This Supplementary Material shows the Core Promoters of Complex II subunits/related genes identified by phylogenetic footprinting. The conserved regions are shown in color codes, which correspond to specific Transcription Factor Binding Sites (TFBS).

The description of the complete description of TFBS can be found in additional file 3 (in the “Matrix Family Library” Excell sheet).

GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites working on promoters.seq (3 seq.)

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1 December 2004 **Wed Jun 8 21:31:13 2005**

Solution parameters:

Sequence file:	promoters.seq (3 seq.)
Type of sequences:	nucleotide sequences
Threshold T:	0.00
'*' signs below alignment denote:	diagonal similarity (max. similarity is represented by 10 '*' signs)
Alignment output:	complete alignment is shown # nucleic acids per line: 50
TF output:	common TF matches located in aligned regions (common to 3 (100.0 %) sequences)
Family matches:	yes
MatInspector library:	Matrix Family Library Version 5.0 (February 2005)
Selected groups (core/matrix sim):	• ALL user_defined.lib (0.75/Optimized) • ALL vertebrates.lib (0.75/Optimized)

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P878032	sym=SDHA|loc=Loc6389|taxid=9606|spec=Homo sapiens|chr=5| ctg=NT_006576|str=(+)|start=207947|end=208947|len=1001| tss=501| comm=succinate dehydrogenase complex, subunit A, flavoprotein (Fp); (NM_004168/501/silver;)	1001 bp
2	P878035	sym=Sdha|loc=Loc66945|taxid=10090|spec=Mus musculus|chr=13| ctg=NT_078713|str=(-)|start=5811894|end=5812912|len=1019| tss=501,502,514,519| comm=succinate dehydrogenase complex, subunit A, flavoprotein (Fp); (AK029520/510/gold;AK010561/522/gold;AK050475/522/gold; AK049590/522/gold;AK075990/527/gold;XM_127445/509/bronze;)	1019 bp
3	P878037	sym=Sdha|loc=Loc157074|taxid=10116|spec=Rattus norvegicus| chr=1|ctg=NW_047549|str=(+)|start=6979031|end=6980031| len=1001|tss=501| comm=succinate dehydrogenase complex, subunit A, flavoprotein (Fp); (NM_130428/501/bronze;)	1001 bp

Alignment (DiAlign format):

Please note that only **upper-case** letters are considered to be **aligned**. For more information, please have a look at the user guide.

V$GLIF V$NRF1 U$NRF1 V$EGRF V$P53F V$INSM V$EREF U$EREF V$RORA

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alignment position 1.........  11........  21........  31........  41........
P878032          1 cactttaagt ttgtttacat gtgacctcc- ---------- ---ACAAACA
P878035          1 ---------- --------- C CTCCAGCTTC CCAGCTGCTG -TAACGAAGA
P878037          1 aggatgacaa caggccggt C CCCGAGCTTT CCAGCAGCTG tTAACGAAGA
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                                                                    *********
alignment position 51........ 61........ 71........ 81........ 91........
P878032        37 CACACAATTA CAAAATAGTT Tagttaat-- ---------- ----------
P878035        31 CGAAAGCTTT GGATATAGTT TCTAGTTCAG TATCCTGGCT TTTACGTAGC
P878037        51 TGAAAGCGAT GGATATAcTT TCTAGTTCAG TATTCTGGAT TCTGCGTAGC
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                                     ** ********** ********** **********
alignment position 101....... 111....... 121....... 131....... 141.......
P878032        65 ---------- ---------- ---------- --CAAGGGAT gtataataaa
P878035        81 CCAGTGCagc tAGCTGCTCC TTGTCCAGCC ACCAAGacAT CATTCCTACC
P878037       101 TCAGTGC--- -AGCTGCTCC TTGTCCAGCC ACCAAGGGAT CATTCCTACC
                  *******      ********** ********** ********** **********
                  *******      ********** ********** ******   ** **********
                  *******      ********** ********** ******   ** **********
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alignment position 151....... 161....... 171....... 181....... 191.......
P878032        83 caagaggtcg gaggcccccgg gccgctcccg cccacctccg cggacgagcg
P878035       131 TACTCTAGAA GTCCAGGGCA GTAtgta--- ---------- ----------
P878037       147 CACAACAGAA GTTCAGGGCG GTAg------ ---------- ----------
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alignment position 201....... 211....... 221....... 231....... 241.......
P878032       133 CCCCCCTCCG ACCCCATTCC CTGCGGTCTG GGCGTTCAgg ccctt cggtc
P878035       158 CCCCCCCCCC CCCCCATTAG TTGAGATTCa AGCGCCCAAC AAAACGGGCT
P878037       171 --------CC CGCCCATTTC TTGAGATTCT AGCGCCCAAC AAAATGGGTT
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alignment position 251....... 261....... 271....... 281....... 291.......
P878032       183 tgggcgatcc cgg------- ---------- ---------- ----------
P878035       208 CTTATGGAGC TTGCGATCtc cgcccc-AGG ACCCTACTTC CATCTCTCCA
P878037       213 CTTATGGAGC TTGCGTTCgc ttccact AGG ACCCTACTTT CATCTGTCCG
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alignment position 301....... 311....... 321....... 331....... 341.......
P878032       196 ---------- ---------- ---------- -AGA---ACC ACCCAcgggg
P878035       257 GATCATCCGA CCCtctcTGT TTTGGCAAAC AAGA---ACC ACCCGAGAAG
P878037       263 GATCCTCGGG CCCggagTGT CTTGGCAAAC AAGAaaaACC ACCCAAGAAG
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                                                             *** **********
alignment position 351....... 361....... 371....... 381....... 391.......
P878032       212 --CTTTAAAA ATGTTGGTGC CCACCACCTC CCCGGAACAG GGC------
P878035       304 CACTTTAAAG ACATTGGCAC CTCACTTACC CCTGGAGCAG AGCCCATCAG
P878037       313 CACTTTAAGG ACATTGGTAC CTCACTTACC CCTGGAGCAA AGCCCATCAG
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alignment position 401....... 411....... 421....... 431....... 441.......
P878032      253 --------CC GCTCTACCTC GGTCGGGgag cgcgggacct cagcgttccc
P878035      354 Cgtt GCTGCC ACCCTACCTC AGACGTGTTG ---------- ----------
P878037      363 Ct aa GCTGAC AGCCTATCTC ACAGGTAATG ---------- ----------
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alignment position 451....... 461....... 471....... 481....... 491.......
P878032      295 ttaacgccaC CGTCCGCGGG TCCGCTTTGC GCAGGCGCGG CGCCCCcact
P878035      384 ---------C CACCGCCGCG TTTaCAGGGC GCAGGCGCAC CACCACTCAC
P878037      393 ---------C CACCGCCGCG TTTGCAGAGC GCAGGCGCAC CACCACTCAG
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alignment position 501....... 511....... 521....... 531....... 541.......
P878032      345 cagtacccgc tccgggcgtg gcatggtgcg caggcgcgat gtcccccact
P878035      425 GCGAGCCAGG AGG------- ---------- ---------- ----------
P878037      434 GCGAGCCAGG AGGa------ ---------- ---------- ----------
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alignment position 551....... 561....... 571....... 581....... 591.......
P878032      395 gcagccccgc tcgactccGG CGTGGTGCGC AGGCGCGGTA TCccccctcc
P878035      438 ---------- --------GG CGTGTTGCGC AGGCGCAGAA TCTTCCAAGC
P878037      448 ---------- ---------G CGTGTTGCGC AGGCGCAGAG CCTTCCAAGC
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alignment position 601....... 611....... 621....... 631....... 641.......
P878032      445 cccgccagct cgacccggt gtGGTGCGCA GGCGCAGTCT G-CGCAGGGA
P878035      470 CCGACACCcG CGCGACTC-- --GGTGCGCA AGCGCAGTCT GTCGCTGGGG
P878037      479 GCCACACCaG CGCGGCTC-- --GGTGCGCA AGCGCAGTCT ATCGCTGAGG
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alignment position 651....... 661....... 671....... 681....... 691.......
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P878032     494 CTGGCGGGAc tgcgcggcgg caacaGCAGA CATGTCGGGG GTCCGGGGCC
P878035     516 CTTGCGGGAA G-------------------GCAGA CATGGCCGGG GTTGGCGCAG
P878037     525 CTTGCGGGAA G-------------------GCAAA CATGGCCGGG GTTGGCGCAG
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alignment position 701....... 711....... 721....... 731....... 741.......
P878032     544 TGTCGCGGCT GCTgagcgct CGGCGCCTGG CGCTGGCCAA GGCGGTGAGT
P878035     552 TTTCGAGGCT TCTTCGCGGG CGGCGCTTGG CGTTAACTGG GGCGGTGAGT
P878037     561 TTTCGAGACT TCTTCGCGGG CGGCGCTTGG CTCTAGCTGG GGCGGTGAGT
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alignment position 751....... 761....... 771....... 781....... 791.......
P878032     594 CCGTGCCGCG gaccggggcg gggcaggcgg ggggccgaggc GGCGGTAGGA
P878035     602 TAGTGCCACG AAATGGCA-- ---------- ---------- GGCGCTAGGA
P878037     611 TAGTGCCACG GTATGGCG-- ---------- ---------- GGCACCAGGA
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alignment position 801....... 811....... 821....... 831....... 841.......
P878032     644 Gcgggacggt cccccagcggg tccgagcgga gcggggcgccg ggtccctgcg
P878035     630 GTGCGcca-- -----CGATT CCACCCGAGT ---------- ----------
P878037     639 ATGCGtctaa tcctgCGATC CCACCCGAGT ---------- ----------
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alignment position 851....... 861....... 871....... 881....... 891.......
P878032     694 ccctcTGTCC CGGGATCGGG AAGGGGCTGA GAGAGccctg ggccggtgcg
P878035     653 -----TGGCC TGAGTCTGGG AAGGTGCAGT GGGCCGAAGC C---------
P878037     669 -----TGAAT TGGATCTGGG AAGGTGCAGC GGGCGGAAGC G---------
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alignment position 901....... 911....... 921....... 931....... 941.......
P878032     744 aggggaagcc gcggggcgga ctcggggacc cggggagctc ggtccttagt
P878035     689 ---------- ---------- ---------- ---------- ----------
P878037     705 ---------- ---------- ---------- ---------- ----------

alignment position 951....... 961....... 971....... 981....... 991.......
P878032     794 agataGTCCG CGTCCGGGTG AAGGTCACAA CCCCGCGGGC ttgctgggcg
P878035     689 -----GACTG CTTTCCGGCG AAGGTCACGA CCCCGAGGTC GCGGGCGTGG
P878037     705 -----GACAC CGTTCCGGCG AAGGTCATGA CCCCGAGGTC GCGGGCATGG
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alignment position 1001..... 1011..... 1021..... 1031..... 1041.....
P878032     844 tcc----CCT CCGCCGCCTT GGTCcgggcc tggggtcctg ggacccccgcg
P878035     734 AGTCTGGCCT TCCCCGTCTT GGTC-TAGCG AAGTTCTCCA AGGTTAAAGG
P878037     750 AGTCTGGCCT TCCCTGTCTT GGTCtTAGCA AAGTTCTCCA AGGTTAACGG
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alignment position 1051..... 1061..... 1071..... 1081..... 1091.....
P878032     890 ggctgaggta gcccctcgcc tcagtgCCTG GCAGGTGGAC TCGGGGAGGA
P878035     783 GAGGGA---- ---------- -------CCGG CCTGTTGCAT TCTGGATGCG
P878037     800 GAGGGA---- ---------- -------CCAG CCTGTgGCAC TCTGGATGTG
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                ******                        **** *****
alignment position 1101..... 1111..... 1121..... 1131..... 1141.....
P878032     940 GTCGTGTCTG Cccaaggtca cccgggcgga tagcggccgg tggccgcccct
P878035     813 GACGGGTCTG CGAgtaATCC GTTGGTAGTC TGGGTGTCGA CACTAAgact
P878037     830 GGCAGATCCG CGA---ATCC GTTGGTAGCC TGGGTGTGGA CACTAA----
                ********** ***    **** ********** ********** ******
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                           ***    **** ********** ********** ******
alignment position 1151..... 1161..... 1171..... 1181..... 1191.....
P878032     990 ggctgggctg gg--------- ---------- ---------- ----------
P878035     863 tataagtgat gagcttacaG GTTTTGTGTA GTGGCCTTAG CTACTGTTTT
P878037     873 ---------- ---------G GTTTTGTGTA GTAGTCTTAG CTACTGTTTT
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alignment position 1201..... 1211..... 1221..... 1231..... 1241.....
P878032    1002 ---------- ---------- ---------- ---------- ----------
P878035     913 TAAATATCAa AGAGATATTT GAAGATACCA GGTGAGACTT CTGCACcGTG
P878037     904 TAAATATCAg AGAGAGATTT GAAAATATCA GGTGAGACTT CTGCACtGTG
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                *********
alignment position 1251..... 1261..... 1271..... 1281..... 1291.....
P878032    1002 ---------- ---------- ---------- ---------- ----------
P878035     963 TTCATCCAGT CTTGCGACTT CT-TTTTGCA TTTGAAGAGG TACACAGtga
P878037     954 TTCATCCAAT TTTGCGGCTT CTgTTTTGCA TTGGAAGAGA GTCACAGa--
```

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                    * * * * * * * * * *  * * * * * * * * * *  * *
alignment  position 1 3 0 1 . . . .
P878032       1002 - - - - - - - -
P878035       1012 c t c a g g g t
P878037       1002 - - - - - - - -
```

Pairwise similarities:

For each pairwise alignment, the similarity (relative to the maximum similarity) and the number of identical nucleic acids (in % of shorter sequence) is given. Maximum values are underlined.

	P878035 (1019 bp)	P878037 (1001 bp)
P878032 (1001 bp)	0.086 29 %	0.075 28 %
P878035 (1019 bp)		1.000 83 %

Please note that the **similarity value 1.000** marks only the two **most similar** sequences, it does not necessarily mean that these sequences are identical.

Extract alignment region	
Positions in alignment	from: to:
Output file	dialign.seq

Extract aligned sequences

For comments, questions or bug reports, please contact support@genomatix.de

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License Agreement

GEMS Launcher 4.1.1

GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites working on promoters_2.seq (3 seq.)

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1 December 2004 **Wed Jun 8 21:35:28 2005**

Solution parameters:

Sequence file:	promoters_2.seq (3 seq.)
Type of sequences:	nucleotide sequences
Threshold T:	0.00
'*' signs below alignment denote:	diagonal similarity (max. similarity is represented by 10 '*' signs)
Alignment output:	complete alignment is shown # nucleic acids per line: 50
TF output:	common TF matches located in aligned regions (common to 3 (100.0 %) sequences)
Family matches:	yes
MatInspector library:	Matrix Family Library Version 5.0 (February 2005)
Selected groups (core/matrix sim):	• ALL user_defined.lib (0.75/Optimized) • ALL vertebrates.lib (0.75/Optimized)

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P876195	sym=SDHB|loc=Loc6390|taxid=9606|spec=Homo sapiens|chr=1| ctg=NT_004610|str=(-)|start=204488|end=205488|len=1001| tss=501| comm=succinate dehydrogenase complex, subunit B, iron sulfur (Ip); (NM_003000/501/bronze;)	1001 bp
2	P876196	sym=Sdhb|loc=Loc67680|taxid=10090|spec=Mus musculus|chr=4| ctg=NT_039267|str=(+)|start=8395078|end=8396196|len=1119| tss=501,608,609,619| comm=succinate dehydrogenase complex, subunit B, iron sulfur (Ip); (AK003052/608/gold;AK009660/609/gold;AK003533/619/gold; NM_023374/501/bronze;)	1119 bp
3	P876197	sym=na|loc=Loc298596|taxid=10116|spec=Rattus norvegicus| chr=5|ctg=NW_047726|str=(+)|start=3781027|end=3782027| len=1001|tss=501| comm=similar to succinate dehydrogenase Ip subunit; (XM_216558/533/bronze;)	1001 bp

Alignment (DiAlign format):

Please note that only **upper-case** letters are considered to be **aligned**. For more information, please have a look at the user guide.

V$ZBPF V$SP1F V$NRF1 U$NRF1 V$EBOX V$P53F V$ETSF U$NRF2 V$CDEF V$EKLF V$MAZF V$E4FF V$YY1F V$MYOD V$EREF U$EREF V$RORA

```
alignment position   1 . . . . . . . . . 11 . . . . . . . . 21 . . . . . . . . 31 . . . . . . . . 41 . . . . . . . .
P876195            1 g t a a t t c c a g c a c t t t g g g a g g c c a a g g t g g g c g g a t c a c g a g g t c a g g a
P876196            1 c t g g c a c c a g c c a c a t a c t a g g t a c c c t t t c t g g c t g c t t t g g t t t t g g t
P876197            1 g c - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
```

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alignment position      51........ 61........ 71........ 81........ 91........
P876195     51 gttcaagacc agtctggcca agatgatgaa acccccgtctc tactaaaaat
P876196     51 tttgtgtgtt t--------- ---------- ---------- ---------- ----------
P876197      3 ---------- ---------- ---------- ---------- ----------

alignment position     101....... 111....... 121....... 131....... 141.......
P876195    101 acaaaaaatt agccgggtgt gatggtgtgc gcctgtaatc ccagctactc
P876196     62 ---------- ---------- ---------- ---------- ----------
P876197      3 ---------- ---------- ---------- ---------- ----------

alignment position     151....... 161....... 171....... 181....... 191.......
P876195    151 gggaggcTGA GGCAGGagaa tcgcgtgaac ccggggaggcg gaggttgcag
P876196     62 -------TGA GGCAGGgtCT CAAGTATCCC AGAT------ ----------
P876197      3 ---------- --------CT CAAGTATCCC AGAT------ ----------
                   *** ******   ** ********** ****
                                ** ********** ****
                                ** ********** ****

alignment position     201....... 211....... 221....... 231....... 241.......
P876195    201 tgagccaaga tcgcgccatt gcactccagc ccggggaaaca gtgcgAGACT
P876196     89 ---------- ---------- ---------- ---------- -----GGACT
P876197     19 ---------- ---------- ---------- ---------- -----AGCCT
                                                                  *****
                                                                  *****
                                                                  *****

alignment position     251....... 261....... 271....... 281....... 291.......
P876195    251 CCATCTCAaa caaacaaaca aaa------- ---------- ----------
P876196     94 CGACCTCATT AAGTAGCggA GGGTGAGCTT GGTTCTCCTA CTGTCTCCAT
P876197     24 CCACCTCACT AAGTAGCcaA GGATGAGCTT GATTCTCCTA CTGCCTCCAC
               ********** *******   * ********** ********** **********
               ********** *******   * ********** ********** **********
               ********** *******

alignment position     301....... 311....... 321....... 331....... 341.......
P876195    274 ---------- -----ATTCC AGGAAT---- ---------- ----------
P876196    144 ATGCCg---- ---------- -GGCATGCAA CTTCTGTACc gacg------
P876197     74 ATGCCaattt ctgggATTCC AGGCATGCAA CTTACGTACa tatttatgaa
               *****      *****     ********** *********
               *****

alignment position     351....... 361....... 371....... 381....... 391.......
P876195    285 ---------- ---------- ---------- ---------- ----------
P876196    173 ---------- ---------- -TGACGTTCA TCTTTtgatc acttcagtca
P876197    124 taaatgaatg agcgacacct tTGACATTCA TTTTTgtgac cgcctcaatc
                                       ********* *****

alignment position     401....... 411....... 421....... 431....... 441.......
P876195    285 ---------- ---------- ---------- ---------- ----------
P876196    202 ctta a-CAAG TGTCCCAATC AGGTAGGGAC TGACAGGTTC TCTAGattta
P876197    174 gctcgcCAAC TGTCTCGCTC AGAGAGGGAC TGACGGGTCC TCTAG-----
                   **** ********** ********** ********** *****
                   **** ********** ********** ********** *****

alignment position     451....... 461....... 471....... 481....... 491.......
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P876195 285 ---------- ---------- ---------- ---------- ----------
P876196 251 gCACAAAGCT GACCAGACAA GAGTCACAGG TGATTGACAG ACACCACTGC
P876197 219 -CACAAAACT GATCAGACAA GAGTCACAGG TGATTGACAG ACACGACTGC
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alignment
position     501...... 511...... 521...... 531...... 541......

P876195 285 ------AAA- GAGGTTGAAA TCGGGGCAGG GACCCGGATA GGATGGCTCC
P876196 301 AAGTAGAGAa GGGTTAAAAA TCACAGCCAC CAGCAGAATA GGAAAGCCCC
P876197 268 AAGTAGAGA- GGGATTAAAA TCACAGCCTT CAGCAAACTA GGAAAGACCC
            *********  ********** ********** ********** **********
            *********  ********** ********** ********** **********
            *********
            *********

alignment
position     551...... 561...... 571...... 581...... 591......

P876195 328 G-CCCcatct aaGTCTTAGC CCCACCCCct gaaagtcgc- ---------C
P876196 351 G-CCCTCCTG --GCCTCTGC CCCGCCCCTC CACGCTACCC TTCC-CTCTC
P876197 317 gcCCCTCCTG --GCCTTTGC CCCACCCCTC CAGGCTACCT TCCCtCTTTC
            * ********   ******** ********** ********** **** *****
              ********   ******** ********** ********** ****     *
              ********   ******** ********** ********** ****

alignment
position     601...... 611...... 621...... 631...... 641......

P876195 367 CTGCCTCTCA GACTCCtccc ctttctgaga aggtcacggg GGAAGCCAAA
P876196 397 CCGCCCCTCA GACTCCAGAG GTCACCTTAG GAACATA--- GGAAGCCCAG
P876197 365 CCGCTGCTCC GACTCCAGAG GTCACCTTAG GAACATA--- GGAAGCCCAG
            ********** ********** ********** *******    **********
            ********** ******        ******* *******    **********
                                     ******* *******    **********
                                     ******* *******    **********
                                                        **********
                                                        **********

alignment
position     651...... 661...... 671...... 681...... 691......

P876195 417 TGGGCATGCG CCgCTACTGC GCTATTGCGC ACGCTCGCTG TGCTTGCCCc
P876196 444 TGGGCATGCG CC-CTACGGG CCGCTGCTGC ACACACGCAC TTCCTGTACA
P876197 412 TGGGCATGCG CC-CTACTGG CCGCTACGGC ACACTCGCAC TTCCTGTCCG
            ********** ** ******* ********** ********** **********
            ********** ** ****  ** ********** ********** **********
            ********** ** ****
            ********** ** ****
            ********** **
            ********** **

alignment
position     701...... 711...... 721...... 731...... 741......

P876195 467 gccttccctc cgcccACCCG G-GAAACCGG AAGCCGCCTC CCACTTGGTT
P876196 493 TTG------- -----GCTCG gaGAAACCGG AAGCGGCCTT CCACTCGTTG
P876197 461 TTT------- -----ACTCG G-GATACCGG AAGCTGCCTT CCACTCGTTG
            ***             ***** * ******** ********** **********
            ***             ***** * ******** ********** **********
                            *****   ******** ********** **********
                                    ******** ********** **********
                                    ******** ********** **********

alignment
position     751...... 761...... 771...... 781...... 791......

P876195 516 GCTCGTACGC GGctagtgGG TCCTCAGtgg atgta---GG CTGGGCGCCG
P876196 531 GCGCTTAGGC GGCTAGC-GG TCCTCAGGGT GAGAGGCCGG CTTCCCACCG
P876197 498 GCTCTTAGGC TGCTAGC-GG ACCTCAAGGG GAGAGGCCGG CTTCCCACCG
```

```
                 * * * * * * * * * *  * * * * * *  * *  * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *
                 * * * * * * * * * *  * * * * * *  * *  * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *
                 * * * * * * * * * *  * *                                     * * * * *  * * * * * * * * * *
                 * *   *                                                     * * * * *  * * * * * * * * * *
                 * *                                                             * *  * * * * * * * * * *
                                                                                 * *  * * * * * * * * * *

alignment
position         8 0 1 . . . . . . .  8 1 1 . . . . . . .  8 2 1 . . . . . . .  8 3 1 . . . . . . .  8 4 1 . . . . . . .

P876195    563   C G A T G T T C G A  C G G G A C A C C G  G C G G a g a g c g  a c c t c g g g g t  T A A G G G G T G G
P876196    580   C G G T G T T C G A  C G G G A T G C C G  G A G G G g - - - -  - - - - - - - - - -  - A A G G G G T G G
P876197    547   C G G T G T T C G A  C G G G A T G C C G  G A G G G - - - - -  - - - - - - - - - -  T A A G G G G T G G
                 * * * * * * * * * *  * * * * * * * * * *  * * * * *                                 * * * * * * * * * *
                 * * * * * * * * * *  * * * * * * * * * *  * * * * *                                 * * * * * * * * * *
                 * * * * * * * * * *  * * * * * * * * * *  * * * * *                                 * * * * * * * * * *
                 * * * * * * * * * *  * * * * * * * * * *  * * * * *                                 * * * * * * * * * *
                 * * * * * * * * * *  * * * * * * * * * *  * * * *                                     * * * * * * * * *
                 * * * * * * * * * *  * * * * * * * * * *  * * * *                                     * * * * * * * * *
                                                                                                       * * * * * * * * *
                                                                                                       * * * * * * * * *
                                                                                                       * * * * * * * * *
                                                                                                       * * * * * * * * *
                                                                                                       * * * * * * * * *

alignment
position         8 5 1 . . . . . . .  8 6 1 . . . . . . .  8 7 1 . . . . . . .  8 8 1 . . . . . . .  8 9 1 . . . . . . .

P876195    613   G G C T G A C G T C  A G G A G C C A A G  A T G G C G G C G G  T G G T C G C C C T  C T C C T T G A G G
P876196    615   G G C T G A C G T C  A G G A G C C A A A  A T G G C G G C G a  c G G T C G G G G T  C T C C T T G A A G
P876197    582   G G C T G A C G T C  A G G A G C C A A A  A T G G C G G C G G  T G G T C G G G G T  C T C C T T G A A G
                 * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *
                 * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *    * * * * * * * *  * * * * * * * * * *
                 * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *    * * * * * * * *  * * * * * * * * * *
                 * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *    * * * * * * * *  * * * * * * * * * *
                 * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * *
                 * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * *
                 * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * *
                 * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * *
                 * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * *

alignment
position         9 0 1 . . . . . . .  9 1 1 . . . . . . .  9 2 1 . . . . . . .  9 3 1 . . . . . . .  9 4 1 . . . . . . .

P876195    663   C G C C G G T T G C  C G G C C A C a a c  c C T T G G C G G A  G C C T G C C T G C  A G G T G A G T C C
P876196    665   C G C G G C T T C C  C G G C T G C C G T  T C T C G G C A G A  G T C G G C C T G C  A G G T G A G C C C
P876197    632   C G C G G C T T T T  C G G C T A C G G C  T C T C G G C A G A  G T C G G C C T G C  A G G T G A G C C C
                 * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *
                 * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *
                 * * * * * * * *      * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *
                 * * * * * * * *      * * * * * * *        * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *
                                      * * * *              * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *
                                                           * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *

alignment
position         9 5 1 . . . . . . .  9 6 1 . . . . . . .  9 7 1 . . . . . . .  9 8 1 . . . . . . .  9 9 1 . . . . . . .

P876195    713   T G G A G C C t c a  g a g a g g g a a a  a g t c a g g a a a  g c - C A C A G A G  A C T G C C T G G a
P876196    715   G G G A G C C G T G  G T T C A G T G G G  G A G C C G T G C C  c G T C A C C G A G  G C T G C C T G G G
P876197    682   C G G A G C C G T A  G T T C A G T G G G  G A A C C G T G C C  g G T C A C C G A G  G C T G C C T G G G
                 * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *    * * * * * * * *  * * * * * * * * * *
                 * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *    * * * * * * * *  * * * * * * * * * *
                 * * * * * * *                                                     * * * * * * * *  * * * * * * * * * *
                   * * * * * *
                   * * * * * *

alignment
position         1 0 0 1 . . . . . .  1 0 1 1 . . . . . .  1 0 2 1 . . . . . .  1 0 3 1 . . . . . .  1 0 4 1 . . . . . .

P876195    762   g c t g a t G G G G  C T G C G G A G A G  A C T G A G G A A G  C A T A G G G C A A  G G C C T C A G g g
P876196    765   T A G A - - G A G G  C C G C G G A G A G  G C G G A A G G A G  C C C G G G T C C A  G G C C T C G G G G
P876197    732   T G G A - - G A G T  C C G C G G A G A A  G C G G A A A G A G  C C C G G G T C C A  G G C C T C A G G A
```

```
                 * * * *    * * * *  * * * * * * * *  * * * * * * * *  * * * * * * * *  * * * * * * * *  * * * * * * * *
                 * * * *    * * * *  * * * * * * * *  * * * * * * * *  * * * * * * * *  * * * * * * * *  * * * * * * * *
                 * * * *    * * * *  * * * * * * * *    * * * * * * * *  * * * * * * * *  * * * * * * * *  * * * * * * * *
                            * * * *  * * * * * * * *    * * * * * * * *  * * * * * * * *  * * * * * * * *

alignment
position         1 0 5 1 . . . . . .  1 0 6 1 . . . . . .  1 0 7 1 . . . . . .  1 0 8 1 . . . . . .  1 0 9 1 . . . . . .

P876195    812   a g a t g g a g g a  c c t c c t c c c c  c t g g t g c a g t  g c t t t g g t t t  g g c t t c G A G C
P876196    813   G A G G A C T T A a  c c c g g c a t c c  t g c t c t T - - -  - - - - - - - - - - -  - - - - - - G A G C
P876197    780   G A G G A C T T A c  c a g c t c c c t g  c c c c - - T - - -  - - - - - - - - - - -  - - - - - - G A G C
                 * * * * * * * * *                          *                                                      * * * *
                 * * * * * * * * *                          *                                                      * * * *
                 * * * * * * * * *                          *                                                      * * * *

alignment
position         1 1 0 1 . . . . . .  1 1 1 1 . . . . . .  1 1 2 1 . . . . . .  1 1 3 1 . . . . . .  1 1 4 1 . . . . . .

P876195    862   A T C C c t g t c a  a g t t a t c t t t  C T G C G C C T C G  C A G C A G C T T -  - - - G T G A G T T
P876196    844   A T C C T T T C A G  A C A G C C A T T -  C C G C G C T T C T  C C a t c a c c g g  a g a G A G A G G C
P876197    809   A T C C T T T C A G  A T A G C C A A C -  C C G C G C T T C T  C C C A A G C T G -  - - - G A G A G T C
                 * * * * * * * * * *  * * * * * * * * *    * * * * * * * * * *  * * * * * * * * *        * * * * * * *
                 * * * * * * * * * *  * * * * * * * * *    * * * * * * * * * *  * *                    * * * * * * *
                 * * * * * * * * * *  * * * * * * * * *    * * * * * * * * * *  * *

alignment
position         1 1 5 1 . . . . . .  1 1 6 1 . . . . . .  1 1 7 1 . . . . . .  1 1 8 1 . . . . . .  1 1 9 1 . . . . . .

P876195    908   A G G G C A C G G g  c a a t t t t t t a  c a g c t a a g g g  t g c g g g g g g g  g g g g a c G T T C
P876196    893   G C G G C C G G G A  G G A G G T T G G A  A g A G A G A A C A  G A A A G A C A G A  - - - - - - G G T C
P876197    854   G C G G C C G G G A  G G A G G T T G G A  A a A G A T A A C G  G A A A G G C A G A  - - - - - - G G T C
                 * * * * * * * * * *  * * * * * * * * * *  *  * * * * * * * *  * * * * * * * * * *          * * * *
                 * * * * * * * * * *  * * * * * * * * * *  *  * * * * * * * *  * * * * * * * * * *          * * * *

alignment
position         1 2 0 1 . . . . . .  1 2 1 1 . . . . . .  1 2 2 1 . . . . . .  1 2 3 1 . . . . . .  1 2 4 1 . . . . . .

P876195    958   A G A A A G G G - G  A C T T G A A T T G  C T C A A G G T C A  C A T G G C A A G C  G A a t g - - - - -
P876196    937   T G G G A G G A g G  A C A G G G A G A G  G T C A A G G T C A  T A G G A T G A G C  G A C C T G T G G T
P876197    898   A G G G A G G A - C  A A G C G A A T T G  G T C A A G G T C A  T A T G A T G G G C  G A C C T G T T G T
                 * * * * * * * *  *  * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *
                 * * * * * * * *                          *  * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *
                                                          *  * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *

alignment
position         1 2 5 1 . . . . . .  1 2 6 1 . . . . . .  1 2 7 1 . . . . . .  1 2 8 1 . . . . . .  1 2 9 1 . . . . . .

P876195   1002   - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -
P876196    987   C G G G A C C C A G  A A T C A A A T C C  T G C T A G T T G T  A C T C C G C C A G  G C T T G T G T g a
P876197    947   T G G A A C C C A G  A A T C A A A T C C  T G A T A T T T G C  A C T C G A C C A A  C C T T G T G T a a
                 * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *  * * * * * * * *
                 * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *  * * * * * * * *
                 * * * * * * * * *

alignment
position         1 3 0 1 . . . . . .  1 3 1 1 . . . . . .  1 3 2 1 . . . . . .  1 3 3 1 . . . . . .  1 3 4 1 . . . . . .

P876195   1002   - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -
P876196   1037   a a g g g a g g c c  t g c g g g g t g t  c t g g g g t g g g  a c c c g g g a g g  c c a g g t c g c a
P876197    997   a a g g g - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -

alignment
position         1 3 5 1 . . . . . .  1 3 6 1 . . . . . .  1 3 7 1 . . . . . .  1 3 8 1

P876195   1002   - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - -
P876196   1087   c c t c c a g g t t  a g g c t g g t c t  g g a t c g g t c a  g g t
P876197   1002   - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - -
```

Pairwise similarities:

For each pairwise alignment, the similarity (relative to the maximum similarity) and the number of identical nucleic acids (in %

of shorter sequence) is given. Maximum values are underlined.

	P876196 (1119 bp)	P876197 (1001 bp)
P876195 (1001 bp)	0.200 34 %	0.209 38 %
P876196 (1119 bp)		1.000 79 %

Please note that the **similarity value 1.000** marks only the two **most similar** sequences, it does not necessarily mean that these sequences are identical.

Extract alignment region	
Positions in alignment	from: to:
Output file	dialign.seq

Extract aligned sequences

For comments, questions or bug reports, please contact support@genomatix.de

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GEMS Launcher 4.1.1

GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites working on promoters_2.seq (3 seq.)

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1 December 2004 **Wed Jun 8 21:41:39 2005**

Solution parameters:

Sequence file:	promoters_2.seq (3 seq.)
Type of sequences:	nucleotide sequences
Threshold T:	0.00
'*' signs below alignment denote:	diagonal similarity (max. similarity is represented by 10 '*' signs)
Alignment output:	complete alignment is shown # nucleic acids per line: 50
TF output:	common TF matches located in aligned regions (common to 3 (100.0 %) sequences)
Family matches:	yes
MatInspector library:	Matrix Family Library Version 5.0 (February 2005)
Selected groups (core/matrix sim):	• ALL user_defined.lib (0.75/Optimized) • ALL vertebrates.lib (0.75/Optimized)

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P876246	sym=SDHC|loc=Loc6391|taxid=9606|spec=Homo sapiens|chr=1| ctg=NT_004487|str=(+)|start=11774025|end=11775026|len=1002| tss=501,502| comm=succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa; (AK131051/502/gold;NM_003001/501/bronze;)	1002 bp
2	P876247	sym=Sdhc|loc=Loc66052|taxid=10090|spec=Mus musculus|chr=1| ctg=NT_039185|str=(-)|start=15061885|end=15062886|len=1002| tss=501,502| comm=succinate dehydrogenase complex, subunit C, integral membrane protein; (AK032458/501/gold;AK012818/501/gold;NM_025321/502/bronze;)	1002 bp
3	P876248	sym=na|loc=Loc289217|taxid=10116|spec=Rattus norvegicus| chr=13|ctg=NW_047399|str=(-)|start=4499141|end=4500141| len=1001|tss=501| comm=similar to integral membrane protein CII-3; (XM_213936/501/bronze;)	1001 bp

Alignment (DiAlign format):

Please note that only **upper-case** letters are considered to be **aligned**. For more information, please have a look at the user guide.

V$SP1F V$ETSF V$YY1F V$EBOX V$E4FF V$MOKF

```
alignment position 1 . . . . . . . . . 11 . . . . . . . . 21 . . . . . . . . 31 . . . . . . . . 41 . . . . . . . .
P876246            1 t c t c g a g g c c c c t c t a c a c a c t c c c c a a c t t a g g t c a c a a t T T A T G T A T C
P876247            1 - - - - - G C T T G C C - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - T A A c a c g - -
P876248            1 a c a g t G C T T G C C - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - T A A T A T C T C
                               * * * * *   *                                                             * * * * * * * * *
```

```
alignment position 51........ 61........ 71........ 81........ 91........
P876246        51 TGTCTGGTTA AAGCTTCGTa ttagaaagg- -------GAG GGAACCCAAA
P876247        15 ---------- ---------- -GGAGGCACC AAGTTCAGAA GAAGGCCAAA
P876248        22 TATAGGGCTG AAGAATCGTg aGGAGGCCCC GAGTTCAGAG GAAAGCCAAA
                  ********** *********    ********** ********** **********
                                          ********** ********** **********
                                                          *** **********

alignment position 101....... 111....... 121....... 131....... 141.......
P876246        93 GTATC-TTTT CTCTTCGGGG TCTCAACCGG CCAACCACca cg-TTTTTAG
P876247        44 CTAGCaTTTT TCCTTGGGTG TCTCAGCCAG CTAACTAGgg ga-TTTTTAA
P876248        72 GGAGC-TTTT TCCTTGGGTG TCTCAGCCAG CTAACTcagg att TTTTTAG
                  *****  **** ********** ********** ********        *******
                  *****  **** ********** ********** ******          *******
                  *****  **** ********** ********** ******          *******
                         **** ********** ********** ******
                         **** ********** ********
                         **** ********** ********

alignment position 151....... 161....... 171....... 181....... 191.......
P876246       141 GCCGACCTGG GAGGCAGGGG GaacgcaacA GACTGCGAAG TCCTTAAGGA
P876247        93 GACAACTTGG AAGGAGGGGG GTGAAGTG-A GCCTCTGAAA TCCTCAGGGA
P876248       121 GACAACTTGG AAGGAGGGGC tTGAAGTG-A GCCTCTGAAA TCCTCCGGGA
                  ********** ********** *********  ********** **********
                  ********** *********    *******  ********** **********
                  ********** *********    *******  ********** **********
                                          *******  ********** **********

alignment position 201....... 211....... 221....... 231....... 241.......
P876246       191 AGAA----TC taaacaagtc cgccgtttgC TGTTTGGGAG TGCGATACAA
P876247       142 ATAAataaGC CGGAGAAGtg gctgc----C TGGCAGAGCG AGCCCTACAA
P876248       170 ATAA----GC CGGCGAAGcc aactgctatC TGGTAGAGCG AGCCCTACAA
                  ****      ** ********           * ********** **********
                  ****                           * ********** **********
                  ****                           * ********** **********
                  ****                                     *** **********

alignment position 251....... 261....... 271....... 281....... 291.......
P876246       237 AATGAATATG TACGCAGGTg gaacgtagac tgcagatttt gagccagcgg
P876247       188 AATAAACACT CGGGCAGGTA AACGCACTAA CggTAACCAC TCGGCGA---
P876248       216 AATAAACACG CAGGCAGGTA AATGCACTAA C--TAATCAC TCGGCGA---
                  ********** ********** ********** *   ******* ********
                  *********     *******              ******* ********
                  *********                          ******* ********
                  *********                          ******* ********

alignment position 301....... 311....... 321....... 331....... 341.......
P876246       287 cgTTTCTGCC GAAATCCTGG CAAATTCC-- --GGTAGAAg tcggctgcag
P876247       235 --TTTTGGCC AAAACTTTGA CAAACGACgc taGCTAGAAA CTGGCGCGTG
P876248       261 --TTTTTGTC AAAACTTAGA CAAACGAC-- --GCTAGAAA CTGGAGCGAG
                    ******** ********** ********       ******** **********
                    ******** ********** ********       ******** **********
                    ******** ********** ********       ******** **********
                    ******** ********** ********       ******** **********

alignment position 351....... 361....... 371....... 381....... 391.......
P876246       333 gaggcggagg aggagactaa ---------- ---------- ----------
P876247       283 AGAGGAAAAC CGAAGAACTG AAaagcaaag caaaacaaaa aactaaaacc
P876248       305 AGAGGAAAAC CGAAGAGCCG AA-------- ---------- ----------
                  ********** ********** **
                  ********** ********** **
                  ********** ********** **
                  ********** ********** **

alignment position 401....... 411....... 421....... 431....... 441.......
P876246       353 ---------- ---------- -AAAACCAGA AAACAACCAG CAAACCAGCT
P876247       333 AAAAAAAACC AAAAAGAACC CAAAACAAAA AAAGTACCAT CCACCAAGCC
P876248       327 AAACAAAATC AAAGGAACAA GCAAACAAAA AGAGGAACcg tctacaaaca
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alignment position  451....... 461....... 471....... 481....... 491.......
P876246     382     AGGCAgagct gagcggagaa gctccagagc ctttaaaaga gactctcGTC
P876247     383     CGGAAcacaa -------AG GAGGTTCCAG CCTAAAAATT CTGAGGTGTC
P876248     377     gcgaactgaa taaccaagAG GAGGTTCCAG CCTAGAAATT CTAAGGTGTC
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alignment position  501....... 511....... 521....... 531....... 541.......
P876246     432     ACATGACACC CCCaaccccg accccccagcc ggcgCGCCTC CGCCCtcg--
P876247     425     ATATGATAGT CCC------- ---------- ----CGCCTC CGCCCCGCCG
P876248     427     ACATGACAgc gtccccccgc- ---------- ---------- --CCCGGCCC
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alignment position  551....... 561....... 571....... 581....... 591.......
P876246     480     ---------- ---------- --------GG TGGCGGGGCc gcctgGCGTC
P876247     454     GCTCCGCC-C CCAAAGGCAG GGCCACACGG GGGGAGgagc gaT--GCGTC
P876248     454     GCTCCGCCgC CCAAAGGGAG GGTTACGCGG GGGCGGGGCg t-T--GGGTC
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alignment position  601....... 611....... 621....... 631....... 641.......
P876246     502     ACTTCCGTCC AGACCGGAAC CCAAGATGGC TGCGCTGTTG CTGAGGTGAC
P876247     501     ATTTCCGTCC AGGCCGGAAC TCAAGATGGC TGCGtTCTTG CTGAGGTGAC
P876248     501     ACTTCCGTCC AGGCCGGAAC TCAAGATGGC TGCGCTCTTG CTGAGGTGAC
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alignment position  651....... 661....... 671....... 681....... 691.......
P876246     552     TTCAG--TGG GACTGGGAGT TGGTGCCTGC GGCCCTCCGG AGATC-TGAA
P876247     551     TTTAGCCTGG GGCTAGGAGT CCACGCCCGC GACCGTTGGG GGAACCTGAA
P876248     551     TTTAGCCTGG GGCTGGGAGT TCGTTCCcgt tactctt-GG GGAGCCTGAA
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alignment position  701....... 711....... 721....... 731....... 741.......
P876246     599     CTGGCCCCTC Acgttttgct gataactgtt tatcctgTGC CTGGGCAGGG
P876247     601     TTAGTCCCTG AGGGGGTGAC AGCGGtGTGT GCCT---TGC GGGGACAGGG
P876248     600     TTGGTCCCTC AGTGGGTAAC AGTGGgGTGT GCCC---TGC GGGAACAGGG
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alignment position 751....... 761....... 771....... 781....... 791.......
P876246       649 AAAGGACCCA TGGGTGTGGA GGCCaagcgC TCGGGGATCC TAGAGACCCC
P876247       648 AAAGGACCTG CGGGTGTGCA GGCCGCGC-C CCTGGGATCT TAGCACCCCC
P876248       647 AAAGGACCTG TGG-TGTGCA GGCCGGGT-C CCTGGGATCT TAGCACCCTC
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alignment position 801....... 811....... 821....... 831....... 841.......
P876246       699 TTTTC-CCgt cccccccagc cgctccggtg cGCTCCGTAG GGCTTCGGGG
P876247       697 TCTTCtCCCC CGGCGGAGAG ---------- -GCTCGGAAG GGCTTAGAGG
P876248       695 TCTTC-CCCC CGGCAGAGAG ---------- -CCTCGGAAA GGCTTAGAGG
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alignment position 851....... 861....... 871....... 881....... 891.......
P876246       748 TCACTgactt cgtatcgagg ggccCTCGGC TCTCGCCCCT TCTGTTTTCC
P876247       736 TCACACTgtg tgtgGCCGAG TGG-CGCGGC TGTCATTGTT TCTGCCTCGC
P876248       733 TCACTCTgtg ta--GCCGAG TGG-CGCGGC TGTCATTGTT TCTGTCTCGC
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alignment position 901....... 911....... 921....... 931....... 941.......
P876246       798 CCACCTCctc tagtacttct aaCGCAAATT GCTCTCGGGC CTGCACCCAG
P876247       785 CCACCTCTAA AGCCTCTT-- --CGAAAACT GCTCTTGTGG CCCCAaaaag
P876248       780 CCACGTCTAA AGCCTCTT-- --CGCAAACT GCTCTTGTGG CCCCACCCAG
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alignment position 951....... 961....... 971....... 981....... 991.......
P876246       848 AGCCGAGCtc tgagaaaaTA ACTTCAAGGT CAGCCACCCA TGGGTCCTAC
P876247       831 ctgctg---- --------TA ACTTCGAGAT CAGCGGGCCC CTAGGCCTGC
P876248       826 GTCCGAGCct caat------ ---------- ---------C CTAGGCCTAC
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                  ********                                 * **********

alignment position 1001...... 1011...... 1021...... 1031...... 1041......
P876246       898 GATTTCGAGA GCGtatttag acatttagct tc-GGAGAGA GAGATCTTCG
P876247       869 AGTTTTGGGG Ggac------ TTAGGGATTG TAGAGGGAGG GGCTCCTTGG
P876248       851 AATTTTGGGG GAGggggat TTAGCGATTG TAGGGGGAGG GGCTCCTTGG
                  ********** ***       ********** ********** **********
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alignment position 1051...... 1061...... 1071...... 1081...... 1091......
P876246       947 TGTATTTTGC CTTTGCTTCG AAtgcctcag acactagct gctcccaccg
P876247       913 AGCACCTAct gggtgc-TTT AACTCCTGGC Aa---TCCTG CTAGCAACCG
P876248       901 AGCACCTAGT CTGTGCTTTT AACTCCTGGC AgctcTACGG CTGGCAGCCT
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alignment position 1101...... 1111...... 1121...... 1131...... 1141......
P876246       997 tgagtg---- ---------- ---------- ---------- ----------
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P876247      959 GTGG AAA CTG  TC g GGC AT CC  TAAT GCA T C C  C T C C C A A G C C  AAG G- - - - - -
P876248      951 GTGG AGA CTG  TC a GGC T T CC  TAAT GCA T C C  C T C C C A T G C C  AAG Gt c a a g a
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alignment  position  1 1 5 1
P876246      1003 -
P876247      1003 -
P876248      1001 a
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Pairwise similarities:

For each pairwise alignment, the similarity (relative to the maximum similarity) and the number of identical nucleic acids (in % of shorter sequence) is given. Maximum values are underlined.

	P876247 (1002 bp)	P876248 (1001 bp)
P876246 (1002 bp)	0.164 35 %	0.186 41 %
P876247 (1002 bp)		1.000 73 %

Please note that the **similarity value 1.000** marks only the two **most similar** sequences, it does not necessarily mean that these sequences are identical.

Extract alignment region	
Positions in alignment	from: to:
Output file	dialign.seq

Extract aligned sequences

For comments, questions or bug reports, please contact support@genomatix.de

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License Agreement

GEMS Launcher 4.1.1

GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites working on promoters_2.seq (3 seq.)

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1 December 2004 **Wed Jun 8 21:46:18 2005**

Solution parameters:

Sequence file:	promoters_2.seq (3 seq.)
Type of sequences:	nucleotide sequences
Threshold T:	0.00
'*' signs below alignment denote:	diagonal similarity (max. similarity is represented by 10 '*' signs)
Alignment output:	complete alignment is shown # nucleic acids per line: 50
TF output:	common TF matches located in aligned regions (common to 3 (100.0 %) sequences)
Family matches:	yes
MatInspector library:	Matrix Family Library Version 5.0 (February 2005)
Selected groups (core/matrix sim):	• ALL user_defined.lib (0.75/Optimized) • ALL vertebrates.lib (0.75/Optimized)

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P876742	sym=SDHD|loc=Loc6392|taxid=9606|spec=Homo sapiens|chr=11| ctg=NT_033899|str=(+)|start=15519538|end=15520538|len=1001| tss=501| comm=succinate dehydrogenase complex, subunit D, integral membrane protein; (AK075360/520/gold;NM_003002/520/bronze;)	1001 bp
2	P876743	sym=Sdhd|loc=Loc66925|taxid=10090|spec=Mus musculus|chr=9| ctg=NT_039473|str=(-)|start=10108845|end=10109850|len=1006| tss=501,506| comm=succinate dehydrogenase complex, subunit D, integral membrane protein; (AK013503/507/gold;AK013962/502/gold;NM_025848/502/bronze;)	1006 bp
3	P876744	sym=Sdhd|loc=Loc363061|taxid=10116|spec=Rattus norvegicus| chr=8|ctg=NW_047799|str=(-)|start=23593559|end=23594559| len=1001|tss=501| comm=succinate dehydrogenase complex, subunit D, integral membrane protein; (XM_343388/519/bronze;)	1001 bp

Alignment (DiAlign format):

Please note that only **upper-case** letters are considered to be **aligned**. For more information, please have a look at the user guide.

V$AREB V$EBOX V$ETSF U$NRF2 V$RORA V$EREF V$HNF4 U$EREF V$SF1F V$YY1F V$FKHD

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alignment position 1 . . . . . . . . . 11 . . . . . . . . . 21 . . . . . . . . . 31 . . . . . . . . . 41 . . . . . . . . .
P876742        1 g c - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P876743        1 c c t g t G C T C C A A G G T C G G A A C C C A G A G A T T C C G A G T G C C A T T c c c g A C C A
P876744        1 - - - - - G C T C C A A G G T C A G A A C C C A G A G A T C C C G A T T G C T A T T t c g a A C C A
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alignment position 51........ 61........ 71........ 81........ 91........
P876742         3 ---------- ---------- ---------G TCGCCCAAAT CTTCCCTGTT
P876743        51 GCGACCAGCT AAT--AACCG CATGCTCCTG TGGCCCAAAC CTTTCCGCTG
P876744        46 GCGACCGGCT AATat AACCG CATGCTTCTG TTGCCCAAAT CTTTCTGCTG
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alignment position 101....... 111....... 121....... 131....... 141.......
P876742        24 TTacacctttt tctttttctCC ACGCTACGCT TATATACCTG GCACcTGAGC
P876743        99 TTTTCgAACC CTTTCCTCCC ACGCAGCGCT TGCCTCCCGG GCAC-TGAGC
P876744        96 CTTTCcAACC CTTTGATCCC ACACAGCGCT TGCCTCACGG GCggtcgcta
                  * * * * *  * * * *  * * * * * * * * * *  * * * * * * * * * *  * * * * * * * * * *  * * * *  * * * * *
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alignment position 151....... 161....... 171....... 181....... 191.......
P876742        74 ACTACCGGTC ACCAGGGaca ggagagccat aactttgtct ttcgtgaggg
P876743       148 ACTGTAGATC ACTGGGGCGG GAGGC----- ---------- ----------
P876744       146 ---------- ----GGGTGG GAGGC----- ---------- ----------
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alignment position 201....... 211....... 221....... 231....... 241.......
P876742       124 gaatgggatG CAGCCGGGAT CGAGcaccag tgagc--CGC CAGTGTACAG
P876743       173 ---------G CAGCCCGGAT CGAGTGGGGC CGCTGTGCc G CAGTGTCCAG
P876744       157 ---------G CAGCCGGGAT CGGGTGGGCC CGCTCTGCTG CAGTGTCCAG
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alignment position 251....... 261....... 271....... 281....... 291.......
P876742       172 ACCTCCGAGC GTGCCCAGGA CCaccaagga aggtgaaact TCCTTTCCCT
P876743       214 AGCTCCGTGA GTGCCCGGGA TCTGCGcCTC ACCC------ TCCTTCCCCT
P876744       198 GGCTCTGTGA GTGCCCGGGA TCTGCGtCTC ACCC------ TCCTTTCCCT
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alignment position 301....... 311....... 321....... 331....... 341.......
P876742       222 TCACCCTCCC CGTCCCCGCA CCTGTGCAGT AAACTGCGCC TTCTGCTGCT
P876743       258 GTTCCTTCCT CATCCTCGTA CCTGCGCAGT GAATTGCGCC TTCTGCTGTT
P876744       242 GTTCt----T CATCCTCGTA CCTGCGCAGT GAACTGTGCC TTCTGCTGTT
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alignment position 351....... 361....... 371....... 381....... 391.......
P876742       272 CGGCGGCCAC CAGGCGCTGC AACTCCGCTT CATCGGCTTC GCCCAGCTCC
P876743       308 CGGCGGCCAC CAGGCGTTGT AACTCCGCTT CGTCCGCTTC ACCAAGCTCG
P876744       288 CGGCGGCCAC CAGGCGTTGT AACTCCGCTT CGTCCGCTTC ACCAAGCTCG
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alignment position 401....... 411....... 421....... 431....... 441.......
P876742      322 GCCATTGTTC GCCTCAGGCT CGCCACcttc cgacagctgt gtttgcgcat
P876743      358 GCCATTGTCG GAGTCAggcg cttcgCTGGG GTGCGCAC-- ----------
P876744      338 GCCATGGTCA GCGTCAATCT GTTCACTGGA GTACGCAC-- ----------
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alignment position 451....... 461....... 471....... 481....... 491.......
P876742      372 GCGCGACGGG TGTGCACCGC CTCTCGACTT CCGGTTCACc cagcatttcc
P876743      396 GCGCGGTGGC AGCGCACCGT CTCCTGCCTT CCGGTTCACG CTTCAGGTTG
P876744      376 GCGCGGTGGC AGAGCACCAC CTCCTGCCTT CCGGTTCACT CTTGAGGTTG
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alignment position 501....... 511....... 521....... 531....... 541.......
P876742      422 tcttccctgt tttcttttcgt cgTCGTGGGT GGGAATTGTC GCCTAAGTGG
P876743      446 CCTCACCGTT CTTTTACgc- ----- GGGGC GGGACTTACT ACATAACTGT
P876744      426 CTTCGCCGTT CTTTTAC--- --TCGGGGGC GGGACTTACG ACATAACTGC
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alignment position 551....... 561....... 571....... 581....... 591.......
P876742      472 TTCCGGGTTG Gt GGATGACC TTGAGCCCTC AGGAACGAGA TGGCGGTTCT
P876743      490 TTCCGGGTTG TAGAGTGACC TTGAGCCCTC GAAAGCGACA TGGCGGTTCT
P876744      471 TTCCGGGccG TAGGGTGACC TTGAGCCCTC AAAAGCGAAA TGGCGGTTCT
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alignment position 601....... 611....... 621....... 631....... 641.......
P876742      522 CTggaggctg agtgccgttT GCGGTGCCCT AGGAGGCCGA GGTGAGGGGT
P876743      540 CTTAAAGCTG GGCGTTCTCT GCAGTGGCCA AGGAGCTCGA GGTGAGGTGT
P876744      521 CTTAAAGCTG GGCGTTCTCT GCAGTGGCCA AGGAGCTCGA GGTGAGGTGT
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alignment position 651....... 661....... 671....... 681....... 691.......
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P876742     572 CTTcccacccc tgAGGTGCTT AGCGTAGCCT CCAGCCAGGG AAGGGGATGg
P876743     590 CTTGGCCATC AAAGGTTCTT GCTGCAGGCT GAAGCAGGGG AGAGGAAGG-
P876744     571 CTTGGCCATC AAAGGTTCTT GCTGCAGCCT GGAGCAGGGG AAAGGAAGG-
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alignment position 701....... 711....... 721....... 731....... 741.......
P876742     622 aAGTGAGGAC TCATCTGCCG GGTGG-GAGA TCTCTTGAGG AGAAGAAAAT
P876743     639 -AGTTAGAGC TCGCCCGCTG GGTGGTGGGA CGTCTTGAGA GGAGGGAACT
P876744     620 -AGTGAGGGC TCGACTGCCG GGTaGTGGGA CGTCTTGAGA GGAAGAAACT
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                                                **** ********** **********
alignment position 751....... 761....... 771....... 781....... 791.......
P876742     671 ACCgaaat-- ---------- ---------- ----CACAGC AATGACCACT
P876743     688 TGCTCTTGTG CCCTcgaggc acCACCTATG CGGACGCAAC GTTGACCGCT
P876744     669 TCCTCTGGTG CCCTcggggg --CACCTCTG CGGACGCAGC GGTGACCGCG
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alignment position 801....... 811....... 821....... 831....... 841.......
P876742     695 GTAGTCTAGG GGTCCAGATG TTTACccgaa ggtatatttca----------
P876743     738 ATAGCCTAAA GGCCCAAGTG TTTACgtgCT GGCTGGTGTC CCCAGCTCGT
P876744     716 GTAGCCCAG- GGCCCAAGTG TTTACaacCT GGCTGGTCTC CCCTGCTCGT
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alignment position 851....... 861....... 871....... 881....... 891.......
P876742     736 ---------- ---------- ---------- ---------- ----------
P876743     788 ACTTTCCGCT TCTGCACTGT GGTTGTGACC CCGGGCTAAT ATGAAACAA
P876744     765 ACTTTTCGCT TCTGGACTGT GGTTGTGACA CCGGGCTAAT GTGAAACAA
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alignment position 901....... 911....... 921....... 931....... 941.......
P876742     736 ---------- ---------- ---------- ---------- ----------
P876743     838 ACTCCTATtt gaGTGTGGAT GGAAGGAGTC CGTTTGATAa tTTGTTCTGA
P876744     815 ACTCCTATcc gtGTGTGGAT GGAAGGAATC TGTTTGATAg -TTGTTTTTA
                ********      ********* ********** ********** *********
                ********      ********* ********** *********
                ********
                ********
alignment position 951....... 961....... 971....... 981....... 991.......
P876742     736 ----CTTGCT G--TGagctg acgagttgag ggaataatca gaaagagagc
P876743     888 GTGGCTTGCT G--TGT---- ---------- ---------- ----------
P876744     864 GTGGCTTGCT ataTGT---- ---------- ---------- ----------
                ********** *   ***
alignment position 1001...... 1011...... 1021...... 1031...... 1041......
P876742     780 tccctctgga agtcgcagtc ctgatgaggc taatccacat agcAGTTCTG
P876743     902 ---------- ---------- ---------- ---------- ---AGTGCTG
P876744     880 ---------- ---------- ---------- ---------- ---AGTTCTG
                                                             *******
alignment position 1051...... 1061...... 1071...... 1081...... 1091......
```

```
P876742      830 TT-TTCt ccc cgttcactgt cccta gaatg ctcccactc gct cccaccc
P876743      909 TC-TTCCTCG ATCTAGCCAT GTAGACAAGA CTAACCTA- - - - - - - - - -
P876744      887 gctTTCCTCG ATCTAGCCAT GTAGACAAGA CTAACCTA- - - - - - - - - -
                 **  ******* ********** ********** ********* *********
                     ******* ********** ********** ********* *********
                     ******* ********** ********** ********* *********
                     ******* ********** ********** ********* *********
                     ******* ********** ********** ********* *********

alignment position 1101..... 1111..... 1121..... 1131..... 1141.....
P876742      879 tgagt cggga aagagggtta gGAGCTTGCC CATTTCTTCT GGAGTTGGTg
P876743      946 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P876744      925 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
                                         ********** ********** ********** ****
                                         *****                              **
                                         *****
                                         *****
                                         *****

alignment position 1151..... 1161..... 1171..... 1181..... 1191.....
P876742      929 tgttt ggatg tgggagtgga gggggggatca gttcgaaaat catttaacct
P876743      974 CCGAGGGCTG CCATAAAAAC CGTGCACCCT CAC- - - - - - - - - - - - - - -
P876744      954 CCGAGTGCTG GCATAACAAC CATGCACCAT CACtcagggc ttcgataa- -
                 ********** ********** ********** ***
                 ********** ********** ********** ***

alignment position 1201..... 1211..... 1221
P876742      979 gggcattt tgt gttacctcag gta
P876743     1007 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P876744     1002 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
```

Pairwise similarities:

For each pairwise alignment, the similarity (relative to the maximum similarity) and the number of identical nucleic acids (in % of shorter sequence) is given. Maximum values are underlined.

	P876743 (1006 bp)	P876744 (1001 bp)
P876742 (1001 bp)	0.215 39 %	0.213 39 %
P876743 (1006 bp)		**1.000** **83 %**

Please note that the **similarity value 1.000** marks only the two **most similar** sequences, it does not necessarily mean that these sequences are identical.

Extract alignment region	
Positions in alignment	from: to:
Output file	dialign.seq

Extract aligned sequences

For comments, questions or bug reports, please contact support@genomatix.de

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GEMS Launcher 4.1.1