**SUPPLEMENTARY MATERIAL**

Supplementary file S1 contains alignments of satDNAs monomers of the nine most abundant non-centromeric satDNAs.

Supplementary file S2 shows periodicity of A/T and G/C nucleotides along the monomer sequence of Cast1-Cast9 satDNAs.

Supplementary file S3 contains results of LOCAL BLAST search and Dot Plot analyses of newly detected satDNAs, and the library of repeat families published previously.

Supplementary file S4 shows consensus sequences of detected satDNAs with indicated primer positions.

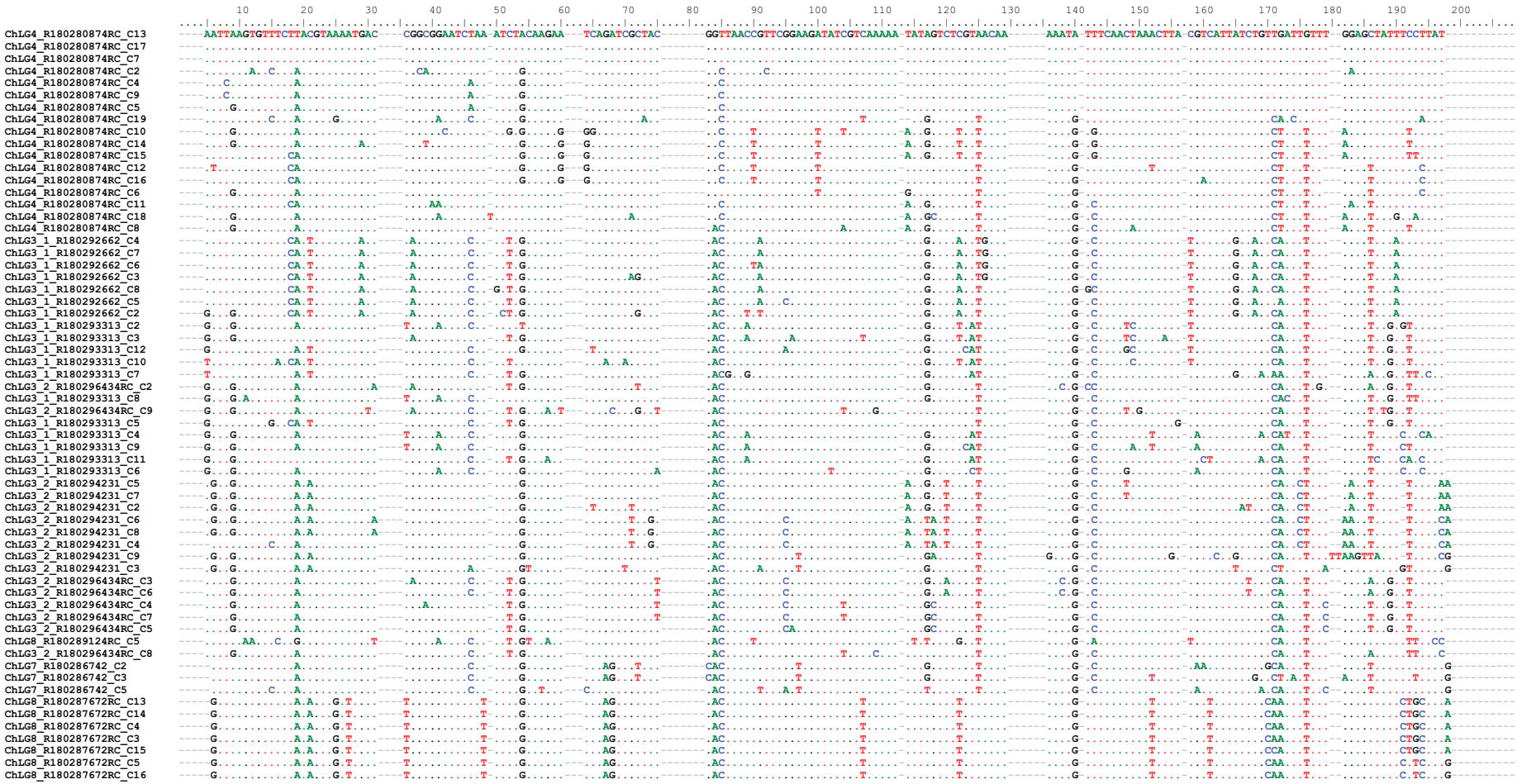
Supplementary file S5 includes phylogenetic trees of all satDNAs.

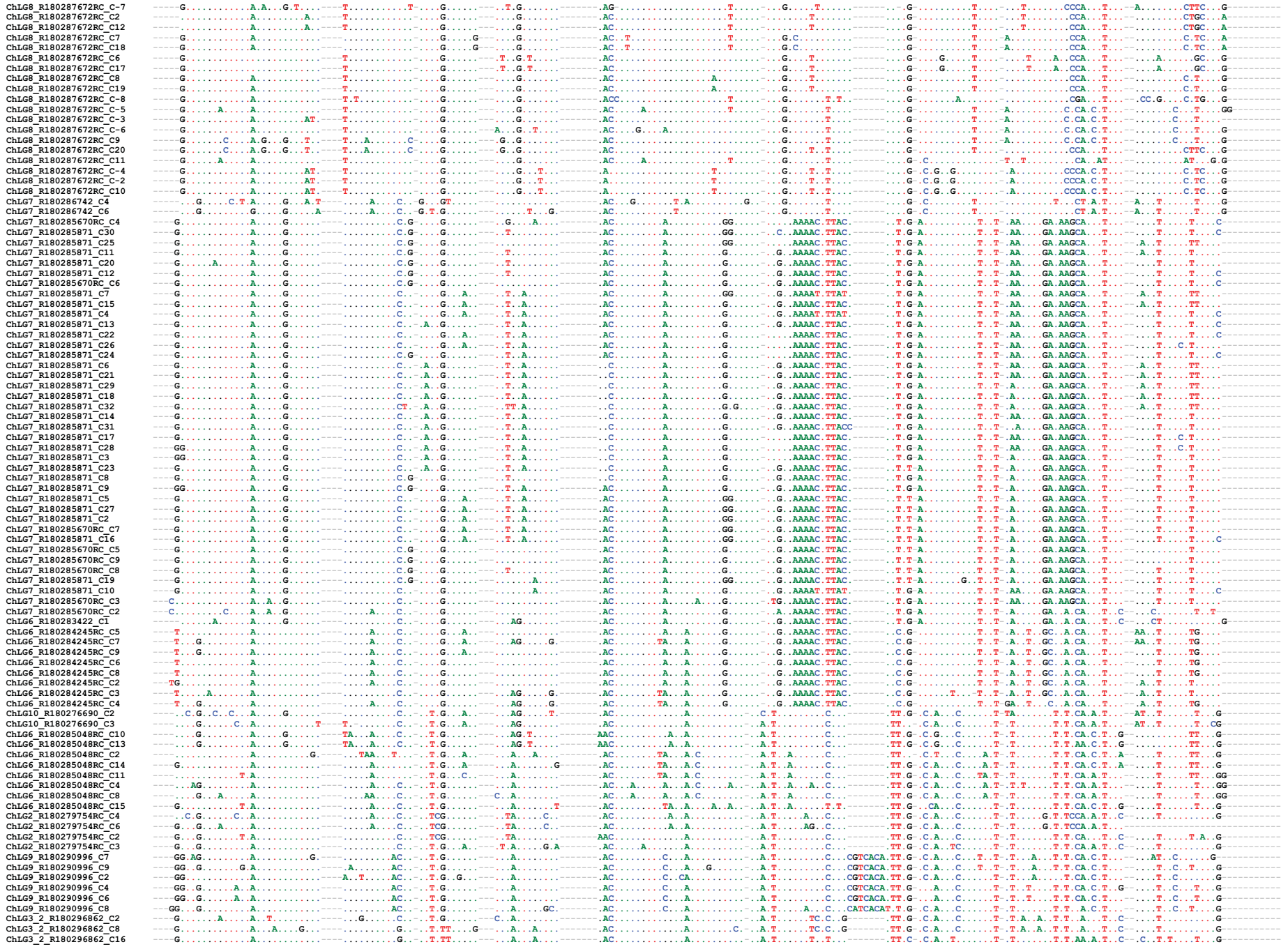
Supplementary file S6 contains alignments of Cast5 flanking regions.

Supplementary file S7 represents the table listing primer sequences.

Additional file 1.Alignments of satDNAs monomers of the nine most abundant non-(peri)centromeric satDNAs obtained by TRF. A) Cast1, B) Cast2, C) Cast3, D) Cast4, E) Cast5, F) Cast6, G) Cast7, H) Cast8 and I) Cast9. All monomers are compared with first sequence and positions identical to the first sequence are shown with dot. Detail descriptions of monomers include chromosome and array origin.

## A. Cast1

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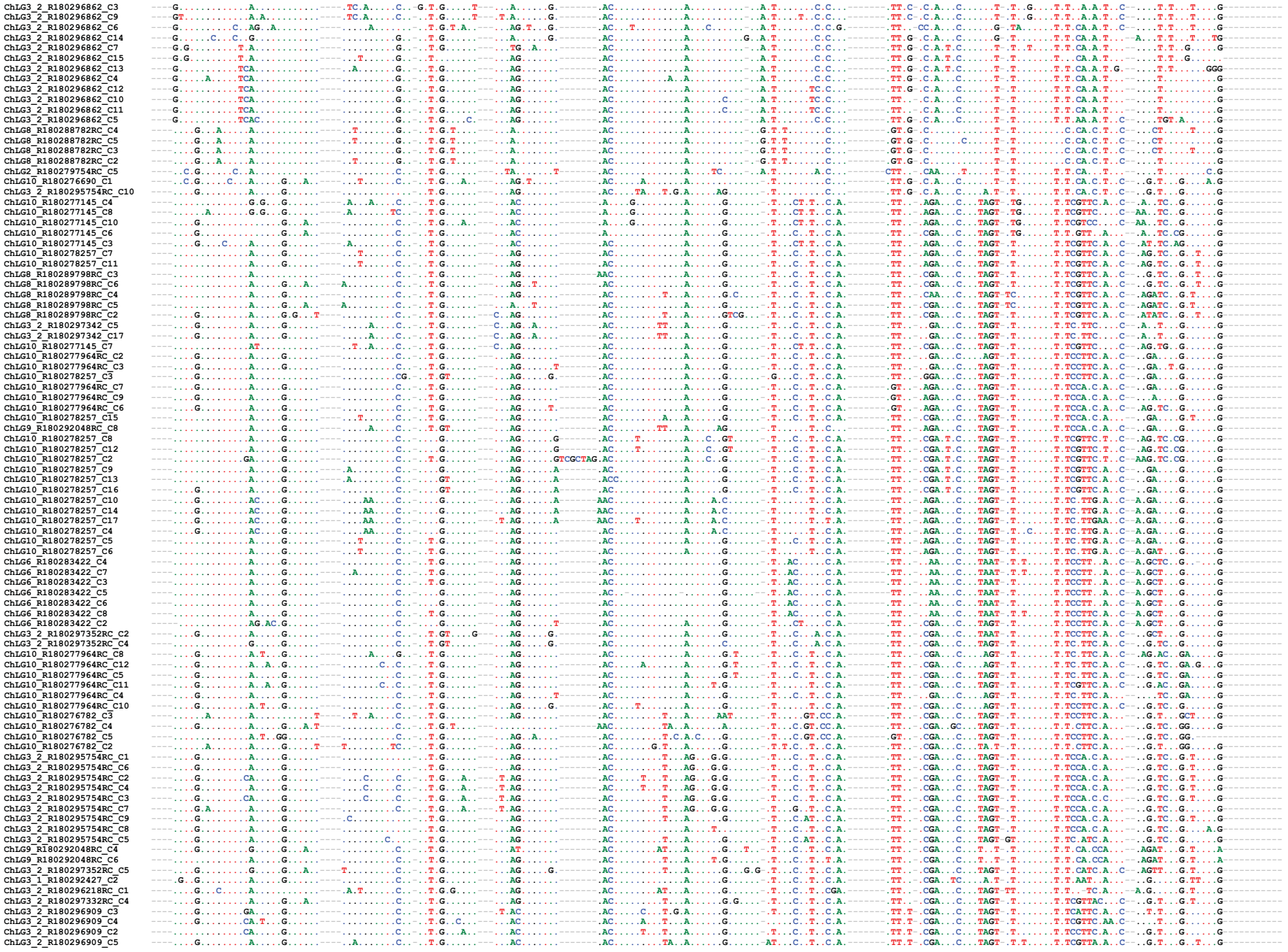
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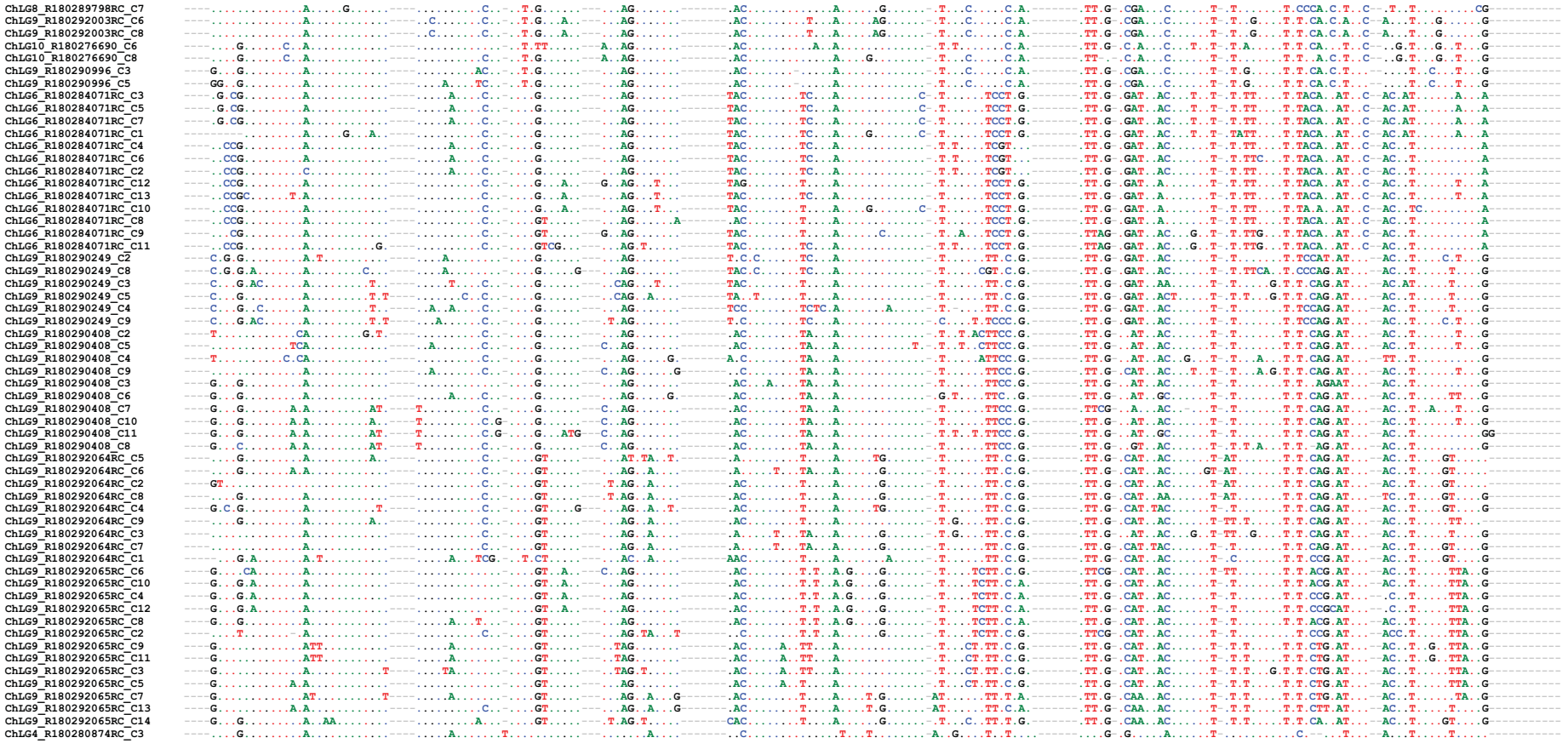
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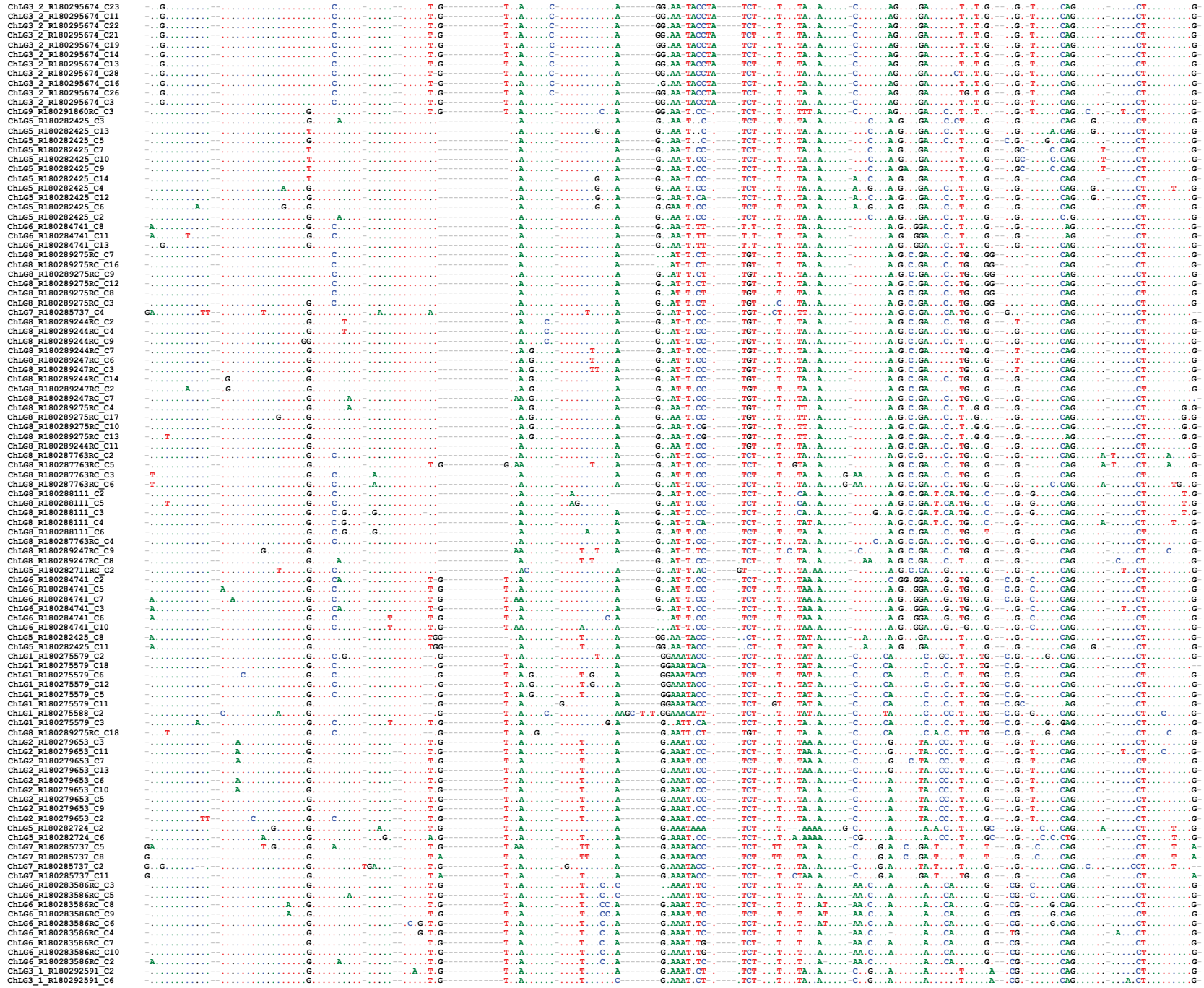
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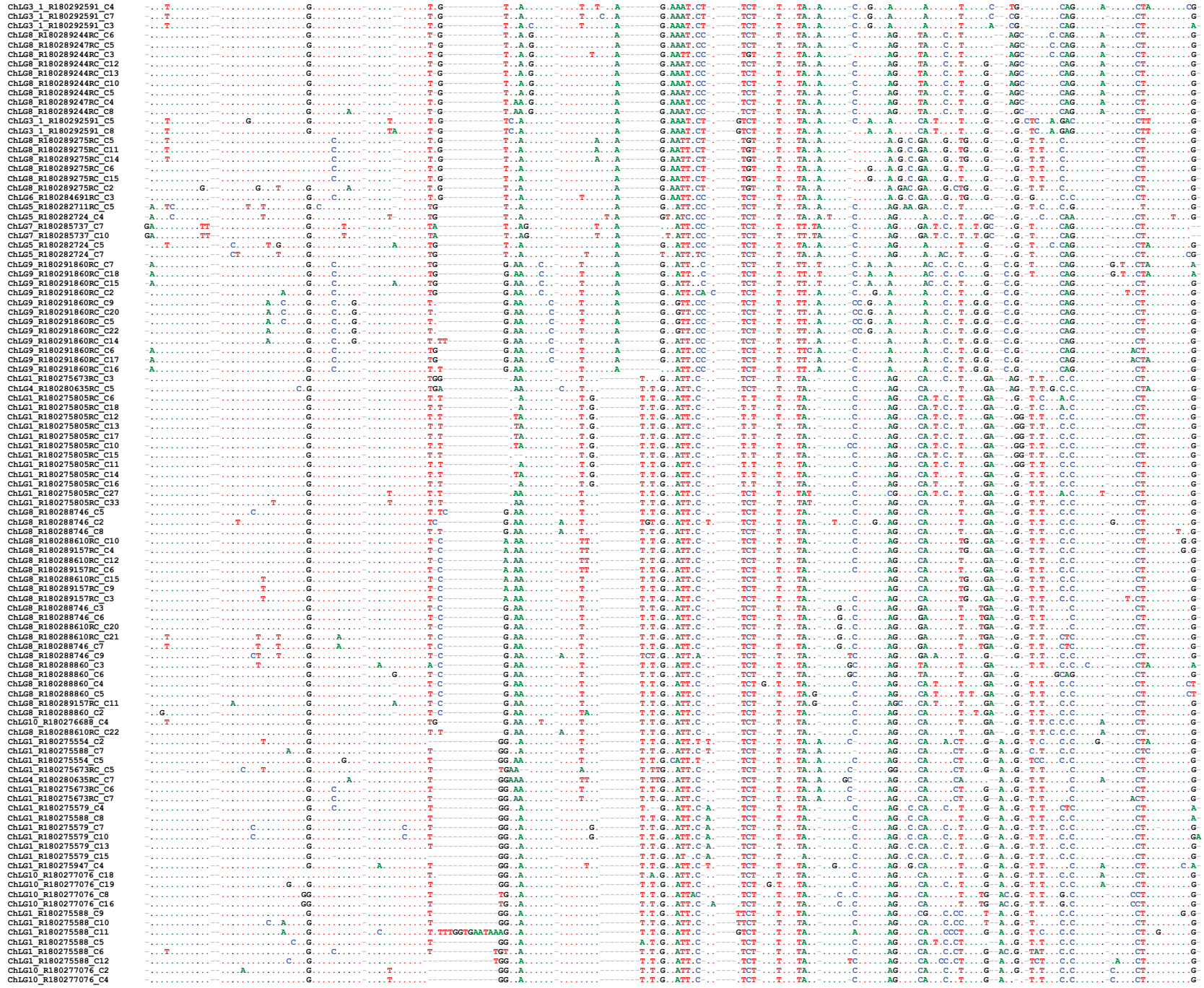
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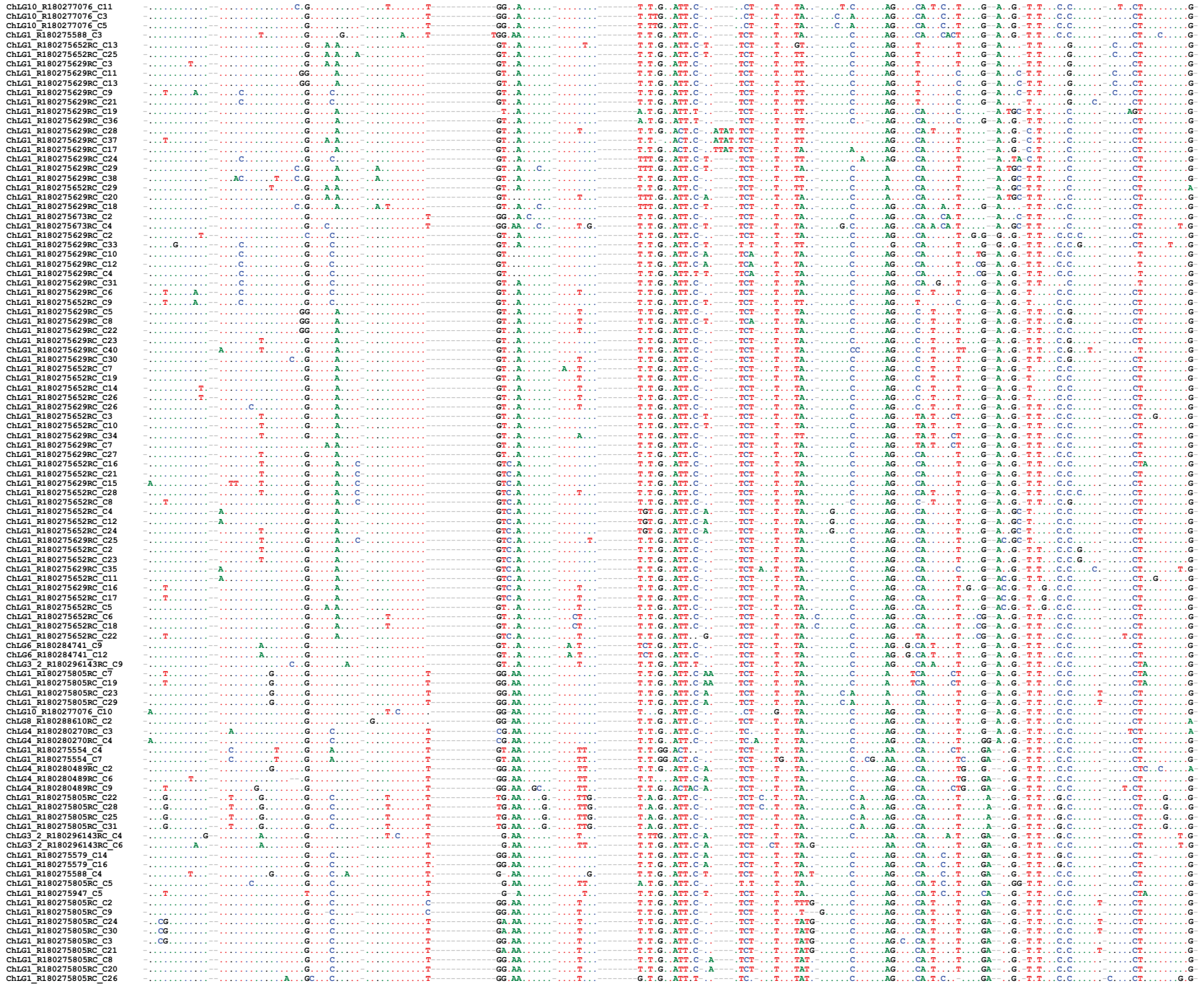
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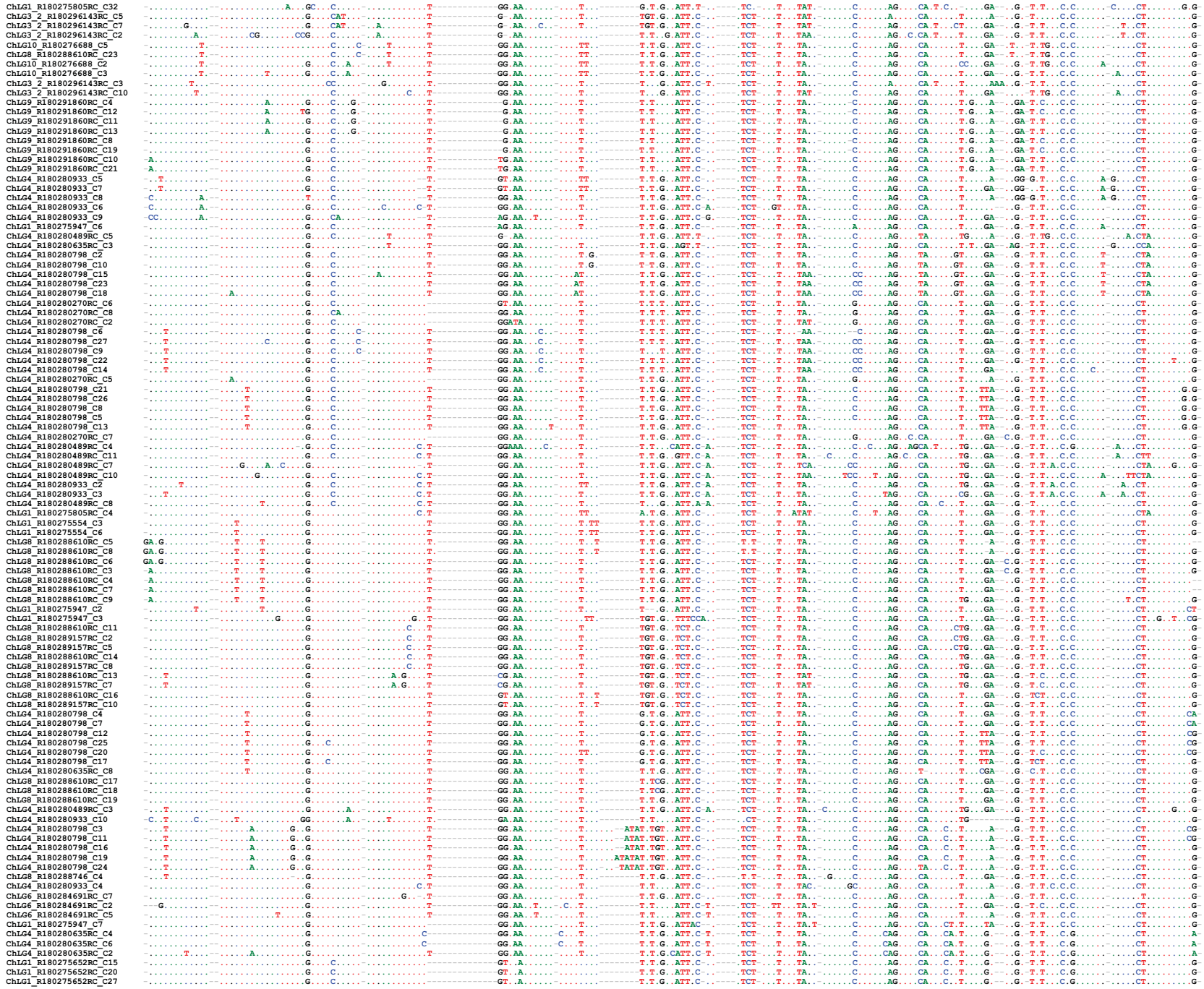
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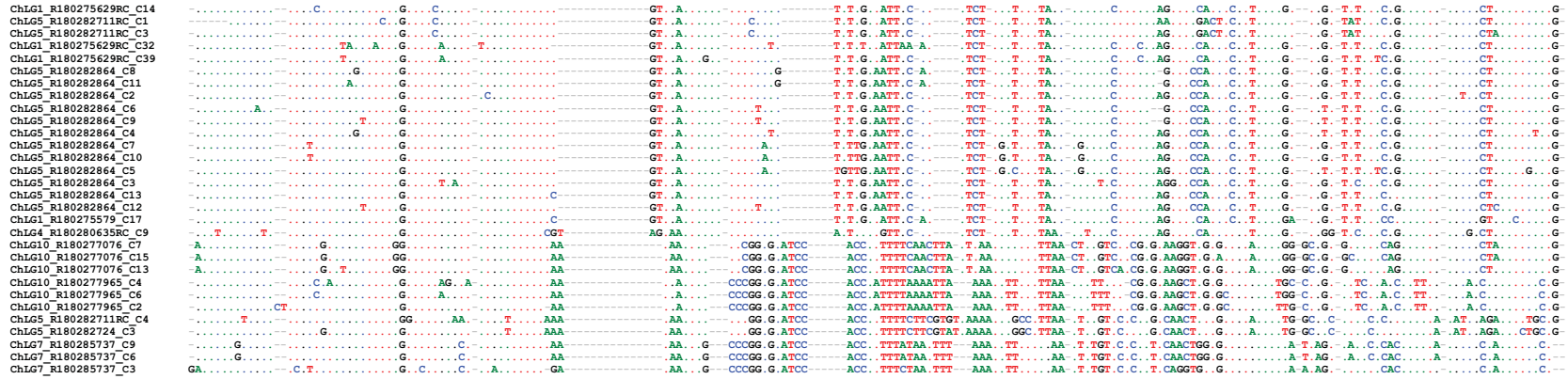
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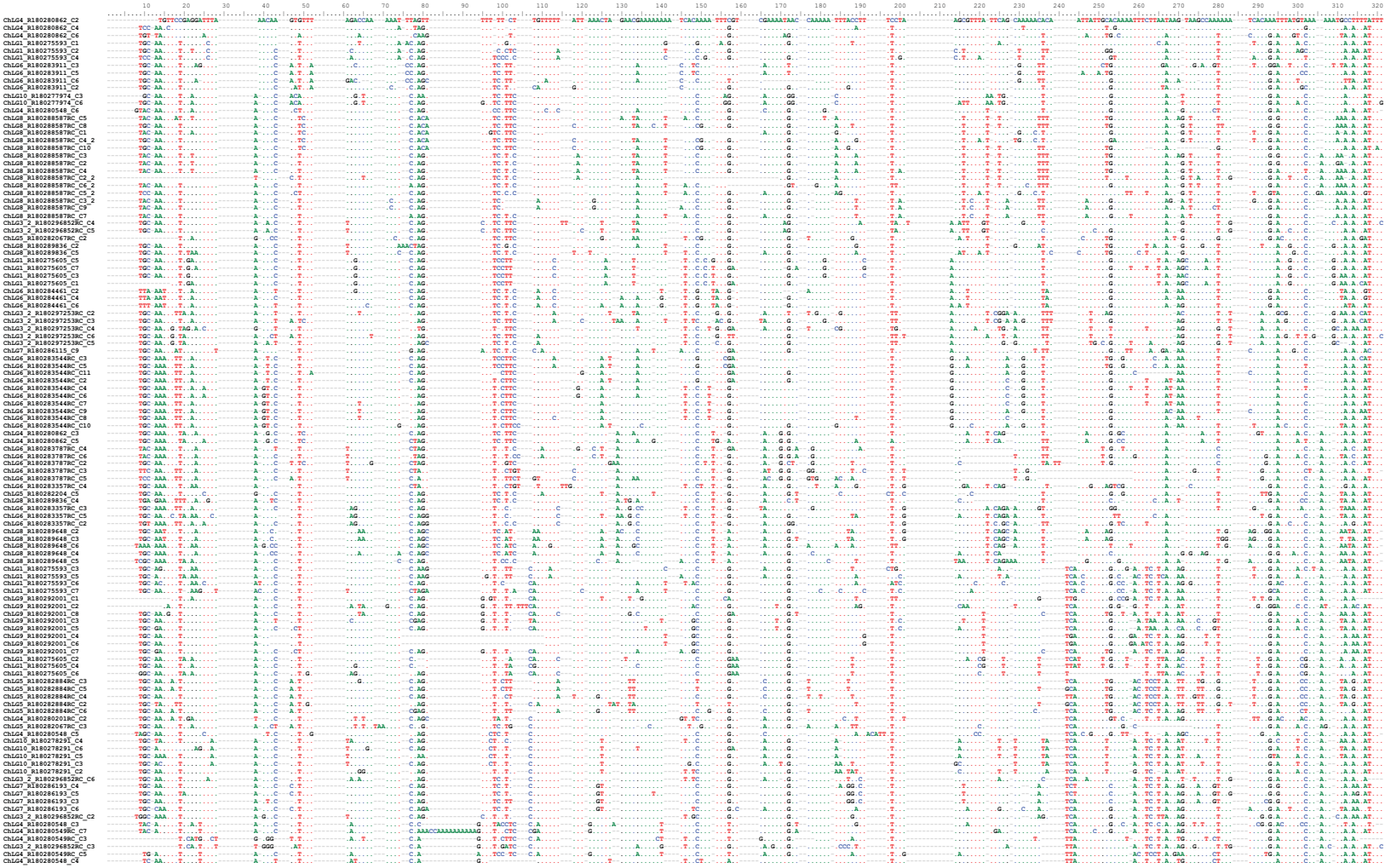

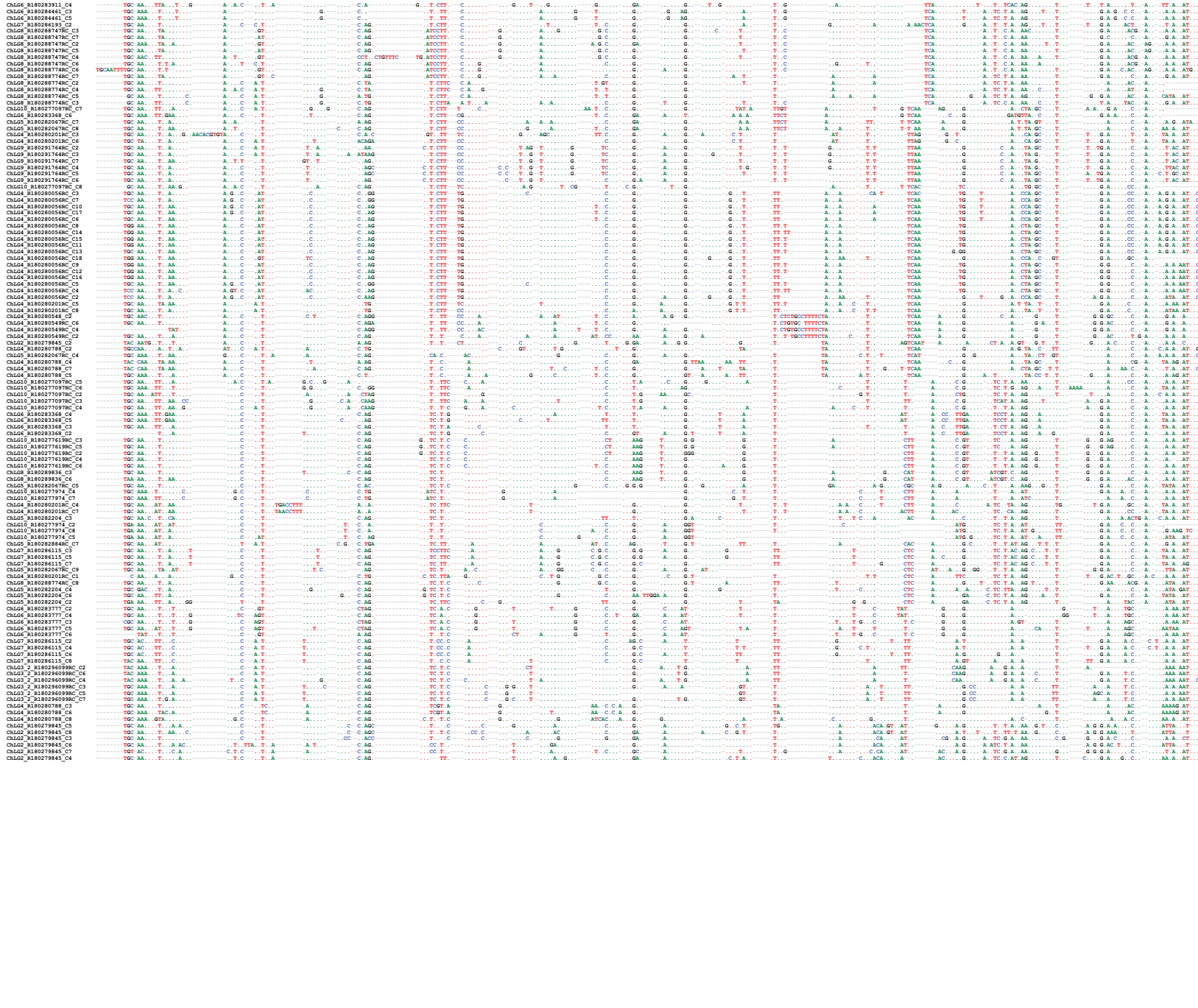

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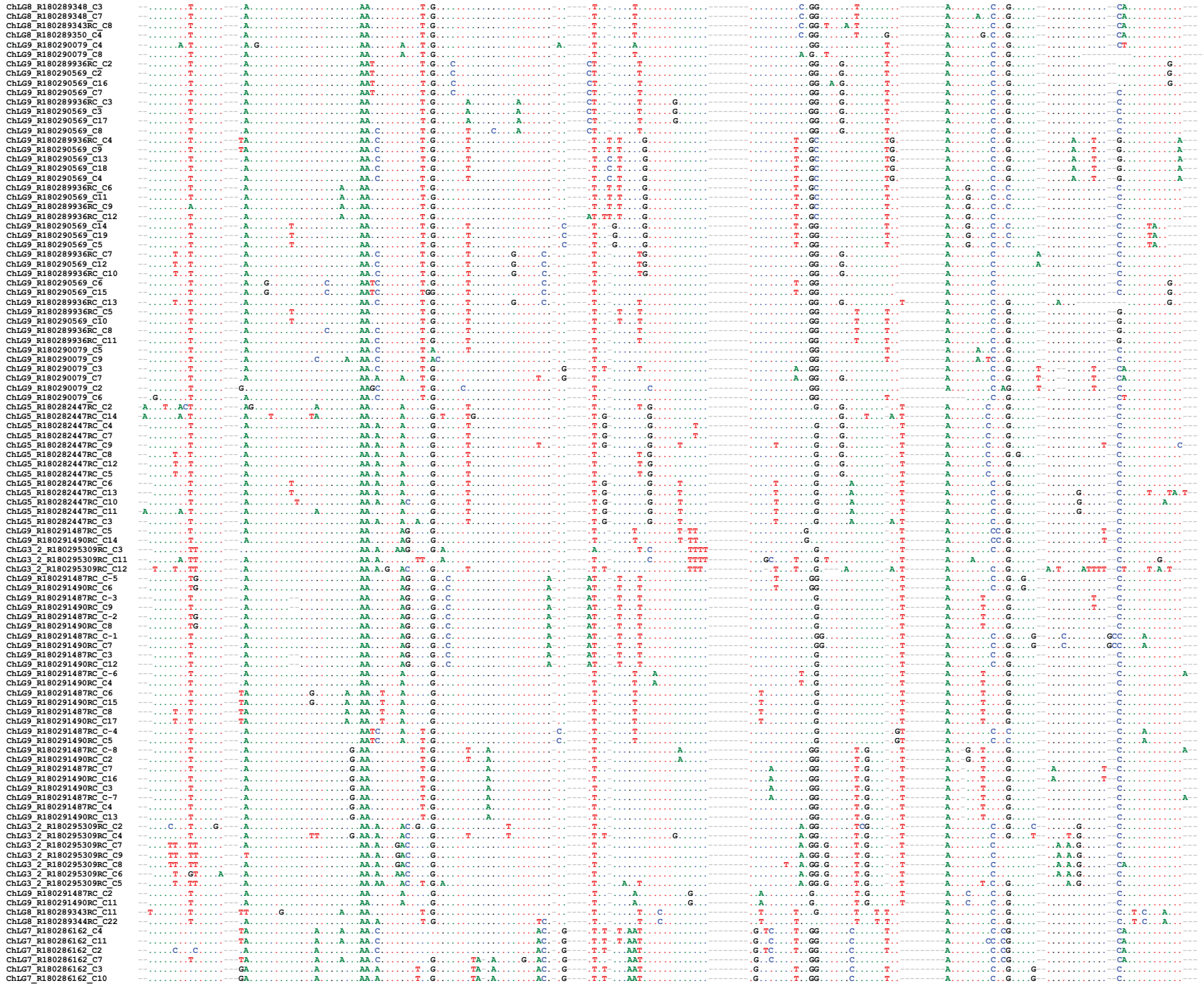
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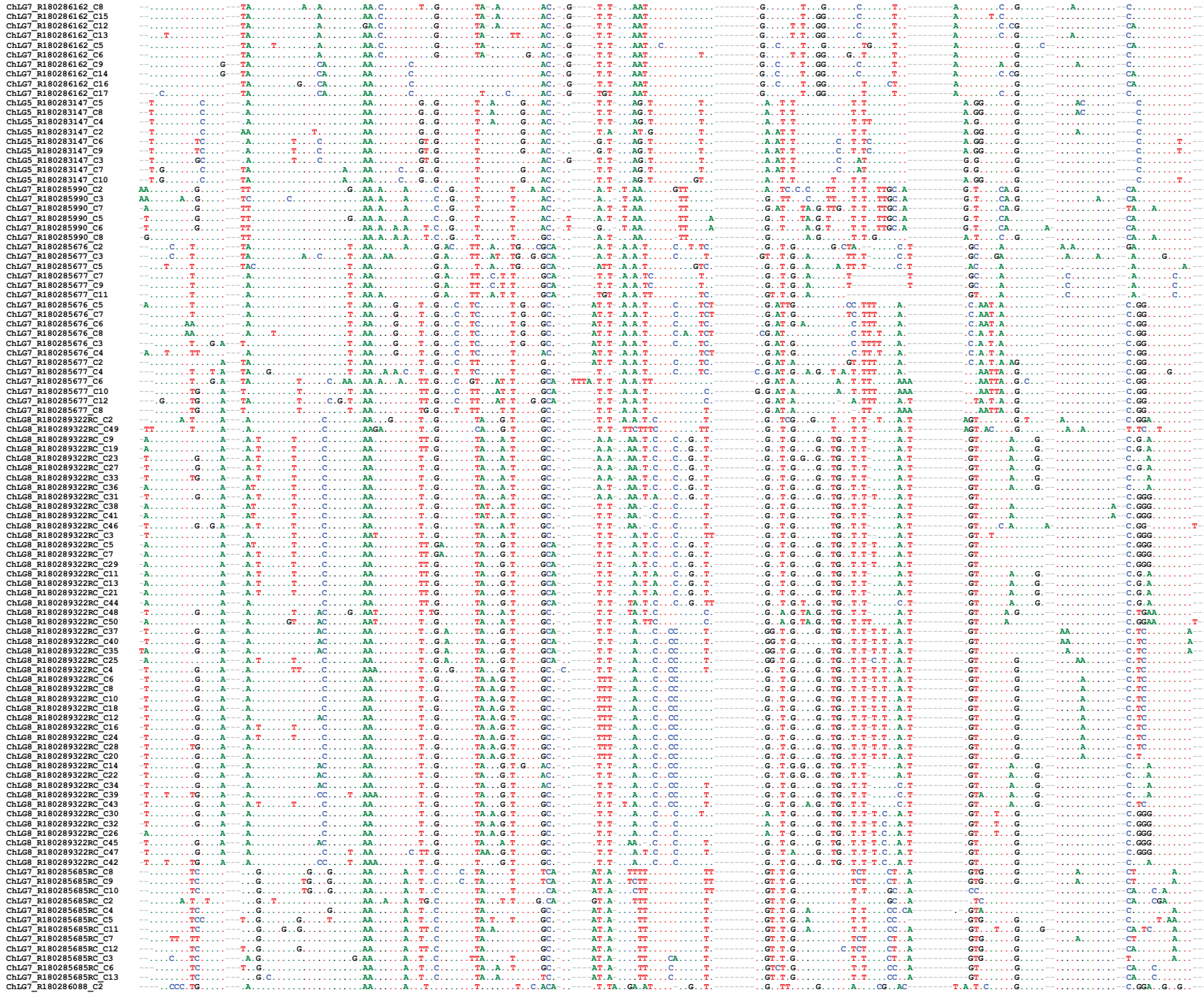
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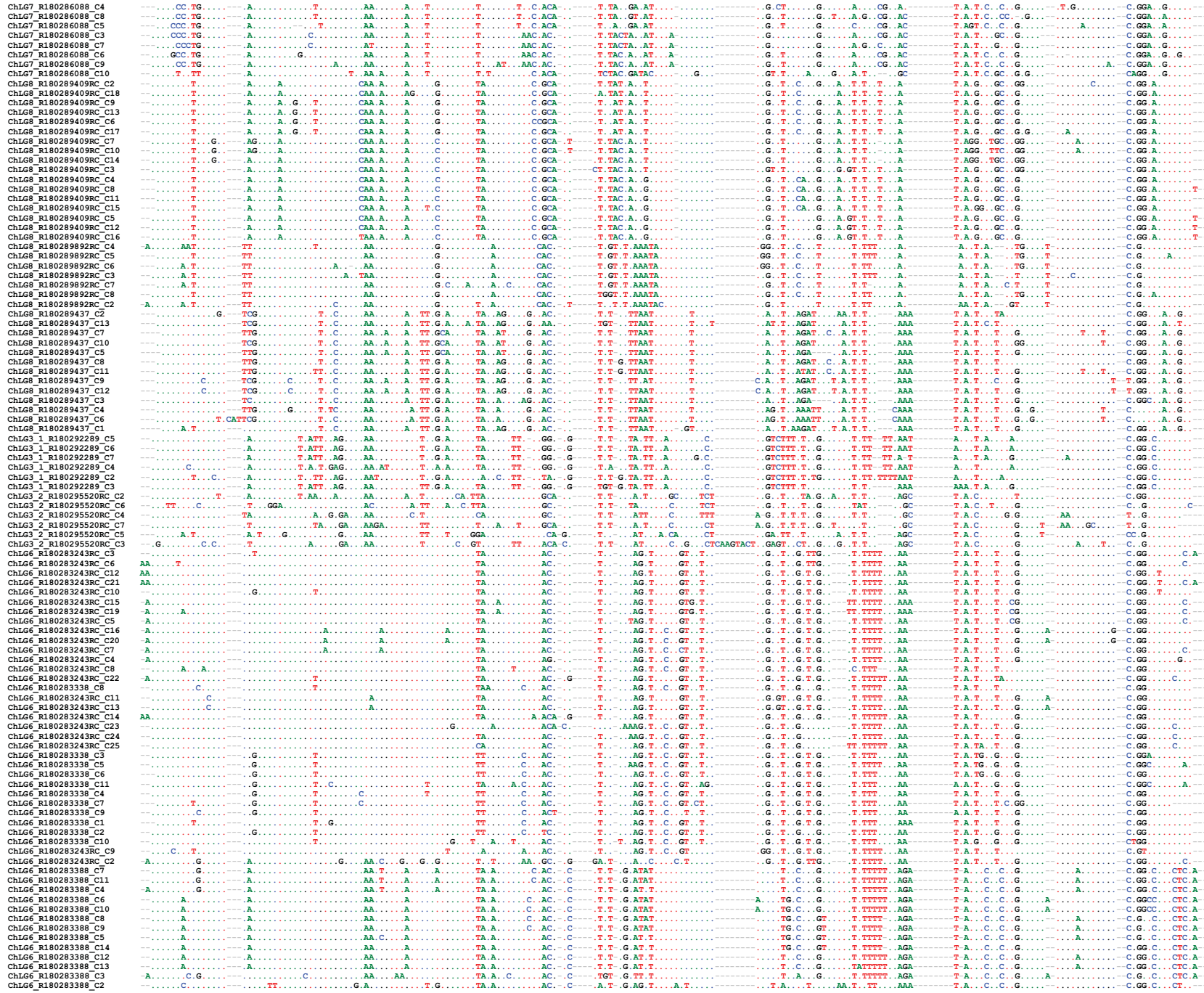
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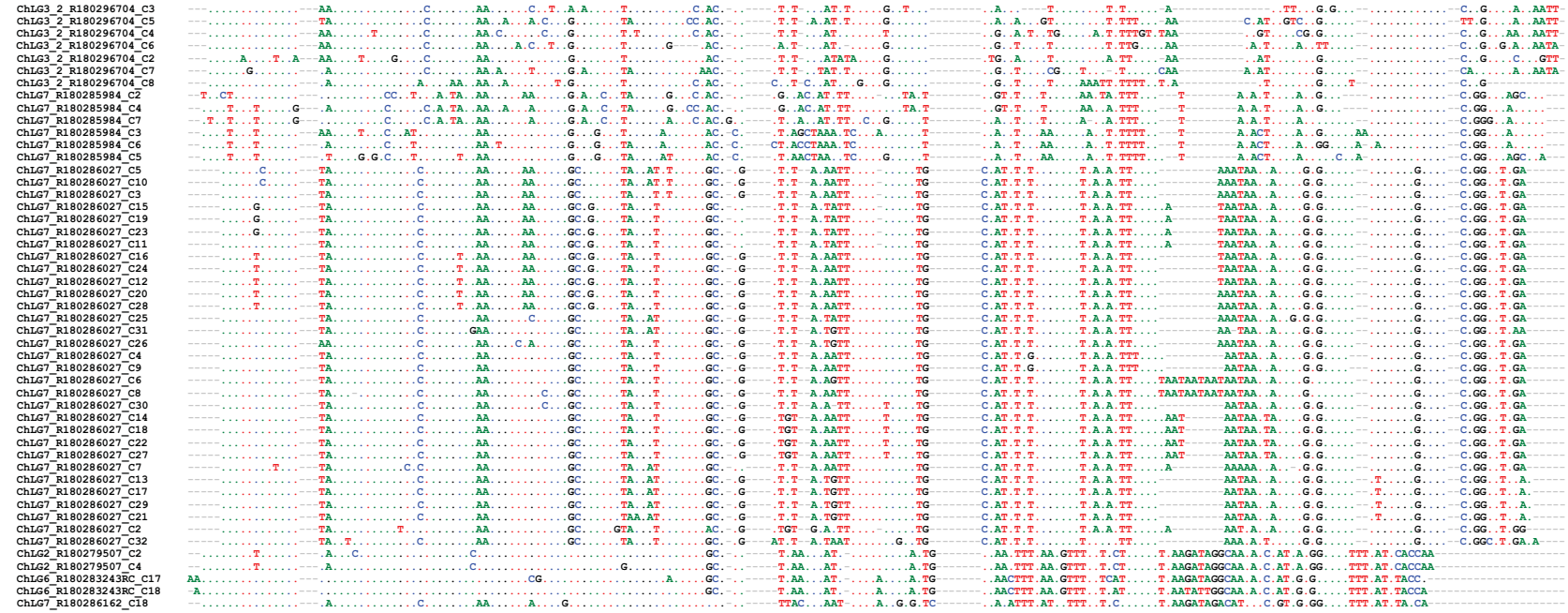
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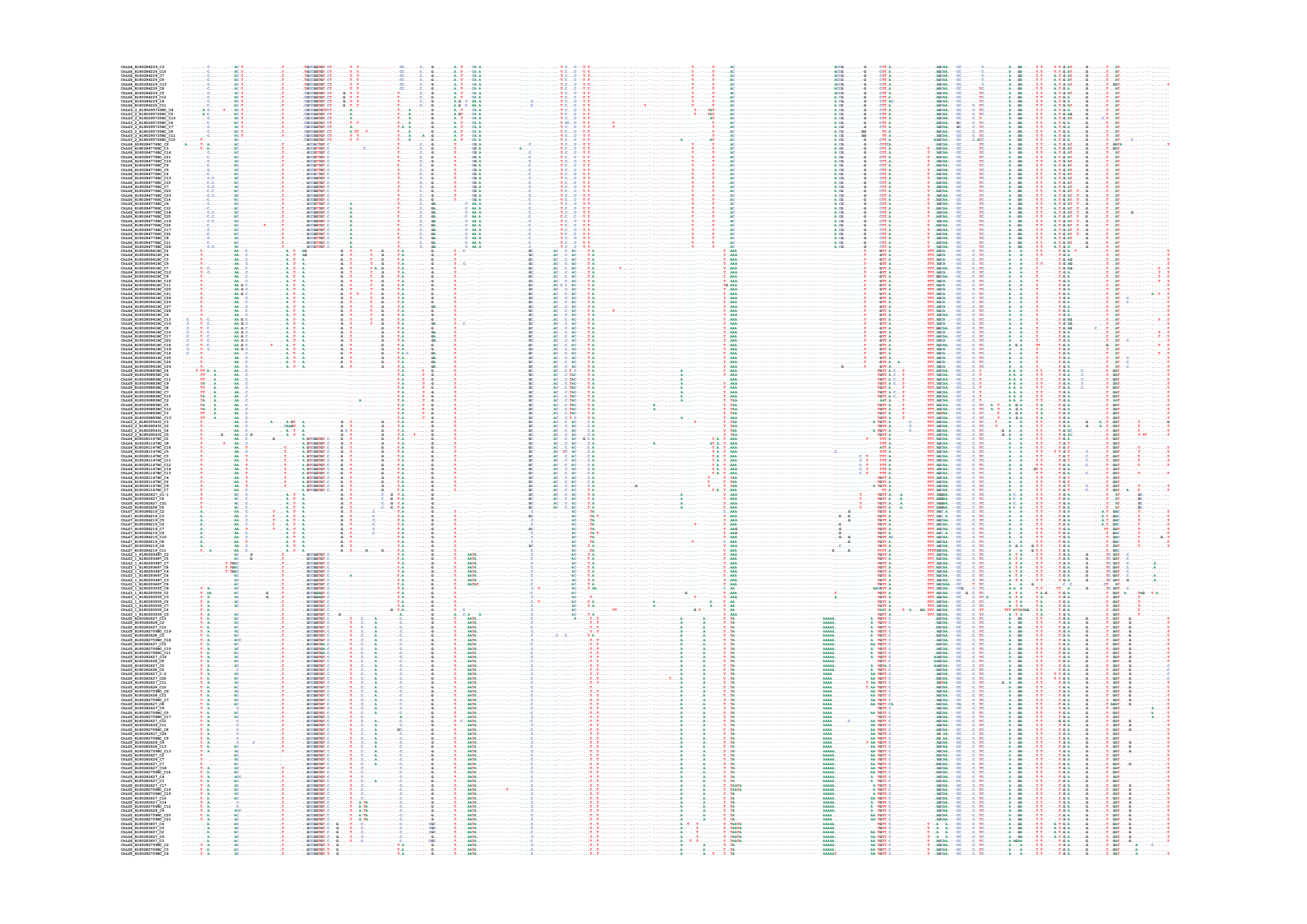
# E. Cast5



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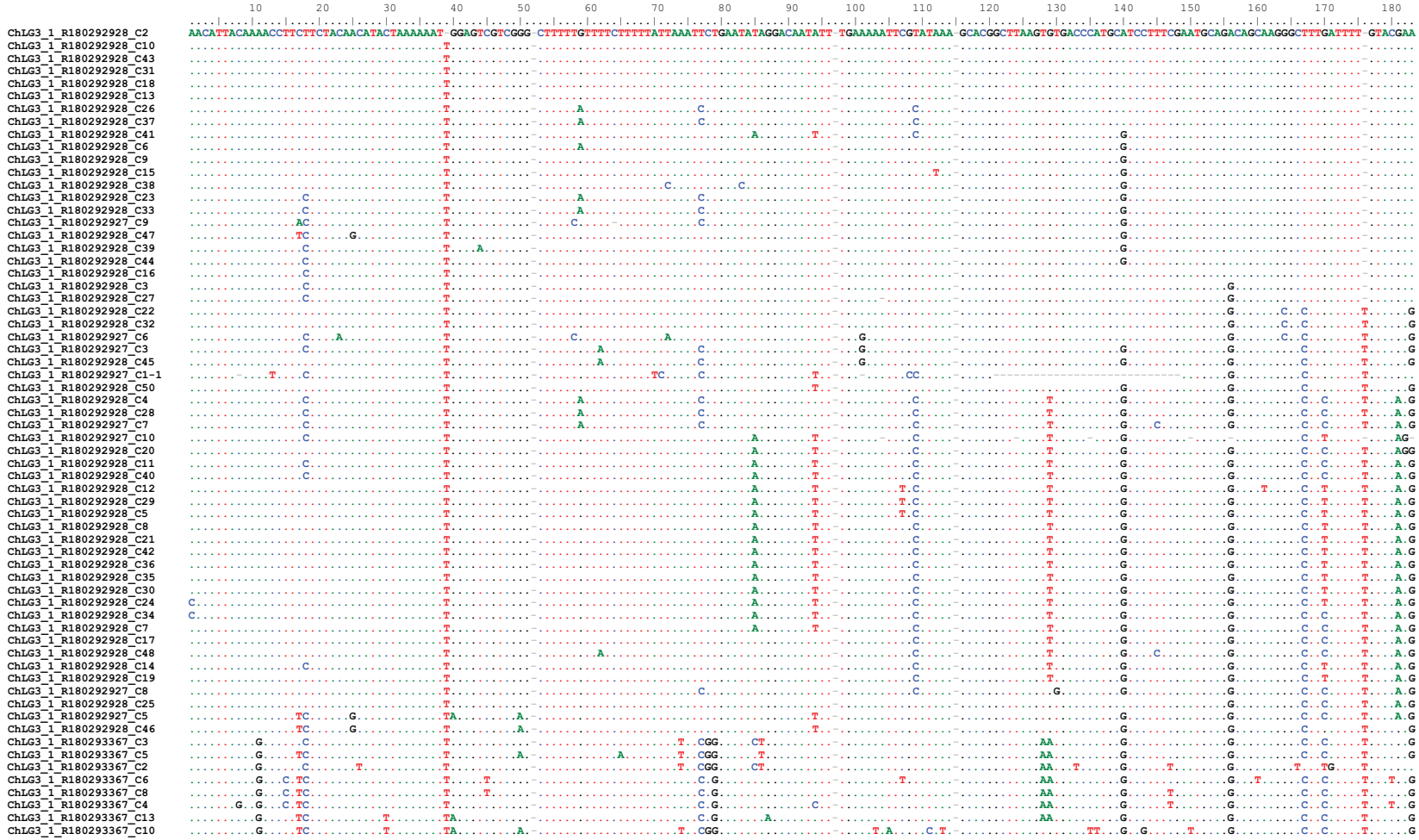
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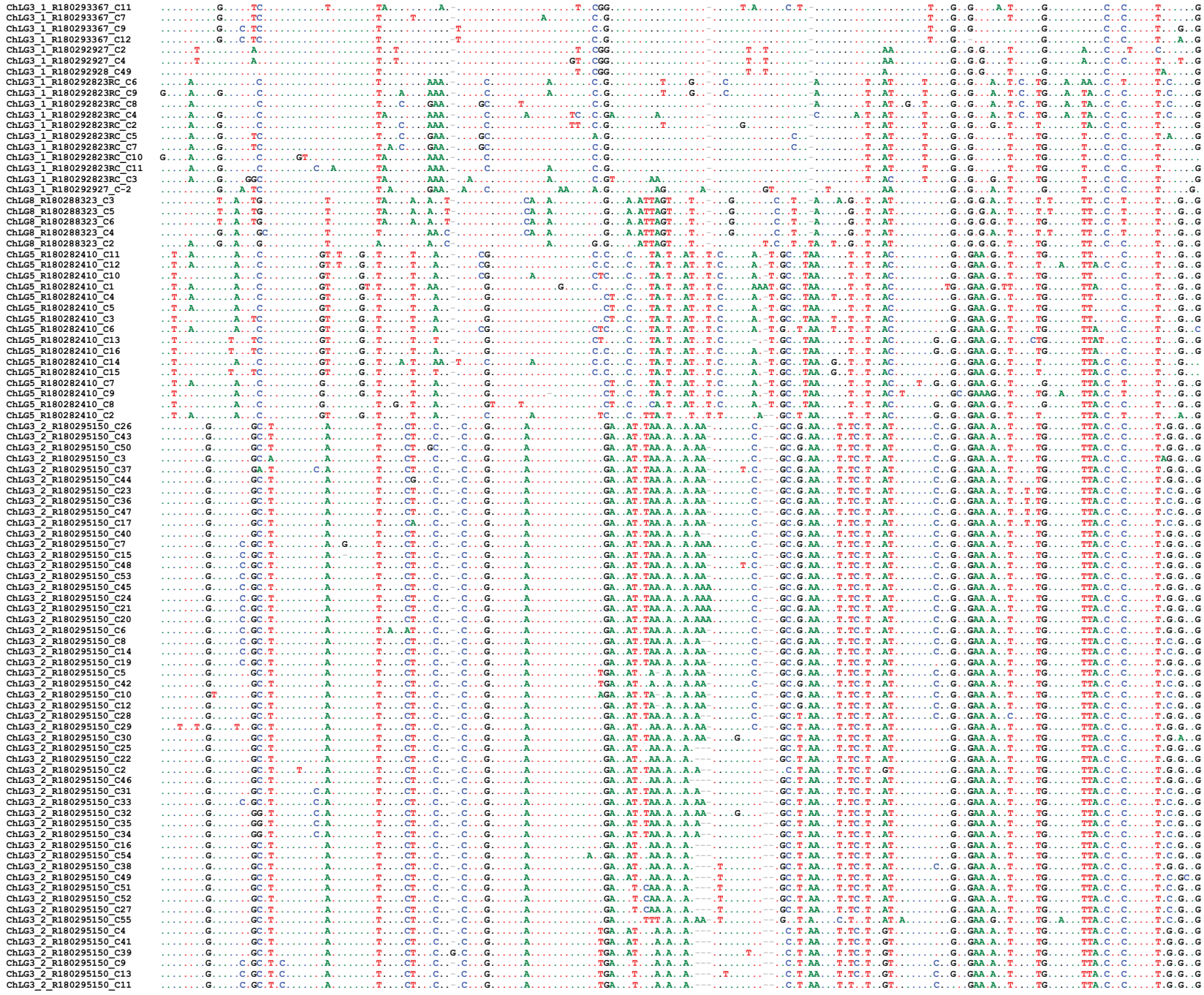
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ChLG3_2_R180295150_C45
ChLG3_2_R180295150_C24
ChLG3_2_R180295150_C21
ChLG3_2_R180295150_C20
ChLG3_2_R180295150_C6
ChLG3_2_R180295150_C8
ChLG3_2_R180295150_C14
ChLG3_2_R180295150_C19
ChLG3_2_R180295150_C5
ChLG3_2_R180295150_C42
ChLG3_2_R180295150_C10
ChLG3_2_R180295150_C12
ChLG3_2_R180295150_C28
ChLG3_2_R180295150_C29
ChLG3_2_R180295150_C30
ChLG3_2_R180295150_C25
ChLG3_2_R180295150_C22
ChLG3_2_R180295150_C2
ChLG3_2_R180295150_C46
ChLG3_2_R180295150_C31
ChLG3_2_R180295150_C33
ChLG3_2_R180295150_C32
ChLG3_2_R180295150_C35
ChLG3_2_R180295150_C34
ChLG3_2_R180295150_C16
ChLG3_2_R180295150_C54
ChLG3_2_R180295150_C38
ChLG3_2_R180295150_C49
ChLG3_2_R180295150_C51
ChLG3_2_R180295150_C52
ChLG3_2_R180295150_C27
ChLG3_2_R180295150_C55
ChLG3_2_R180295150_C4
ChLG3_2_R180295150_C41
ChLG3_2_R180295150_C39
ChLG3_2_R180295150_C9
ChLG3_2_R180295150_C13
ChLG3_2_R180295150_C11

# G. Cast7

ChLG3_2_R180295150_C18
ChLG5_R180282547RC_C2
ChLG5_R180282547RC_C4
ChLG3_1_R180293225_C2
ChLG3_1_R180293225_C6
ChLG3_1_R180293225_C4
ChLG4_R180280157_C1
ChLG4_R180280157_C3
ChLG4_R180280157_C5
ChLG4_R180280157_C7
ChLG8_R180288349RC_C3
ChLG8_R180288349RC_C5
ChLG3_2_R180297093RC_C4
ChLG3_2_R180297093RC_C13
ChLG3_2_R180297093RC_C7
ChLG3_2_R180297093RC_C10
ChLG3_2_R180297093RC_C12
ChLG3_2_R180297093RC_C5
ChLG3_2_R180297093RC_C11
ChLG3_2_R180297093RC_C8
ChLG3_2_R180297093RC_C2
ChLG3_2_R180297093RC_C3
ChLG3_2_R180297093RC_C6
ChLG3_2_R180297093RC_C9
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ChLG3_2_R180294957_C11
ChLG4_R180280157_C-4
ChLG4_R180280157_C-2
ChLG3_2_R180296303_C7
ChLG3_2_R180296303_C9
ChLG3_2_R180296303_C2
ChLG3_2_R180296303_C3
ChLG3_2_R180296303_C8
ChLG3_2_R180296303_C10
ChLG3_2_R180296303_C4
ChLG3_2_R180296303_C5
ChLG3_2_R180296303_C6
ChLG4_R180280157_C-3
ChLG5_R180282191RC_C3
ChLG5_R180282191RC_C8
ChLG5_R180282191RC_C12
ChLG5_R180282191RC_C5
ChLG5_R180282191RC_C2
ChLG5_R180282191RC_C6
ChLG5_R180282191RC_C10
ChLG5_R180282191RC_C9
ChLG5_R180282191RC_C13
ChLG5_R180282191RC_C7
ChLG5_R180282191RC_C11
ChLG5_R180282191RC_C4
ChLG8_R180288349RC_C2
ChLG8_R180288349RC_C6
ChLG8_R180288349RC_C4
ChLG4_R180280157_C2
ChLG4_R180280157_C4
ChLG4_R180280157_C8
ChLG4_R180280157_C6
ChLG8_R180289864_C4
ChLG8_R180289864_C5
ChLG8_R180289864_C6
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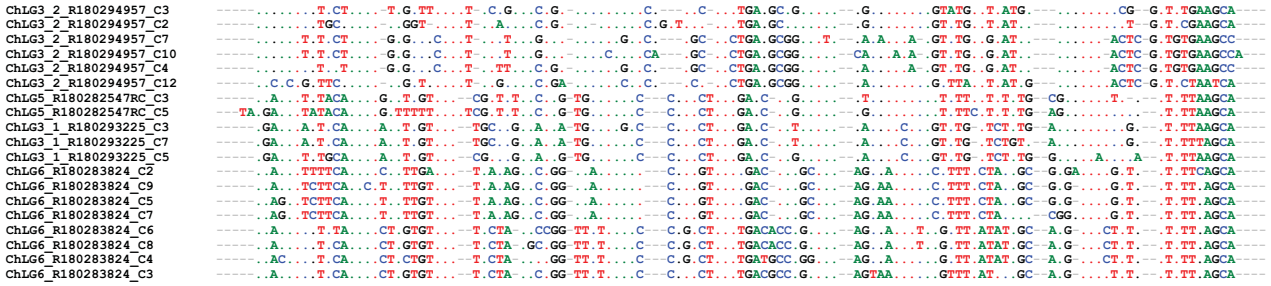
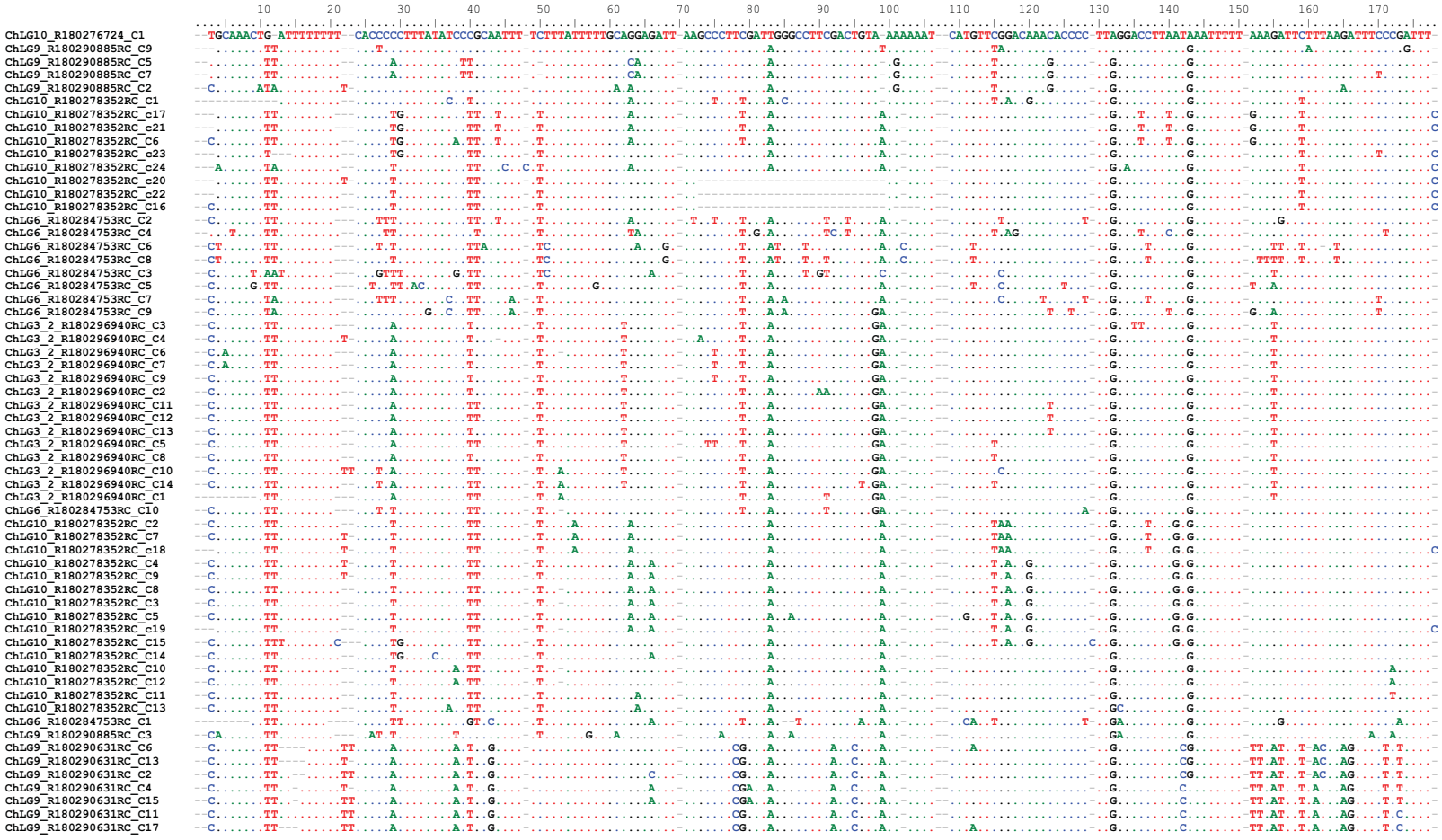
ChLG8_R180289864_C2
ChLG3_2_R180294957_C6
ChLG3_2_R180294957_C9


ChLG3_2_R180294957_C3
ChLG3_2_R180294957_C2
ChLG3_2_R180294957_C7
ChLG3_2_R180294957_C10
ChLG3_2_R180294957_C4
ChLG3_2_R180294957_C12
ChLG5_R180282547RC_C3
ChLG5_R180282547RC_C5
ChLG3_1_R180293225_C3
ChLG3_1_R180293225_C7
ChLG3_1_R180293225_C5
ChLG6_R180283824_C2
ChLG6_R180283824_C9
ChLG6_R180283824_C5
ChLG6_R180283824_C7
ChLG6_R180283824_C6
ChLG6_R180283824_C8
ChLG6_R180283824_C4
ChLG6_R180283824_C3

# H. Cast8


10
20
30
40
50
60
70
80
90
100
110
120
130
140
150
160
170
ChLG10_R180276724_C1
ChLG9_R180290885RC_C9
ChLG9_R180290885RC_C5
ChLG9_R180290885RC_C7
ChLG9_R180290885RC_C2
ChLG10_R180278352RC_C1
ChLG10_R180278352RC_c17
ChLG10_R180278352RC_c21
ChLG10_R180278352RC_C6
ChLG10_R180278352RC_c23
ChLG10_R180278352RC_c24
ChLG10_R180278352RC_c20
ChLG10_R180278352RC_c22
ChLG10_R180278352RC_C16
ChLG6_R180284753RC_C2
ChLG6_R180284753RC_C4
ChLG6_R180284753RC_C6
ChLG6_R180284753RC_C8
ChLG6_R180284753RC_C3
ChLG6_R180284753RC_C5
ChLG6_R180284753RC_C7
ChLG6_R180284753RC_C9
ChLG3_2_R180296940RC_C3
ChLG3_2_R180296940RC_C4
ChLG3_2_R180296940RC_C6
ChLG3_2_R180296940RC_C7
ChLG3_2_R180296940RC_C9
ChLG3_2_R180296940RC_C2
ChLG3_2_R180296940RC_C11
ChLG3_2_R180296940RC_C12
ChLG3_2_R180296940RC_C13
ChLG3_2_R180296940RC_C5
ChLG3_2_R180296940RC_C8
ChLG3_2_R180296940RC_C10
ChLG3_2_R180296940RC_C14
ChLG3_2_R180296940RC_C1
ChLG6_R180284753RC_C10
ChLG10_R180278352RC_C2
ChLG10_R180278352RC_C7
ChLG10_R180278352RC_c18
ChLG10_R180278352RC_C4
ChLG10_R180278352RC_C9
ChLG10_R180278352RC_C8
ChLG10_R180278352RC_C3
ChLG10_R180278352RC_C5
ChLG10_R180278352RC_c19
ChLG10_R180278352RC_C15
ChLG10_R180278352RC_C14
ChLG10_R180278352RC_C10
ChLG10_R180278352RC_C12
ChLG10_R180278352RC_C11
ChLG10_R180278352RC_C13
ChLG6_R180284753RC_C1
ChLG9_R180290885RC_C3
ChLG9_R180290631RC_C6
ChLG9_R180290631RC_C13
ChLG9_R180290631RC_C2
ChLG9_R180290631RC_C4
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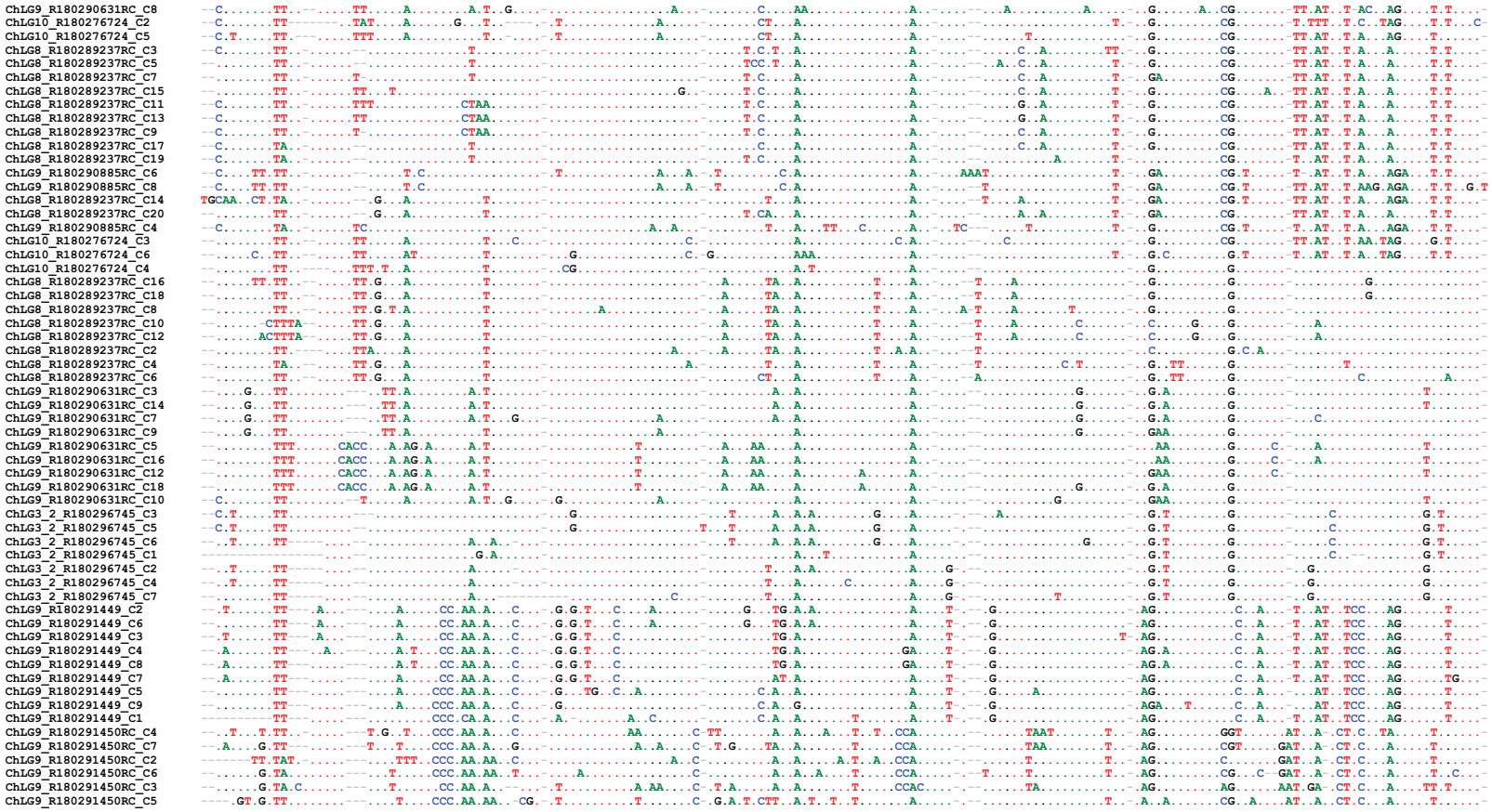
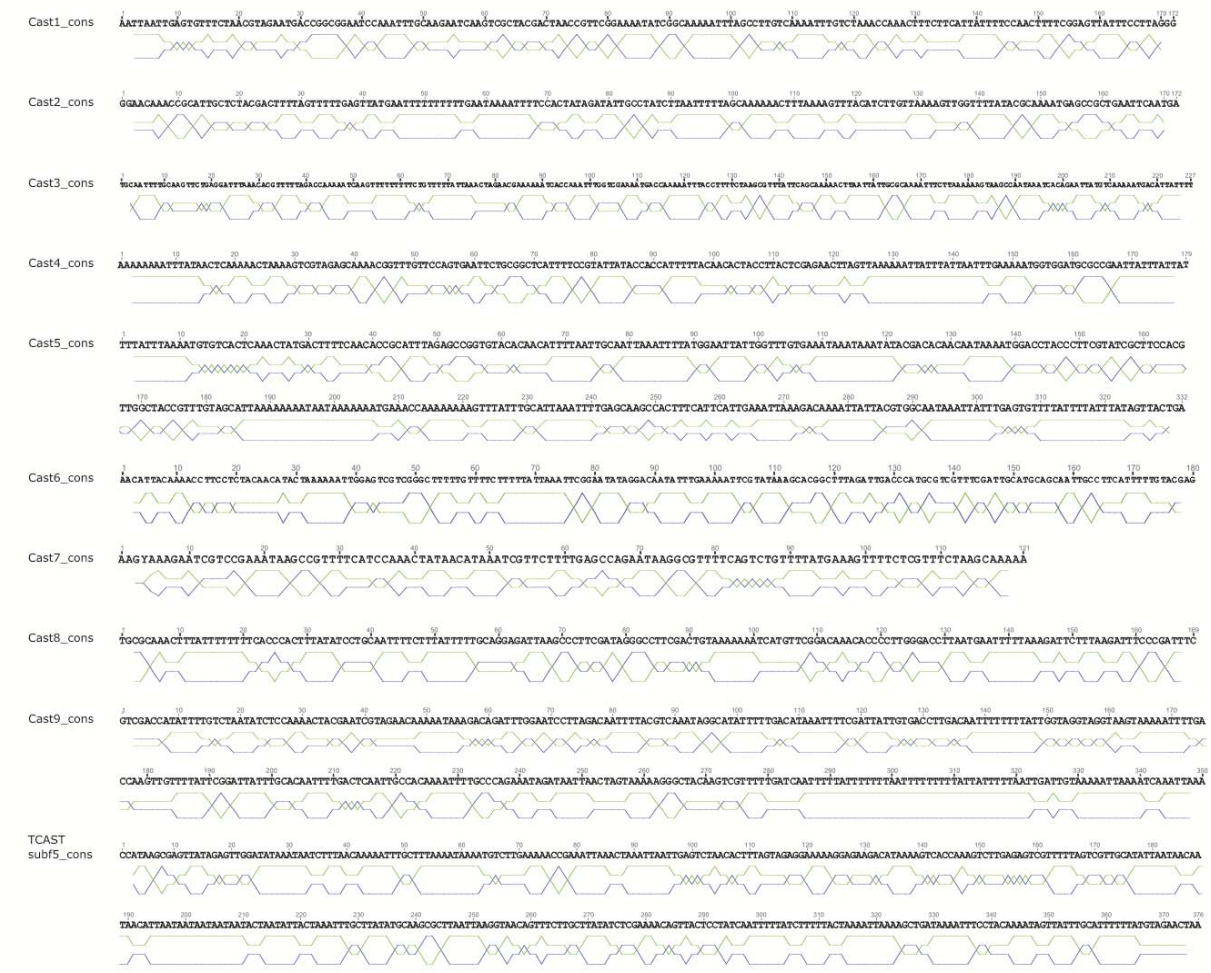
ChLG9_R180290631RC_C11
ChLG9_R180290631RC_C17


ChLG9_R180290631RC_C8
ChLG10_R180276724_C2
ChLG10_R180276724_C5
ChLG8_R180289237RC_C3
ChLG8_R180289237RC_C5
ChLG8_R180289237RC_C7
ChLG8_R180289237RC_C15
ChLG8_R180289237RC_C11
ChLG8_R180289237RC_C13
ChLG8_R180289237RC_C9
ChLG8_R180289237RC_C17
ChLG8_R180289237RC_C19
ChLG9_R180290885RC_C6
ChLG9_R180290885RC_C8
ChLG8_R180289237RC_C14
ChLG8_R180289237RC_C20
ChLG9_R180290885RC_C4
ChLG10_R180276724_C3
ChLG10_R180276724_C6
ChLG10_R180276724_C4
ChLG8_R180289237RC_C16
ChLG8_R180289237RC_C18
ChLG8_R180289237RC_C8
ChLG8_R180289237RC_C10
ChLG8_R180289237RC_C12
ChLG8_R180289237RC_C2
ChLG8_R180289237RC_C4
ChLG8_R180289237RC_C6
ChLG9_R180290631RC_C3
ChLG9_R180290631RC_C14
ChLG9_R180290631RC_C7
ChLG9_R180290631RC_C9
ChLG9_R180290631RC_C5
ChLG9_R180290631RC_C16
ChLG9_R180290631RC_C12
ChLG9_R180290631RC_C18
ChLG9_R180290631RC_C10
ChLG3_2_R180296745_C3
ChLG3_2_R180296745_C5
ChLG3_2_R180296745_C6
ChLG3_2_R180296745_C1
ChLG3_2_R180296745_C2
ChLG3_2_R180296745_C4
ChLG3_2_R180296745_C7
ChLG9_R180291449_C2
ChLG9_R180291449_C6
ChLG9_R180291449_C3
ChLG9_R180291449_C4
ChLG9_R180291449_C8
ChLG9_R180291449_C7
ChLG9_R180291449_C5
ChLG9_R180291449_C9
ChLG9_R180291449_C1
ChLG9_R180291450RC_C4
ChLG9_R180291450RC_C7
ChLG9_R180291450RC_C2
ChLG9_R180291450RC_C6
ChLG9_R180291450RC_C3
ChLG9_R180291450RC_C5

# I. Cast9

ChLG8_R180289192_C8
ChLG8_R180289192_C2
ChLG8_R180289192_C4
ChLG8_R180289192_C7
ChLG8_R180289192_C9
ChLG8_R180289192_C3
ChLG8_R180289192_C6
ChLG3_2_R180297062_C2
ChLG3_2_R180297062_C6
ChLG3_2_R180297062_C3
ChLG3_2_R180297062_C4
ChLG3_2_R180297062_C5
ChLG3_2_R180297062_C1
ChLG3_2_R180297062_C7

# Additional file S2



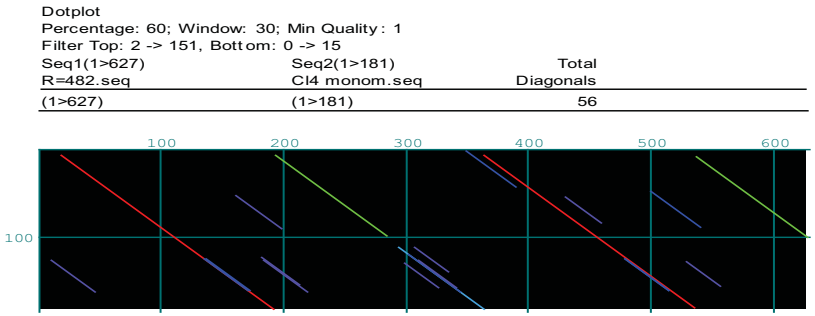

Additional file 2. Periodicity of A/T and G/C nucleotides along the monomer sequences. Proportion of AT nucleotides are indicate with green line while blue line represent GC nucleotides.

Additional file 3. Results of LOCAL BLAST search of new TRF satDNAs with RepeatScout library repeat families published in Wang et al 2008 (A and C). Comparison of obtained RepeatScout repeat families with new satDNAs by dot plot analyses (B and D)

## A. BLAST with Cast4

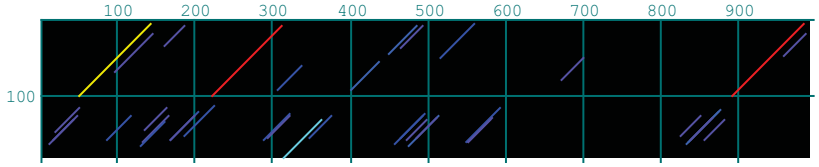
| | | |
|---|---|---|
| R=482\|TRF=0.000\|NSEG=0.429\|HighB | 151 | 7e-038 |
| R=135\|TRF=0.000\|NSEG=0.444\|HighB | 151 | 7e-038 |
| R=0\|TRF=0.080\|NSEG=0.370\|HighB-dispearsed dimer | 151 | 7e-038 |
| R=2036\|TRF=0.000\|NSEG=0.341\|Low-part of monomer+ flanking | 143 | 2e-035 |
| R=1766\|TRF=0.000\|NSEG=0.306\|Mid- part of monomer+flanking | 127 | 1e-030 |
| R=692 (RR=689. TRF=0.000 NSEG=0.388part of monomer+flanking | 127 | 1e-030 |
| R=3699\|TRF=0.000\|NSEG=0.242\|Low | 125 | 4e-030 |

## B. DotPlot analyses of Cast4 and similar RepeatScout repeat families



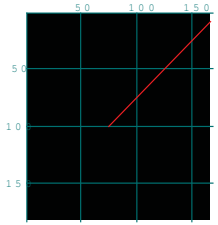
Dotplot
Percentage: 60; Window: 30; Min Quality: 1
Filter Top: 1 -> 25, Bottom: 1 -> 75

| Seq1(1>992) | Seq2(1>181) | Total |
|---|---|---|
| R=135.seq | Cl4 monom.seq | Diagonals |
| (1>992) | (1>181) | 89 |



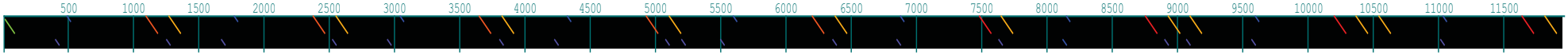

Dotplot
Percentage: 70; Window: 30; Min Quality
Filter Top: 0 -> 0, Bottom: 56 -> 56

| Seq1(1>167) | Seq2(1>181) | Tot |
|---|---|---|
| R2036.seq | Cl4 monom.seq | Diagor |
| (1>167) | (1>181) | 1 |



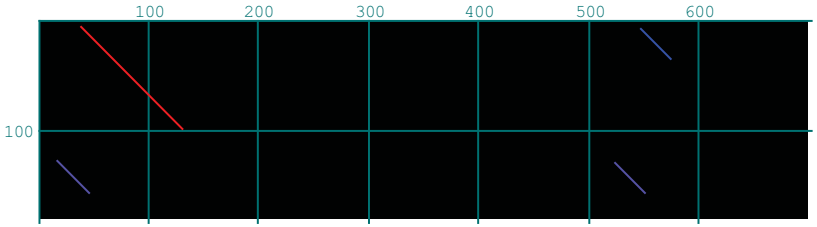
Dotplot
Percentage: 70; Window: 30; Min Quality: 1
Filter Top: 1 -> 73, Bottom: 1 -> 14

| Seq1(1>11954) | Seq2(1>181) | Total |
|---|---|---|
| R=0.seq | Cl4 monom.seq | Diagonals |
| (1>11954) | (1>181) | 95 |



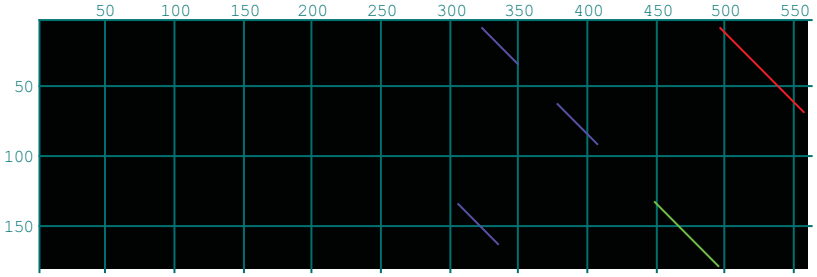

Dotplot
Percentage: 70; Window: 30; Min Quality: 1
Filter Top: 1 -> 62, Bottom: 2 -> 3

| Seq1(1>698) | Seq2(1>181) | Total |
|---|---|---|
| R=1766.seq | Cl4 monom.seq | Diagonals |
| (1>698) | (1>181) | 6 |

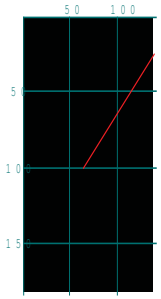



Dotplot
Percentage: 70; Window: 30; Min Quality: 1
Filter Top: 1 -> 41, Bottom: 5 -> 5

| Seq1(1>560) | Seq2(1>181) | Total |
|---|---|---|
| R=692.seq | Cl4 monom.seq | Diagonals |
| (1>560) | (1>181) | 6 |



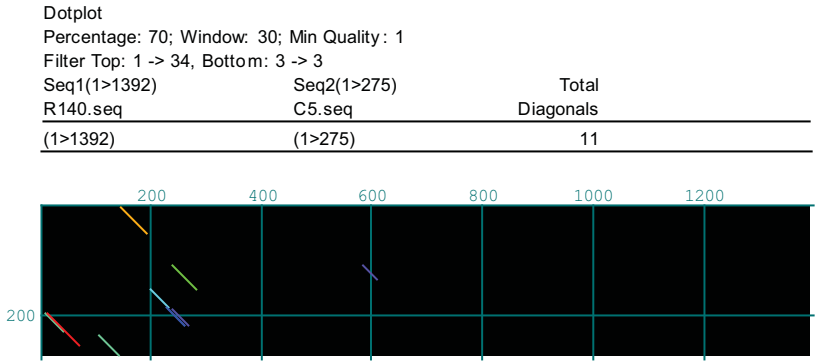
Dotplot
Percentage: 70; Window: 30; Min (
Filter Top: 0 -> 0, Bottom: 39 -> 3
Seq1(1>139) Seq2(1>181) Tot
R3699.seq Cl4 monom.s@qiago
(1>139) (1>181) 1



## C. BLAST with Cast5

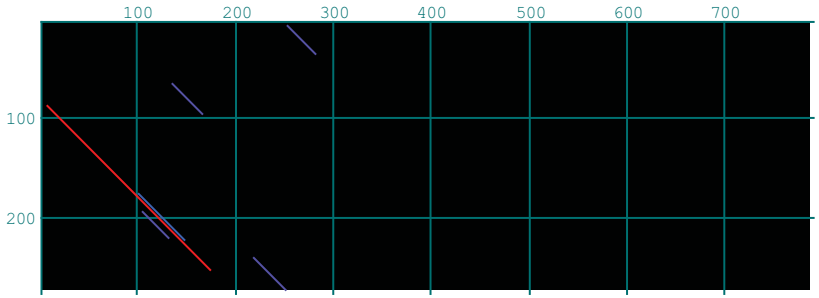
```
R=1877|TRF=0.000|NSEG=0.261|Mid                                  172   4e-044
R=66|TRF=0.034|NSEG=0.471|HighA                                  131   1e-031
R=140|TRF=0.000|NSEG=0.215|Mid                                    92   1e-019
```

## D. DotPlot analyses of Cast4 and similar RepeatScout repeat families



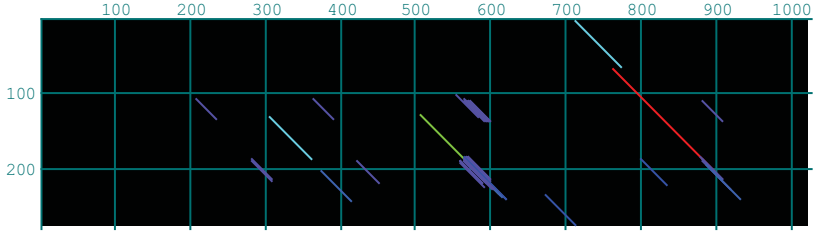
Dotplot
Percentage: 70; Window: 30; Min Quality: 1
Filter Top: 2 -> 123, Bottom: 0 -> 0

| Seq1(1>787) | Seq2(1>275) | Total |
|---|---|---|
| R1877.seq | C5.seq | Diagonals |
| (1>787) | (1>275) | 6 |

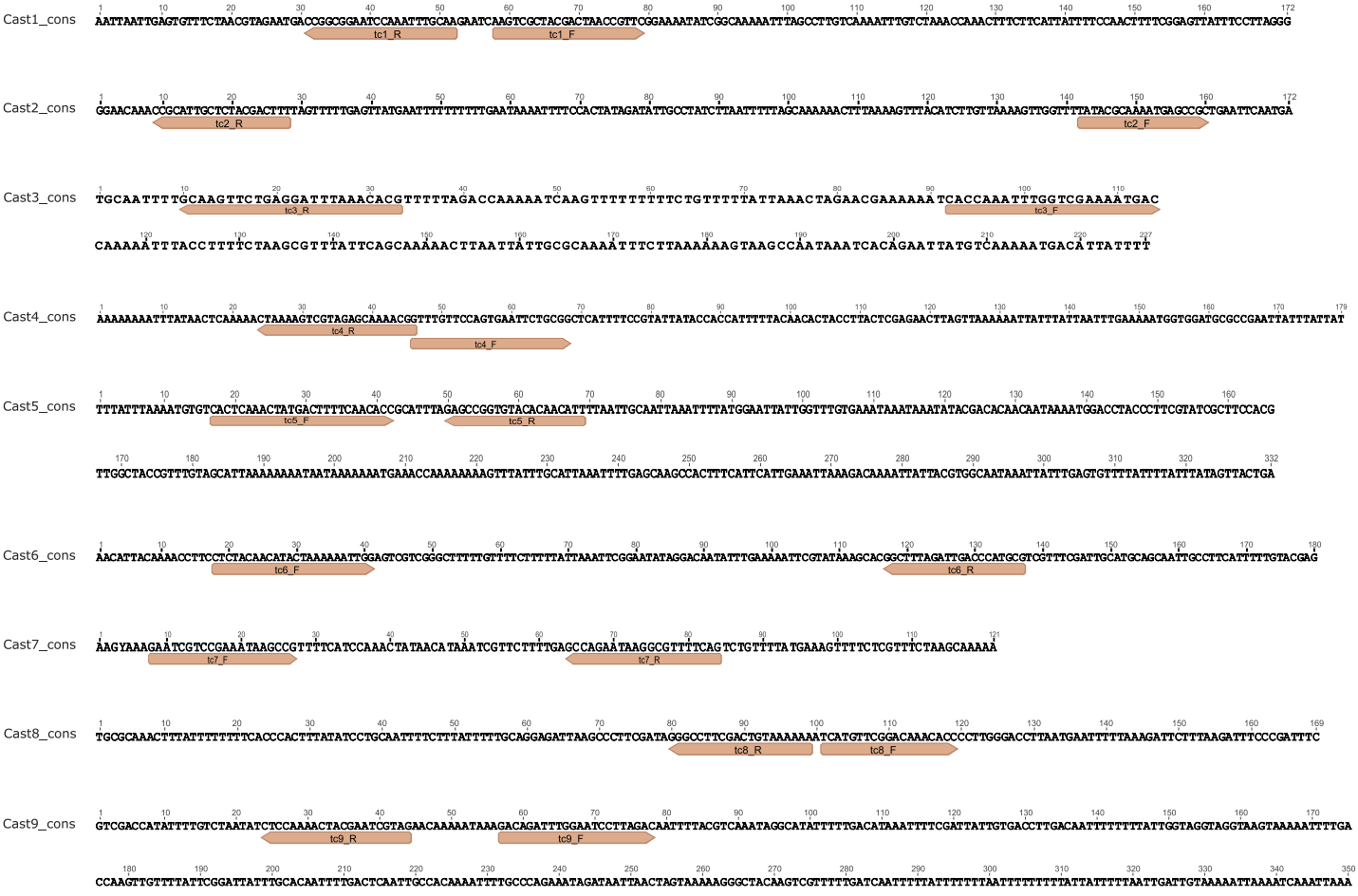



Dotplot
Percentage: 70; Window: 30; Min Quality: 1
Filter Top: 1 -> 110, Bottom: 1 -> 6

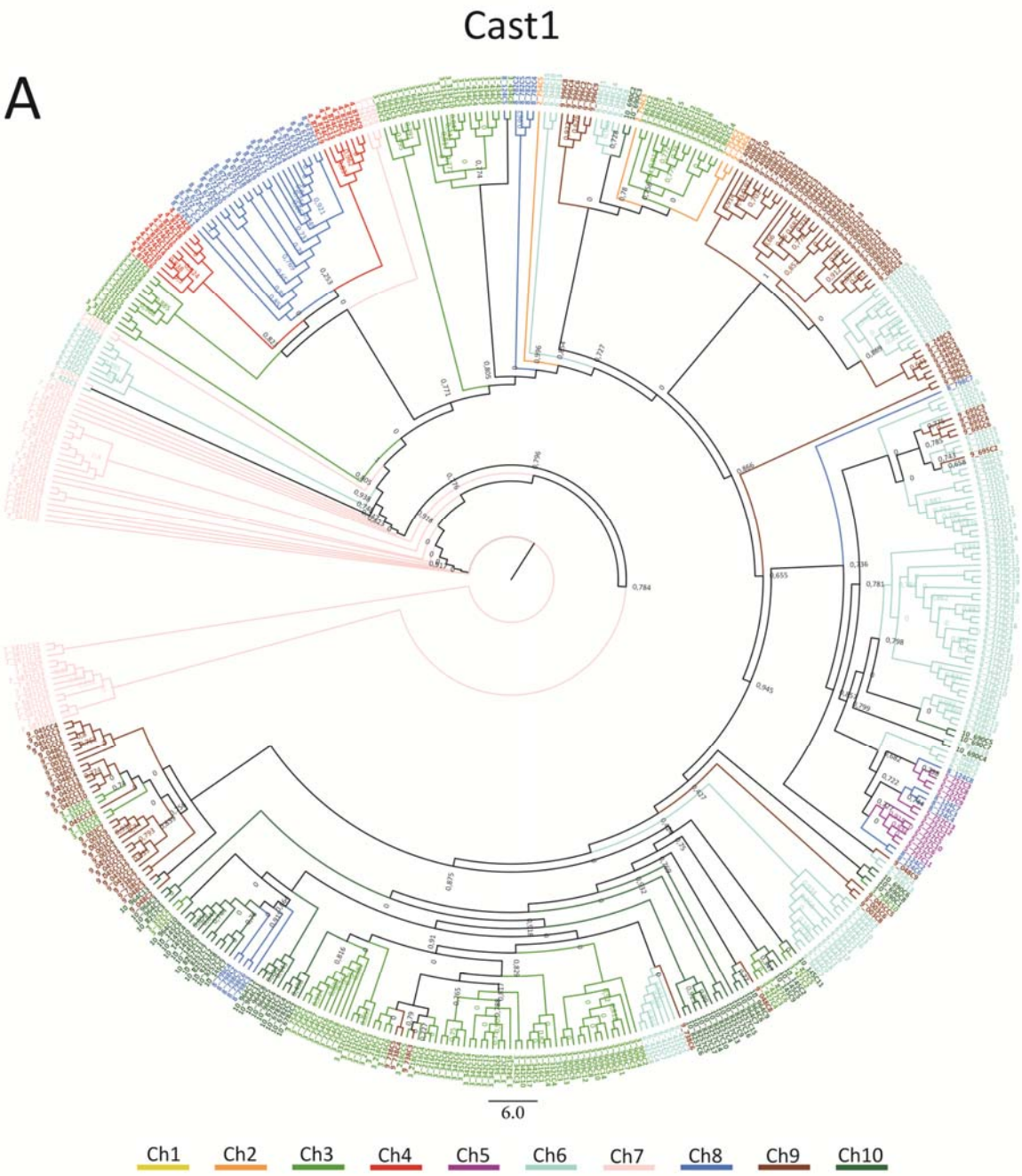
| Seq1(1>1025) | Seq2(1>275) | Total |
|---|---|---|
| R66.seq | C5.seq | Diagonals |
| (1>1025) | (1>275) | 50 |

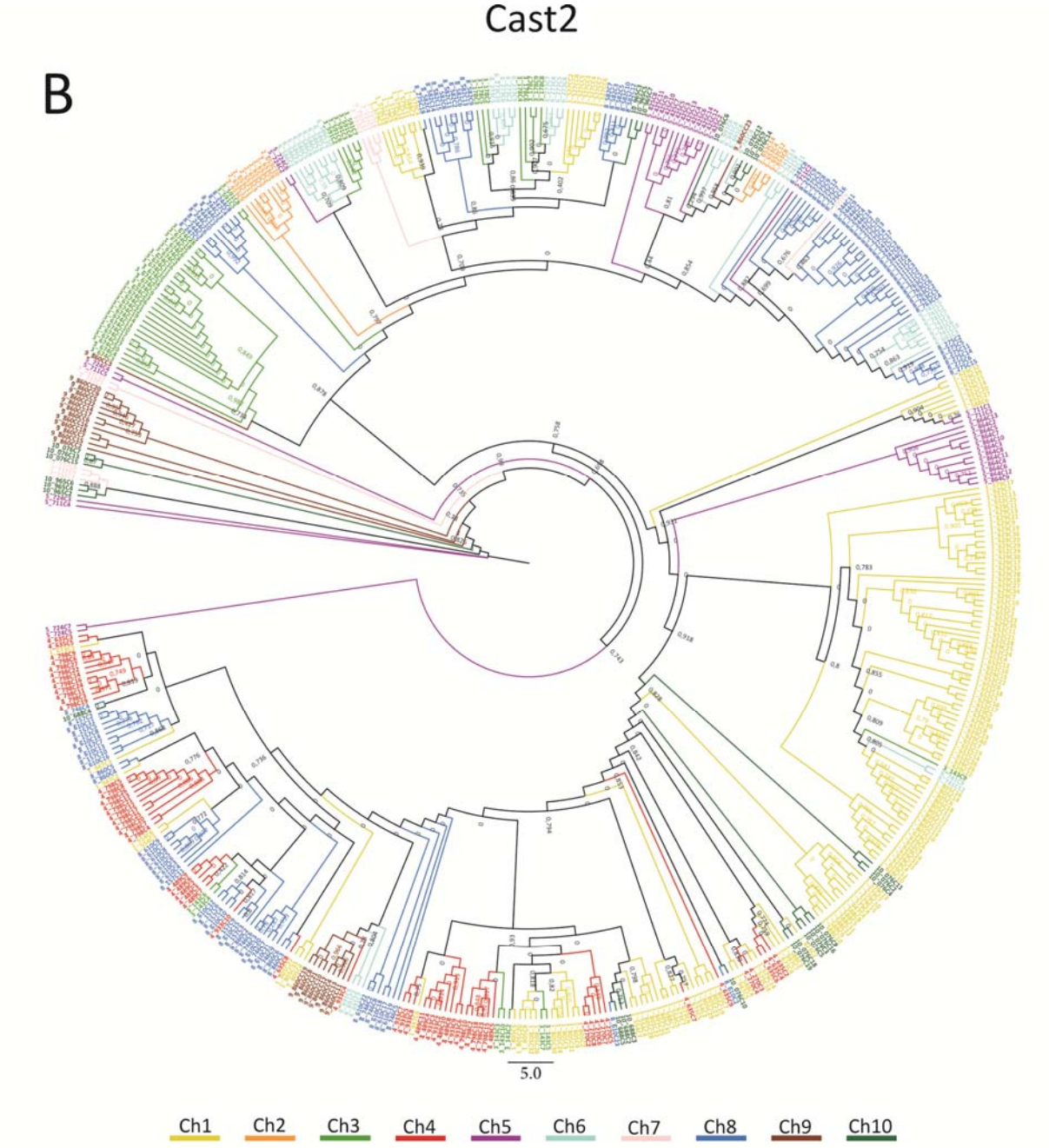


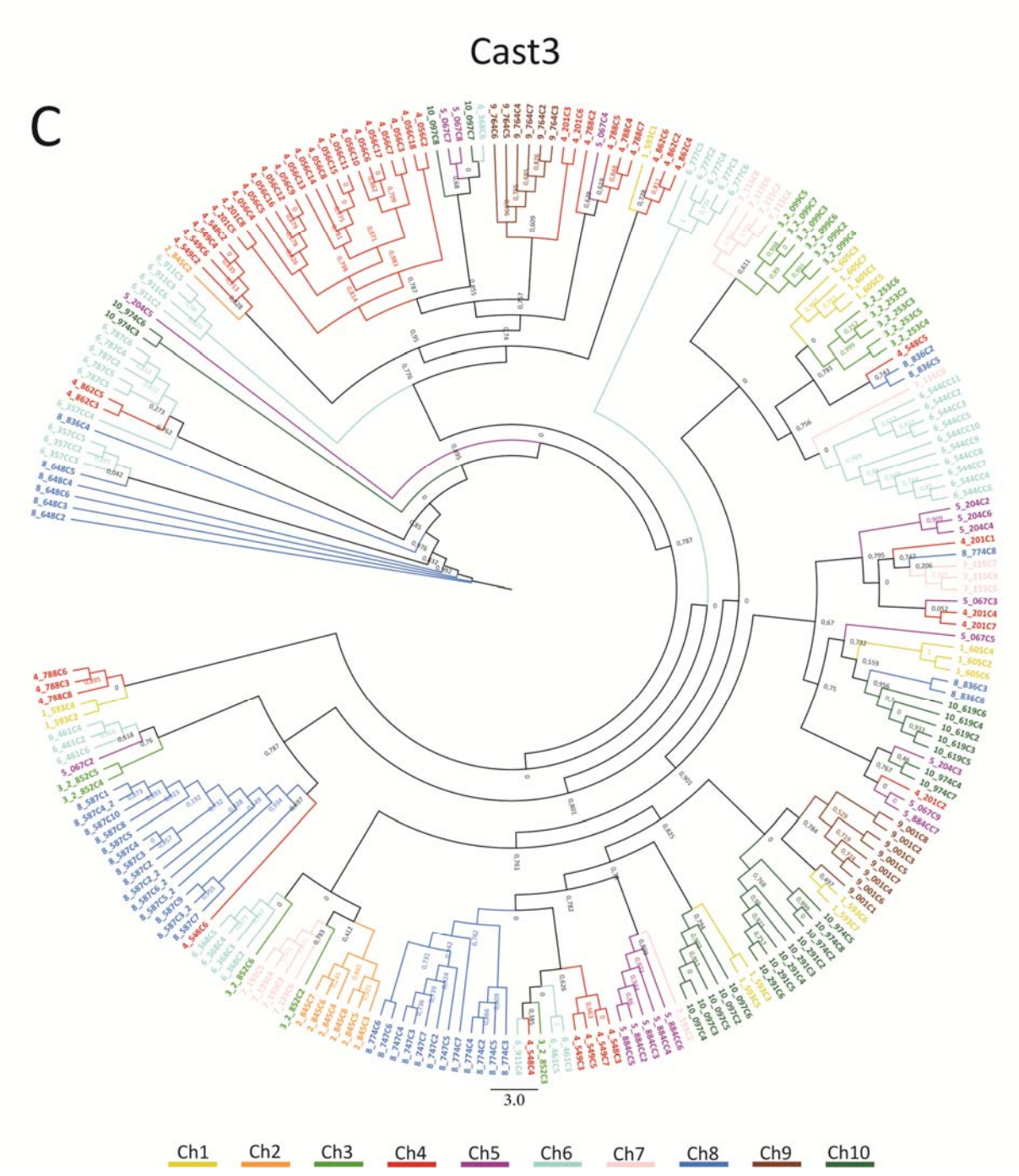
Additional file 4. Consensus sequences of Cast1-Cast9 satDNAs with primer positions

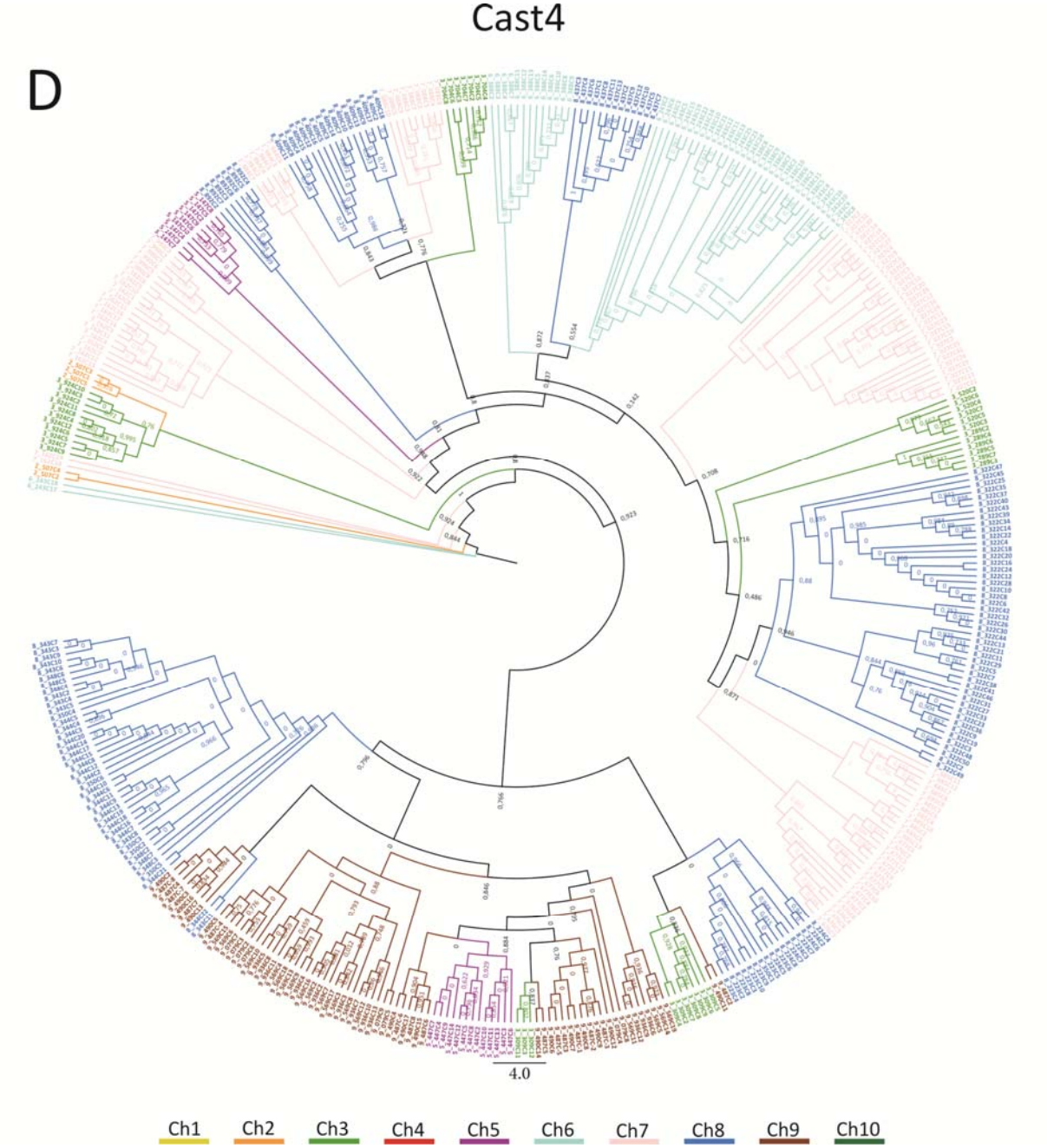


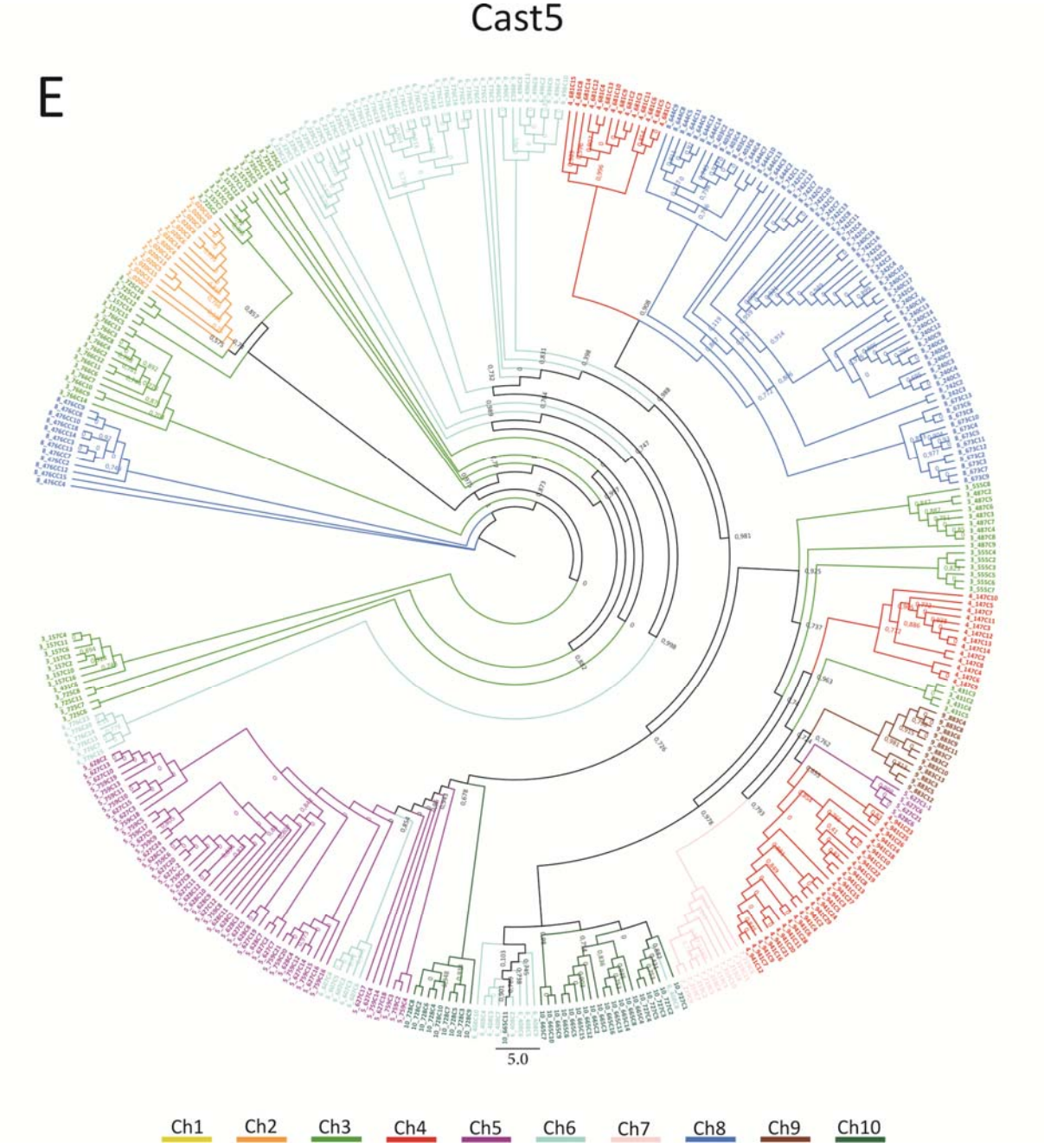
Additional file 5. Phylogenetic relationships of monomers of Cast1-Cast9 satDNAs (A-I) presented in ML trees. Detail descriptions of monomers include chromosome and array origin. Terminal branches are colored according to the chromosome of origin. Numbers at nodes indicate branch support values.




Cast2
B
5.0
Ch1
Ch2
Ch3
Ch4
Ch5
Ch6
Ch7
Ch8
Ch9
Ch10

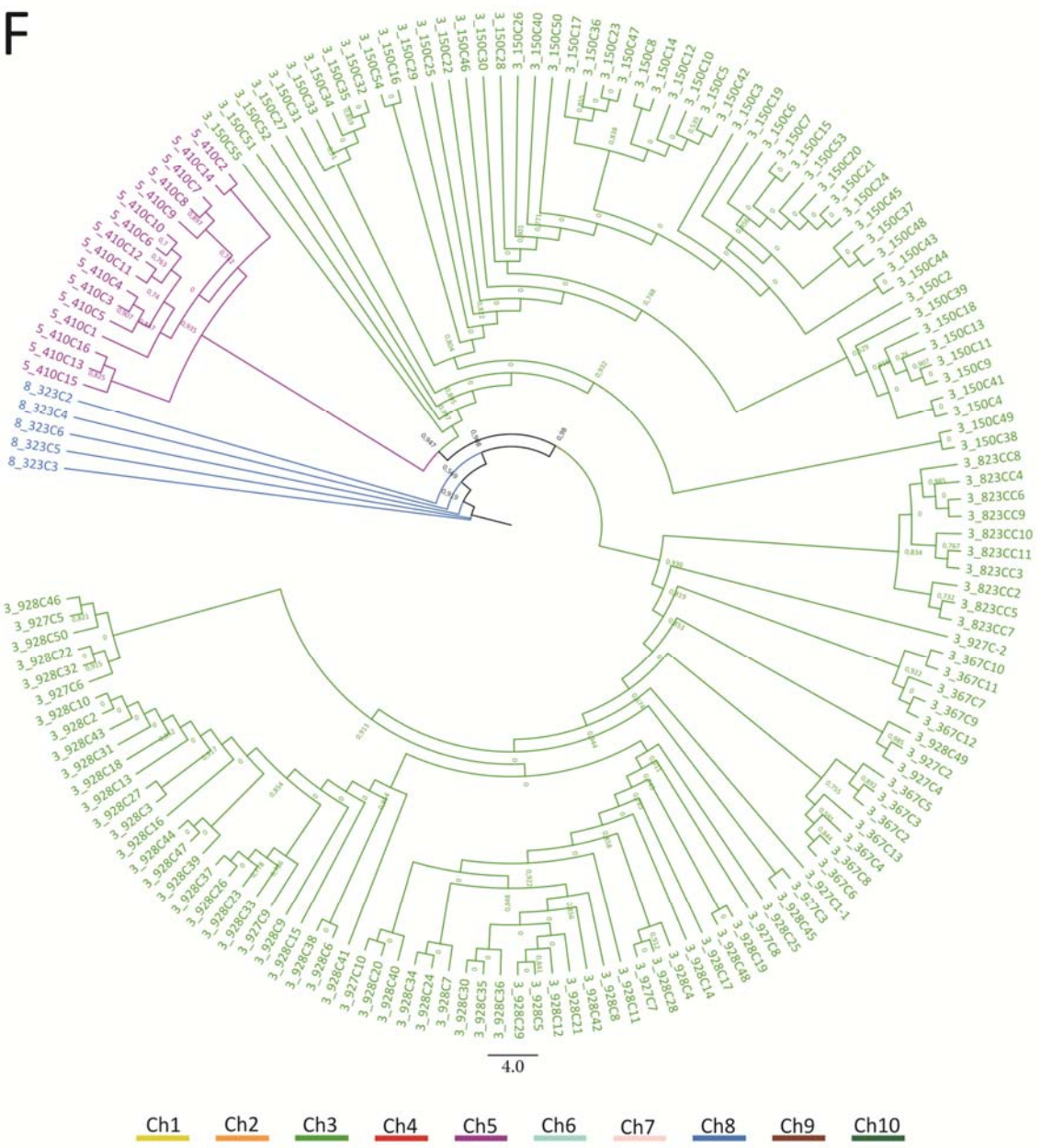

Cast3
C
3.0
Ch1
Ch2
Ch3
Ch4
Ch5
Ch6
Ch7
Ch8
Ch9
Ch10

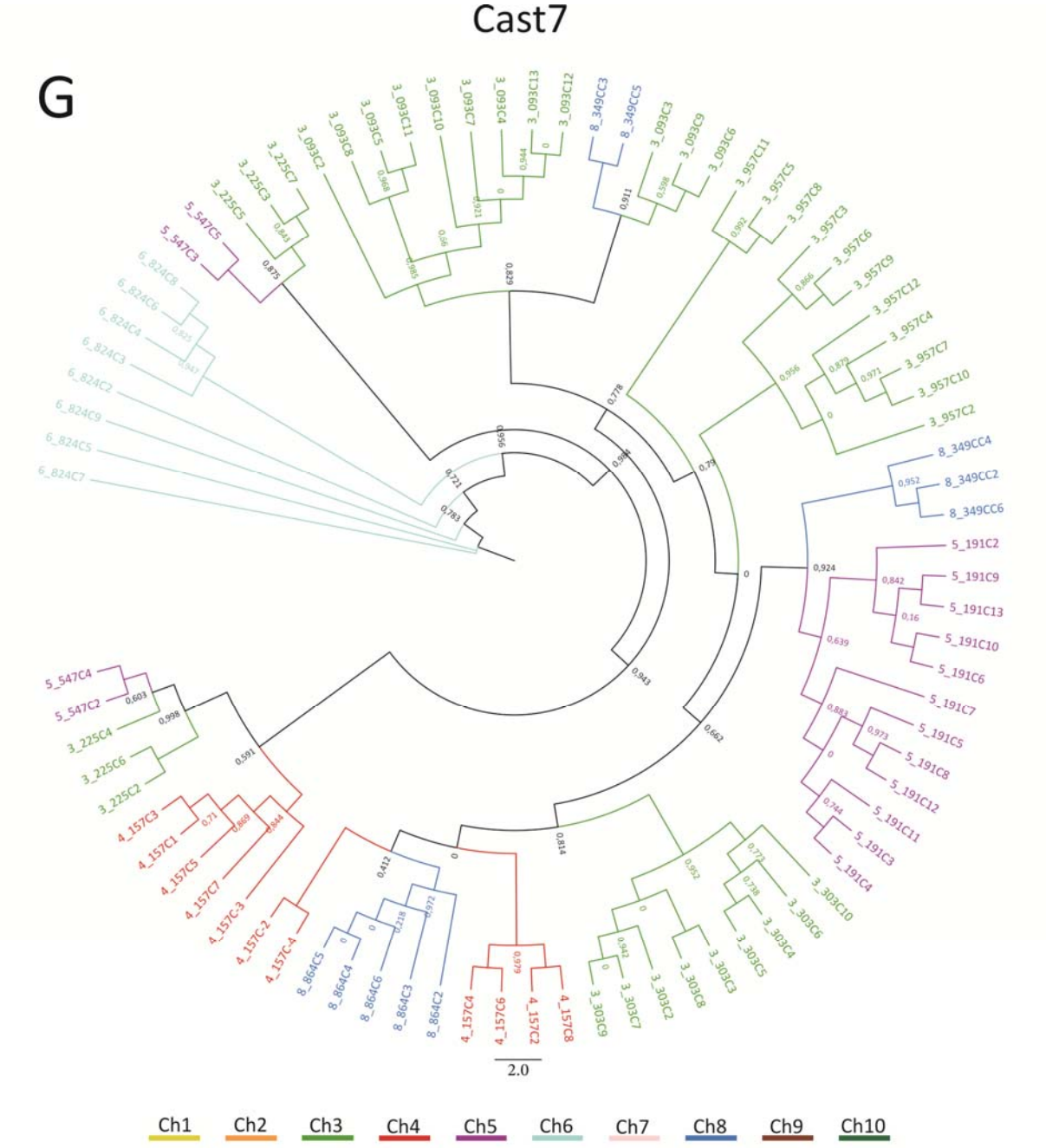

Cast4
D
4.0
Ch1
Ch2
Ch3
Ch4
Ch5
Ch6
Ch7
Ch8
Ch9
Ch10


Cast5
E
5.0
Ch1
Ch2
Ch3
Ch4
Ch5
Ch6
Ch7
Ch8
Ch9
Ch10

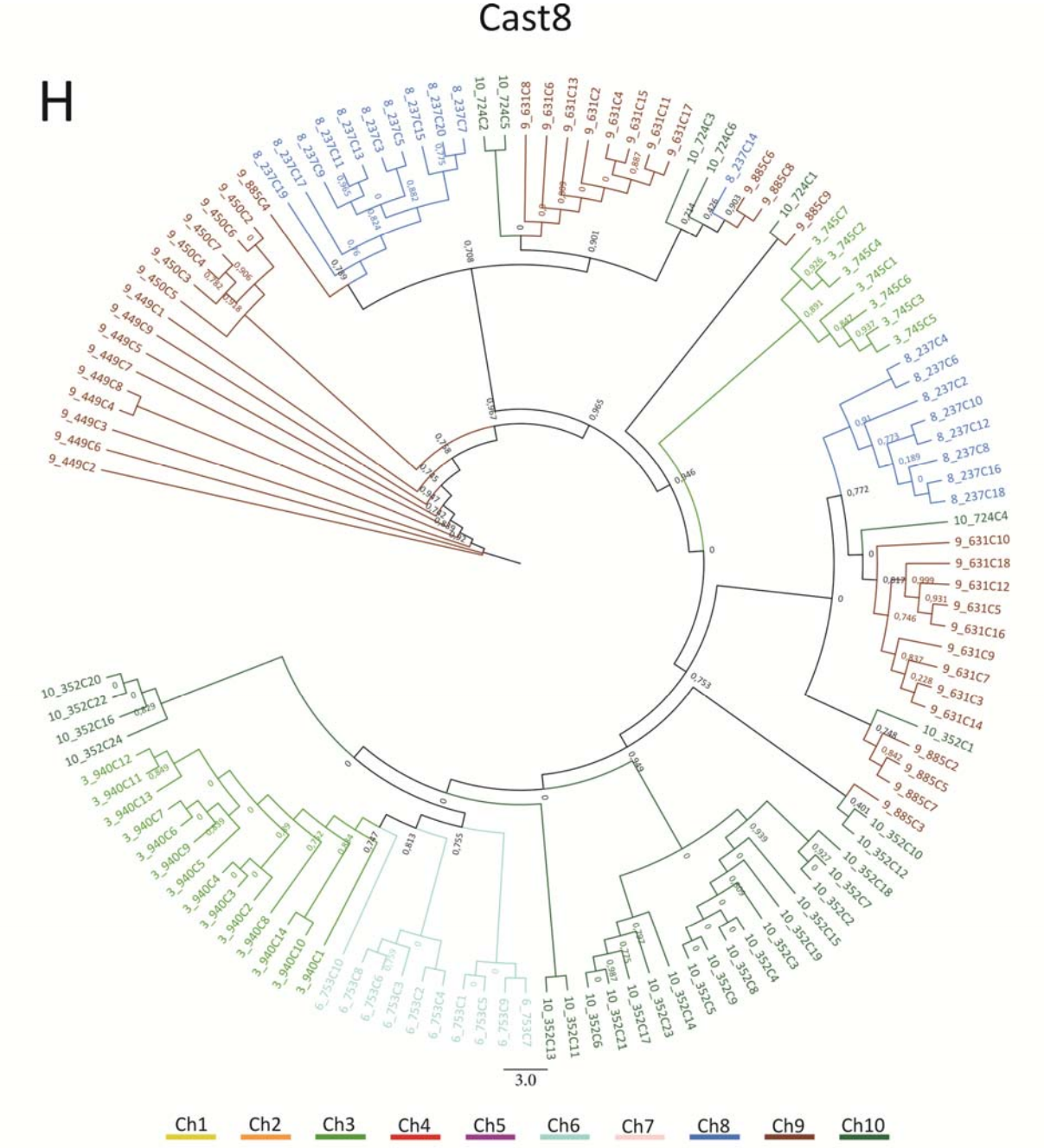
Cast6

F

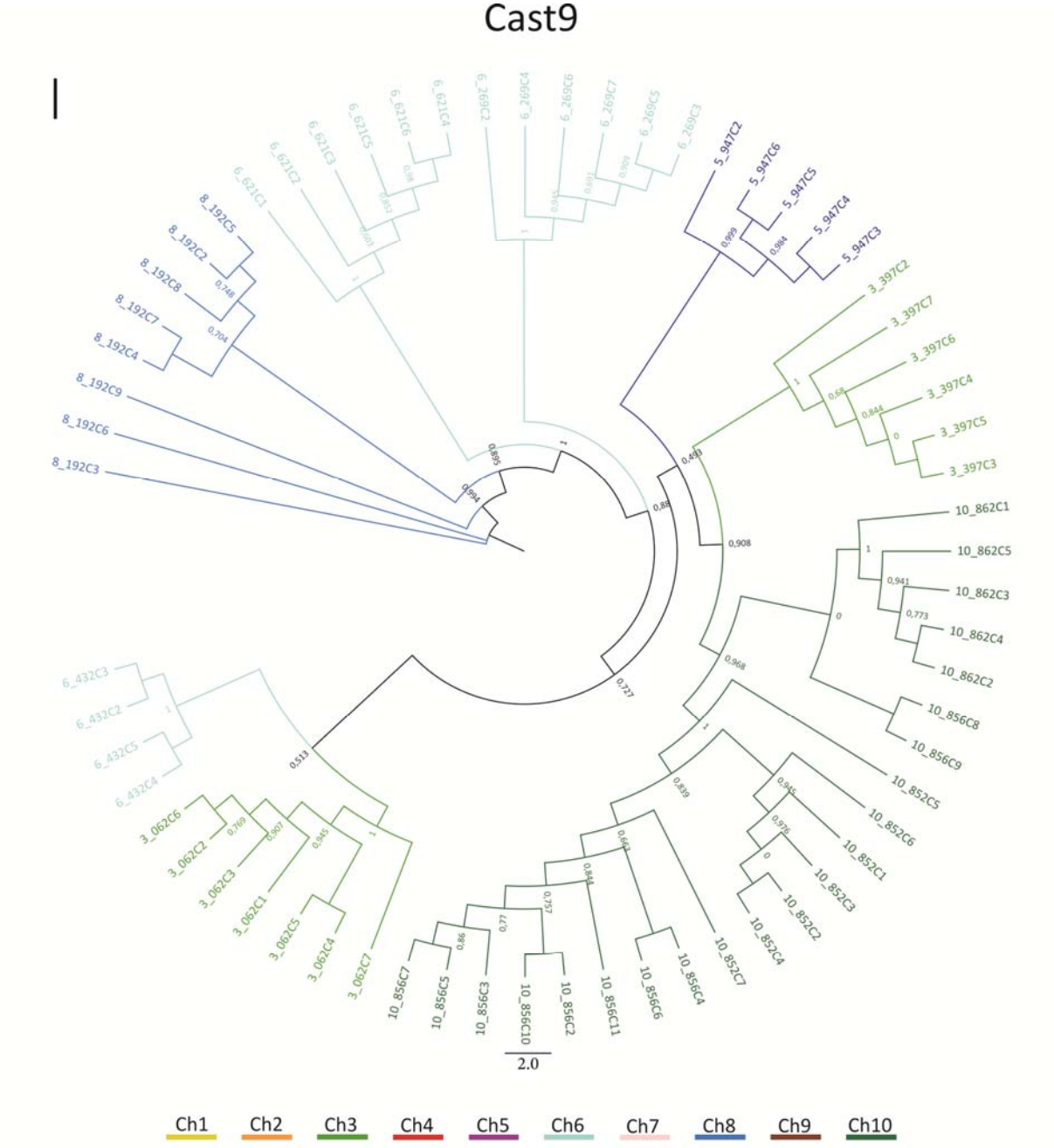



Cast7
G
3_093C13
3_093C12
8_349CC3
8_349CC5
3_093C3
3_093C9
3_093C6
3_957C11
3_957C5
3_957C8
3_957C3
3_957C6
3_957C9
3_957C12
3_957C4
3_957C7
3_957C10
3_957C2
8_349CC4
8_349CC2
8_349CC6
5_191C2
5_191C9
5_191C13
5_191C10
5_191C6
5_191C7
5_191C5
5_191C8
5_191C12
5_191C11
5_191C3
5_191C4
3_303C10
3_303C6
3_303C4
3_303C5
3_303C8
3_303C3
3_303C2
3_303C7
3_303C9
4_157C4
4_157C6
4_157C2
4_157C8
8_864C2
8_864C3
8_864C6
8_864C4
8_864C5
4_157C-4
4_157C-2
4_157C-3
4_157C7
4_157C5
4_157C1
4_157C3
3_225C4
3_225C6
3_225C2
5_547C4
5_547C2
6_824C7
6_824C5
6_824C9
6_824C2
6_824C3
6_824C4
6_824C6
6_824C8
5_547C3
5_547C5
3_225C3
3_225C5
3_225C7
3_093C2
3_093C8
3_093C5
3_093C11
3_093C10
3_093C7
3_093C4
2.0
Ch1
Ch2
Ch3
Ch4
Ch5
Ch6
Ch7
Ch8
Ch9
Ch10

# Cast8



# Cast9


6_269C2
6_269C4
6_269C6
6_269C7
6_269C5
6_269C3
6_621C4
6_621C6
6_621C5
6_621C3
6_621C2
6_621C1
8_192C5
8_192C2
8_192C8
8_192C7
8_192C4
8_192C9
8_192C6
8_192C3
5_947C2
5_947C6
5_947C5
5_947C4
5_947C3
3_397C2
3_397C7
3_397C6
3_397C4
3_397C5
3_397C3
10_862C1
10_862C5
10_862C3
10_862C4
10_862C2
10_856C8
10_856C9
10_852C5
10_852C6
10_852C1
10_852C3
10_852C2
10_852C4
10_852C7
10_856C4
10_856C6
10_856C11
10_856C2
10_856C10
10_856C3
10_856C5
10_856C7
3_062C7
3_062C4
3_062C5
3_062C1
3_062C3
3_062C2
3_062C6
6_432C4
6_432C5
6_432C2
6_432C3
2.0
Ch1
Ch2
Ch3
Ch4
Ch5
Ch6
Ch7
Ch8
Ch9
Ch10

Additional file 6. Alignments of Cast5 flanking regions with R=66 (A) and with R=140/R=1877 (B) sequence from repetitive library in Wang et al. 2008. Positions identical to the first sequence are shown in gray, differences are shown in color and deletions are indicated with dash. Positions of R66_F and R66_R primers are marked. Green arrow indicates start of satDNA arrays. Boxes denote domain with sequence similarity between Mariner/Tc1 (non-autonomous transposon from RepBase) and R140-like flanking regions.

Additional file 7. List of primer sequences

| **Sequence name** | **Primer name** | **Sequence 5'-3'** |
|---|---|---|
| Cast1 | tc1_F | AAGTCGGCTACGACTAACCGTTC |
| | tc1_R | TTGCAAATTTGGATTCCGCCCGG |
| Cast2 | tc2_F | TATACGCAAAATGAGCCGC |
| | tc2_R | AAAGTCGTAGAGCAATGCGG |
| Cast3 | tc3_F | CACCAAATTTGGTCGAAAATGAC |
| | tc3_R | CGTGTTTAAATCCTCAGAACTTGC |
| Cast4 | tc4_F | GTTTGTTCCAGTGAATTCTGCGG |
| | tc4_R | CCGTTTTGCTCTACGACTTTTAG |
| Cast5 | tc5_F | GGTGTTGAAAAGTCATAARTTGAGTG |
| | tc5_R | GAGCCGGTGTACACAACATT |
| Cast6 | tc6_F | CGACGCATGGGTCAATCTAAGACA |
| | tc6_R | ATTCGAAACTTTTCAAAAAAATTGG |
| Cast7 | tc7_F | GAATCGTCCGAAATAAGCCG |
| | tc7_R | CTGAAAACGCCTTATTCTGGC |
| Cast8 | tc8_F | TCATGTTCGGACAAACACC |
| | tc8_R | TTTTTTACAGTCGAAGGCCC |
| Cast9 | tc9_F | GACAGATTTGGAATCCTTAGAC |
| | tc9_R | CTACGATTCGTAGTTTTGGAG |
| R66-like | R66_F | TTCATATGGCTTCTCCGTTGG |
| | R66_R | TATTTACTGAGGTATTGAATTTGAT |