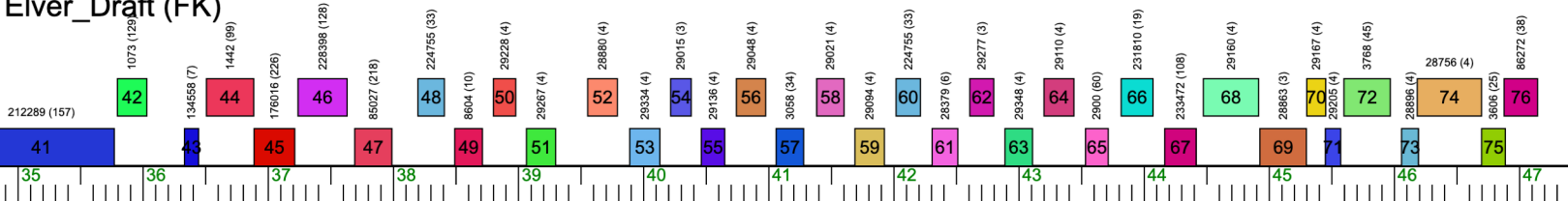
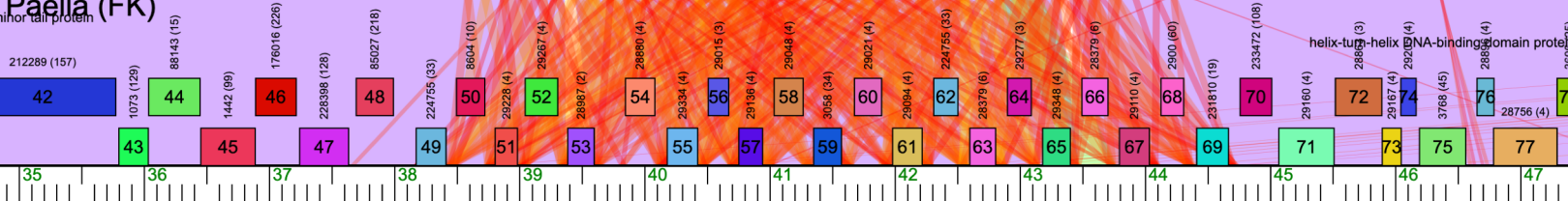


FKPHAGES REGULATORY REGION

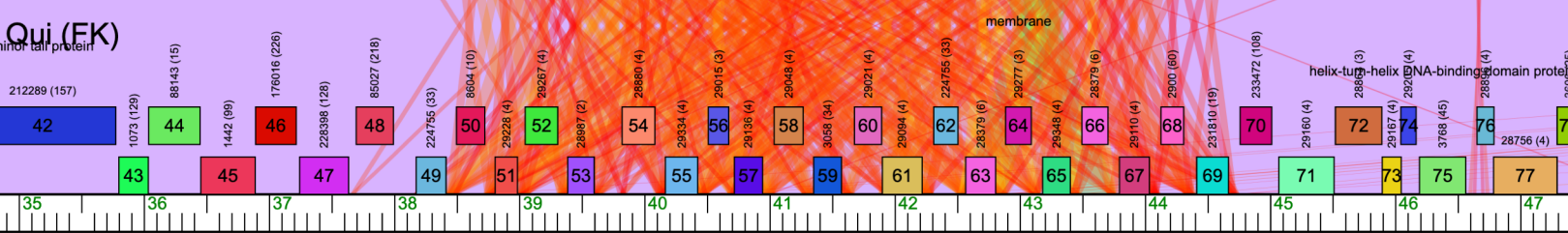
Elver_Draft (FK)



Paella (FK)



Qui (FK)



FK PHAGES REGULATORY REGION

FK Phage NKF cluster with repeated upstream regulatory regions GENES 49-67

```

>Elver_49
    AAAACGGAGGGCCTAACAAGCCCTCTCTTTTTTCGCAGGAATCACATAGGTAATAATGAGAACCCCTATGAAAGGATTTACCATG
>Elver_50
    AAAACGGAGGGCCTAACAAGCCCTCTCTTTTTTCGCTAAATCACAAGGACTTATAATGAGAACCAATTCTAAAGGAGAACCTAATG
>Elver_51
    AAAAGATAAGCGGAGGGCCTAACAAGCCCTCTCTTTTTTCGACTCGCGATATTCACAAGGGTAATAATGAGAACCCCTATGAAAGGAATCATTATG
>Elver_52
    ATAAGAGCGACTTCTCCCCGCCTATATTTTTTGACCAGTTCGTAGGATTCACAAGTCTTATAATGAGAACCACTACGAAAGGAAATACCATG
>Elver_53
    AAAACTCGGAGGCCCTAACACGGCCTCTAGTTTTCTCTCGGTCGCGATATTTACAAAGACTTATAATGAGAACCCCTATGAAAGGAAAGACAATG
>Elver_54
    AAAACGGAGGGCCTAACAAGCCCTCTCTTTTTTCGCGAATTTACAAGGCGTATAATGAGAACCCCTATGAAAGGAATTAAGTCATG
>Elver_55
    AAAACCAACCACTAAAGCGGAGGGCCTAACAAGCCCTCTCTTTTTTCGCGGGAATCACATGGCATATATTGAGAACCCCTATGAAAGGAACATCATG
>Elver_56
    AAAACGGAGGGCCTAACAAGCCCTCTCTTTTTTCTCGGTCGCGAAAATCACAAGGTGTATAGTGAGAACCCCTCTATGAAAGGAACATAATG
>Elver_57
    AAAACGGAGGGCCTAACAAGCCCTCTCTTTTTTCTCGCGATATTTACAGCGCCTATAATGAGAACCCCACTAGAAAGGAACTGTAATG
>Elver_58
    AAGGAGAAGAGGCCTAACAAGCCCTCTCTTTTTTCTCGGGTTTCGAGAGATCACAAGGACTTATAATGAGAGAAAATCAATGAAAGGAATCTAATG
>Elver_59
    AAATGAGGGGCGCTAACACCGCCTCTTATTTTTTCGTAGGAATCACATTGCCTATAATGAGAACCCCTATGAAAGGAAGTACCATG
>Elver_60
    AAAAGCGGGGCCTAACAAGCCCTCTCTTTTTTCTCTAAGTCGAGGATCACAAGGACTTATATTGAGAACCCCTACGAAAGGAATTAGCATG
>Elver_61
    AAAACGGAGGCCTAACACGGCCTCTCTTTTTTCGCAGAAATCACAGGGCTATAATGAGAGAAAATCCCTATGAAAGGAACCAATCATG
>Elver_62
    AAAAAGGGGCGCTAACACCGCCTCTTATTTTTTCGCAGAAATCACAGGGCATATAATGAGAGAAAATCCCTATGAAAGGAATTATTATG
>Elver_63
    AAAACGGAGGCCTAACACGGCCTCTCTTTTTTCGCAGAAATCACAGGGCTATAATGAGAGAAAATCCCTATGAAAGGAACCAAAATG
>Elver_64
    AATAAGAGGCGCTAACACCGCCTCTTATTTTTTCGCACAATTCACAAGGCTATAATGAGAACCCCTTATTAATGAAAGGAACCAAAATG
>Elver_65
    AATTAAAGAGATAAGAGACCCTAACCCGGCCTCTTATTTTTTCTCTTTTCGACAATTCACAAAGTGTATAATGAGAACCTATGAAAGGACATATTATG
>Elver_66
    AAAATAAGGAGGTCTACAAGACCTCTTATTTTTTCTCGAGAAATACAGGGCTATAATGAGAACCCCTCTATGAAAGGAATTACCCTAATG
>Elver_67
    AAAGTTGAGGGCCTAACAAGCCCTCTCTTTTTTGTTTTCTCGCATAAATACATGGCCTATAATGAGAGAAAATTCAACTATTTAAGGAGAACCCATG

```

ATG = correct start to annotate (all have highest RBS scores)

ATG/GTG/TTG = longer starts that should not be annotated.