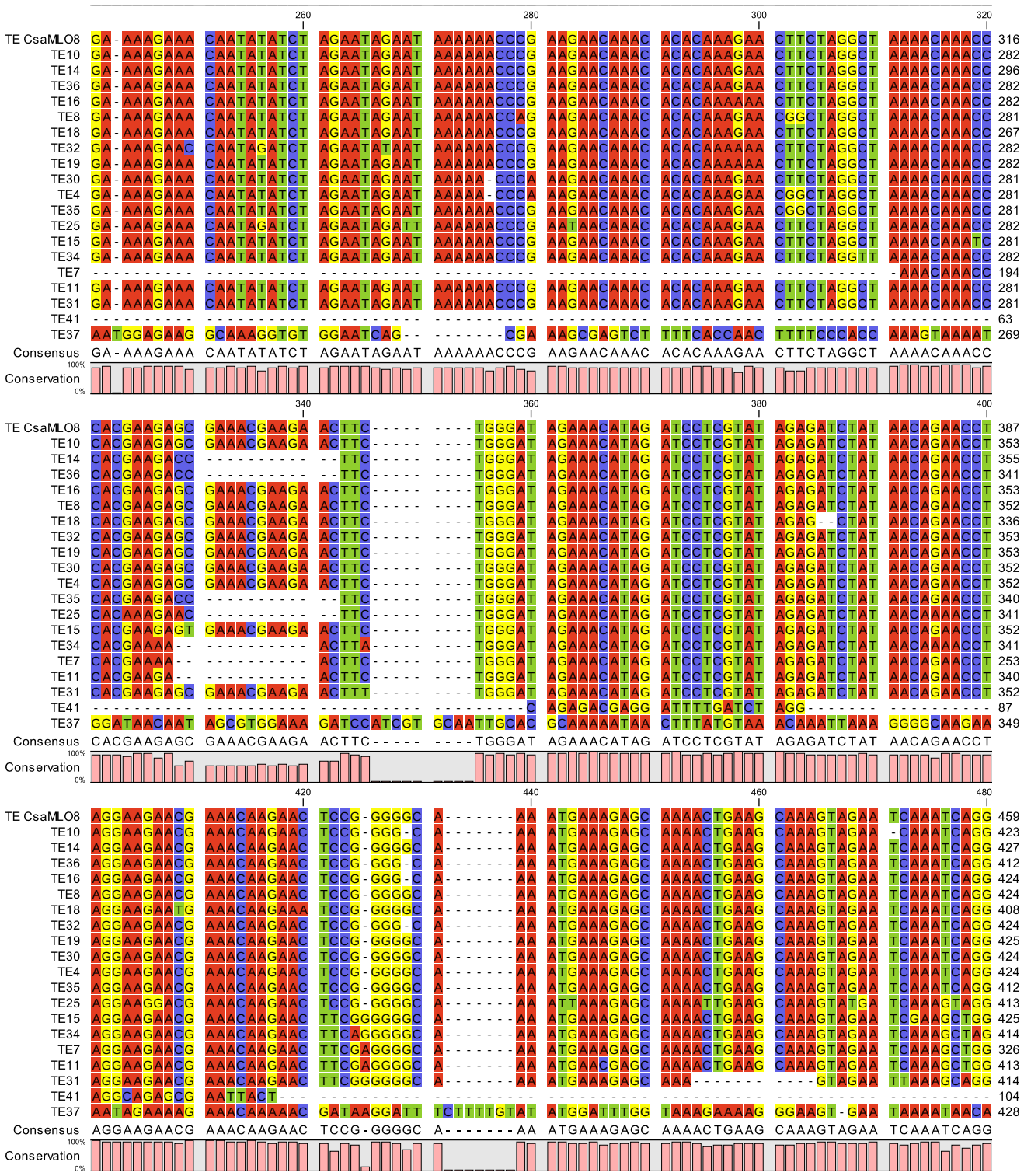
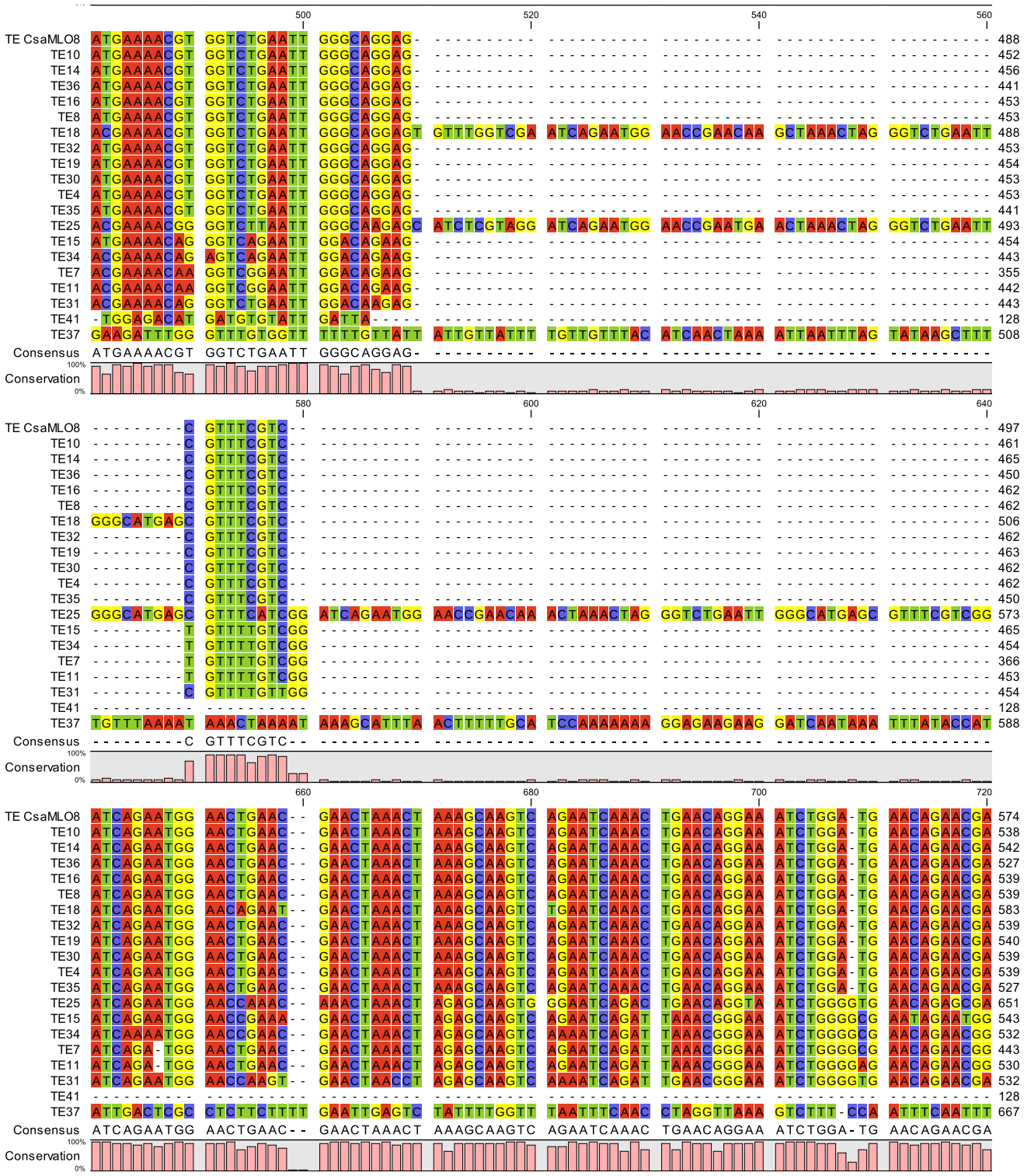
```
                                   20                                  40                                  60                                  80
                                    |                                   |                                   |                                   |
TE CsaMLO8   TGTTGATTTT  ATGGAATCAA  TCTATAT-TT  CATTCATTAC  TTAATAGAGA  TACAAGCCTA  TATATAACCA  TAGAGAAATA  79
TE10         TGTTGATTTT  ATGGAATTAA  TCTATAT-TT  CATTTATTAC  TTAATAGAGA  TACAAGCCTA  TATATAACCA  TAGAGAAATA  79
TE14         -GTTGATTTT  ATGGAATAAA  TCTATAT-TT  CATTCATTAC  TTAATAGAGA  TACAAGCCTA  TATATA-CCA  TAGAGAAATA  77
TE36         TGTTGATTTT  ATGGAATCAA  TCTATAT-TT  CATTCATTAC  TTAATAGAGA  TACAAGCCTA  TATATAACCA  TAGAGAAATA  79
TE16         TGTTGATTTT  ATGGAATTAA  TCTATAT-TT  CATTAATTAC  TTAATAGAGA  TACAAGCCTA  TATATAACCA  TAGAGAAATA  79
TE8          -GTTGATTTT  ATGGAATAAA  TCTATAT-TT  CATTTCTTAT  TTAGTAGAGA  TACAAGCCTA  TATATAACCA  TAGAGAAATA  78
TE18         ----------  -----ATCAA  TCTATAT-TT  CCTTAATTAC  TTAATAGAGA  TACAAGCCTA  TATATAACCA  TAGAGAAATA  64
TE32         TGTTGATTGT  ATGGAATAAA  TCTATAT-TT  CATTTATTAT  TTAGTAGAGA  TACAAGCCTA  TATATAACCA  TAGAGAAATA  79
TE19         TGTTGATTTT  ATGGAATAAA  TCTATAT-TT  CATTCATTAT  TTAATAGAGA  TACAAGCCTA  TATATAACCA  TAGAGAAATA  79
TE30         TGTTGATTTT  ATGGAATAAA  TCTATAT-TT  CTTTTATTAT  TTAGTAGAGA  TACAAGCCTA  TATATAACCA  TAGAGAAATA  79
TE4          TGTTGATTTT  ATGGAATAAA  TCTATAT-TT  CATTTATTAT  TTAGTAGAGA  TACAAGCCTA  TATATAACCA  TAGAGAAATA  79
TE35         -GTTGATTTT  ATGGAATTAA  TCTATAT-TT  CATTCATTAT  TTAATAGAGA  TACAAGCTTA  TATATAACCA  TAGAGAAATA  78
TE25         GTTGTTTTAT  ATGGAATGAA  TCTCTAT-TT  CCTTAATCAT  TTAATAGAGG  TACAAGCCTA  TATATAACCA  TAGAGAAATA  79
TE15         -GTTGATTTT  ATGGAATTAA  TCTATAT-TT  CATTCATTAT  TTAGTAGAGA  TACAAGCCTA  TATATAACCA  TAGAGAAATA  78
TE34         TGTTGATTTT  ATGGAATTAA  TCTATAT-TT  CATTCATTAT  TTAGTAGAAA  TACAAGCCTA  TATATAACCA  TAGAGAAATA  79
TE7          TGTTGATTTT  ATGGAATAAA  TCTATATATT  CATTTATTAT  TTAGTAGAGA  TAAAAGCCTA  TATATAACCA  TAGAGAAATA  80
TE11         -GTTGATTTT  ATGGAATTAA  TCTATAT-TT  CATTCATTAT  TTAGTAGAGA  TACAAGCCTA  TATATAACCA  TAGAGAAATA  78
TE31         -GTTGATTTT  ATGGAATTAA  TCTCTAT-TT  CATTAATTAT  TTAGTAGAGG  TACAAGTTTA  TATATAACCA  TAGAGAAATA  78
TE41         TGTTGATTTT  ATGGAATCAA  TCTATAT-TT  CATTAATTAC  TTAATATGG-  ----------  ----CGGCGG  CAGCAGAAT-  63
TE37         -GTTGATTTT  ATGGAATAAA  TCTATAT-TT  CATTTATTAT  TTAGTAGAGA  TAAAAGCCTA  TATATAACCA  TAGAGAAATA  78
Consensus    TGTTGATTTT  ATGGAATAAA  TCTATAT-TT  CATTCATTAT  TTANTAGAGA  TACAAGCCTA  TATATAACCA  TAGAGAAATA
100%
Conservation
0%

                                  100                                 120                                 140                                 160
                                    |                                   |                                   |                                   |
TE CsaMLO8   CACTTAAGGA  AATAATATCA  AATAATATCT  CCTAAGAATA  ATATCTCCTA  AGAATAATAT  CTCCTAAGAA  TAATATCTCC  159
TE10         CACTTAAGCA  AATAATATCA  AATAATATCT  CC--------  ----------  AGAATAATAT  CTCCTAA---  ----------  128
TE14         CACTTAAGGA  AATAATATCA  AATAATATCT  CC--------  ----------  AGAATAATAT  CTCCTAACAA  TAATATCTCC  139
TE36         CACTTAAGCA  AATAATATCA  AATAATATCT  CC--------  ----------  AGAATAATAT  CTCCTAA---  ----------  128
TE16         CACTTAAGGA  AATAATATCA  AATAATATCT  CC--------  ----------  AGAATAATAT  CTCCTAA---  ----------  128
TE8          CACTTAAGGA  AATAATATCA  AATAATATCT  CT--------  ----------  AGAATTATAT  CTCCTAAT--  ----------  128
TE18         CACTTAAGGA  AATAATATCA  AATAATATCT  CT--------  ----------  AGAATTATAT  CTCCTAAT--  ----------  114
TE32         CACTTAAGGA  AATAATATCA  AATAATATCT  CT--------  ----------  AGAATTATAT  CTCCTAAT--  ----------  129
TE19         CACTTAAGGA  AATAATATCA  AATAATATCT  CT--------  ----------  AGAATAATAT  CTCCTAA---  ----------  128
TE30         TACTTAAGGA  AATAATATCA  AATAATATCT  CC--------  ----------  AGAATAATAT  CACCTAA---  ----------  128
TE4          CACTTAAGGA  AATAATATCA  AATAATATCT  CT--------  ----------  AGAATTATAT  CTCCTAAT--  ----------  129
TE35         CACTTAAGGA  AATAATATCA  AATAATATCT  CC--------  ----------  AGAATAATAT  CTCCTAA---  ----------  127
TE25         CACTTAAGGA  AATAATATCA  AATAATATCT  TC--------  ----------  ATAATAATAT  CACCTAA---  ----------  128
TE15         CACTTAAGGA  AATAATATCA  AATAATATCT  CC--------  ----------  AGAATAATAT  CTCCTAA---  ----------  127
TE34         CACTTAAGGA  AATAATATCA  AATAATATCT  CC--------  ----------  AAAATAATAT  CTCCTAA---  ----------  128
TE7          CA--------  AATAATATCA  AATAATATCT  CT--------  ----------  AGAATTATAT  CTCCTAA---  ----------  121
TE11         CACTTAAGGA  AATAATATCA  AATAATATCT  CC--------  ----------  AAAATAATAT  CTCCTAA---  ----------  127
TE31         CACTTAAGGA  CATAATATCA  AATAATATCT  CA--------  ----------  TGAATAATAT  CACCTAA---  ----------  127
TE41         ----------  ----------  ----------  ----------  ----------  ----------  ----------  ----------  63
TE37         CACTTAAGGA  AATAATATCA  AATAATATCT  CT--------  ----------  AGAATTATAT  CTCCTAAT--  ----------  128
Consensus    CACTTAAGGA  AATAATATCA  AATAATATCT  CC--------  ----------  AGAATAATAT  CTCCTAA---  ----------
100%
Conservation
0%

                                  180                                 200                                 220                                 240
                                    |                                   |                                   |                                   |
TE CsaMLO8   TAAGAATAAT  CTAATTATAT  TAATACCCTC  CCTCAAACTC  AAGGTTGAAA  TCA--CAAAC  TTGAGTTTGC  TAAGAACTAA  237
TE10         ---GAATAAT  CTAATTATAT  TAATACCCTC  CCTCAAACTC  AAGGTTGAAA  TCA--CAAAC  TTGAGTTTGC  TAAGAACTAA  203
TE14         TAAGAATAAT  CTAATTATAT  TAATACCCTC  CCTCAAACTC  AAGGTTGAAA  TCA--CAAAC  TTGAGTTTGC  TAAGAACTAA  217
TE36         ---AAATAAT  CTAATTATAT  TAATACCCTC  CCTCAAACTC  AAGGTTGAAA  TCA--CAAAC  TTGAGTTTGC  TAAGAACTAA  203
TE16         ---GAATAAT  CTAATTATAT  TAATACCCTC  CCTCAAACTC  AAGGTTGAAA  TCA--CAAAC  TTGAGTTTGC  TAAGAACTAA  203
TE8          ----AATAAT  CTAATTATAT  TAATACCCTC  CCTCAAACTC  AAGGTTGAAA  TCA--CAAAC  TTGAGTTTGC  TAAGAACTAA  202
TE18         ----AATAAT  CTAATTATAT  TAATACCCTC  CCTCAAACTC  AAGGTTGAAA  TCA--CAAAC  TTGAGTTTGC  TAAGAACTAA  188
TE32         ----AATAAT  CTAATTATAT  TAATACCCTC  CCTCAAACTC  AAGGTTGAAA  TCA--CAAAC  TTGAGTTTGC  TAAGAACTAA  203
TE19         ---GAATAAT  CTAATTATAT  TAATACCCTC  CCTCAAACTC  AAGGTTGAAA  TCA--CAAAC  TTGAGTTTGC  TAAGAACTAA  203
TE30         ---GAATAAT  CTAATTATAT  TAATACCCTC  CCTCAAACTC  AAGGTTGAAA  TCA--CAAAC  TTGAGTTTGC  TAAGAACTAA  203
TE4          ----AATAAT  CTAATTATAT  TAATACCCTC  CCTCAAACTC  AAGGTTGAAA  TCA--CAAAC  TTGAGTTTGC  TAAGAACTAA  203
TE35         ---GAATAAT  CTAATTATAT  TAATACCCTC  CCTCAAACTC  AAGGTTGAAA  TCA--CAAAC  TTGAGTTTGC  TAAGAACTAA  202
TE25         ---GAATAAT  CTAATTACAT  TAATACCCTC  CCTCAAACTT  AAGGTTGAAA  TCA--CAAAC  TTGAGTTTGC  TAAGAACTAA  203
TE15         ---GAATAAT  CTAATTATAT  TAATACCCTC  CCTCAAACTC  AAGGTTGAAA  TCA--CAAAC  TTGAGTTTGC  TAAGAACTAA  202
TE34         ---GAATAAT  CTAATTATAT  TAATACCCTC  CCTCAAACTC  AAGGTTGAAA  TCA--CAAAC  TTGAGTTTGC  TAAGAACTAA  203
TE7          ---GAATAAT  CTAATTATAT  TAATACCCTC  CCTCAAACTC  AAGGTTGAAA  TCTTTCAACC  TTGAGTT---  ----------  185
TE11         ---GAATAAT  CTAATTATAT  TAATACCCTC  CCTCAAACTC  AAGGTTGAAA  TCA--CAAAC  TTGAGTTTGC  TAAGAACTAA  202
TE31         ---GAATAAT  CTAATTATAT  TAATACCCTC  CCTCAAACTC  AAGGTTGAAA  TCA--CAAAC  TTGAGTTTGC  TAAGAACTAA  202
TE41         ----------  ----------  ----------  ----------  ----------  ----------  ----------  ----------  63
TE37         ----AATAAT  CTAATTATAT  TAATACTCTT  ----AAACAC  TGTATC--AT  TTAGGAAAGA  CTAATTTGAA  TGAAAGGTAA  198
Consensus    ---GAATAAT  CTAATTATAT  TAATACCCTC  CCTCAAACTC  AAGGTTGAAA  TCA--CAAAC  TTGAGTTTGC  TAAGAACTAA
100%
Conservation
0%
```


TE CsaMLO8
TE10
TE14
TE36
TE16
TE8
TE18
TE32
TE19
TE30
TE4
TE35
TE25
TE15
TE34
TE7
TE11
TE31
TE41
TE37
Consensus
Conservation
100%
0%


TE CsaMLO8
TE10
TE14
TE36
TE16
TE8
TE18
TE32
TE19
TE30
TE4
TE35
TE25
TE15
TE34
TE7
TE11
TE31
TE41
TE37
Consensus
Conservation
100%
0%

```
                                   740       760       780       800
TE CsaMLO8  AAACTGAAGA GAACTGAGAG GTTGAGTAGA TAGAGAACTT T--------- -----GCGGC GTTCTTCGCA AA-------A 633
TE10        AAACTGAAGA GAACTGAGAG GTTGAGTAGA TAGAGAACTT T--------- -----GCGGC GTTCTTCGCA AA-------A 597
TE14        AAACTGAAGA GAACTGAGAG GTTGAGTAGA TAGAGAACTT T--------- -----GCGGC GTTCTTCGCA AA-------A 601
TE36        AAACTGAAGA GAACTGAGAG GTTGAGTAGA TAGAGAACTT T--------- -----GCGGC GTTCTTCGCA AA-------A 586
TE16        AAACTGAAGA GAACTGAGAG GTTGAGTAGA TAGAGAACTT T--------- -----GCGGC GTTCTTCGCA AA-------A 598
TE8         AAACTGAAGA GAACTGAGAG GTTGAGTAGA TAGAGAACTT T--------- -----GCGGC GTTCTTCGCA AA-------A 598
TE18        AAACTGAAGA GAACTGAGAG GTTGAGTAGA TAGAGAACTT T--------- -----GCGGC GTTCTTCGCA AA-------A 642
TE32        AAACTGAAGA GAACTGAGAG GTTGAGTAGA TAGAGAACTT T--------- -----GCGGC GTTCTTCGCA AA-------A 598
TE19        AAACTGAAGA GAACTGAGAG GTTGAGTAGA TAGAGAACTT T--------- -----GCGGC GTTCTTCGCA AA-------A 599
TE30        AAACTGAAGA GAACTGAGAG GTTGAGTAGA TAGAGAACTT T--------- -----GCGGC GTTCTTCGCA AA-------A 598
TE4         AAACTGAAGA GAACTGAGAG GTTGAGTAGA TAGAGAACTT T--------- -----GCGGC GTTCTTCGCA AA-------A 598
TE35        AAACTGAAGA GAACTGAGAG GTTGAGTAGA TAGAGAACTT T--------- -----GCGGC GTTCTTCGCA AA-------A 586
TE25        AAACTGAACA GAGTTGAGAG GTTGAGCGGA TAGAGGGCTA T--------- -----GCGGC GTTCTTCGCA AA-------C 710
TE15        AAACTGAACT GAA-------- -TGGAGCATA AAG---GCTT A--------- -----GCGGA TTTGAACAAA AA-------C 591
TE34        AAACTGAACT GAA-------- -TGGAGCAGA GAG---GCTT A--------- -----GCGGA TCTGAACAAA AA-------C 580
TE7         AAACTGAACT GAA-------- -TGGAGCAGA GAG---GCTT A--------- -----GCGGA TCTGAACAAA AA-------C 491
TE11        AAGCTGCACT GAA-------- -TGGAGCAGA GAG---GCTT A--------- -----GCGGA TCTGAACAAA AA-------C 578
TE31        AAACCGAACT GAA-------- -TGGAGTAGA GAG---GCCT A--------- -----GCGGA TCTGAACAAA AA-------C 580
TE41        ---CTGATG- ---------- ---------- ---------- ---------- ---------- ---------- ---------- 134
TE37        ACGTTAAAGA TAATTATGCT AATTAGCTTG AAATAACTTT TTTTCTTTTT TTCCGATTGG TCTCTTAGGA AATTCAGTTA 747
Consensus   AAACTGAAGA GAACTGAGAG GTTGAGTAGA TAGAGAACTT T--------- -----GCGGC GTTCTTCGCA AA-------A
100%
Conservation
0%

                                   820       840       860       880
TE CsaMLO8  AGAGAAGATG CGTTTCATGA CGGCGAGCTT C-----ACAA ATGGAGAGCG GACA---AAG ----CCGAAC CTGTGCGTCG 701
TE10        AGAGAAGATG CGTTTCATGA CGGCGAGCTT C-----ACAA ATGGAGAGCG GACA---AAG ----CCGAAC CTGTGCGTCG 665
TE14        AGAGAAGATG CGTTTCATGA CGGCGAGCTT C-----ACAA ATGGAGAGCG GACA---AAG ----CCGAAC CTGTGCGTCG 669
TE36        AGAGAAGATG CGTTTCATGA CGGCGAGCTT C-----ACAA ATGGAGAGCG GACA---AAG ----CCGAAC CTGTGCGTCG 654
TE16        AGAGAAGATG CGTTTCATGA CGGCGAGCTT C-----ACAA ATGGAGAGCG GACA---AAG ----CCGAAC CTGTGCGTCG 666
TE8         AGAGAAGATG CGTTTCATGA CGGCGAGCTT C-----ACAA ATGGAGAGCG GACA---AAG ----CCGAAC CTGTGCGTCG 666
TE18        AGAGAAGATG CGTTTCATGA CGGCGAGCTT C-----ACAA ATGGAGAGCG GACA---AAG ----CCGAAC CTGTGCGTCG 710
TE32        AGAGAAGATG CGTTTCATGA CGGCGAGCTT C-----ACAA ATGGAGAGCG GACA---AAG ----CCGAAC CTGTGCGTCG 666
TE19        AGAGAAGATG CGTTTCATGA CGGCGAGCTT C-----ACAA ATGGAGAGCG GACA---AAG ----CCGAAC CTGTGCGTCG 667
TE30        AGAGAAGATG CGTTTCATGA CGGCGAGCTT C-----ACAA ATGGAGAGCG GACA---AAG ----CCGAAC CTGTGCGTCG 666
TE4         AGAGAAGATG CGTTTCATGA CGGCGAGCTT C-----ACAA ATGGAGAGCG GACA---AAG ----CCGAAC CTGTGCGTCG 666
TE35        AGAGAAGATG CGTTTCATGA CGGCGAGCTT C-----ACAA ATGGAGAGCG GACA---AAG ----CCGAAC CTGTGCGTCG 654
TE25        AGAGAAGATG GGTTTCATGG CGGCGAGCTT C-----ACGA ACGGAGAGCA GACG---GAG ----CCGAAC TTGCGCGTTG 778
TE15        AGAAACGAGG CGTCGT-TGG ATCTGGGCTT CGATCTAAAC TTTGAAGGCA GACATGAAGG ----ATGGGT TTGAATGAAA 666
TE34        AGAAACGAGG CGTCGT-TGG ATCTGGGCTT CGATCTAAAC TTTGAAGGCA GACATGTAGG ----ATAGGT CTGAACGAAA 655
TE7         AGAATGGAGG CGTCGT-TGG ATCTGGGCTT CGATCTAAAC TTCAAAGGCA GACATGAAGA ----ATGGGT CTGAATGAAA 566
TE11        AGAAACGAGG CGTCGT-TGG ATCTGGGCTT CGATCTAAAC TTTGAAGGCA GACATGAAGG ----ATGGGT CTGAACGAAA 653
TE31        AAAATCGAGG CGCCGT-TGG ATTTGGGCTT CGATCTAAAC TTCAAAGGCA GACATGAAGG ----ATGGGT CTGAACGAAA 655
TE41        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- 134
TE37        TGAAAACAAA TATAATGCAA GAATGACATT CTAAGGTTGC AT-GAGATCG GATGTGGAAA ATATCCAAAC TATTAAATTC 826
Consensus   AGAGAAGATG CGTTTCATGA CGGCGAGCTT C-----ACAA ATGGAGAGCG GACA---AAG ----CCGAAC CTGTGCGTCG
100%
Conservation
0%

                                   900       920       940       960
TE CsaMLO8  TCGGCTGTGA GTGGAGCGGA ---GCGGTGG AT-CA-TGGA TCTGA----A CAAA--GATT CACCCTCTTC ---AGGATCG 767
TE10        TCGGCTGTGA GTGGAGCGGA ---GCGGTGG AT-CA-TGGA TCTGA----A CAAA--GATT CACCCTCTTC ---AGGATCG 731
TE14        TCGGCTGTGA GTGGAGCGGA ---GCGGTGG AT-CA-TGGA TCTGA----A CAAA--GATT CACCCTCTTC ---AGGATCG 735
TE36        TCGGCTGTGA GTGGAGCGGA ---GCGGTGG AT-CA-TGGA TCTGA----A CAAA--GATT CACCCTCTTC ---AGGATCG 720
TE16        TCGGCTGTGA GTGGAGCGGA ---GCGGTGG AT-CA-TGGA TCTGA----A CAAA--GATT CACCCTCTTC ---AGGATCG 732
TE8         TCGGCTGTGA GTGGAGCGGA ---GCGGTGG AT-CA-TGGA TCTGA----A CAAA--GATT CACCCTCTTC ---AGGATCG 732
TE18        TCGGCTGTGA GTGGAGCGGA ---GCGGTGG AT-CA-TGGA TCTGA----A CAAA--GATT CACCCTCTTC ---AGGATCG 776
TE32        TCGGCTGTGA GTGGAGCGGA ---GCGGTGG AT-CA-TGGA TCTGA----A CAAA--GATT CACCCTCTTC ---AGGATCG 732
TE19        TCGGCTGTGA GTGGAGCGGA ---GCGGTGG AT-CA-TGGA TCTGA----A CAAA--GATT CACCCTCTTC ---AGGATCG 733
TE30        TCGGCTGTGA GTGGAGCGGA ---GCGGTGG AT-CA-TGGA TCTGA----A CAAA--GATT CACCCTCTTC ---AGGATCG 732
TE4         TCGGCTGTGA GTGGAGCGGA ---GCGGTGG AT-CA-TGGA TCTGA----A CAAA--GATT CACCCTCTTC ---AGGATCG 732
TE35        TCGGCTGTGA GTGGAGCGGA ---GCGGTGG AT-CA-TGGA TCTGA----A CAAA--GATT CACCCTCTTC ---AGGATCG 720
TE25        TCGTCTATGA GTGGGGTGGA ---GCTGTGG AT-CA-TGGA TCTGA----A CAGA--GATT CAGCTTCTTC GTCAGGATTG 847
TE15        TTAGACAGAC ---------- TTGGAGGCGG ATGCG-AGGA TCTGAGGACA TGGG--GTTT CATGGGTTTT GTCGAGA--- 730
TE34        TTAGACAGAT CTGGAACAGA TTGGAGGCAG ACGCG-AGGA TCTGAGGACA TGGG--GTTT CATGG-TTTT GTTGGAA--- 728
TE7         TCATACAGGT CTGGAACAAA TTGGAGGCGG ACGCG-AGGA TCTGAGGACA TGGG--GTTT CATGG-TTTT GTTGGGA--- 639
TE11        TTAGACAGAT CTGGAACAGA TTGAAGGCAG ACGCG-AGGA TCTGAGGACA TGGG--GTTT CATGG-TTTT GTTGGGA--- 726
TE31        TCAGACAGAC CTGGGATAGA TTGAAGGCGG ACACG-AGGA TCTGAGGACA TGGG--GTTT CGTTGGTTTT GTCGGGA--- 729
TE41        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- 134
TE37        TAATCTTTAT CTAAATCCTA TGTTTAGGCA TTACAATAAA TCTTAAGTCA CCATTTAATA TATTCTCTTG ATAAATACCT 906
Consensus   TCGGCTGTGA GTGGAGCGGA ---GCGGTGG AT-CA-TGGA TCTGA----A CAAA--GATT CACCCTCTTC ---AGGATCG
100%
Conservation
0%
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                                980       1,000     1,020     1,040
TE CsaMLO8  GGAGTCTTCA ATCTAAAGAG ATTGTCTGGT ACGAGTAAAG GGCGGCGGCG GCAGGTCGGT CTGATCTTGA ACAGT--ATG 845
TE10        GGAGTCTTCA ATCTAAAGAG ATTGTCTGGT ACGAGTAAAG GGCGGCGGCG GCAGGTCGGT CTGATCTTGA ACAGT--ATG 809
TE14        GGAGTCTTCA ATCTAAAGAG ATTGTCTGGT ACGAGTAAAG GGCGGCGGCG GCAGGTCGGT CTGATCTTGA ACAGT--ATG 813
TE36        GGAGTCTTCA ATCTAAAGAG ATTGTCTGGT ACGAGTAAAG GGCAGCGGCG GCAGGTCGGT CTGATCTTGA ACAGT--ATG 798
TE16        GGAGTCTTCA ATCTAAAGAG ATTGTCTGGT ACGAGTAAAG GGCGGCGGCG GCAGGTCGGT CTGATCTTGA ACAGT--ATG 810
TE8         GGAGTCTTCA ATCTAAAGAG ATTGTCTGGT ACGAGTAAAG GGCAGCGGCG GCAGGTCGGT CTGATCTTGA ACAGT--ATG 810
TE18        GGAGTCTTCA ATCTAAAGAG ATTGTCTGGT ACGAGTAAAG GGCGGCGGCG GCAGGTCGGT CTGATCTTGA ACAGT--ATG 854
TE32        GGAGTCTTCA ATCTAAAGAG ATTGTCTGGT ACGAGTAAAG GGCGGCGGCG GCAGGTCGGT CTGATCTTGA ACAGT--ATG 810
TE19        GGAGTCTTCA ATCTAAAGAG ATTGTCTGGT ACGAGTAAAG GGCGGCGGCG GCAGGTCGGT CTGATCTTGA ACAGT--ATG 811
TE30        GGAGTCTTCA ATCTAAAGAG ATTGTCTGGT ACGAGTAAAG GGCGGCGGCG GCAGGTCGGT CTGATCTTGA ACAGT--ATG 810
TE4         GGAGTCTTCA ATCTAAAGAG ATTGTCTGGT ACGAGTAAAG GGCGGCGCA-- ---------- ---------- ---------- 780
TE35        GGAGTCTTCA ATCTAAAGAG ATTGTCTGGT ACGAGTAAAG GGCGGCGGCG GCAGGTCGGT CTGATCTTGA ACAGT--ATG 798
TE25        GGAGTTTTCA ACCAAAAGGA GTCATCTGGT ACGAGTAAGG GGCAGTGGTA GCGGGTCGGT CTGATCTGGA ACAGT--ATG 925
TE15        --------CA ACATAAAAAG ATGG---AGC AACGACAATG AAACGCAGCG GCGAGCGGAG CT--TCTTGG ACGATGGACC 797
TE34        --------CA ACGTAAGGAG ATGG---AGC AACGACAACG AAACGCAACG GCGAGCGGAT CT--TCTTGG ACGACGGACA 795
TE7         --------CA GCGTAAGGAG ATGG---AGC AACGGCAACG AAACGCAGCG GCGAGCGGAG CT--TCTTGG ACGATGGACA 706
TE11        --------CA GCGCAAGGAG ATGG---AGC AACGGCAACT TTATGTTGCG GCGAGCAGAG CT--TCTTGG ACGACGAACA 793
TE31        --------CA GCGTAAGCAG ATGG---AGC AACGACAACG AAACGCAGCG GCGAGCGGAG CT--TCTTAG ACGACGGACA 796
TE41        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- 134
TE37        AACAT----G GATTTATGTA ACTCTAATAT ATGATGAAAT AGCTATATTA GTATACATAT TTGAAATCTT GTATCTATTT 982
Consensus   GGAGTCTTCA ATCTAAAGAG ATTGTCTGGT ACGAGTAAAG GGCGGCGGCG GCAGGTCGGT CTGATCTTGA ACAGT--ATG
100%
Conservation
0%

                                1,060     1,080     1,100     1,120
TE CsaMLO8  ATTCGAAGG- ---------- ---------- --CGAAAGAT GAAA--TAAA ACACGGATCT GGAAGTCGAA GACACGAACA 900
TE10        ATTCGAAGG- ---------- ---------- --CGAAAGAT GAAA--TAAA ACACGGATCT GGAAGTCGAA GACACGAACA 864
TE14        ATTCGAAGG- ---------- ---------- --CGAAAGAT GAAA--TAAA ACACGGATCT GGAAGTCGAA GACACGAACA 868
TE36        ATTCGAAGG- ---------- ---------- --CGAAAGAT GAAA--TAAA ACACGGATCT GGAAGTCGAA GACACGAACA 853
TE16        ATTCGAAGG- ---------- ---------- --CGAAAGAT GAAA--TAAA ACACGGATCT GGAAGTCGAA GACACGAACA 865
TE8         ATTCGAAGG- ---------- ---------- --CGAAAGAT GAAA--TAAA ACACGGATCT GGAAGTCGAA GACACGAACA 865
TE18        ATTCGAAGG- ---------- ---------- --CGAAAGAT GAAA--TAAA ACACGGATCT GGAAGTCGAA GACACGAACA 909
TE32        ATTCGAAGG- ---------- ---------- --CGAAAGAT GAAA--TAAA ACACGGATCT GGAAGTCGAA GACACGAACA 865
TE19        ATTCGAAGG- ---------- ---------- --CGAAAGAT GAAA--TAAA ACACGGATCT GGAAGTCGAA GACACGAACA 866
TE30        ATTCGAAGG- ---------- ---------- --CGAAAGAT GAAA--TAAA ACACGGATCT GGAAGTCGAA GACACGAACA 865
TE4         ------AAAA ---------- ---------- --CAAGAGGT CGGA--CGAA GAACTATGAA GGAGATGGCC GCCGCGGACG 830
TE35        ATTCGAAGG- ---------- ---------- --CGAAAGAT GAAA--TAAA ACACGGATCT GGAAGTCGAA GACACGAACA 853
TE25        GTTCGAAGGA GGACAGGATC GATAGATCTG GGCGGAAGAC GAAA--TAAG ACACGAATCT GGAAGTCGGA GACATGAACG 1003
TE15        AAACCGAAAC TCTTCGGCTG GGCGTTCGGC TTCAACTGAC AAAGGTTCAA TCGGCTGCTT GGCTAATGGA AAAACAAGAG 877
TE34        AAATTGAAAC TCTTTGATTG GGCGTTCGGC TTCAACTGAC AGAGGTTCAA TCGGCTGCTT GGCTGACGAA AAAACAAAAG 875
TE7         AAACCGAAAC TCTTCGGCTG GGCGTTCGGC TTCAACTGAC AGAGG----- ---GTTGCTT GGCTAACGGA AAAACAAGAG 778
TE11        AAACCGAAAC TCTTTGGCTG GGCGTTCGAC TTCAACTGAC AGAGGTTCAA TCGGCTGGTT GGCTAAAAGA AAAACAAGAG 873
TE31        AAACCAAAAC TCTTTGGTTG GGCGTTCGGC TTCAACTGAT AGAGGTTCAA TCAATTACCT GGCTAACAGA AAAACAAGAG 876
TE41        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- 134
TE37        ATTAAAAG-- ---------- ----CTAAAT TTTAAAGAAC ATCTGTTTTA AGTTTTGTTT AAAAAAAAAT CGTTCANAAA 1046
Consensus   ATTCGAAGG- ---------- ---------- --CGAAAGAT GAAA--TAAA ACACGGATCT GGAAGTCGAA GACACGAACA
100%
Conservation
0%

                                1,140     1,160     1,180     1,200
TE CsaMLO8  GA-------- ---------- ---------- ---------- ---------- ---GATGCAC GAACAAATCG GTGCTTGCAA 929
TE10        GA-------- ---------- ---------- ---------- ---------- ---GATGCAC GAACAAATCG GTGCTTGCAA 893
TE14        GA-------- ---------- ---------- ---------- ---------- ---GATGCAC GAACAAATCG GTGCTTGCAA 897
TE36        GA-------- ---------- ---------- ---------- ---------- ---GATGCAC GAACAAATCG GTGCTTGCAA 882
TE16        GA-------- ---------- ---------- ---------- ---------- ---GATGCAC GAACAAATCG GTGCTTGCAA 894
TE8         GA-------- ---------- ---------- ---------- ---------- ---GATGCAC GAACAAATCG GTGCTTGCAA 894
TE18        GA-------- ---------- ---------- ---------- ---------- ---GATGCAC GAACAAATCG GTGCTTGCAA 938
TE32        GA-------- ---------- ---------- ---------- ---------- ---GATGCAC GAACAAATCG GTGCTTGCAA 894
TE19        GA-------- ---------- ---------- ---------- ---------- ---GATGCAC GAACAAATCG GTGCTTGCAA 895
TE30        GA-------- ---------- ---------- ---------- ---------- ---GATGCAC GAACAAATCG GTGCTTGCAA 894
TE4         CT-------- ---------- ---------- ---------- ---------- ---AGTGAAA AACAAATGGG GTTTCTGGGG 859
TE35        GA-------- ---------- ---------- ---------- ---------- ---GATGCAC GAACAAATCG GTGCTTGCAA 882
TE25        GA-------- ---------- ---------- ---------- ---------- ---GATGCGC AGACAAATCG GTGGTTGCAA 1032
TE15        GTCGAACGAA GAACTACGAA GGAGATGGCC A--------- --CCGTGGAC GCTAGTGAAA AACGAATGGG GTTTCTGGGG 946
TE34        GTCGAACGAA GAACTATGAA GGAGATGGCC G--------- --CCGTGGAC GCTAGTGAAA AATGAGTGGG GTTTCTGGGG 944
TE7         GTCGGACGAA GAACTATGAA GGAGATGGCC G--------- --CCGCGGAC GCTAGTGAAA AACGAATGGG GTTTCTGGGG 847
TE11        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- 873
TE31        GTCAGACGAA GAACTATGAA GGAGACGGCC GGGAAGCAAG GGCGGCGGAT GCTAGTGAAA A-TGAATGGG GTTTCTGAGG 955
TE41        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- 134
TE37        TATTATAATT ATATTGTGCA AA------TT GGAAAGAATA TTTCCACCTG ATTTTTTCAG CATCATGGTA CACCTTGTAG 1120
Consensus   GA-------- ---------- ---------- ---------- ---------- ---GATGCAC GAACAAATCG GTGCTTGCAA
100%
Conservation
0%
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                                   1,220                   1,240                   1,260                   1,280
TE CsaMLO8  TGTGCGCACA AGTAGATCTA AGTGAGGACG AATGGAGA-G CGGATATGGG T-CGAGAGTG CGACGAACTG GGTCGAGAGT 1007
TE10        TGTGCGCACA AGTAGATCTA AGTGAGGACG AATGGAGA-G CGGATATGGG T-CGAGAGTG CGACGAACTG GGTGGA---- 967
TE14        TGTGCGCACA AGTAGATCTA AGTGAGGACG AATGGAGA-G CGGATATGGG T-CGAGAGTG CGACGAACTG GGTGGA---- 971
TE36        TGTGCGCACA AGTAGATCTA AGTGAGGACG AATGGAGA-G CGGATATGGG T-CGAGAGTG CGACGAACTG GGTGGA---- 956
TE16        TGTGCGCACA AGTAGATCTA AGTGAGGACG AATGGAGA-G CGGATATGGG T-CGAGAGTG CGACGAACTG GGTGGA---- 968
TE8         TGTGCGCACA AGTAGATCTA AGTGAGGACG AATGGAGA-G CGGATATGGG T-CGAGAGTG CGACGAACTG GGTGGA---- 968
TE18        TGTGCGCACA AGTAGATCTA AGTGAGGACG AATGGAGA-G CGGATATGGG T-CGAGAGTG CGACGAACTG GGTGGA---- 1012
TE32        TGTGCGCACA AGTAGATCTA AGTGAGGACG AATGGAGA-G CGGATATGGG T-CGAGAGTG CGACGAACTG GGTGGA---- 968
TE19        TGTGCGCACA AGTAGATCTA AGTGAGGACG AATGGAGA-G CGGATA---- ---------- ---------- ---------- 940
TE30        TGTGCGCACA AGTAGATCTA AGTGAGGACG AATGG----- ---------- ---------- ---------- ---------- 929
TE4         TTTGGTTGGT GGCAGATTTG AACAGCAATG AGTGGCAA-A GGGA------ ---------- ---------- ---------- 902
TE35        TGTGCGCACA AGTAGATCTA AGTGAGGACG AATGGAGA-G CGGATATGGG T-CGAGAGTG CGACG----- ---------- 945
TE25        TGTGTGAATA GGTAGATTTG AGCGAGGACG AATGGAGACG CAGATCTGGG CACGAGAATG CGACAAACTG TGTGAATGGA 1112
TE15        TTTGGATGGT GGCAGATTTG AACAGCAATG AGTGGCAAAG GGAAGGTG-- ---------- ---------- ---------- 994
TE34        TTTGGATGGT GGCAGATTTG AACAGCAATG AGTGGCAAAG GGAAGGTG-- ---------- ---------- ---------- 992
TE7         TTTGGATGGT GGCAGATTTG AACAGCAATG AGTGGCAAAG GGAAGGTG-- ---------- ---------- ---------- 895
TE11        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- 873
TE31        TTTGGATGGT GGCAGATTTG AGCGGCAATG AGCGGCAAAG GGAATGTG-- ---------- ---------- ---------- 1003
TE41        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- 134
TE37        TTCACTTGCC ATATGA---- GATAAAAGTT ACTGGAGGTT GGTAACTGGG TTCTAGTGAA GCACAGGCCT -----AAACT 1191
Consensus   TGTGCGCACA AGTAGATCTA AGTGAGGACG AATGGAGA-G CGGATATGGG T-CGAGAGTG CGACG--C-- -----A----
100%
Conservation
0%
                                   1,300                   1,320                   1,340                   1,360
TE CsaMLO8  GCGACGAACT GTGTGGATGG AAGGAGCAGT GATGGCGGAA GGAGCAGTGA TGGCAGAAGG AGTAGTGGCG GCGGCAGCAG 1087
TE10        ---------- ---------- ---------- -----TGGAA GGAGCAGTGA TGGCAGAAGG AGTAGTGGCG GCGGCAGCAG 1012
TE14        ---------- ---------- ---------- -----TGGAA GGAGCAGTGA TGGCAGAAGG AGTAGTGGCG GCGGCAGCAG 1016
TE36        ---------- ---------- ---------- -----TGGAA GGAGCAGTGA TGGCAGAAGG AGTAGTGGCG GCGGCAGCAG 1001
TE16        ---------- ---------- ---------- -----TGGAA GGAGCAGTGA TGGCAGAAGG AGTAGTGGCG GCGGCAGCAG 1013
TE8         ---------- ---------- ---------- -----TGGAA GGAGCAGTGA TGGCAGAAGG AGTAGTGGCG GCGGCAGCAG 1013
TE18        ---------- ---------- ---------- -----TGGAA GGAGCAGTGA TGGCAGAAGG AGTAGTGGCG GCGGCGGCAG 1057
TE32        ---------- ---------- ---------- -----TGGAA GGAGCAGTGA TGGCAGAAGG AGTAGTGGCG GCGGCAGCAG 1013
TE19        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- 940
TE30        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- 929
TE4         ---------- ---------- ---------- ---------- ---------- ---------- AGGTGCAACG ACAACGGCAG 922
TE35        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- 945
TE25        AGGA------ ---------- ---------- -GTAGTGGTG GCGGCAGTTG CGGCGGAAGG AGTAGTGGCG GCGGCGGCAG 1165
TE15        ---------- ---------- ---------- ---------- ---------- ---------- -----CAACG ACAACGACGG 1009
TE34        ---------- ---------- ---------- ---------- ---------- ---------- -----CAACG ACAACGGCAA 1007
TE7         ---------- ---------- ---------- ---------- ---------- ---------- -----CAACG ACAACGGCAA 910
TE11        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- 873
TE31        ---------- ---------- ---------- ---------- ---------- ---------- -----CGACG ACGGCGGTGA 1018
TE41        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- 134
TE37        ATTGCCAAAG TTTAAACGGG CAAACTTATC CTCTCTGCAA ATTCCAGCAA GGGC------ ---------- ---------- 1245
Consensus   ---------- ---------- ---------- ------G--- ----CAG--- -GGC------ AG--GTGGCG GCGGCNGCAG
100%
Conservation
0%
                                   1,380                   1,400                   1,420                   1,440
TE CsaMLO8  AATCAGAGAC GAGGATTTTG ATCTAGGAGG CA------GA GCGAA----- ---------TT ACTTGGAGAC A---TGATGT 1145
TE10        AATCAGAGAC GAGGATTTTG ATCTAGGAGG CA------GA GCGAA----- ---------TT ACTTGGAGAC A---TGATGT 1070
TE14        AATCAGAGAC GAGGATTTTG ATCTAGGAGG CA------GA GCGAA----- ---------TT ACTTGGAGAC A---TGATGT 1074
TE36        AATCAGAGAC GAGGATTTTG ATCTAGGAGG CA------GA GCGAA----- ---------TT ACTTGGAGAC A---TGATGT 1059
TE16        AATCAGAGAC GAGGATTTTG ATCTAGGAGG CA------GA GCGAA----- ---------TT ACTTGGAGAC A---TGATGT 1071
TE8         AATCAGAGAC GAGGATTTTG ATCTAGGAGG CA------GA GCGAA----- ---------TT ACTTGGAGAC A---TGATGT 1071
TE18        AATCAGAGAC GAGGATTTTC ATCTATCGGG CA------GA GCGAA----- ---------CT ACTTGGAGAC A---TGATGT 1115
TE32        AATCAGAGAC GAGGATTTTG ATCTAGGAGG CATTTGCAGA TCTAAGGGGT GGCTTCGGCT AATGGGAGAT GATTTTGCCT 1093
TE19        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- 940
TE30        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- 929
TE4         ATTTGCAGA- ---------- -TCTAAGGGG CGGCTTCGG- ---------- ---------- ---------- ---------- 949
TE35        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- 945
TE25        AATCAGAGAC GAGGATTTT- ATCTATCGGG TA-------- ---------- -AAGCGAACT ACTTGGAGGA A---TGATTT 1222
TE15        ATTTGCAGA- ---------- -TCTAAGGGA CGGCTTCGG- ---------- ---------- ---------- ---------- 1036
TE34        ATTTGCAGA- ---------- -TCTAAGGGG CGGCTTCAG- ---------- ---------- ---------- ---------- 1034
TE7         ATTTGCAGA- ---------- -TCTAAGGGG TGGCTTCGG- ---------- ---------- ---------- ---------- 937
TE11        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- 873
TE31        ATTTGCAGA- ---------- -TCTAAGGTC CGGCTTCGG- ---------- ---------- ---------- ---------- 1045
TE41        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- 134
TE37        ---------- ---------- ---------- ---------- ---------- ---------- -TCTGGAGAG TTCTTCATAT 1264
Consensus   AATCAGAGA- ---------- -TCTAGGAGG CA------G- ---------- ---------- ----GGAG-- ----T----T
100%
Conservation
0%
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                                  1,460                                   1,480                                   1,500                                   1,520
TE CsaMLO8  GTATTGATTA CTGATG-GGT AT-------- GGCTCTGCCT CCGTCGACGA AT---CAACG GAGGCAGAC- --G--AGCGG 1208
TE10        GTATTGATTA CTGATG-GGT AT-------- GGCTCTGCCT CCGTCGACGA AT---CAACG GAGGCAGAC- --G--AGCGG 1133
TE14        GTATTGATTA CTGATG-GGT AT-------- GGCTCTGCCT CCGTCGACGA AT---CAACG GAGGCAGAC- --G--AGCGG 1137
TE36        GTATTGATTA CTGATG-GGT AT-------- GGCTCTGCCT CCGTCGACGA AT---CAACG GAGGCAGAC- --G--AGCGG 1122
TE16        GTATTGATTA CTGATG-GGT AT-------- GGCTCTGCCT CCGTCGACGA AT---CAACG GAGGCAGAC- --G--AGCGG 1134
TE8         GTATTGATTA CTGATG-GGT AT-------- GGCTCTGCCT CCGTCGACGA AT---CAACG GAGGCAGAC- --G--AGCGG 1134
TE18        GTATTGATTA CTGATG-GAT AT-------- GGCTCTGCCT CCGTCGACGA AT---CAACA GATGCAGAC- --G--AAAGG 1178
TE32        CCGTTGATGG CTAATGAGAG AT-------- GATTCTGCCT CCGTTGATGA ATGATCAACG GAGGCAGAG- --ATCAAACG 1162
TE19        ---------- -------GAG AT-------- GATTCTGCCT CCGTTGATGA ATGATCAACG GAGGCAGAG- --ATCAAACG 992
TE30        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- 929
TE4         ---------- CTAATGGGAG AT-------- GATTCTGCCT CCGTTGATGA ATGATCAACG GAGGCAGAG- --ATCAAACG 1008
TE35        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- 945
TE25        GTATTAATTA CCGATGGGA- AT-------- GGCTCTGCCT CCGTCGACGA AT---CAACG GAGGCAGAC- --G--AATGG 1285
TE15        ---------- CTAATGGGAG AT-------- GATTCTGCCT CTGTTGATGA ATGATCAACG GAGGCAGAG- --ATCAAACG 1095
TE34        ---------- CTAATGGGAG AT-------- GATTCTGCCT CCGTTGATGA ATGATCAACG GAGGCAGAG- --ATCAAACG 1093
TE7         ---------- CTAATGGGAG AT-------- GATTCTGCCT CCGTTGATGA ATGATCAACG GAGGCAGAG- --ATCAAACG 996
TE11        ---------- ---------- ---------- -ATTCTGCCT CCGTTGATGA ATGATCAACG GAGGCAGAG- --ATCAAACG 919
TE31        ---------- CTAATGGGGG AT-------- GATTCTGCCT CCGTTAAT-- ---------- ---------- ----CGAACG 1081
TE41        ---------- -------GGT AT-------- GGCTCTGCCT CCGTCGACGA AT---CAACG GAGGCAGAC- --G--AGCGG 181
TE37        CTTTTGAGTT CAGATAGTCC ATTAACCTCA AGTTCTAGCT CTAGGGGAGG ATTGCCTCCT AGACCAAATT CAGTAAAAAC 1344
Consensus   ---TT-A--- CTGATG-GNT AT-------- GGNTCTGCCT CCGTCGACGA AT---CAACG GAGGCAGAC- --G--AAAGG
100%
Conservation
0%

                                  1,540                                   1,560                                   1,580                                   1,600
TE CsaMLO8  GGATGTGACG GCTAGAA--- -TACAAGGAG ACTAAAACCC TATAGCTCTG ATACCATGTT GATTT-TATG GAATCAATCT 1283
TE10        GGATGTGACG GCTAGAA--- -TACAAGGAG ACTAAAACCC TATAGCTCTG ATACCATGTT GATTT-TATG GAATTAATCT 1208
TE14        GGATGTGACG GCTAGAA--- -TACAAGGAG ACTAAAACCC TATAGCTCTG ATACCATGTT GATTT-TATG GAATCAATCT 1212
TE36        GGATGTGACG GCTAGAA--- -TACAAGGAG ACTAAAACCC TATAGCTCTG ATACCATGTT GATTT-TATG GAATCAATCT 1197
TE16        GGATGTGACG GCTAGAA--- -TACAAGGAG ACTAAAACCC TATAGCTCTG ATACCATGTT GATTT-TATG GAATCAATCT 1209
TE8         GGATGTGACG GCTAGAA--- -TACAAGGAG ACTAAAACCC TATAGCTCTG ATACCATGTT GATTT-TATG GAATCAATCT 1209
TE18        GGATGTGACG GCTAGAA--- -TACAAGGAG ACTAAAACCC TATAGCTCTG ATACCATGTT GATTT-TATG GAATCAATCT 1253
TE32        GGATGTGGAG GCTAGAA--- -TTCAATAAG GCGAAAACCC TAGAGCTCTG ATACCATGTT GATTT-TATG GAATAAATCT 1237
TE19        GGATGTGGAG GCTAGAA--- -TTCAATAAG GCGAAAACCC TAGAGCTCTG ATACCATGTT GATTT-TATG GAATAAATCT 1067
TE30        ---------- ---------- ---CAAGGAA ACTAAAACCC TATAGCTCTG ATACCATGTT GATTT-TATG GAATTAATCT 985
TE4         GGATGTGGAG GCTAGAA--- -TTCAATAAG GCGAAAACCC TAGAGCTCTG ATACCATGTT GATTT-TATG GAATAAATCT 1083
TE35        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- 945
TE25        GGATGTGACG ACTAGAA--- -TACAAGGAG GCTAAAACCC TATAGCTCTG ATACCATGTT GTTTTCTATG GAATGAATCT 1361
TE15        GGATGTGGAG GCTAGAA--- -TTCAATAAG GCGAAAACCC TAGAGCTCTG ATACTATGTT GATTT-TATG GAATTAATCT 1170
TE34        GGATGTGGAG GCTAGAA--- -TTCACTAAG GAGAAAACCC TAGAGCTCTG ATACCATGTT GATTT-TATG GAATTAATCT 1168
TE7         GGATGTGGAG GCTAGAA--- -TTCAATAAG GCGAAAACCC TAGAGCTCTG ATACCATGTT GATTT-TATG GAATAAATCT 1071
TE11        GGATGTGGAG GCTAGAA--- -TTCAATAAG GCGAAAACCC TAGAGCTCTG ATACCATGTT GATTT-TATG GAATTAATCT 994
TE31        GGATGTGGAG GCTAGAA--- -TTCAATGAG GCGAAAACCC TATAGCTCTG GTACCATGTT GATTT-TATG GAATTAATCT 1156
TE41        GGATGTGACG GCTAGAA--- -TACAAGGAG ACTAAAACCC TATAGCTCTG ATACCATGTT GATTT-TATG GAATTAATCT 256
TE37        CAAATCTTCG GTGAGAAGCT TTGGAGCAAA ACGATCTTTC CCAGGTGGAG ACATCATTGT TGATTTTATG GAATAAATCT 1424
Consensus   GGATGTGACG GCTAGAA--- -TACAAGGAG ACTAAAACCC TATAGCTCTG ATACCATGTT GATTT-TATG GAATTAATCT
100%
Conservation
0%

                                  1,620                                   1,640                                   1,660                                   1,680
TE CsaMLO8  ATAT-TTCAT TCATTACTTA ATAGAGATAC AAGCCTATAT ATAACCATAG AGAAATACAC TTAAGGAAAT AATATCAAAT 1362
TE10        ATAT-TTCAT TAATTACTTA ATAGAGATAC AAGCCTATAT ATAACCATAG AGAAATACAC TTAAGGAAAT AATATCAAAT 1287
TE14        ATAT-TTCAT TAATTACTTA ATAGAGATAC AAGCCTATAT ATAACCATAG AGAAATACAC TTAAGGAAAT AATATCAAAT 1291
TE36        ATAT-TTCAT TCATTACTTA ATAGAGATAC AAGCCTATAT ATAACCATAG AGAAATACAC TTAAGCAAAT AATATCAAAT 1276
TE16        ATAT-TTCAT TAATTACTTA ATAGAGATAC AAGCCTATAT ATAACCATAG AGAAATACAC TTAAGGAAAT AATATCAAAT 1288
TE8         ATAT-TTCAT TCATTACTTA ATAGAGATAC AAGCCTATAT ATAACCATAG AGAAATACAC TTAAGGAAAT AATATCAAAT 1288
TE18        ATAT-TTCAT TAATTACTTA ATAGAGATAC AAGCCTATAT ATAACCATAG AGAAATACAC TTAAGGA--C AATA------ 1324
TE32        ATAT-TTCAT T------TTA ATAGAGATAC AAGCCTATAT ATAACCATAG AGAAATACAC TTAAGAAAAT AATATAAAAT 1310
TE19        ATAT-TTCAT TCATTATTTA ATAGAGATAC AAGCCTATAT ATAACCATAG AGAAATACAC TTAAGGAAAT AATATCAAAT 1146
TE30        ATAT-TTCAT TAATTACTTA ATAGAGATAC AAGCCTATAT ATAACCATAG AGAAATACAC TTAAGGAAAT AATATCAAAT 1064
TE4         ATAT-TTCAT TTATTATTTA GTAGAGATAC AAGCCTATAT ATAACCATAG AGAAATACAC TTAAGGAAAT AATATCAAAT 1162
TE35        ---------- ---------- ATAGAGATAC AAGCCTATAT ATAACCATAG AGAAATACAC TTAAGGAAAT AATATCAAAT 1005
TE25        CTAT-TTCAT TAATCATTTA GGAGAGGTAC AAGCCTATAT ATAACCATAG AGAAATACAC TTAAGGAAAT AATATCAAAT 1440
TE15        ATATATTTCAT TCATTATTTA GTAGAGATAC AAGCCTATAT ATAACCATAG AGAAATACAC TTAAGGAAAT AATATCAAAT 1250
TE34        ATAT-TTCAT TCATTATTTA GTAGAGATAC AAGCCTATAT ATAACCATAG AGAAATACAC TTAAGGAAAT AATATCAAAT 1247
TE7         ATATATTTCAT TTATTATTTA GTAGAGATAC AAGCCTATAT ATAACCATAG AGAAATACA- -------AAT AATATCAAAT 1143
TE11        ATAT-TTCAT TCATTATTTA GTAGAGATAC AAGCCTATAT ATAACCATAG AGAAATACAC TTAAGGAAAT AATATCAAAT 1073
TE31        ATAT-TTCAT TAATTATTTA GTAGAGGTAC AAGTCTCTAT ATAACCATAG AGAAATACAC TTAAGAAAAT AATATCAAAT 1235
TE41        ATAT-TTCAT TAATTACTTA ATAGAGATAC AAGCCTATAT ATAACCATAG AGAAATACAC TTAAGGAAAT AATATCAAAT 335
TE37        ATAT-TTCAT TTATTATTTA GTAGAGATAC AAGCCTATAT ATAACCATAG AGAAATACAC TTAAGGAAAT AATATCAAAT 1503
Consensus   ATAT-TTCAT TAATTANTTA ATAGAGATAC AAGCCTATAT ATAACCATAG AGAAATACAC TTAAGGAAAT AATATCAAAT
100%
Conservation
0%
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                                   1,700                                   1,720                                   1,740                                   1,760
                                     |                                       |                                       |                                       |
TE CsaMLO8  A---------- ---------- ---------- ------ATATC TCCTAAGAAT AATAT-CTCC TAAGAATAAT ATC-------- 1400
TE10        A---------- ---------- ---------- ------ATATC TCC--AGAAT AATAT-CTCC TAAGAATAAT ATC-------- 1323
TE14        A---------- ---------- ---------- ------ATATC TCC--AGAAT AATAT-CTCC TAAGAATAAT ATC-------- 1327
TE36        A---------- ---------- ---------- ------ATATC TCC--AGAAT AATAT-CTCC TAAGAATAA- ---------- 1308
TE16        A---------- ---------- ---------- ------ATATC TCC--AGAAT AATAT-C--- ---------- ---------- 1308
TE8         ATTTCATTCA TTATTTAGTA GAGTTACAAG CCTATATATA ACCATAGAGA AATACACTTA AGGAAATAAT ATCAAATAAT 1368
TE18        ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- 1324
TE32        A---------- ---------- --ATAATATA AAATAATATC TCC--AGAAT AATAT-CTCC TAAGAATAA- ---------- 1355
TE19        A---------- ---------- ---------- -------ATA TCTCTAGAAT AATAT-CTCC TAATAATAA- ---------- 1178
TE30        AATATCTCCA GAAT------ ---------- ----AATATC TCCTAAGAAT AATAT-CTCC TAAGAATAAT TTC-------- 1116
TE4         A---------- ---------- ---------- -------ATA TCTCTAGAAT TATAT-CTCC TAATAATAA- ---------- 1194
TE35        A---------- ---------- ---------- -------ATA TCTCCAGAAT AATAT-CTCC TAAGAATAAT ---------- 1038
TE25        A---------- ---------- ---------- -------ATA TGTCCAGAAT AATAT-CACC TAAGAATAA- ---------- 1472
TE15        A---------- ---------- ---------- -------ATA TCTCCAAAAT AATAT-CTCC TAAGAATAAT ---------- 1283
TE34        A---------- ---------- ---------- -------ATA TCTCCAGAAT AATAT-CTCC TAAGAATAA- ---------- 1279
TE7         A---------- ---------- ---------- -------ATA TCTCTAGAAT TATAT-CTCC TAAGAATAA- ---------- 1175
TE11        A---------- ---------- ---------- -------ATA TCTCTAGAAT AATAT-CTCC TAAGAATAAT ---------- 1106
TE31        A---------- ---------- ---------- -------ATA TCTCCAGAAT AATAT-CACC TAAGAATAAT ---------- 1268
TE41        A---------- ---------- ---------- -------ATA TCTCCAGAAT AATAT-CTCC TAAGAATAA- ---------- 367
TE37        A---------- ---------- ---------- -------ATA TCTCTAGAAT TATAT-CTCC TAATAATAAT ---------- 1536
Consensus   A---------- ---------- ---------- -------ATA TCTCNAGAAT AATAT-CTCC TAAGAATAAT ----------
100%
Conservation
0%

                                   1,780                                   1,800
                                     |                                       |
TE CsaMLO8  -TCCTAAGAA TAATATCTCC TAAGAATAAT CTAATTATAT TAATAATTAT 1449
TE10        -TCCTAAGAA TAATATCTCC TAAGAATAA- ---------- ---------- 1351
TE14        -TCCTAAGAA TAATATCTCC TAAGAATAAT ---------- ---------- 1356
TE36        ---------- ---------- ---------- ---------- ---------- 1308
TE16        ---------- ---------- ---------- ---------- ---------- 1308
TE8         ATCTCTAGAA TTATATCTCC TAATAATAAT ---------- ---------- 1398
TE18        ---------- ---------- ---------- ---------- ---------- 1324
TE32        ---------- ---------- ---------- ---------- ---------- 1355
TE19        ---------- ---------- ---------- ---------- ---------- 1178
TE30        ---------- ---------- ---------- ---------- ---------- 1116
TE4         ---------- ---------- ---------- ---------- ---------- 1194
TE35        ---------- ---------- ---------- ---------- ---------- 1038
TE25        ---------- ---------- ---------- ---------- ---------- 1472
TE15        ---------- ---------- ---------- ---------- ---------- 1283
TE34        ---------- ---------- ---------- ---------- ---------- 1279
TE7         ---------- ---------- ---------- ---------- ---------- 1175
TE11        ---------- ---------- ---------- ---------- ---------- 1106
TE31        ---------- ---------- ---------- ---------- ---------- 1268
TE41        ---------- ---------- ---------- ---------- ---------- 367
TE37        ---------- ---------- ---------- ---------- ---------- 1536
Consensus   ---------- ---------- ---------- ---------- ----------
100%
Conservation
0%
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