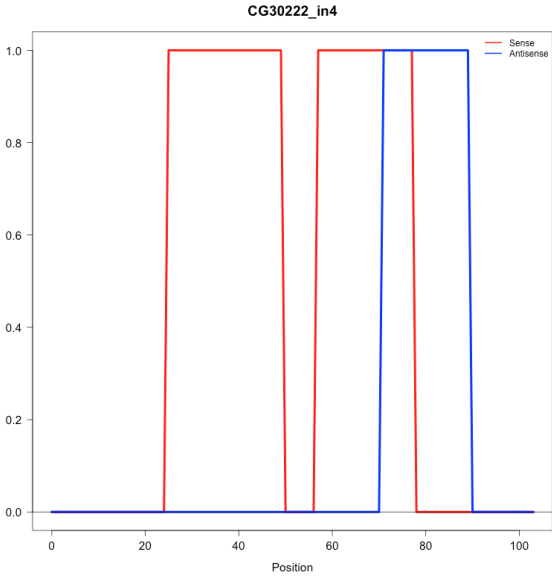
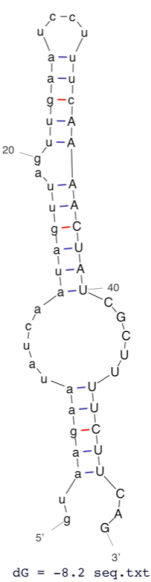


Output of mc_graph (1)
by G. Serrat and M. Zuker



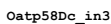
CG30222_in4

[chr2R 17472230-17472333 +](#)

TTTCAACTTGCCTGAATTTGATTGTAAGAATATCAATAGTTAGTTGAATCCTTTCAAACTATCGCTTTTCTTCAGATGATCACTACTTTTATAGTTTGCT
.....((((((.....((((((.....((((((.....)))))))))).....)))))).....
Plus strand

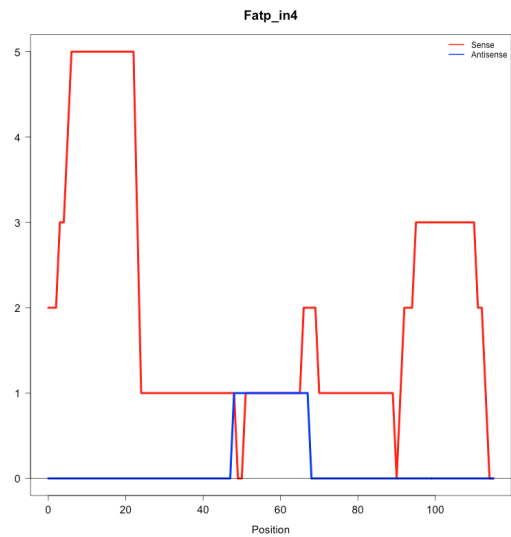
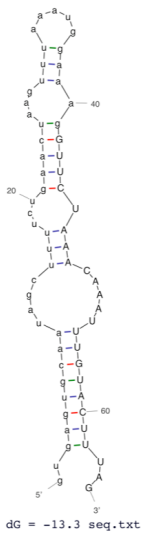
	Size	Blast	Total Norm	# of libraries
.....GTAAGAATATCAATAGTTAGTTGAA.....	25	1	1.00	1
.....AAAACTATCGCTTTTCTTCAG.....	21	1	1.00	1

dg - 36.5 seq.txt

[illegible]

	Size	Blast	Total Norm	# of libraries
.....TTATCCTTTTATTACTGCGCA.....	21	1	2.00	1
.....ATTATCCTTTTATTACTGCGCAG.....	23	1	2.00	2
.....ATTATCCTTTTATTACTGCGCA.....	22	1	2.00	2

Output of seq.graph (R)
by G. Smeets and M. Zuker



Fatp_in4

[chr2L_10512844-10512959 -](#)

AGGCTGCGGTTATCTCTCACTCCCGGTGAGTGCAATAGCTTTTCTGAACTAAGTTTAAATGGAAAGGTTCTAAACAAATTGTACTTTAGTTATCTGTTTATCGCTGCTGGCATC
.....(((((((.....(((((((.....((((.....)))))).....)))))).....)))))).....
Plus strand

	Size	Blast	Total Norm	# of libraries
AGGCTGCGGTTATCTCTCACTCC.....	23	1	2.00	1
...CTGCGGTTATCTCTCACTCCC.....	21	1	1.00	1
.....AGTTTAAATGGAAAGGTTCT.....	19	1	1.00	1
.....ATCTGTTTATCGCTGCTGG.....	19	1	1.00	1
.....CGGTTATCTCTCACTCCCG.....	19	1	1.00	1
.....GTTCTAAACAAATTGTACTTTAG.....	24	1	1.00	1
.....GTGAGTGCAATAGCTTTTCTGAAC.....	24	1	1.00	1
.....TATCTGTTTATCGCTGCTGGCAT.....	23	1	1.00	1
.....GCGGTTATCTCTCACTCCC.....	19	1	1.00	1
.....TGTTTATCGCTGCTGGCA.....	18	1	1.00	1

Eaat2_in6

Position

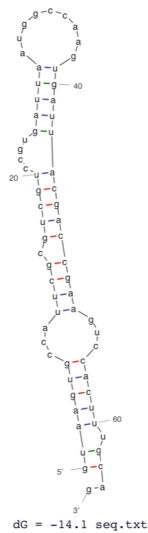
Sense
Antisense

Position	Sense	Antisense
0 - 10	0.0	0.0
10 - 45	1.0	0.0
45 - 70	0.0	0.0
70 - 85	0.0	1.0
85 - 90	1.0	1.0
90 - 115	1.0	0.0
115 - 120	0.0	0.0

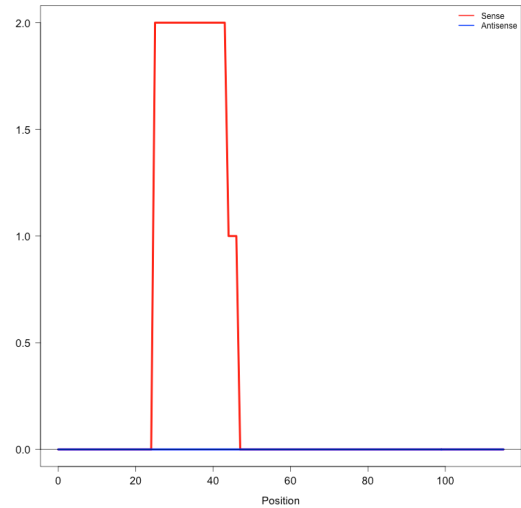
chr2L 738410-738532 -

	Size	Blast	Total Norm	# of libraries
.....CCTTGCAAGGATCGGATTGCGACC.....	24	1	1.00	1
..STGAGTATGGAATCAATTTGT.....	21	1	1.00	1
.....CGCCGTGGACTGGTTTGT.....	18	1	1.00	1

Output of seq.graph (R)
by G. Reinert and M. Zacher



Lip1_in2



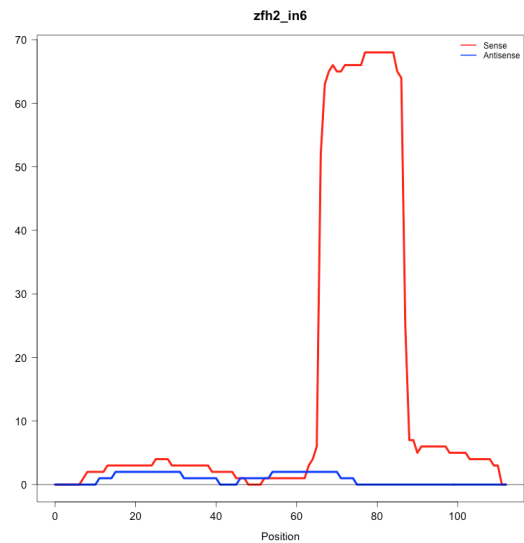
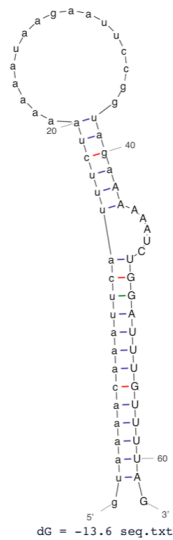
Lip1_in2

[chr2L 10700626-10700741 -](#)

GTAATGGGGCCCAACGTGAGCCTGGGTAAGTGCCATTTCGCGTCGTCGGTGATTAATGGCCAAGTGATTACGCCGAAGTCCACTTGCAGCCTACTTGCTGGCCGACCACAACATA
.....(((((((.....(((((((.....((((.....)))))))))))).....)))))).....
Plus strand

	Size	Blast	Total Norm	# of libraries
.....TAAGTGCCATTTCGCGTCG.....	19	1	1.00	1
.....TAAGTGCCATTTCGCGTCGTC.....	22	1	1.00	1

Output of seq.graph.RS
by G. Smeets and M. Zuker



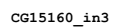
zfh2_in6

[chr4 551694-551806 +](#)

GCGGAGTCCCATGCAGTAGAAAGAGGTAAACAAATTCATTCTAAAAATAAGAATCCGGTAGAAAAAATCTGGATTGTTTTAGAAAGTTTCAGGAAGTGATGTCTCGCC
.....((((((((((((((((((((.....)))))))))))))))).....)))))))))))))))).....
Plus strand

	Size	Blast	Total Norm	# of libraries
.....AAAAATCTGGATTGTTTTAG.....	21	1	31.00	13
.....AAAAATCTGGATTGTTTTAGA.....	22	1	10.00	6
.....AAAATCTGGATTGTTTTAGA.....	21	1	7.00	7
.....AAAATCTGGATTGTTTTAG.....	20	1	4.00	1
.....AAAAATCTGGATTGTTTT.....	19	1	2.00	2
.....AAAAATCTGGATTGTTTTAGAAG.....	24	1	2.00	1
.....TTCAGGAAGTGATGTCTCGC.....	20	1	2.00	1
.....AAAAATCTGGATTGTTTTAG.....	22	1	2.00	2
.....CCCATGCAGTAGAAAGAG.....	18	1	1.00	1
.....CAGTAGAAAGAGGTAAACAAATTC.....	26	1	1.00	1
.....GAAAAAATCTGGATTGTTTT.....	21	1	1.00	1
.....AAAAATCTGGATTGTTTTA.....	20	1	1.00	1
.....TAGAAGTTTCAGGAAGTGATGTCTCGC.....	27	1	1.00	1
.....AGAATTCGGTAGAAAA.....	18	1	1.00	1
.....AAATCTGGATTGTTTTAGA.....	20	1	1.00	1
.....GTAAACAAATTCATTCTA.....	20	1	1.00	1
.....GTAAACAAATTCATTCTAAAA.....	23	1	1.00	1
.....TTTGTTTTAGAAGTTTCAGGAAGTGA.....	26	1	1.00	1
.....TTTAGAAGTTTCAGGAAGTGATGTCTC.....	27	1	1.00	1
.....TTTGTTTTAGAAGTTTCAGGA.....	21	1	1.00	1
.....CCATGCAGTAGAAAGAGGTAA.....	21	1	1.00	1
.....AGAAAAAATCTGGATTGTTTT.....	21	1	1.00	1
.....AAATCTGGATTGTTTTAG.....	19	1	1.00	1
.....CTGGATTGTTTTAGAGT.....	19	1	1.00	1
.....AATCTGGATTGTTTTAG.....	18	1	1.00	1
.....AGAAAAAATCTGGATTGT.....	19	1	1.00	1

dG = -8.6 seq.t.txt

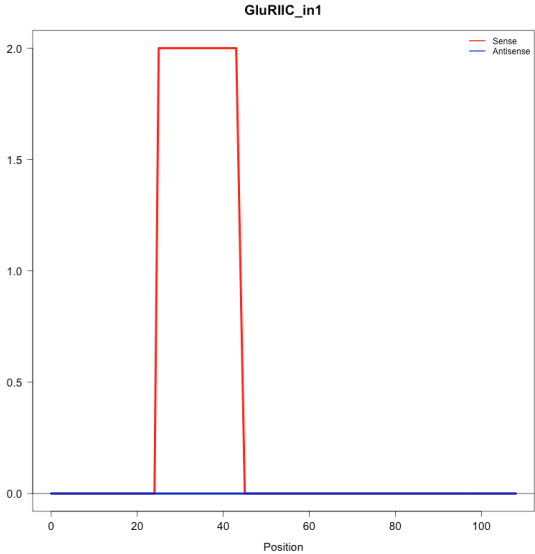
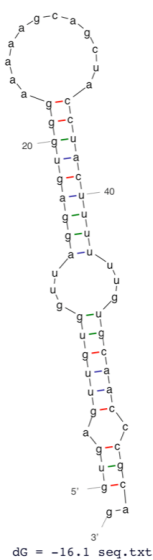


[chr2L 18592093-18592201 +](#)

AAAGGAAGTCAAAGTGGTAGCCAGTGTAAAGTTAAATCTATTAAAGCTATCAAGATTACGAAGTCTAAATAAATTTTAATCTTACAGGCGCTATAAGAGCTTTGGCAGCGCA
.....(((((((((((.((((.((((.(.....))))).)))))....))))).))))
Plus strand

	Size	Blast	Total Norm	# of libraries
.....GTAAGTTAAATCTATTAAGCT.....	21	1	2.00	1
.....TCTAAATAATTTAATCTTACAG.....	22	1	1.00	1
AAAGGAAGTCAAAGTGGTAGCC.....	22	1	1.00	1
.....TCTAAATAATTTAATCTTA.....	19	1	1.00	1
.....ATTAAGCTATCAAGATTACGA.....	21	1	1.00	1
.....TCTAAATAATTTAATCTTACA.....	21	1	1.00	1

Output of `ss_graph.RS`
by G. Smeets and M. Zuker



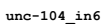
GluRIIC_in1

[chr2L 914254-914362 +](#)

AGCCGGGGGCAACAAATCAACATTG**GTGAGTTGTGGTTAGGAGTGGGAAAAAGCAGCTACCTACTTTTTGTGCAACCCGCAG**GCGCCTTCTTCTACGACGATGAGCT
.....(((.((((((.....)))))))).)).....
Plus strand

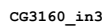
	Size	Blast	Total Norm	# of libraries
..... GTGAGTTGTGGTTAGGAGT	19	1	1.00	1
..... GTGAGTTGTGGTTAGGAGTG	20	1	1.00	1

dG = -11.4 seq.txt



TCATTGATGAAGGCAACAAGCTCG**G**TGAGTATTATTATAAATATGGTTTAAATCTTATCATCTTATTATATATACTATTAAATAACTTTCAGAACGTGGCAGCTACTAACATGAAC
.....(((.(.((((((.((((.(...(((.(.....)))))).)))))..))))).)).....
Plus strand

	Size	Blast	Total Norm	# of libraries
GTGAGTATTATTATAAATATG.....	21	1	1.00	1

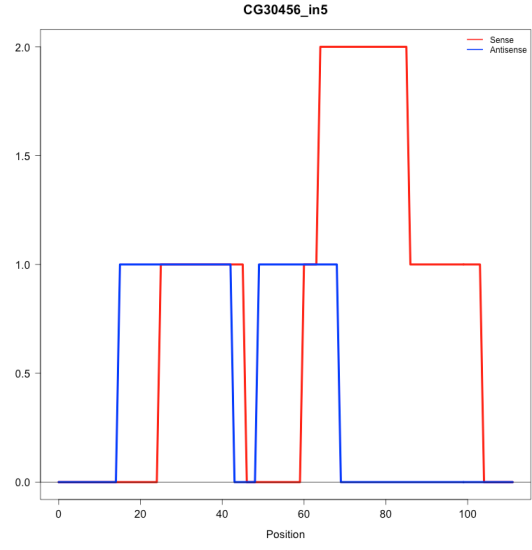
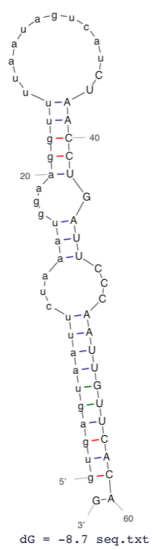


chrX 5582177-5582279 -

GCAGACGGCATTGTCTACCTTTGTG**CTAAGTTGCATTGTATTCTAAGCAGTAGTAATAACAATGATATACTTACAG**AAGCCTCGAAGGCGCTCAGCAGAATA
(((((((((.((((((((((((((.....))))).)))))))).)).....)))))).
 Plus strand

	Size	Blast	Total Norm	# of libraries
.....GTAAGTTGCATGTGATTCTAAGCAC.....	25	1	4.00	3
.....GTAAGTTGCATGTGATTCTAAG.....	22	1	2.00	2
.....GTAAGTTGCATGTGATTCTAAGC.....	23	1	2.00	2
.....GTAAGTTGCATGTGATTCTAAGCACT.....	26	1	2.00	2
.....AAATACAAATGATATACTTACA.....	22	1	1.00	1

Output of seq_graph (R)
by G. Simon and B. Zaker



CG30456_in5

chr2R 12993850-12993961 +

TTTGC TGT CAC GCG AGT CATT AAT GTG AGT AAT TCT AAA TGA AGG TTT TTA TAG TCA TCT AAC CTG ATT CCC AAT TGT TCA CAG ACC TTCTT CAAGA ACC GTG ACATAG
.....(((((((((((.....(((.....((((.....)))))).)))).)))))).....
Plus strand

	Size	Blast	Total Norm	# of libraries
.....CCTGATTCCCAATTGTTACAG.....	22	1	1.00	1
GTGAGTAATTCTAAATGGAAG.....	21	1	1.00	1
.....CTAACCTGATTCCCAATTGTTACAG.....	26	1	1.00	1
.....ACCTTCTTCAAGAACGT.....	18	1	1.00	1

dG = -14.2 seq.txt

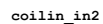


chr2R 7918364-7918476 +

CGAGC GCGGACTCAAGTTGTGGGCC**G**TGAGTATAGAGATAA**A**TTTAAGTTATGATACAGAAATCCATTGAT**G**CTTTTATAC**TGCAG**ATGCTTTTCATACGCTCTTTTCGGCTC
.....(((((((((((.....((((((...(((.....)))..))))))....))))))))).....
Plus strand

	Size	Blast	Total Norm	# of libraries
CGAGCGCGGACTCAAGTTGTTGGC.....	24	1	2.00	1
.....TTGATTGCCTTTATACTTGCA..	20	1	1.00	1
.....TGATTGCCTTTATACTTGCA..	21	1	1.00	1
GTGAGTATAGAGATAATTAAAGT.....	23	1	1.00	1
.....TTTGATTGCCTTTATACTTGCA..	21	1	1.00	1
CGAGCGCGGACTCAAGTTGTTGG.....	23	1	1.00	1

5' -15.5 seq.txt



GACTCTGTGATATTGAACCGATTCCAGTGTGAGATACGAGGCATTTTAAATGGTAGATGTATGCTTATGAGTGCCTTGACATCTTATAGTAGAGAAAATAGGCAATCTTTGGA
(((((((((.....((((.....)))))))))..)))))).....
 Plus strand

	Size	Blast	Total Norm	# of libraries
.....GTGAGATACGAGGCATTAAATGG.....	24	1	6.00	4
.....ATGGTAGATGTATGCTTATGAGTGC.....	25	1	1.00	1
.....TTAAATGGTAGATGTATGCT.....	21	1	1.00	1
.....TTAAATGGTAGATGTATGCT.....	20	1	1.00	1
.....TATGAGTGCCCTTGACATCTTAGT.....	24	1	1.00	1
.....TATGAGTGCCCTTGACATCTT.....	21	1	1.00	1
.....GGTAGATGTATGCTTATGAGTGC.....	23	1	1.00	1
.....TTAAATGGTAGATGTATGCTTA.....	23	1	1.00	1
.....GTGAGATACGAGGCATTAAATGGTA.....	26	1	1.00	1

	Size	Blast	Total Norm	# of libraries
GTGAGTAGCTGTCGTGTTAGT	21	1	15.00	2
GTGAGTAGCTGTCGTGTTAG	20	1	7.00	3
GTGAGTAGCTGTCGTGTTAGTAGC	24	1	6.00	4
GTAGCTCCATTGCTAACAGCA	21	1	5.00	1
GTGAGTAGCTGTCGTGTTAGTA	22	1	3.00	1
GCTGAGTAGCTGTCG	18	1	2.00	1
GTGAGTAGCTGTCGTGTT	18	1	2.00	1
GTGAGTAGCTGTCGTGTTA	19	1	2.00	1
CGTGTAGTAGCTCCATTGCT	21	1	1.00	1
CTGTCGTGTAGTAGCTC	18	1	1.00	1
TTCTGCACAGATCACCATT	20	1	1.00	1
CACAGATCACCATTCCACCGT	21	1	1.00	1
GTGAGTAGCTGTCGTGTAGTAGCTCCATTGCTAA	35	1	1.00	1
GATTGTGCTCTCCTCGCT	19	1	1.00	1
CGGATTGTGCTCTCCTC	18	1	1.00	1
GAGTAGCTGTCGTGTTAGT	19	1	1.00	1
TCCTGCACAGATCACCATTCCACCGTG	27	1	1.00	1
CGGATTGTGCTCTCCTCGCT	22	1	1.00	1
CGGATTGTGCTCTCCTCGC	20	1	1.00	1
AACAGCACGAGATTCTGACAG	23	1	1.00	1
AACAGCACGAGATTCTGCACA	22	1	1.00	1
GTGAGTAGCTGTCGTGTAGTAGTCC	27	1	1.00	1
GTGAGTAGCTGTCGTGTAGTAGCTC	26	1	1.00	1



[chr3R 23763034-23763177 -](#)

	Size	Blast	Total Norm	# of libraries
.....GCGCTGTGTGCTGCTTTAG.....	20	1	19.00	1
.....GTGTGCGCGCTGTGTGTGCTGCTTT..	24	1	7.00	1
..ACAGCGTGTGTCCATGGTGAAC.....	22	1	3.00	1
..CAGCGTGTGTCCATGGTGAAC.....	21	1	2.00	2
..AACAGCGTGTGTCCATGGTG... ..	20	1	1.00	1
.....TGCGCCTGTGTGTGCTGCTTTAG.....	23	1	1.00	1
.....CGCCTGTGTGTGCTGCTTT..	19	1	1.00	1
..AACAGCGTGTGTCCATGGTGA.. ..	22	1	1.00	1

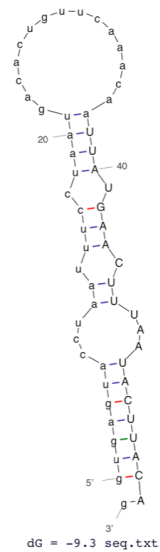


chr2L 10212238-10212351 +

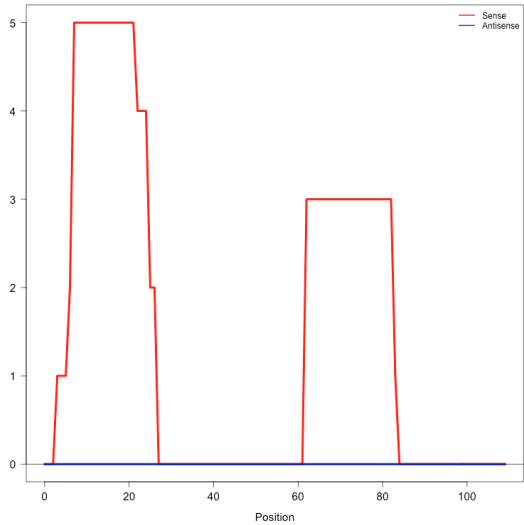
ACATACACCGCACCCTCCGAAAAA**TAGGGTCGTGATGATATATATTACACTTCTAGTATTATATATATGTGTACATTATTACAG**CCACGACGTTGTGATATTCTTAACC
.....(((((((((((((((((((((.(.(((.(....))..))..)))))))))).)))..)).....
Plus strand

	Size	Blast	Total Norm	# of libraries
GTAGGTCCTGATGATATATA	19	1	70.00	3
GTAGGTCCTGATGATATATAT	20	1	70.00	3
GTAGGTCCTGATGATATAT	18	1	26.00	3
GTAGGTCCTGATGATATATATA	21	1	21.00	3
GTAGGTCCTGATGATATA	18	1	15.00	3
GTAGGTCCTGATGATATATATAT	22	1	11.00	3
GTAGGTCCTGATGATATAT	19	1	6.00	2
GTAGGTCCTGATGATATATATATT	23	1	3.00	3
GTAGGTCCTGATGATATATATATTT	24	1	1.00	1
AAAGTAGGTCCTGATGATATAT	23	1	1.00	1
ACGACGTGTTGATATTCTTAACC	23	1	1.00	1
GTAGGTCCTGATGATATATATATTTACA	27	1	1.00	1
CGACGTGTTGATATTCT	18	1	1.00	1
GTAGGTCCTGATGATATATATATTTACACTT	31	1	1.00	1
TATATTTACACTTACTGATT	20	1	1.00	1
GTAGGTCCTGATGATATATAT	21	1	1.00	1

Output of m_gmsh R3
by G. Stewart and M. Zuker



Mtp_in3

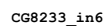


Mtp_in3

[chr2L 20920201-20920310 -](#)

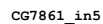
AACTACAATGTGCTGGGACAAAAGG**GTGAGTACCTAATTTCTTAATGACACTGTTCAAACAATTATGAACTTTAATACTTACAG**GTCTTACGACAGTCCTCACCCTGCA
.....(((((((.....(((.....))))).)).....)))).....
Plus strand

	Size	Blast	Total Norm	# of libraries
.....ATGTGCTGGGACAAAAGG.....	18	1	2.00	1
.....TTATGAACTTTAATACTTACA.	21	1	2.00	2
.....TTATGAACTTTAATACTTACAG	22	1	1.00	1
.....AATGTGCTGGGACAAAAGG GT	21	1	1.00	1
..TACAATGTGCTGGGACAAA.. GT	19	1	1.00	1
.....ATGTGCTGGGACAAAAGG GT	20	1	1.00	1



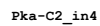
chr2R 10036659-10036763 -

	Size	Blast	Total Norm	# of libraries
GTGCGTTAAGTGTTATGTTTATA.....	24	1	8.00	8
GTGCGTTAAGTGTTATGTT.....	20	1	5.00	3
GTGCGTTAAGTGTTATGTT.....	19	1	4.00	3
GTGCGTTAAGTGTTATGTTTAT.....	23	1	2.00	2
GTGCGTTAAGTGTTAIGG.....	18	1	2.00	1
GTGCGTTAAGTGTTATGTTTATATAC.....	27	1	2.00	2
GTGCGTTAAGTGTTATGTTTATATA.....	26	1	1.00	1
.....TTAATTAAACATTTTCGCAG	21	1	1.00	1
.AGGCGGATAAGGATATTAAAC.....	21	1	1.00	1
...CGGATAAGGATATTAAACCAG.....	21	1	1.00	1
GTGCGTTAAGTGTTATGTTT.....	21	1	1.00	1
GTGCGTTAAGTGTTATGTTTATAT.....	25	1	1.00	1



GCTTCACAATCCCATTTGGGAATGAGGTAGGGCGAGCGTTTTTTGGCACTAAAAAATTACTGTCATAATGTTATCCTCGCAGCTGATGCGTTTAACGAGCTGGACA
 ((((((.((((((..... ((((((.((((((.....)))))).)))))).)))))).))))).
 Plus strand

	Size	Blast	Total Norm	# of libraries
.....GTTATCCTCGCAGGCTGA.....	18	1	1.00	1
.....ATTTGAATGAGTAGGG.....	18	1	1.00	1
.....GCTGATGCGTTTAACGAGCT.....	20	1	1.00	1
.....GTAGGGCAGCGTTTTTTTGGCACT.....	24	1	1.00	1

[illegible]

[chr3R 26521561-26521673 -](#)

TCATCGAGGTGGACACCTCAAAGCG**G**TAGTGGAGTGGGAGTGGGTCAAGGTGCTTCCAATGCAGTGCTCATGCCACCCCTTCTCAGTTTAGGAAACTCGAACGACGGCTCC
(((.(.(.(((.(.(((.(.(...(((.....)))))))))))).))))).))))).))))).
 Plus strand

	Size	Blast	Total Norm	# of libraries
GTGAGTGGAGTGGGAGTG	18	1	2.00	2
GTGAGTGGAGTGGGAGTGGG	20	1	2.00	1
AGGTGGACACCTCAAAGCC	19	1	1.00	1
TGCAGGTGGACACCTCAAAGCC	22	1	1.00	1
TGCAGGTGGACACCTCAAAGC	21	1	1.00	1
GTGAGTGGAGTGGGAGTGG	19	1	1.00	1
TAGGAAACTCGAACGACGGCTCC	23	1	1.00	1

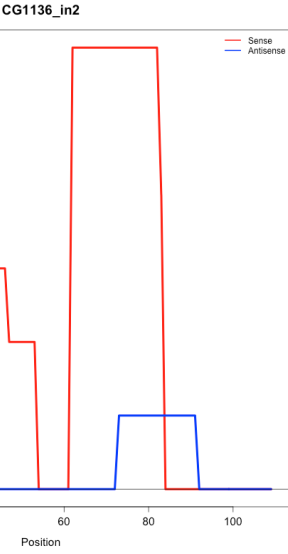
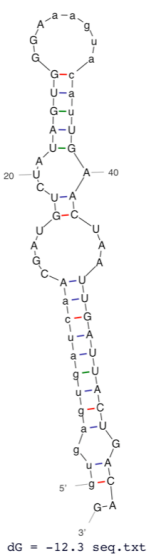


[chr2R 18492658-18492792 -](#)

TCCGCCAATTGGCACAATCAATACA**GTAAGCAATACGTTGGGGTCTACGCATTAGATAAAGGGGGTCTCATAATGGGTCTGTGAACTTATGCATATTGCCATTGCGAG**ATTACCCGAAGCCTGTACCGCGGTT
(((((((((((.(((((((((((.(((.((((.....(.(.....)).)))))).)))))).)))))).)))))).))))))
 Plus strand

	Size	Blast
.....GTAAGCAATACGTTGGGTICTA.....	22	1
.....TTACCCGAAGCCTGTACCGC.....	20	1
.....TAATGGGCTGTGAACTTATGCA.....	24	1
.....TAAGCAATACGTTGGGTICTAC.....	22	1
.....GTAAGCAATACGTTGGGTICT.....	21	1

Output of mfold R2
by D. Bryant and M. Zuker



CG1136_in2

[chr3L 4057390-4057499 +](#)

CGGCTGCAGGATGGCACAGTCATCGGTGAGTGATCAACGATGTCTATAGTGGGAAAGTACATTGAACTAATTGATTACTGACAGGAAGTGAAGCCTGGATCGATCGCGC
.....(((.(((((((.....(((.....))))))..)).....)))))).....
Plus strand

	Size	Blast	Total Norm	# of libraries
.....TGAAGTAATTGATTACTGACAG.....	22	1	4.00	4
.....ACGATGTCTATAGTGGGA.....	18	1	2.00	1
.....TGAAGTAATTGATTACTGACA.....	21	1	2.00	2
GTGAGTGATCAACGATGTCTAT.....	22	1	1.00	1

[illegible]

	Size	Blast	Total Norm	# of libraries
.....TTTCCCAACCGCCTTCCA.....	21	1	8.00	4
GTAGGTTGAATCGGTGGGGAA.....	21	1	5.00	2
.....TCCCAACCGCCTTCCAG.....	20	1	3.00	1
GTAGGTTGAATCGGTGGGGAAC TG.....	24	1	2.00	1
GTAGGTTGAATCGGTGGGGA.....	20	1	2.00	2
.....ATTCCCAACCGCCTTCCA.....	22	1	1.00	1
.....CATTCCCTGGAGATCGG.....	18	1	1.00	1
.....TGGAGATCGGTAGGTTGAAT.....	21	1	1.00	1