

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 corresponds 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
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TGTAATCAGGC
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>CT3134:tll:CG1378 8926
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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

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CTTCTTTGTTCC
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GTTTTTAAGAGA
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ATTTTTTTGCGC
ATTTTTTTGGCC
ATTTTTTGTTTC
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GTTTTTTGGCAT
GTTTTTTGGGCA
CTTTTTAAGCTA
ATTTTTTTCCCA
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GTTTTTGTTAAG
CTTTTTCACTCC
CTTTTTGGCTTT
CTTTTTATGAAT
ATTTTATTGAGT
ATTTTTGTATGC
ATTTTTTATAAC
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ATTTTTTTGGCA
ATTTTAAACAGC
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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

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TAGGAAAGTAGATCA
AAAAAAAGTAGCGCA
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GAGGATCGTAAAAAA
GGAGGTCGTAAACCC
TAAAAAACGGACGGA
GAGGATGGCAGAGCA
TTTGAAGTGAACGGG
TTGACACCGAAGTGA
TCATAAAGTAGATCT
TTCGACCCGGGATCG
TAAAAAACGGACGGA
TGAGAACCCGAAAGA
TGGAACAATAAAGTT
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TGCACTTCTAAAAAA
GTAGGAAGTTAAGCG
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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

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GACCGGGTT
GAAGGGATT
AACTGGGTT
AAACGGGTT
CAAAGAGTT
CCACGGATT
GATAGAGTT
GAAAGAGGT
CAACGGGTT
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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

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ATTTGACTT
CTTAGGATT
AGTTGCCTT
ATTAGACTC
CTTTCACCC
CATTGTCTT
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ATTAGTTTT
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CCTTGACTT
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CCTTGACTT

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CAUDAL															
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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

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 CCGTTTTTTAAGCC
 GAACTGATTTGAAC
 CAACTCTTTCGGGT
 CGGATTTTACAACC
 TAAAGTTTTTGACC
 CGATTTTTTAAAAT
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 TCTTTATTTGGCA
 GAATTTATTAGGTT
 CCACATTTTTTGAT
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DORSAL

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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

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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

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 CGACAGTTGTTAATGAAGAGATA