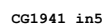
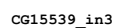


[illegible][illegible]

	Size	Blast	Total Norm	# of libraries
.....ATTGTATCCGGTCTTCATTTTAG	23	1	16.00	11
.....ATTGTATCCGGTCTTCATTT...	20	1	6.00	3
.....ATTGTATCCGGTCTTCATTTT..	21	1	5.00	4
GTAGGTTGAAATCGGATACAACATA.....	24	1	4.00	4
.....TTAATTGTATCCGGTCTTCAT....	21	1	2.00	1
GTAGGTTGAAATCGGATACAACAT.....	23	1	2.00	2
..AGGTTGAAATCGGATACAACAT.....	21	1	1.00	1
.....ATTGTATCCGGTCTTCATTTTTA..	22	1	1.00	1
..TAGGTTGAAATCGGATACAACAT.....	22	1	1.00	1
.....TTGTATCCGGTCTTCATTTTAG	22	1	1.00	1
..GGTTGAAATCGGATACAACATA.....	21	1	1.00	1
.....ATCCGGTCTTCATTTTAGG.....	19	1	1.00	1

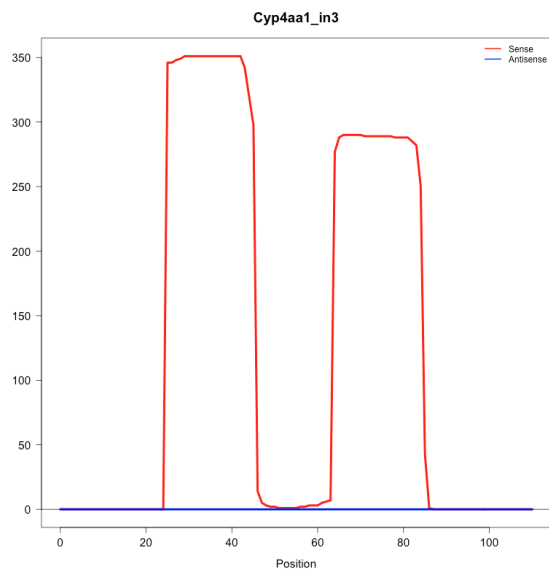
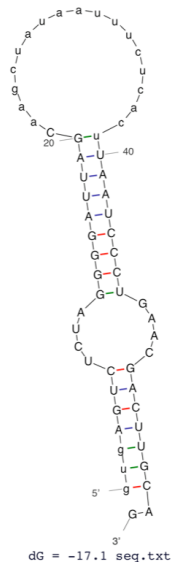
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TTCTGTCGAGATTCAAGATGAACCTG**GTAGGATTTTAAGCATTAAAGCATGTATATAGTTTTTGTCTGCTCATAAAGTTCTATAAG**GTTCTCGATACTTGGCCATGAGTGA
 ((((((((((((((((((((.....(((.....((.....)).....)))))))))).....)))))))))).....
 Plus strand

	Size	Blast	Total Norm	# of libraries
.....CTGTGCTCATAAAGTTCTATAG.....	22	1	3.00	3
GTAGGATTTTAAGCATTAAAGCA.....	22	1	1.00	1
.....TAGTTTTTGTGTGCTCATAAAGT.....	24	1	1.00	1
.....TGTGCTCATAAAGTTCTATAG.....	21	1	1.00	1

Output of ss_graph (2)
by D. Stewart and M. Zuker



Cyp4aa1_in3

[chr2R_11833366-11833476 +](#)

AACTGTGTACTGGACATACTAAATG**GTGAGTCTCTAGGGGATTAGCAAGCTATAATTTCTCACTTAATCCCTGAACGACTTGCAG**AGGCCGTTTGGGTGTGCCGATCAA
.....(((((((.....(((((((.....)))))))))).....)))))).....
Plus strand

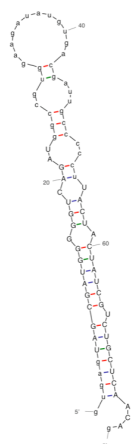
	Size	Blast	Total Norm	# of libraries
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.....TAATCCCTGAACGACTTGCAG	21	1	201.00	54
.....TAATCCCTGAACGACTTGCAG A.....	22	1	36.00	21
.....TAATCCCTGAACGACTTGC A.....	20	1	30.00	15
..... GTGAGTCTCTAGGGGATTA	19	1	23.00	11
..... GTGAGTCTCTAGGGGATTAG	20	1	22.00	12
..... GTGAGTCTCTAGGGGATT	18	1	9.00	4
..... GTGAGTCTCTAGGGGATTAGCA	22	1	8.00	5
.....AATCCCTGAACGACTTGCAG A.....	21	1	6.00	5
.....AATCCCTGAACGACTTGCAG	20	1	5.00	5
.....TAATCCCTGAACGACTTGC	19	1	2.00	2
.....ACTTAATCCCTGAACGACTTG	21	1	2.00	1
.....ATCCCTGAACGACTTGCAG	19	1	2.00	2
..... GTGAGTCTCTAGGGGATTAGCAA	23	1	2.00	2
.....CTTAATCCCTGAACGACTTG	20	1	1.00	1
.....GCAAGCTATAATTTCTCACTTAATCCC	27	1	1.00	1
.....GAGTCTCTAGGGGATTAGC	19	1	1.00	1
.....TAATCCCTGAACGACTTGCAG AG.....	23	1	1.00	1
.....GTCTCTAGGGGATTAGCA	18	1	1.00	1
.....GAGTCTCTAGGGGATTAGCAAGCT	24	1	1.00	1
.....TTCTCACTTAATCCCTGAACGACTTGC	27	1	1.00	1
.....TTAATCCCTGAACGACTTGC A.....	21	1	1.00	1
.....CTCACTTAATCCCTGAACGA	20	1	1.00	1
.....AGTCTCTAGGGGATTAGC	18	1	1.00	1
.....GTCTCTAGGGGATTAGCAAG	20	1	1.00	1



[chr3R 4134127-4134232 -](#)

CGAGCAGCGGTCGCACATGTCTAAGGTGAGCAGCATGGCCACATTATTGGGCAACCAATGAATTCGCCGCTGCCACAGGTTCACTCGGTCTGCTGGAATCGCG
(((.....(((.....((((((((.....)))))))))).....)))))).....))
 Plus strand

	Size	Blast	Total Norm	# of libraries
GTGAGCACGATGCCACATTTATT	24	1	42.00	17
GTGAGCACGATGCCACATTTATTGGA	21	1	12.00	9
GTGAGCACGATGCCACATTTATTGGA	20	1	7.00	5
GTGAGCACGATGCCACATTTATTGGA	18	1	4.00	4
GTGAGCACGATGCCACATTTATTGGA	27	1	4.00	3
GTGAGCACGATGCCACATTTATTG	23	1	3.00	2
GTGAGCACGATGCCACATTTATTGGA	26	1	2.00	2
GTGAGCACGATGCCACATTTATTGGA	19	1	2.00	1
GTGAGCACGATGCCACATTTATTGGA	19	1	2.00	2
GTGAGCACGATGCCACATTTATTG	22	1	2.00	2
GTGAGCACGATGCCACATTTATTGGA	21	1	1.00	1
GTGAGCACGATGCCACATTTATTGGA	18	1	1.00	1
GTGAGCACGATGCCACATTTATTGGA	26	1	1.00	1
GTGAGCACGATGCCACATTTATTGGA	21	1	1.00	1
GTGAGCACGATGCCACATTTATTGGA	25	1	1.00	1
GTGAGCACGATGCCACATTTATTGGA	18	1	1.00	1

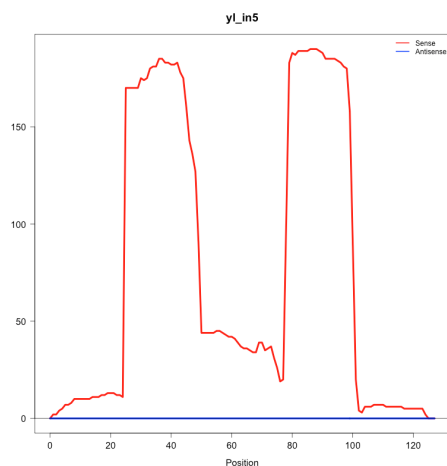


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y1 in5      dG = -23.9 seq.txt
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chrX_14093552-14093679_+

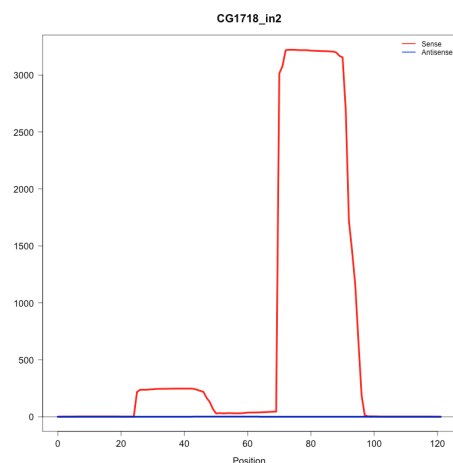
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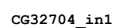
5'	strand	3'	Size	Blast	Total	# of libraries
.....		TACTATATGTTCTGCTCAAA.....	22	1	48.00	23
.....		GGATAGATAGGTTGGTCAATG.....	25	1	47.00	10
.....		GGATAGATAGGTTGGTCAATG.....	24	1	39.00	15
.....		TACTACTATATGTTCTGCTCAAA.....	22	1	39.00	17
.....		TACTACTATATGTTCTGCTCAAA.....	21	1	23.00	13
.....		TACTACTATATGTTCTGCTCAAA.....	21	1	19.00	4
.....		TACTACTATATGTTCTGCTCAAA.....	23	1	15.00	13
.....		TACTACTATATGTTCTGCTCAAA.....	21	1	18.00	9
.....		TACTACTATATGTTCTGCTCAAA.....	20	1	15.00	5
.....		GGATAGATAGGTTGGTCAATG.....	22	1	12.00	7
.....		TACTACTATATGTTCTGCTCAAA.....	26	1	10.00	7
.....		TACTACTATATGTTCTGCTCAAA.....	23	1	9.00	7
.....		TACTACTATATGTTCTGCTCAAA.....	19	1	6.00	5
.....		TACTACTATATGTTCTGCTCAAA.....	23	1	6.00	4
.....		ATCTATATGTTCTGCTCAAA.....	20	1	5.00	2
.....		TACTACTATATGTTCTGCTCAAA.....	18	1	5.00	4
.....		TACTACTATATGTTCTGCTCAAA.....	24	1	4.00	4
.....		CTGGAGATATGTTCTGCTCAAA.....	23	1	4.00	3
.....		CTGGAGATATGTTCTGCTCAAA.....	25	1	4.00	4
.....		TACTACTATATGTTCTGCTCAAA.....	24	1	4.00	2
.....		TACTACTATATGTTCTGCTCAAA.....	20	1	3.00	2
.....		TACTACTATATGTTCTGCTCAAA.....	22	1	3.00	2
.....		TACTACTATATGTTCTGCTCAAA.....	27	1	3.00	2
.....		TACTACTATATGTTCTGCTCAAA.....	20	1	3.00	3
.....		TACTACTATATGTTCTGCTCAAA.....	18	1	3.00	1
.....		CTGGAGATATGTTCTGCTCAAA.....	26	1	3.00	3
.....		TACTACTATATGTTCTGCTCAAA.....	26	1	2.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	22	1	2.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	24	1	2.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	21	1	2.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	26	1	2.00	2
.....		TACTACTATATGTTCTGCTCAAA.....	24	1	2.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	26	1	2.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	26	1	2.00	2
.....		TACTACTATATGTTCTGCTCAAA.....	19	1	2.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	24	1	2.00	2
.....		TACTACTATATGTTCTGCTCAAA.....	24	1	2.00	2
.....		TACTACTATATGTTCTGCTCAAA.....	22	1	2.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	25	1	1.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	26	1	1.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	21	1	1.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	19	1	1.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	20	1	1.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	24	1	1.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	18	1	1.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	25	1	1.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	25	1	1.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	18	1	1.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	26	1	1.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	19	1	1.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	23	1	1.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	26	1	1.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	26	1	1.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	19	1	1.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	25	1	1.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	22	1	1.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	27	1	1.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	21	1	1.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	18	1	1.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	24	1	1.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	21	1	1.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	28	1	1.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	20	1	1.00	1
.....		TACTACTATATGTTCTGCTCAAA.....	24	1	1.00	1



Plus strand

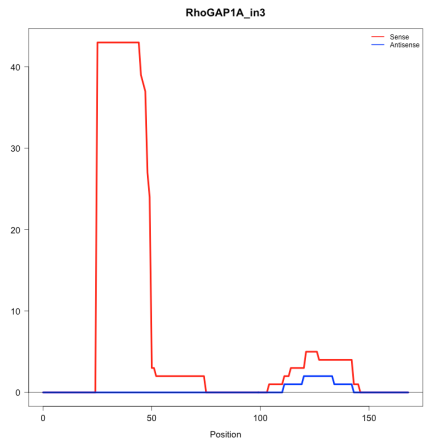
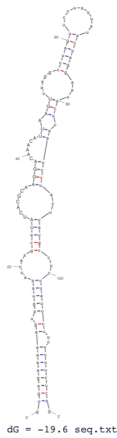
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.....ACTCAGGATTTCATTCACTT.....	21	1	463.00	64
.....ACTCAGGATTTCATTCACTGAG.....	26	1	434.00	67
.....ACTCAGGATTTCATTCACTGCGA.....	25	1	428.00	59
.....ACTCAGGATTTCATTCACTTTC.....	24	1	276.00	48
.....ACTCAGGATTTCATTCACTGTT.....	23	1	258.00	39
.....ACTCAGGATTTCATTCACTGAGT.....	27	1	115.00	44
.....CTAAGTCACTATCGGATTGTGTG.....	25	1	53.00	28
.....CTAAGTCACTATCGGATTG.....	24	1	52.00	21
.....CTAAGTCACTATCGGATTG.....	22	1	50.00	18
.....TCAGGCGATTTCATTCACTGCGA.....	23	1	43.00	24
.....TCAGGCGATTTCATTCACTGAGT.....	25	1	41.00	28
.....TCAGGCGATTTCATTCACTGCGAG.....	24	1	29.00	16
.....CTCAGGCGATTTCATTCACTG.....	23	1	28.00	20
.....ACTCAGGCGATTTCATTCA.....	19	1	28.00	14
.....CTCAGGCGATTTCATTCACTGCGA.....	24	1	19.00	12
.....TCAGGCGATTTCATTCACTGTC.....	22	1	14.00	9
.....CTCAGGCGATTTCATTCACTGCGAG.....	26	1	14.00	12
.....TTATTGAACCTAGAGGCTCTCTC.....	20	1	14.00	8
.....ACTCAGGCGATTTCATTCACT.....	20	1	12.00	8
.....CTCAGGCGATTTCATTCACTGCGAG.....	25	1	12.00	11
.....CTAAGTCACTATCGGATT.....	20	1	10.00	5
.....TCAGGCGATTTCATTCACTTT.....	20	1	9.00	2
.....CTAAGTCACTATCGGATTGTG.....	22	1	8.00	6
.....ACTCAGGCGATTTCATTCTC.....	18	1	8.00	2
.....CTAAGTCACTATCGGATTCT.....	21	1	8.00	8
.....ACTCAGGCGATTTCATTCACTGCGAT.....	28	1	8.00	2
.....CTCAGGCGATTTCATTCACTGTC.....	19	1	8.00	8
.....CTCAGGCGATTTCATTCACTGTC.....	23	1	7.00	7
.....CTCAGGCGATTTCATTCACTGTC.....	23	1	6.00	6
.....CTCAGGCGATTTCATTCACTTT.....	21	1	5.00	3
.....CTCAGGCGATTTCATTCACTGTT.....	22	1	4.00	3
.....CTAAGTCACTATCGGATTGTGTG.....	26	1	4.00	3
.....CTAAGTCACTATCGGATTG.....	21	1	3.00	3
.....CTAAGTCACTATCGGATTGTGTG.....	24	1	3.00	3
.....CATTTCATTCACTGCGAGT.....	19	1	3.00	2
.....TCAGGCGATTTCATTCACTGTT.....	21	1	3.00	3
.....TTATTGAACCTAGAGGCTCTCACTAGAG.....	27	1	2.00	2
.....CAGGCGATTTCATTCACTGCGAG.....	24	1	2.00	2
.....TCAGGCGATTTCATTCACTGCGAG.....	18	1	2.00	2
.....CTCAGGCGATTTCATTCACTCT.....	20	1	2.00	2
.....TAGCGCGCGCACTCAGGCGATTGAG.....	26	1	2.00	1
.....CTAAGTCACTATCGGATTGTG.....	20	1	2.00	2
.....TTATTGAACCTAGAGGCTCTCACTAG.....	25	1	2.00	2
.....AGGCGATTTCATTCACTCTT.....	18	1	1.00	1
.....GACTATCGGCGATTGTGTGTT.....	21	1	1.00	1
.....GACTATCGGCGATTGTG.....	27	1	1.00	1
.....GACTATCGGCGATTGTG.....	18	1	1.00	1
.....TATTGAACCTAGAGGCTCTCACTAGAG.....	26	1	1.00	1
.....GACTCAGGCGATTTCATTCACTGCGA.....	26	1	1.00	1
.....AGCGCGCGCACTCAGGCGATTCACTGCGA.....	30	1	1.00	1
.....ATGCGCGGATTGTGTGTTATTGAACCT.....	25	1	1.00	1
.....ATTTCATTCACTGCGAGT.....	18	1	1.00	1
.....GGCGGATTGTGTGTTATTG.....	19	1	1.00	1
.....TTAGCGCTCTCACTCAAGGCG.....	20	1	1.00	1
.....GTGATATCGGCGATTGTGTGTT.....	23	1	1.00	1
.....CGTCTCACTCAAGGCGATTCACT.....	24	1	1.00	1
.....TGCACTCAGGCGATTTCATTCACTGCGAG.....	29	1	1.00	1
.....TCGCGCTCAAGGATTT.....	18	1	1.00	1
.....TGAACTTAGCGCTCTCACTCAAGGCG.....	25	1	1.00	1
.....TGAACTTAGCGCTCTCACTCAAGGCGA.....	26	1	1.00	1
.....TTATTGAACCTAGAGGCTCTC.....	19	1	1.00	1
.....CTGACGCTACAGTACACTAAG.....	19	1	1.00	1
.....TGATATCGGCGATTGTGTGTT.....	21	1	1.00	1
.....TTATTGAACCTAGAGGCTCTC.....	19	1	1.00	1
.....TTAGCGCTCTCACTCAAGGCGATTCTCA.....	26	1	1.00	1
.....CTTAGCGCTCTCACTCAAGGATTT.....	25	1	1.00	1
.....TAGCGCGCGCACTCAAGGCG.....	19	1	1.00	1
.....CTCAGGCGATTTCATTCACTGCGAT.....	27	1	1.00	1
.....ACTATCGGCGATTGTGTGTTATT.....	23	1	1.00	1
.....TAGCGCTCTCACTCAAGGCGAT.....	21	1	1.00	1
.....CTAAGTCACTATCGGCGATTGTGTGTT.....	27	1	1.00	1
.....TAGCGCTCTCACTCAAGGCGA.....	20	1	1.00	1
.....CAGGCGATTTCATTCACTGCGA.....	22	1	1.00	1
.....CTGCACTCAAGGCGATTTCATTCTCA.....	23	1	1.00	1
.....ATCCCTGCGACGTACACTCA.....	18	1	1.00	1
.....TCAGGCGATTTCATTCACTGCGATCATC.....	30	1	1.00	1
.....GCACTCAGGCGATTTCATTCACTGCGAT.....	29	1	1.00	1
.....TTTAGAGCTTAGCGCTCTCACTCAAGGCGA.....	27	1	1.00	1





GCTGGCTCGGAAGTACTCAAGATAA**G**TGGGTGTTCTTGGAATTCGCCTCGATCGGTAGCTAAATTCTGTA**A**CTCCTAA**AAG**CCTTTGGATTGAGCCTGTTCACG
(((.(.((((((((.(.(.....))).....)))))))).).)))).
 Plus strand

	Size	Blast	Total Norm	# of libraries
.....AAATTTCGTATTACTCCTAAAA.....	22	1	9.00	5
.....AAATTTCGTATTACTCCTAA.....	20	1	7.00	3
GTGGGTGTTCTTGGAAATTCGC.....	22	1	5.00	5
.....AAATTTCGTATTACTCCTAAA.....	21	1	4.00	3
.....AAATTTCGTATTACTCCTAAAAG.....	23	1	2.00	2
.....CCTTTTGGATTGAGCCTG.....	18	1	2.00	2
GTGGGTGTTCTTGGAAATTCG.....	21	1	1.00	1
GTGGGTGTTCTTGGAAATTC.....	20	1	1.00	1



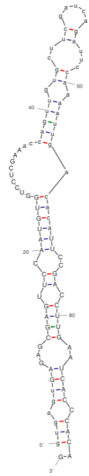
RhoGAP1A_in3

chrX 29746-29914 +

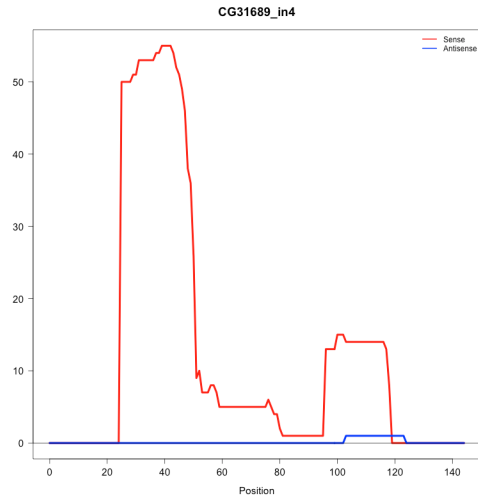
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Plus strand

	Size	Blast	Total Norm	# of libraries
GTGAGAAAAGTAGTAAATTAAAGCA.....	25	1	23.00	10
GTGAGAAAAGTAGTAAATTAAAG.....	23	1	10.00	6
GTGAGAAAAGTAGTAAATT.....	20	1	4.00	4
GTGAGAAAAGTAGTAAATTAAAGC.....	24	1	3.00	3
.....CCTCTTATCTCTTTTCTCAG	22	1	2.00	2
.....TATCACGCCAAGGACAAACATTAAAGT.....	25	1	2.00	1
.....ACTTATGCTCTTATCTCTTTTCTCAG	29	1	1.00	1
GTGAGAAAAGTAGTAAATTAA.....	21	1	1.00	1
GTGAGAAAAGTAGTAAATTAA.....	22	1	1.00	1
.....CCTACTTATGCTCTTATCTCTTTTCTCAGACC.....	35	1	1.00	1
GTGAGAAAAGTAGTAAATTAAAGCATA.....	27	1	1.00	1
.....ACTCAATCCTACTTATGCTCTT.....	23	1	1.00	1



dG = -18.3 seq.txt

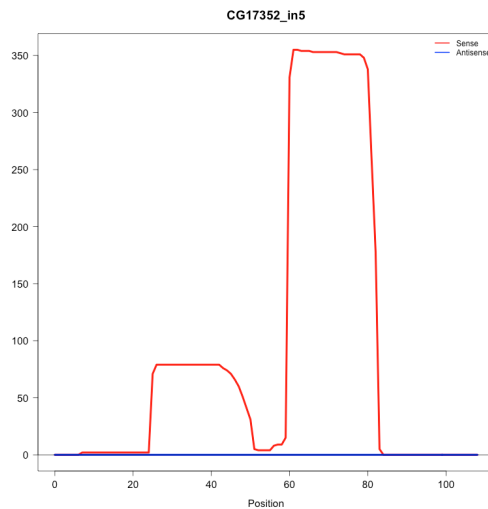
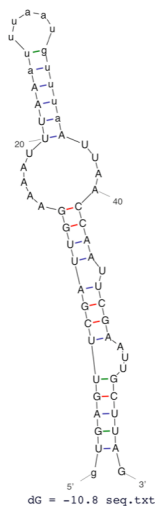


CG31689_in4

chr2L 2737542-2737686 +

[illegible]

	Size	Blast	Total Norm	# of libraries
GTGAGTGAGAGCGAGTTCCAATGTGG	26	1	18.00	11
GTGAGTGAGAGCGAGTTCCAATGTG	25	1	9.00	7
GTGAGTGAGAGCGAGTTCCAATG	23	1	8.00	6
.TTCCGACCTTGAATCACCACAG	23	1	8.00	6
GTGAGTGAGAGCGAGTTCCAATGTGGTC	28	1	3.00	1
.TTCCGACCTTGAATCACCACA	22	1	3.00	3
GTGAGTGAGAGCGAGTTCCAAT	22	1	3.00	3
.GACCTTGAATCACCACA	18	1	2.00	1
GTGAGTGAGAGCGAGTTCCAA	21	1	2.00	2
.GAGAGCGAGTTCCAATGTGGTCTCTGAA	28	1	2.00	1
GTGAGTGAGAGCGAGTTCCAATGT	24	1	2.00	2
.CCTCGAAACCAGTTGTGCTTCGATCAGA	28	1	2.00	1
GTGAGTGAGAGCGAGTTCC	19	1	2.00	2
.GAGTTCCAATGTGGTCTCTG	20	1	1.00	1
.GTGAGAGCGAGTTCCAATGTG	21	1	1.00	1
GTGAGTGAGAGCGAGTTC	18	1	1.00	1
GTGAGTGAGAGCGAGTTCCAATGTGGT	27	1	1.00	1
.CAGATTCCAAAATTGACACATTCGGAC	27	1	1.00	1
.GAAACCAGTTGTGCTTCGATCAGAT	25	1	1.00	1
.TCTCGAAACCAGTTGTGCTTCGATCA	27	1	1.00	1
GTGAGTGAGAGCGAGTTCCA	20	1	1.00	1
.TTCCGACCTTGAATCACCAC	21	1	1.00	1
.GTTCCAATGTGGTCTCTGA	19	1	1.00	1
.AAACCAGTTGTGCTTCGATC	20	1	1.00	1



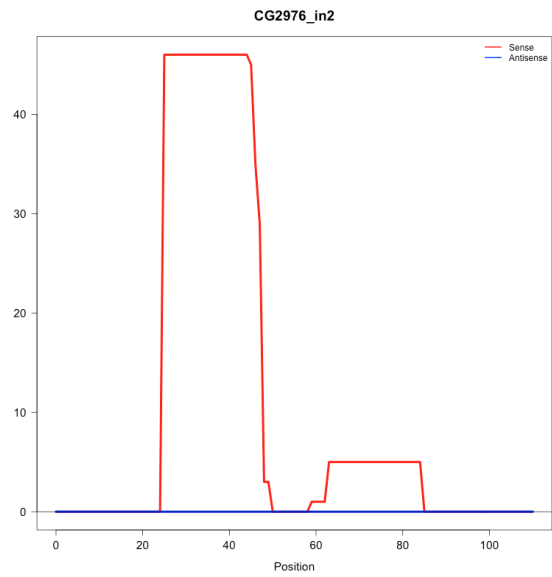
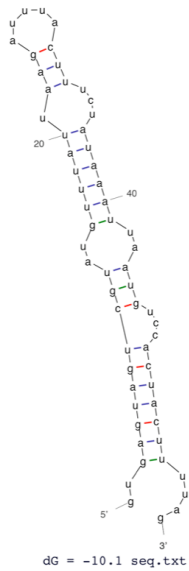
CG17352_in5

[chr3L 8347258-8347366 -](#)

[illegible]

	Size	Blast	Total Norm	# of libraries
.....ATTAACCAATTCGAATTGCTTAG.....	23	1	153.00	58
.....ATTAACCAATTCGAATTGCTTA.....	22	1	76.00	33
.....ATTAACCAATTCGAATTGCTT.....	21	1	76.00	36
GTGAGTTCGATTGGAAAATTTAAT.....	26	1	27.00	12
.....TTAACCAATTCGAATTGCTTAG.....	22	1	19.00	10
GTGAGTTCGATTGGAAAATTTA..	24	1	10.00	4
GTGAGTTCGATTGGAAAATTTAAT.....	25	1	10.00	4
.....ATTAACCAATTCGAATTGCT.....	20	1	7.00	4
GTGAGTTCGATTGGAAAA.....	18	1	5.00	3
GTGAGTTCGATTGGAAAATTTA.....	23	1	5.00	5
.....TGAGTTCGATTGGAAAATTTA.....	22	1	4.00	3
GTGAGTTCGATTGGAAAATTTA.....	22	1	4.00	3
GTGAGTTCGATTGGAAAATTT.....	21	1	3.00	3
GTGAGTTCGATTGGAAAATT.....	20	1	3.00	2
.....TTAACCAATTCGAATTGCTTAG.....	23	1	3.00	3
.....AATTAACCAATTCGAATTGCTT.....	22	1	3.00	3
.....TGAGTTCGATTGGAAAATTTA.....	21	1	2.00	2
GTGAGTTCGATTGGAAAAT.....	19	1	2.00	2
.....GCCTGTTCAACTACTTGA.....	18	1	2.00	2
.....ATTAACCAATTTCGAATTGC.....	19	1	2.00	1
.....ATTAACCAATTTCGAATTGCTTAG.....	24	1	2.00	2
.....TGAGTTCGATTGGAAAATTT.....	20	1	2.00	2
.....TTTAATTAAACCAATTTCGAATTGCT.....	24	1	2.00	2
GTGAGTTCGATTGGAAAATTTAATTT.....	27	1	2.00	1
.....AATTAACCAATTTCGAATTGC.....	20	1	1.00	1
.....TTTAAATTTAATGTTTAATTAAC.....	23	1	1.00	1
.....TTTAAATTTAATGTTTAATT.....	20	1	1.00	1
.....TTAACCAATTTCGAATTGCTTA.....	21	1	1.00	1
.....TAATGTTTAATTAACCAATTTCG.....	22	1	1.00	1
.....AATGTTTAATTAACCAATTTCGA.....	22	1	1.00	1
.....TTAATTAACCAATTTCGAATTGCTTAG.....	26	1	1.00	1
.....TTAACCAATTTCGAATTGCTT.....	20	1	1.00	1
.....TTTAATTAACCAATTTCGAATTGCTTA.....	26	1	1.00	1
.....AATTAACCAATTTCGAATTGCT.....	21	1	1.00	1
.....AATTAACCAATTTCGAATTGCTTA.....	23	1	1.00	1

Output of `ss_graph` (R)
by D. Sievert and M. Zuber

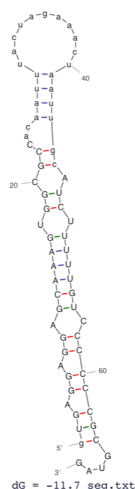


CG2976_in2

[chr2L 4829954-4830064](#) -

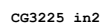
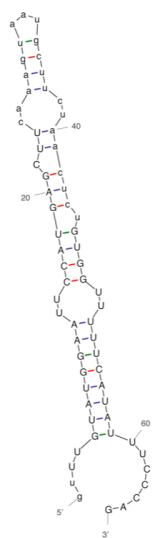
GCCAGTGGGCCATTGCGAGCTTTAA**GTGAGTAGTCGTATGTTTATTAAGATTACTTTCTATAAAATTAATGTCCACTACTTTTAG**TCTCTATGACGATGAACTTAGCTTT
.....(((((((.(.(((((((((.....)))))).....)))))).....)))))).....
Plus strand

	Size	Blast	Total Norm	# of libraries
..... GTGAGTAGTCGTATGTTTATTA	23	1	26.00	8
..... GTGAGTAGTCGTATGTTTATT	21	1	10.00	8
..... GTGAGTAGTCGTATGTTTATTA	22	1	6.00	5
.....AATTAATGTCCACTACTTTTAG	22	1	4.00	3
..... GTGAGTAGTCGTATGTTTATTAAGA	25	1	3.00	3
.....TATAAATTAATGTCCACTACTTTTAG	26	1	1.00	1
..... GTGAGTAGTCGTATGTTTAT	20	1	1.00	1



chr3R 11661983-11662101 -

Sequence	Size	Blast	Total Norm	# of libraries
.....ATCTTTTGTCCCCCGCGTAG.....	22	1	38.00	14
GTGAGGAGGACAAAGTGGCGC.....	22	1	13.00	5
.....AGGAAGCCTGTCCCGTGGACG.....	21	1	9.00	1
.....ATCTTTTGTCCCCCGCGTA.....	21	1	7.00	4
GTGAGGAGGACAAAGTGGCGCC.....	23	1	5.00	3
.....GAAGCCTGTCCCGTGGACGCCA.....	22	1	3.00	3
GTGAGGAGGACAAAGTGGCGCCA.....	24	1	3.00	2
..ATCTACTCGGATTCTGTCAG.....	21	1	3.00	3
.....AGGAAGCCTGTCCCGTGGACGCC.....	23	1	2.00	2
.....ATCTTTTGTCCCCCGCGT.....	20	1	2.00	1
.....AAGCCTGTCCCGTGGACGCCA.....	21	1	2.00	1
.....TGTCCTGGTGGACGCCATC.....	18	1	2.00	1
GTGAGGAGGACAAAGTGGCGCCAC.....	25	1	1.00	1
GTGAGGAGGACAAAGTGG.....	19	1	1.00	1
.....AGCCTGTCCCGTGGACGCCA.....	20	1	1.00	1
..GCATCTACTCGGATTCTGTCAG.....	24	1	1.00	1
..TGAGGAGGACAAAGTGGCG.....	20	1	1.00	1
.....GGAAGCCTGTCCCGTGGACGCCATC.....	25	1	1.00	1
..TGAGGAGGACAAAGTGGCGCC.....	22	1	1.00	1
GTGAGGAGGACAAAGTG.....	18	1	1.00	1
.....TTTGTCCCCCGCGTAG.....	18	1	1.00	1
..TGATCTACTCGGATTCTGTCAG.....	18	1	1.00	1
.....GGAAGCCTGTCCCGTGGACGCCA.....	23	1	1.00	1
.....GAAGCCTGTCCCGTGGACGCCATC.....	24	1	1.00	1
.....AAGCCTGTCCCGTGGACGCC.....	20	1	1.00	1
.....TTTACTAGAACTAATTGCATCT.....	23	1	1.00	1
GTGCATCTACTCGGATTCTGTCAGGTGAGGAG.....	33	1	1.00	1
GTGAGGAGGACAAAGTGGCGCCACA.....	26	1	1.00	1
.....GCCTGTCCCGTGGACGCC.....	18	1	1.00	1
GTGAGGAGGACAAAGTGGCGG.....	21	1	1.00	1
..TGATCTACTCGGATTCTGTCAG.....	25	1	1.00	1
.....AGCCTGTCCCGTGGACGCC.....	19	1	1.00	1
.....ACTCGGATTCTGTCAGS.....	18	2	0.50	1



chr2L 4817790-4817906 -

TCATACTAGTGGGTGAACAGGCAGC**GTTTGATGGAATTC**CATGAGCT**TCAAAGTAATGCTTCTAACTCTG**TGGT**TTTTCATATTCCCA**GTTGCAAGAGCACCCAGGTGCCACAG
 ((((((((((. ((((((((. ((. ((((.))))).)))))).)))))).)))))).
 Plus strand

Sequence	Size	Blast	Total Norm	# of libraries
GTTTGTATGGAATTCATGAG.....	21	1	535.00	74
GTTTGTATGGAATTCATGA.....	20	1	33.00	20
GTTTGTATGGAATTCATG.....	19	1	13.00	9
GTTTGTATGGAATTCATGAGCTTC.....	25	1	9.00	6
.....GTGGTTTTTCATATTCCAG.....	21	1	7.00	1
GTTTGTATGGAATTCATGAGCTTCA.....	26	1	6.00	5
GTTTGTATGGAATTCATGAGCT.....	23	1	6.00	4
..TTGTATGGAATTCATGAGCTT.....	22	1	6.00	5
GTTTGTATGGAATTCATGAGC.....	22	1	4.00	4
..TTGTATGGAATTCATGAGC.....	20	1	3.00	3
..TTTGTATGGAATTCATGAGC.....	21	1	2.00	2
.....AAAGTAATGCTTCTAACTCTGT.....	22	1	2.00	1
..TTTGTATGGAATTCATGAG.....	20	1	2.00	2
.....AGTGGCAAGAGCACCAGGTGCCACA.....	26	1	1.00	1
..TTGTATGGAATTCATGAG.....	19	1	1.00	1
.....CTTCAAAGTAATGCTTCTAACTCT.....	24	1	1.00	1
.....CTGTGGTTTTTCATATTCCCA.....	22	1	1.00	1
GTTTGTATGGAATTCATGAGCTTCAAAG.....	29	1	1.00	1
...TGTATGGAATTCATGAGCTT.....	21	1	1.00	1
..TTTGTATGGAATTCATGAGCTTCAAAGT.....	29	1	1.00	1
.....CTCTGTGGTTTTTCATATTCC.....	22	1	1.00	1
..TTTGTATGGAATTCATGAGCTTCAAAG.....	28	1	1.00	1
.....CAAAGTAATGCTTCTAACTCTGTGG.....	25	1	1.00	1