File 2: Experimentally known binding sites and weight matrix construction for the gap genes

File 2: For each transcription factor (bicoid, caudal, dorsal, hunchback, knirps, Kruppel, tailless, torRE) the following data are shown:

(1) the frequency matrix obtained by running WCONSENSUS
(2) the alignment of the binding sites from the same WCONSENSUS run
(3) the experimental binding site data. The heading for each site contains the annotated transcript ID (CT number), gene ID (CG number), and gene name. The last number correponds to the distance of the site to 10000 bases upstream of translation start of that gene.

BICOID

```
A |   2   5   3  27  30   0   1   3   4   2   6
C |  10  12   0   0   0   0  29  13  15   9  14
G |  10   4   0   3   0   7   0   3  11  13   6
T |   8   9  27   0   0  23   0  11   0   6   4
```

```
TCTGAGCTCCG
CCTAATCTGGC
TCTAATCTCGC
CTTAAGCTCGC
CGTAATCTGCT
TTTAATCCGTT
AATAATCCAGC
CTTAATCACCA
TTAAATCCCTC
GTTAATCTCCG
CTAAATCCGGC
GTTAATCCGTT
AATAATCTCGC
TATAATCGCAC
GCTAATCCCAG
CGTAATCCCCA
TCTAATCCAGA
TCTAATCCCTT
GCTAAGCTGGC
GCTAAGCTCCC
GATGATCCGGG
CCTAAGCCAGC
CGAAATCGCTG
CCTAATCGCGG
GCTGATCCCGC
CCTAAGCTGCA
GATAATCTGCA
GTTAATCAATA
TGTAATCAGGC
GTTAAGACGCC
```

```
>CT3134:tll:CG1378 8926
AAAATAAAAAACAAATATTTGCATTTC
>CT3134:tll:CG1378 8921
GCTAAGAAATGCAAATATTTGTTTTTT
>CT3134:tll:CG1378 8844
ATTAAAAACGCAATCTGAGCTCCGCA
>CT3134:tll:CG1378 8829
```

```
TGCGTTTTTAATAATAATTTTTATAAA
>CT3134:tll:CG1378 8799
TTACTTTAAAATAATTTTATTTATTAA
>CT3134:tll:CG1378 8696
AAGGCAACGCCTAATCTGGCTCAGCCG
>CT3134:tll:CG1378 8671
CCACTTGAATCCTAAAGGCTCTCAAAA
>CT3134:tll:CG1378 8644
ACAGTGCCTCTAATCTCGCTTGGTCCT
>CT3134:tll:CG1378 8596
CGATTCCTCGACTTAAGCTCGCCGCTT
>CT3134:tll:CG1378 8574
ATCTAAAATCCGTAATCTGCTTAAGCG
>CT11169:Kr:CG3340 5900
AAAATTTAATCCGTTTCTGAAGGTAGGC
>CT11169:Kr:CG3340 5930
CAGACAAATAATCCAGCCTTAAGCATGGTGAT
>CT11169:Kr:CG3340 5951
TCAAGCTTAATCACCATGCT
>CT11169:Kr:CG3340 6001
TTTTCCTTAAATCCCTCTGTT
>CT11169:Kr:CG3340 6013
CCCTCTGTTAATCTCCGGCTT
>CT11169:Kr:CG3340 6337
TAACTGAACTAAATCCGGCTTAG
>CT7758:eve:CG2328 5113
CCGTGTTAATCCGTTTGCC
>CT7758:eve:CG2328 5132
TTGACTAATAATCTCGCTGAT
>CT7758:eve:CG2328 5283
CTGGACTATAATCGCACAACGA
>CT7758:eve:CG2328 5377
CCCTTGGCTAATCCCAGCAA
>CT27633:hb:CG9786 9273
GACCAACGTAATCCCCATAGAAAACCG
>CT27633:hb:CG9786 9382
TTTCTGCTCTAATCCAGAATGGATC
>CT27633:hb:CG9786 9488
TGCCCATCTAATCCCTTGACGCGTG
>CT27633:hb:CG9786 9314
GCTCGCTGCTAAGCTGGCCAT
>CT27633:hb:CG9786 9330
GCCATCCGCTAAGCTCCCGGA
>CT27633:hb:CG9786 9343
TGGATTTGGATGATCCGGGAG
>CT15191:kni:CG4717 6930
GGGTACCTAAGCCAGCGAT
>CT15191:kni:CG4717 6940
AGGTAACGAAATCGCTGGC
>CT15191:kni:CG4717 6951
CGTTACCTAATCGCGGGA
>CT15191:kni:CG4717 6961
GGTAAGCTGATCCCGCGA
>CT15191:kni:CG4717 6972
GCTTACCTAAGCTGCAGA
>CT15191:kni:CG4717 6983
CCTAGGATAATCTGCAG
>CT15191:kni:CG4717 8186
TAGAAGTTAATCAATAAGAG
>CT15191:kni:CG4717 8624
TTCCCTGTAATCAGGCTATT
```

```
>CT3134:tll:CG1378 7154
AATGAAAGGGTTAAATAGCTG
>CT3134:tll:CG1378 7205
GAGAAAAGGGTTAAGACGCCAC
```

HUNCHBACK

```
A |  17   0   0   0   0   1  11   7   3  11   5   8
C |  12   0   1   1   0   0   3   8   6  11   9  18
G |  14   4   0   0   0   0   5   8  25   7  10   4
T |   0  39  42  42  43  42  24  20   9  14  19  13
```

```
AGTTTTTTGTTT
ATTTTTGTGCCC
CTCTTTACGGTT
CTTCTTTGTTCC
ATTTTTATGGGT
CGTTTTTTGTTC
CTTTTTTCGCTG
GTTTTTTTCCCC
ATTTTTTAATTC
GTTTTTAAGATC
GTTTTTACGAGC
CTTTTTATGATC
ATTTTTTTGCTT
CTTTTTCTTTTC
ATTTTTTCAGAC
GTTTTTTCGCGA
GTTTTTTTTTTC
GTTTTTAAGAGA
ATTTTTTGTTGT
GTTTTTACTTTG
ATTTTTTGCATT
GTTTTTATGACT
ATTTTTTTGCGC
ATTTTTTTGGCC
ATTTTTTGTTTC
CGTTTTGCGTTT
GTTTTTTGGCAT
GTTTTTTGGGCA
CTTTTTAAGCTA
ATTTTTTTCCCA
GTTTTTTTTTTT
GTTTTTGTTAAG
CTTTTTCACTCC
CTTTTTGGCTTT
CTTTTTATGAAT
ATTTTATTGAGT
ATTTTTGTATGC
ATTTTTTATAAC
GTTTTTTTGCTA
CTTTTTCCGCGG
GGTTTTTGGGTA
ATTTTTTTGGCA
ATTTTTAACAGC
```

```
>CT7758:eve:CG2328 2812
GATCAGTTTTTTGTTTTGGCCG
```

```
>CT7758:eve:CG2328 2832
CGACCGATTTTTGTGCCCGGTG
>CT7758:eve:CG2328 2848
CCGGTGCTCTCTTTACGGTTTATG
>CT7758:eve:CG2328 2887
CCCAGCTTCTTTGTTCCGGGCT
>CT7758:eve:CG2328 2936
TGCAGATTTTTATGGGTCCCG
>CT7758:eve:CG2328 3038
ATCACGTTTTTTGTTCCCATTG
>CT7758:eve:CG2328 3059
GTGCGCTTTTTTCGCTGCGCT
>CT7758:eve:CG2328 3076
CGCTAGTTTTTTTCCCCGAACC
>CT7758:eve:CG2328 3108
CTCTAATTTTTTAATTCTTCACG
>CT7758:eve:CG2328 3212
CTCTCGTTTTTAAGATCCGTT
>CT7758:eve:CG2328 3260
ATTCACGTTTTTACGAGCTCGT
>CT11169:Kr:CG3340 5802
CAAATTGCTTTTTATGATCATGCAT
>CT11169:Kr:CG3340 5830
CAATTTATATTTTTTTGCTTTTCCT
>CT11169:Kr:CG3340 5875
TTACACTTTTTCTTTTCTGATCCA
>CT11169:Kr:CG3340 5917
GATTAAATTTTTTCAGACAAATA
>CT11169:Kr:CG3340 6038
CGCGACGCGTTTTTTCGCGACTCC
>CT11169:Kr:CG3340 6063
CCTGCATTGTTTTTTTTTTCAGTTTCTT
>CT11169:Kr:CG3340 6281
TTTGTTGTTTTTAAGAGAAAT
>CT11169:Kr:CG3340 6291
CTTTGACATTTTTTGTTGTTTT
>CT11169:Kr:CG3340 6305
TTGCATTGTTTTTACTTTGACA
>CT11169:Kr:CG3340 6315
TACACATATTTTTTGCATTGTTTT
>CT7758:eve:CG2328 5469
ATTATGTGTTTTTATGACTTTC
>CT7758:eve:CG2328 5551
ACTGGGTTATTTTTTTGCGCCG
>CT7758:eve:CG2328 5634
ACCCCACGATTTTTTTGGCCAA
>CT27633:hb:CG9786 9365
GTGCGCATAATTTTTTGTTTCTGCTCTA
>CT27633:hb:CG9786 8881
CCCTTTTTCCCGTTTTGCGTTTTTAATA
>CT27633:hb:CG9786 5895
CTCTTTGCCGTTTTTTGGCATCTCCGCT
>CT27633:hb:CG9786 5801
TCGCCAATTGTTTTTTGGGCAACTTTAA
>CT27633:hb:CG9786 5590
CTGTATTCCACCTTTTTAAGCTAATTTCG
>CT27633:hb:CG9786 5489
TTTAGACCAATTTTTTTCCCAAGCGGAA
>CT27633:hb:CG9786 5405
TAATAGTTTTTTTTTTTAGTCCAAAATT
>CT15191:kni:CG4717 7488
```

```
TAACGAGTTTTTGTTAAGAGTA
>CT15191:kni:CG4717 7568
CTTGACTTTTTCACTCCGAAGT
>CT15191:kni:CG4717 7692
GTTCTTTCTTTTTGGCTTTGAGC
>CT15191:kni:CG4717 7724
TTAACTCTTTTTATGAATATTT
>CT15191:kni:CG4717 7833
ATTTGTATTTTATTGAGTATAA
>CT15191:kni:CG4717 8012
AAACCTATTTTTGTATGCTATT
>CT15191:kni:CG4717 8102
ATAGTATTTTTTATAACTTTTC
>CT15191:kni:CG4717 8153
ACTATCGTTTTTTTGCTATGAA
>CT15191:kni:CG4717 8309
CAAAACCTTTTTCCGCGGGAAA
>CT15191:kni:CG4717 8367
CCGCCGGTTTTTGGGTACATTT
>CT15191:kni:CG4717 8458
TGCTCATTTTTTTGGCATGGGC
>CT15191:kni:CG4717 8476
GACTTCATTTTTAACAGCTGCT
```

```
            KNIRPS

A |   5  11  11   9  18  18  11   4   2  14  17  13  10   7  19
C |   0   1   3   0   5   2  14  13   3   0   0  12   0  11   1
G |   7   8  12  13   4   0   1   7   8   9  10   1  10   5   5
T |  15   7   1   5   0   7   1   3  14   4   0   1   7   4   2
```

```
TAGAAAACTAGATCA
AGAGCACCGGGCACA
TGGGAAATGGGAACG
TAGGAAAGTAGATCA
AAAAAAACTAGCGCA
GTGTAACTGAACTAA
GAGGATCGTAAAAAA
GGAGGTCGTAAAACC
TAAAAAACGGACGGA
GAGGATGGCAGAGCA
TTTGAACTGAACGGG
TTGACACCGAACTGA
TCATAAAGTAGATCT
TTCGACCCGGGATCG
TAAAAAACGGACGGA
TGAGAACCCGAAAGA
TGGAACAATAAAGTT
AAAAATCGCTACACA
TGCACTTCTAAAAAA
GTAGGAACTTAAGCG
GAGAAACCTAATAAA
TAGGCAAAAGGCTTA
AGATGTCCTTAGGAA
TGGGAACAAGACAAA
ATATCACGTGGCGTG
TTGTGAACTTACAAA
GACGATCATAAAGTA
```

```
>CT7758:eve:CG2328 2797
TGCATTAGAAAACTAGATCAGTTTTT
>CT7758:eve:CG2328 2841
AACCGTAAAGAGAGCACCGGGCACAAA
>CT7758:eve:CG2328 2864
TGGGAAATGGGAACGCGGCCATAAACC
>CT7758:eve:CG2328 3022
CGTATTAGGAAAGTAGATCACGTTT
>CT7758:eve:CG2328 3067
GAAAAAAACTAGCGCAGCGAAAA
>CT11169:Kr:CG3340 6333
TGTGTAACTGAACTAAATCCGGCTTAGG
>CG6494:h:CT20229 2620
GTTGAGGATCGTAAAAAACTGC
>CG6494:h:CT20229 2639
GACGGAGGTCGTAAAACCCGTT
>CG6494:h:CT20229 2652
GGCTTAAAAAACGGACGGAGGT
>CG6494:h:CT20229 2673
CAGAGGATGGCAGAGCAGAAAG
>CG6494:h:CT20229 2693
CTGATTTGAACTGAACGGGTCA
>CG6494:h:CT20229 2708
AGAGTTGACACCGAACTGATTT
>CG6494:h:CT20229 3137
GATCATAAAGTAGATCTTAACC
>CG6494:h:CT20229 2606
TTCGACCCGGGATCGCAGTTTTTT
>CG6494:h:CT20229 2648
CTTAAAAAACGGACGGAGGTCGTA
>CG6494:h:CT20229 2725
CCCGCTATGAGAACCCGAAAGAGT
>CG6494:h:CT20229 2755
AATCCGGCTGGAACAATAAAGTTT
>CG6494:h:CT20229 2791
TAAAAAATCGCTACACACTTCCCG
>CG6494:h:CT20229 2836
AATAAAGATTGCACTTCTAAAAAA
>CG6494:h:CT20229 2864
CAAATTGTAGGAACTTAAGCGGAA
>CG6494:h:CT20229 2886
AAATTCCGAGAAACCTAATAAATT
>CG6494:h:CT20229 2915
TTTTTTGATTAGGCAAAAGGCTTA
>CG6494:h:CT20229 2980
TAAAGAAGATGTCCTTAGGAAACT
>CG6494:h:CT20229 3041
TTTTTTATGGGAACAAGACAAAAA
>CG6494:h:CT20229 3077
AGATATCACGTGGCGTGGTATCAG
>CG6494:h:CT20229 3113
GACATGTTGTGAACTTACAAAGAC
>CG6494:h:CT20229 3127
TTACAAAGACGATCATAAAGTAGA
```

```
         KRUPPEL

A |  10  19  17  12   0   4   3   0   0
C |   3   1   2   6   0   0   2   0   2
G |   7   0   0   1  20  16  15   2   0
```

```
T |   0   0   1   1   0   0   0  18  18

AAACGGATT
GACCGGGTT
GAAGGGATT
AACTGGGTT
AAACGGGTT
CAAAGAGTT
CCACGGATT
GATAGAGTT
GAAAGAGGT
CAACGGGTT
GAAAGGCTT
GAACGGGTC
GAAAGAGTT
AAAAGGCTT
AAAAGGGTT
AAAAGGGGC
AAAAGGGTT
AAAAGGGTT
AAAAGGGTT
AAAAGGGTT

>CT7758:eve:CG2328 4976
GCGCAATATAACCCAATAATTT
>CT7758:eve:CG2328 5112
ATGGCAAACGGATTAACACGGC
>CT7758:eve:CG2328 5300
AACGAGACCGGGTTGCGAAGTC
>CT7758:eve:CG2328 5494
GATGTCGAAGGGATTAGGGGCGC
>CT7758:eve:CG2328 5545
TAGCGAACTGGGTTATTTTTTT
>CT7758:eve:CG2328 5588
GGCTCAAAACGGGTTAAGCTCGC
>CG6494:h:CT20229 5901
CTGCCTGATTCGCAAAGAGTTT
>CG6494:h:CT20229 6013
GAGTTTCCACGGATTAGACCTC
>CG6494:h:CT20229 6035
GTTCTCTCTGGGATAGAGTTTA
>CG6494:h:CT20229 6054
TAGTCTCGCGCCGAAAGAGGTT
>CG6494:h:CT20229 2633
ATCCTCAACGGGTTTTACGACC
>CG6494:h:CT20229 2661
GAGCAGAAAGGCTTAAAAAACG
>CG6494:h:CT20229 2686
GAACTGAACGGGTCAGAGGATG
>CG6494:h:CT20229 2724
GCTATGAGAACCCGAAAGAGTT
>CG6494:h:CT20229 2924
TAGGCAAAAGGCTTAAAAAACA
>CG6494:h:CT20229 2950
GCAACCTTGGTGTTAATTGAGA
>CG6494:h:CT20229 3057
GACAAAAAAGGGTTTTGCGGAG
>CT27633:hb:CG9786 9185
ATTTAGTTAAGTCCCGCAATCCTT
>CT27633:hb:CG9786 8868
GGGAAAAAGGGGCATTTACGGAAT
```

```
>CT15191:kni:CG4717 7663
CGGCATAAAAGGGTTAAACAGGTAGCTC
>CT15191:kni:CG4717 7633
GCCCATAAAAGGGTTAAGCACATC
>CT15191:kni:CG4717 7604
GTACCAAAAGGGTTGTTCAGAC
>CT15191:kni:CG4717 7800
CTTTTAAAAGGGTTACAATTAA
```

TAILLESS

```
A |  12   1   1   5   2  11   1   0   0
C |   8   2   2   1   3   1  17   2   3
G |   0   2   1   0  15   5   0   1   2
T |   0  15  16  14   0   3   2  17  15
```

```
CTTTAACTT
ATTAAATTT
ATTTGTCTG
ATTACGCCC
CTCCGGCTT
ATTTGACTT
CTTAGGATT
AGTTGCCTT
ATTAGACTC
CTTTCACCC
CATTGTCTT
CTTTGGCGG
ATTAGTTTT
ATATGGCTT
ATGTCACTT
ATTTGACTT
AGCTGACTT
CCTTGACTT
ATTTGACTT
CCTTGACTT
```

```
>CT11169:Kr:CG3340 5777
TGAAAACTGCTTTAACTTAATCGACATG
>CT11169:Kr:CG3340 5912
AAACGGATTAAATTTTTTCAGA
>CT11169:Kr:CG3340 5930
AAGGCTGGATTATTTGTCTG
>CT11169:Kr:CG3340 5981
AATCCGTCAATATTACGCCCCT
>CT11169:Kr:CG3340 6013
CCCTCTGTTAATCTCCGGCTTAGA
>CT11169:Kr:CG3340 6259
TTTAAGAGAAATTTGACTTCTTAATTGCCGACGA
>CT11169:Kr:CG3340 6354
GCTTAGGATTCTTGCGTCATA
>CT27633:hb:CG9786
GCAAAGCGAGTTGCCTTCATAAAATCTCGTGGCGTGTCGACTGGAA
>CT27633:hb:CG9786
TCTAATGACCATTAGACTCATAGATATTGTA
>CT27633:hb:CG9786
TTTTTTGTGCGCGACCTCAACCCTTTCACCCAT
>CT27633:hb:CG9786
GTTTCCACCTAATGTCGGCGTCATTGTCTTCTTTATGACG
```

```
>CT27633:hb:CG9786
CAACCCTTTGGCGGACGAGAAAGTTGCTAGGA
>CT27633:hb:CG9786
CAAGCCGCGATCTTCTTGGAATTAGTTTTGGTC
>CT27633:hb:CG9786
ATATTCATAAAGTTATATATGGCTTTTAA
>CT27633:hb:CG9786
TAACTACATGTCACTTTCAGGTTTTTACATT
>CT15191:kni:CG4717 7442
TTCCATTTGACTTTCATTTGT
>CT15191:kni:CG4717 7466
CGTTAGCTGACTTCCCAGAAG
>CT15191:kni:CG4717 7568
GGAACCTTGACTTTTTCACTC
>CT15191:kni:CG4717 7448
TTCCATTTGACTTTCATTTGT
>CT15191:kni:CG4717 7574
GGAACCTTGACTTTTTCACTC


            CAUDAL
A |   0   8   7   2   1   1   2   0   3   8   8   5   5   2
C |  12   4   0   7   0   1   1   0   0   3   1   0   8   9
G |   2   6   7   1   1   1   0   1   0   0   7  12   2   1
T |   5   1   5   9  17  16  16  18  16   8   3   2   4   7

CAGTTTTTTACGAT
CGGGTTTTACGACC
CCGTTTTTTAAGCC
GAACTGATTTGAAC
CAACTCTTTCGGGT
CGGATTTTACAACC
TAAAGTTTTTGACC
CGATTTTTTAAAAT
TGTTTTTTTTAGAA
TCTTTATTTTGGCA
GAATTTATTAGGTT
CCACATTTTTTGAT
CTGTTTTTTAAGCC
CATCTTCTTTATCT
TATCTTTTTAAGTC
CGATTTTTTATGGG
CAGTTTTTTTTTTC
CGTCTTTGTAAGTT
TCGCTTTTATGGCC

>CG6494:h:CT20229 2617
ATCGCAGTTTTTTACGATCCTCA
>CG6494:h:CT20229 2636
CTCAACGGGTTTTACGACCTCCG
>CG6494:h:CT20229 2657
CGTCCGTTTTTTAAGCCTTTCTG
>CG6494:h:CT20229 2698
ACCGAACTGATTTGAACTGAACG
>CG6494:h:CT20229 2719
GTGTCAACTCTTTCGGGTTCTCA
>CG6494:h:CT20229 2743
CCAGCCGGATTTTACAACCCGCT
>CG6494:h:CT20229 2762
CTGGAACAATAAAGTTTTTGACC
>CG6494:h:CT20229 2801
```

```
GTAGCGATTTTTTAAAATGTTTT
>CG6494:h:CT20229 2829
TTTTGTTTTTTTTAGAAGTGCAA
>CG6494:h:CT20229 2845
AGTGCAATCTTTATTTTGGCAAATTGT
>CG6494:h:CT20229 2878
TTAAGCGGAATTTATTAGGTTTC
>CG6494:h:CT20229 2897
TTTCTCGGAATTTCCACATTTTTTGATTAGGCAA
>CG6494:h:CT20229 2928
CGGGCTGTTTTTTAAGCCTTTTG
>CG6494:h:CT20229 2971
GGACATCTTCTTTATCTATCCAT
>CG6494:h:CT20229 2992
CCTTAGGAAACTATCTTTTTAAGTCGAAAA
>CG6494:h:CT20229 3035
ATGCGATTTTTTATGGGAACAA
>CG6494:h:CT20229 3098
CAGTTTTTTTTTTCCGACATGTT
>CG6494:h:CT20229 3121
TATGATCGTCTTTGTAAGTTCAC
>CT3134:tll:CG1378 7083
TCGCTTTTATGGCCCAAAAGTTGCC
```

DORSAL

```
A |   5   0   1   5  15   5   4   1   0   0   0   3   9
C |   5   2   3   1   1   2   0   1  13  30  20  19   0
G |   5  18  23  24   2   1   0   1   2   0   4   6  10
T |  15  10   3   0  12  22  26  27  15   0   6   2  11
```

```
GGGGATTTCCCCG
TGGGATATTCCCG
CGGGAATTCCCTT
TGGGTATACCCGT
TGCGATTTTCTCG
TTCGATTTTCTCG
TTGGGTTTTCTCT
TTGACTTTTCGCT
TGGATTTTTCTGT
AGGCATTTTCCCA
CTGGATTTTCGGA
AGGGTTTTGCCCT
GTGGAGTTCCCCT
TGGGTTATTCTTT
CTGGTTTTCCCGA
CTGGATTTCCCAA
TGGGTTTCTCCCA
TTGGTTTTCCCAG
AGTGTTTTCCGCT
AGGGTTTTCCCCA
TCGGGTTGGCCCG
GCGGATTTTCCCG
TGGGTCATCCCGG
AGTAATTTCCCAT
TTCGTATTTCCCT
TTGGAATTCCGCG
GGAAACTTTCCCA
TGTGTTTTTCCCA
GCGGAATTTCCTG
GGGGAAATTCCCG
```

```
>sog 705 up transl start
ATTACGGGGATTTCCCCGCACC
>sog 795 up transl start
GGACATGGGATATTCCCGACGGC
>sog 879 up transl start
GAAAGCGGGAATTCCCTTCCGC
>sog 958 up transl start
CCATTTGGGTATACCCGTATCT
>CT10023:twi:CG2956 8781
CGCCTGCGATTTTCTCGGTACGT
>CT10023:twi:CG2956 9660
GGATTTCGATTTTCTCGAGCGGC
>CT10023:twi:CG2956 9542
TTCTTTGGGTTTTCTCTCGATTT
>CT10023:twi:CG2956 8727
AAATTTGACTTTTCGCTCGTATT
>CT10023:twi:CG2956 9572
GCTCTGGATTTTTCTGTTTCTCT
>CT10023:twi:CG2956 9526
TCCCAGGCATTTTCCCAAATCGA
>CT10023:twi:CG2956 8740
CGCTCGTATTTTTCTGGATTTTCGGAGCTCCG
>CT10023:twi:CG2956 8531
CCAACAGGGTTTTGCCCTGTCCC
>CT10023:twi:CG2956 8841
TTTCGTGGAGTTCCCCTCGGTT
>CT10023:twi:CG2956 9556
TTTCTGTTTCTCTTGGGTTATTCTTTGGG
>CT1179:zen:CG1046 2615
AGTATCTGGTTTTCCCGAAAATC
>CT1179:zen:CG1046 2889
GACTTCTGGATTTCCCAAAACT
>CT1179:zen:CG1046 2938
TTGATTGGGTTTCTCCCAGTTAT
>CT1179:zen:CG1046 3007
AGAGCTTGGTTTTCCCAGGACA
>CT13146:sna:CG3956 4726
TGGCGGCCAGTGTTTTCCGCTTCATTCA
>CT13146:sna:CG3956 4691
CCCCCGAAAGGGTTTTCCCCAAAATAAT
>CT13146:sna:CG3956 4766
TTCCTGGTCGGGTTGGCCCGCTCATTAG
>CT13146:sna:CG3956 4831
CGACAAGTGCGGATTTTCCCGCGACATCA
>CT13146:sna:CG3956 4997
CTACCTGGTGGGTCATCCCGGATATCTC
>CT13146:sna:CG3956 5109
GGATTTAAAGTAATTTCCCATCTTATCC
>CT13146:sna:CG3956 5174
TTTCCATTTCGTATTTCCCTGCAATGGA
>CT13146:sna:CG3956 5262
GCGGGGAATTGGAATTCCGCGCTGGAAT
>CT13146:sna:CG3956 5460
ACTATCGATGGGAAACTTTCCCAACTCCCAC
>CT1008:rho:CG1004 6356
CGATGTGTGTTTTTCCCACCGCA
>CT1008:rho:CG1004 6492
GGCGGGCGGAATTTCCTGATTCG
>CT1008:rho:CG1004 6551
TTTTGGGGGAAATTCCCGGGCGA
```

TORSO RESPONSE ELEMENT

```
A |   0   0   0   0   0   6   6   0   0   6   6
C |   0   1   5   0   5   0   0   0   0   0   0
G |   0   4   1   0   0   0   0   1   6   0   0
T |   6   1   0   6   1   0   0   5   0   0   0

TCCTCAAGGAA
TGCTCAATGAA
TGCTCAATGAA
TGCTCAATGAA
TGCTCAATGAA
TTGTTAATGAA

>CT3134:tll:CG1378 7370
TTTTCGTCCTCAAGGAACTTTGT
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>tll Dvir D3 LiawPNAS 90 858 1993
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>tll Dvir distal LiawGen&dev1995
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