1 AAAAGTGCAAGAAGACAGGCATGTCTTTGACCCAGGAATGATCATTGCTGAAGATGGTGTCAAGTGAACCTAGATTAA
Tug1 -----TTTATTGAGAGATGATGA--TAATTACAGCATTGTCTAATGAAGTTTATTAA

3841-3920

TUG1 CAGCCCTCCACTCCAGATGGATATCCAGTGATTCCTAGAATGGGATATAGCCAGAGAACAATTC-TATGCACCCTACACT
Tug1 TAGCATTCCATCCAAGTGGAC-----TTCTGGAGTTGGATATAACCAGAGCAATTCATATGTATCCTACACT

3921-4000

TUG1 GACGACTCCCTTAAGCAACACCAGATGCT--CTACTGGTACTTGAAGTACATGACTTTGAAGTCTTGACCCTCCATGAA
Tug1 GAAGAACACCATTAACCTTTCAGCAACCTATAGCTAGTGGTACTAGAAGTACGTGTCTTGAAGTCT-----ATGA-

4001-4080

TUG1 TACCTGAATTATCAGCAAGCGGTTTTGAAGCTGGTGCCTCATTGAGGCCATATTAGAGCAACTTGTACATTTGACCTCT
Tug1 -----GAGCTGGTATTGAAGCTGATGCCTCCTTAAGGCCATCTTAGACCAAGTTGTTGTTGACCTCT

4081-4160

TUG1 TGTTATCAGCCATGGTACTCTACTTCGTGTGCAAGAGATAACTATGAAAGCCAAATTCAAATACTGGCAACATTTCTTAA
Tug1 CCTCATTAACATATGG-----AGCAGAATTGAAATAC---AAATTTTCTTAA

4161-4240

TUG1 AGGGGCTCAATATCTATCATTTCGTCTCTTTTCCAAACTACACATCACTGTATGACTCAACCAGTAGCAGTTATATTGCC
Tug1 AGGGACTTGAACCTGGTTATCATTCAATATCTCAAGTTCAAGTCAT--GTTGATGCAACCAGTAGTTATTAACCTGCT

4241-4320

TUG1 CCTTGGTTTTTATTCAGTTAACTACTGTTTCCAAGATAAATGAGCTAATAAGCTTTAAAAAAAAAAAAAAAAAGGCTG
Tug1 CCATGGTTTTTGTTA--TTAATACTTTTCCAGGG-----CTTAAAAAAAAAAAAATTA---CTTAA

4321-4400

TUG1 AATTCTTTTTTCTTCATCACTGGCATATCTGCCTATTCTCCAGAATTATTATGACTATTAGCTCACTTT--AACAGTTG
Tug1 -----TTTCTCCAACACGTCTATACTGTCTGTTCAAAAG-----TAACTACTACCACTATATGGAACAGATG

4401-4480

TUG1 AACTTCAAGCGACAATCTTTGAACACCCCTTCTCA---TGTGATTTAAATGAAACCATTTGGAAAAGTTCTTCTAGC
Tug1 ATTCTGAAG---ACACTCTGAGCATCCTTATGATATTTGTGACTTAAATGTGGC---TGGAAATTTCTTCTTACC

4481-4560

TUG1 CAGTAATAGATTTTTTTTTTAATTGCTCTGCCTTGTGCCGAGAGATGTTCTTTTAAAGATGAATCTTTTGATGTCTGATAC
Tug1 CAGTGAAATATTTAATGATTAG-----TCTTCATGCCTGATAC

4561-4640

TUG1 CACCAA---ATATAGGTGGTAGGGAGAGTTGGAGGCTGGCCCTTTGAGC-AGGCCATTAGCTTACTTGCTGGGCATTTT
Tug1 CATCAACTGTATATGCGTGATAGGCAAAGTTGACATAGGCATTTGACTCTAGGCTAT--GATAGCTTGCTAGTAACTTC

4641-4720

TUG1 CGATAGCTTATTGCCTACCTTTTTGCTGAAA---CAAAGTATTGAAAAACAAATCTATGAAGACTGCAGCTAAGGAT
Tug1 AAGTAGCATATTGTCAACCTGTTGCTGAAAAGTAGAGTAACTTGGAAAAAAACT-----AAATGGCAGCTAAGGAT

4721-4800

TUG1 TTTATCGGTAGACTTAAGAGCTTTTGTCTTGTGGATATTTAGTGAACCACATCAGTCTCAATACTGTCAATTTTACAC
Tug1 TTTTTCA-GTATTCCTGAGTTTCTGTCTTG-GGATATTTCAATGAAATTTTAC-----CTGTCTTCACTT

4801-4880

TUG1 TGACTCAGAGCAGCTGACTTCATTCCCTTGCCATGATATATATTTAAGGCAGGCATTGTAACAGACATAAAGACAACCTTAT
CelF1 AA---CAGAGTGACTGAC-----TCCTTACTATGAAGTATTCTTA-----AGACATTAAGATTACTTTT

4881-4960

TUG1 CTGTTTCAGCAGGAAGGATTTCAGTTTATGAACTCTCAGACCAGATCATGTTGAACAAGGAGACTTTGATGTGTGCATGA
Tug1 -----GTAGAAAGGATAAAATTCCTGACCATCCAAATC--ATCATAGTGAACA---AGACTTCAATTTGTGACCTGA

4961-5040

TUG1 GAAAACCTC--ATTCTTTACTTCCCAGTCAATTTAAAGGCCAGCTATCCTGAGCTACTCGAATGAATGCACTGGTTAAACA
Tug1 GAAAATCTCATTCTCTACTTTCGTAGTCAATGTAAGGGCCAA--TGCTATCAGCTACTC---TGAGTGCACTGGGTAAACG

5041-5120

TUG1 TTGGAATAGTTTGTATATCCTTGCTCTCT---CTCTAGGCCAATTGTGATTACATGACTCGACTCTACATCTCGTCA
Tug1 TTGGAAGTGCCTTCTTTATATCATTACTTTTTATCCTCTAAATTAATCATGGTTATGTAATTC--TCGCCACAAATCAGCA

5121-5200

TUG1 AACAAGGCCTAGGTCTGGTTGCTGTAGACTGCTCGCCCTCAACAAAT-AAAATCTGGTTGACTAGCCTCCTGTATATAC
Tug1 AATCAGACTCAGATCTGGTTATCTAGACTGCTCACAGTTAACAAATCAAACCTCTGGATGACT--TCTGCTGTATATGC

5201-5280

TUG1 AACTATTATTTGTTAAGAAGAAATTCGTCATTTTCTACTACCTTCCAATTGTCAGCTCTTTTTTCTCTCTGGTTT
Tug1 AACTACTATTTGTAAGAAGAAATTCGTCATTTTCTACTACCTTCCAATTGTCAGCTCTTTTTTCTCTCTGGTTT---

5281-5360

TUG1 TTCTTACTTTACAGAAAAAGACATTGATCTATACTGCCATCCCTCTAATCCTGCCATACTCAGTCAAAAGGAATGAC
Tug1 -----TATTAACAAACAAAAATAAGCTACACTGCCAGCTATCC--CTCCTGCCATACTCAGTCAAAAGGAATGAC---

5361-5440

TUG1 TTAAGATGAAGATGATCATCTGCTCGAGTCTAAAATATACATTGTATATAAGAATTGGTGATTAGAAAAGCAAAAACCT
Tug1 -----GAATCGGGAATCTAACCAGT-----GAATGGATAAGTAGAAAAAACTAAAACCT

5441-5520

TUG1 -----AAAACCTAAATCTAGGAGTCTGTATACTGTCTCCATGTCTCCATGCCTCAGATCTCATCTAAATCTTTGAACAG
Tug1 AAGGCAAAAGCCTTAATCTAGGGCCTTTTCTACTATCTTCATGT-----CTTGGATTTTCATCTAAAATC---AACAG

5521-5600

TUG1 CACCATTCAACCAATCTGAGGCCTTGACTTGCTTGAAGATGATTCTCAGAGATCGGCTGAGTAAAAAAGATGACGACT
Tug1 TGCCACCAACCAGTCTGAGGCTTGACTTGCTTGAAGATGATTCTTAGAGATGGGCTGATTACAGAAGGTGAAGACT

5601-5680

TUG1 TGATTACCAAGAAAGTAGGGCCAACCTTTGACAAATCTGGCTCTGCTGACCCTGTCACTCC **CAGATGTAGC** ATAGACTCC
Tug1 TGATTACCAAGAAAGTAGAGCCAACCTTTGACAAACCTGGCTCTAC--AATCTATTGCTTC **CAGATGTAGC** ATAGACTCA

5681-5760

TUG1 TAAACAGAACCTCAAGTCTG-ATTGAGGATAAAGGCCTTCTCCTGAGCTGAAAGTTCTT-TGGCAGATGAGCAAGAAACTG
Tug1 TAACTAGAACCTCAAGTCTGCATTGAGGATATAGCCTT---CTAAGCTGACAGTCTTGCAACAGGTGAGCAAGAAAATG

5761-5840

TUG1 AAAGCTGATGTACCTGACTGGCTCTGTAAGATCAGAAAACCTGTATCCAGAATAAGCCCTATGGATTAACCCCTGAGTACC
Tug1 AAAGCTGTTATACCCAACCTGGCCCTTAAAGATCCAAAATAATGTCTGGACTAAACCCCTATG-----GAGTACC

5841-5920

TUG1 CAGAGTAAAACTAATTTACAGAACTTCCTTATTGATCTGCTGGTCTTCCAGATCATATTCTGGCTATTGGTATGGCTG
Tug1 CAGGACAAAACTAATTTACAGAGCTTCATTATTAATCTGCCTGTTCTTAG-----CTTAATTATTGGTATGGCTG

5921-6000

TUG1 GCCTTTCTGAAGGTACCCTGCTTGTCTATTTTCTGAC-TCAGCTCTTG--CCTGCCTTTTTCACATGTTGCTGCAATTA
Tug1 GCCCTACTGAAG-----TAGTTTGTCTGTTTACCTGCTTCAGCTCTAACCTGGCTATTTTGACATGCTACTGCAATTA

6001-6080

TUG1 GACTCAC-----CGTGAGGACTACAGTCAATTTAGTCTATCTTGTGCCAA-TACAACAAGGATTTTAAATAGTAACA
Tug1 GACTAACTGGCTTTGAGAAGACTACAATCAGTTTCAGCTCTCCTTTGCCAATTTACCAAGGAATTTTGATAAGAGGA

6081-6160

TUG1 ACCCACACCTCACCCTAGGACTCAATGTTACAAACAGGAAGGACCATTGCTGCATACTCCTTGACCAGCAACTTTTTT
Tug1 ACCCATACCTCACCC-----CACCAGAACAGAAAGGACCA-TGCTGCATATTCCTTGACCAGCAAC-----

6161-6240

TUG1 GAAGATATTTTAAAGTGCAGAGTAGGCCTCTATTCTGTATGTAATTGTTTATTTCAGCACCTGGAACCTCATCTATCG
Tug1 -----TTTAAAGTAGAGAACAACCC-----TGCTTGTTTTCAACATCTGAAACACCATT-----

6241-6320

TUG1 GGTCTGGAAGGAATACAGCAGTTCGAAAGCCGCTCCATTTCT--CTCCTCAGTAGTGCAGAAATGAGTCCGATTACC
Tug1 GATCTAATAGGAGTATAGAAGGTTGACAGCAGAGTACTACTTACTTCTTTCATAACTCAGAAATGAATATGACTGGCC

6321-6400

TUG1 AGTACACACAGAAGTGTACCAGTTCAACCTAGCAAAAAGA-----AGAAAAGTTTCCACTGTACTTAAAATTTACAG
Tug1 -----CAGAAGT-TGTAAGTTCACCTTGACAAGAAACAGCAACACCAGAAGTTTACTGCTGAACTT--AACTTGCCA

6401-6480

TUG1 CTGACTCAAATTCCTCACAGAATTAATTTG--ATGTAGAAGGCTAGTTGTCTTACTTCAGATCAGCAGGACAGTTGGGCT
Tug1 CTTACTCGAATAGTCTCACAGACCTGCTTGCCAAGTAGGAGGCTAGTTTTCTGCTTCATATCACCATTGGAGTGGGGCT

6481-6560

TUG1 C--TCAGACTCATG--ACCACTGAGTTG-----CTTGTGTTGAAACTGTGGTTTCATCCAACATATGCTATTGGAC
Tug1 CAATGGGGTCAATGTTAATACTGACTTGAATGGGGACCTTATGGTGAATCCTAGACTATG-----AGGCTAATGGAA

6561-6640

TUG1 ATGATTATTATTCCATTCAAATGGATTACAGACTTCTTGAGGACAGGACAAACTTATCTCTCATGGTGTTTTTTTAGAAAT
Tug1 ATTATTG----TCTATTCAAGTGGATTATAGATTTCTTGAGGACAGAACAGAC--ATCACTCCTGGTGATTTTTAGAA--

6641-6720

TUG1 ACCTTTATAACCAAGGAAGAAACCATGCCAGCTGTTACCATTCAACTTCTTAAGCAGAGATTAAGCTTTTTTCATATCTGT
Tug1 --CTTGATTACCAAGGAAGAA---ATACCAGCTGCTAACAGTCAACTTCATGGGCAAAGATTAAGCTCTCT-ATATCTGG

6721-6800

TUG1 TCTTATCCTGGACATCAGTAGTTTTTAATTGCCAGCATCCG-TTCCATCTTGTA-ACAACTCCCTGATGTTTCTTAAAA
Tug1 TCGTATCCTGGATGC---TAGTTTTTTATTGCCAGTGACCATTCCATCTCACGCTTAACTTCCTGATGTTTTTTGGAA

6801-6880

TUG1 CCACCTCTTCTATTTTCAGTCT--GTGGTTGGACAGTCTGACCCAACCTTGAGCTTTGTGGGTGAACATGTAATTCAG
Tug1 CCATCTCTTCCAATTTTCAGTCTGGTGATTTAGACAGTCT-----TTTCATGCTGGACATTTTGTGCA

6881-6960

TUG1 ACCTCATCAATCA---GCAAATCCATCTGAACT-----
Tug1 ACCTCATCAATCACAGCAAAGTCCATCTTGACTTTAGTGATTAGTTCAGGAATGGATGCATGATTCAAGTTGTCCAATG

6961-7040

TUG1 -----GTGGAGGAGAAGCTCTCTTTACTGAGGGTGCTTTAGCTTTGTAGGATGAAAACCT
Tug1 ATAATCAACCCTAGGTGTTTTCTCAGTTGTGGAGAAGTCTCTT-----AGATGCTTTAGCTTTGTAGGA--GAAAACCT

7041-7120

TUG1 CAAACTAACAGGGCCTA-----
Tug1 CAAACCAACAGGGCTACCTACTATGTTGAATGATTGTAGGAGAAAACTCAAACCAACCAGGGCTACCTACTATGTTGAA

7121-7200

TUG1 ----CCATGTAGAGAATGAAGCCAGTGCAGGGGAAAGCAGAGCCAAAATATGGAGAGACTTGAATCCTGATGACAGCGTT
Tug1 TGAGCCAGGCAGAAAATGAAGCCAGTACAGAGGAAATGGAGCCAAAAGGAAGAGACTTGAGTTCTGATGATCACATT

7201-7280

TUG1 TGTGCCCTGGATCCAACCGTGCCTGAAGC---TAGAATATCCCCTGGACTTTTCAGTTATGTGAACCAATAAATACCCT
Tug1 TATGCCCTGTATCCAACGTGCCTGAAGCTAATAGTACATCACCTGGACTTTTCAGTTATGTGAACCAATAAATCCCC

7281-7360

TUG1 TTTTTGCTTAAGTTACTTTGAGTTGGGTTTCTGTTACTTGAATTGAATCCACACTAATATATCTACCAACATTGAGACT
Tug1 TTTTTGTTAAGTTACTTTGAGTT-----

7361-7440

TUG1 TGACAGATCCAAGTATTTATTAAGCTAGAGGTCATGGTCACTGAAATTACTTTCCAAAGTGAAGACAAAATGAAACAGG
Tug1 -----

7441-7520

TUG1 AACTGAGGGAATATTTAAGATCCCACAGAAGCGTAAAAATGACATGGTAGAAAGTAATAGAAAACCTAAATGTCTGTGCAT

Tug1 -----

7521-7600

TUG1 TAAAGGATAGGTTAAGGTGTGGTTCAGCCATATAGGAATATCTCGTATCTGTTAAAATGAATAAAGTACATTCATTGTGT

Tug1 -----

7601-7680

TUG1 ATGGAAAAATGGCCATGATACATTAGGTGAAACAAGTTATTAATAGAAAAGTGTACAGTGTGAACTCATTTTAAAATGTG

Tug1 -----

7681-7760

TUG1 TGTGCTTATGTTTATAAATGCATAGAAAGGTCTATTACAGCTTTCTTTGAACAGTGTAGATCACATGAAACTTTCAACT

Tug1 -----

7761-7840

TUG1 TTATACATTTCTGTATTAATATTTTACACTACCCACATTATTTTAAACTTTATTTTAAATAAAGAATTTTAAAATTA

Tug1 -----

7841

TUG1 A

Tug1 -

Sequence Alignment 3

**Homo sapiens CUGBP Elav-like family member 1 (CELF1), transcript variant 1,
mRNA**

Sequence ID: NM_006560.4

Length: 4594 bp

**Mus musculus CUGBP, Elav-like family member 1 (Celf1), transcript variant 1,
mRNA**

Sequence ID: NM_017368.3

Length: 4873 bp

CELF1 sequence has 97.8% homology with Celf1 (5' – 3'):

1-80

```
CELF1      GGC-----  
Celf1      CGCCGCGGTGGTACGTTCCCTTCGCCGCCGCCCCCTCCGCGGCGGCCCTCCCCGCCGTGGTAGGTGCCGAAGTGCC
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81-160

```
CELF1      -----AGCGGCAGCGGCGGGACGCGGAGGCTCCCCCGG  
Celf1      GCCATTTGGGGTGTCTGCTCTGGCGGCAGCGGCAGCGGCAGAGGCGGCGGCGGGACGCGGAGGCTCCCCCGG
```

161-240

```
CELF1      GATTCGGCCTCAGCAGCGAGGCGGCGGCGGCTGCGGAGGCGC-AGGCAGCAACTGAGGCAGCGGAGGCTCAGGTGC  
Celf1      GATTCGGCCTCAGCAGCGA--GGCAGCGGCGGCTGCGGAGGAGCAAGGCAGCAGCTGAGGCAGCGGCGGCTCAGGTGC
```

241-320

```
CELF1      AGCCGCTG-----  
Celf1      AGCCGCTGGAAGCTAAAGCTGTGTATATTTGTGGATCAGACAAGTGCAAGTATTATCATTGGCTTCTGAAGGGGAG
```

321-400

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CELF1      -----  
Celf1      AGTGAGGTGATGGCTGCGTTTAAGTTGGATTTCCAGAAATGATGGTGGATCATTGCTCTTTGAATTCAGTCTCTGT
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401-480

CELF1 CTCAAAGAAAATGAACGGCACCTGGACCACCCAGACCAACCAGATCTTGATGCTATCAAGATGTTTGTGGGCCAGGTTCC
Ce1f1 CTCAAAGAAAATGAACGGCACCTGGACCACCCAGACCAACCAGATCTTGATGCTATCAAGATGTTTGTGGGCCAGGTTCC

481-560

CELF1 CAAGGACCTGGTCTGAAAAGGACTTGCGGAACTCTTCAACAGTATGGTGTGTGTATGAAATCAACGTCCTAAGGGAT
Ce1f1 CAAGGACCTGGTCTGAGAAAGACTTGAGGGAGCTTTTGGAGCAGTATGGTGTGTCTATGAAATCAACATCCTAAGGGAT

561-640

CELF1 AGGAGCCAAAACCCGCTCAGAGCAAAGGGTGTGTTTTGTTACATTTTACACCCGTAAAGCTGCATTAGAAGCTCAGAA
Ce1f1 AGGAGCCAAAACCCCTCCTCAGAGCAAAGGGTGTGTTTTGTTACATTTTACACCCGTAAAGCTGCATTAGAAGCTCAGAA

641-720

CELF1 TGCTCTTACAACATGAAAGTCCTCCAGGGATGCATCACCCATACAGATGAAACCTGCTGACAGTGAGAAGAACAATG
Ce1f1 TGCTCTCCATAACATGAAGGTCCTCCCTGGGATGCATCACCCATACAGATGAAGCCTGCTGACAGTGAAAAGAACAATG

721-800

CELF1 CAGTGAAGACAGGAAGCTGTTTATTGGTATGATTTCCAAGAAGTCACTGAAAATGACATCCGAGTCATGTTCTCTTCG
Ce1f1 CTGTGAAGACAGGAAGCTCTTATTGGTATGATTTCCAAGAAGTGTACTGAAAATGACATCCGAGTCATGTTTCTCTTCG

801-880

CELF1 TTTGGACAGATTGAAGAATGCCGGATATTGCGGGGACCTGATGGCCTGAGCCGAGGTTGTGCATTTGTGACTTTTACAAC
Ce1f1 TTTGGACAGATTGAAGAGTGCCGGATATTGCGGGGACCTGATGGCCTGAGCAGAGGTTGTGCATTTGTGACTTTTACTAC

881-960

CELF1 AAGAGCCATGGCACAGACGGCTATCAAGCAATGCACCAAGCACAGACCATGGAGGGTTGCTCATCACCATGGTGGTAA
Ce1f1 AAGAACCATGGCACAGACAGCTATCAAAGCAATGCACCAAGCACAAACCATGGAGGGTTGCTCATCCCAATGGTGGTAA

961-1040

CELF1 AATTTGCTGATACAGAAGGACAAAGAACAGAAGAGaatggccagcagctccagcagCAGATGCAGCAAAATCAGCGCA
Ce1f1 AGTTTGCCGACACCAGAAGGACAAAGAACAGAAGAGAATGGCCAGCAGCTCCAGCAGCAGATGCAGCAGATCAGTGCA

1041-1120

CELF1 GCATCTGTGTGGGAAACCTTGCTGGTCTAAATACTCTTGACCCAGTATTAGCA-----CTCCTTCAGCA
Ce1f1 GCGTCTGTGTGGGAAACCTTGCTGGTCTGAACACACTTGACCCAGTACTTAGCACTTTATTTGCAGCTCTACAGCA

1121-1200

CELF1 GACTGCCTCCTCTGGGAACCTCAACACCCTGAGCAGCCTCCACCCAATGGGAGGGTTGAATGCAATGCAGTTACAGAATT
Ce1f1 GACTGCCTCCTCTGGGAACCTCAACACCCTGAGCAGCCTCCACCCAATGGGAGGGTTAAATGCAATGCAGTTACAGAATT

1201-1280

CELF1 TGGCTGCACTAGCTGCTGCAGCTAGTGCAGCTCAGAACACACCAAGTGGTACCAATGCTCTCACTACATCCAGCAGTCCC
Ce1f1 TGGCTGCACTAGCTGCTGCAGCTAGTGCAGCTCAGAACACACCAAGTGGTACCAATGCTCTCACTACATCCAGCAGTCCC

1281-1360

CELF1 CTCAGCGTGCTCACTAGTTCAGGGTCCTCACCTAGCTCTAGCAGCAGTAATTCTGTCAACCCCATAGCCTCACTTGGAGC
Ce1f1 CTCAGCGTACTCACCAGTTCAGGGTCTTCACCGAGCTCCAGCAGCAGTAATTCTGTCAACCCCATAGCCTCACTTGGAGC

1361-1440

CELF1 CCTGCAGACATTAGCTGGAGCAACGGCTGGCCTCAATGTTGGCTCTTTGGCAGGAATGGCTGCCTTAAATGGTGGCCTGG
Ce1f1 CCTGCAAACATTGGCCGGAGCAACAGCTGGCCTCAACGTTGGCTCATTGGCAGGGATGGCTGCCTTGAATGGTGGTCTGG

1441-1520

CELF1 GCAGCAGTGGCCTTTCCAATGGCACCAGGGAGCACCATGGAGGCCCTCACTCAGGCCTACTCGGGTATCCAGCAATATGCT
Ce1f1 GCAGCAGTGGCCTTTCCAATGGCACTGGGAGTACCATGGAAGCCCTCACCAGGCGTATTCTGGTATCCAGCAATATGCT

1521-1600

CELF1 GCTGCTGCGCTCCCCTCTGTACAACCAGAATCTTCTGACACAGCAGAGTATTGGTGCCTGGAAGCCAGAAGGAAGG
Ce1f1 GCTGCAGCCCTCCCCTCTGTACAACCAGAATTTATTGACACAGCAGAGTATTGGTGCCTGGAAGCCAGAAGGAAGG

1601-1680

CELF1 TCCAGAGGGAGCCAACCTGTTTACCTACACCTGCCCCAGGAGTTTGGTGATCAGGACCTGCTGCAGATGTTTATGCCCT
Ce1f1 TCCAGAAGGAGCCAACCTGTTTACCTATCACCTGCCCCAGGAGTTTGGAGACCAGGACTTACTGCAGATGTTTATGCCCT

1681-1760

CELF1 TTGGGAATGTCGTGTCTGCCAAGGTTTTTCATAGACAAGCAGACAAAACCTGAGCAAGTGTTTTGGTTTTGTAAGTTACGAC
Ce1f1 TTGGGAATGTCGTGTCTGCCAAGGTTTTTCATAGACAAGCAGACAAAACCTGAGCAAGTGTTTTGGTTTTGTAAGTTATGAC

1761-1840

CELF1 AATCCTGTTTTCGGCCAAGCTGCCATCCAGTCCATGAACGGCTTTCAGATTGGCATGAAGCGGCTTAAAGTGCAGCTCAA
Ce1f1 AATCCTGTCTCAGCTCAAGCTGCCATCCAGTCCATGAACGGCTTTCAAATGGAATGAAGAGGCTTAAAGTGCAGCTCAA

1841-1920

CELF1 ACGTTTGAAGAATGACAGCAAGCCCTACTGAGCGTGCTCCCCTCTGAGACTGGAGTGAGAGGGTCTTCTGATTCTCTGCCG
Ce1f1 ACGTTTGAAGAATGATAGTAAGCCCTACTGA--GTGCTCCCCTCTGAGACTGGAGTGAGAAGATCTTCTGATTCTCTGCCG

1921-2000

CELF1 TTTGTTTCATCGTTGTGCCTAAAGCATGTCGATGTGGCGTCAAGTACATCGTCCAAATCCCTGTCTCTTCAGCTTCTCTGA
Ce1f1 TTTGTTTCATCGTTGTGCCTAAAGCATGTCGATGTGGCGTCAAGTACATCGTCCAAATCCCTGTCTCTTCAGCTTCTCTGA

2001-2080

CELF1 TGCTTGAACCTCTCACCTTTGACCTTGTTGACCTTTGATGCTGATGTGATTTTTATTATGTTTGTCTTTCTTCTCGTT
Ce1f1 TGCTTGAACCTCTCACCTTTGACCTTGTTGACCTTTGATGCTGATGTGTA-TTTTATTATGTTTGTCTTTCTTCTTGT

2081-2160

CELF1 TTTTTTCTTTTTTCTTTCCCTTTTTTTTCCCTTTTGTGCTGCCAAATGGTTTTGCTAGAACGACTGCTGAAGGGGAAA
Ce1f1 TTTTCTTTTTTCTTTCTTT-TTTTTTTTCCCTTTTGTGCTGCCAAATGGTTTTGCTAGAACGACTGCTGAAGGGGAAA

2161-2240

CELF1 TATTTAAACTGCATTTGAATAT-AAAAAAATCTATTTTCTAGAACTTCATAAGATAAACCACTTGATTTGTGATTCC
Ce1f1 TATTTAAACTGCATTTGAATATAAAAAAAATCTATTTTCTAGAACTTCATAAGATAAACCACTTGATTTGTGATTCC

2241-2320

CELF1 AATTCTTTGTAATTGTCTTCAGAGCAGCCCTACTAGCACATACCGCGTGGTGTGTTGTATTCTGTGAACACACAGCCAGT
Ce1f1 AATTCTTTGTAACGTGC-TCAGAGCAGCCCTACTAGCACATGCGGTGGTGTGTTGTATCCTTGTGAACACACAGCCAGT

2321-2400

CELF1 CCGTTTCTAGGCTTTGTTTCTCTGTGTGCTTAGTTTTAAAGACAACCTTGAAGTAAACAATGAAATAAAAGATGTCACCTA
Ce1f1 CCGCTCCAGGCTTTGTTCTCTGTGTGCTTAGTTTTAAAGACAACCTTGAATAAACAATGAAATAAAAGATGTCACCTA

2401-2480

CELF1 AAACCTCTGAGGCTCCTGAGCACATTTGCTGATACAGTCTGTGGGCTTGAGGAGACCGCATGTATTGTTCTTCTTTT
Ce1f1 AAATCTTTGAGGCTCCTGAACACATTTGCTGACATAGTTT-TGGGGCTTGAGGAGACCGCATG--TTGTTATTAATTT-

2481-2560

CELF1 GTTTTTCTTCTGAGTTCTCAACTGCGGAGA-----GCACCTGAACCCCTTTCCTTTTGGACCGAGGCTGCA
Ce1f1 -TTGTTTTCTGAGTTCTCAACTGCAGAAAATGCTGAAATACACCCTTACCCCATTCCTTTTACTGAATGCTGAG

2561-2640

CELF1 CTTTGGGCCCAGCCAGCCCTTTTCTTTTTCTTTTTCTTTTGTGGTTCTTCCCTGGAGCGACTCT---GGGGAGTCTCTG
Ce1f1 GTTTGGGCCCAGCTAGCC-----TTTTTCTTTTTCTTTTGTGGTTCTT-CCTGAAGCAGCCCTGCAGGAAGCCCTA

2641-2720

CELF1 GA--TATCCCGCCTGCCCTTCCCCTCAGC-----CCCATGCTTGTCCAACAGTCTCCACAGCAAAATGT
Ce1f1 GGGTCCCTCTTCCCCTCCCCTCCCCTCGGCTCAGCCAGCTCACACCCGTGCTTCTTCTACAGTCTCCACAGCAAAATGT

2721-2800

CELF1 GATGCTTTGATTTTTTTGTTGTTGTTTTGTTTTGTTTGTATTGTTTTGTTTGTGTTTTGTTTTGAAATTTTTCTTTCTACTA
Ce1f1 GATGCTTTCAACTT-----TTTTGGGTTTTGTTT-CTTTGCCTTTTTGTTTTGAA-TTTTTCTTTCTACTA

2801-2880

CELF1 AGATTATGCCAGAAAA---AAGTTTTGCATGTTTCTGCTGTTTCTTACACCTTCGTATATATCACCTTCACCTCTCT
Ce1f1 AGATTATGCCAGAAAAACAAGTTGTCATGTTTCTGCTGTTTCTTACACCTTCGTATATATCACCTTCACCTCTCT

2881-2960

CELF1 GTTTTCTATAGTTTGTGCAAAAAGTATCGATTTAAAGGGTTTCAAAGAAGCTGTTTTAAATTGTTGTAGGGTTGATTA
Ce1f1 GTTTTCTATAGTTTGTGCAAAAAGTACTGATTTAAAGGGTTTCAAAGAAGATGTTTTAAATTGTTATGGGGTTGATTT

2961-3040

CELF1 TTTTTTCAAGATTGATTTGTTAATTTTGAAGTGGCAACTTTCCTCTATTGCCCTTAGAGCGTTTGCCTGTGCACTT
Ce1f1 TTTTTCTCAAGATTGATCGTTTTATTTTGAAGTGGCAACTTTCCTCTATTGCCCTTAGAGTGTGTTGCCTGTGCACTT

3041-3120

CELF1 AGACTGTCACTTCGT---GTGGCCTCCAGGTCTTACCGGGGCTCCGGGAGGCTGGCTGCTTTGCTCAGAGAGGGTGGGA
Ce1f1 AGACTGTCACTCTTTGTGGTGGCTCCAGGTCTCAGTGGGGATCCAGGAGGCTGGCTGCTCTGCTCAGGGAGTACAGGG

3121-3200

CELF1 AGGGGGCCTGGAGAGACACGAGAAGCAGAGGTAGAGCCTAGAAGGTGGCAGCAGGTGGGTAAGAGGCTTATTTAGCACAT
Ce1f1 GG-----CCAGAGGCAGAAGCAGAACC--AAAGGTGGCTGTGGGTAGGCAGGA----TGCTTAGGGCAT

3201-3280

CELF1 TAGGGGCAGTGAGCACCTGGAGGAA-----GGAGGGCGCTCCCAATCACCCGTAGGAGGCCATCTGCACACCAAGCG
Ce1f1 CAAGGCTAGATCACGGAGGGAGGGAGGGCAGGCGGGCAGTACTTCTGATTACCCAGAGGAGGCCATCGGTGCACTGAGTG

3281-3360

CELF1 GCAAT----TCACCTGCTGGCGCTTTTCTAGGTGACAAGCAC----AATACTACAGTCTTCACACTGTTTACAGCCCTG
Ce1f1 GCAATATACCTGCCTGCCTGGCTTTCCCTAGGTGACAAGCACAATAAATACTACAGTCTTCACACTGTTTACAGCTCTG

3361-3440

CELF1 GGCACCAGCCACCCGGCACTGGCTCTTCATCACAGCTCTGCTCTTGCTTAGCTAGTGGGGTGGGGAAAGGGCAGGGATT
Ce1f1 GGCACCAACCACCCGGCACTGGCTCTTCACTATGGCTCTGCTCTTACTTAGCTAATAGAGTTGGGGTAAGGGCAAGAAAC

3441-3520

CELF1 TGTTTTTTTAATTGGGTGGAGAGCCAAACAGCTACTGTCCCTGGGTGCCAAGCAAGCCAGTTTTTTGGTTCCTGAGGGA
Ce1f1 TG-TTTTTAAATTGGGTGAAGAGCCAGATAGCTACTGTTCCTGGGTGCCAGGCCAGCCAGTTCTTTGGTTCCTAAGGGA

3521-3600

CELF1 AACTGACCTCCTCTCTTGTGGCACCATCCAGCCTCAGGGTCTTGGAGACTTGAGTAAGAATGTGAGTGGAGGGGAGAG
Ce1f1 AACTTACCTCCTCTCTTGTAGCACCATCCAGCCTCAGGGTCTTGGGACTTGG--AAGAATGTAATAGAGGAGGAGAG

3601-3680

CELF1 GT--GAGGAGAGGAGCACA---GGTGGATCTGTGGAGGAAGAGGTTACAGGGGAGGAGCTGATGATAGATCCCACCC
Ce1f1 GCTAGAGGAAATGAGTAGACAGGGATGGATCTGTGAAGAGCAGAGGCTGCAGGG---AGGATTTTACAGATCCCCTG

3681-3760

CELF1 AGACTTAAGCTGCTGGTGGTGGGTGAGCTGGGAAGTAGGACTGTCCAGGGAAGGGTGGAGAGATGTAGCTAGGGGCTGG
Ce1f1 AGACTTAAGC-ACTGGTGGGAGGAAAGT--GGAAGCAAGGTTGTCCAGGAAAGGGTGGCAAGGTGCAGCAAAGGATGGG

3761-3840

CELF1 GGAGGGGAGGTGGAAGCGCTATTGAGCATCTCCACCAAGGTTGATGAAGGAAGGGATCCCAGCAGGGTTTCTGCTC
Ce1f1 GGTGGGGAG---AGAAGCACGGTCTGGCATCATCCACTCTCTGCCTGGTG--TTGAAGGAACTCCAGCACAGTTTCTGCTC

3841-3920

CELF1 TGGGG--CTGGCAGGTTGCCTG--GTATTATGCCAAGGCCCTCTGCTGGGGAAAGGGCAGCCAGGCAGAGGCCCCAG
Ce1f1 TGGGACCCCTACAGGTTGCCAATATATTATGCTTGAGGCCACCTTACTAGGAAGAAATGGCAGCCAAAGTGGGGGAC---

3921-4000

CELF1 TGCTCTGGTAGGCTGCTGAATTCCTGGAAGGGGTGATTGGATGGAAAGAGGCCAGAAACCCAGCCTGAGAGA--CTGCT
Ce1f1 --TTAAGTATGCTGCTTAAGGTCTGGAAGGGGTGGTAGGATGCCAGCG-----CCTAGCATGAGAGAGCCTGCT

4001-4080

CELF1 GTGCACCCACAGTCTGACTGCACAGAGCCGCTCTGTGGCAGGAGGCACTGAGGCTCCCTTCCTGTGTATTGAGAAG
Ce1f1 GTGTG-CCCACAGTCTGACTGCACAGAG-CGCTCTGTGGCAGGAGGTGCTGCGG-TCCCTTCCTGTGTACTGAGAAG

4081-4160

CELF1 CAGTGTTTGCCAATATATTTTGCTTTCAATTCCAAGAGGAGCTCTGGGAAAACCTGTGGATAAAACCAAATGCCAAATGT
Ce1f1 CTGGGCTTGCCAATATAGTTTGCTTTGATTCCAAGAGGAGCTCTGGGAAAACCTGTGGATAAAACCAAATGCCAAATGT

4161-4240

CELF1 TGGACGTTGTTTCCTTTTCCTTTCTCTCTGATTGTTTAAATTGTTCTGTGGTGGTTTAAATGGATTTGAGACCCTGG
Ce1f1 TGGACATTGTTTCCTTTTCCTTT--TCTCTCTGATTGTTTAAATTGTTCCGTAGTGGTTTAAATGGATTTGAGACCCTGG

4241-4320

CELF1 AGCGGCAGCTGCCTTTCTGATTTCAGCTGCTTTTTGTGAATAATTTAAAAAGAAAAAAAAAAAAAGAACTTTACATTTTG
Ce1f1 AGCGGCAGCTGCCTTTCTGATTTCAGCTGCTTTTTGTGAATAATTTAAAAAG-AAAAAAAAAAAAAGAACTTTACATTTTG

4321-4400

CELF1 GAGACAAACCTGTGTGAGTTTTTATTGGTACAAACGTTGTATTTAACACTAGGGGTTTTGTACAGTTTTTTGCCTTTTC
Ce1f1 GAGACAAACCTGTGTGAGTTTTTATTGGTACAAACGTTGTATTTAACACTAGGGGTTTTGTACAGTTTTTTGCCTTTTC

4401-4480

CELF1 TACTAGAAAACAATGTAAGTGATTTCACAATGTGAAGAGAAAAAAATGCCACTATGACCAAACGCACAGTCTGTTC
Ce1f1 TACTAGAAAACAATGTAAGTGATTTCACAATGTGAAGAG--AAAAAATGCCACTATGACCAAACGCACAGTCTGTTC

4481-4560

CELF1 TGCAGCAACAACGGGATTCAATCAACT--AGTCGTATTAGCCGTAGAAATGCTTTTCCTTTATCTGTTTGTAGCTTT
Ce1f1 TGCAGCAACAACGGGATTCAATCAACTCAAAGTCGTATTAGCCGTAGAAATGCTTTT-CCTGACCTTGTGTAGCTTT

4561-4640

CELF1 TCCTTTCTTTCTGTTTTGATTGCAAAAGAAAATGCTTTTTTGTGTGAACTTGTGTTGACTCTGTAGAAAATTATGG
Ce1f1 --CCTTTTCTCTG-TTTGATTATAAAAG--ATGCTTTTGTGTGAACTTGTGTTGACTCTGTAGAAAATTATGG

4641-4720

CELF1 ATTTTACTTTAATGGTTT-----AAAAAAGGCAAGGAGAGCCCTCGTCGCTTTTCTTACCTAATCACAGAGTTTGT
Ce1f1 ATTTTGTCTTAATGGTTTTTAAAAAAGGCAAGGAGAGCCCGTGTGCTTTTCTTACCTAATCAC--AGTTTGT

4721-4800

CELF1 GTAGTGAATTTAAAAAGAAAAAAATTTGTTATAAGTTTGGAGCAAGGGAGTATGTGTTTCAAAGGAATCTCCTTCCTTT
Ce1f1 GTAGTGGATT--AAAAAAGAAAAAGTTGTTATAAGTTTGGAGCAAGGGAGTATGTGTTTAAAAAGACTCTCCTTC--T

4801-4880

CELF1 TTTTGTGTGTTTTTCCTTTTGTCCAATGGGGAACCTAAATCTGTTTAAATTGCACAGACACATGGACAAAAAGTCATT

Ce1f1 TTTTGTGTGTTTTTCCTTTTGTCCAATGGGGAACCTAAATCTGTTTAAATTGCACAGACACAGACAAAAAGTCATT

4881-4960

CELF1 TGTATCTGCCAAGTGTGGTACCTTCCTTTGTTTATTGCTATTAAACTGTTGAGAAGAACTGA-----

Ce1f1 TGTATCTGCCAAGTGTGGTACCTTCCTTTGTTTATTGCTATTAAACTGTTGAGAAGAAAAAAAAAAAAAAAAAAAAA

References

Madeira, et al., The EMBL-EBI search and sequence analysis tools APIs in 2019, *Nucleic Acids Res*, 47 (2019) W636-W641.DOI: 10.1093/nar/gkz268.