AT1G76680.1-2

```
                                                                                                  GSM366866 GSM304283 GSM366870 GSM304284 Total
GTAAGCACATTTTGGATTTGGA                                                                            0.86      0         0         0         0.86
    GCACATTTTGGATTTGGA                                                                            0         0.68      0         0         0.68
                                                                                  TGTGTCCTTGTTGTTGCAG 0         0         1.74      0         1.74
                                                                                   TGTGTCCTTGTTGTTGCA 0         0         0         3.67      3.67
GTAAGCACATTTTGGATTTGGAATTCAAGAAGCTGAAACCATTCAAGATTCTTATATGTGTCCTTGTTGTTGCAG
-13.10  ....(((((....((((.....((..(((((..((((....))))...)))))..))..))))....))).))..   []
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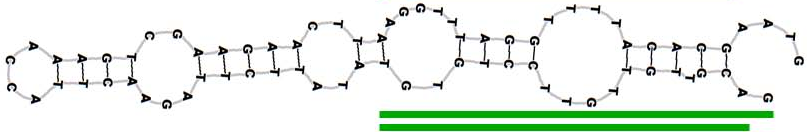

AT2G10921.1-2

	GSM343001	GSM518432	GSM442934	GSM342999	GSM456945	GSM442932	GSM257235	GSM442935	GSM253623	GSM442933	GSM343002	GSM366870	GSM343005	GSM343004	GSM642338	GSM366865	GSM366868	GSM304285	GSM304284	GSM304282	GSM154336	GSM343000	Total
ATCGAATCTCCTGTTATTATGAAC	0.81	0	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.07
ATCGAATCTCCTGTTATTATGA	0	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.24
CTCCTGTTATTATGAACATGGTAT	1.21	0	0	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.59
CTCCTGTTATTATGAACATGGTA	0	0	0	0	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15
TCCTGTTATTATGAACATGGTATA	0	0	0	0	0	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.28
CCTGTTATTATGAACATGGTATA	0	0	0	0	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15
ATTATGAACATGGTATATAGAATG	0	0	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.26
ATTATGAACATGGTATATAGAAT	0	0	0	0	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15
ATGAACATGGTATATAGAATGGA	0	0	0	0	0	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.55
ATGAACATGGTATATAGAATGGAT	0	0	0.26	0	0	0.28	13.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	13.85
TGAACATGGTATATAGAATGGATA	0	0	0	0	0	0	0	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.27
TGAACATGGTATATAGAATGGA	0	0	0	0	0	0	0	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.27
GAACATGGTATATAGAATGG	0	0	0.26	0	0	0	0	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.53
GAACATGGTATATAGAATGGATA	0	0	0.26	0	0	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.81
GAACATGGTATATAGAATGGATAT	0	0	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.26
ACATGGTATATAGAATGGATATG	0	0	0.53	0	0	0	0	0	0	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0.82
ACATGGTATATAGAATGGATA	0	0	0	0	0	0.28	0	0.54	7.32	0	0	0	0	0	0	0	0	0	0	0	0	0	8.14
ACATGGTATATAGAATGGATATGA	0	0	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.26
CATGGTATATAGAATGGATATGAA	0	0	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.26
ATGGTATATAGAATGGATATGAAT	0	0	0.26	0.38	0.15	0.28	0	0.27	0	0	0.28	0	0	0	0	0	0	0	0	0	0	0	1.62
ATGGTATATAGAATGGATA	0	0	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.26
ATGGTATATAGAATGGATATGAA	0	0	0	0	0	0	0	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.27
TGGTATATAGAATGGATATGAA	0	0	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.26
ATATAGAATGGATATGAATCA	0	0	0.26	0	0	0	26.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	26.89
ATATAGAATGGATATGAATCAATA	0	0	0.26	0	0	0.28	26.63	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	27.71
TATAGAATGGATATGAATCAATA	0	0	0	0	0	0	13.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	13.31
AGAATGGATATGAATCAATAA	0	0	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.26
AATGGATATGAATCAATAAAAGGT	0	0	0	0	0	0	13.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	13.31
AAAGGTTTCTGAATGGATAT	0	0	0	0	0	0	0	0	7.32	0	0	0	0	0	0	0	0	0	0	0	0	0	7.32
AAAGGTTTCTGAATGGATATA	0	0	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.26
AAAGGTTTCTGAATGGATATATA	0	0	0.26	0	0	0	0	0.54	0	0.29	0	0	0	0	0	0	0	0	0	0	0	0	1.09
AAGGTTTCTGAATGGATA	0	0	0	0	0	0	0	0	0	0	0	1.74	0	0	0	0	0	0	0	0	0	0	1.74
AAGGTTTCTGAATGGATATA	0	0	0	0	0	0	0	0	0	0	0	0	0.36	0	0	0	0	0	0	0	0	0	0.36
AGGTTTCTGAATGGATAT	0	0	0	0	0	0.28	0	0	0	0	0	0	0.36	0	0	0	0	0	0	0	0	0	0.64
GGTTTCTGAATGGATATATAA	0	0	0	0	0	0	0	0	0	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0.29
ATATAAATAGACTCGTTATTATGG	0	0	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.26
ATAAATAGACTCGTTATTATGGAC	0	0	0.26	0	0	0	0	0.27	0	0	0	0	0.36	0.3	0	0	0	0	0	0	0	0	1.19
AAATAGACTCGTTATTATGGACAT	0	0	0	0	0	0	0	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.27
AAATAGACTCGTTATTATGGA	0	0	0	0	0	0	0	0	0	0	0	0	0.36	0	0	0	0	0	0	0	0	0	0.36
AAATAGACTCGTTATTATGGACA	0	0	0.53	0	0	0.55	0	0.27	0	0.29	0	0	0	0	0	0	0	0	0	0	0	0	1.64
AATAGACTCGTTATTATGGACATC	0	0	0.26	0	0	0.28	0	0	0	0	0.28	0	0.36	0	0	0	0	0	0	0	0	0	1.18
ATAGACTCGTTATTATGGACATC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.1	0	0	0	0	0	0	0	0.1
TAGACTCGTTATTATGGACATCA	0	0	0.53	0	0.15	0.28	0	0.27	0	0.87	0	0	0.72	0	0	0	0	0	0	0	0	0	2.82
AGACTCGTTATTATGGACATCAAA	0	0	0	0	0	0	0	0.54	0	0	0.57	0	0	0	0	0	0	0	0	0	0	0	1.11
AGACTCGTTATTATGGACATC	0	0	0	0	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15
ATGGACATCAAAAAATTGTTTGTT	0	0	0	0	0	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.28
GGACATCAAAAAATTGTTTGTTGA	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0.6
CAAAAAATTGTTTGTTGATTTTT	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.58	0	0	0	0	0	0	0.58
AAATTGTTTGTTGATTTTT	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.44	0	0	0	0	0	1.44
AATTGTTTGTTGATTTTTCTT	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.22	0	0	0	0	1.22
ATTGTTTGTTGATTTTTCTTT	0	0	0	0	0	0	0	0	0	0	0	0	0	0.3	0	0	0	0	0	0	0	0	0.3
ATTGTTTGTTGATTTTTC	0	0	0	0	0	0	0	0	0	0	0	0	0.36	0	0	0	0	0	0	0	0	0	0.36
TGTTTGTTGATTTTTCTTTCA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3.67	0	0	0	3.67
TTGTTGATTTTTCTTTCAGTTT	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.46	0	0	1.46
TTGTTGATTTTTCTTTCAGTTTGC	0	0	0	0.38	0	0	0	0	0	0	0.28	0	0	0	0	0.58	0	0	0	0	0	0	1.24
TGTTGATTTTTCTTTCAGTTTGCA	0	0.48	0	0.76	0	0	0	0	0	0	0	0	0.36	0	0	0	0	0	0	0	0	0	1.6
GTTGATTTTTCTTTCAGTTTGCAG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	12.72	0	12.72
GTTGATTTTTCTTTCAGTTTGCA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.81	0.81

```
GTTAATCGAATCTCCTGTTATTATGAACATGGTATATAGAATGGATATGAATCAATAAAAGGTTTCTGAATGGATATATAATAAATAGACTCGTTATTATGGACATCAAAAAATTGTTTGTTGATTTTTCT
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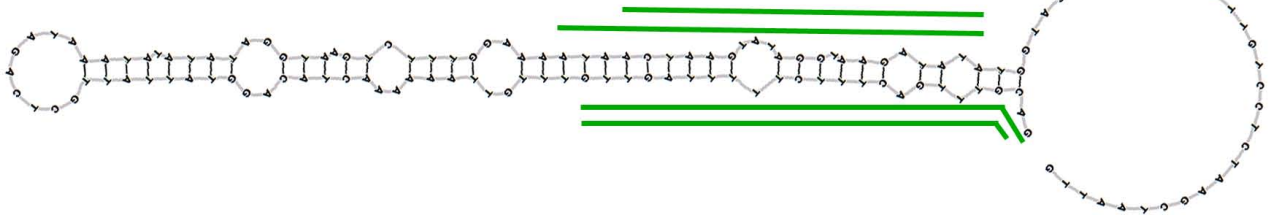

AT3G60950.1-15

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     
GTTCATTGTTTAAACATGTGGGAC
 TTCATTGTTTAAACATGTGGGAC
  TCATTGTTTAAACATGTGGGACA
    ATTGTTTAAACATGTGGGACATTT
    ATTGTTTAAACATGTGGGAC
    ATTGTTTAAACATGTGGGACA
          AAACATGTGGGACATTTTTGT
            ACATGTGGGACATTTTTGTATTT
              ATGTGGGACATTTTTGTATTTGT
                                TTGTGTTACAATTGTTTTGGTTA
                                 GTGTTACAATTGTTTTGGTTA
                                              GTTTTGGTTATAGAAAAGTTGG
                                               TTTGGTTATAGAAAAGTTGGGCTC
                                                          ATAGAAAAGTTGGGCTCCCTGTGA
GTTCATTGTTTAAACATGTGGGACATTTTTGTATTTGTGTTACAATTGTTTTGGTTATAGAAAAGTTGGGCTCCCTGTGAAAG
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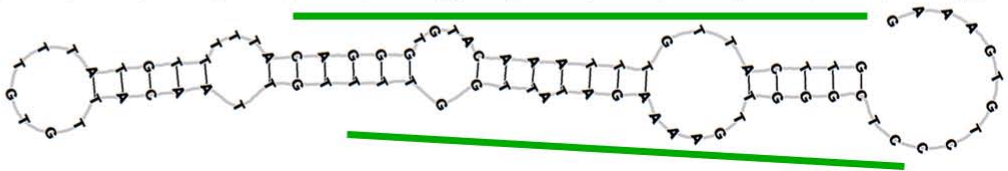
	GSM343002	GSM366867	GSM518432	GSM342999	GSM343004	GSM442934	GSM343005	GSM304283	GSM442935	GSM642338	GSM642337	GSM366866	GSM442933	GSM642335	GSM366865	Total
	0.28	1.14	0	0	0	0	0	0	0	0	0	0	0	0	0	1.42
	0	0	0.24	0.38	0	0	0	0	0	0	0	0	0	0	0	0.62
	0	0	0	0	0.91	0	0	0	0	0	0	0	0	0	0	0.91
	0	0	0	0	0	0.53	0	0	0	0	0	0	0	0	0	0.53
	0	0	0	0.38	0	0	0.36	0	0	0	0	0	0	0	0	0.74
	0	0	0	0	0	0	0	0.68	0	0	0	0	0	0	0	0.68
	0	0	0	0	0	0	0	0	0.27	0	0	0	0	0	0	0.27
	0	0	0	0	0	0	0	0	0	0.15	0	0	0	0	0	0.15
	0	0	0	0	0	0	0	0	0	0	0.13	0	0	0	0	0.13
	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.28
	0	0	0	0	0	0	0	0	0	0	0	0.43	0	0	0	0.43
	0	0	0	0	0	0	0	0	0	0	0	0	0.29	0	0	0.29
	0	0	0	0	0	0	0	0	0	0	0	0	0	0.76	0	0.76
	0	0	0	0	0	0	0	0.68	0	0	0	0	0	0	0.58	1.26



AT4G05280.1-2

	GSM442935	GSM442934	GSM304282	GSM642338	GSM343004	GSM456945	GSM253624	GSM304284	GSM257237	GSM343000	GSM343002	GSM642337	GSM442933	GSM366868	GSM518432	GSM442932	GSM342999	GSM366865	GSM304283	GSM366870	GSM253622	Total
AGGAGGAGGAAAGCATGGAGGG	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.54
AGGAGGAGGAAAGCATGGAGGGGT	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.54
GAGGAGGAAAGCATGGAGGGGTG	0	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.26
AGGAGGAAAGCATGGAGGGGTGGA	0	0	1.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.46
GAGGAAAGCATGGAGGGGTGGAAG	0	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.26
AGGAAAGCATGGAGGGGTGGA	0	0	0	0.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.1
AAAGCATGGAGGGGTGGAAGCA	0	0	1.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.46
AAAGCATGGAGGGGTGGAAGCAA	0	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.26
AAAGCATGGAGGGGTGGAAGCAAC	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.27
AAGCATGGAGGGGTGGAAGCAACT	0.54	0	0	0.05	0.3	0.3	2.81	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4
AAGCATGGAGGGGTGGAAG	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.27
AAGCATGGAGGGGTGGAAGCAA	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.27
AAGCATGGAGGGGTGGAAGCA	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.27
AAGCATGGAGGGGTGGAAGCAAC	0	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.26
AGCATGGAGGGGTGGAAGCAACT	0.27	0	0	0	0	0	0	3.67	0	0	0	0	0	0	0	0	0	0	0	0	0	3.94
AGCATGGAGGGGTGGAAGCAAC	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.27
AGCATGGAGGGGTGGAAGCAA	0	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.26
CATGGAGGGGTGGAAGCAACTGGC	0	0	0	0	0	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15
ATGGAGGGGTGGAAGCAACTGGC	0	0	0	0	0	0.15	0	0	18.72	0	0	0	0	0	0	0	0	0	0	0	0	18.87
ATGGAGGGGTGGAAGCAACTGGCA	0	0	0	0	0	0.15	0	0	0	0.81	0	0	0	0	0	0	0	0	0	0	0	0.96
ATGGAGGGGTGGAAGCAACTG	0	0	0	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15
TGGAGGGGTGGAAGCAACTGGC	0	0	0	0	0	0	0	0	0	0	0.28	0	0	0	0	0	0	0	0	0	0	0.28
TGGAGGGGTGGAAGCAACTGGCA	0	0.53	0	0	0	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.68
TGGAGGGGTGGAAGCAACTGGCAC	0	0	0	0	0.3	0.89	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.19
GGAGGGGTGGAAGCAACTGGCA	0	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.26
GAGGGGTGGAAGCAACTGGCA	0	0	0	0	0	0.3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.3
GAGGGGTGGAAGCAACTGGCAC	0	0	0	0	0	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15
GAGGGGTGGAAGCAACTGGCACTA	0	0	0	0	0	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15
AGGGGTGGAAGCAACTGGCAC	0	0	0	0	0	0	0	0	0	0	0	0.13	0	1.44	0	0	0	0	0	0	0	1.57
AGGGGTGGAAGCAACTGGCACTAT	0	0	0	0	0	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.45
AGGGGTGGAAGCAACTGGCACTA	0	0	0	0	0	0.15	0	0	0	0	0	0	0.29	0	0	0	0	0	0	0	0	0.44
GGGGTGGAAGCAACTGGCA	0	0	0	0	0	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15
GGGTGGAAGCAACTGGCACTATCT	0.27	0.26	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.13
GGGTGGAAGCAACTGGCAC	0	0	0	0	0	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15
GGGTGGAAGCAACTGGCACTATC	0	0	0	0	0	0.3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.3
GGGTGGAAGCAACTGGCACTAT	0.27	0	0	0	0	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.42
GGTGGAAGCAACTGGCACTATCTC	0	0	0	0	0	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15
GGTGGAAGCAACTGGCACTATC	0	0	0	0	0	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15
GGTGGAAGCAACTGGCACTAT	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.27
GTGGAAGCAACTGGCACTATCTCT	0	0	0	0	0	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15
TGGAAGCAACTGGCACTATCTCTT	0.27	0	0	0	0	0.3	0	0	0	0.81	0	0	0	0	0	0	0	0	0	0	0	1.38
TGGAAGCAACTGGCACTATCTC	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.27
GGAAGCAACTGGCACTATCTCTTT	0	0	0	0	0	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15
GGAAGCAACTGGCACTATCTCTT	0	0	0	0	0	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15
GAAGCAACTGGCACTATCTCTT	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.27
GAAGCAACTGGCACTATCTCTTT	0	0	0	0	0	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15
TCTTTTTATTTTGGTTGACGGT	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.48	0	0	0	0	0	0	0.48
CTTTTTATTTTGGTTGACGGTGTG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.28	0	0	0	0	0	0.28
TTTTATTTTGGTTGACGGTGTG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.76	0	0	0	0	0.76
TTTATTTTGGTTGACGGTGTGGTA	0	0	0	0	0	0	0	0	0	0	0	0	0	1.44	0	0	0	0	0	0	0	1.44
TTATTTTGGTTGACGGTGTGGTA	0	0	0	0	0	0	0	0	0	0	0	0	0	1.44	0	0	0	0.58	0	0	0	2.02
TATTTTGGTTGACGGTGTGGTAGC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.48	0	0	0	0	0	0	0.48
ATTTTGGTTGACGGTGTGGTAGCG	0	0	0	0	0	0	2.81	0	0	0	0	0.13	0	0	0	0	0	0	0	0	0	2.94
ATTTTGGTTGACGGTGTGGTA	0	0	0	0.2	0	0	0	0	0	0	0	0	0	1.44	0.72	0	0	0	0.68	1.74	0	4.78
ATTTTGGTTGACGGTGTGGTAGCGG	0	0	0	0.05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.05
ATTTTGGTTGACGGTGTGGTAGC	0	0	0	4.45	0	0	0	0	0	0	0	5.91	0	0	0.48	0	0	0	0	0	0	10.84
ATTTTGGTTGACGGTGTGGTAG	0	0	0	1.1	0	0	0	0	0	0	0	0.53	0	0	0	0	0	0	0	0	0	1.63
ATTTTGGTTGACGGTGTGGT	0	0	0	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.35
TTTTGGTTGACGGTGTGGTAGC	0	0	0	0	0	0	0	0	0	0.41	0	0	0	0	0	0	0	0	0	0	0	0.41
TTTGGTTGACGGTGTGGTAGC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.19	1.19
TTTGGTTGACGGTGTGGTAGCGGC	0	0	0	0	0.3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.3
TTGGTTGACGGTGTGGTAGCG	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.27
TTGGTTGACGGTGTGGTAGCGG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.59	0.59
TTGGTTGACGGTGTGGTAGCGGCC	0	0	0	0	0	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15
TGGTTGACGGTGTGGTAGCGGCCC	0.27	0	0	0	0	0.3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.57
GGTTGACGGTGTGGTAGCGGCC	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.27
GGTTGACGGTGTGGTAGCG	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.27
GGTTGACGGTGTGGTAGCGGCCCA	0	0.26	0	0	0	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.41
GGTTGACGGTGTGGTAGC	0	0	0	0	0	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15
GGTTGACGGTGTGGTAGCGGCCC	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.27
GTTGACGGTGTGGTAGCGGCCCA	0.54	0.53	0	0	0	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.22
GTTGACGGTGTGGTAGCGGCC	0	0	0	0	0	0.3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.3
GTTGACGGTGTGGTAGCGGCCC	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.27
TTGACGGTGTGGTAGCGGCCCACA	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.27
TTGACGGTGTGGTAGCGGCCC	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.27
TTGACGGTGTGGTAGCGGCCCA	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.27
TGACGGTGTGGTAGCGGC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.24	0	0	0	0	0	0	0.24
ACGGTGTGGTAGCGGCCCACAG	0	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.26
CGGTGTGGTAGCGGCCCA	0	0	0	0	0	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15

GTAGGAGGAGGAAAGCATGGAGGGGTGGAAGCAACTGGCACTATCTCTTTTTATTTTGGTTGACGGTGTGGTAGCGGCCCACAG

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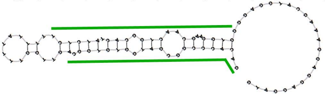

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	GSM642338	GSM442934	Total
GTAAATAAAGACTGAAACTTTCC	0.2	0	0.2
GTAAATAAAGACTGAAACTTTCCCAGATC	0.05	0	0.05
ATAAAGTTTGCTTCTTTGTTACAG	0	0.26	0.26
AAAGTTTGCTTCTTTGTTACAG	0.6	0	0.6

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        GTAAATAAAGACTGAAACTTTCCCAGATCCAAATTCGTTAAAATTGAAATCAAAATCTGATAAAGTTTGCTTCTTTGTTACAG
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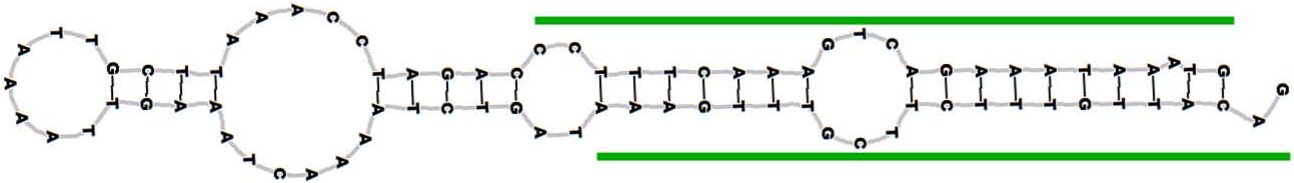

LOC_Os02g13250.1-5

		GSM278572	GSM693279	GSM693280	GSM520635	GSM520636	GSM278571	GSM520639	GSM455965	GSM686039	GSM686040	Total
	GTGCAATTTGTGGCATCAGTCGGG	0.67	0	0	0	0	0	0	0	0	0	0.67
	GTGCAATTTGTGGCATCAGT	0	0.1	0	0	0	0	0	0	0	0	0.1
	TGCAATTTGTGGCATCAGTCGGG	0.33	0	0	0	0	0	0	0	0	0	0.33
	GCAATTTGTGGCATCAGTCGGGTC	0.33	0	0	0	0	0	0	0	0	0	0.33
	CAATTTGTGGCATCAGTCGGGTC	0	0	0.11	0	0	0	0	0	0	0	0.11
	AATTTGTGGCATCAGTCGGGTCAG	0	0	0	0.16	0	0.31	0	0	0	0	0.47
	AATTTGTGGCATCAGTCGGGTCA	0	0	0	0	0.23	0	0	0	0	0	0.23
	AATTTGTGGCATCAGTCGGGT	0	0	0.11	0	0	0	0	0	0	0	0.11
	TTTGTGGCATCAGTCGGGTCAGAC	0	0.1	0	0	0	0	0	0	0	0	0.1
	GGCATCAGTCGGGTCAGACAAAGA	0	0	0	0.16	0	0	0	0	0	0	0.16
	ATCAGTCGGGTCAGACAAAGAAGA	0	0.1	0	0.33	0.23	0	0.44	0.25	0	0	1.35
	TCAGTCGGGTCAGACAAAGAAGAA	0	0	0	0	0	0.31	0	0	0	0	0.31
	TCGGGTCAGACAAAGAAGAAGTAC	0	0	0.11	0	0	0	0	0	0	0	0.11
	AGAAGTACTAGGATTGGAATGGGA	0.33	0	0	0.16	0	0	0	0	0	0	0.49
	AGAAGTACTAGGATTGGAATGGG	0	0	0	0	0	0	0	0	0.08	0	0.08
	GAAGTACTAGGATTGGAATGGGA	0	0.1	0	0	0	0	0	0	0	0	0.1
	AGTACTAGGATTGGAATGGGACGG	0	0	0	0	0	0	0	0	0.08	0.08	0.16
	AGGATTGGAATGGGACGGTACAG	0	0	0	0	0	0	0	0	0	0.08	0.08
	GATTGGAATGGGACGGTACAG	0	0	0	0	0	0	0	0	0.08	0	0.08
	ATTGGAATGGGACGGTACA	0	0	0	0	0	0	0	0	0	0.08	0.08
	GTGCAATTTGTGGCATCAGTCGGGTCAGACAAAGAAGAAGTACTAGGATTGGAATGGGACGGTACAG											
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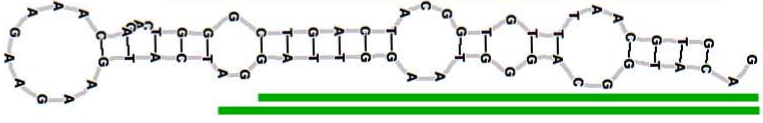

LOC_Os02g52100.1-2

	GSM520635	GSM520636	GSM278571	GSM693280	GSM693279	GSM571078	GSM520638	GSM520637	GSM686039	GSM520634	GSM278572	GSM409318	GSM686040	GSM455965	Total
GTTGCATGGCCGCCCTAAGTCGGT	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0.66
ATGGCCGCCCTAAGTCGGTTCA	0	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0.23
CGCCCTAAGTCGGTTCATATCGAG	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0.33
CCCTAAGTCGGTTCATATCGAGGC	0	0	0.31	0.11	0	0	0	0	0	0	0	0	0	0	0.42
CCTAAGTCGGTTCATATCGA	0	0	0	0	0.1	0	0	0	0	0	0	0	0	0	0.1
CCTAAGTCGGTTCATATCGAGGCT	0	0	0	0	0.1	0.24	0	0	0	0	0	0	0	0	0.34
CTAAGTCGGTTCATATCGAGGCT	0	0	0	0.11	0.1	0	0	0	0	0	0	0	0	0	0.21
CTAAGTCGGTTCATATCGA	0	0	0	0.11	0.1	0	0	0	0	0	0	0	0	0	0.21
CTAAGTCGGTTCATATCGAGG	0	0	0	0	0	0	0.2	0	0	0	0	0	0	0	0.2
CTAAGTCGGTTCATATCG	0	0	0	0	0.1	0	0	0	0	0	0	0	0	0	0.1
CTAAGTCGGTTCATATCGAG	0	0	0	0.11	0	0	0	0	0	0	0	0	0	0	0.11
TAAGTCGGTTCATATCGAG	0	0	0	0.11	0	0	0	0	0	0	0	0	0	0	0.11
TAAGTCGGTTCATATCGAGGCT	0	0	0	0	0.1	0	0	0	0	0	0	0	0	0	0.1
TAAGTCGGTTCATATCGAGGC	0	0	0	0	0.1	0	0.2	0.44	0	0	0	0	0	0	0.74
TAAGTCGGTTCATATCGAGGCTGG	0	0	0	0.11	0.1	0	0.2	0	0	0	0	0	0	0	0.41
TAAGTCGGTTCATATCGA	0	0	0	0.11	0	0	0	0	0	0	0	0	0	0	0.11
AAGTCGGTTCATATCGAG	0	0	0	0.11	0.1	0	0	0	0	0	0	0	0	0	0.21
AAGTCGGTTCATATCGAGGCT	0	0	0	0.11	0.1	0	0	0	0	0	0	0	0	0	0.21
AAGTCGGTTCATATCGAGGC	0	0	0	0.11	0	0.24	0	0	0.08	0	0	0	0	0	0.43
AAGTCGGTTCATATCGAGGCTGGG	0	0	0	0	0	0	0	0	0	0.37	0	0	0	0	0.37
AGTCGGTTCATATCGAGGCTGG	0	0	0	0	0	0	0.2	0	0	0	0	0	0	0	0.2
AGTCGGTTCATATCGAGGCTGGGG	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0.16
TCGGTTCATATCGAGGCTGGG	0	0	0	0	0	0	0	0	0	0	0.33	17.53	0	0	17.86
CATATCGAGGCTGGGGGAGAAGGC	0	0	0	0	0.2	0	0	0	0	0	0	0	0.08	0	0.28
AGGCGCTACCCTTATTTAAGCTCC	0	0	0	0.11	0	0	0	0	0	0	0	0	0	0	0.11
GCGCTACCCTTATTTAAGCTCCTC	0	0	0	0	0	0.24	0	0	0	0	0	0	0	0	0.24
TAAGCTCCTCAAACGCTCCGGGCC	0	0	0	0	0	0	0	0	0	0	0	0	0	0.25	0.25
TAAGCTCCTCAAACGCTCCGGG	0	0	0	0	0	0	0	0	0	0	0	0	0	0.25	0.25
AAGCTCCTCAAACGCTCCGGGCCG	0.16	0	0.31	0	0	0	0	0	0	0	0	0	0.08	0	0.55
GCTCCTCAAACGCTCCGGGCCGTT	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0.16
GCTCCGGGCCGTTTACTTGGACGG	0	0	0	0.11	0	0	0	0	0	0	0	0	0.08	0	0.19
CGGGCCGTTTACTTGGACGGAG	0	0	0	0	0.1	0	0	0	0	0	0	0	0.08	0	0.18
CGGGCCGTTTACTTGGACGGA	0	0	0	0	0.1	0	0	0	0	0	0	0	0	0	0.1

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GTTGCATGGCCGCCCTAAGTCGGTTCATATCGAGGCTGGGGGAGAAGGCGCTACCCTTATTTAAGCTCCTCAAACGCTCCGGGCCGTTTACTTGGACGGAG
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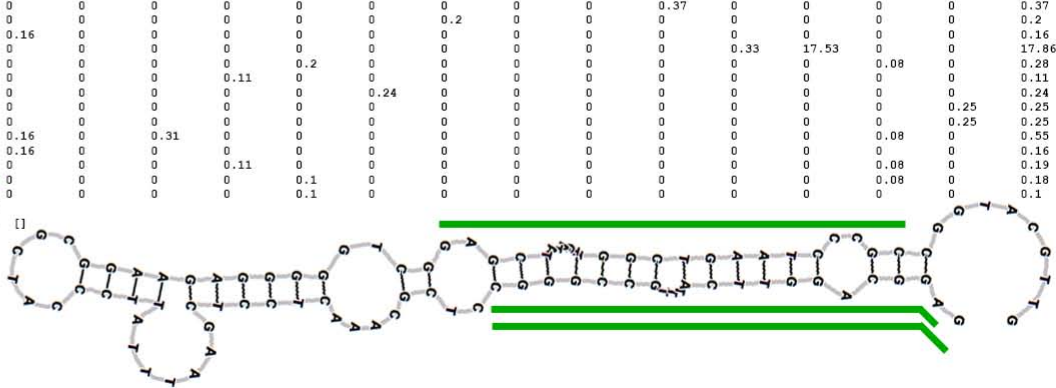

LOC_Os03g06520.1-6

	GSM520640	GSM520638	GSM455965	GSM520636	GSM520637	GSM520635	GSM520634	GSM520639	GSM686039	GSM693279	GSM409322(Leaf 1)	Total
GTATGCACATTCGTGGTAG	0.2	0.2	0.5	0	0	0	0	0	0	0	0	0.9
GTATGCACATTCGTGGTAGCCAGGAT	0.2	0	0	0	0	0	0	0	0	0	0	0.2
GTATGCACATTCGTGGTAGCCAGG	0	0.2	0	0.23	0	0.16	0	0	0	0	0	0.59
GTATGCACATTCGTGGTAGCCAGGA	0.2	0	0.5	0	0.22	0.16	0	0	0	0	0	1.08
GTATGCACATTCGTGGTAGCC	0	0.41	0	0	0	0	0	0	0	0	0	0.41
GTATGCACATTCGTGGTAGCCA	0	0	0	0.23	0	0	0	0	0	0	0	0.23
GTATGCACATTCGTGGTAGCCAG	0	0.2	0	0	0	0	0	0	0	0	0	0.2
TAGCCAGGATTCGAACTCGAGACC	0	0	0	0	0	0.16	0	0	0	0	0	0.16
AGCCAGGATTCGAACTCGAGACC	0	0	0.5	0	0	0.16	0.37	0	0	0	0	1.03
AGCCAGGATTCGAACTCGAGAC	0	0.2	0	0	0	0	0	0	0	0	0	0.2
AGCCAGGATTCGAACTCGAGACCT	0	0	0.74	0	0.22	0.99	0	0	0	0	0	1.95
AGCCAGGATTCGAACTCGAGACCTCT	0.2	0	0	0	0	0	0	0	0	0	0	0.2
GCCAGGATTCGAACTCGAGACCTC	0.2	0	0.74	0	0.22	0.33	0	0	0	0	0	1.49
GCCAGGATTCGAACTCGAGACCT	0	0	0.25	0	0	0	0	0	0	0	0	0.25
CCAGGATTCGAACTCGAGACCTC	0	0	0	0	0	0	0	0.22	0	0	0	0.22
CAGGATTCGAACTCGAGACCTC	0.2	0.2	0.25	0	0.22	0	0	0	0.08	0	0	0.95
AGGATTCGAACTCGAGACCTCTGG	0.39	0.2	0.25	0	0	0	0.73	0.66	0.08	0	11.76	14.07
AGGATTCGAACTCGAGACCTC	0	0	0	0	0	0	0	0	0	0.1	0	0.1
AGGATTCGAACTCGAGACCTCT	0	0.2	0	0	0	0	0	0	0	0	0	0.2
GATTCGAACTCGAGACCTCTGG	0	0	0	0	0	0.16	0	0	0	0	0	0.16
GATTCGAACTCGAGACCTC	0	0	0.25	0	0	0	0	0	0	0	0	0.25
GATTCGAACTCGAGACCTCTG	0	0.2	0	0	0	0	0	0	0	0	0	0.2
ATTCGAACTCGAGACCTCTGGGTT	0	0	0	0	0.22	0	0	0	0	0	0	0.22
ATTCGAACTCGAGACCTCTGGGTTTCT	0.2	0	0	0	0	0	0	0	0	0	0	0.2
TTCGAACTCGAGACCTCTGGGTT	0	0	0.25	0	0	0	0	0	0	0	0	0.25
TCGAACTCGAGACCTCTGGGTTTCT	0	0	0.25	0	0	0	0	0	0	0	0	0.25
TCGAACTCGAGACCTCTGGGTTT	0	0	0.25	0	0	0	0	0	0	0	0	0.25
TCGAGACCTCTGGGTTTCTGA	0	0.2	0	0	0	0	0	0	0	0	0	0.2
TCTGATACCATGTGTGTATGCA	0	0	0.74	0	0	0	0	0	0	0	0	0.74
CTGATACCATGTGTGTATGCA	0.2	0	0	0	0	0	0	0	0	0	0	0.2
TGATACCATGTGTGTATGCAG	0	0	0.25	0	0	0	0	0	0	0	0	0.25
GATACCATGTGTGTATGCA	0	0	0.25	0	0	0	0	0	0	0	0	0.25

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GTATGCACATTCGTGGTAGCCAGGATTCGAACTCGAGACCTCTGGGTTTCTGATACCATGTGTGTATGCAG
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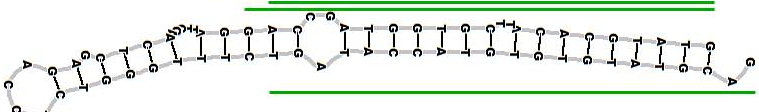

LOC_Os03g36170.1-6

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   TATGCTTGATGAATATGGTGTT
    ATGCTTGATGAATATGGTGTT
      CTTGATGAATATGGTGTTTCCGA
                                  CTTGCCATGCAACCAATAGGCTT
                                                                  TCTACGAGCTAATTGTTGG
                                                                     GAGCTAATTGTTGGGAGGAAG
                                                                       CTAATTGTTGGGAGGAAGCCAAAT
                                                                                                  CTAACCAAATTTAAAAGTCGGTGT
                                                                                                   AACCAAATTTAAAAGTCGGTGTGA
                                                                                                            AAAGTCGGTGTGATGAAGGGTTTC
                                                                                                           AAGTCGGTGTGATGAAGGGTTT
                                                                                                             CGGTGTGATGAAGGGTTTCTTCTA
GTACTATGCTTGATGAATATGGTGTTTCCGATACCTTTTGGGTGGAAGCCATAAACACTGCTTGCCATGCAACCAATAGGCTTTATTTGCATCATCTCTTGATAGACTTTCTACGAGCTAATTGTTGGGAGGAAGCCAAATATTGCCTATTTTTGAGTTTTTGGTTGCAAGTGTTATATTTACCGAAAGGGAGTTAGACTAACCAAATTTAAAAGTCGGTGTGATGAAGGGTTTCTTCTAG
-64.10 .((((..(((((..(((((...((..((.(((((((.(((((((.......(((((((((..(((((...(((((((((((..(((((((.(..(((((..(((((.((((.....)))).....))))).)))))).))))))...))))).))).))))).))))))...))))))..))..))))).))))))...))))))..))...))))).))))).))))).))))..................  []
```

GSM520635	GSM455965	GSM520636	GSM693279	GSM693280	GSM686039	GSM455962	GSM278572	GSM686040	GSM409313	Total
0.16	0	0	0	0	0	0	0	0	0	0.16
0	0.25	0	0	0	0	0	0	0	0	0.25
0	0	0.23	0	0	0	0	0	0	0	0.23
0	0	0	0.1	0	0	0	0	0	0	0.1
0	0	0	0.1	0	0	0	0	0	0	0.1
0	0	0	0	0.11	0	0	0	0	0	0.11
0	0	0	0	0	0.08	0	0	0	0	0.08
0	0	0	0	0	0	3.96	0	0	0	3.96
0	0	0	0	0	0	0	0.33	0	0	0.33
0	0	0	0	0.11	0	0	0	0	0	0.11
0	0	0	0	0	0.08	0	0	0	0	0.08
0	0	0	0	0	0.16	0	0	0	0	0.16
0	0	0	0	0.11	0	0	0	0	0	0.11
0	0	0	0	0	0	0	0	0.08	0	0.08
0	0	0	0	0	0	0	0	0	10.05	10.05

LOC_Os03g57750.2-1

GTGTGAGACGAATTGTTGGT

CGAACAGTAGGAATTCGACA

	GSM520637	GSM278572	GSM409321	Total
	0.22	0	0	0.22
	0.22	0	0	0.22
TCCGGCAATCGTCTCATCTG	0	0.33	0	0.33
CGGCAATCGTCTCATCTGCAG	0	0	7.33	7.33

```
        GTGTGAGACGAATTGTTGGTTCAGCTTCGCTGATCAAATCGAATTGACTTCCTCTTTTTTTTCCTTTCTCTGCACATTAGCTCTTGTTAGAATCGAACAGTAGGAATTCGACAAATTCTGTTCTCGCGTTCTTCTTCATCAATCATCTTCGTGATCCGGCAATCGTCTCATCTGCAG
-38.16  (((((((((.(((((((((.(((....(((.((.((.......((((.(((((((.(((..(((.........((......)).........)))..)))).)).)))))).))))).......)).)).)).))).....................))).))))))))))))))..))..  []
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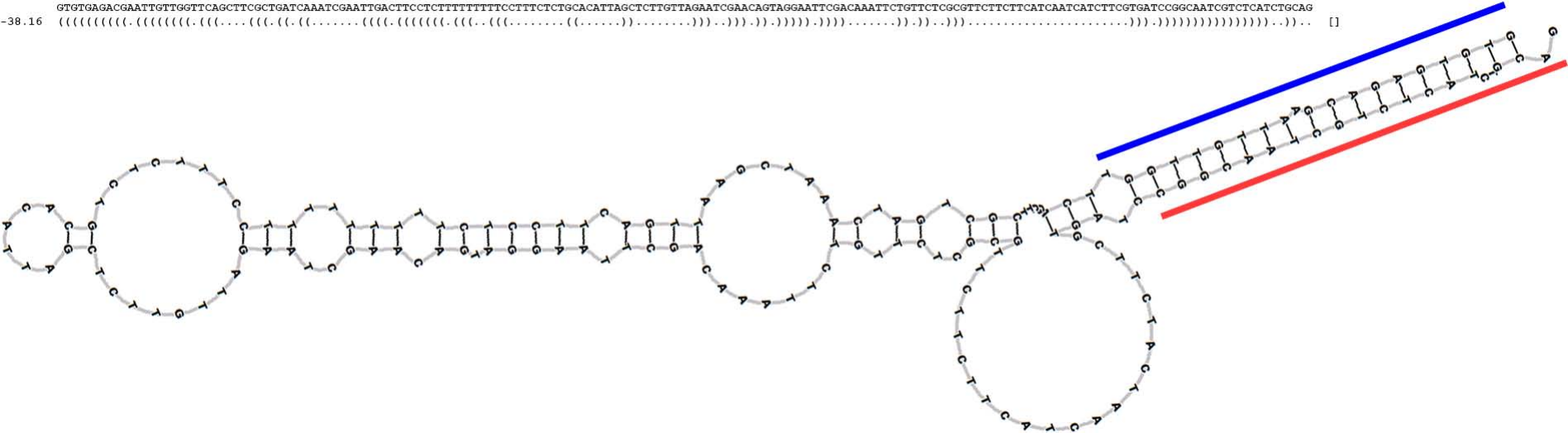

LOC_Os04g09380.1-5

	GSM693280	GSM693279	GSM571078	GSM278572	GSM278571	GSM520635	GSM520637	GSM520634	GSM520638	GSM686039	GSM520636	Total
GTGGAGCACGTGGATGATCAGGAA	0.75	1.1	0.49	0.33	0.92	0	0	0	0	0	0	3.59
GTGGAGCACGTGGATGATCAGGA	0.11	0.1	0	0	0	0	0	0	0	0	0	0.21
TGGAGCACGTGGATGATCAGGAA	0.11	0.1	0	0	0	0	0	0	0	0	0	0.21
TGGAGCACGTGGATGATCAG	0.11	0	0	0	0	0	0	0	0	0	0	0.11
TGGAGCACGTGGATGATCAGGA	0.22	0	0	0.33	0	0	0	0	0	0	0	0.55
TGGAGCACGTGGATGATCA	0.11	0	0	0	0	0	0	0	0	0	0	0.11
TGGAGCACGTGGATGATCAGG	0	0	0	0	0.31	0	0	0	0	0	0	0.31
TGGAGCACGTGGATGATCAGGAAA	0.32	0	0	0.33	0	0	0	0	0	0	0	0.65
GGAGCACGTGGATGATCAGGAAAC	0.11	0	0	0	0	0	0	0	0	0	0	0.11
GAGCACGTGGATGATCAGGAAACT	0	0	0	0	0.31	0	0	0	0	0	0	0.31
AGCACGTGGATGATCAGGAAACT	0	0	0	0	0.31	0	0	0	0	0	0	0.31
AGCACGTGGATGATCAGGAAAC	0	0.1	0	0	0	0	0	0	0	0	0	0.1
GGATGATCAGGAAACTAAAATTGT	0	0	0	0	0	0.16	0	0	0	0	0	0.16
AATAATGTTCATGATACTGTTCAG	0	0	0	0	0	0	0.22	0	0	0	0	0.22
ATGATACTGTTCAGCACTCACCTC	0	0	0	0	0	0	0	0.37	0.2	0	0	0.57
GATACTGTTCAGCACTCACCTCCT	0	0	0	0	0	0.16	0	0	0	0	0	0.16
TACTGTTCAGCACTCACCTCCTGT	0	0	0	0	0	0	0	0	0	0.08	0	0.08
ACTGTTCAGCACTCACCTCCTGTT	0	0	0	0	0	0.16	0	1.47	0	0	0.94	2.57

```
        GTGGAGCACGTGGATGATCAGGAAACTAAAATTGTTGATAATAATGTTCATGATACTGTTCAGCACTCACCTCCTGTTTTGTAG
-13.61  ..((((...(((..(((.(((.........(((((.....)))))..........))).))).))).....)))).........  []
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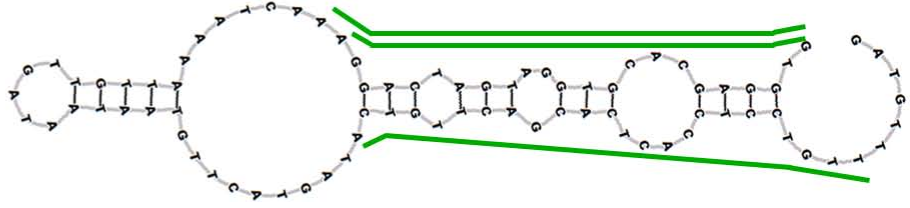

LOC_Os04g45540.1-3

	GSM520636	GSM520635	GSM693280	GSM278571	GSM693279	GSM571078	GSM520638	GSM520637	GSM686039	GSM520634	GSM520639	GSM686040	GSM409321	GSM409318	GSM278572	GSM409324	GSM455965	GSM571077	GSM520640	Total
ATGGCCGCCCTAAGTCGGTTCA	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.23
CGCCCTAAGTCGGTTCATATCGAG	0	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.33
CCCTAAGTCGGTTCATATCGAGGC	0	0	0.11	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.42
CCTAAGTCGGTTCATATCGAGGCT	0	0	0	0	0.1	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0.34
CCTAAGTCGGTTCATATCGA	0	0	0	0	0.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.1
CTAAGTCGGTTCATATCGA	0	0	0.11	0	0.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.21
CTAAGTCGGTTCATATCGAG	0	0	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.11
CTAAGTCGGTTCATATCGAGGCT	0	0	0.11	0	0.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.21
CTAAGTCGGTTCATATCGAGG	0	0	0	0	0	0	0.2	0	0	0	0	0	0	0	0	0	0	0	0	0.2
CTAAGTCGGTTCATATCG	0	0	0	0	0.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.1
TAAGTCGGTTCATATCGAGGC	0	0	0	0	0.1	0	0.2	0.44	0	0	0	0	0	0	0	0	0	0	0	0.74
TAAGTCGGTTCATATCGAGGCTGG	0	0	0.11	0	0.1	0	0.2	0	0	0	0	0	0	0	0	0	0	0	0	0.41
TAAGTCGGTTCATATCGAGGCT	0	0	0	0	0.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.1
TAAGTCGGTTCATATCGA	0	0	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.11
TAAGTCGGTTCATATCGAG	0	0	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.11
AAGTCGGTTCATATCGAGGC	0	0	0.11	0	0	0.24	0	0	0.08	0	0	0	0	0	0	0	0	0	0	0.43
AAGTCGGTTCATATCGAGGCT	0	0	0.11	0	0.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.21
AAGTCGGTTCATATCGAG	0	0	0.11	0	0.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.21
AAGTCGGTTCATATCGAGGCTGGG	0	0	0	0	0	0	0	0	0	0.37	0	0	0	0	0	0	0	0	0	0.37
AGTCGGTTCATATCGAGGCTGGGA	0	0	0	0	0	0	0	0	0	0	0.66	0	0	0	0	0	0	0	0	0.66
AGTCGGTTCATATCGAGGCTGG	0	0	0	0	0	0	0.2	0	0	0	0	0	0	0	0	0	0	0	0	0.2
TCGGTTCATATCGAGGCTGGGAGA	0	0	0.11	0	0.1	0.24	0	0	0	0	0	0.08	0	0	0	0	0	0	0	0.53
TCGGTTCATATCGAGGCTGGGA	0	0	0	0	0	0	0	0	0	0	0	0	7.33	0	0	0	0	0	0	7.33
TCGGTTCATATCGAGGCTGGG	0	0	0	0	0	0	0	0	0	0	0	0	0	17.53	0.33	0	0	0	0	17.86
CGGTTCATATCGAGGCTGGGAGAG	0	0	0	0	0.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.1
CGGTTCATATCGAGGCTGGGAGA	0	0	0	0	0.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.1
GTTCATATCGAGGCTGGGAGAGAA	0	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.16
TTCATATCGAGGCTGGGAGAGAAG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.33	0	0	0	0	0.33
TCATATCGAGGCTGGGAGAGAAGG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.33	9.04	0	0	0	9.37
CATATCGAGGCTGGGAGAGAAGGC	0	0.16	1.29	2.76	1.99	0.49	0	0	2.58	0	0	6.78	0	0	1.67	0	0.25	0.79	0	18.76
CATATCGAGGCTGGGAGAGAAGG	0	0	0.11	0	0	0	0	0	0.16	0	0	0.15	0	0	0	0	0	0	0	0.42
CATATCGAGGCTGGGAGAGAAG	0	0	0	0	0	0	0	0	0.08	0	0	0.3	0	0	0	0	0	0	0	0.38
CATATCGAGGCTGGGAGAGAAGGCG	0	0	0	0	0	0	0	0	0.08	0	0	0.08	0	0	0	0	0	0	0	0.16
ATATCGAGGCTGGGAGAGAAGGC	0	0	0.11	0	0	0	0	0	0	0	0	0.15	0	0	0	0	0	0	0.2	0.46
ATATCGAGGCTGGGAGAGAAGGCG	0	0	0	0	0.5	0	0	0	0.23	0	0	0.08	0	0	0	0	0	0	0	0.81
ATATCGAGGCTGGGAGAGAAGG	0	0	0.11	0	0	0	0	0	0	0	0	0	0	0	0.33	0	0	0.26	0	0.7
TATCGAGGCTGGGAGAGAAGGCG	0	0	0.11	0	0.2	0	0	0	0	0	0	0.08	0	0	0	0	0	0	0	0.39
TATCGAGGCTGGGAGAGAAGGCGC	0	0	0.22	0.61	0.4	0.24	0	0	0	0	0	0.38	0	0	0	0	0	0	0	1.85
TATCGAGGCTGGGAGAGAAGGC	0	0	0.11	0	0	0	0	0	0.23	0	0	0.38	0	0	0.33	0	0	0	0	1.05
TATCGAGGCTGGGAGAGAAGGCGCT	0	0	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.11
ATCGAGGCTGGGAGAGAAGGCGC	0	0	0	0	0	0	0	0	0.08	0	0	0	0	0	0	0	0	0	0	0.08
ATCGAGGCTGGGAGAGAAGGC	0	0	0	0	0	0	0	0	0.16	0	0	0.15	0	0	0	0	0	0	0	0.31
ATCGAGGCTGGGAGAGAAGGCGCT	0	0	0	0	0	0	0	0	0	0	0	0.23	0	0	0	0	0	0	0	0.23
TCGAGGCTGGGAGAGAAGGCGC	0	0	0.11	0	0	0	0	0	0	0	0	0.08	0	0	0	0	0	0	0	0.19
TCGAGGCTGGGAGAGAAGGCGCGCTA	0	0	0.11	0.31	0.7	0.24	0	0	0	0	0	0.3	0	0	0	0	0	0	0	1.66
TCGAGGCTGGGAGAGAAGGCGCT	0	0	0	0	0.1	0	0	0	0.08	0	0	0	0	0	0	0	0	0	0	0.18
TCGAGGCTGGGAGAGAAGGCG	0	0	0	0	0	0	0	0	0.08	0	0	0	0	0	0	0	0	0	0	0.08
TCGAGGCTGGGAGAGAAGGC	0	0	0	0	0	0	0	0	0.08	0	0	0	0	0	0	0	0	0	0	0.08
CGAGGCTGGGAGAGAAGGCGCTA	0	0	0	0	0	0	0	0	0	0	0	0.15	0	0	0	0	0	0	0	0.15
CGAGGCTGGGAGAGAAGGC	0	0	0	0	0.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.1
CGAGGCTGGGAGAGAAGGCGCT	0	0	0	0	0	0	0	0	0.08	0	0	0	0	0	0	0	0	0	0	0.08
CGAGGCTGGGAGAGAAGGCGCTAC	0	0	0	0	0.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.2
GAGGCTGGGAGAGAAGGCGCT	0	0	0.11	0	0.2	0	0	0	0.16	0	0	0	0	0	0	0	0	0	0	0.47
GAGGCTGGGAGAGAAGGCGCTAC	0	0	0	0	0	0	0	0	0	0	0	0.08	0	0	0	0	0	0	0	0.08
GAGGCTGGGAGAGAAGGCGCTACC	0	0.66	0	0	0.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.76
GAGGCTGGGAGAGAAGGCGCTA	0	0	0	0	0.4	0	0	0	0.08	0	0	0.08	0	0	0	0	0	0	0	0.56
GAGGCTGGGAGAGAAGGC	0	0	0	0	0	0	0	0	0	0	0	0.08	0	0	0	0	0	0	0	0.08
GAGGCTGGGAGAGAAGGCG	0	0	0	0	0	0	0	0	0.08	0	0	0	0	0	0	0	0	0	0	0.08
GAGGCTGGGAGAGAAGGCGC	0	0	0	0	0	0	0	0	0.08	0	0	0	0	0	0	0	0	0	0	0.08
AGGCTGGGAGAGAAGGCGCTA	0	0	0	0	0.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.2
AGGCTGGGAGAGAAGGCGCTACCC	0	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.33
GCTCCGGGCCGTTTATCTGGACGG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.25	0	0	0.25
CCGGGCCGTTTATCTGGACGGAG	0	0	0	0	0	0	0	0	0	0	0	0.08	0	0	0	0	0	0	0	0.08

GTATGGCCGCCCTAAGTCGGTTCATATCGAGGCTGGGAGAGAAGGCGCTACCCCTATTTAAACTCGTCAAACGCTCCGGGCCGTTTATCTGGACGGAG

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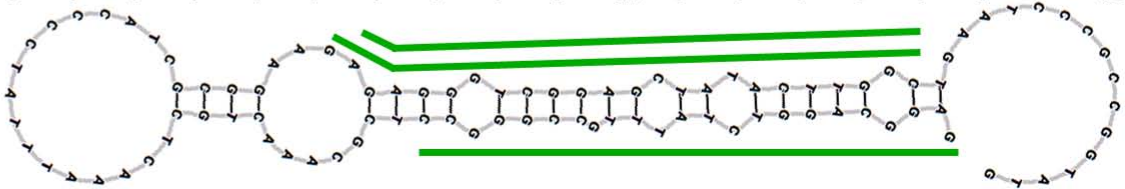

LOC_Os06g23260.1-5

	GSM693279	GSM455965	GSM693280	GSM520640	GSM520635	GSM520638	GSM686040	GSM686039	GSM520636	GSM520634	GSM520637	GSM278572	GSM278571	GSM571078	Total
GTCATCGATCCGGATAGATTAGA	0.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.1
GTCATCGATCCGGATAGATTAGAA	0.2	0.25	0	0.59	0.16	0	0	0	0	0	0	0	0	0	1.2
GTCATCGATCCGGATAGATTA	0.1	0	0.11	0	0	0	0	0	0	0	0	0	0	0	0.21
GTCATCGATCCGGATAGATTAG	0.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.1
CATCGATCCGGATAGATTAGAA	0	0	0	0	0	0.2	0	0	0	0	0	0	0	0	0.2
ATCGATCCGGATAGATTAGAA	0	0	0	0	0	0	0.08	0	0	0	0	0	0	0	0.08
ATCGATCCGGATAGATTAGAAG	0	0	0	0	0	0.2	0	0	0	0	0	0	0	0	0.2
TCGATCCGGATAGATTAGAAG	0	0	0	0	0	0.41	0	0	0	0	0	0	0	0	0.41
TCCGGATAGATTAGAAGCCCT	0	0	0.11	0	0	0	0	0	0	0	0	0	0	0	0.11
TCCGGATAGATTAGAAGCCC	0	0	0	0	0	0	0	0.08	0	0	0	0	0	0	0.08
AGAATGATGTGGTGCAAT	0.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.1
AATGATGTGGTGCAATGTCTCGTC	0	0	0	0.2	0	0	0	0	0.23	0	0	0	0	0	0.43
ATGATGTGGTGCAATGTCTCGTCA	0	0	0	0	0	0	0	0	0	0.37	0	0	0	0	0.37
GATGTGGTGCAATGTCTCGTCAGT	0	0.25	0	0	0.16	0	0	0	0	0	0	0	0	0	0.41
TGCAATGTCTCGTCAGTTTTGAGT	0	0	0	0	0	0	0	0	0	0	0.22	0	0	0	0.22
GCAATGTCTCGTCAGTTTTG	0	0	0	0	0	0	0	0	0	0	0	0.33	0	0	0.33
AATGTCTCGTCAGTTTTGAGTTGA	0	0	0	0.59	0.16	0.2	0	0	0.94	0	0.44	0	0	0	2.33
AATGTCTCGTCAGTTTTGAGT	0	0	0	0	0	0.2	0	0	0	0	0	0	0	0	0.2
ATGTCTCGTCAGTTTTGAGTTGAT	0	0	0	0.2	0	0.2	0	0	0	0	0	0	0	0	0.4
GTCTCGTCAGTTTTGAGTTGATATT	0	0	0	0	0	0.2	0	0	0	0	0	0	0	0	0.2
TCAGTTTTGAGTTGATATTTCCAC	0	0	0	0	0	0	0	0	0	0	0	0.33	0.31	0	0.64
ATTTTTCAATATAATGACGCAT	0	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0.25
TTTTTCAATATAATGACGCATCT	0	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0.25
TTTCAATATAATGACGCATCTGCT	0	0	0	0	0	0	0.15	0	0	0	0	0	0	0	0.15
TTCAATATAATGACGCATCTGCTT	0	0	0.11	0	0	0	0	0	0	0	0	0	0	0	0.11
TTCAATATAATGACGCATCTGC	0	0	0.11	0	0	0	0	0	0	0	0	0	0	0	0.11
TCAATATAATGACGCATCTGCTTT	0	0	0	0	0	0	0	0	0	0	0	0.33	0	0	0.33
CAATATAATGACGCATCTGCTTTG	0	0	0	0	0	0	0.08	0	0	0	0	0	0	0	0.08
AATATAATGACGCATCTGCTTTGT	0	0	0	0	0	0	0	0	0	0	0	0.33	0	0	0.33
ATATAATGACGCATCTGCTTTGT	0	0	0	0.2	0	0	0	0	0	0	0	0	0	0	0.2
ATAATGACGCATCTGCTTTGTCAC	0	0	0	0	0	0	0	0	0	0	0	0	0	0.24	0.24
ATAATGACGCATCTGCTTTGT	0	0	0	0	0	0	0.08	0.08	0	0	0	0	0	0	0.16
ATAATGACGCATCTGCTTT	0	0	0	0	0	0.2	0	0.08	0	0	0	0	0	0	0.28
GCATCTGCTTTGTCACCTTGTGA	0	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0.25
CTGCTTTGTCACCTTGTGAAAGAG	0.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.1

GTCATCGATCCGGATAGATTAGAAGCCCTTTAGAATGATGTGGTGCAATGTCTCGTCAGTTTTGAGTTGATATTTCCACATTCATTTTTCAATATAATGACGCATCTGCTTTGTCACCTTGTGAAAGAG

-26.77 .(((.(((....((((((.((((.((.....((((((((((...((((((...((.....)).....)))))))).)))))).))))))).....)).)))).)))))))...))))))..... []

LOC_Os06g29760.1-1

	GSM455965	GSM520635	GSM686040	GSM693280	GSM693279	GSM520637	GSM520640	GSM686039	GSM278572	GSM278571	GSM571077	GSM520636	GSM520638	GSM329298	GSM520639	Total
GTTAGATTGTAAATAGGAAAGCGC	0.25	1.81	0.38	0.32	0.9	0.22	0.99	0.08	0.67	0.61	0	0	0	0	0	6.23
GTTAGATTGTAAATAGGAAAGC	0	0	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0.15
GTTAGATTGTAAATAGGAAA	0	0.16	0	0	0	0	0	0.08	0	0	0	0	0	0	0	0.24
GTTAGATTGTAAATAGGAAAG	0	0	0	0	0.1	0	0	0	0	0	0	0	0	0	0	0.1
TTAGATTGTAAATAGGAAAGCGCGCT	0	0	0	0	0	0.44	0	0	0	0	0	0	0	0	0	0.44
TTAGATTGTAAATAGGAAAGC	0	0	0	0	0.2	0	0	0.08	0.33	0	0	0	0	0	0	0.61
TTAGATTGTAAATAGGAAAG	0	0	0	0	0	0	0	0.08	0	0	0	0	0	0	0	0.08
TTAGATTGTAAATAGGAAAGCG	0	0	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0.08
TTAGATTGTAAATAGGAAAGCGCG	0	0	0	0.22	0	0	0	0	0.33	0	0	0	0	0	0	0.55
TTAGATTGTAAATAGGAAAGCGC	0	0	0	0	0.1	0	0	0.08	0.33	0	0	0	0	0	0	0.51
TAGATTGTAAATAGGAAAG	0	0	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0.08
TAGATTGTAAATAGGAAAGCGCG	0	0	0.08	0	0.2	0	0	0	0.33	0	0.26	0	0	0	0	0.87
TAGATTGTAAATAGGAAAGCGCGC	0	0	0.45	0.32	1	0.22	0	0.08	1	0.61	0.26	0	0	0	0	3.94
TAGATTGTAAATAGGAAAGC	0	0	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0.08
TAGATTGTAAATAGGAAAGCGC	0	0	0	0.32	0	0	0	0	0.33	0	0	0	0	0	0	0.65
TAGATTGTAAATAGGAAAGCG	0	0	0	0	0.1	0	0	0	0	0	0	0	0	0	0	0.1
AGATTGTAAATAGGAAAGCGCG	0	0	0	0.11	0	0	0	0	0	0	0	0	0	0	0	0.11
AGATTGTAAATAGGAAAGCGCGCT	0	0.33	0.08	0.11	0.2	0	0	0.23	0	0.31	0.26	0	0	0	0	1.52
AGATTGTAAATAGGAAAGC	0	0	0	0	0.2	0	0	0	0	0	0	0	0	0	0	0.2
GATTGTAAATAGGAAAGCGCGCTC	0	1.64	0.23	0	0.2	0	0	0	0.33	0	0	0.23	0	0	0	2.63
ATTGTAAATAGGAAAGCGCGCTC	0	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0.16
ATTGTAAATAGGAAAGCGCGCT	0	0	0	0	0	0	0	0.08	0	0	0	0	0	0	0	0.08
TTGTAAATAGGAAAGCGCGCT	0	0	0	0	0	0	0	0	0	0	0.26	0	0	0	0	0.26
TGTAAATAGGAAAGCGCGCTCATC	0	0.16	0	0	0.2	0	0	0	0.33	0.31	0	0	0	0	0	1
GTAAATAGGAAAGCGCGCTCATCA	0	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0.16
GTAAATAGGAAAGCGCGC	0	0	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0.08
TAAATAGGAAAGCGCGCTCATCAC	0	0	0	0	0.1	0	0	0	0	0	0	0	0	0	0	0.1
AAATAGGAAAGCGCGCTCATCACC	0	0	0	0.11	0.1	0	0	0	0.33	0	0	0	0	0	0	0.54
AAATAGGAAAGCGCGCTCATC	0	0	0	0	0	0	0	0	0.33	0	0	0	0	0	0	0.33
AATAGGAAAGCGCGCTCATCACCT	0	0	0	0	0.1	0	0	0	0	0	0	0	0.2	0	0	0.3
ATAGGAAAGCGCGCTCATCACC	0	0	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0.08
ATAGGAAAGCGCGCTCATCACCTT	0	0	0	0	0.1	0	0	0	0	0	0	0	0	0	0	0.1
TAGGAAAGCGCGCTCATCACCTT	0	0	0	0	0	0	0	0.08	0	0	0	0	0	0	0	0.08
TAGGAAAGCGCGCTCATCACC	0	0	0	0	0	0	0	0.23	0	0	0	0	0	0	0	0.23
AGGAAAGCGCGCTCATCACCTTTC	0	0	0	0.11	0.1	0	0	0	0	0	0	0	0	0	0	0.21
AGGAAAGCGCGCTCATCAC	0	0	0.08	0	0	0	0	0	0	0	0	0	0	3.46	0	3.54
AGGAAAGCGCGCTCATCACC	0	0	0	0	0	0	0	0	0	0	0	0	0.2	0	0	0.2
AAAGATATCTTTGCATGGAAACCA	0	0	0	0.11	0	0	0	0	0	0	0	0	0	0	0	0.11
GGAAACCATCTGATATGCCCGGTAT	0	0	0	0	0.1	0	0	0	0	0	0	0	0	0	0	0.1
GGAAACCATCTGATATGCCCGGTA	0	0.16	0.15	0	0.2	0	0.2	0	0	0	0.26	0	0	0	0	0.97
GAAACCATCTGATATGCCCGGTAT	0	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0.89	1.22
GAAACCATCTGATATGCCCGGTATT	0	0	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0.08
GAAACCATCTGATATGCCCGGT	0	0	0	0	0	0	0	0	0	0	0	0	0.2	0	0	0.2
CATCTGATATGCCCGGTATTCCT	0	0	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0.08
ATCTGATATGCCCGGTATTCCTAG	0	0.16	0.08	0	0	0	0	0.08	0	0	0	0	0	0	0	0.32
ATCTGATATGCCCGGTATTCC	0	0	0	0	0	0	0	0.08	0	0	0	0	0	0	0	0.08
GATATGCCCGGTATTCCTAG	0	0	0	0	0.1	0	0	0	0	0	0	0	0	0	0	0.1

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      GTTAGATTGTAAATAGGAAAGCGCGCTCATCACCTTTCTTCAAAACAATAAAGATATCTTTGCATGGAAACCATCTGATATGCCCGGTATTCCTAG
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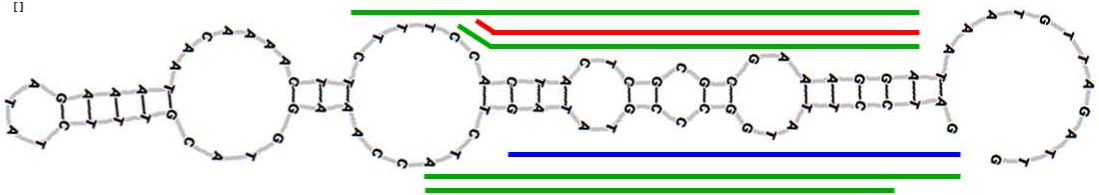

LOC_Os06g31910.1-2

	GSM686040	GSM686039	GSM278572	GSM455965	GSM520635	GSM520638	GSM693279	GSM571077	Total
GTAGACGAGCAGTTAGTAGGCTT	0.08	0.08	0.33	0	0	0	0	0	0.49
GTAGACGAGCAGTTAGTAGGCTTG	0	0	0	0.25	0	0	0	0	0.25
TAGACGAGCAGTTAGTAGGCTT	0	0	0	0	0.16	0	0	0	0.16
TAGACGAGCAGTTAGTAGGCT	0	0	0	0	0	0.2	0	0	0.2
GACGAGCAGTTAGTAGGCTT	0	0	0	0	0	0	0.1	0	0.1
TCTTCTCGTTTGTTTTTCTGCTAG	0	0	0	0	0	0	0	0.26	0.26

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        GTAGACGAGCAGTTAGTAGGCTTGCGTGTGTGTTCTTCTCGTTTGTTTTTCTGCTAG
-11.90  (((((.(((((((..((.(((..(((....)))..)))))...)))))).)))))...  []
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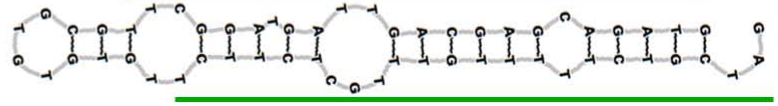
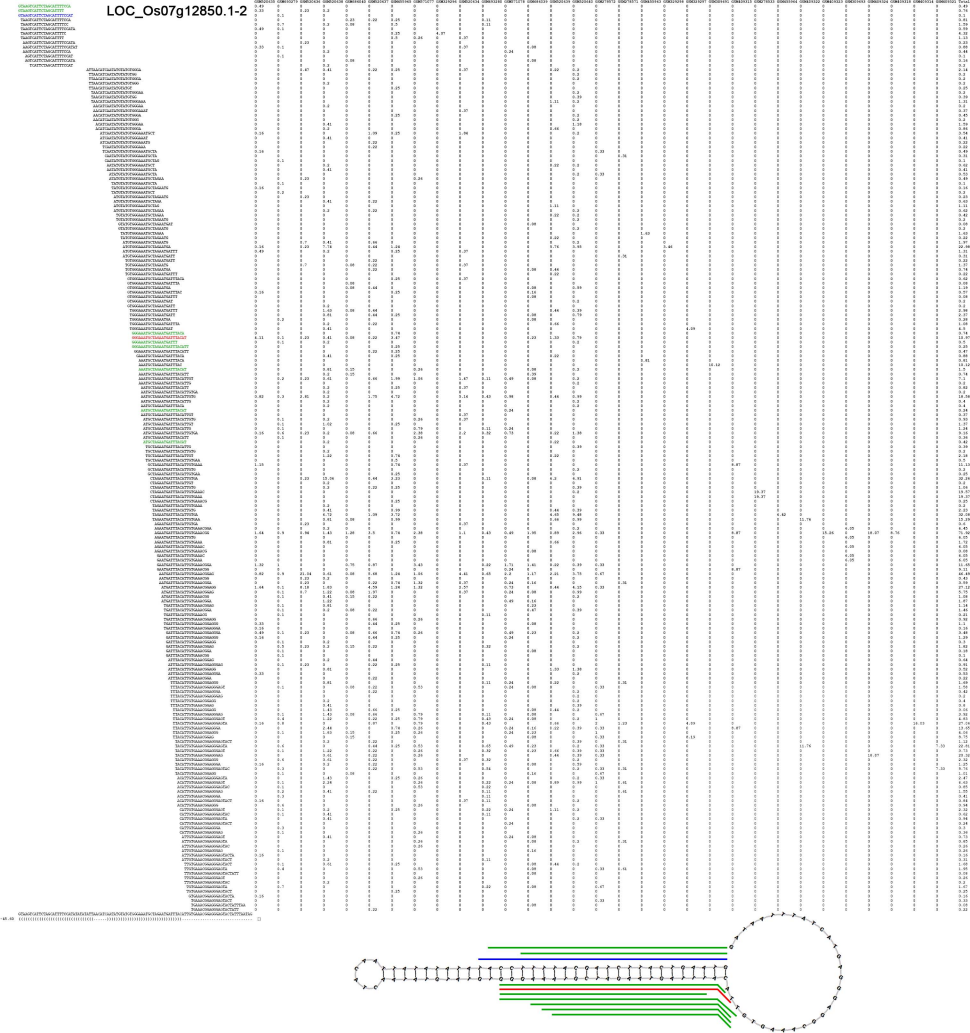


LOC_Os07g12850.1-2



LOC_Os07g32220.1-5

	GSM520635	GSM455965	GSM693280	GSM520634	GSM520640	GSM686039	GSM520637	GSM693279	GSM278572	GSM278571	GSM520636	GSM520638	Total
GTTGGTGGTCTCAATTGTGATAGA	0.16	0	0	0	0	0	0	0	0	0	0	0	0.16
TGGTGGTCTCAATTGTGATAGACT	0	0.25	0	0	0	0	0	0	0	0	0	0	0.25
GTGGTCTCAATTGTGATAGACTAA	0	0	0.11	0	0	0	0	0	0	0	0	0	0.11
ATTTTAGTACTTATATATGATCGA	0	0	0.32	0.37	0.2	0.08	0	0	0	0	0	0	0.97
TTTTAGTACTTATATATGATCGA	0	0	0.11	0	0	0	0	0	0	0	0	0	0.11
TTTAGTACTTATATATGATCG	0	0	0	0	0	0	0.22	0	0	0	0	0	0.22
TTAGTACTTATATATGATCGAT	0	0	0	0	0	0	0.22	0	0	0	0	0	0.22
TAGTACTTATATATGATCGATCAA	0	0	0.65	0	0	0	0	0.3	0	0	0	0	0.95
AGTACTTATATATGATCGATCAAC	0	0	0.32	0	0	0	0	0	0	0	0	0	0.32
TACTTATATATGATCGATCAACT	0	0	0.11	0	0	0	0	0	0	0	0	0	0.11
ACTTATATATGATCGATCAACTAA	0	0	0.22	0	0	0	0	0.1	0.67	0	0	0	0.99
ACTTATATATGATCGATCAACTAAT	0	0	0	0	0	0	0	0	0	0.31	0	0	0.31
ACTTATATATGATCGATCAACTA	0	0	0.11	0	0	0	0	0	0	0	0	0	0.11
TTATATATGATCGATCAACTAA	0	0	0	0	0	0	0	0.1	0	0	0	0	0.1
TTATATATGATCGATCAACTAATC	0	0	0.11	0	0	0	0	0	0.67	0	0	0	0.78
ATATATGATCGATCAACTAATC	0	0	0.97	0	0	0	0	0.4	0	0	0	0	1.37
ATATATGATCGATCAACTAATCT	0	0	0.11	0	0	0	0	0	0	0	0	0	0.11
ATATATGATCGATCAACTA	0	0	0	0	0	0	0	0	0.33	0	0	0	0.33
ATATATGATCGATCAACTAAT	0	0	0.11	0	0	0	0	0	0	0	0	0	0.11
ATATATGATCGATCAACTAA	0	0	0	0	0	0	0	0	0	0.31	0	0	0.31
TATATGATCGATCAACTAATCT	0	0	0.11	0	0	0	0	0	0	0	0	0	0.11
TATATGATCGATCAACTAATC	0	0	0.75	0	0	0	0	0.2	0	0	0	0	0.95
TATATGATCGATCAACTAATCTGG	0	0	0.11	0	0	0	0	0	0	0	0	0	0.11
ATATGATCGATCAACTAATCTGGAA	0	0.25	0	0	0	0	0	0	0	0	0	0	0.25
ATATGATCGATCAACTAATCTGGA	0	0.25	0	0	0	0	0	0	0	0	0	0	0.25
ATATGATCGATCAACTAATC	0	0	1.72	0	0	0	0	0.7	0	0	0	0	2.42
ATATGATCGATCAACTAATCT	0	0	0	0	0	0.08	0	0	0	0	0	0	0.08
TATGATCGATCAACTAATC	0	0	0.22	0	0	0	0	0.5	0	0	0	0	0.72
TATGATCGATCAACTAATCTGGAA	0	0	0	0	0	0	0.66	0	0	0	0	0	0.66
ATGATCGATCAACTAATCTGGAAT	0.16	0	0	0	0	0	0	0	0	0	0.23	0	0.39
GATCAACTAATCTGGAATTATGAC	0	0	0	0.37	0	0	0	0	0	0	0	0	0.37
ATCAACTAATCTGGAATTATGACA	0	0	0.11	0	0	0	0	0	0	0	0	0	0.11
TCAACTAATCTGGAATTATGA	0	0.25	0	0	0	0	0	0	0	0	0	0	0.25
TCAACTAATCTGGAATTATGAC	0	0	0	0	0	0	0	0	0	0	0	0.41	0.41
ACTAATCTGGAATTATGACAATGT	0	0	0.11	0.73	0.2	0	0.22	0	0	0	0	0	1.26

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       GTTGGTGGTCTCAATTGTGATAGACTAACTATATTTTAGTACTTATATATGATCGATCAACTAATCTGGAATTATGACAATGTAG
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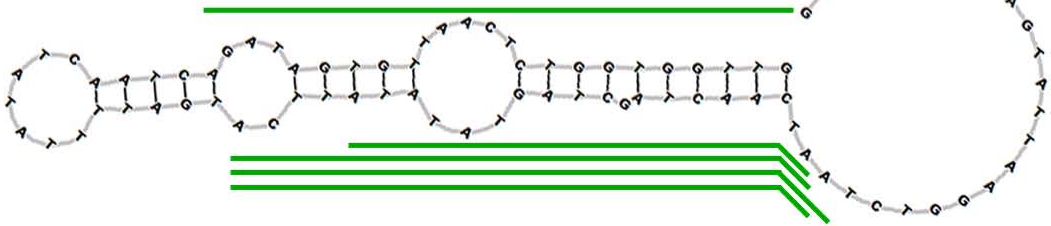

LOC_Os08g04190.1-1
(osa-MIR1429)

	GSM455965	GSM571078	GSM686039	GSM520634	GSM571077	GSM686040	GSM409323	GSM409322	GSM409320	GSM520640	GSM520637	GSM520638	GSM520639	GSM520635	GSM520636	GSM409319	GSM693279	GSM329297	GSM693280	GSM329298	GSM278571	GSM278572	GSM278532	GSM329294	GSM409316	GSM409317	Run1	GSM407071	GSM329299	GSM409318	GSM407072	Run2	GSM409324	GSM309691	GSM278533	GSM455963	GSM455962	GSM455964	Total
GTAATATACTAATCCGTGCATCCA	81.15	3.3	2.38	3.3	10.29	4.67	0	35.29	0	29.62	24.26	0.41	24.13	268.46	6.31	13.71	5.78	12.28	7.97	10.38	1.54	1.67	70.37	40.73	39.12	42.11	0	0	0	0	0	0	0	0	0	0	0	0	736.23
GTAATATACTAATCCGTGCATCC	0.5	0.24	0.23	0	0.26	0.23	15.26	0	0	0	0.22	0.2	0	0.33	0	0	0.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	17.67
GTAATATACTAATCCGTGCA	0	0	0.16	0	0.26	0	0	0	0	0.2	0	0	0.22	0.33	0	0	0.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.37
GTAATATACTAATCCGTG	0	0	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.08
GTAATATACTAATCCGTGCAT	0	0	0.08	0.37	0.26	0.08	0	0	0	0	0	0	0	0.16	0	0	0	0	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.06
GTAATATACTAATCCGTGCATCCAT	0.25	0	0	0	0	0	0	0	0	0.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.45
GTAATATACTAATCCGTGCATCC	0.25	0	0	0	0.26	0.08	0	0	36.87	0	0.22	0.2	0	0.49	0	0	0	0	0.11	3.46	0	0	0	4.07	0	0	0	0	0	0	0	0	0	0	0	0	0	0	46.01
AATATACTAATCCGTGCATCCA	0	0	0	0	0	0	0	0	0	0	0	0	0	0.82	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.04
ATATACTAATCCGTGCATCCA	0	0	0.08	0	0	0	0	0	0	0.2	0.66	0	0.44	0	0	0	0.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.48
TATACTAATCCGTGCATCCA	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.41
ATACTAATCCGTGCATCCA	0	0	0	0	0	0	0	0	0	0	0.22	0	0.22	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.77
ACGTCATGTGGAACGTGCATCGGT	0	0	0	0	0	0	0	0	0	0	0	0	0	0.16	0	0	0	0	0	0	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.47
CGTCATGTGGAACGTGCATCGGT	0	0	0	0	0	0	0	0	0	0	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.22
ACGTGCATCGGTTCATAAGTGTGT	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.25
TGGTGCACGGGTTGTATGTGTGCA	0	0	0	0	0	0	0	0	0	0	0	0.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.2
GGTGCACGGGTTGTGTAT	0	0	0	0	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.26
GTGCACGGGTTGTATGT	0	0	0.08	0	0	0	0	0	0	0.2	0.44	0	0	1.15	0	0	0.5	0	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2.48
GTGCACGGGTTGTATGTGTGC	0.99	0	0	0	0	0	0	0	0	1.78	0.87	0	1.77	0.99	0	0	0.1	0	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6.61
GTGCACGGGTTGTATGTG	0	0	0.16	0	0	0.15	0	0	0	0	0	0	0	0	0	0	0.1	0	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.63
GTGCACGGGTTGTATGTGTGCAG	54.85	53.68	40.53	0.37	39.59	47.25	30.52	58.81	0	39.5	15.08	1.02	29.44	80.43	2.34	20.57	154.36	118.73	84.77	65.74	26.46	28.9	234.6	44.8	13.04	14.06	28.16	28.16	32.73	8.76	90.76	90.76	45.19	10.12	174.36	0	0	0	1808.42
GTGCACGGGTTGTATGTGTGCA	2.48	0.98	0	0	0.26	0.15	0	0	0	2.57	1.31	0.2	1.33	4.77	0	0	0.7	0	0.75	3.46	0	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	19.29
GTGCACGGGTTGTATGTG	0	0	0.16	0	0.26	0.08	0	0	0	0.2	0.22	0	0.22	0.66	0	0	0.5	0	0.43	3.46	0	0	0	12.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	18.41
GTGCACGGGTTGTATGTT	0	0	0	0	0	0.15	0	0	0	0.99	0.22	0	0	0.33	0	0	2.89	0	2.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7.06
TTGCACGGGTTGTATGTGC	1.49	0	0	0	0	0	0	11.76	0	0.2	0	2.65	0.89	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.51	11.08	0	112.58
TTGCACGGGTTGTATGTGTGCA	0.99	0	0.08	0	0.53	0	0	0	0	0.79	0.66	1.03	0.89	0.16	0	0	0.2	0	0.32	0	0	0	0	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6.45
TTGCACGGGTTGTATGTGTGCAG	0.25	1.22	0.39	0	1.32	0.6	0	0	0	0	0	0.41	0.22	0.16	0	0	3.48	0	0.43	3.46	0.41	0.33	23.46	0.15	0	0	0	0	0	8.76	0	0	0	0	0	0	0	0	53.46
TTGCACGGGTTGTATGTTG	0.25	0.24	0	0	0	0	0	0	0	0	0	0.81	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.38	0	5.14	95.82
TTGCACGGGTTGTATGTT	0.25	0	0	0	0	0	0	0	0	0	0	0.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.45
TGCACGGGTTGTATGTGT	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.1
TGCACGGGTTGTATGTGTGCAG	0	0.24	0	0	0	0	0	0	0	0.2	0	0	0	0	0	0	0.1	0	0	0	0	0	0	4.07	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4.61
TGCACGGGTTGTATGTGCA	0.25	0.24	0	0	0	0	0	0	0	0	0	0.2	0	0	0	0	0.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.79
GCACGGGTTGTATGTGTGCAG	0	0	0	0	0.26	0	0	0	0	0.39	0.44	0	0.66	0.16	0	0	0	4.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6
CACGGGTTGTATGTGTGCAG	0	0	0	0	0	0.15	0	0	0	0.59	0.22	0	0.22	0	0	0	0	4.09	0	0	0	0	0	0	0	0	0	0	10.91	0	0	0	0	0	0	0	0	0	16.18
ACGGGTTGTATGTGTGCAG	0.25	0	0	0	0	0	0	0	0	5.33	1.97	0.41	1.11	0	0	0	0	4.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	13.16

```
GTAATATACTAATCCGTGCATCCATCGTAATCTTACACGTCATGTAATCTTACACGTCATGTAAACGTGCATCGGTTCATAATGTGTGTTTATAATGTTAATGGTATGTGTGGTTGCACGGGTTGTATGTGTGCAG
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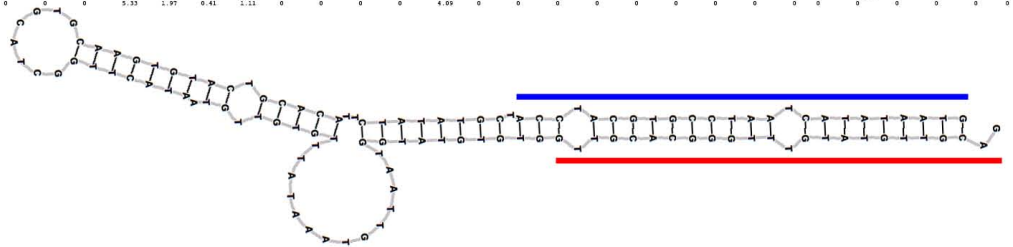
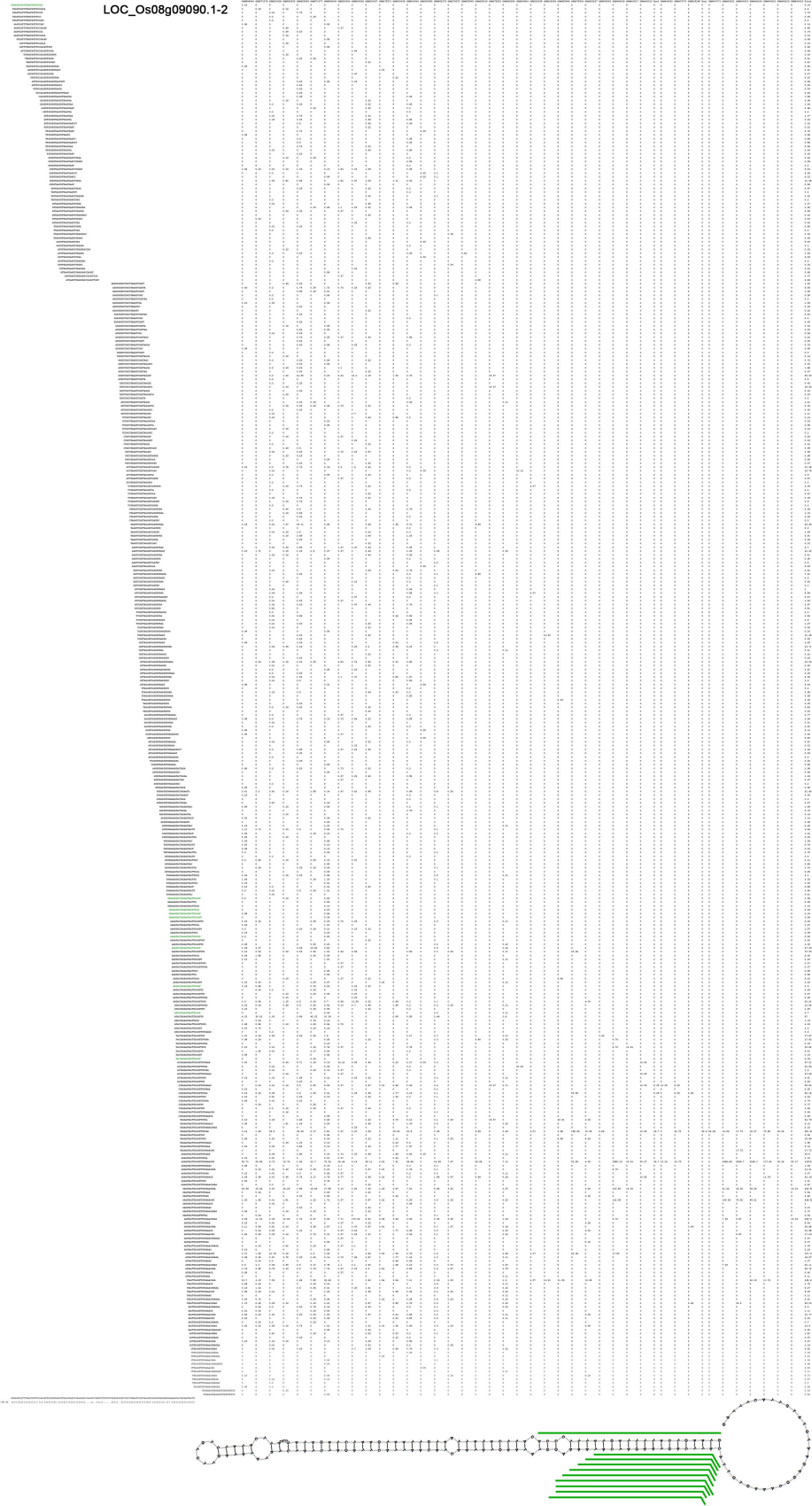


LOC_Os08g09090.1-2



LOC_Os08g42590.1-4

	GSM520637	GSM520638	GSM520640	GSM455965	Total
GTAAGTTGAACAAAATCATCAACA	0.66	0	0	0	0.66
TTGATGCTGATTTTGCGCATTTGTAG	0	0.2	0.59	0.25	1.04
TGATGCTGATTTTGCGCATTTGTAG	0	0.41	0.2	0	0.61
GATGCTGATTTTGCGCATTTGTAG	0.22	0	0.2	0	0.42
GCTGATTTTGCGCATTTGTA	0	0	0.2	0	0.2

```
       GTAAGTTGAACAAAATCATCAACATGGTTCATGCCCCATTTCTTGCAATCTTGATGCTGATTTTGCGCATTTGTAG
-12.80 .((((.((..(((((((((.((.((.((((((.............)).)))).)).)).)))))))))..)))))).... []
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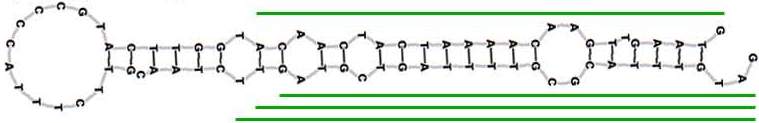

LOC_Os09g04260.1-13

	GSM686040	GSM693279	GSM329296	Total
CAAGACCAAGTTGATTATGCCG	0.08	0	0	0.08
ATGCCTTGATCAACCAATCT	0	0.1	0	0.1
CCTTGATCAACCAATCTGGAG	0	0	8.15	8.15

```
      GTGCACAAATTTCCAAGACCAAGTTGATTATGCCGTACAACATGCCTTGATCAACCAATCTGGAG
-12.20 ...........(((.(((....(((((((.((..........)).)))))))...))))))).  []
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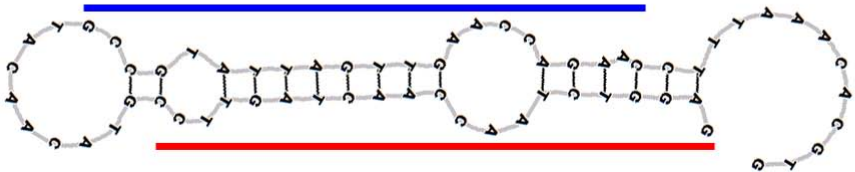

LOC_Os11g26670.1-2

	GSM686040	GSM686039	GSM278572	GSM455965	GSM520635	GSM520638	GSM693279	GSM571077	Total
GTAGACGAGCAGTTAGTAGGCTT	0.08	0.08	0.33	0	0	0	0	0	0.49
GTAGACGAGCAGTTAGTAGGCTTG	0	0	0	0.25	0	0	0	0	0.25
TAGACGAGCAGTTAGTAGGCTT	0	0	0	0	0.16	0	0	0	0.16
TAGACGAGCAGTTAGTAGGCT	0	0	0	0	0	0.2	0	0	0.2
GACGAGCAGTTAGTAGGCTT	0	0	0	0	0	0	0.1	0	0.1
TCTTCTCGTTTGTTTTTCTGCTAG	0	0	0	0	0	0	0	0.26	0.26

```
        GTAGACGAGCAGTTAGTAGGCTTGCGTGTGTGTTCTTCTCGTTTGTTTTTCTGCTAG
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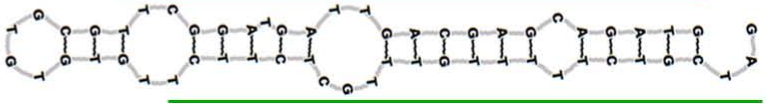
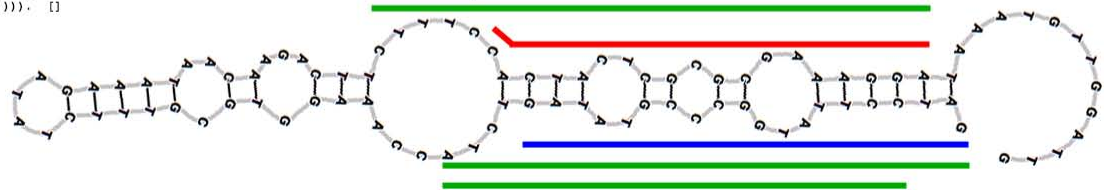


LOC_Os12g18060.1-1

	GSM571077	GSM520635	GSM693279	GSM278571	GSM278572	GSM686040	GSM693280	GSM520638	GSM686039	GSM329298	GSM455965	GSM520636	GSM520640	GSM520639	Total
TTGTAAATAGGAAAGCGCGCT	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0.26
TGTAAATAGGAAAGCGCGCTCATC	0	0.16	0.2	0.31	0.33	0	0	0	0	0	0	0	0	0	1
GTAAATAGGAAAGCGCGC	0	0	0	0	0	0.08	0	0	0	0	0	0	0	0	0.08
GTAAATAGGAAAGCGCGCTCATCA	0	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0.16
TAAATAGGAAAGCGCGCTCATCAC	0	0	0.1	0	0	0	0	0	0	0	0	0	0	0	0.1
AAATAGGAAAGCGCGCTCATC	0	0	0	0	0.33	0	0	0	0	0	0	0	0	0	0.33
AAATAGGAAAGCGCGCTCATCACC	0	0	0.1	0	0.33	0	0.11	0	0	0	0	0	0	0	0.54
AATAGGAAAGCGCGCTCATCACCT	0	0	0.1	0	0	0	0	0.2	0	0	0	0	0	0	0.3
ATAGGAAAGCGCGCTCATCACCTT	0	0	0.1	0	0	0	0	0	0	0	0	0	0	0	0.1
ATAGGAAAGCGCGCTCATCACC	0	0	0	0	0	0.08	0	0	0	0	0	0	0	0	0.08
TAGGAAAGCGCGCTCATCACC	0	0	0	0	0	0	0	0	0.23	0	0	0	0	0	0.23
TAGGAAAGCGCGCTCATCACCTT	0	0	0	0	0	0	0	0	0.08	0	0	0	0	0	0.08
AGGAAAGCGCGCTCATCAC	0	0	0	0	0	0.08	0	0	0	3.46	0	0	0	0	3.54
AGGAAAGCGCGCTCATCACCTTTC	0	0	0.1	0	0	0	0.11	0	0	0	0	0	0	0	0.21
AGGAAAGCGCGCTCATCACC	0	0	0	0	0	0	0	0.2	0	0	0	0	0	0	0.2
ACCTTTCTTCAGAACAATAAAGAT	0	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0.16
CTTCAGAACAATAAAGATATCTTT	0	0	0	0	0	0	0	0	0	0	0.25	0	0	0	0.25
AAAGATATCTTTGCGTGGAAACCA	0	0	0	0	0.33	0	0.11	0	0	0	0	0	0	0	0.44
AGATATCTTTGCGTGGAAACCATC	0	0	0	0	0	0	0	0	0	0	0	0.23	0	0	0.23
GGAAACCATCTGATATGCCCGGTAT	0	0	0.1	0	0	0	0	0	0	0	0	0	0	0	0.1
GGAAACCATCTGATATGCCCGGTA	0.26	0.16	0.2	0	0	0.15	0	0	0	0	0	0	0.2	0	0.97
GAAACCATCTGATATGCCCGGTAT	0	0.33	0	0	0	0	0	0	0	0	0	0	0	0.89	1.22
GAAACCATCTGATATGCCCGGTATT	0	0	0	0	0	0.08	0	0	0	0	0	0	0	0	0.08
GAAACCATCTGATATGCCCGGT	0	0	0	0	0	0	0	0.2	0	0	0	0	0	0	0.2
CATCTGATATGCCCGGTATTCCT	0	0	0	0	0	0.08	0	0	0	0	0	0	0	0	0.08
ATCTGATATGCCCGGTATTCC	0	0	0	0	0	0	0	0	0.08	0	0	0	0	0	0.08
ATCTGATATGCCCGGTATTCCTAG	0	0.16	0	0	0	0.08	0	0	0.08	0	0	0	0	0	0.32
GATATGCCCGGTATTCCTAG	0	0	0.1	0	0	0	0	0	0	0	0	0	0	0	0.1

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GTTAGGTTGTAAATAGGAAAGCGCGCTCATCACCTTTCTTCAGAACAATAAAGATATCTTTGCGTGGAAACCATCTGATATGCCCGGTATTCCTAG
-15.80  .............((((((..((.((..((((.....(((...((..(((((....)))))).)).)))......))))..)).)).)...)))))).  []
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