Supplementary information

Web Table 1. Number of cytosines methylated in different sequence contexts within 15 cloned PCR products of bisulfite treated DNA.

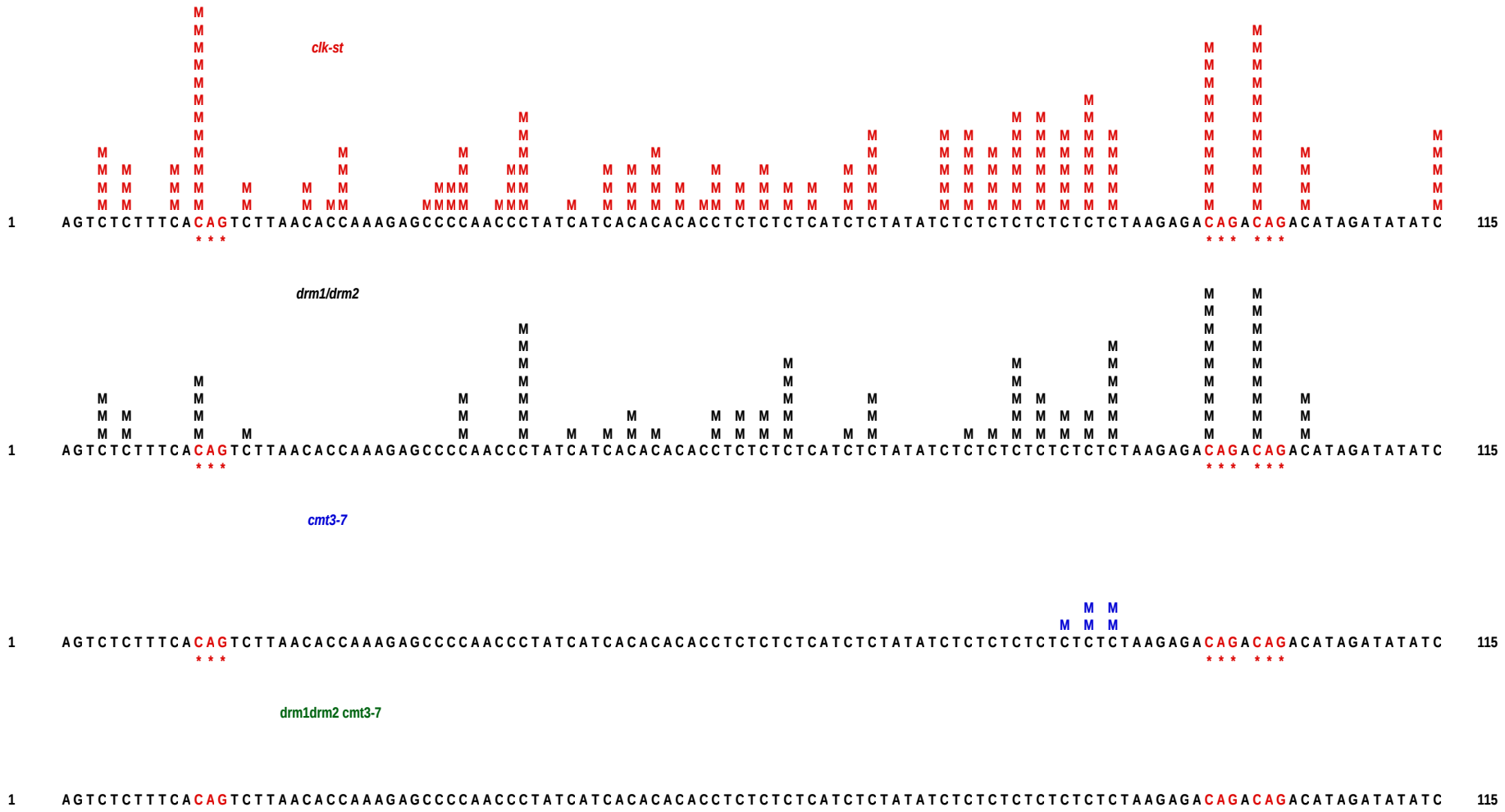
FWA 500 nt.	CpG	CpNpG*	Asym[†]
Total number of sites	300	210	990
Number methylated			
WS (wild type)	266 (89%)	38 (18%)	42 (4.2%)
drm1 drm2	243 (81%)	0 (0%)	0 (0%)
cmt3-7	279 (93%)	6 (2.9%)	63 (6.4%)
drm1 drm2 cmt3-7	263 (88%)	0 (0%)	0 (0%)

MEA-ISR 219 nt.	CpG	CpNpG	Asym
Total number of sites	135	15	255
Number methylated			
WS (wild type)	118 (87%)	7 (47%)	47 (18.4%)
drm1 drm2	117 (87%)	0 (0%)	0 (0%)
cmt3-7	120 (89%)	2 (13%)	32 (12.5%)
drm1 drm2 cmt3-7	117 (87%)	0 (0%)	0 (0%)

SUPERMAN region 1028 nt.	CpG	CpNpG	Asym
Total number of sites	135	405	3060
Number methylated			
Line *clk-st(*wild type*)*	22 (16%)	221 (55%)	497 (16%)#
drm1 drm2	19 (14%)	158 (39%)	266 (8.7%)
cmt3-7	12 (8.9%)	0 (0%)	175 (5.7%)#
drm1 drm2 cmt3-7	14 (10%)	0 (0%)	0 (0%)

[*] CpGpG sites are counted as CpG sites and not included in the CpNpG category.
[†]Asym (Asymmetric) is defined by cytosines within the context CpHpH, where H = A, T, or C. # Derived from previously published data (Lindroth et al., Science 292, 2077-2080).

Web Figure 1: Detailed methylation pattern at the *SUP* locus for *clk-st* (red), *drm1 drm2* (black) *cmt3-7* (blue), and *drm1 drm2 cmt3-7* (green). "M's" denote methylated cytosines from 15 individual cloned PCR products of bisulfite treated genomic DNA. The 27 CpNpG sites are shown in red and highlighted by red asterisks. The 9 CpG sites are shown in blue and highlighted by blue asterisks. The 1028 nucleotide sequence shown was assembled from 30 clones arising from two separate PCR products, which overlap by 78 base pairs. The two sequences were joined together at nucleotide 284.


clk-st
1 AGTCTCTTTCACAGTCTTAACACCAAAGAGCCCCAACCCTATCATCACACACACCTCTCTCTCATCTCTATATCTCTCTCTCTCTCTCTAAGAGACAGACAGACATAGATATATC 115
drm1/drm2
1 AGTCTCTTTCACAGTCTTAACACCAAAGAGCCCCAACCCTATCATCACACACACCTCTCTCTCATCTCTATATCTCTCTCTCTCTCTCTAAGAGACAGACAGACATAGATATATC 115
cmt3-7
1 AGTCTCTTTCACAGTCTTAACACCAAAGAGCCCCAACCCTATCATCACACACACCTCTCTCTCATCTCTATATCTCTCTCTCTCTCTCTAAGAGACAGACAGACATAGATATATC 115
drm1drm2 cmt3-7
1 AGTCTCTTTCACAGTCTTAACACCAAAGAGCCCCAACCCTATCATCACACACACCTCTCTCTCATCTCTATATCTCTCTCTCTCTCTCTAAGAGACAGACAGACATAGATATATC 115

clk-st

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116   TTAGATTTTTCCCAGGGGAAAAAAGTGAGTTCATCTTTTCAGATCTTACAAACACTTTGCTTTTATAAACTGATGTACCACAAATCATTACTAGTACTATCTTAATTATCTTTAC   230
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drm1/drm2

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116   TTAGATTTTTCCCAGGGGAAAAAAGTGAGTTCATCTTTTCAGATCTTACAAACACTTTGCTTTTATAAACTGATGTACCACAAATCATTACTAGTACTATCTTAATTATCTTTAC   230
```

cmt3-7

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116   TTAGATTTTTCCCAGGGGAAAAAAGTGAGTTCATCTTTTCAGATCTTACAAACACTTTGCTTTTATAAACTGATGTACCACAAATCATTACTAGTACTATCTTAATTATCTTTAC   230
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drm1drm2 cmt3-7

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116   TTAGATTTTTCCCAGGGGAAAAAAGTGAGTTCATCTTTTCAGATCTTACAAACACTTTGCTTTTATAAACTGATGTACCACAAATCATTACTAGTACTATCTTAATTATCTTTAC   230
```

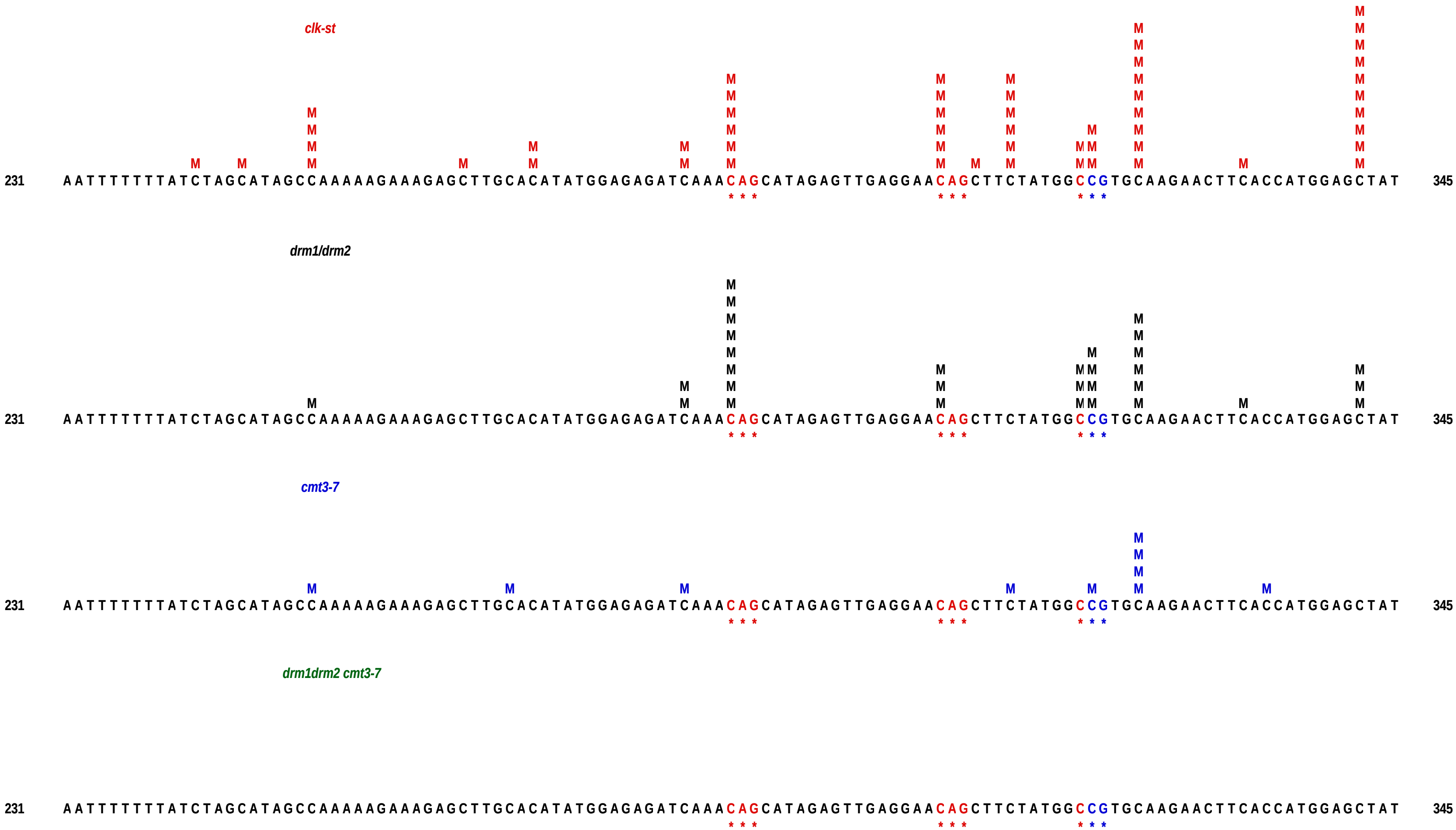
clk-st
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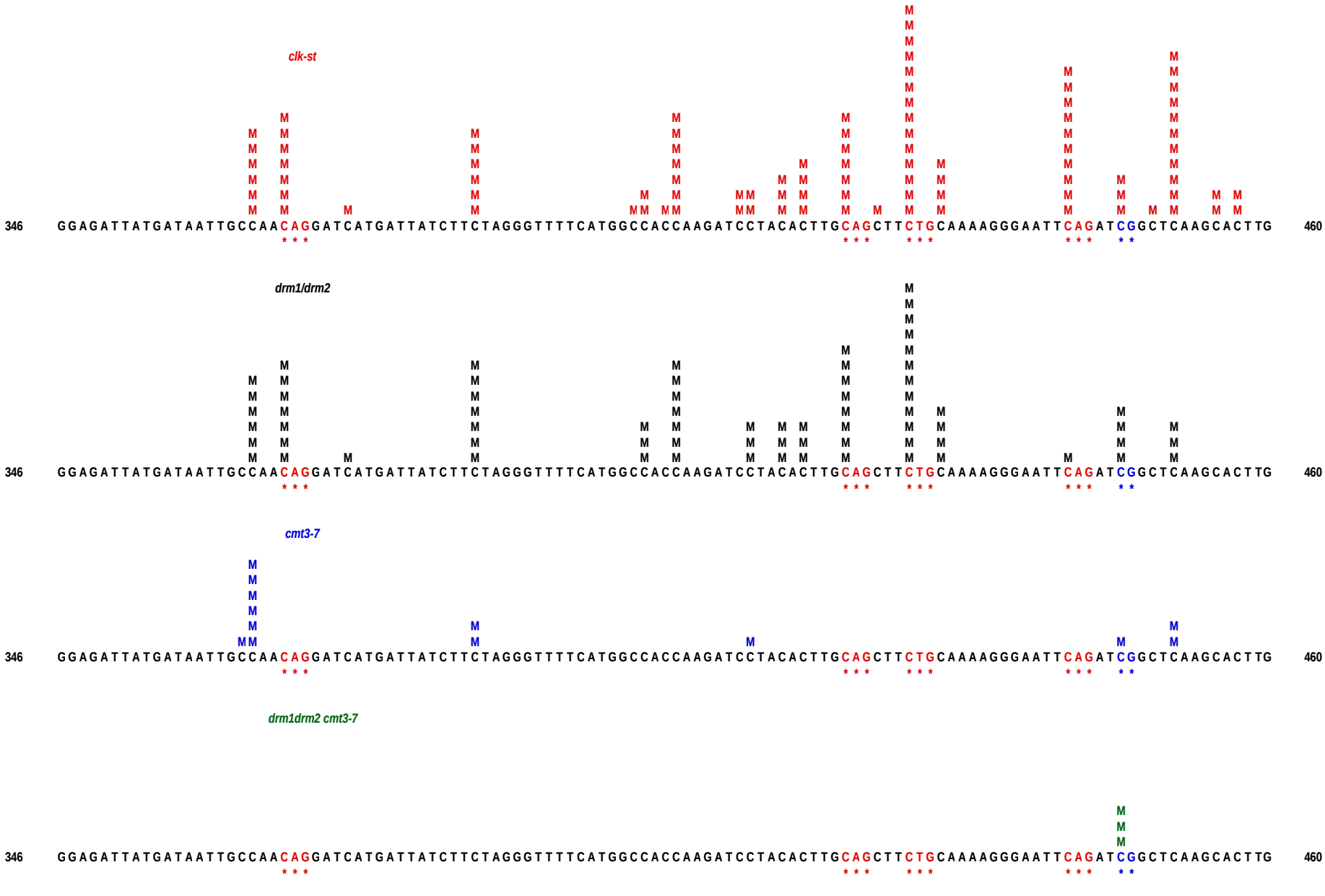
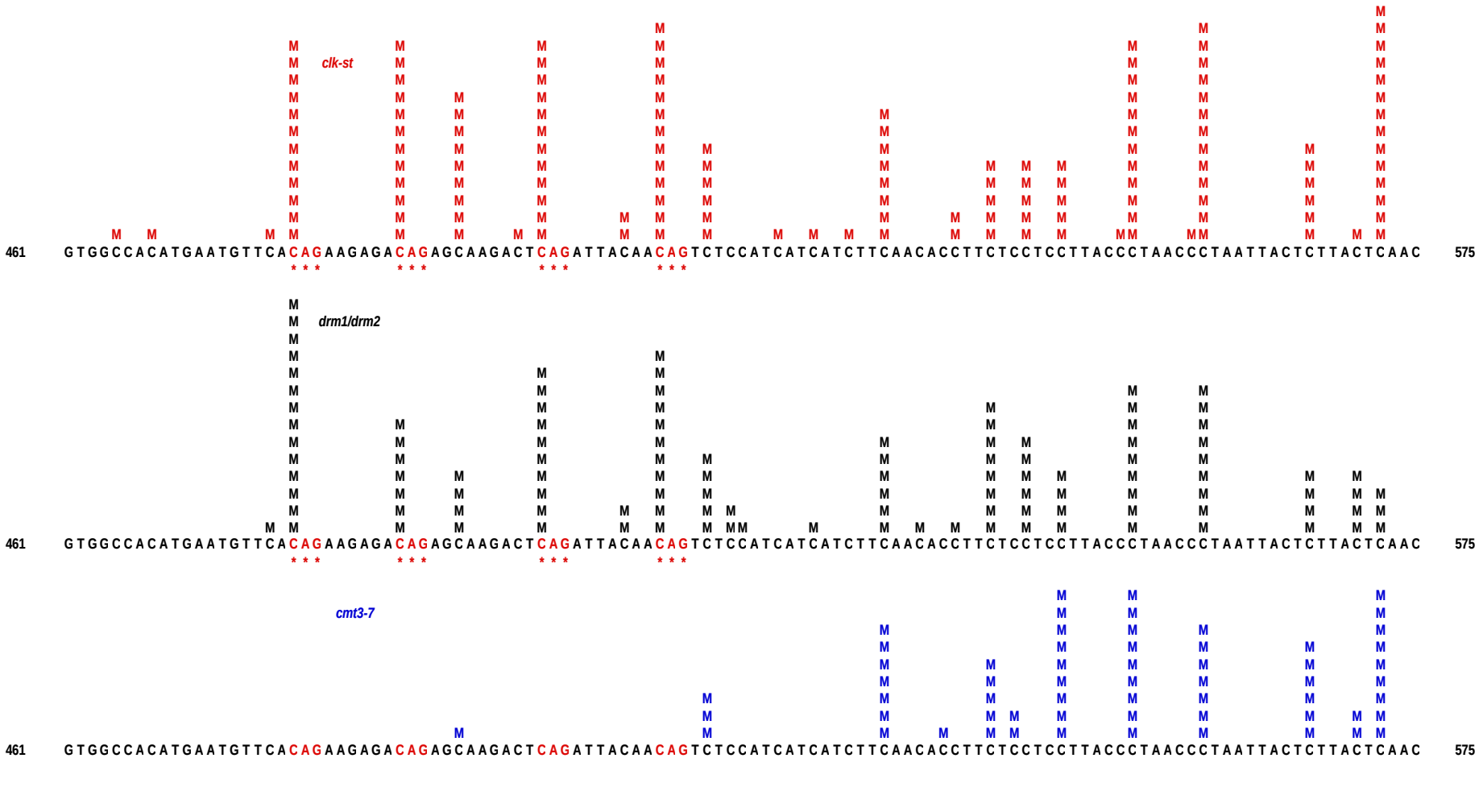
drm1/drm2
231 AATTTTTTTATCTAGCATAGCCAAAAAGAAAGAGCTTGCACATATGGAGAGATCAAACAGCATAGAGTTGAGGAACAGCTTCTATGGCCGTGCAAGAACTTCACCATGGAGCTAT 345
cmt3-7
231 AATTTTTTTATCTAGCATAGCCAAAAAGAAAGAGCTTGCACATATGGAGAGATCAAACAGCATAGAGTTGAGGAACAGCTTCTATGGCCGTGCAAGAACTTCACCATGGAGCTAT 345
drm1drm2 cmt3-7
231 AATTTTTTTATCTAGCATAGCCAAAAAGAAAGAGCTTGCACATATGGAGAGATCAAACAGCATAGAGTTGAGGAACAGCTTCTATGGCCGTGCAAGAACTTCACCATGGAGCTAT 345


clk-st
drm1/drm2
cmt3-7
drm1drm2 cmt3-7
346 GGAGATTATGATAATTGCCAACAGGATCATGATTATCTTCTAGGGTTTTCATGGCCACCAAGATCCTACACTTGCAGCTTCTGCAAAAGGGAATTCAGATCGGCTCAAGCACTTG 460


clk-st
461 GTGGCCACATGAATGTTCACAGAAGAGACAGAGCAAGACTCAGATTACAACAGTCTCCATCATCATCTTCAACACCTTCTCCTCCTTACCCTAACCCTAATTACTCTTACTCAAC 575
drm1/drm2
461 GTGGCCACATGAATGTTCACAGAAGAGACAGAGCAAGACTCAGATTACAACAGTCTCCATCATCATCTTCAACACCTTCTCCTCCTTACCCTAACCCTAATTACTCTTACTCAAC 575
cmt3-7
461 GTGGCCACATGAATGTTCACAGAAGAGACAGAGCAAGACTCAGATTACAACAGTCTCCATCATCATCTTCAACACCTTCTCCTCCTTACCCTAACCCTAATTACTCTTACTCAAC 575
drm1drm2 cmt3-7
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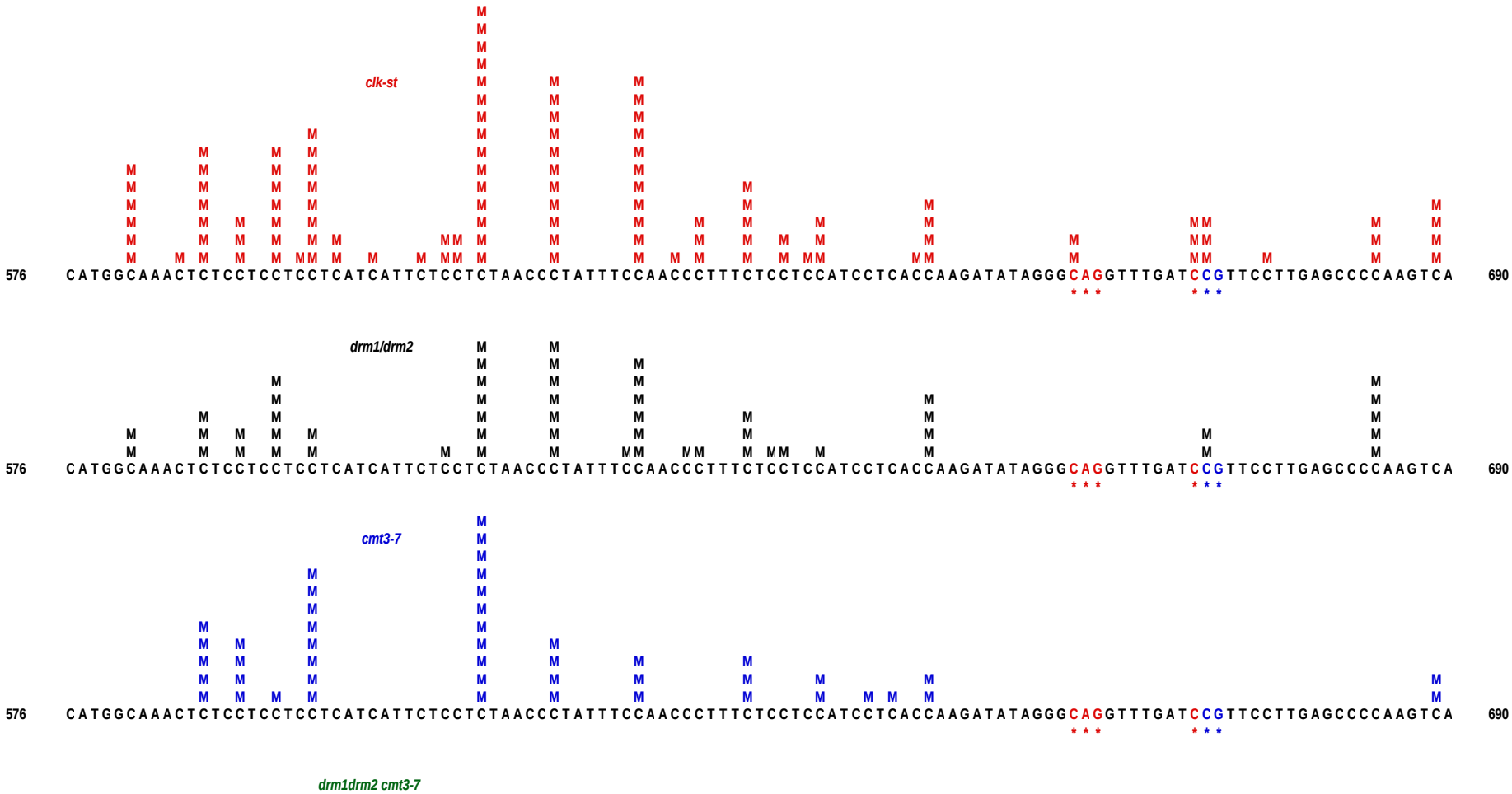
clk-st
576 CATGGCAAACTCTCCTCCTCCTCATCATTCTCCTCTAACCCTATTTCCAACCCTTTCTCCTCCATCCTCACCAAGATATAGGGCAGGTTTGATCCGTTCCTTGAGCCCCAAGTCA 690
drm1/drm2
576 CATGGCAAACTCTCCTCCTCCTCATCATTCTCCTCTAACCCTATTTCCAACCCTTTCTCCTCCATCCTCACCAAGATATAGGGCAGGTTTGATCCGTTCCTTGAGCCCCAAGTCA 690
cmt3-7
576 CATGGCAAACTCTCCTCCTCCTCATCATTCTCCTCTAACCCTATTTCCAACCCTTTCTCCTCCATCCTCACCAAGATATAGGGCAGGTTTGATCCGTTCCTTGAGCCCCAAGTCA 690
drm1drm2 cmt3-7
576 CATGGCAAACTCTCCTCCTCCTCATCATTCTCCTCTAACCCTATTTCCAACCCTTTCTCCTCCATCCTCACCAAGATATAGGGCAGGTTTGATCCGTTCCTTGAGCCCCAAGTCA 690

clk-st

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691   AAACATACACCAGAAAACGCTTGTAAGACTAAGAAATCATCTCTTTTAATGGAGGCTGGAGAGGCTACAAGGTTCACCAGTAAAGATGCTTGCAAGATCCTGAGGAATGATGAAA   805
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drm1/drm2

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691   AAACATACACCAGAAAACGCTTGTAAGACTAAGAAATCATCTCTTTTAATGGAGGCTGGAGAGGCTACAAGGTTCACCAGTAAAGATGCTTGCAAGATCCTGAGGAATGATGAAA   805
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cmt3-7

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691   AAACATACACCAGAAAACGCTTGTAAGACTAAGAAATCATCTCTTTTAATGGAGGCTGGAGAGGCTACAAGGTTCACCAGTAAAGATGCTTGCAAGATCCTGAGGAATGATGAAA   805
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drm1drm2 cmt3-7

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691   AAACATACACCAGAAAACGCTTGTAAGACTAAGAAATCATCTCTTTTAATGGAGGCTGGAGAGGCTACAAGGTTCACCAGTAAAGATGCTTGCAAGATCCTGAGGAATGATGAAA   805
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clk-st

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        M                                       M           M
        M                                       M           M                M
        M                                       M           M                M
        M                                       M           M     M     M    M           M
        M                                       M           M     M     M  MM           M  M
        M                               M       M     M     M     M     M  MM           M  M                    M     MM
806     TCATCAGCTTGGAGCTTGAGATTGGTTTGATTAACGAATCAGAGCAAGATCTGGATCTAGAACTCCGTTTGGGTTTCGCTTAATTAGATGGTAATAACTTTATCCATAAAGGATT    920
        * * *                               * *   * * *         * * *             * * *          * *
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drm1/drm2

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                                                M
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                                                M           M                           M
        M                                       M           M                           M
        M           M                           M           M                MM         M
806     TCATCAGCTTGGAGCTTGAGATTGGTTTGATTAACGAATCAGAGCAAGATCTGGATCTAGAACTCCGTTTGGGTTTCGCTTAATTAGATGGTAATAACTTTATCCATAAAGGATT    920
        * * *                               * *   * * *         * * *             * * *          * *
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cmt3-7

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                                                                                    M
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                                                                                    M
                                        M                       M         M         M  M
806     TCATCAGCTTGGAGCTTGAGATTGGTTTGATTAACGAATCAGAGCAAGATCTGGATCTAGAACTCCGTTTGGGTTTCGCTTAATTAGATGGTAATAACTTTATCCATAAAGGATT    920
        * * *                               * *   * * *         * * *             * * *          * *
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drm1drm2 cmt3-7

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                                                                                    M
806     TCATCAGCTTGGAGCTTGAGATTGGTTTGATTAACGAATCAGAGCAAGATCTGGATCTAGAACTCCGTTTGGGTTTCGCTTAATTAGATGGTAATAACTTTATCCATAAAGGATT    920
        * * *                               * *   * * *         * * *             * * *          * *
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clk-st

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                    M                           M
                    M                       M   M
    M               M                       M   M
    M         M     M                   M   M   M                       M   M                           M               M
921 CGAAGTTCACAATTCTAGAAGATATGATGCTTCTCTAAGGTTAATTAGTTTCATCCATATGAAATTCTCTAAGCTTGCTATTTAGTAGAACGTTATAGTTGATTATAT 1028
    * *                                                                                                         * *
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drm1/drm2

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                                                M
                                                M
    M                                           M
    M                                       M   M                                                               M
921 CGAAGTTCACAATTCTAGAAGATATGATGCTTCTCTAAGGTTAATTAGTTTCATCCATATGAAATTCTCTAAGCTTGCTATTTAGTAGAACGTTATAGTTGATTATAT 1028
    * *                                                                                                         * *
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cmt3-7

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                    M                           M
                    M                       M   M
                    M                       M   M                                                   M
    M               M                       M   M                                                   M
    M               M                       M   M                                       M           M
    M               M                       M   M                                       M           M
921 CGAAGTTCACAATTCTAGAAGATATGATGCTTCTCTAAGGTTAATTAGTTTCATCCATATGAAATTCTCTAAGCTTGCTATTTAGTAGAACGTTATAGTTGATTATAT 1028
    * *                                                                                                         * *
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drm1drm2 cmt3-7

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    M
    M
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    M
    M
    M
    M
921 CGAAGTTCACAATTCTAGAAGATATGATGCTTCTCTAAGGTTAATTAGTTTCATCCATATGAAATTCTCTAAGCTTGCTATTTAGTAGAACGTTATAGTTGATTATAT 1028
    * *                                                                                                         * *
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