Figures S1–S37. ORF maps of PB2, NP, M1, M2, M42, NS1, NS2, NS3, H1–H18 and N1–N11 transcripts. Symbols and legends used are as defined in Figure 1. Briefly, the putative ORFs are graphed in 3 forward-reading frames: F1, F2 and F3. Each colored box represents the start codon of an ORF, with red, green and blue indicating strong, medium and weak Kozak sequences, respectively. Numbers from 1 indicate the positions of start codons. For ORFs with mixed populations of different Kozak strengths, multiple colors indicate the population proportions. F2 and F3 ORFs of major prevalence (>50%) are additionally labelled by their frequencies. ORFs of lower prevalence (<95% for F1, <50% for F2/F3) are grey-labelled. Each ORF ends with a solid line. For F2/F3 ORFs of various sizes, the corresponding dominant length is used to close the ORF. For overlapping ORFs, an asterisk (*) accompanying the start position is additionally labelled in grey to mark the end of the ORF.

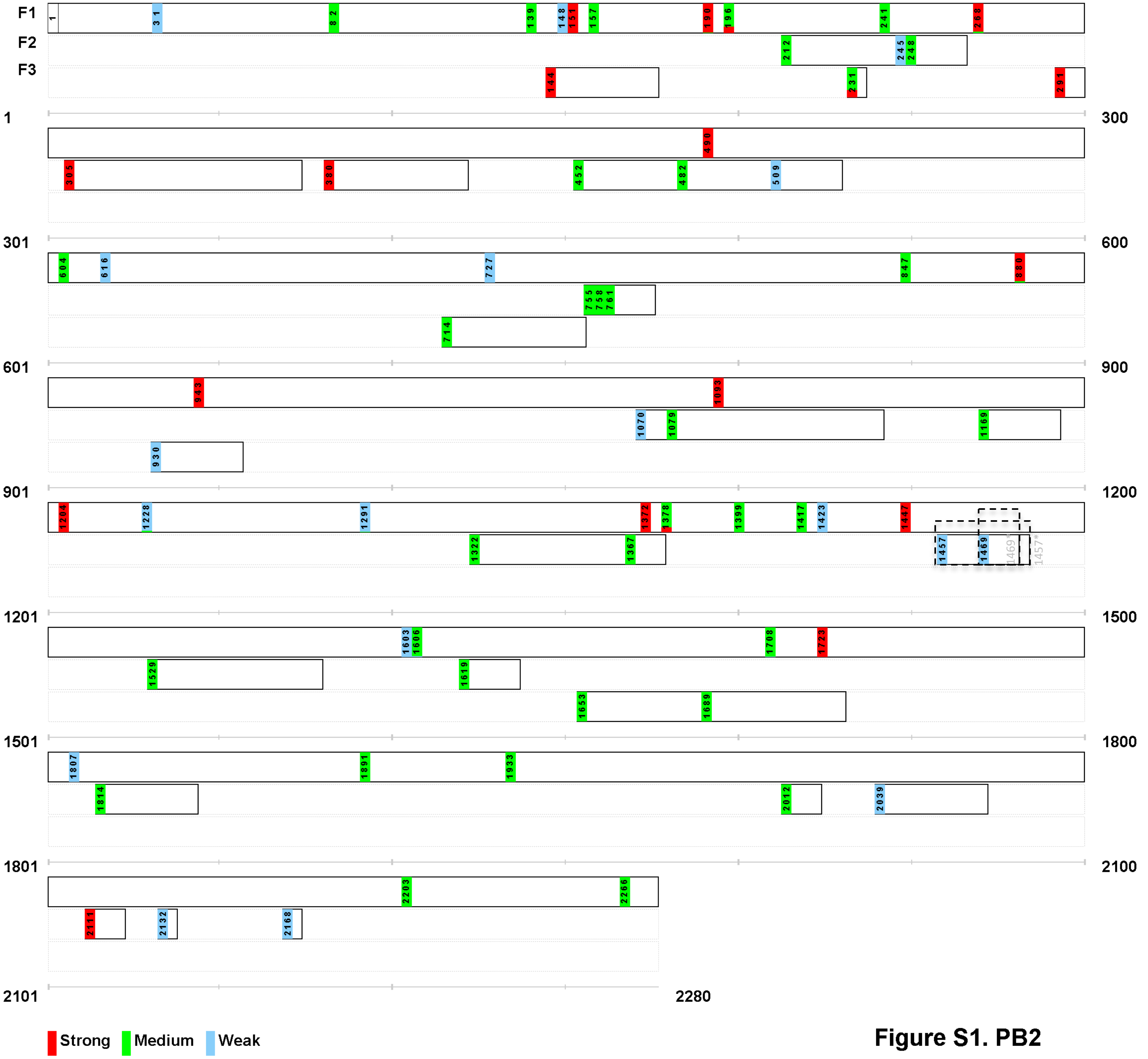
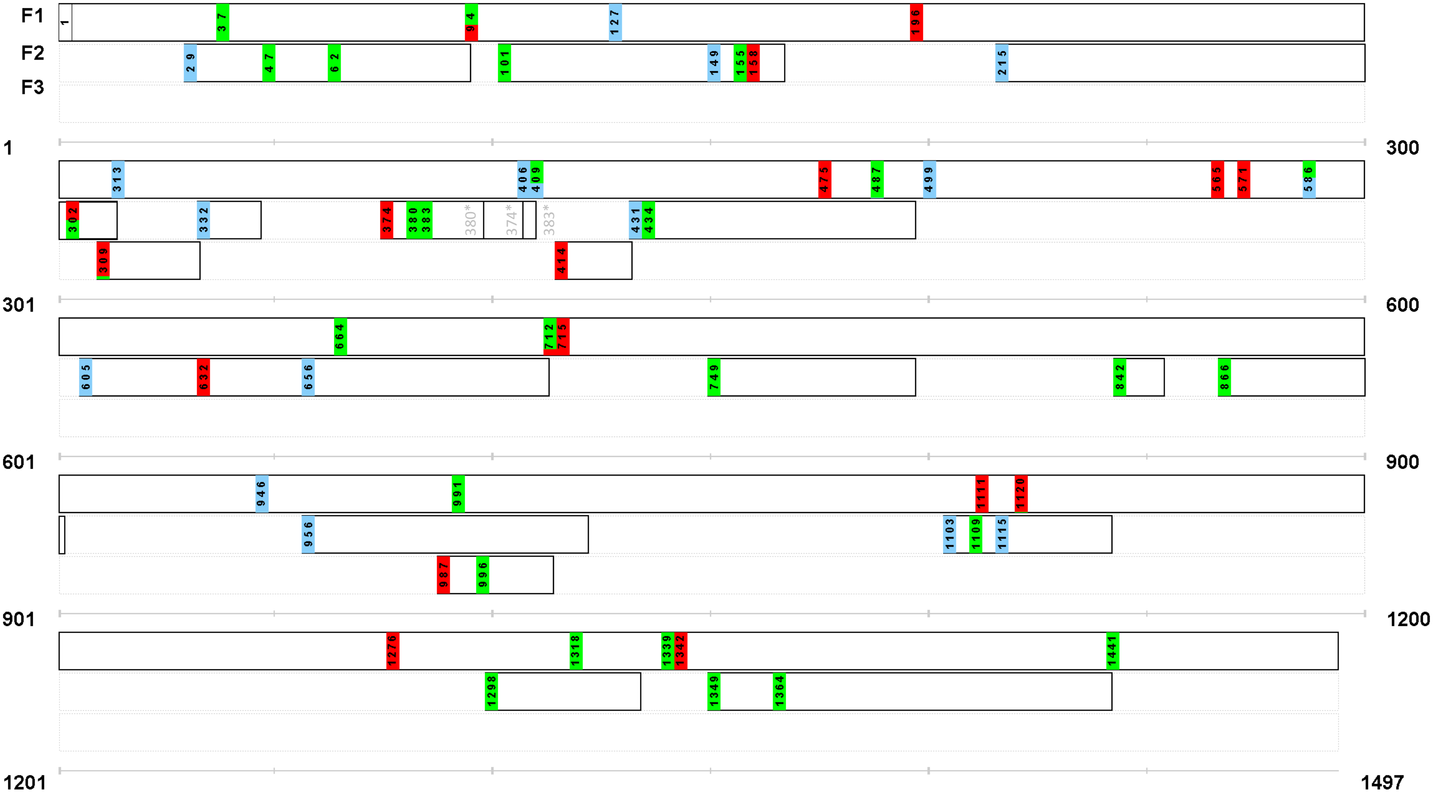
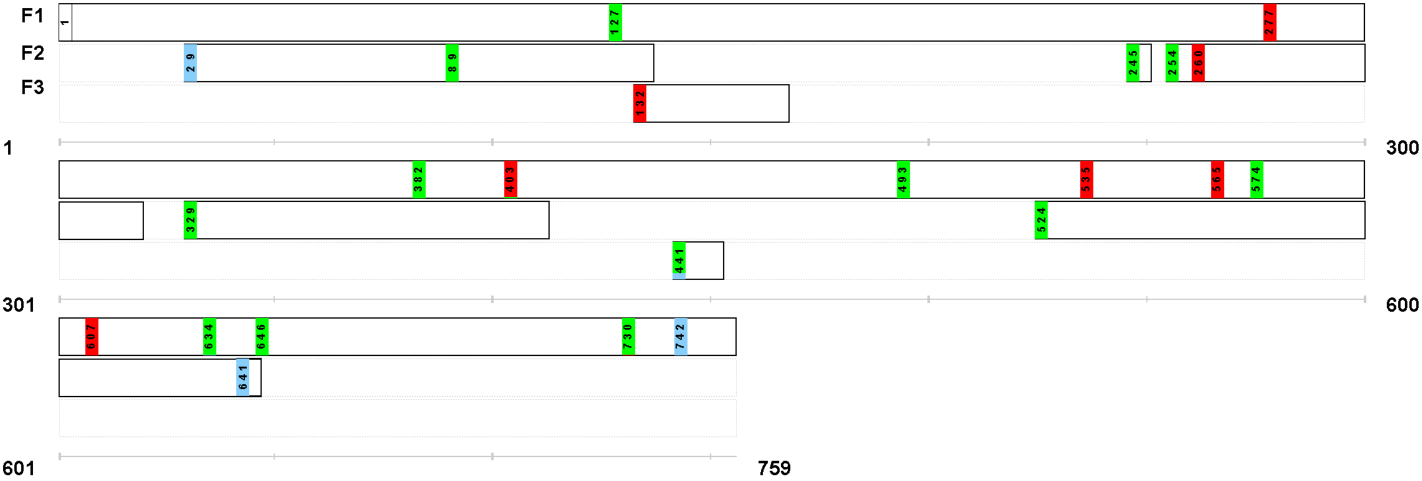


Figure S1. PB2



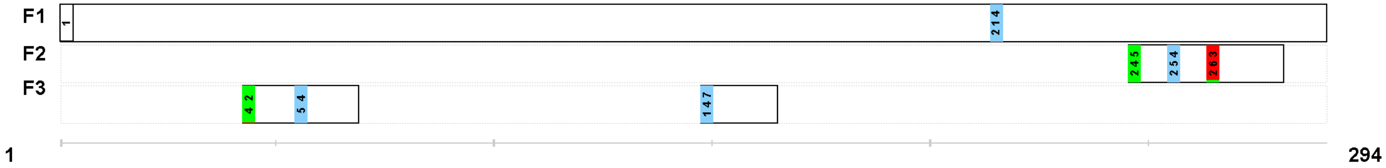
🟥 Strong 🟩 Medium 🟦 Weak

Figure S2. NP


F1
F2
F3
1
127
277
29
89
245
254
260
132
1
300
382
403
493
535
565
574
329
524
441
301
600
607
634
646
730
742
641
601
759

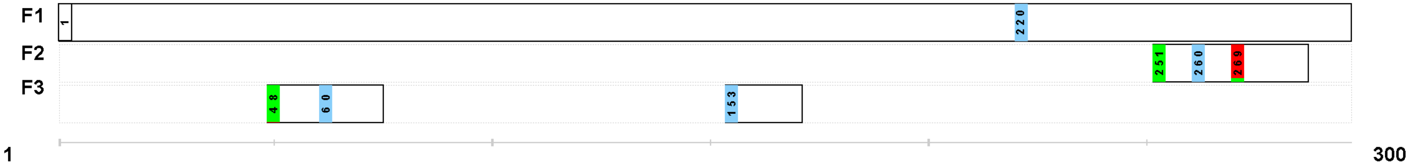
🟥 Strong
🟩 Medium
🟦 Weak

Figure S3. M1



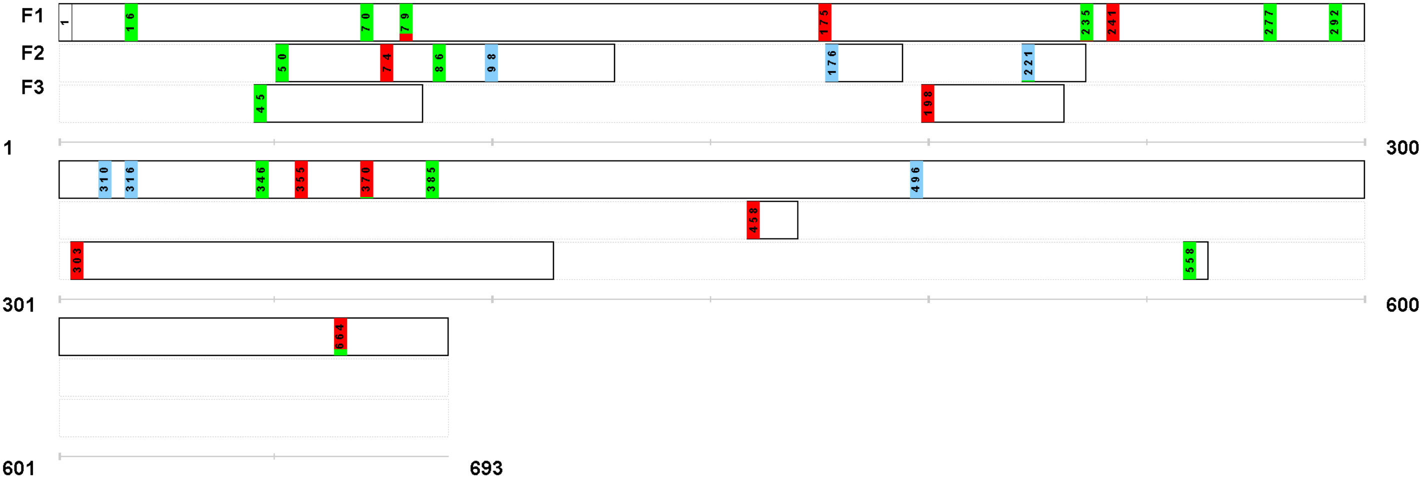
🟥 Strong 🟩 Medium 🟦 Weak

Figure S4. M2



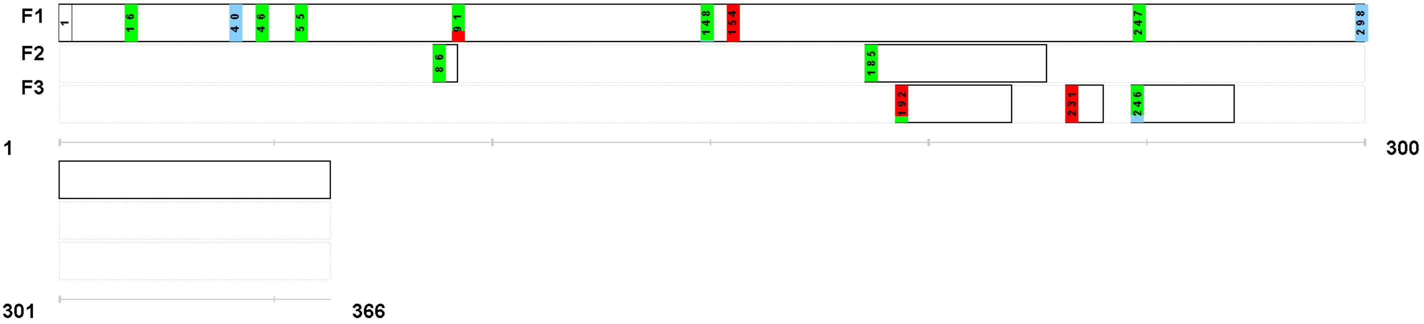
🟥 Strong 🟩 Medium 🟦 Weak

Figure S5. M42



🟥 Strong 🟩 Medium 🟦 Weak

Figure S6. NS1



🟥 Strong 🟩 Medium 🟦 Weak

Figure S7. NS2

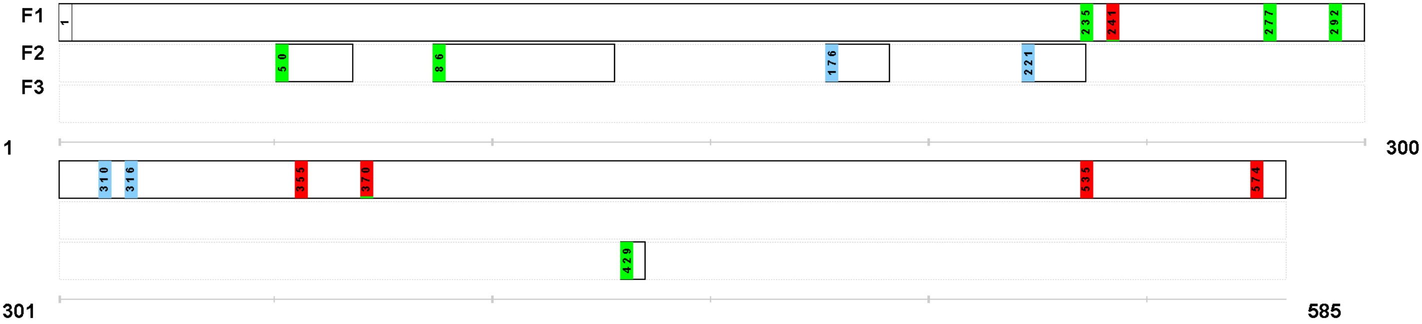


Figure S8. NS3

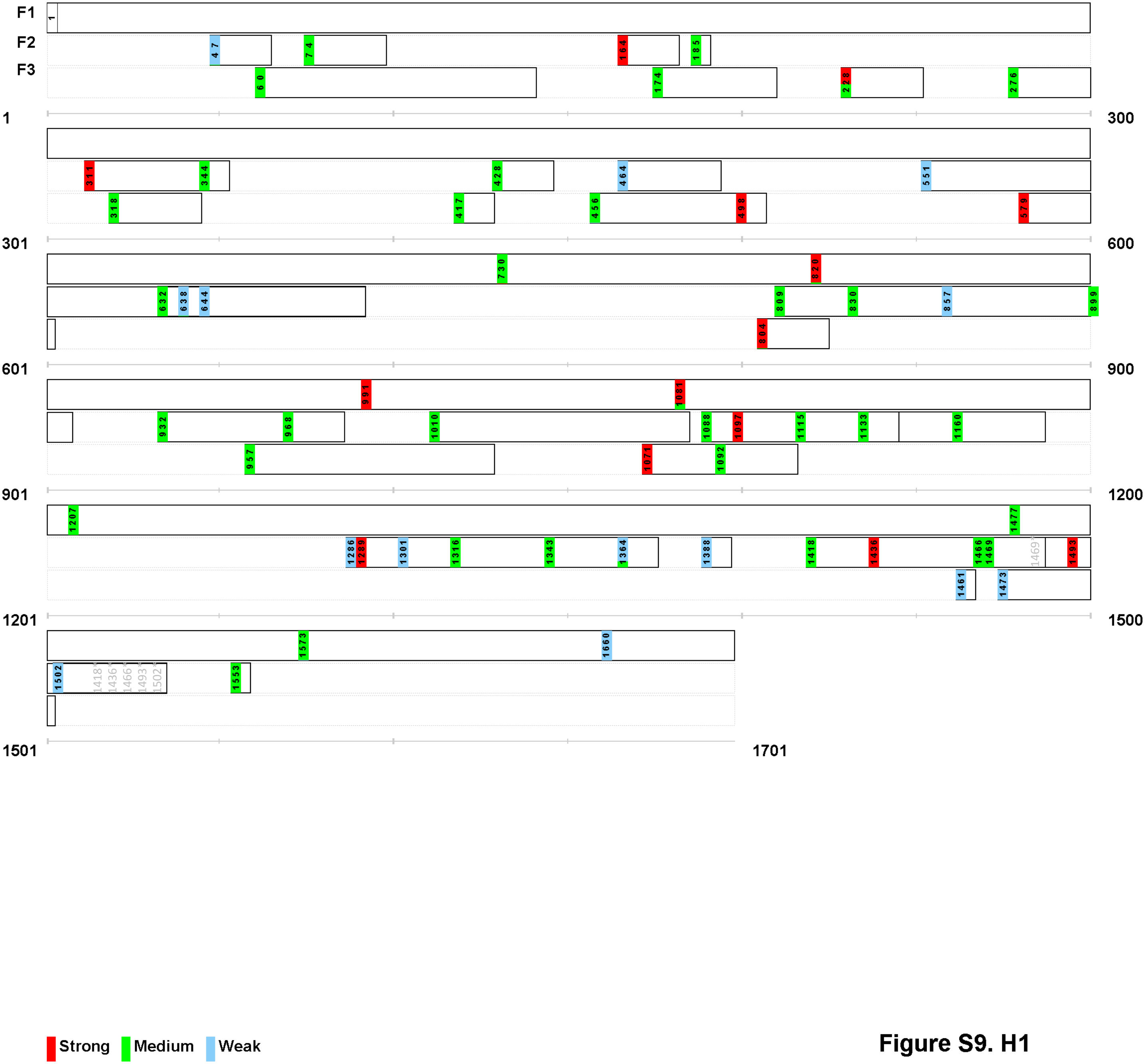
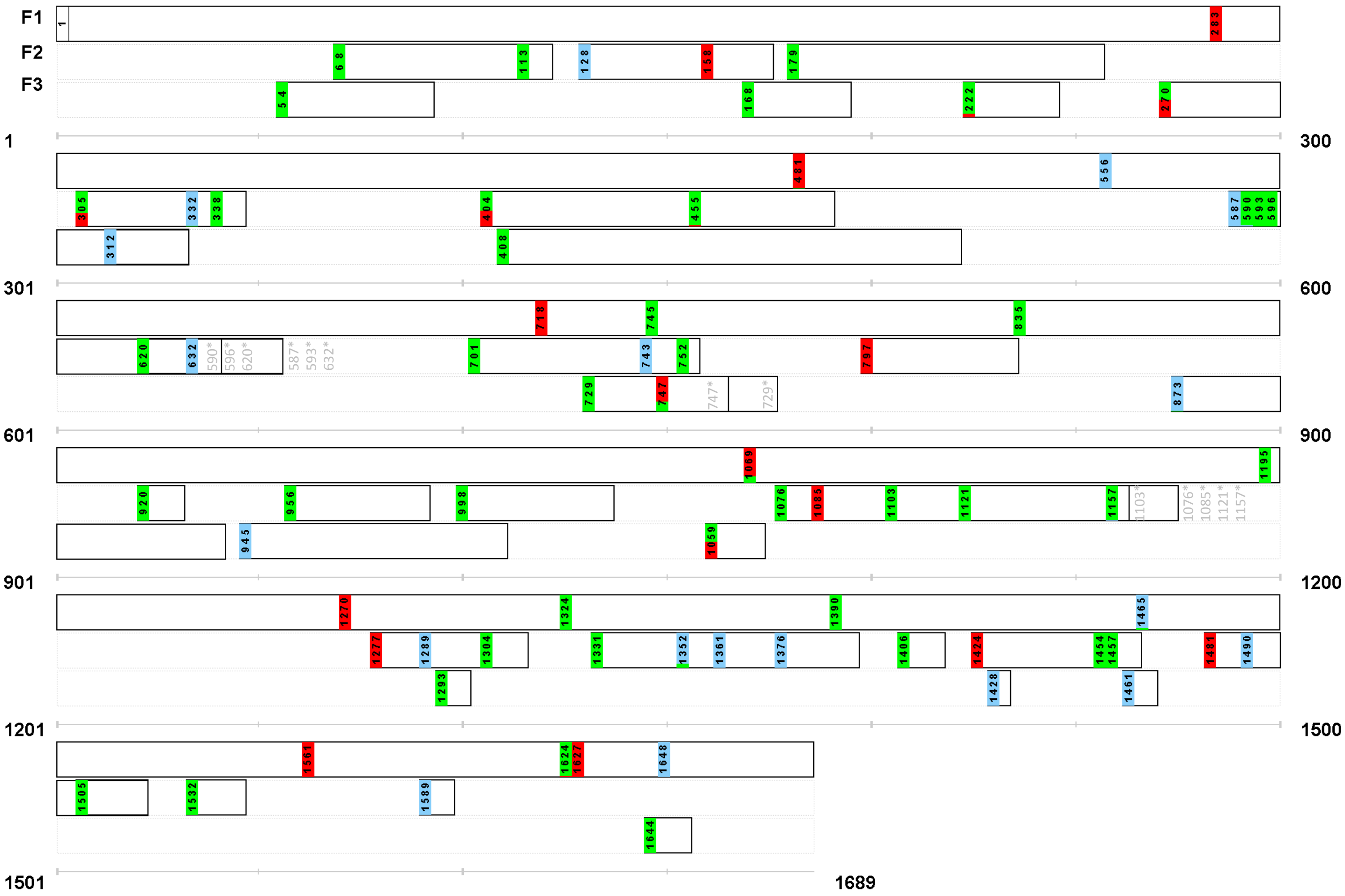

F1
F2
F3
1
47
74
164
185
60
174
228
276
1
300
311
344
428
464
551
318
417
456
498
579
301
600
730
820
632
638
644
809
830
857
899
804
601
900
991
1081
932
968
1010
1088
1097
1115
1133
1160
957
1071
1092
901
1200
1207
1477
1286
1289
1301
1316
1343
1364
1388
1418
1436
1466
1469
1469
1493
1461
1473
1201
1500
1573
1660
1502
1418
1436
1466
1493
1502
1553
1501
1701
Strong
Medium
Weak

Figure S9. H1



🟥 Strong 🟩 Medium 🟦 Weak

Figure S10. H2

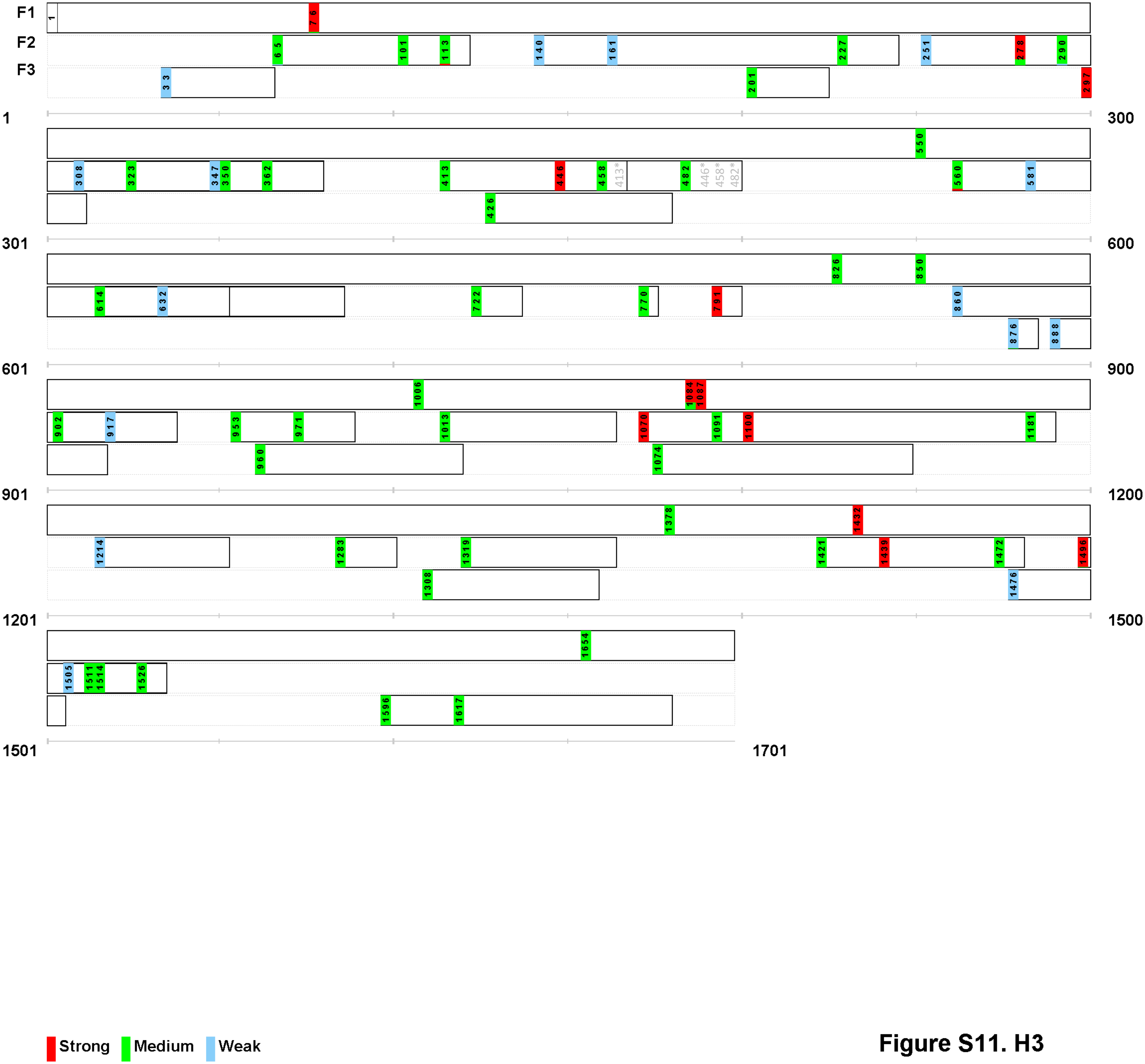
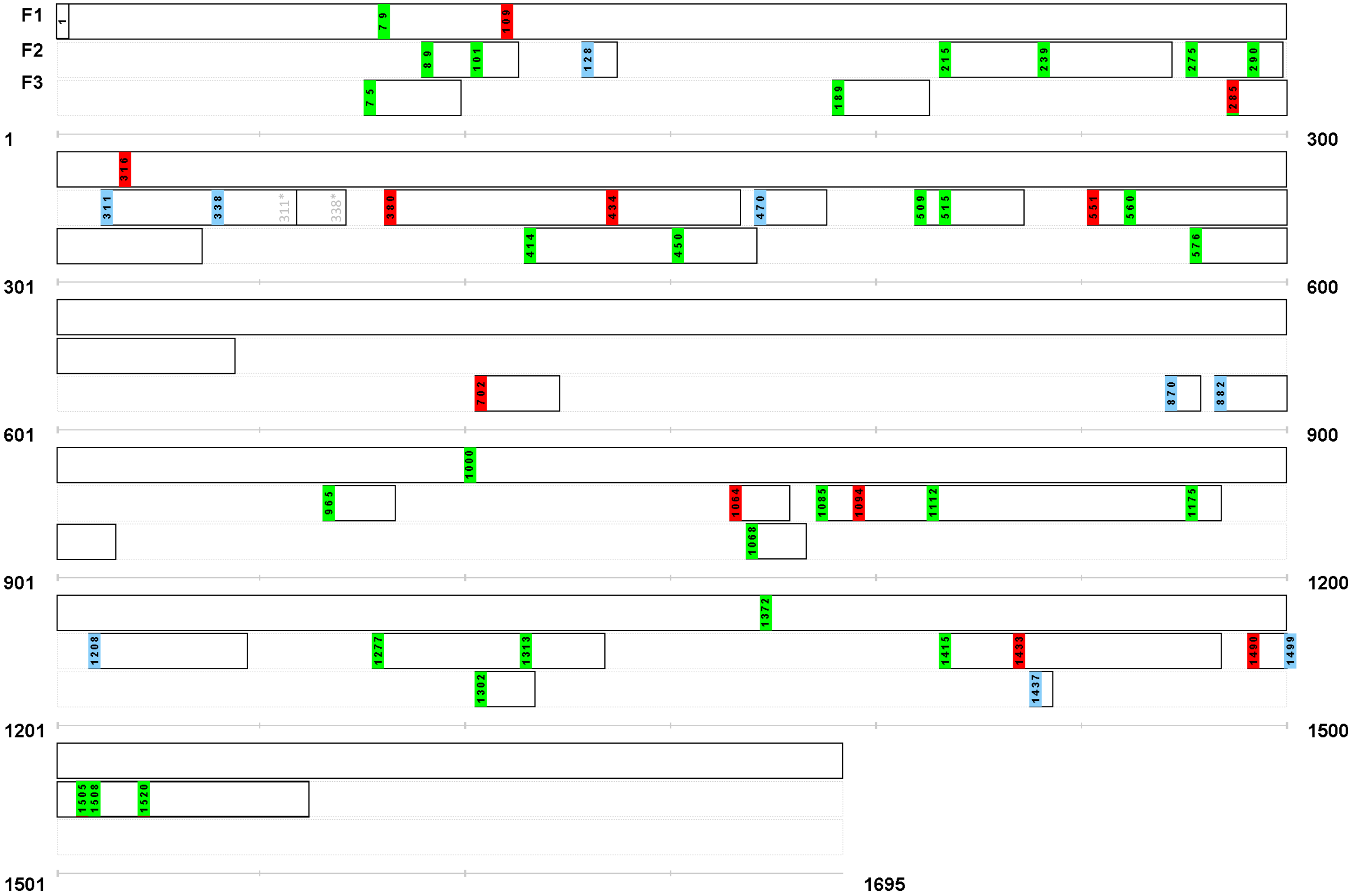


Figure S11. H3



🟥 Strong 🟩 Medium 🟦 Weak

Figure S12. H4

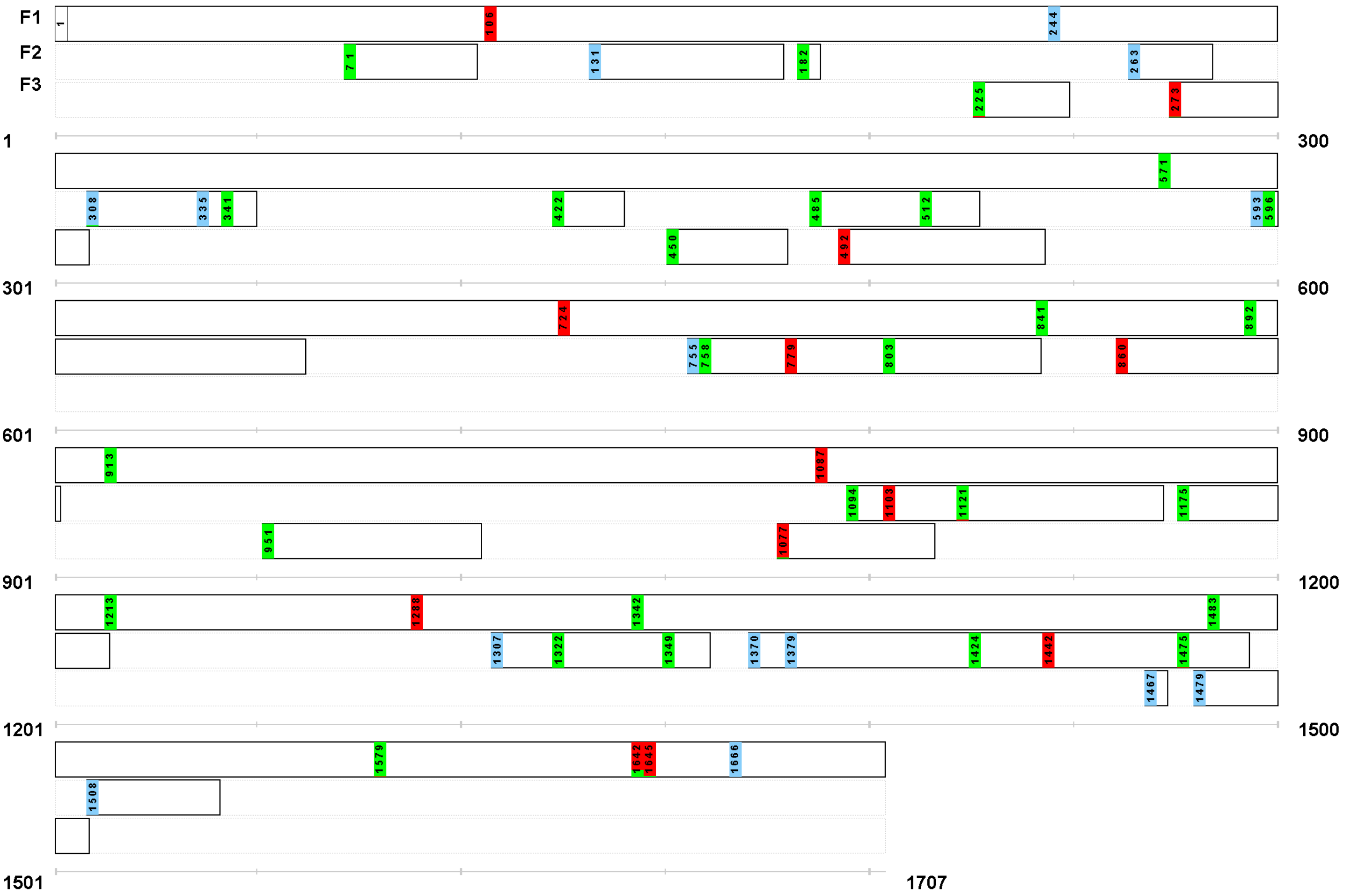
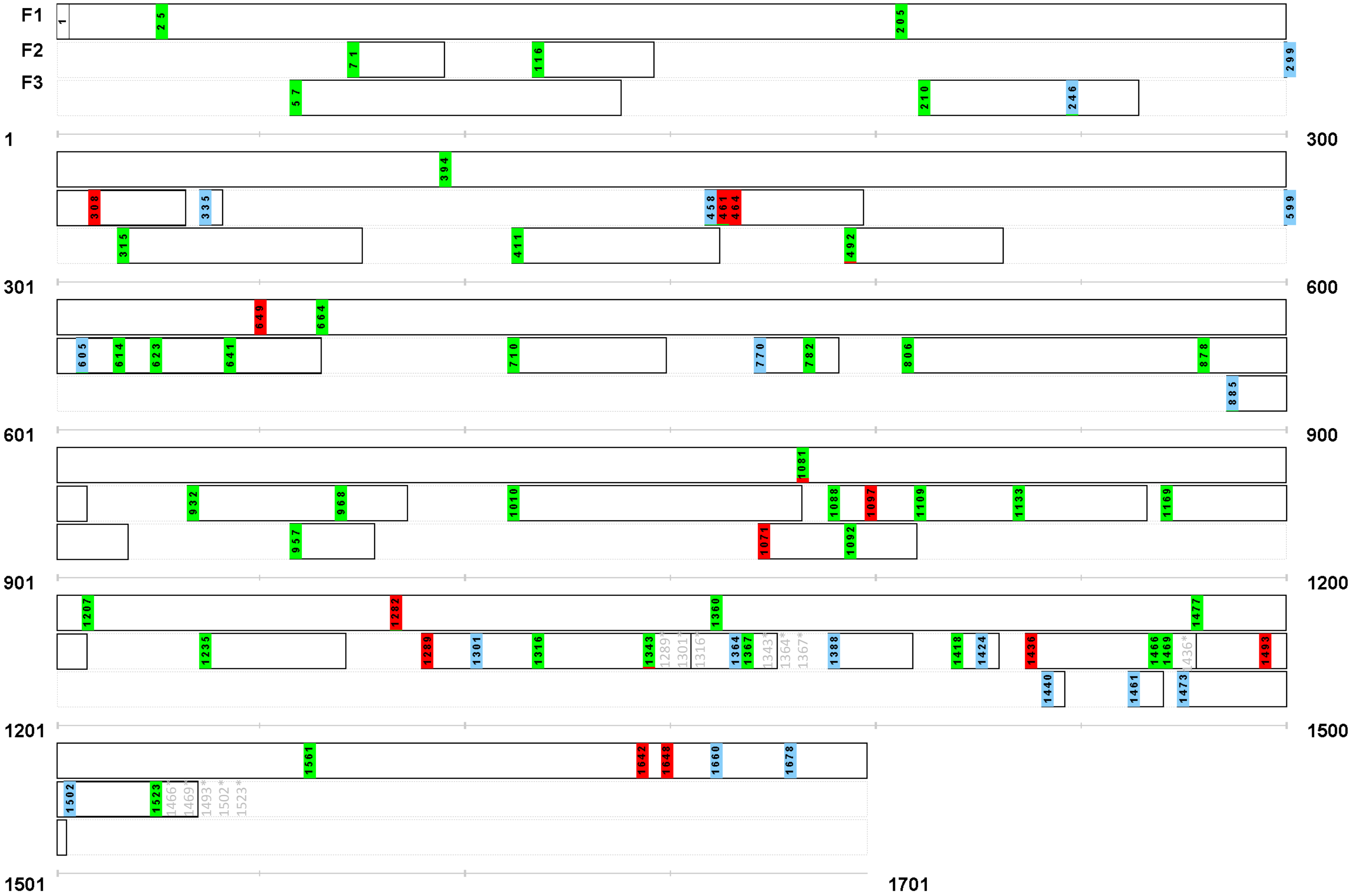


Figure S13. H5



🟥 Strong 🟩 Medium 🟦 Weak

Figure S14. H6

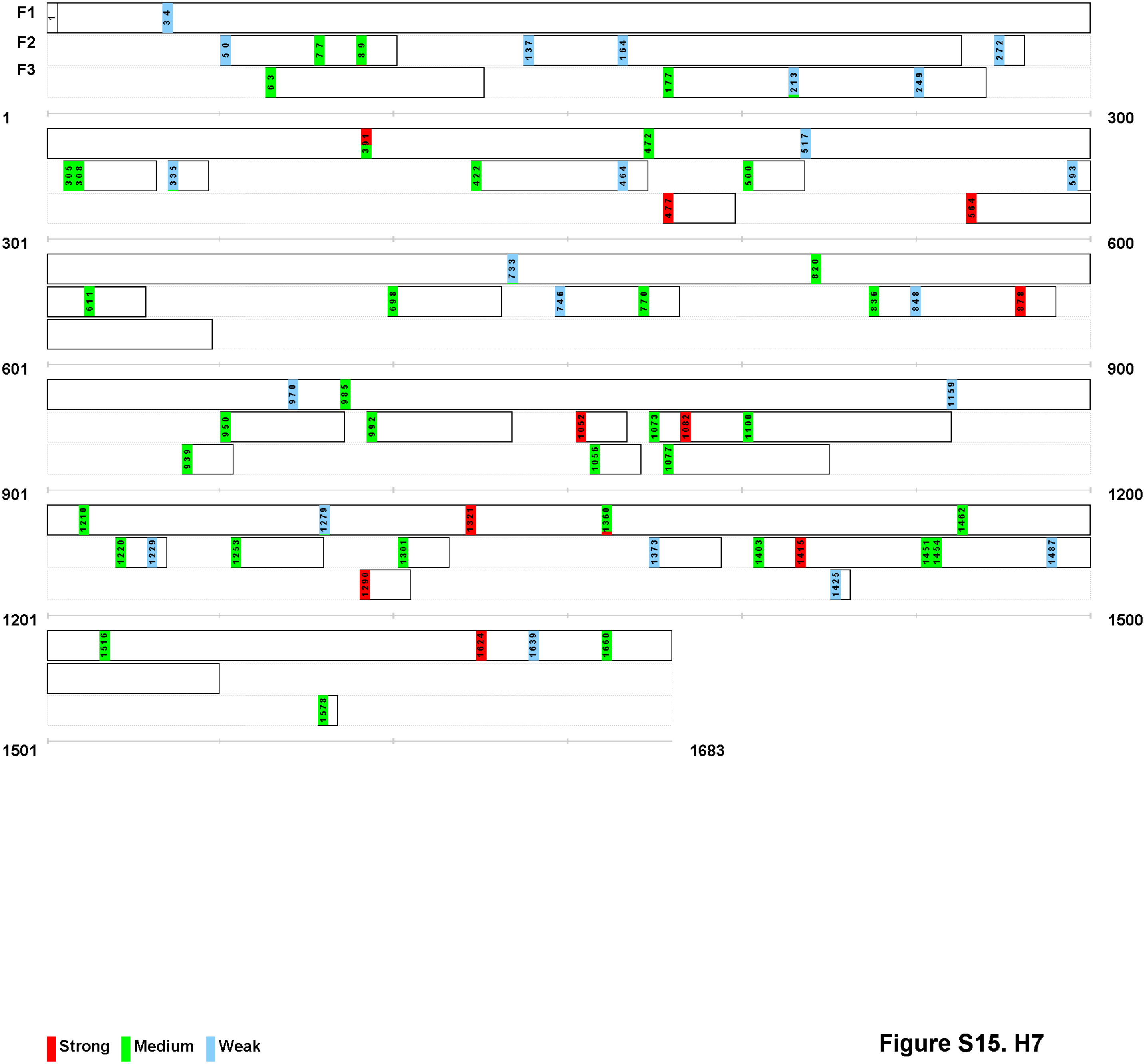
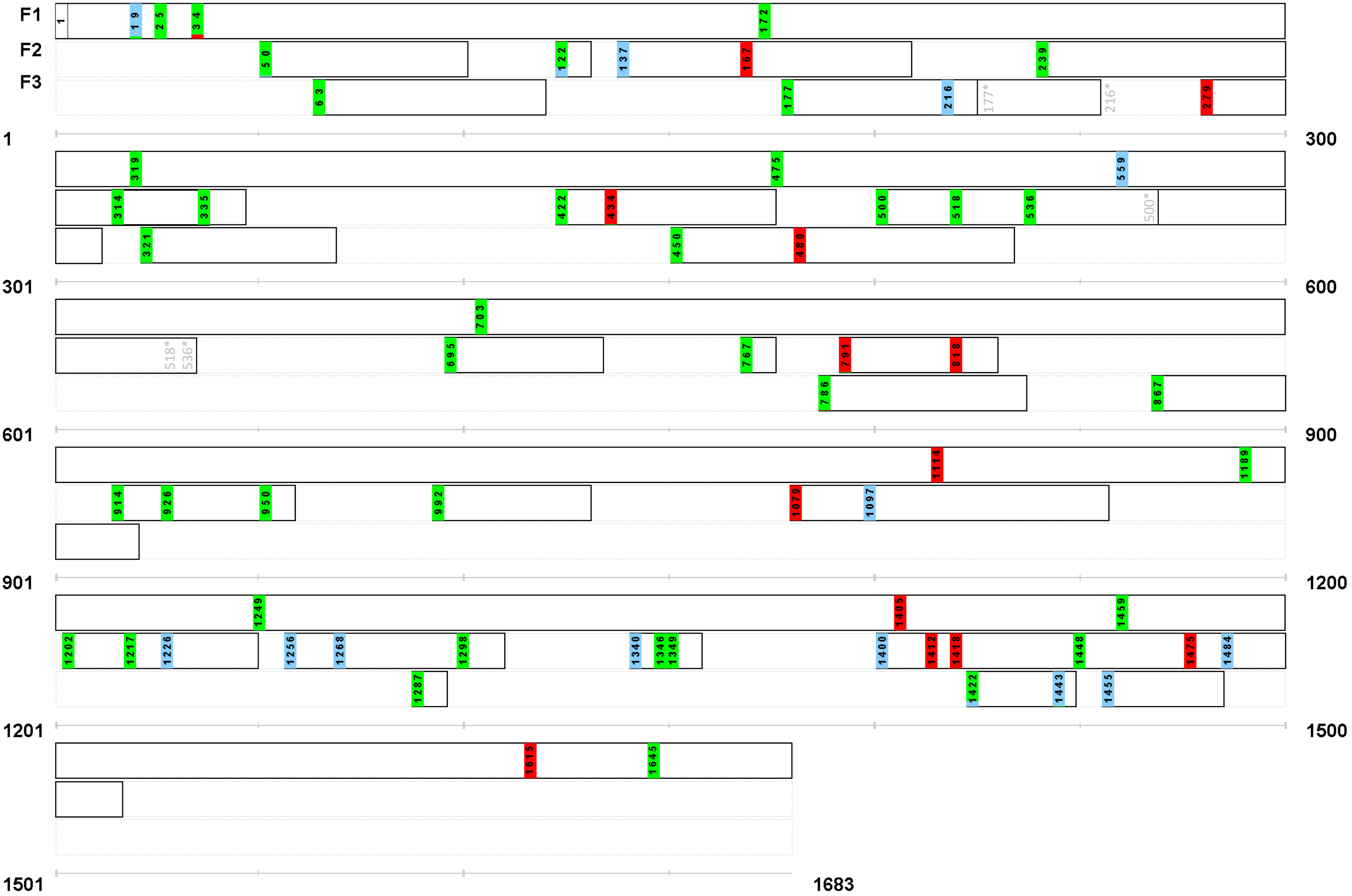


Figure S15. H7

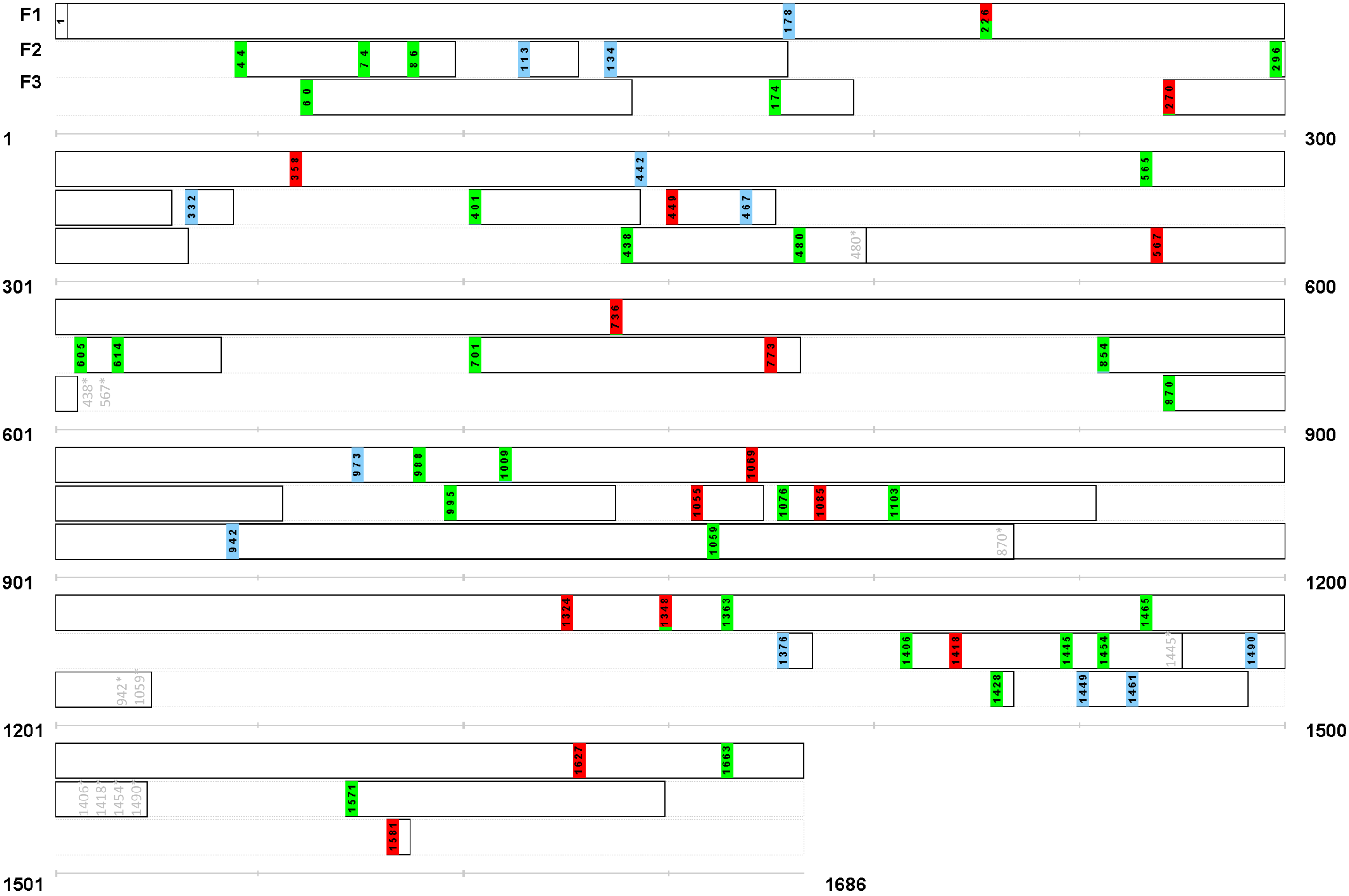
🟥 Strong 🟩 Medium 🟦 Weak

Figure S16. H8



🟥 Strong 🟩 Medium 🟦 Weak

Figure S17. H9



🟥 Strong 🟩 Medium 🟦 Weak

Figure S18. H10

Figure S19. H11

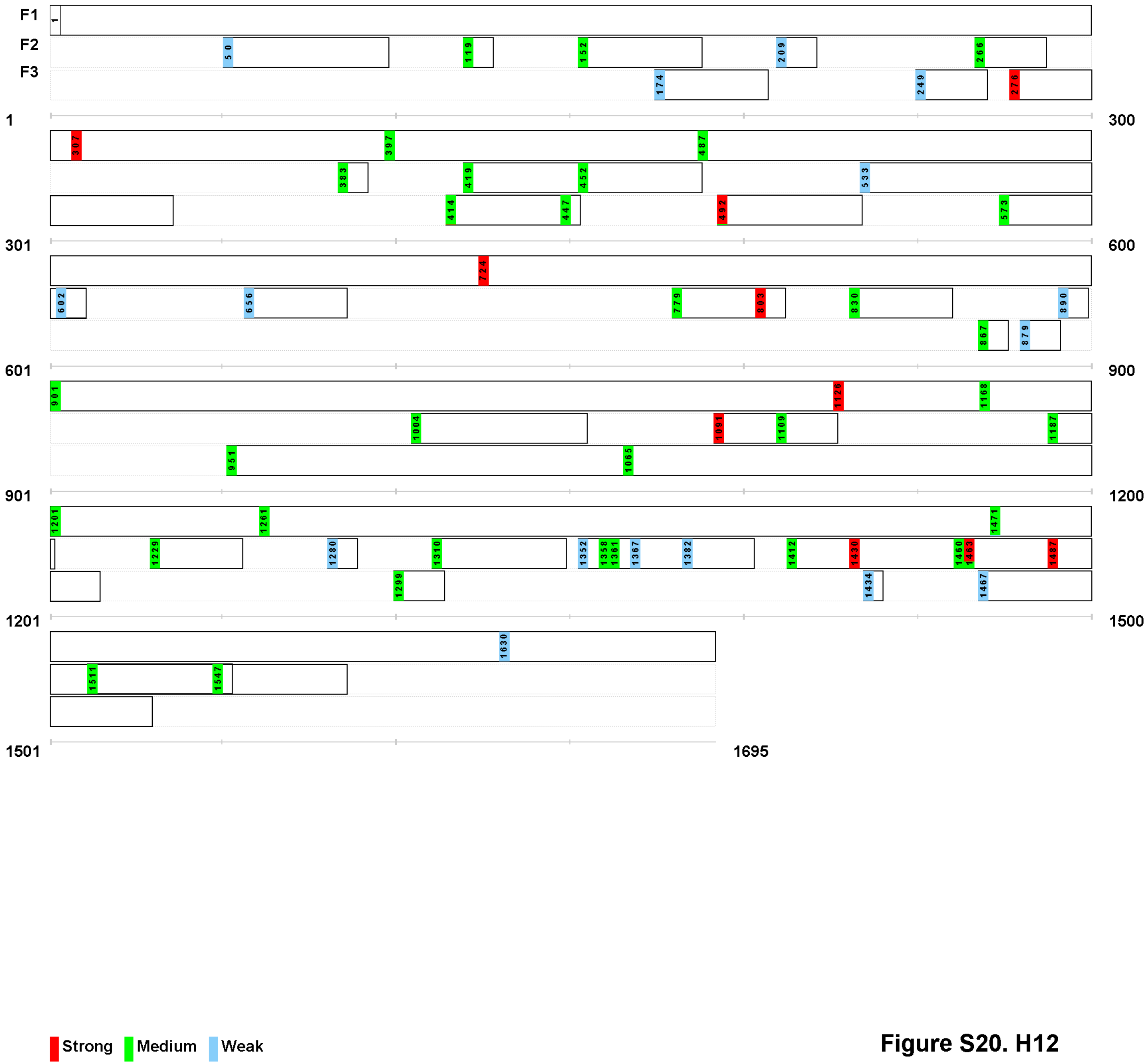
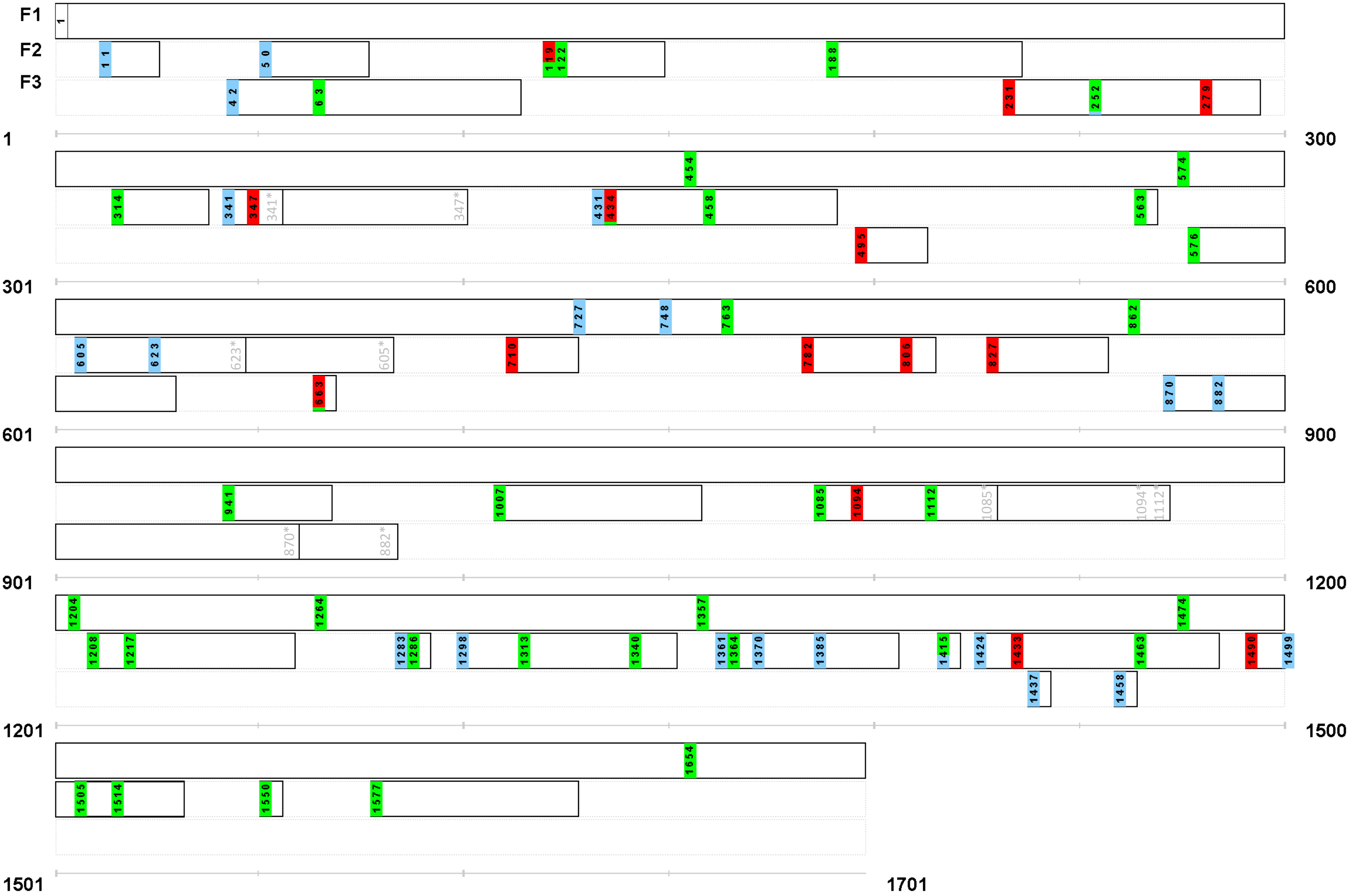
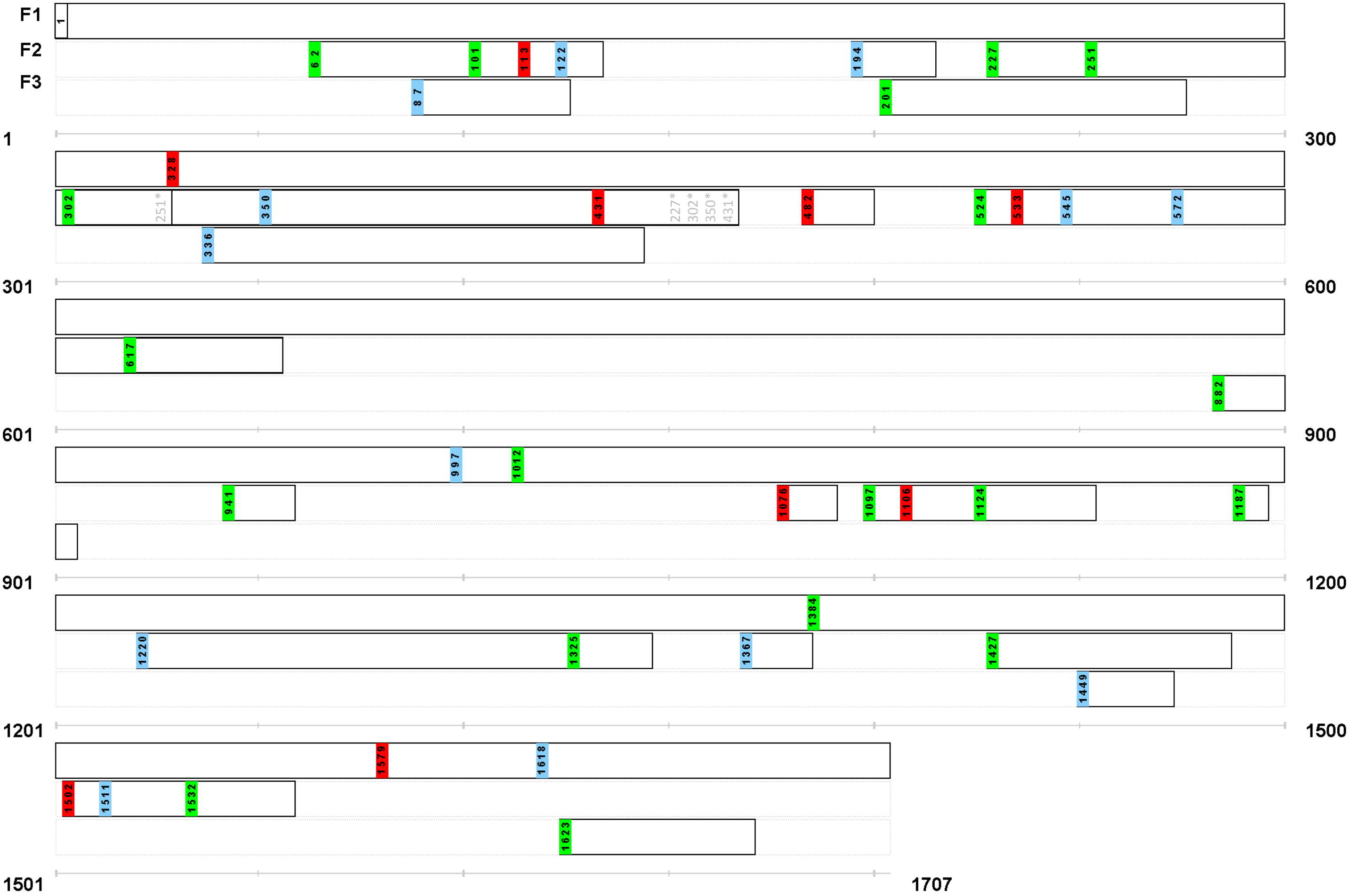


Figure S20. H12



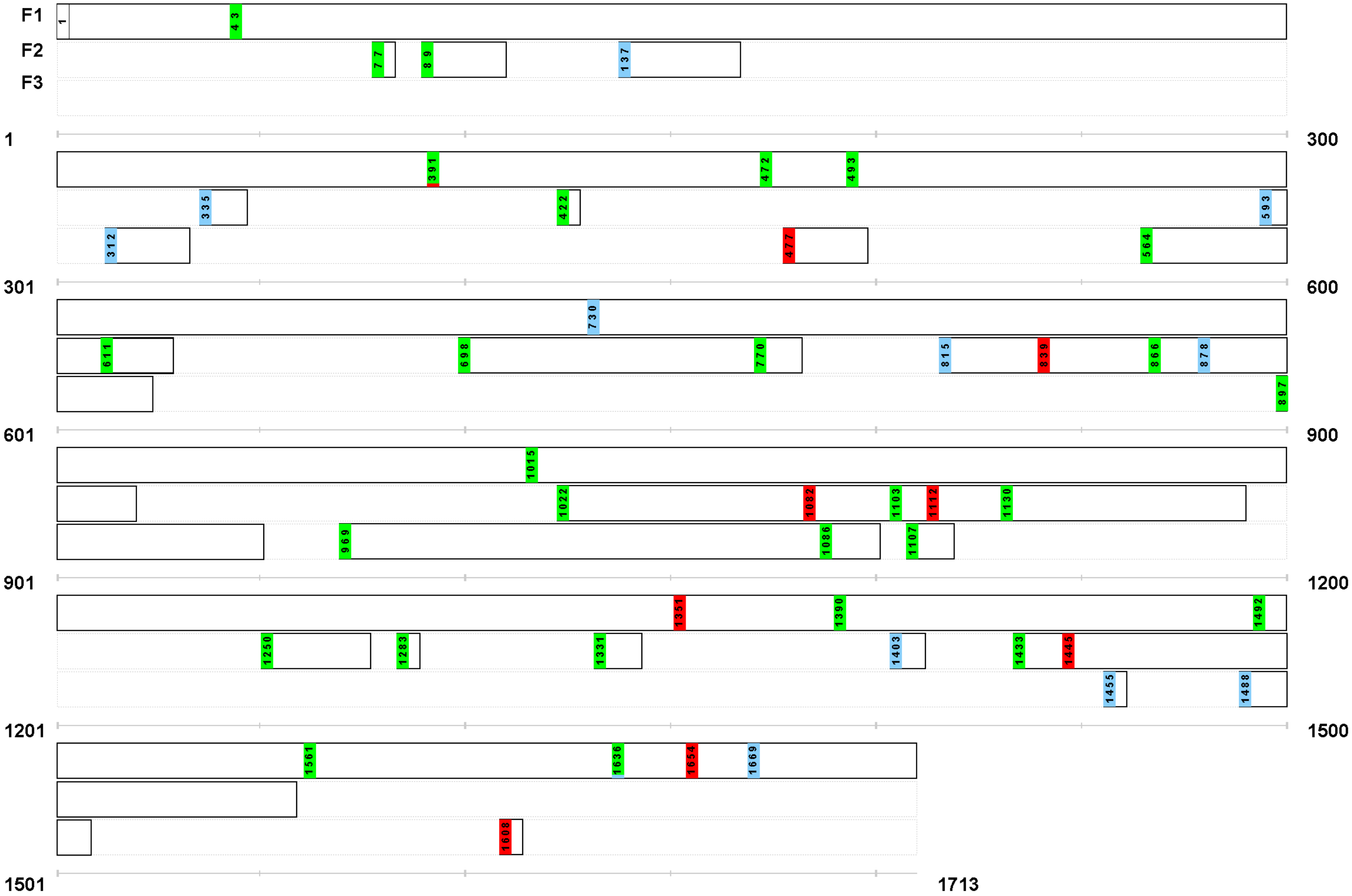
🟥 Strong 🟩 Medium 🟦 Weak

Figure S21. H13



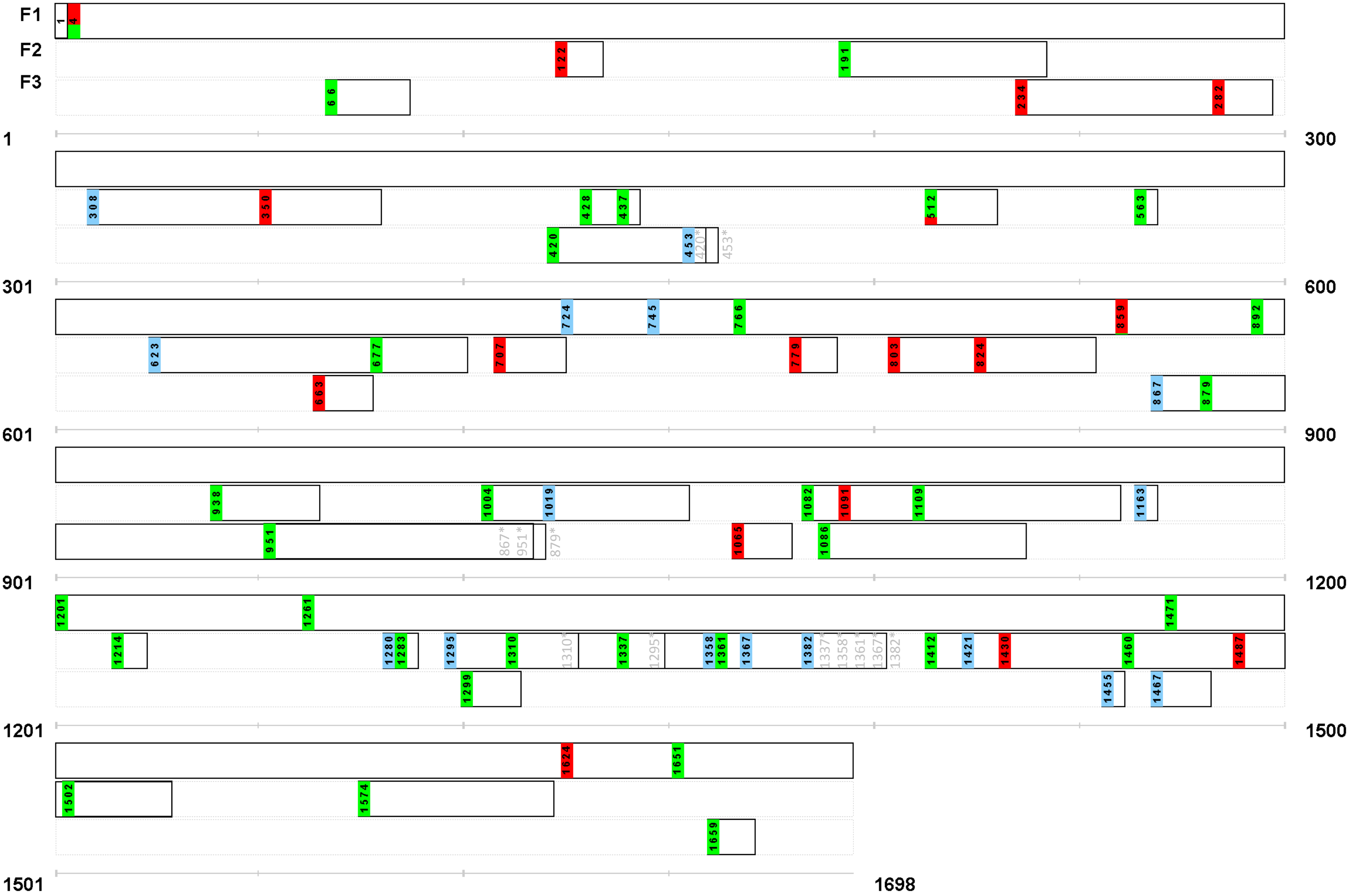
🟥 Strong 🟩 Medium 🟦 Weak

Figure S22. H14



🟥 Strong 🟩 Medium 🟦 Weak

Figure S23. H15



🟥 Strong 🟩 Medium 🟦 Weak

Figure S24. H16

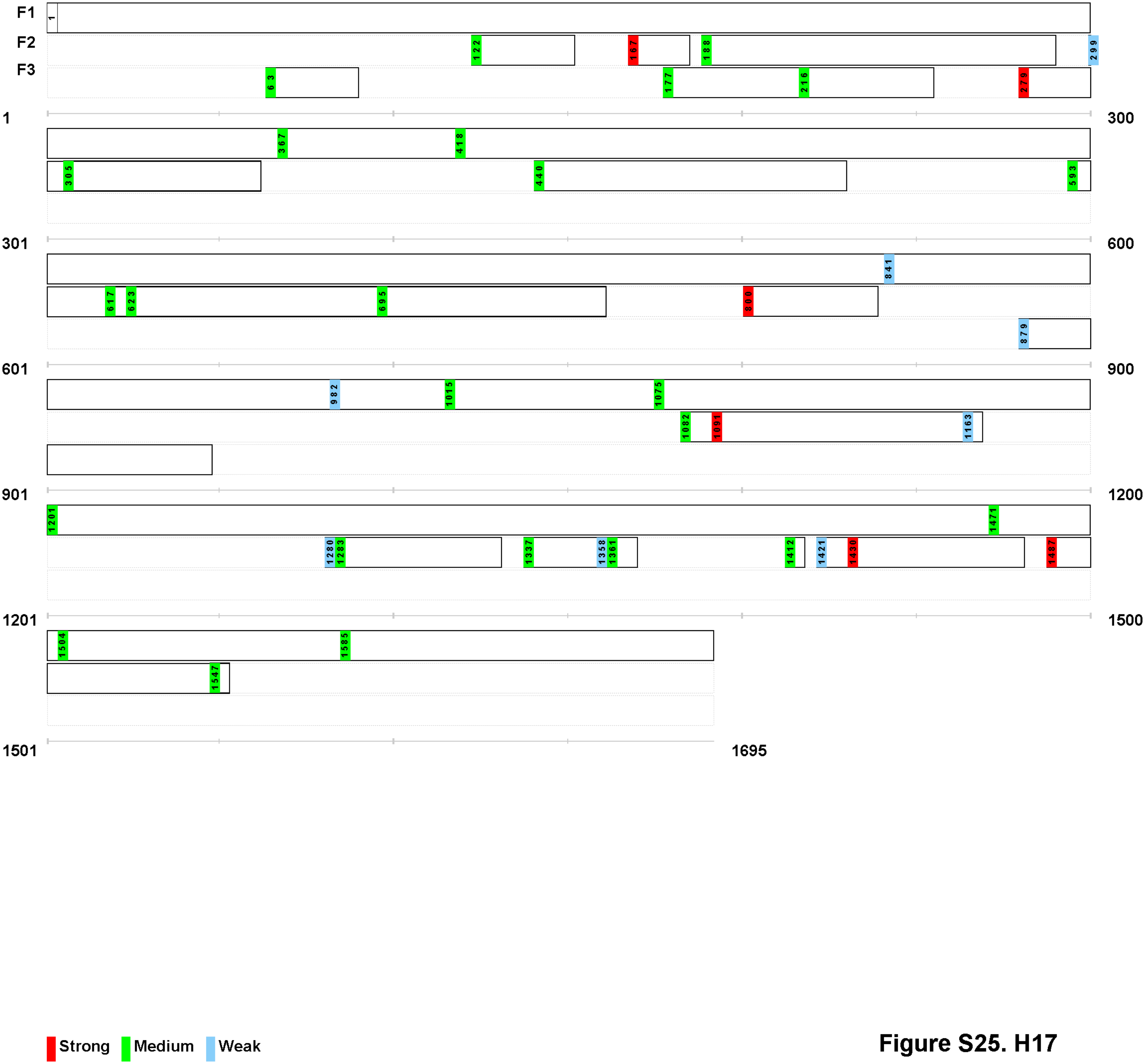


Figure S25. H17

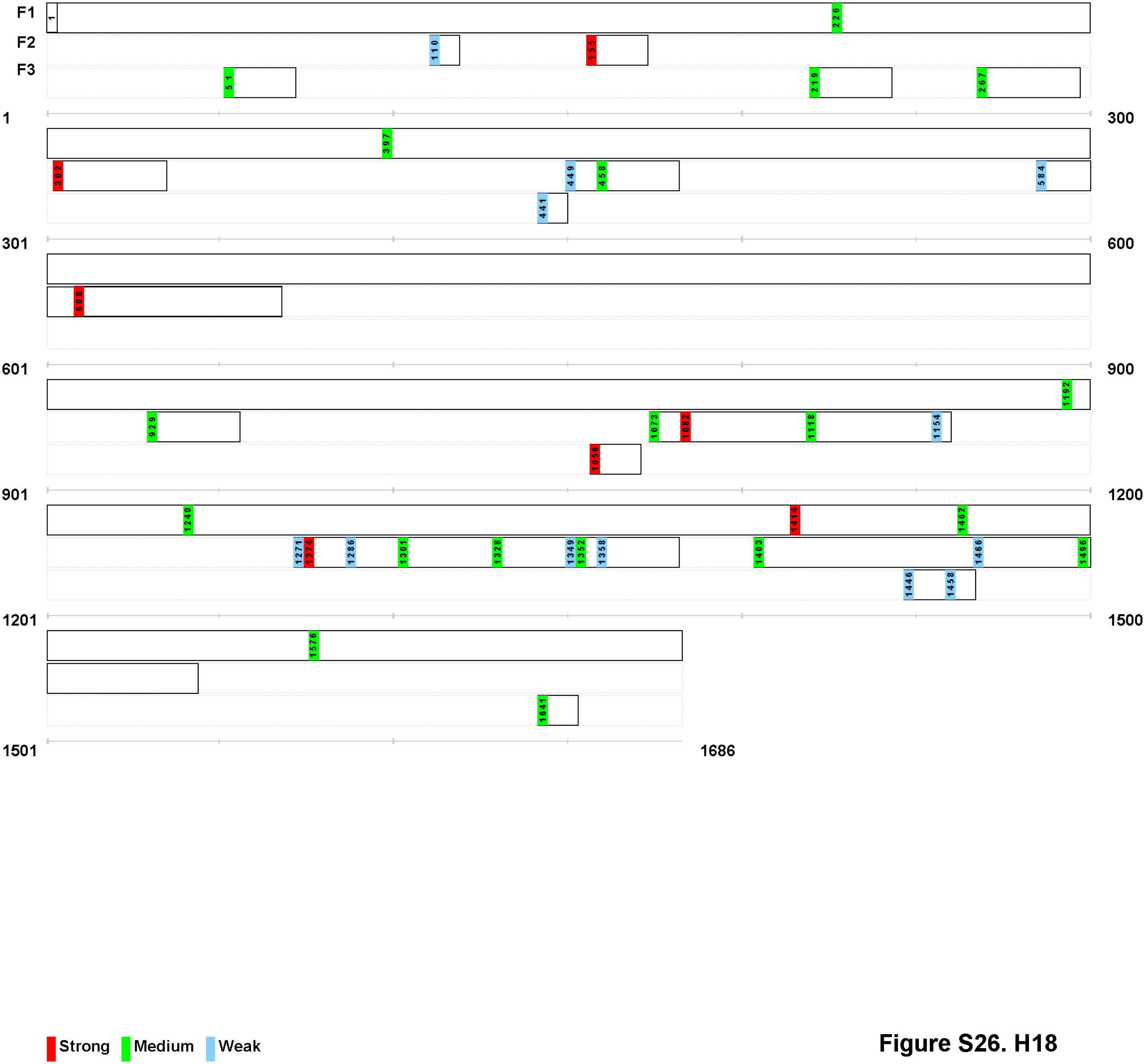
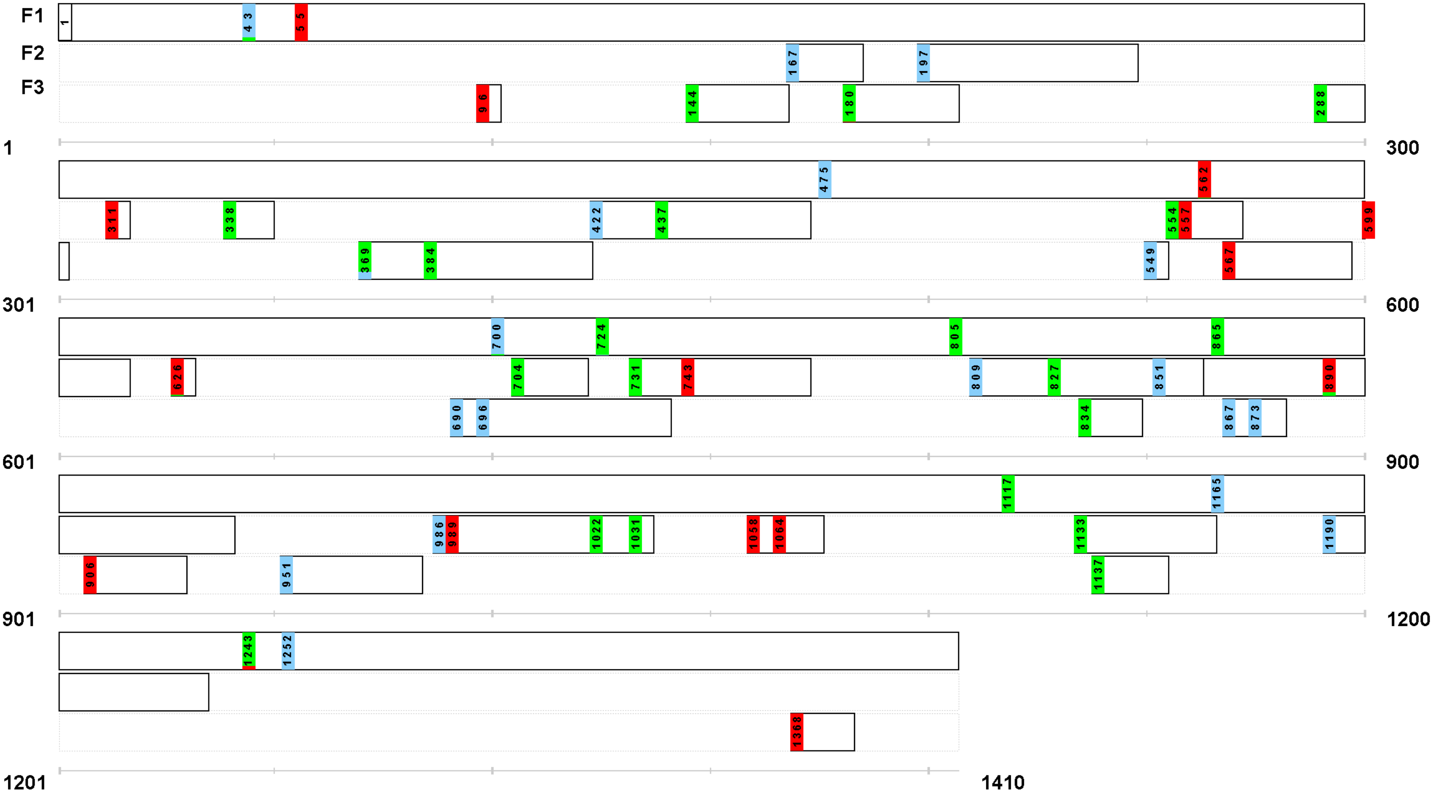
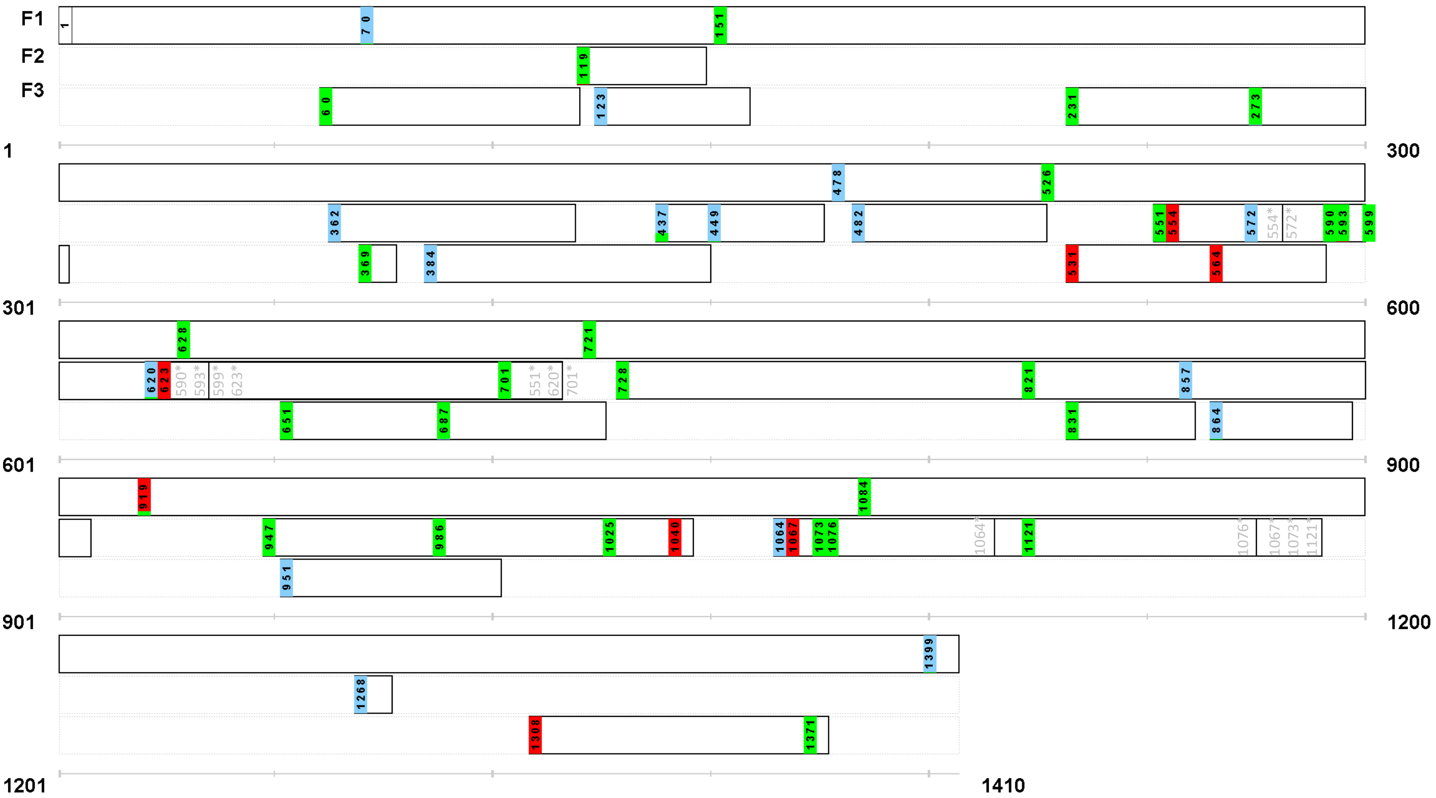


Figure S26. H18



🟥 Strong 🟩 Medium 🟦 Weak

Figure S27. N1



🟥 Strong 🟩 Medium 🟦 Weak

Figure S28. N2

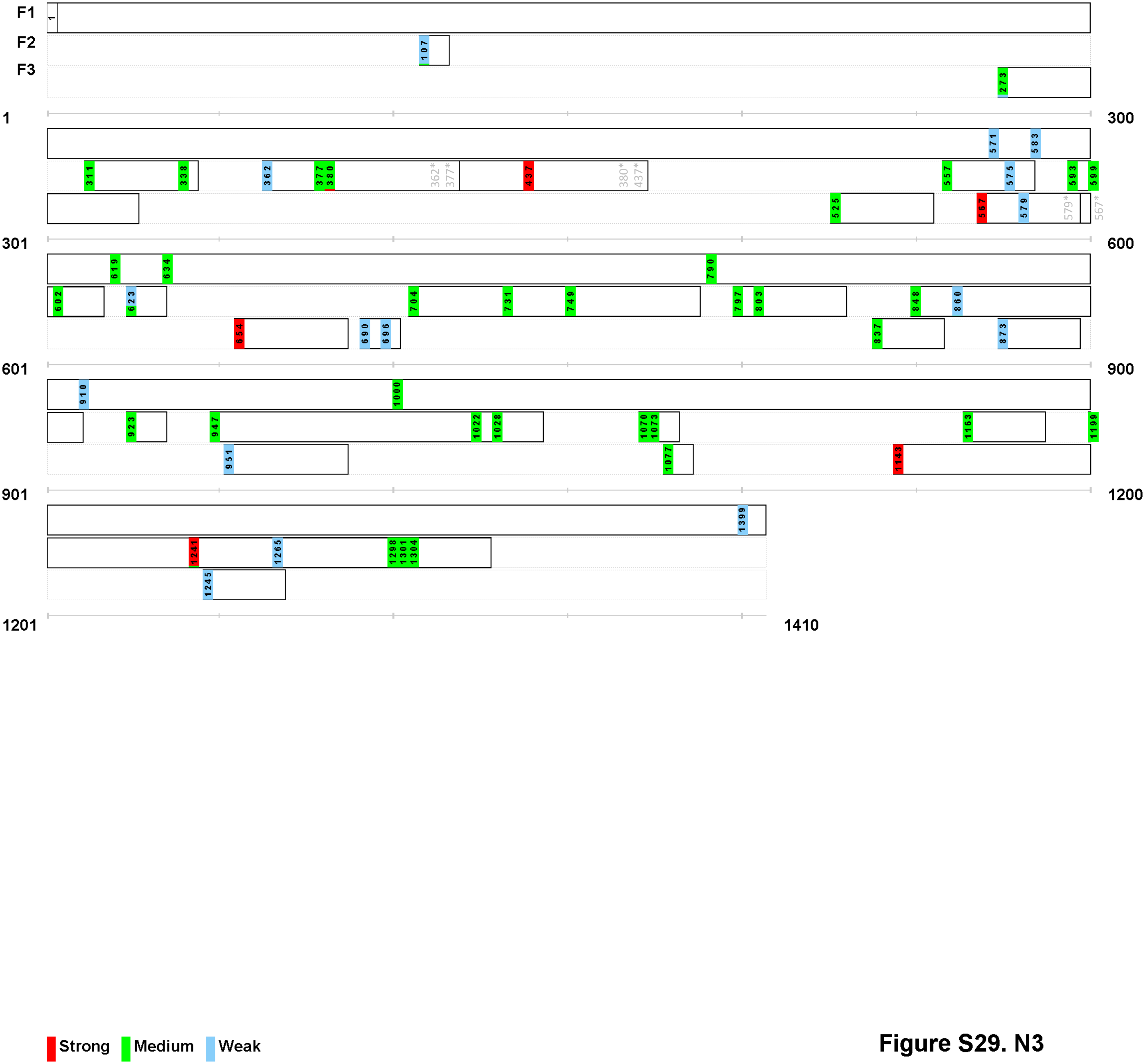
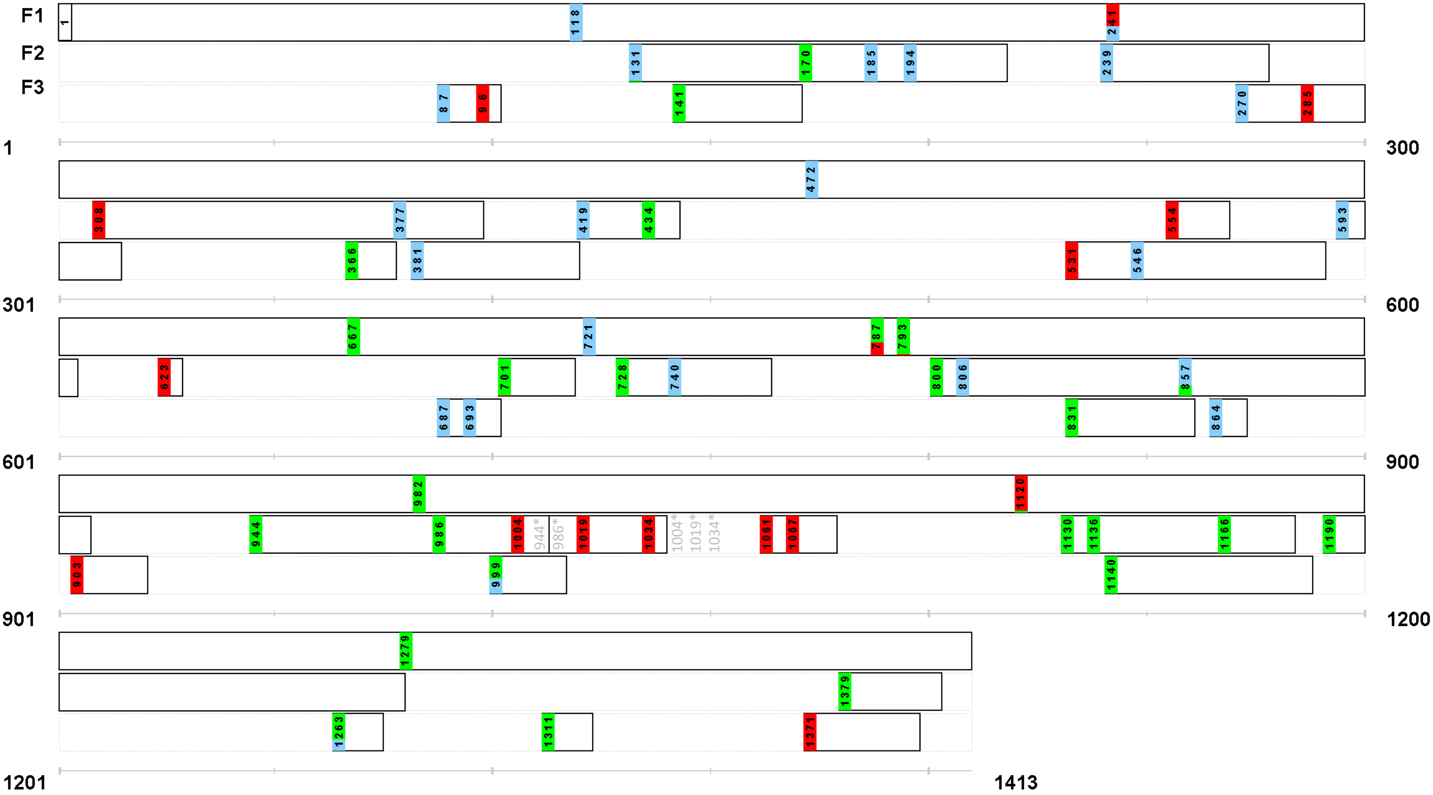


Figure S29. N3



🟥 Strong 🟩 Medium 🟦 Weak

Figure S30. N4

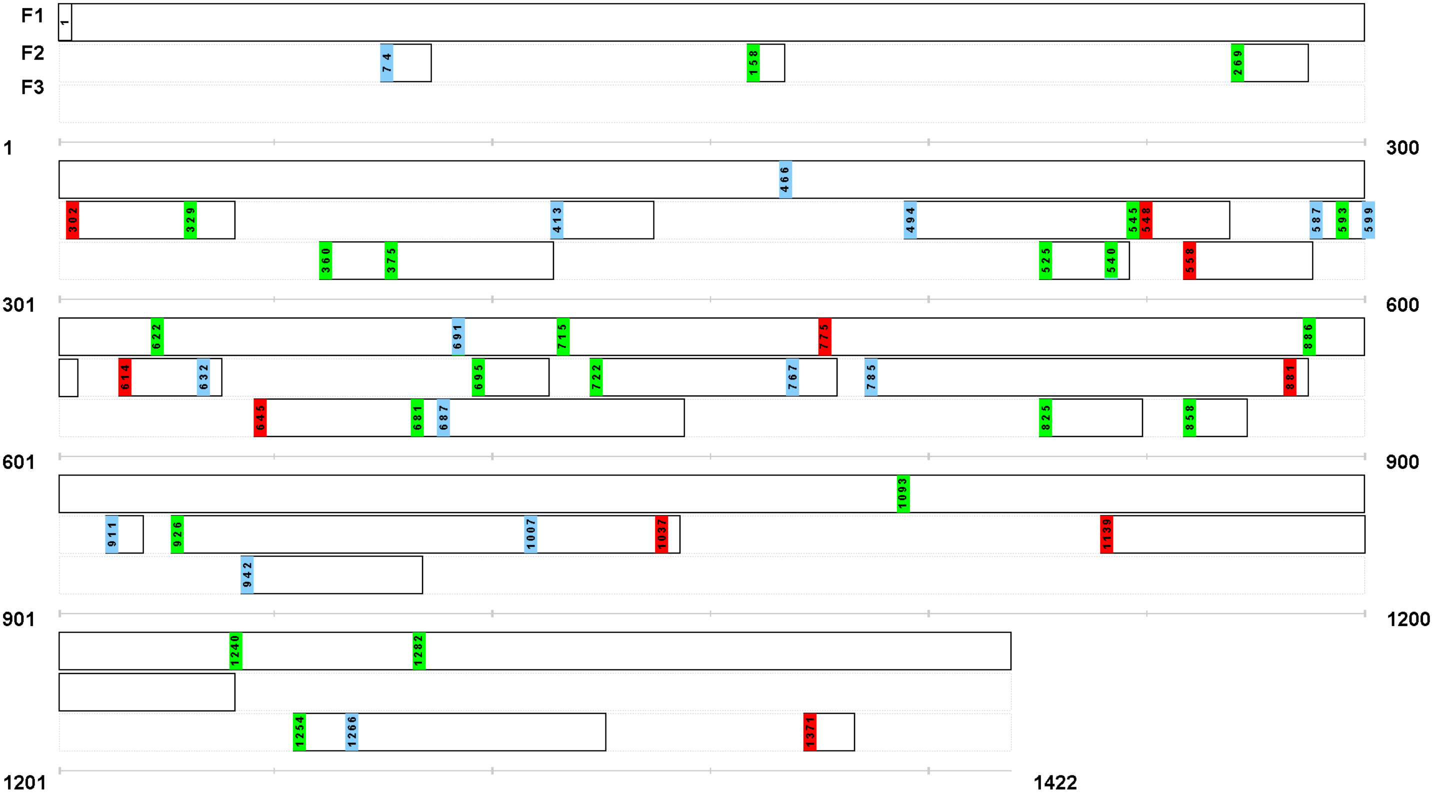
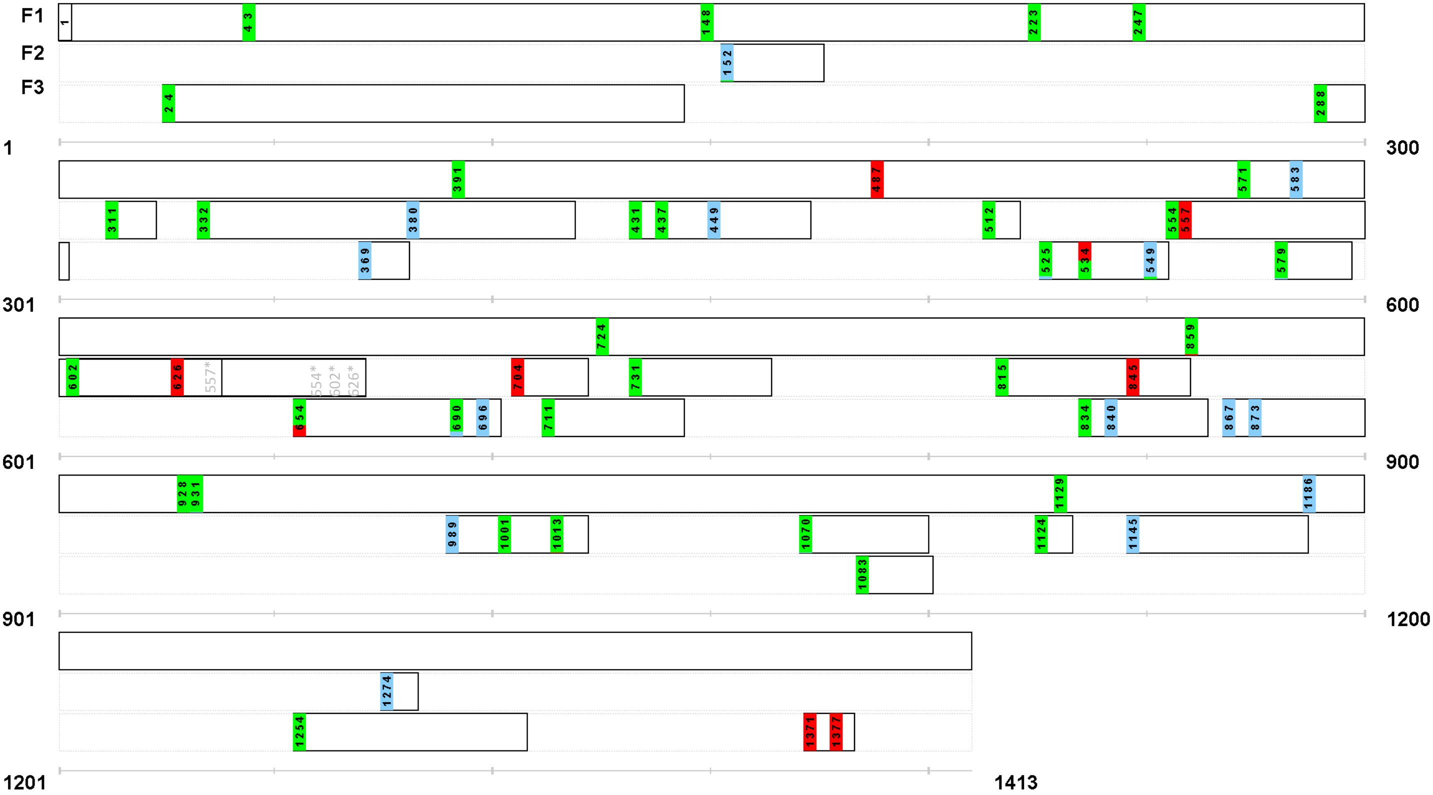
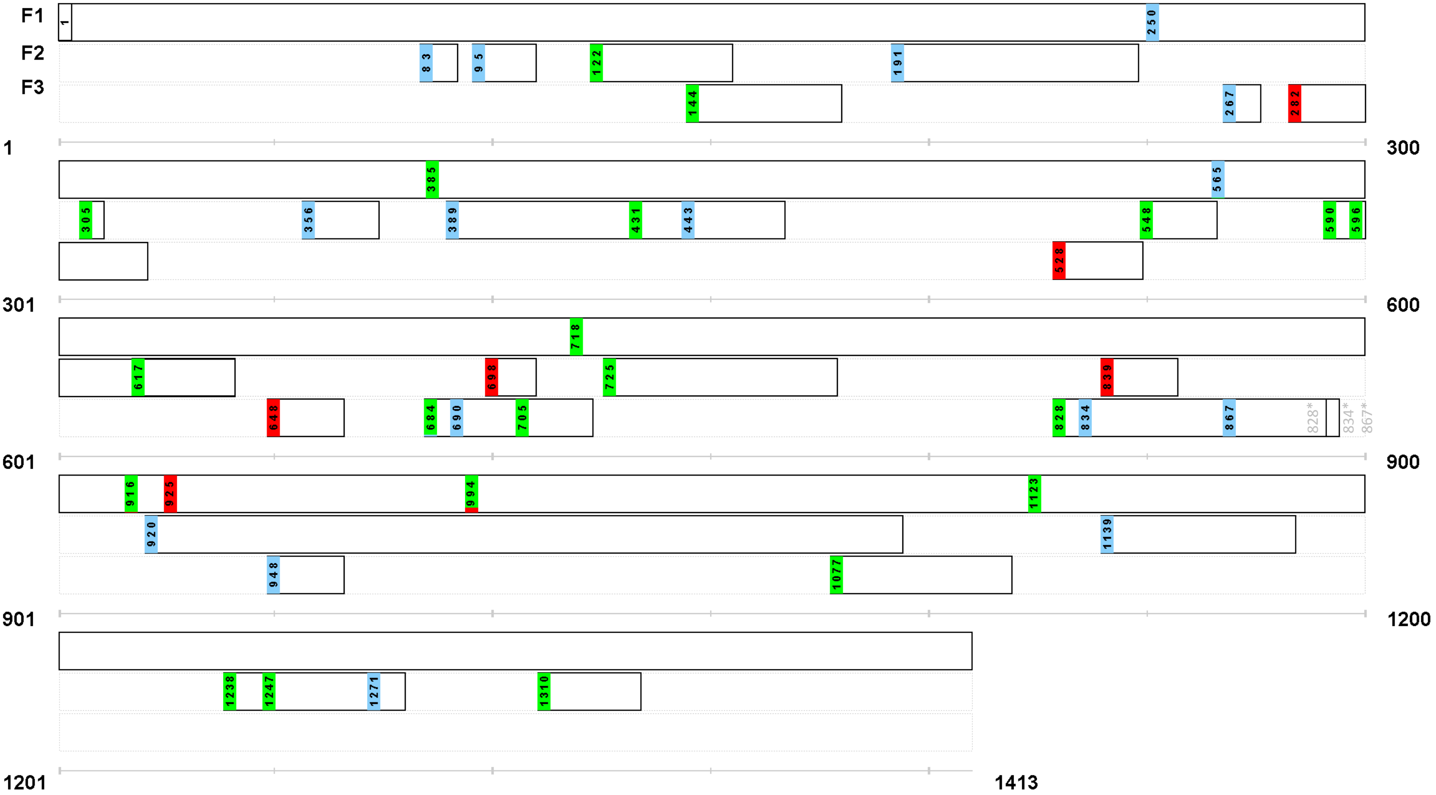


Figure S31. N5



🟥 Strong 🟩 Medium 🟦 Weak

Figure S32. N6



🟥 Strong 🟩 Medium 🟦 Weak

Figure S33. N7

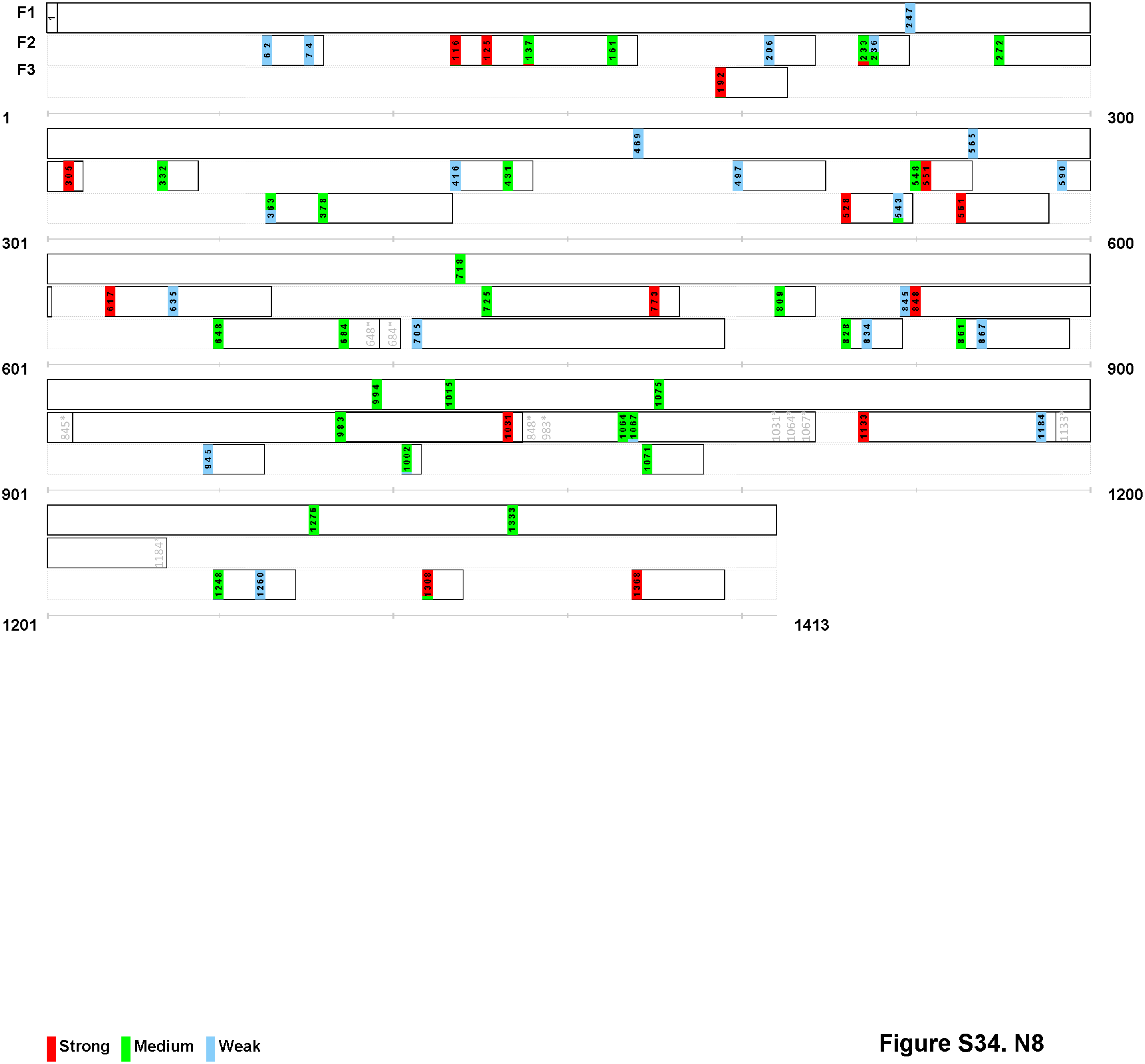
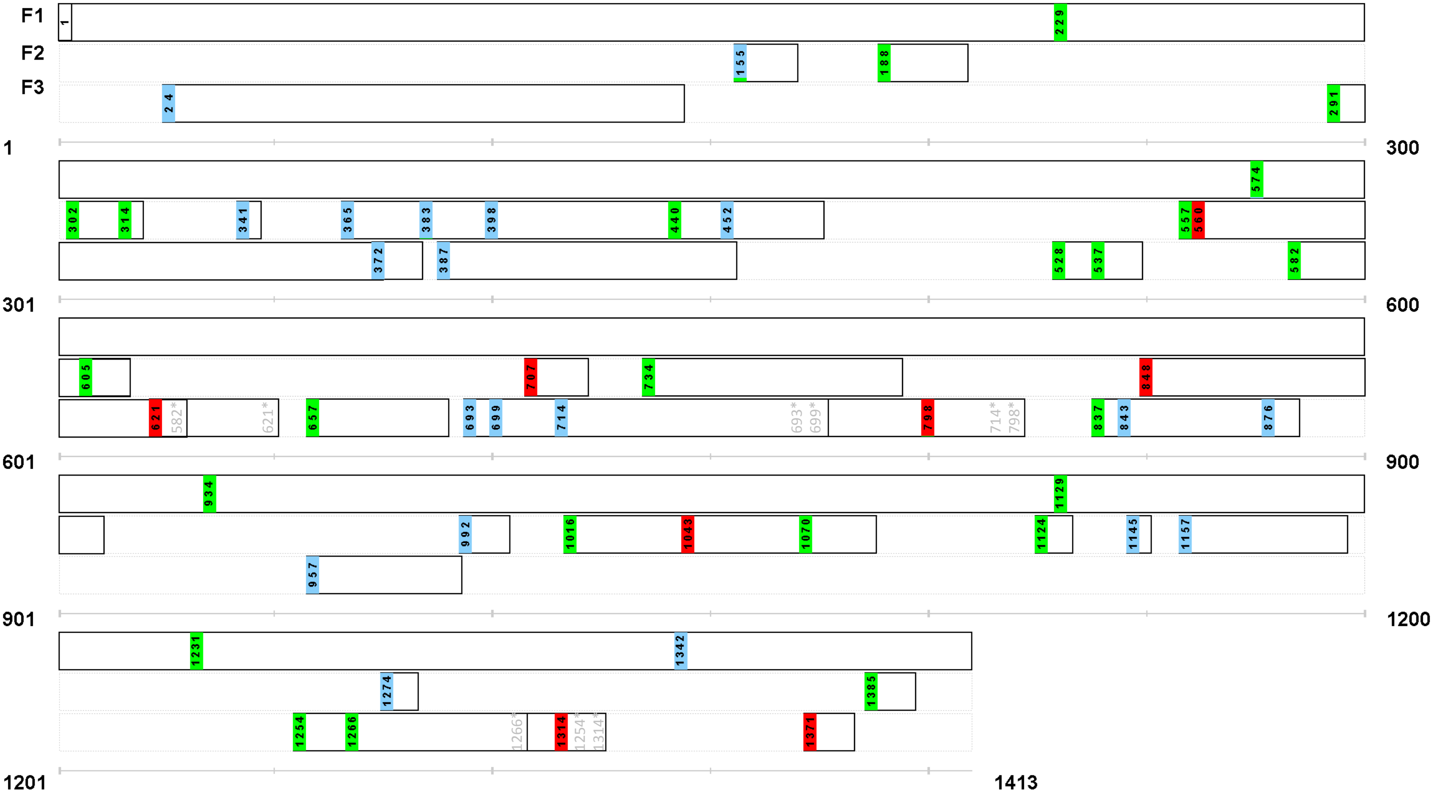


Figure S34. N8



🟥 Strong 🟩 Medium 🟦 Weak

Figure S35. N9

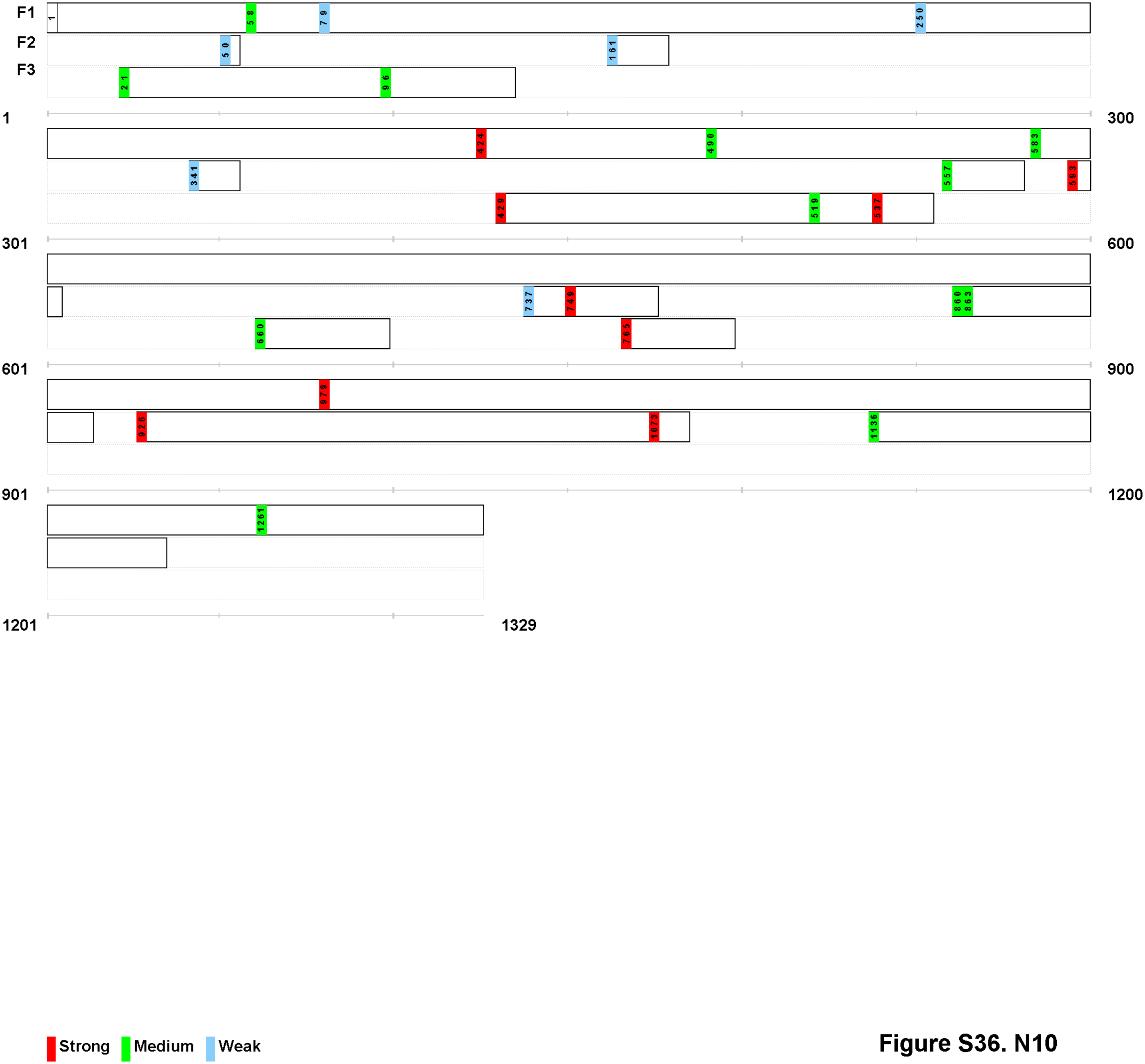


Figure S36. N10

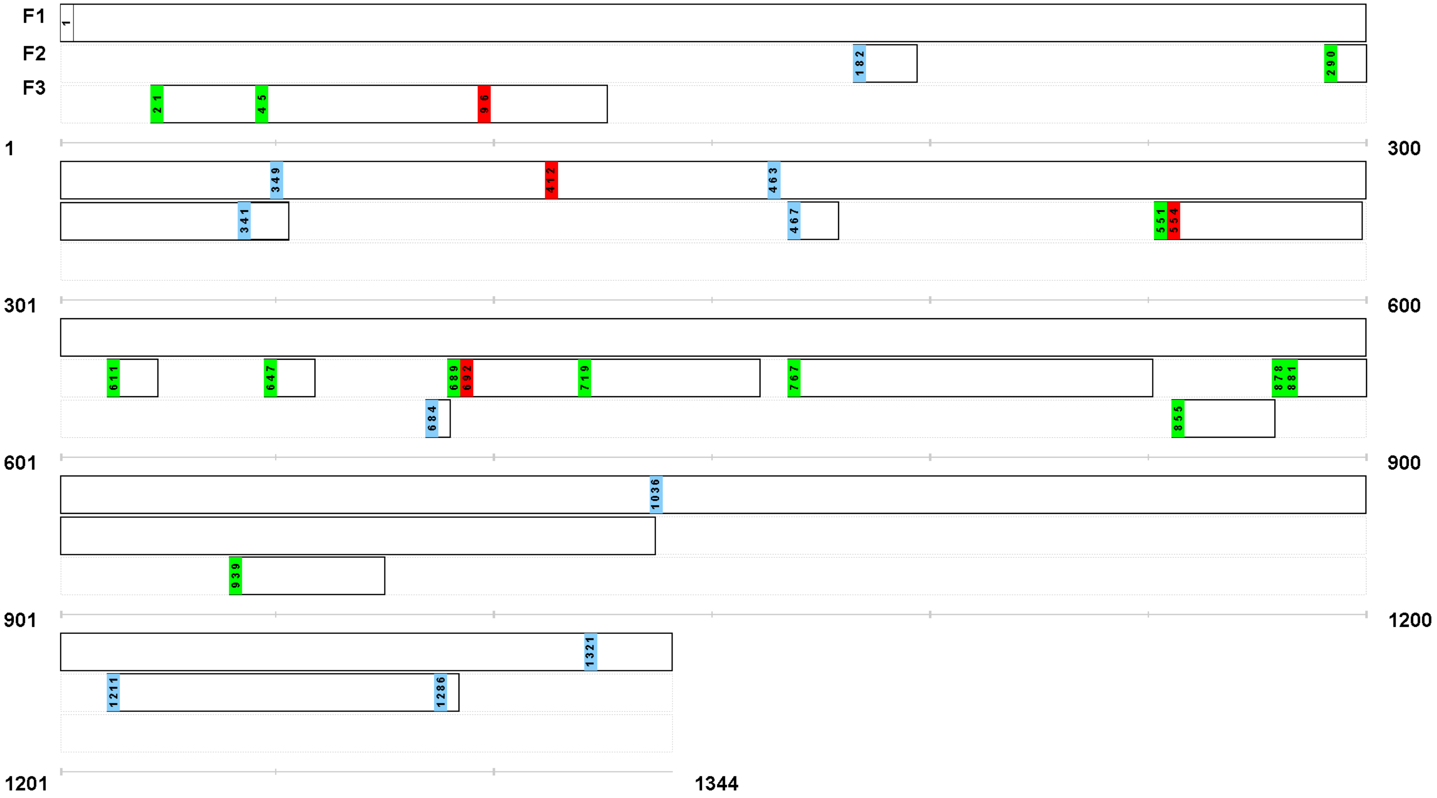


Figure S37. N11

Figures S38. Nucleotide alignments for the BLASTP reports. Four nt sequence alignments are used to illustrate the single nt insertions or deletions (red) that disturbed the reading frames, producing database hits to the ORFs (Table 3). (a) Corresponds to Case 5 in Table 3. Query = JN087010, which translates into AEI29961 in Table 3. Sbjct = HM145493, the second-closest hit in the NT database, excluding the query sequence itself. b) Corresponds to Case 6 in Table 3. Query = AY790308, which translates into AAV68025 in Table 3. Sbjct = AY862651, the second-closest hit in the NT database, excluding the query sequence itself. c) Corresponds to Case 7 in Table 3. Query = M25291, which translates into AAA43224 in Table 3. Sbjct = CY005956, the second-closest hit in the NT database, excluding the query sequence itself. d) Corresponds to Case 8 in Table 3. Query = EU429730, which translates into ACA04672 in Table 3. Sbjct = EU429760, the second-closest hit in the NT database, excluding the query sequence itself.

(a)

```
Query 1681 TGCCATAGGGGTGATACACAAATTCAAACGAGAGAGATCATTCGAGCTGAAGAAGCTGTG 1740
Sbjct 1681 TGCCATAGGGGTGATACACAAATTCAAACAAG-GAGATCATTCGAGCTGAAGAAGCTGTG 1739
...
Query 1801 TATCCGGAATCTCCACATCCCAGAGGTCTGCTTGAAGTGGGAACTAGATGGATGAAGATT 1860
Sbjct 1800 TATCCGGAATCTCCACATCCCAGAGGTCTGCTTGAAGTGGGAACTA-ATGGATGAAGATT 1858
Query 1861 ATCAGGGTAGGCTGTGTAATCCTTCTGAACCCATTTGTCAGTCATAAGGAAATTGAGTCT 1920
Sbjct 1859 ATCAGGGTAGGCTGTGTAATCCTT-TGAACCCGTTTGTCAGTCATAAGGAAATTGAGTCT 1917
```

(b)

```
Query  646 ATTGACGATCGGATTTTCTGGAGAGGTGAAAATGGACCAAAGAACAAGGGATTGCATATG 705
Sbjct  601 ATTAACGATCGGAATTTCTGGAGAGGTGAAAATGGACGAA-GAACAA-GGATTGCCTATG 658
```

(c)

```
Query 1260 AACAAGTAGAGGGAAGGATCCAAGACTTAGAGAAGTATGTTGAAGACAC-AAGATTGACT 1318
Sbjct 1260 AACAAGTAGAGGGAAGAATTCAAGACTTAGAGAAGTATGTTGAAGACACAAAGATTGACC 1319
```

(d)

```
Query  721 TGGGAAC-TGTACAGTAGTAATGACTGATGGAAAGTGCATCAGGAAGGGGCTGATACTAG 779
Sbjct  721 TGG-AACTTGTACGGTAGTAATGACTGATGG-AAGTGCATCAGGAA-GGGCTGATACTAG 777
Query  780 AATATTATTCGTTAAAGAGGGGAAAATCGTGCATATCAGCCCACTATCAGGGAAGTGCCC 839
Sbjct  778 AATATTATTCGTTAAAGAGGGGAAAATCGTGCATATCAGCCCACTATCA-GGAAGTGCCC 836
```