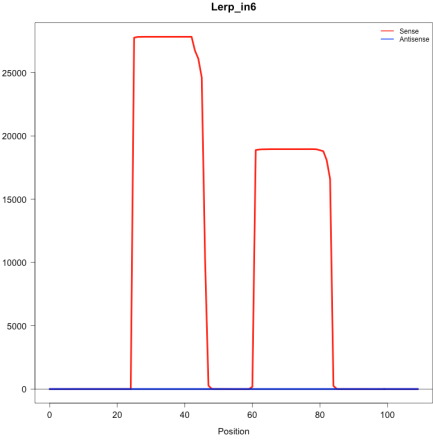
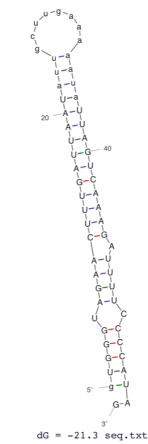


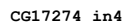


Lerp_in6

chr3R 22687045-22687154 =

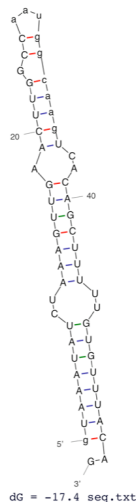
GTAAAGCCACAATCCAAAGAACCGTGGGTAGAACTTTGATTAAATTTGCTTGAATAATATTAGTCAAGATTTTCCCCATAGATTATCAATTCCGCAATGTACAA
.....(((L(((L(((L(((L(((L.....)))))))))))))))))).....
Plus strand

	Size	Blast	Total Norm	# of libraries
.....TTAGTCAAGATTTTCCCCATAG.....	23	1	16207.00	169
.....TTGGGTAGAACTTTGATTAAAT.....	21	1	14334.00	162
.....TTGGGTAGAACTTTGATTAAATA.....	22	1	9972.00	164
.....TTGGGTAGAACTTTGATTAA.....	20	1	1468.00	109
.....TTAGTCAAGATTTTCCCCATA.....	22	1	1453.00	131
.....TTGGGTAGAACTTTGATT.....	18	1	1089.00	84
.....TTAGTCAAGATTTTCCCCAT.....	21	1	658.00	104
.....TTGGGTAGAACTTTGATTAA.....	19	1	638.00	77
.....TTGGGTAGAACTTTGATTAAATAT.....	23	1	250.00	76
.....TTAGTCAAGATTTTCCCCATAG.....	24	1	232.00	70
.....ATTAGTCAAGATTTTCCCCATAG.....	24	1	100.00	51
.....TTAGTCAAGATTTTCCCCATA.....	20	1	78.00	29
.....TTAGTCAAGATTTTCCCC.....	19	1	62.00	19
.....ATTAGTCAAGATTTTCCCCAT.....	22	1	40.00	21
.....TAGTCAAGATTTTCCCCATAG.....	22	1	31.00	18
.....TTGGGTAGAACTTTGATTAAAT.....	20	1	30.00	15
.....TTGGGTAGAACTTTGATTAAATA.....	21	1	22.00	15
.....ATTAGTCAAGATTTTCCCCATA.....	23	1	19.00	18
.....TTAGTCAAGATTTTCCCC.....	18	1	13.00	8
.....AGTCAAGATTTTCCCCATAG.....	21	1	10.00	8
.....ATTAGTCAAGATTTTCCCC.....	20	1	8.00	6
.....TAGTCAAGATTTTCCCCATA.....	21	1	7.00	3
.....GTTAGAACTTTGATTAAATA.....	19	1	6.00	3
.....TTAGTCAAGATTTTCCCCATAGAT.....	25	1	5.00	4
.....TTGGGTAGAACTTTGATTAAATAT.....	22	1	5.00	4
.....CAAAGATTTTCCCCATAG.....	18	1	4.00	4
.....ATTAGTCAAGATTTTCCCCATAG.....	25	1	4.00	4
.....TTGGGTAGAACTTTGATTAAATATT.....	23	1	3.00	1
.....TCAAAGATTTTCCCCATAG.....	19	1	3.00	3
.....TTGGGTAGAACTTTGATTAAATATTCCTT.....	29	1	3.00	3
.....TAGTCAAGATTTTCCCCATAG.....	23	1	3.00	3
.....ATTAGTCAAGATTTTCCCCA.....	21	1	3.00	3
.....TTGGGTAGAACTTTGATTAAATATT.....	24	1	3.00	3
.....GTTAGAACTTTGATTAAAT.....	18	1	3.00	3
.....TTGGGTAGAACTTTGATTAAAT.....	19	1	3.00	2
.....AGTCAAGATTTTCCCCATA.....	20	1	2.00	1
.....TCAAAGATTTTCCCCATAG.....	20	1	2.00	2
.....CACAAATCCAAAGAACG.....	18	1	2.00	1
.....TAGTCAAGATTTTCCCCAT.....	20	1	2.00	2
.....TTGGGTAGAACTTTGATTAAATATTCCT.....	27	1	2.00	2
.....GTCAAAGATTTTCCCCATAG.....	20	1	2.00	2
.....TTGGGTAGAACTTTGATTAA.....	19	1	1.00	1
.....AGCCCAAATCCAAAGAAC.....	20	1	1.00	1
.....TCAAAGATTTTCCCCATA.....	18	1	1.00	1
.....TCCCCATAGATTATCAATT.....	20	1	1.00	1
.....TTGGGTAGAACTTTGATTAAATA.....	23	1	1.00	1
.....AAAGATTTTCCCCATAG.....	18	1	1.00	1
.....ATTAGTCAAGATTTTCC.....	18	1	1.00	1
.....TATTAGTCAAGATTTTCC.....	20	1	1.00	1
.....GTCAAAGATTTTCCCCATA.....	19	1	1.00	1
.....AGTCAAGATTTTCCCCATAG.....	22	1	1.00	1
.....TTGGGTAGAACTTTGATTAAATATTC.....	26	1	1.00	1
.....AGTCAAGATTTTCCCCAT.....	19	1	1.00	1



AACCATGGACATTCTGACCGTGCAGCTGAGTGTGAGCCAGGAATATAGTCTCTTATTATGGTTCAAATCGCTCGCAGAAATCCACCCCTGGCAAAATCCTTACCA
(((((((.....))))))))).....
 Plus strand

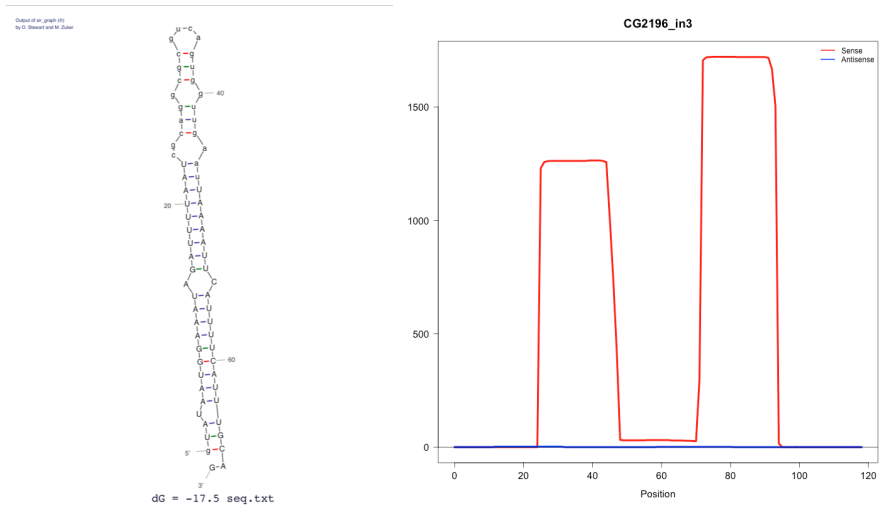
	Size	Blast	Total Norm
.....TTATTGGTTCAAATCGCTCGCAG.....	23	1	122.00
.....TTATTGGTTCAAATCGCTCGCA.....	22	1	64.00
.....TTATTGGTTCAAATCGCTCGC.....	21	1	20.00
.....ATTGGTTCAAATCGCTCGCAG.....	21	1	10.00
.....TTATTGGTTCAAATCGCTCG.....	20	1	6.00
.....TATTGGTTCAAATCGCTCGCAG.....	22	1	5.00
GTGAGTTTTGGAGCCAGGAATA.....	22	1	4.00
.....ATTGGTTCAAATCGCTCGC.....	19	1	3.00
.....ATTGGTTCAAATCGCTCGCAGA.....	22	1	3.00
.....TTATTATTGGTTCAAATCGCTCG.....	23	1	2.00
.....ATTGGTTCAAATCGCTCGCA.....	20	1	2.00
GTGAGTTTTGGAGCCAGGAAT.....	21	1	2.00
.....ATTGGTTCAAATCGCTCG.....	18	1	2.00
.....GGTTCAAATCGCTCGCAG.....	18	1	1.00
.....TATTGGTTCAAATCGCTCGCA.....	21	1	1.00
.....TTATTGGTTCAAATCGCTCGCAGA.....	24	1	1.00
.....TATTATTGGTTCAAATCGCTC.....	21	1	1.00



chr2R 6773012-6773119 +

GAAGAAGCTGAAGTTCCTCATCTATGTAAATATCTAAAGTTGAACTTGGCCAATGGCAAGTCACAGCTTTTGTGTTTACAGGAGAACGAGTACTTCCAGGATCTAT
(((((((..(((((((.((((((..(-..))))))..))))))..)))))).....
 Plus strand

Strand		Size	Blast	Total Norm	# of libraries
	TCACAGCTTTTGTGTTTACAG.....	22	1	6579.00	154
	TCACAGCTTTTGTGTTTACAG.....	21	1	5859.00	147
	GTAAATATCTAAAGTTGAACT.....	21	1	1262.00	111
	TCACAGCTTTTGTGTTTAC.....	20	1	958.00	72
	TCACAGCTTTTGTGTTT.....	18	1	126.00	38
	ACAGCTTTTGTGTTTACAG.....	20	1	99.00	36
	TCACAGCTTTTGTGTTTAC.....	19	1	63.00	28
	GTAAATATCTAAAGTTGAAC.....	20	1	50.00	29
	CACAGCTTTTGTGTTTACAG.....	21	1	49.00	19
	AGCTTTTGTGTTTACAG.....	18	1	37.00	28
	GTCACAGCTTTTGTGTTTACAG.....	22	1	37.00	19
	ACAGCTTTTGTGTTTACAG.....	19	1	35.00	27
	CACAGCTTTTGTGTTTACAG.....	20	1	32.00	14
	TCACAGCTTTTGTGTTTACAGG.....	23	1	24.00	22
	GTAAATATCTAAAGTTGAACTTGG.....	24	1	19.00	2
	GTAAATATCTAAAGTTGAACTTGGC.....	25	1	16.00	9
	CAGCTTTTGTGTTTACAG.....	19	1	8.00	6
	CACAGCTTTTGTGTTTAC.....	19	1	5.00	3
	ACAGCTTTTGTGTTTAC.....	18	1	3.00	3
	GTAAATATCTAAAGTTGAACTTGGCC.....	26	1	3.00	3
	GTAAATATCTAAAGTTGAAG.....	19	1	3.00	2
	GTAAATATCTAAAGTTGAACTT.....	22	1	3.00	2
	GTAAATATCTAAAGTTGAACTTG.....	23	1	2.00	2
	TAAATATCTAAAGTTGAACTTGGCC.....	25	1	2.00	1
	AATATCTAAAGTTGAACTTGGC.....	22	1	1.00	1
GAAGAAGCTGAAGTTCCTCATCTAT	TGGCAAGTCACAGCTTTTGTGTTTACAG.....	25	1	1.00	1
	TGGCAAGTCACAGCTTTTGTGTTTACAG.....	29	1	1.00	1
	TCACAGCTTTTGTGTTTACAGAG.....	24	1	1.00	1
	CAGCTTTTGTGTTTACAG.....	18	1	1.00	1
	GTCACAGCTTTTGTGTTTACAG.....	23	1	1.00	1
	AGTCACAGCTTTTGTGTTTAC.....	21	1	1.00	1
	AGTCACAGCTTTTGTGTTTACAG.....	23	1	1.00	1
	TAAATATCTAAAGTTGAACTTG.....	22	1	1.00	1
	GTAAATATCTAAAGTTGAACTTGGCCAA.....	28	1	1.00	1
	GTCACAGCTTTTGTGTTTAC.....	20	1	1.00	1
	GTAAATATCTAAAGTTGAACTTGGCCA.....	27	1	1.00	1
	TGGCCAATGGCAAGTCACAGCTTTTGTGTTTAC.....	34	1	1.00	1



CG31772_in12

Y-axis: Expression level (0 to 5000). X-axis: Position (0 to 120).

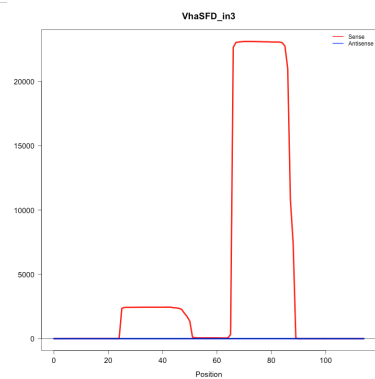
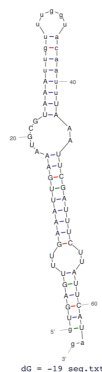
Legend: Sense (red line), Antisense (blue line).

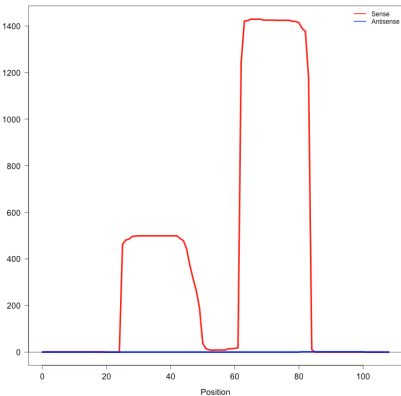
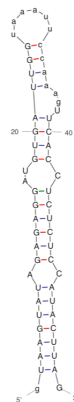
Position	Sense	Antisense
0	0	0
25	0	0
26	900	0
45	900	0
46	0	0
70	0	0
71	5100	0
90	5100	0
91	0	0
120	0	0

AGGACAACCAAGTGGCTGGACAAAAGGTTGGGGGACATTGATCTCGGAGACGGCGGTTTAACTGATCCATTCTCTCACATCACTTCCCTCACAGTGCACGGTGCTTGTACCAGAGTCC

	Size	Blast	Total Norm	# of libraries
.....TCTCACATCACTTCCTCCACAG.....	22	1	3715.00	69
.....TCTCACATCACTTCCTCCACA.....	21	1	788.00	44
GTTGGGGACATTGATCTCGGAG.....	23	1	416.00	35
.....CTCACATCACTTCCTCCACAGT.....	22	1	389.00	43
GTTGGGGACATTGATCTCGGAGA.....	24	1	334.00	25
GTTGGGGACATTGATCTCGGA.....	22	1	70.00	18
.....TCTCACATCACTTCCTCCAC.....	20	1	68.00	23
GTTGGGGACATTGATCTCGG.....	21	1	39.00	18
.....CTCACATCACTTCCTCCACAG.....	21	1	35.00	15
.....TCACATCACTTCCTCCACAGT.....	21	1	33.00	13
.....TCTCACATCACTTCCTCTCA.....	19	1	21.00	14
.....TCTCACATCACTTCCTCT.....	18	1	12.00	3
.....CTCACATCACTTCCTCCACA.....	20	1	12.00	9
GTTGGGGACATTGATCTCGGAGACG.....	26	1	12.00	6
.....CACATCACTTCCTCCACAG.....	19	1	9.00	9
.....TCACATCACTTCCTCCACAG.....	20	1	6.00	4
.....TCTCACATCACTTCCTCCACAGT.....	23	1	6.00	6
.....CACATCACTTCCTCCACAGT.....	20	1	5.00	4
.....CGGCGGTTTAAGTATCCATT.....	22	1	5.00	4
...GGGGACATTGATCTCGGAGA.....	21	1	3.00	1
GTTGGGGACATTGATCT.....	18	1	3.00	3
.....CTCACATCACTTCCTCCACAGTG.....	23	1	3.00	2
..TTGGGGACATTGATCTCGGAGA.....	23	1	3.00	3
.....TCTCACATCACTTCCTCCACAGTCA.....	26	1	2.00	1
.....CTCACATCACTTCCTCCAC.....	19	1	2.00	1
GTTGGGGACATTGATCTC.....	19	1	1.00	1
..TGGGGACATTGATCTCGG.....	19	1	1.00	1
.....CTCACATCACTTCCTCTCA.....	18	1	1.00	1
.....CTCTCACATCACTTCCTCCACAG.....	23	1	1.00	1
.....GACGCGGTTTAAGTATCCATT.....	24	1	1.00	1
GTTGGGGACATTGATCTCGGAGACG.....	27	1	1.00	1
.....ACATCACTTCCTCCACAG.....	18	1	1.00	1
.....ACATCACTTCCTCCACAGT.....	19	1	1.00	1
GTTGGGGACATTGATCTCG.....	20	1	1.00	1
.....CGGCGGTTTAAGTATCCATT.....	21	1	1.00	1
..TTGGGGACATTGATCTCGGAG.....	22	1	1.00	1
.....TCACATCACTTCCTCCACA.....	19	1	1.00	1
.....TCTCTCACATCACTTCCTCCACAG.....	24	1	1.00	1
GTTGGGGACATTGATCTCGGAGAC.....	25	1	1.00	1
.....GCACGGTGCTGTACACAGA.....	19	1	1.00	1

Plus strand

[illegible]



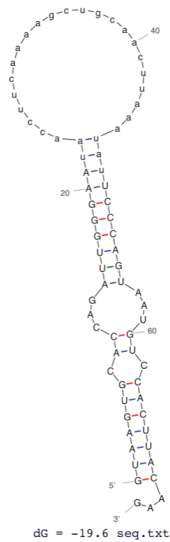
chr2R 10120609-10120717 -

TCCTTAAGAACTCCAAGCTTTTCCAAGTAAGTATAGAGAGGATGTGATTGGTAAATCCAAAGATTCACCTCTCTCCATACTAGTCGTCGAGGGGTATCATGCCCAT
(((((((.(((((.(((((((.....))))))..))))..)))))).....
 Plus strand

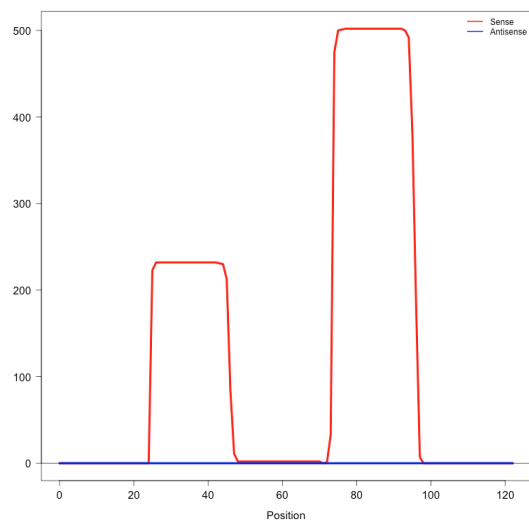
5' strand	Size	Blast	Total Norm	# of libraries
.....TTCACTCTCTCCACTACTTAGT.....	22	1	1014.00	108
.....TTCACTCTCTCCACTACTTAG.....	21	1	173.00	29
.....TCACCTCTCTCCACTACTTAGT.....	21	1	145.00	46
GTAAGTATAGAGAGGATGTGATTGG.....	25	1	144.00	21
GTAAGTATAGAGAGGATGTGATTC.....	24	1	72.00	18
GTAAGTATAGAGAGGATGTGA.....	21	1	64.00	35
GTAAGTATAGAGAGGATGTGATT.....	23	1	48.00	24
GTAAGTATAGAGAGGATGTGAT.....	22	1	46.00	22
GTAAGTATAGAGAGGATGTG.....	20	1	36.00	17
.....TTCACTCTCTCCACTACTCT.....	19	1	25.00	12
GTAAGTATAGAGAGGATGTGATTGGT.....	26	1	25.00	12
.....TCACCTCTCTCCACTACTTAG.....	20	1	18.00	8
.....TTCACTCTCTCCACTACTTA.....	20	1	12.00	9
GTAAGTATAGAGAGGATG.....	18	1	12.00	8
.....TCACCTCTCTCCACTACTTAGTC.....	22	1	11.00	5
GTAAGTATAGAGAGGATGT.....	19	1	11.00	9
.....ACCTCTCTCCACTACTTAGT.....	19	1	6.00	5
.....TTCACTCTCTCCACTACTCT.....	18	1	5.00	4
TAAGTATAGAGAGGATGTGATTGG.....	24	1	5.00	3
TAAGTATAGAGAGGATGTGA.....	20	1	5.00	4
.....AAAGTTCACCTCTCTCCACTACTTAG.....	25	1	5.00	2
GTAAGTATAGAGAGGATGTGATTGGTA.....	27	1	4.00	3
...AGTATAGAGAGGATGTGAT.....	19	1	4.00	4
...GATTGGTAAATCCAAAGTTCACCT.....	25	1	4.00	1
TAAGTATAGAGAGGATGTGATT.....	22	1	3.00	2
...AGTATAGAGAGGATGTGA.....	18	1	3.00	3
...AAGTATAGAGAGGATGTGAT.....	20	1	2.00	2
TAAGTATAGAGAGGATGT.....	18	1	2.00	1
.....AAATTCCAAAGTTCACCTCTCTCCATA.....	27	1	2.00	1
...AGTATAGAGAGGATGTGATTGGTAA.....	25	1	2.00	1
.....GTTCACCTCTCTCCACTACTTAGT.....	23	1	2.00	2
.....CACCTCTCTCCACTACTTAG.....	19	1	2.00	2
TAAGTATAGAGAGGATGTGAT.....	21	1	2.00	2
...AAGTATAGAGAGGATGTGATTGG.....	23	1	2.00	2
...GTATAGAGAGGATGTGAT.....	18	1	2.00	2
TAAGTATAGAGAGGATGTGATTG.....	23	1	1.00	1
.....AGTTCACCTCTCTCCACTACTTAGT.....	24	1	1.00	1
.....AGTTCACCTCTCTCCATA.....	18	1	1.00	1
...TTGGTAAATCCAAAGTTCACCTCTCT.....	27	1	1.00	1
TAAGTATAGAGAGGATGTGATTGGT.....	25	1	1.00	1
...AGTATAGAGAGGATGTGATTG.....	21	1	1.00	1
.....TTCCAAAGTTCACCTCTCTCCATAC.....	25	1	1.00	1
.....TAAATTCCAAAGTTCACCTCTCTCCATA.....	28	1	1.00	1
..CTTTAAGACTCCAAAGCTT.....	19	1	1.00	1
.....TATAGAGAGGATGTGATT.....	18	1	1.00	1
...AGTATAGAGAGGATGTGATTGG.....	22	1	1.00	1

[illegible]

Output of seq-graph (3)
by D. Stewart and M. Zuker



CG17560_in3



CG17560_in3

[chr3R_12444484-12444606 +](#)

CTGTCCATCTTCGACCGCGATCA**GTAAGTGCACCAGATTGGGAATAACCTTCAAAAAGCTGCAACTTAAATATTTCCAGTAATGTCCACTTACAAG**GAGCCCTCGTTGGATGGTGGACA
.....(((((((.....((((((((.....))))))))).....)))))).....)))))).....
Plus strand

	Size	Blast	Total Norm	# of libraries
.....TCCAGTAATGTCCACTTACA..	22	1	180.00	24
.....TCCAGTAATGTCCACTTACAAG	23	1	159.00	31
GTAAGTGCACCAGATTGGGA..	21	1	129.00	19
.....TCCAGTAATGTCCACTTACA..	21	1	90.00	22
GTAAGTGCACCAGATTGGGAAT..	22	1	68.00	16
GTAAGTGCACCAGATTGGGA..	20	1	17.00	9
.....TTCCAGTAATGTCCACTTACA..	22	1	17.00	5
.....CCAGTAATGTCCACTTACAAG	22	1	14.00	7
.....TTCCAGTAATGTCCACTTACA..	23	1	12.00	7
GTAAGTGCACCAGATTGGGAATA..	23	1	7.00	5
TAAGTGCACCAGATTGGGAAT..	21	1	6.00	3
.....CCAGTAATGTCCACTTACA..	21	1	6.00	3
.....TCCAGTAATGTCCACTTAC..	20	1	6.00	4
.....TCCAGTAATGTCCACTTACAAGG..	24	1	5.00	2
.....CCAGTAATGTCCACTTACA..	20	1	3.00	3
.....TCCAGTAATGTCCACTTA..	19	1	2.00	2
.....TTCCAGTAATGTCCACTTAC..	21	1	2.00	1
TAAGTGCACCAGATTGGGAATA..	22	1	2.00	1
.....CCAGTAATGTCCACTTACAAGG..	23	1	2.00	1
TAAGTGCACCAGATTGGGA..	20	1	1.00	1
.....TAACCTTCAAAAAGCTGCAACTTAAA..	25	1	1.00	1
.....TTCCAGTAATGTCCACTTACAAG	24	1	1.00	1
GTAAGTGCACCAGATTGG..	18	1	1.00	1
.....AACCTTCAAAAAGCTGCAACTTAAA..	24	1	1.00	1
GTAAGTGCACCAGATTGGG..	19	1	1.00	1
.....CCAGTAATGTCCACTTACA..	19	1	1.00	1
.....CAGTAATGTCCACTTACA..	19	1	1.00	1
.....ATTCCAGTAATGTCCACTTACA..	23	1	1.00	1

dG = -18.3 seq.txt



[chr3R 26617332-26617443 -](#)

	Size	Blast	Total Norm	# of libraries
.....ATAAAGTATGCCGAACTCGC.....	21	1	1361.00	129
.....ATAAAGTATGCCGAACTCGCAG.....	23	1	1281.00	120
.....ATAAAGTATGCCGAACTCG.....	20	1	1048.00	112
.....TAAAGTATGCCGAACTCGCAG.....	22	1	302.00	81
.....ATAAAGTATGCCGAACTCGCA.....	22	1	288.00	74
.....TAAAGTATGCCGAACTCGCA.....	21	1	69.00	30
.....TAAAGTATGCCGAACTCGC.....	20	1	34.00	18
.....AAAAGTATGCCGAACTCGCAG.....	21	1	33.00	20
.....ATAAAGTATGCCGAACTC.....	19	1	25.00	17
GTGAGTTTCGTACACTTAATT.....	21	1	22.00	13
GTGAGTTTCGTACACTTAATTA.....	22	1	11.00	8
.....TAATAGGATCGGCCGTTAAT.....	20	1	6.00	5
.....AATAGGATCGGCCGTTAAT.....	19	1	6.00	5
.....ATAAAGTATGCCGAACTC.....	18	1	6.00	4
.....AATAAAGTATGCCGAACTCGC.....	22	1	6.00	4
GTGAGTTTCGTACACTTAAT.....	20	1	5.00	5
.....TAAAGTATGCCGAACTCG.....	19	1	4.00	4
.....AGTATGCCGAACTCGCAG.....	18	1	4.00	2
.....AATAGGATCGGCCGTTAA.....	18	1	3.00	3
.....GCCACCGTGCTGGAGAG.....	18	1	3.00	2
.....AAAGTATGCCGAACTCGCAG.....	20	1	3.00	3
GTGAGTTTCGTACACTTA.....	18	1	3.00	3
.....AAGTATGCCGAACTCGCAG.....	19	1	2.00	1
GTGAGTTTCGTACACTTAATTAATAGG.....	27	1	2.00	2
.....GGCAGCGGATGCGCGATCACC.....	21	1	2.00	1
GTGAGTTTCGTACACTTAATTAATAGGAT.....	29	1	2.00	2
.....TAGGATCGGCCGTTAATAAA.....	20	1	1.00	1
.....TAAAGTATGCCGAACTC.....	18	1	1.00	1
.....TAATAGGATCGGCCGTTAATAAAGT.....	26	1	1.00	1
.....TTAATAGGATCGGCCGTTAAT.....	21	1	1.00	1
.....AAAAGTATGCCGAACTCGCAGG.....	22	1	1.00	1
.....GATGCGCGATCACCAAGA.....	19	1	1.00	1
.....ATAAAGTATGCCGAACTCGCAGG.....	24	1	1.00	1
.....AATAAAGTATGCCGAACTCG.....	21	1	1.00	1
.....AATAAAGGATCGGCCGTTAATA.....	24	1	1.00	1
GACCGAAGCCACCGTGC.....	18	1	1.00	1

[illegible]

	Size	Blast	Total Norm	# of libraries
GTAAGCATTGCAAAATGTAGTTGTT.....	25	1	120.00	42
.....CAACATTTACAATGTTTGCA	21	1	85.00	40
.....ACAACATTTACAATGTTTGC..	20	1	81.00	17
.....CAACATTTACAATGTTTGCA..	20	1	53.00	22
.....CAACATTTACAATGTTTGC..	19	1	50.00	11
GTAAGCATTGCAAAATGTAGTTG.....	23	1	47.00	13
.....ACAACATTTACAATGTTTGCA..	21	1	45.00	16
GTAAGCATTGCAAAATGTAGTTGTTA.....	26	1	41.00	21
GTAAGCATTGCAAAATGTAGTT.....	22	1	27.00	19
.....ACAACATTTACAATGTTTGCA	22	1	15.00	10
GTAAGCATTGCAAAATGTAGTTGT.....	24	1	6.00	5
GTAAGCATTGCAAAATGTAGT.....	21	1	5.00	5
.....CAACATTTACAATGTTTGCA	22	1	4.00	3
.....ACAACATTTACAATGTTTG...	19	1	4.00	1
.....AATTCGCTCTTCAATCATT.....	20	1	2.00	2
GTAAGCATTGCAAAATGTAGTTGTTAA.....	27	1	2.00	1
AGACATCCGGGATAAGCA.....	18	1	1.00	1
.....TGTTTGCA	19	1	1.00	1
TAAGCATTGCAAAATGTAGTTG.....	22	1	1.00	1
.....AAATTCGCTCTTCAATCATTAA.....	22	1	1.00	1
GTAAGCATTGCAAAATGTAGTTGTTAAA.....	28	1	1.00	1
..AAGCATTGCAAAATGTAGTTGT.....	22	1	1.00	1
.....TGTTTGCA	21	1	1.00	1
GTAAGCATTGCAAAATGTAGTTGTTAAAT.....	29	1	1.00	1
.....AACATTTACAATGTTTGCA	20	1	1.00	1
.....AAATTCGCTCTTCAATCATT.....	20	1	1.00	1

dg = -15.5 seq.txt



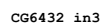
GCCATGATGCCACCATTCTGACCTG**TGAGTGTGATCGATTTCGAGGTTTGGCACACGAATATAATCTGGAATCTTTAATCTCGCAG**TCCCAACCGAAATGTCAGTGTTCGT
 ((((((((((.(((((((.(((((((.(((((((.)))))))))))))))))))))))))).....
 Plus strand

	Size	Blast	Total Norm	# of libraries
.....TCTGGAATCTTTAATTTCGCAG.....	21	1	3208.00	118
.....TCTGGAATCTTTAATTTCGCAGT.....	22	1	1270.00	107
.....TCTGGAATCTTTAATTTCGCA.....	20	1	424.00	90
GTGAGTTGATCGATTTCGAGGTT.....	23	1	381.00	52
.....TCTGGAATCTTTAATTTCGC.....	19	1	141.00	34
.....TCTGGAATCTTTAATTTCGCAGTT.....	23	1	113.00	47
GTGAGTTGATCGATTTCGAGGT.....	22	1	20.00	12
.....TCTGGAATCTTTAATTTCG.....	18	1	19.00	13
.....CTGGAATCTTTAATTTCGCAG.....	20	1	15.00	7
.....CTGGAATCTTTAATTTCGCAGT.....	21	1	5.00	5
GTGAGTTGATCGATTTCGAGGTTT.....	24	1	5.00	3
.....ATCTGGAATCTTTAATTTCGCAG.....	22	1	3.00	3
GTGAGTTGATCGATTTCGAGG.....	21	1	3.00	3
GTGAGTTGATCGATTTCGA.....	19	1	3.00	2
.....TGGAATCTTTAATTTCGCAGT.....	20	1	2.00	2
.....TGGAATCTTTAATTTCGCAG.....	19	1	2.00	2
.....GATTTCGAGGTTTTTGGCACA.....	20	1	2.00	1
.....ATCTGGAATCTTTAATTTCGCAGT.....	23	1	1.00	1
GTGAGTTGATCGATTTCGAGTTTT.....	25	1	1.00	1
.....TTCCCACCGAAATGTCAGTGT.....	21	1	1.00	1
GTGAGTTGATCGATTTCGAG.....	20	1	1.00	1
.....GGAATCTTTAATTTCGCAGT.....	19	1	1.00	1
.....GTTTGGCACACGAATATAA.....	20	1	1.00	1



AAATACATTTAGCAATAAGTTAGAC**GTGAGTATGGCTATACAATCATCTGGAAACGTAACTCTAATGTATGTAATTGTATGTTGTATTTCGAG**TTTTATGATAGCAAAAGGTCCTCATG
 ((((((((((.(((((((.((((((((((.....)))))).....)))..))))).....)))))).....)))))).....)))))).....)))))).....
 Plus strand

	Size	Blast	Total Norm	# of libraries
.....TATTGTATGTTGTAATTGCAGT.....	22	1	1381.00	84
.....TATTGTATGTTGTAATTGCAG.....	21	1	710.00	78
.....TATTGTATGTTGTAATTGCA.....	20	1	179.00	37
.....TATTGTATGTTGTAATTGC.....	19	1	28.00	16
GTGAGTATGGCTATACAAATCATCTGGA.....	28	1	16.00	4
.....ATTGTATGTTGTAATTGCAG.....	20	1	7.00	6
.....TATTGTATGTTGTAATTGCAGTT.....	23	1	6.00	6
.....TATTGTATGTTGTAATTG.....	18	1	5.00	3
.....ATTGTATGTTGTAATTGCAGTT.....	21	1	4.00	4
.....TGTATGTTGTAATTGCAGT.....	19	1	4.00	4
.....TGTATGTTGTAATTGCAG.....	19	1	4.00	3
.....TGTATGTTGTAATTGCAGT.....	20	1	4.00	2
.....GTATGTTGTAATTGCAGT.....	18	1	3.00	3
.....AATCATCTGGAACGTAAGTT.....	20	1	3.00	3
GTGAGTATGGCTATACAAATCATCTGGAA.....	29	1	3.00	2
.....ATCATCTGGAACGTAAGTT.....	19	1	3.00	2
GTGAGTATGGCTATACAAATCATC.....	24	1	3.00	2
GTGAGTATGGCTATACAAATCA.....	22	1	2.00	2
.....TAAGTTCTAATGTATGTATTGTA.....	23	1	2.00	2
GTGAGTATGGCTATACAAA.....	19	1	2.00	2
.....TGTATGTTGTAATTGCAG.....	18	1	2.00	2
.....TGTATGTATTGTATGTGTGTT.....	19	1	2.00	2
.....TGTATTGTATGTTGTAATTGCAGT.....	24	1	2.00	1
.....TAAGTTCTAATGTATGTATTGTATG.....	25	1	2.00	2
.....AAATCATCTGGAACGTAAGTT.....	21	1	2.00	2
GTGAGTATGGCTATACAAATCATCTGG.....	27	1	1.00	1
TAAGTTAGACGTGAGTATGGCTATACAAA.....	29	1	1.00	1
.....TGTATGTTGTAATTGCAGTT.....	20	1	1.00	1
.....TGTATGTATTGTATGTTGTAATTGCAGT.....	28	1	1.00	1
.....ATTGTATGTTGTAATTGCA.....	19	1	1.00	1
.....TACAAATCATCTGGAACGTAAGTTCTAAT.....	29	1	1.00	1
.....TCATCTGGAACGTAAGTTCTAATGTATG.....	28	1	1.00	1
.....TCTAATGTATGTATTGTATGT.....	21	1	1.00	1
.....ATGTATGTATTGTATGTTGT.....	20	1	1.00	1
GTGAGTATGGCTATACAA.....	18	1	1.00	1
.....GTATTGTATGTTGTAATTGCAG.....	22	1	1.00	1
.....TGTATGTATTGTATGTTGTAATTGCAG.....	27	1	1.00	1
TACATTAGCAATAAGTTAGACGTGAGT.....	28	1	1.00	1
.....GCTATACAAATCATCTGGAACGTAAG.....	26	1	1.00	1
.....ATACAAATCATCTGGAACGTAAGTTCTA.....	28	1	1.00	1
.....TTGCAGTTTATGATAGCAAAGGT.....	24	1	1.00	1



GCCTTGCCACATCATGGGCTACGACG**GTGAGTAGTCGCCAGTTAGCTTGGCTGAGTGAGGATTTAAGTCCTGGGACATCTCTCTGCGAG**TCAAGATCCTGAAGCGGACGGCAG
 ((((((((((((((((((((((((((((((((((((((((((((((((.....
 Plus strand

	Size	Blast	Total Norm	# of libraries
.....TCCTGGGACATCTCTCTTGCAG.....	22	1	418.00	37
.....TCCTGGGACATCTCTCTTGC..	21	1	133.00	24
.....TCCTGGGACATCTCTCTTGCAGT.....	23	1	64.00	21
GTGAGTGATGCTCCAGTTAGCT.....	22	1	44.00	21
.....TGGCTGAGTGAGGATTTAAG.....	20	1	43.00	12
GTGAGTGATGCTCCAGTTAGC.....	21	1	24.00	13
GTGAGTGATGCTCCAGTTAGCTT.....	23	1	19.00	9
.....TCCTGGGACATCTCTCTTGC..	20	1	17.00	9
GTGAGTGATGCTCCAGTTAG.....	20	1	16.00	7
.....GTCCTGGGACATCTCTCTTGC..	21	1	15.00	12
GTGAGTGATGCTCCAGTTAGCTTG.....	24	1	9.00	8
.....AGTCCTGGGACATCTCTCTTGC..	22	1	9.00	5
.....TCCTGGGACATCTCTCTTG... ..	19	1	6.00	6
.....TCCTGGGACATCTCTCTTGCAGTC.....	24	1	4.00	2
.....AGTCCTGGGACATCTCTCTTG... ..	21	1	3.00	2
.....GTCCTGGGACATCTCTCTTG... ..	20	1	3.00	2
GTGAGTGATGCTCCAGTTA.....	19	1	2.00	2
GTGAGTGATGCTCCAGTT.....	18	1	2.00	1
.....GTCCTGGGACATCTCTCTTGC..	22	1	1.00	1
.....GGACATCTCTCTTGCAGTCAAGATC.....	25	1	1.00	1
.....CCACTCATGGGCTACGACG.....	19	1	1.00	1
.....TCCTGGGACATCTCTCTT.....	18	1	1.00	1
.....TCCTGGGACATCTCTCTTGCAGTCAAGATCCTGA.....	34	1	1.00	1
.....CCTGGGACATCTCTCTTGCAGTC.....	23	1	1.00	1
GTGAGTGATGCTCCAGTTAGCTTG.....	25	1	1.00	1
.....AGTCCTGGGACATCTCTCTT.....	20	1	1.00	1

