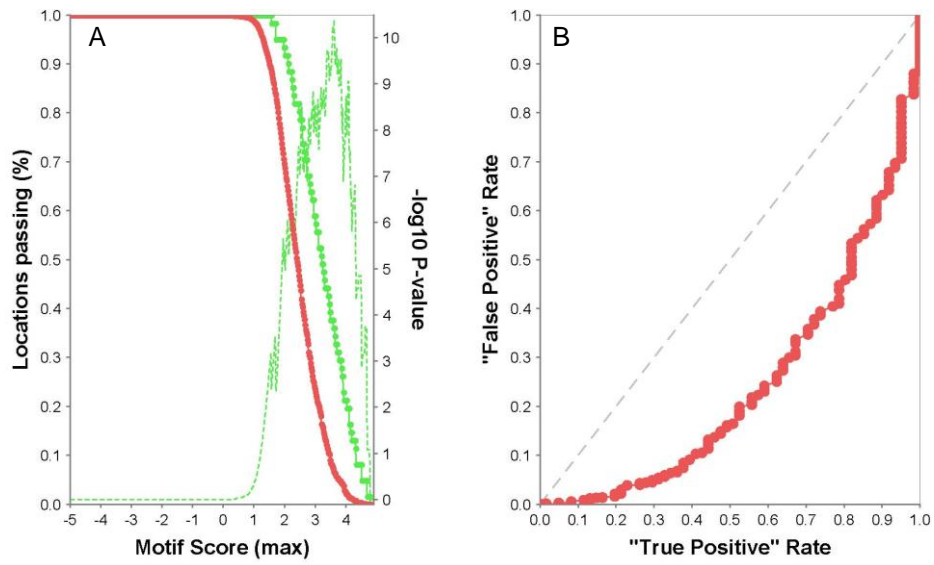


Data File S2

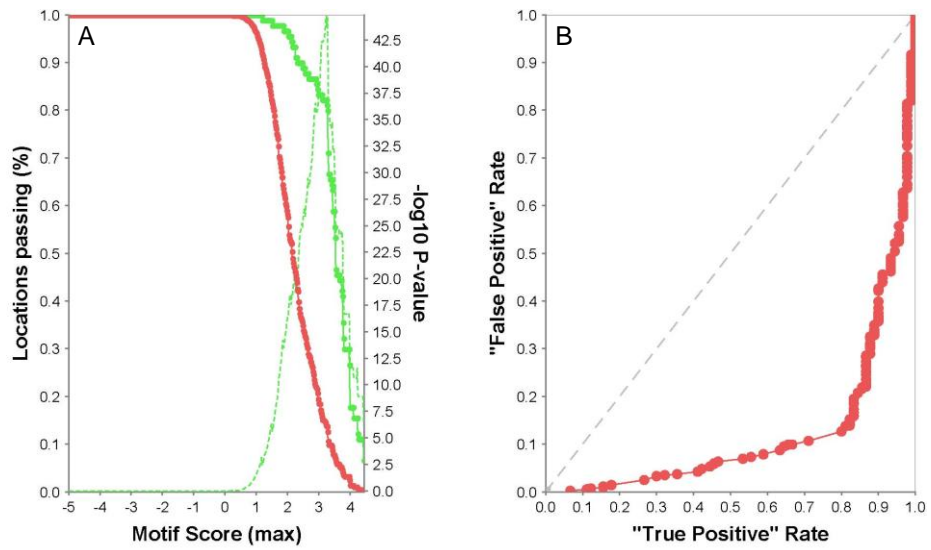
Motif Finding and Assessment

Motif analysis was performed with MochiView's "motif finder" function using 250 bp centered on the midpoint of half of the extracted peaks for each factor, and analyzed for significance of enrichment in the remaining half of extracted peaks for that factor using MochiView's "enrichment" function. This utility assesses the likelihood of finding the identified motif by chance in random intergenic regions of the same length (500 bp). Motif enrichment plots are shown below for each regulator. In panel A, the red line indicates the percentage of 500 bp random intergenic regions that contain the indicated motif, and the green line shifted to the right of it, indicates the percentage of 500 bp extracted peaks that contain the indicated motif. The dashed green line reflects the negative \log_{10} -transformed p-value for the motif in the 500 bp extracted peaks with values corresponding to the y-axis legend displayed on the right side of the plot in panel A. These p-values were calculated using a one-tailed Fisher's Exact test comparing the number of 500 bp random intergenic regions passing and missing the cutoff to those of the 500 bp extracted peaks. Panel B is a Receiver Operating Characteristic (ROC) plot displaying the percentage of 500 bp extracted peaks passing the cutoff as the "True positive rate" (x-axis) and the percentage of random 500 bp random intergenic regions passing the cutoff as the "False-positive rate" (y-axis). The significantly enriched, de novo-generated motifs from our ChIP-chip data for each regulator are shown as graphic logos below the plots.

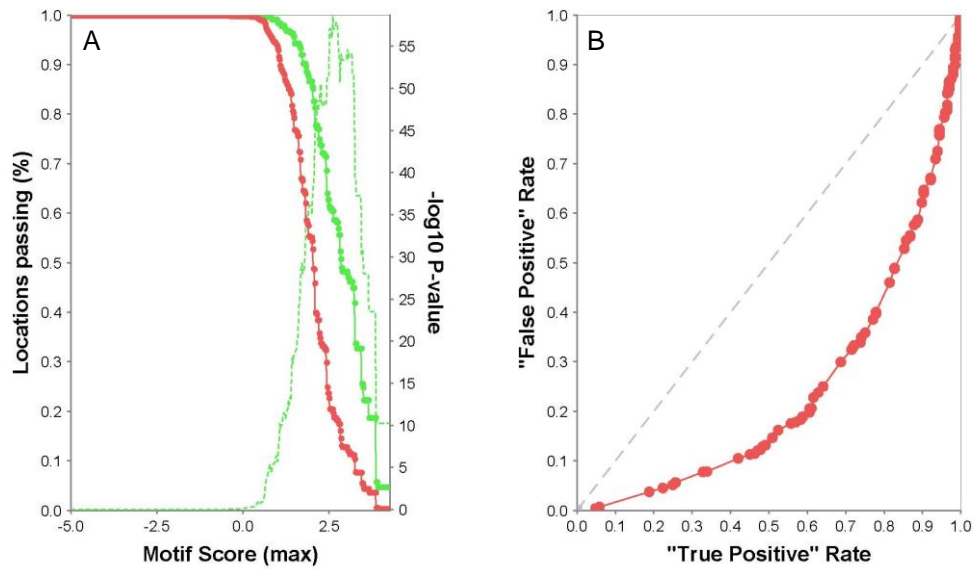
Bcr1



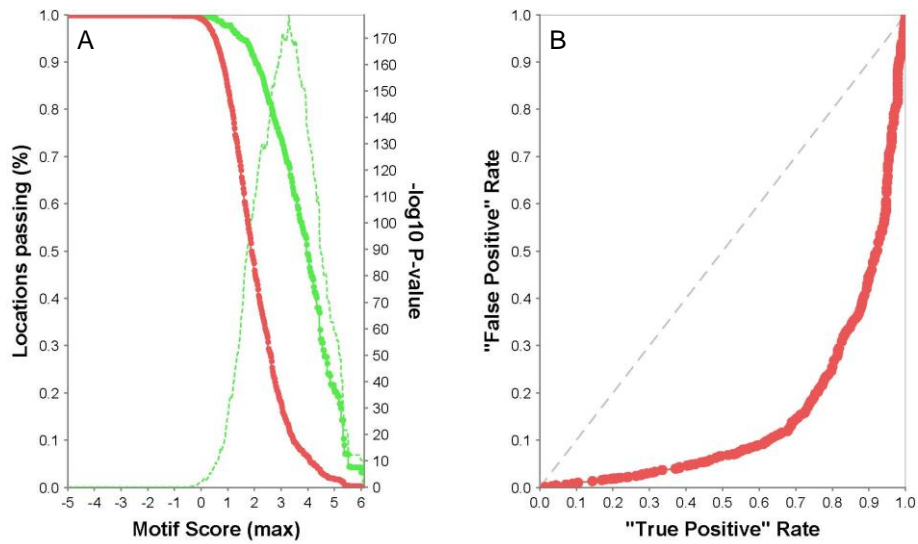
Tec1



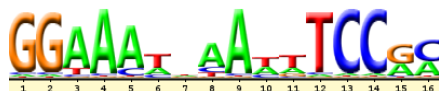
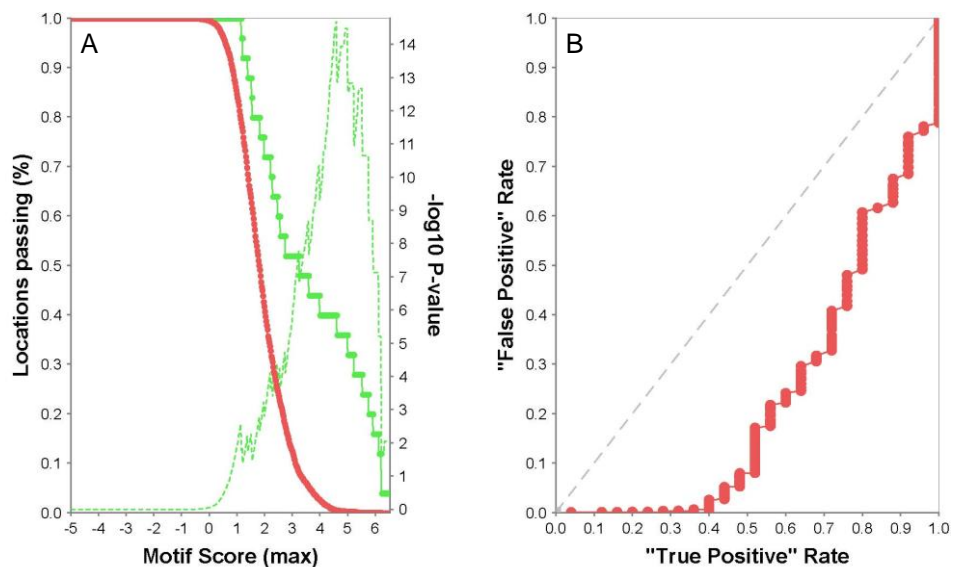
Efg1



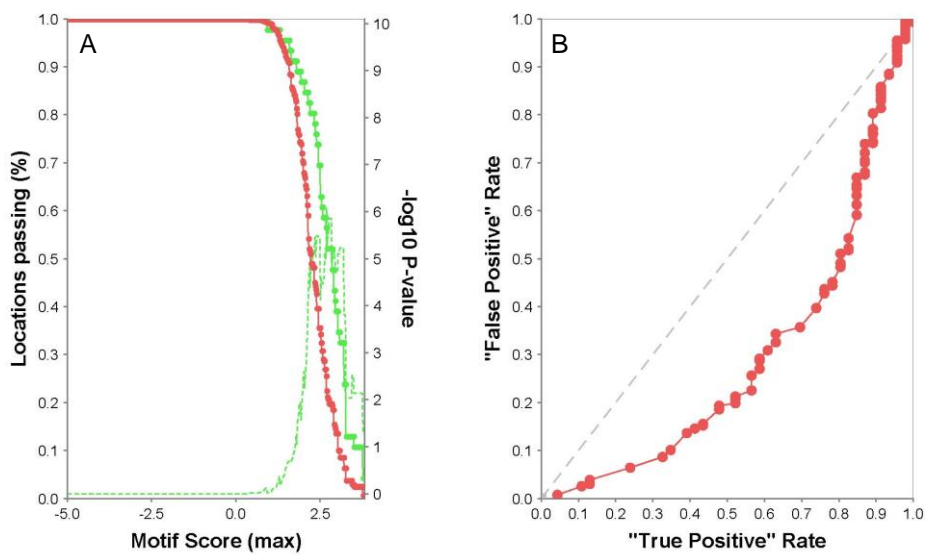
Ndt80



Rob1

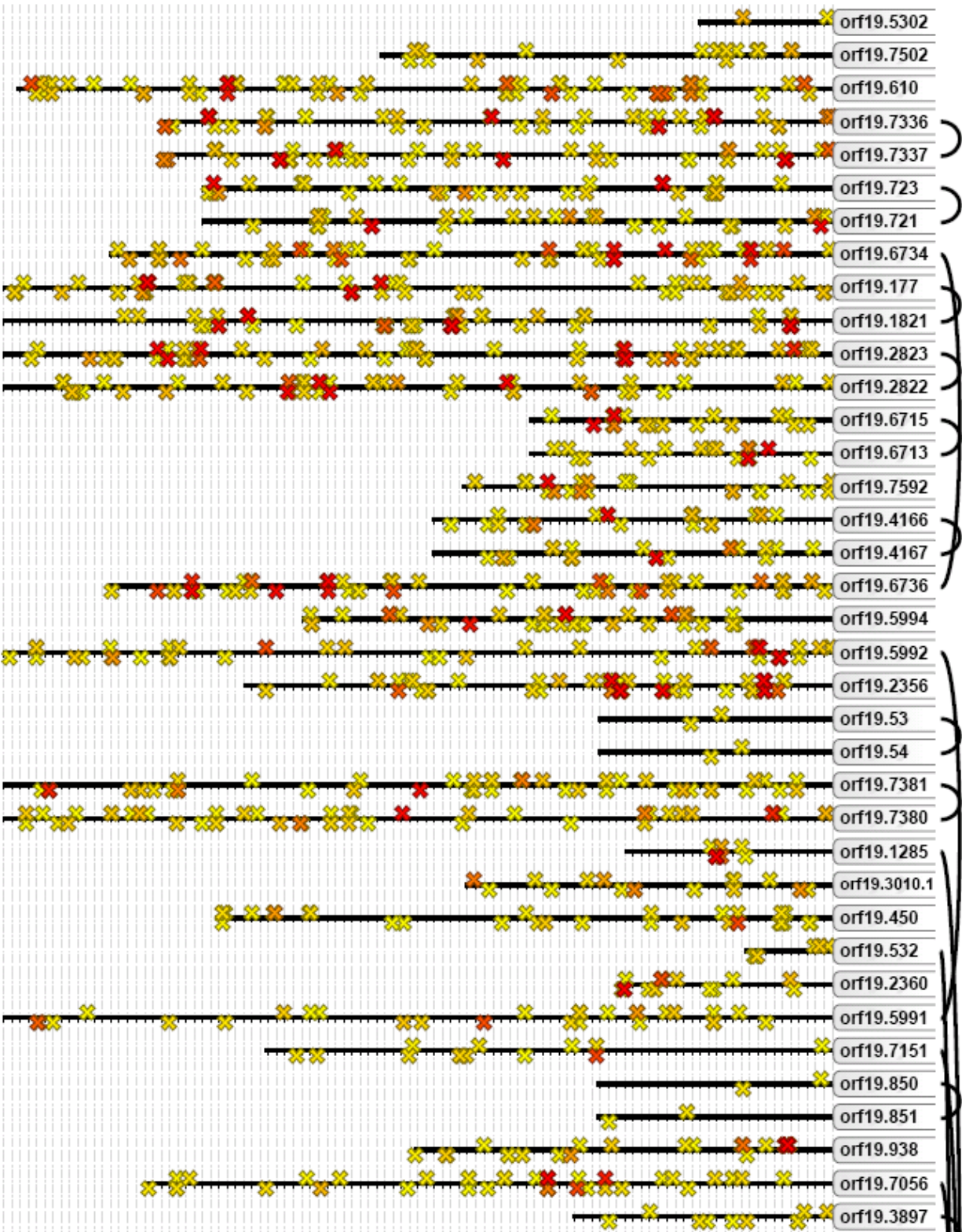


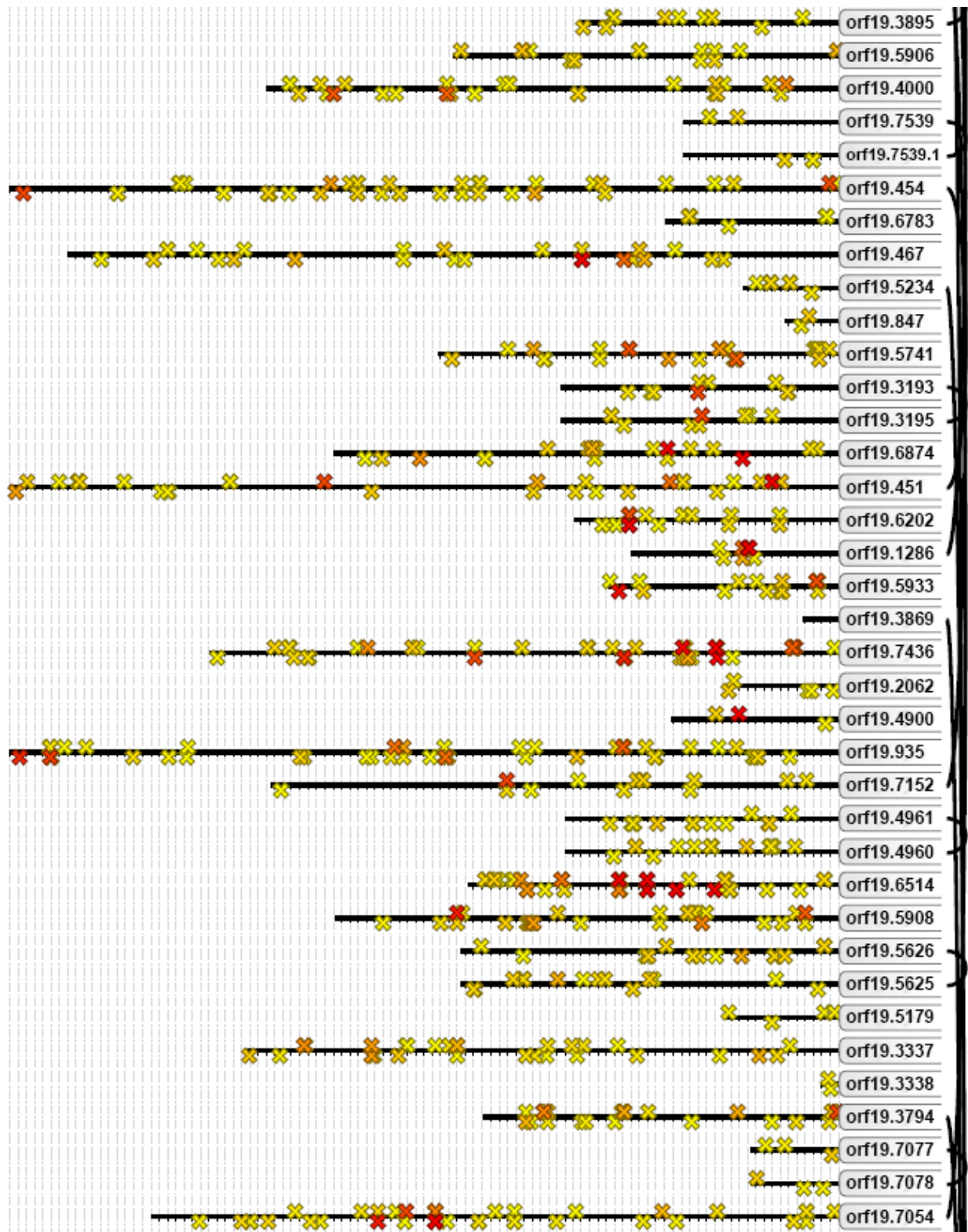
Brg1

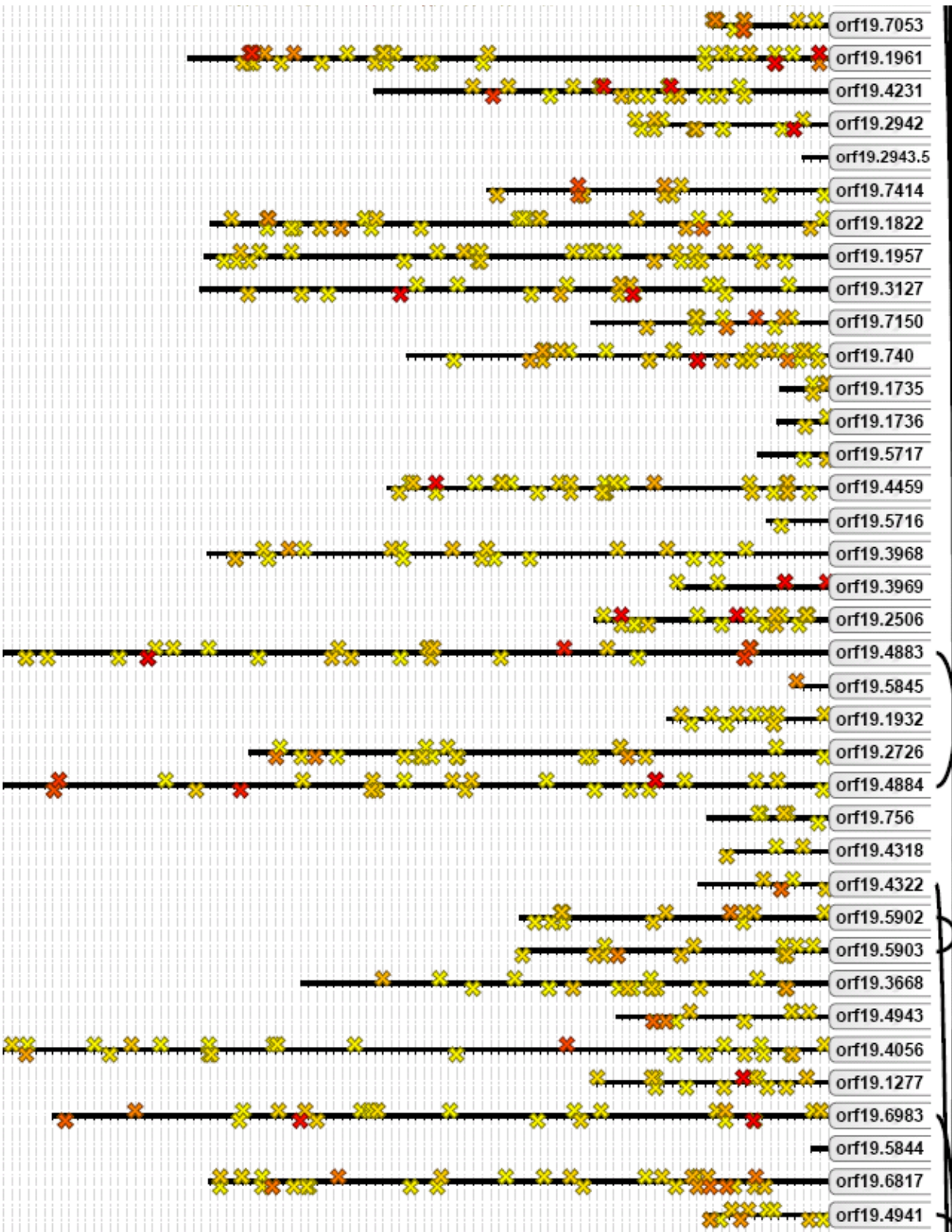


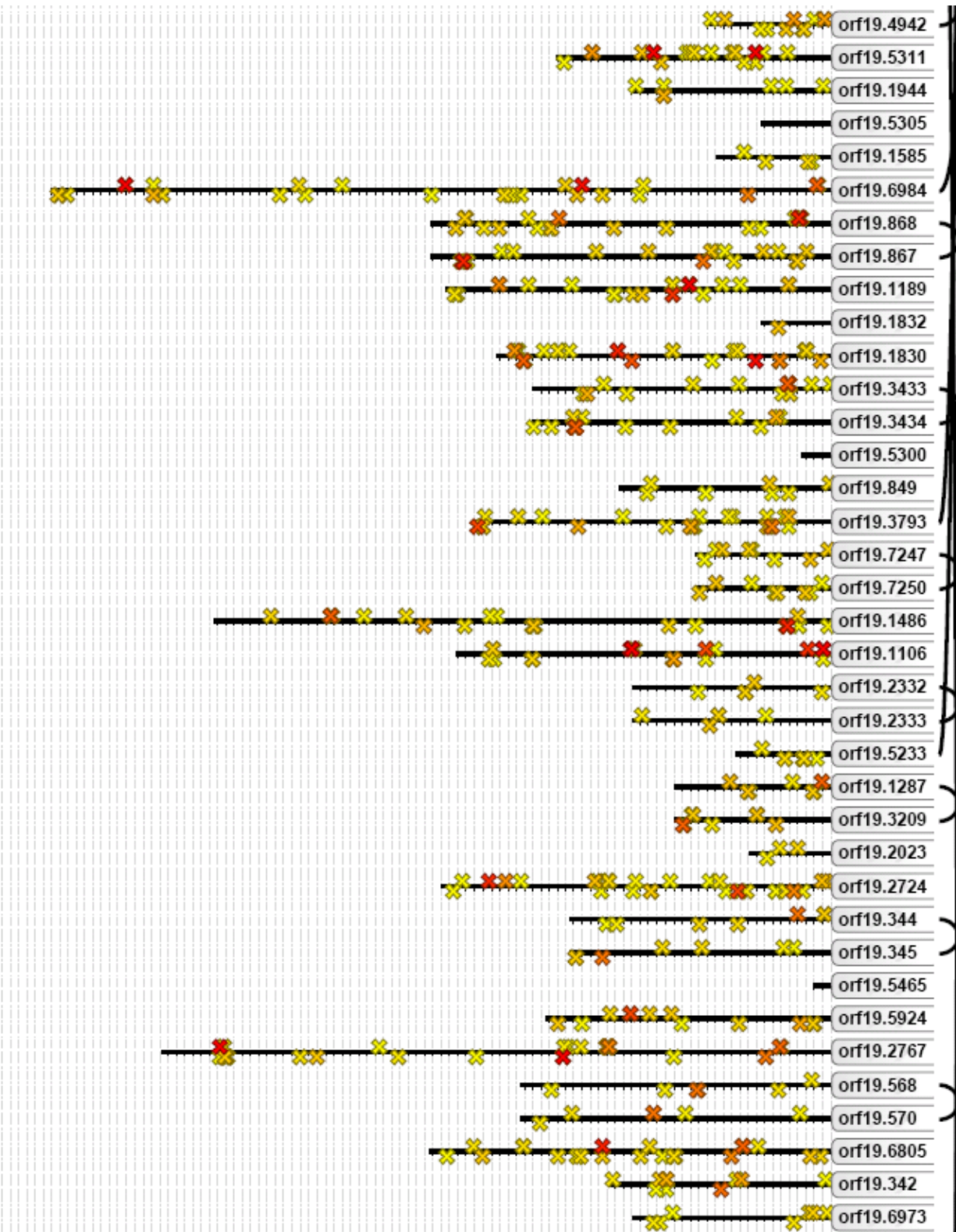
Motif Distribution Summary

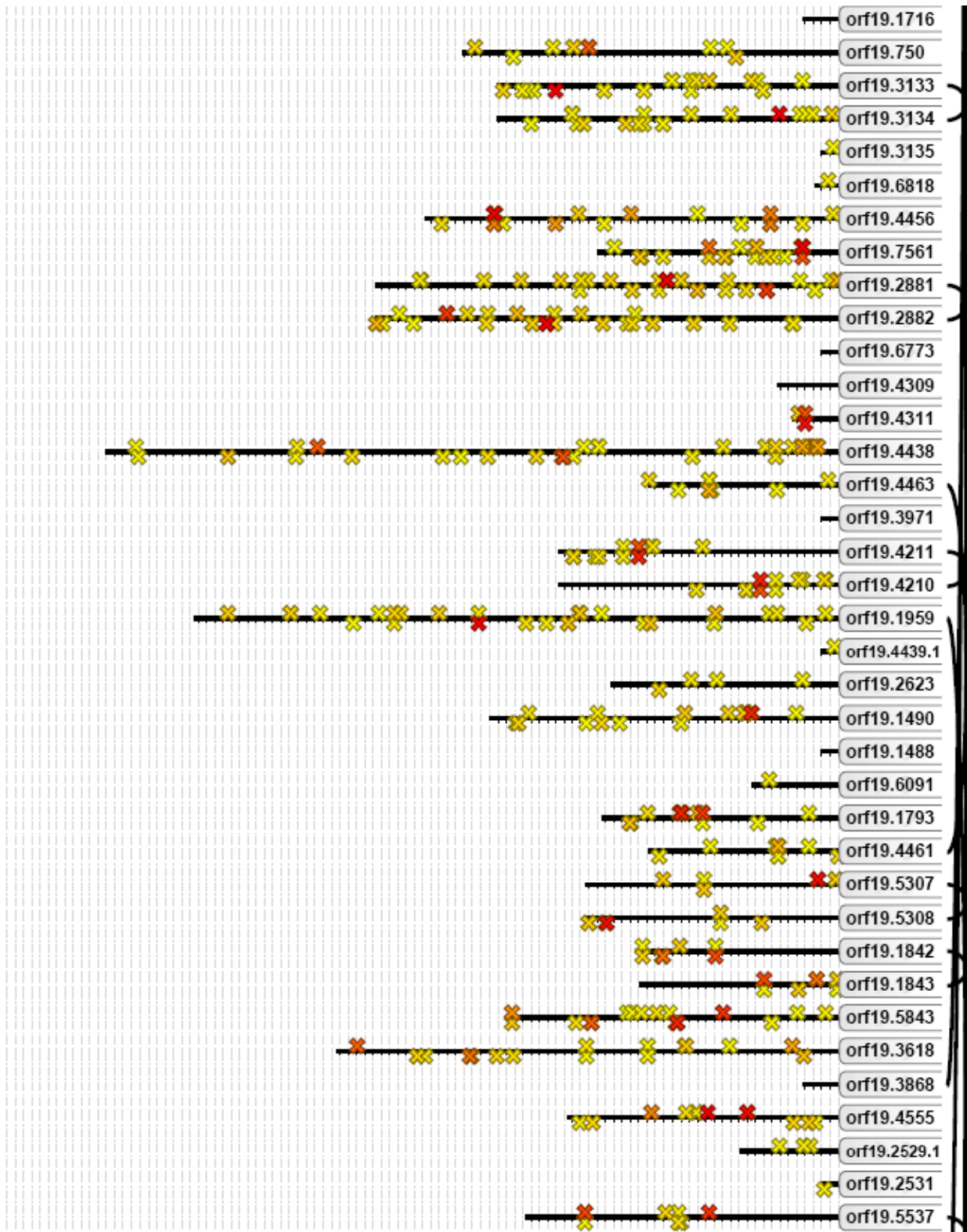
Motif distribution visual summary plots for Bcr1 were constructed with MochiView's "compact motif/data/location plot" function using the minimum LOD score cutoffs established from the enrichment plots. A LOD score cutoff of 3 was used for the Bcr1 motif. Shown are the upstream promoter regions of the direct targets of Bcr1. The motifs for Bcr1 are indicated by the colored "x," where the increasing color scale from light yellow to red indicates the minimum to maximum LOD score value.

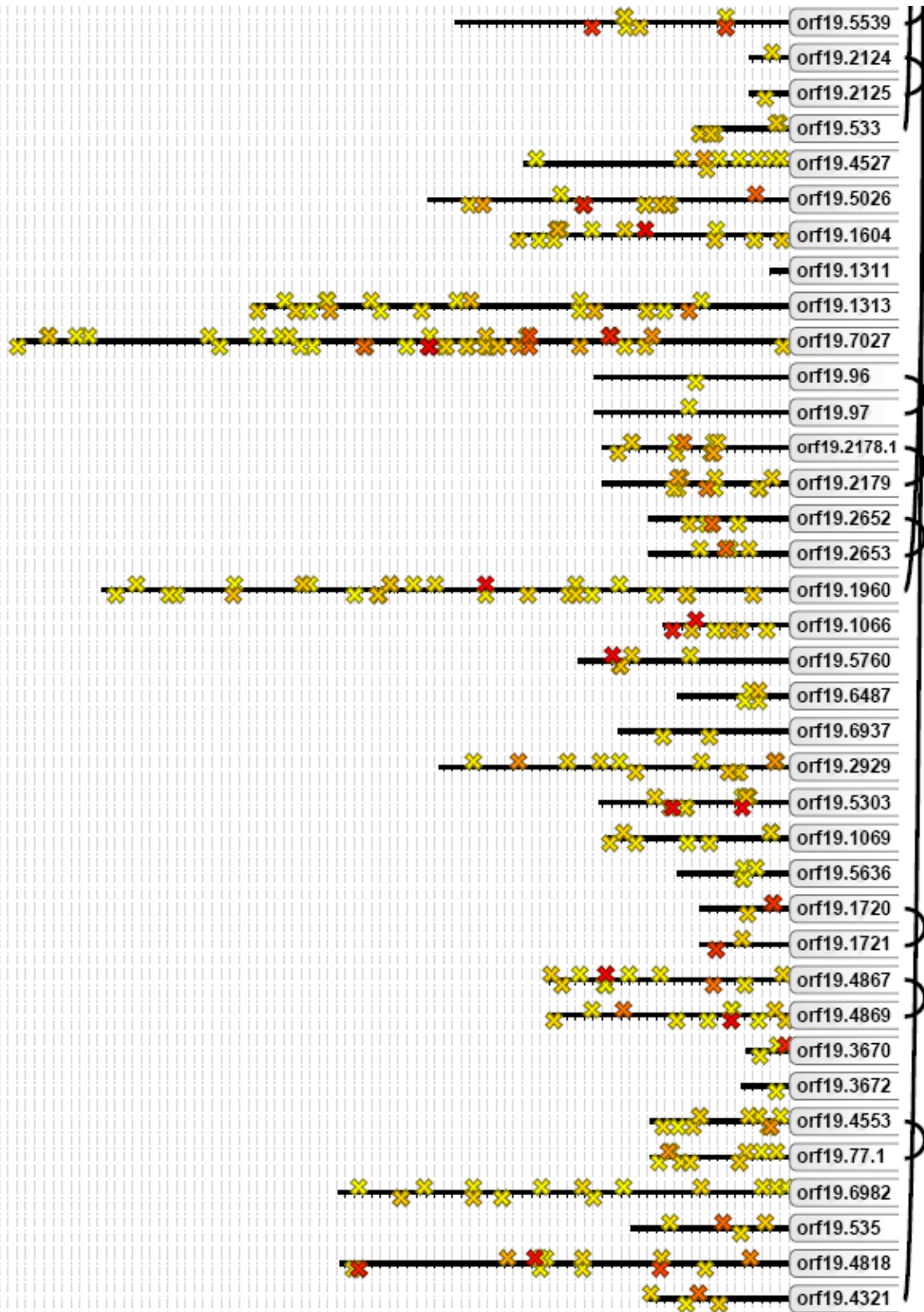


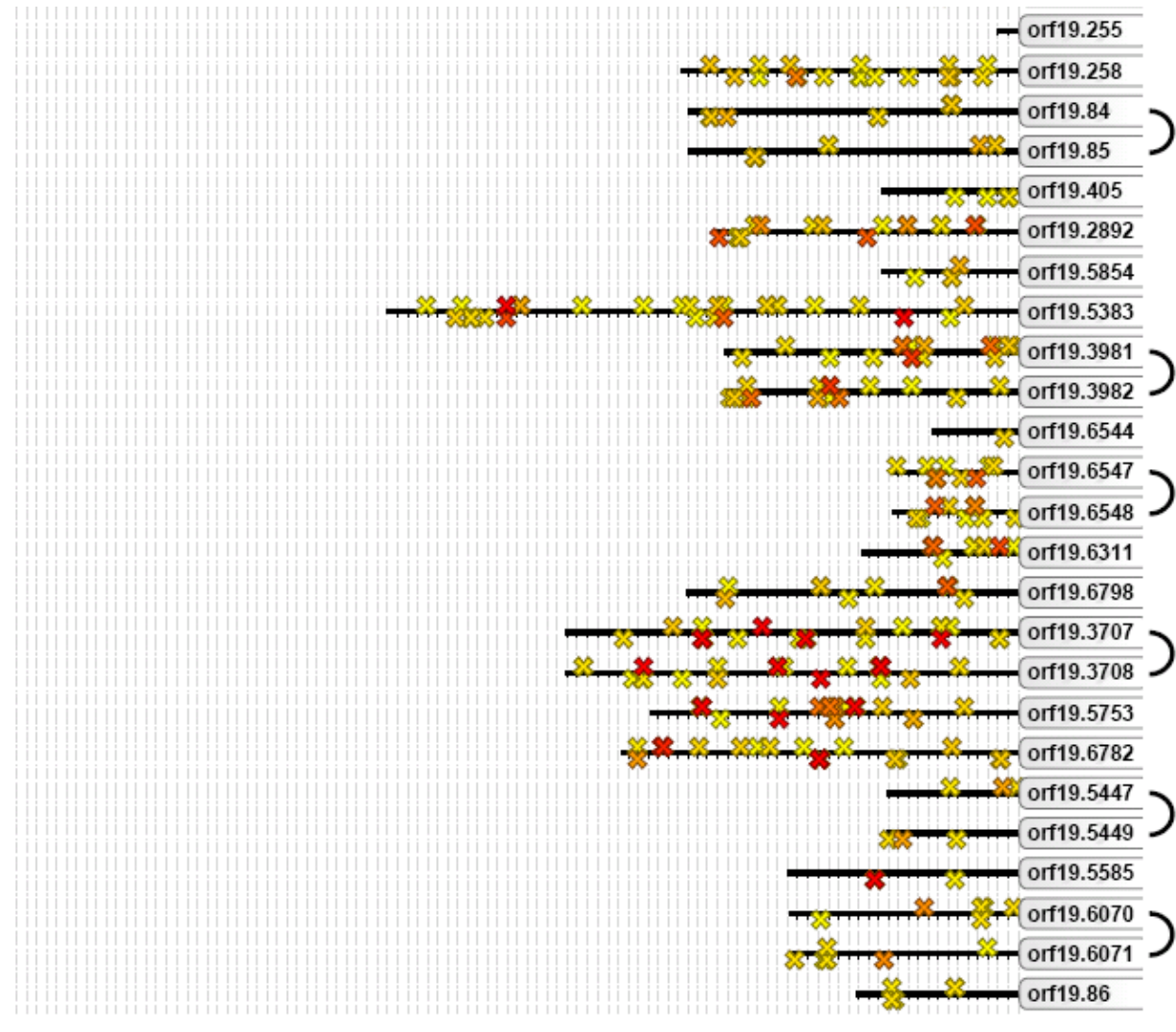








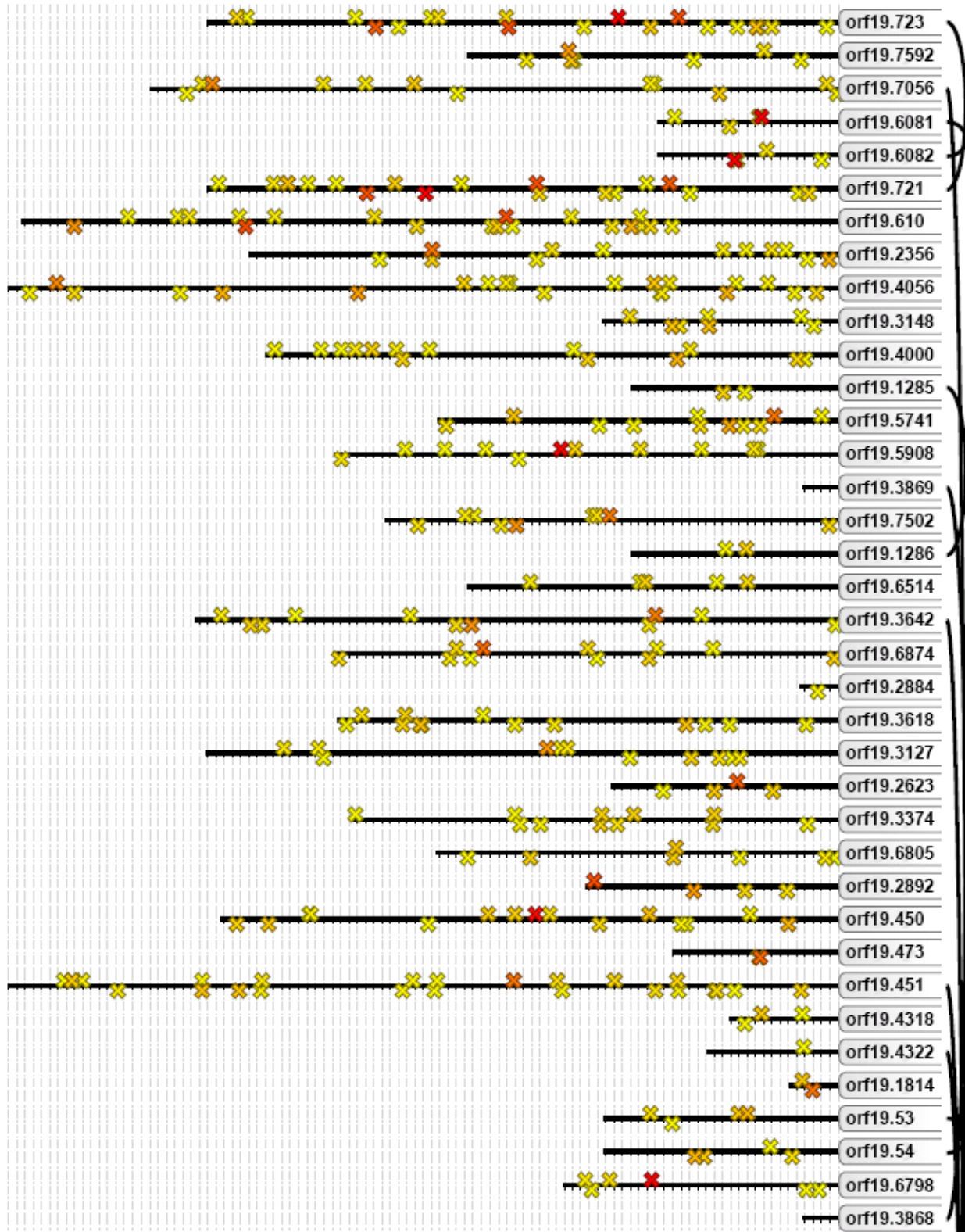


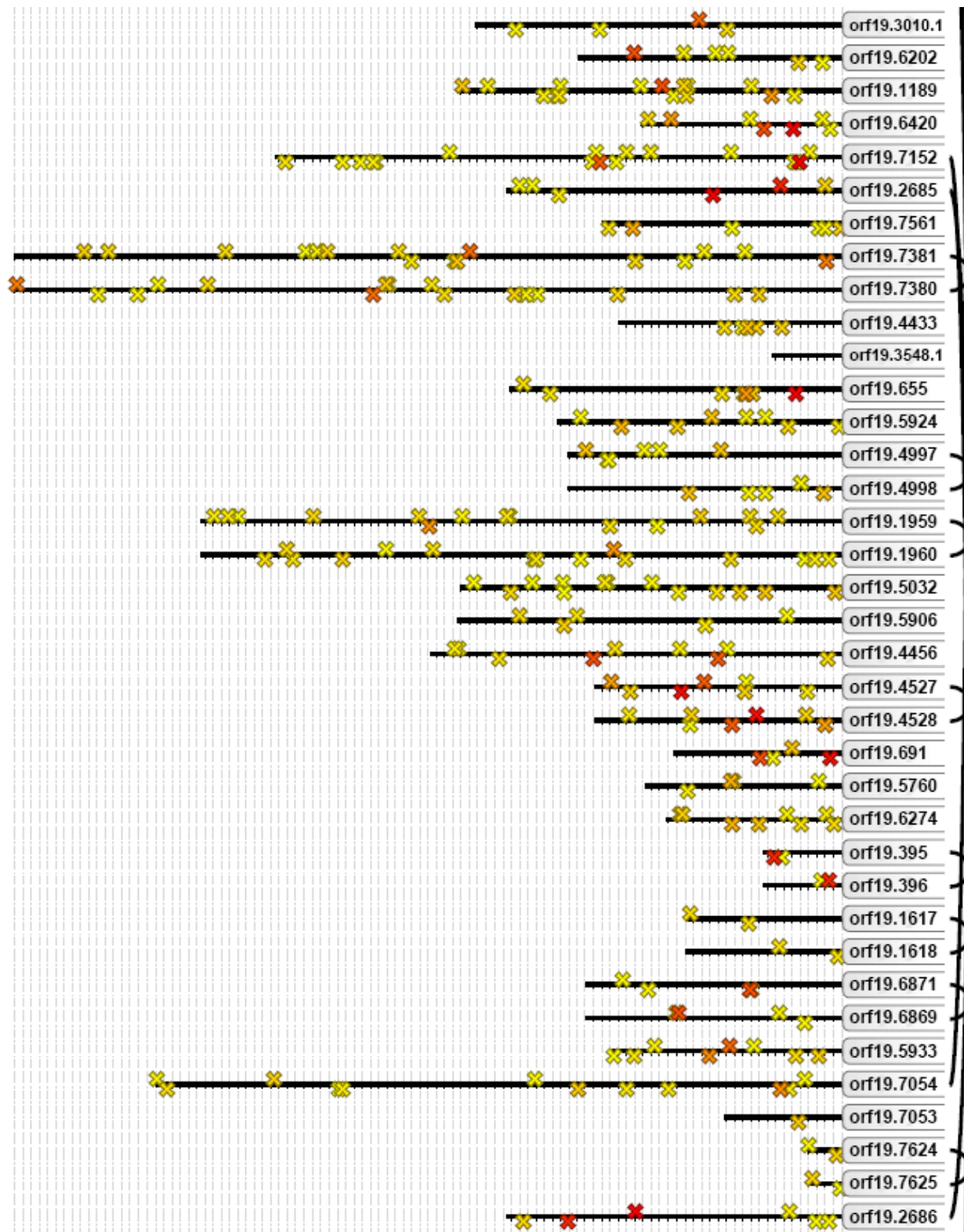


Bcr1 Motif

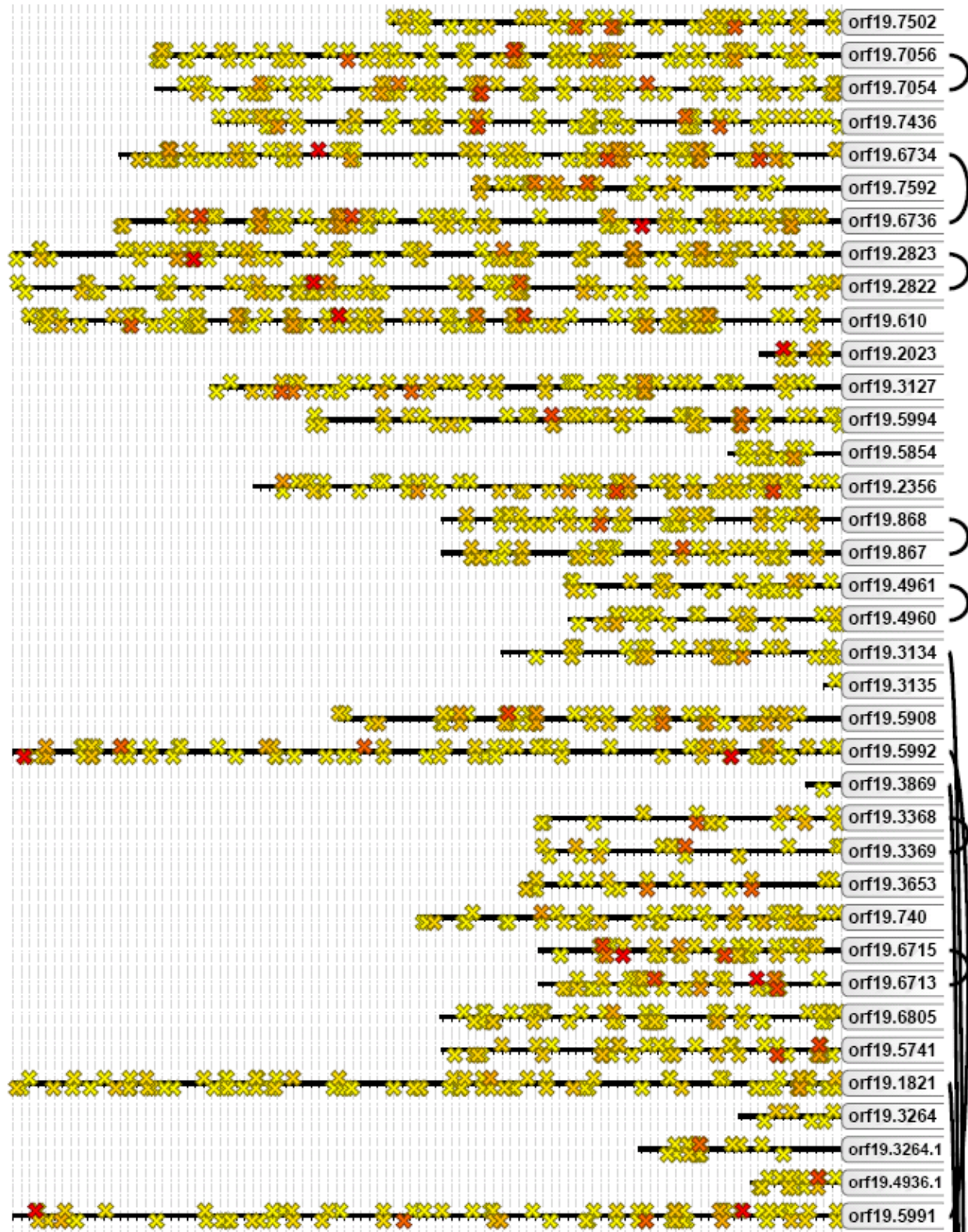


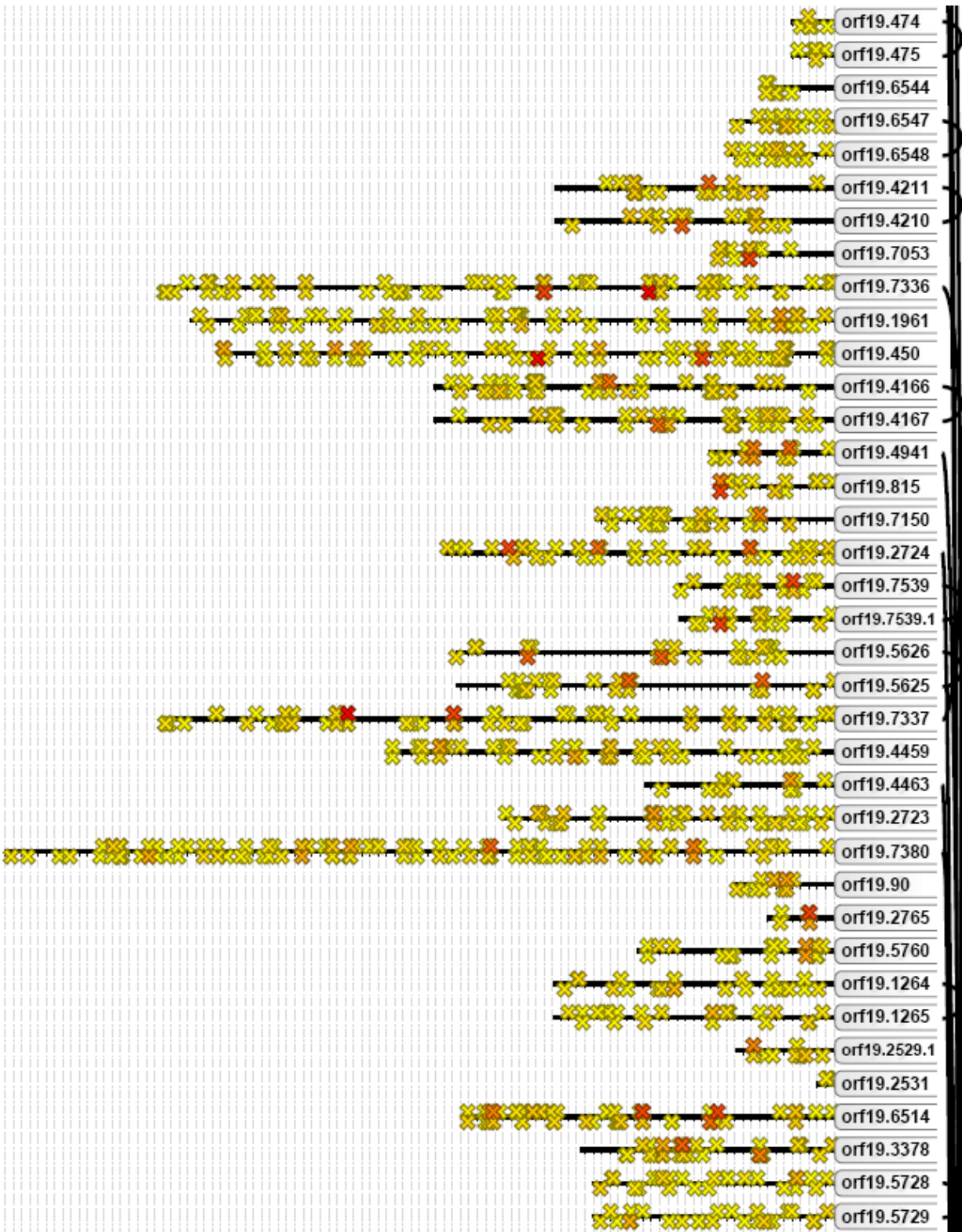
Motif distribution visual summary plots for Tec1 were constructed with MochiView's "compact motif/data/location plot" function using the minimum LOD score cutoffs established from the enrichment plots. A LOD score cutoff of 3 was used for the Tec1 motif. Shown are the upstream promoter regions of the direct targets of Tec1. The motifs for Tec1 are indicated by the colored "x," where the increasing color scale from light yellow to red indicates the minimum to maximum LOD score value.

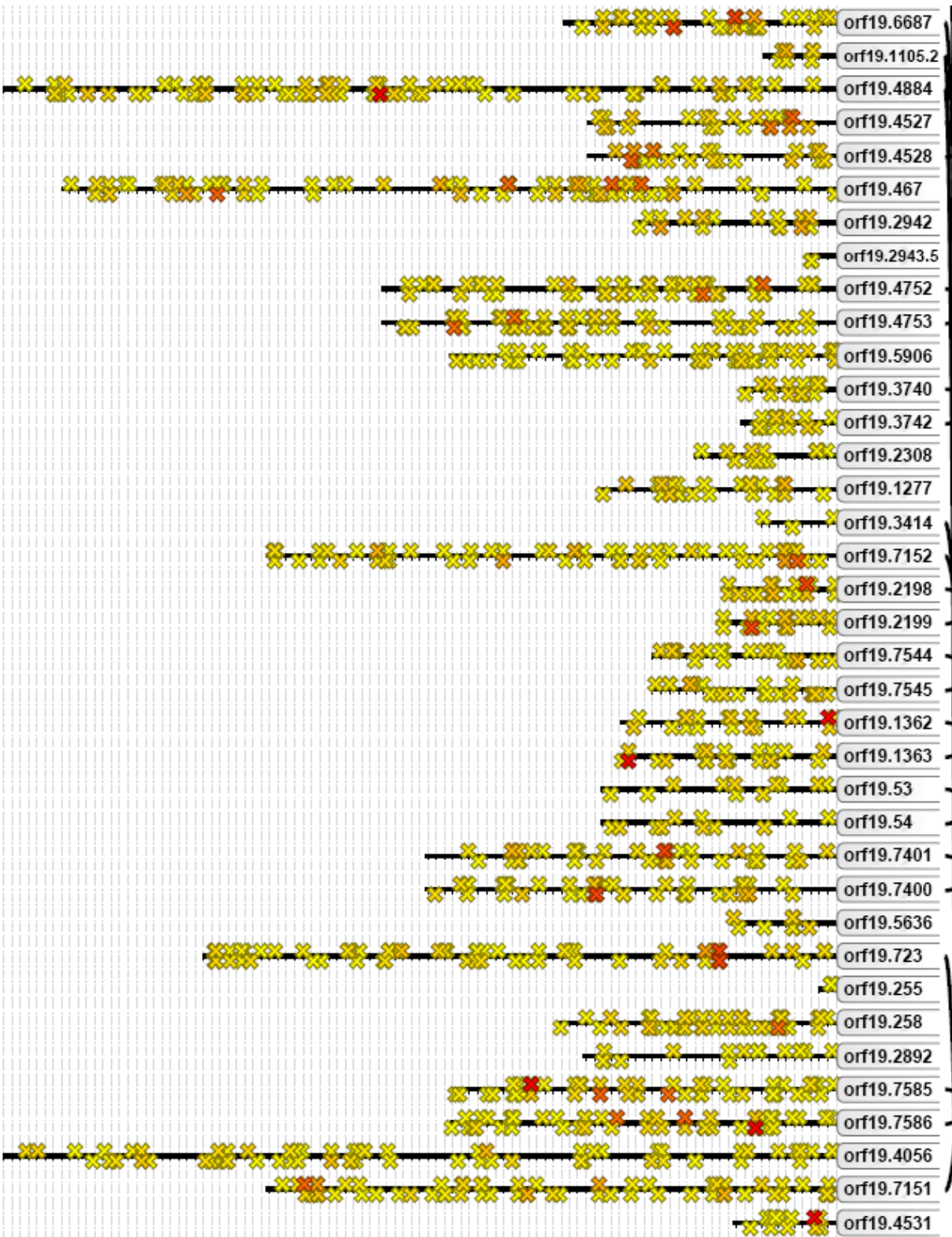


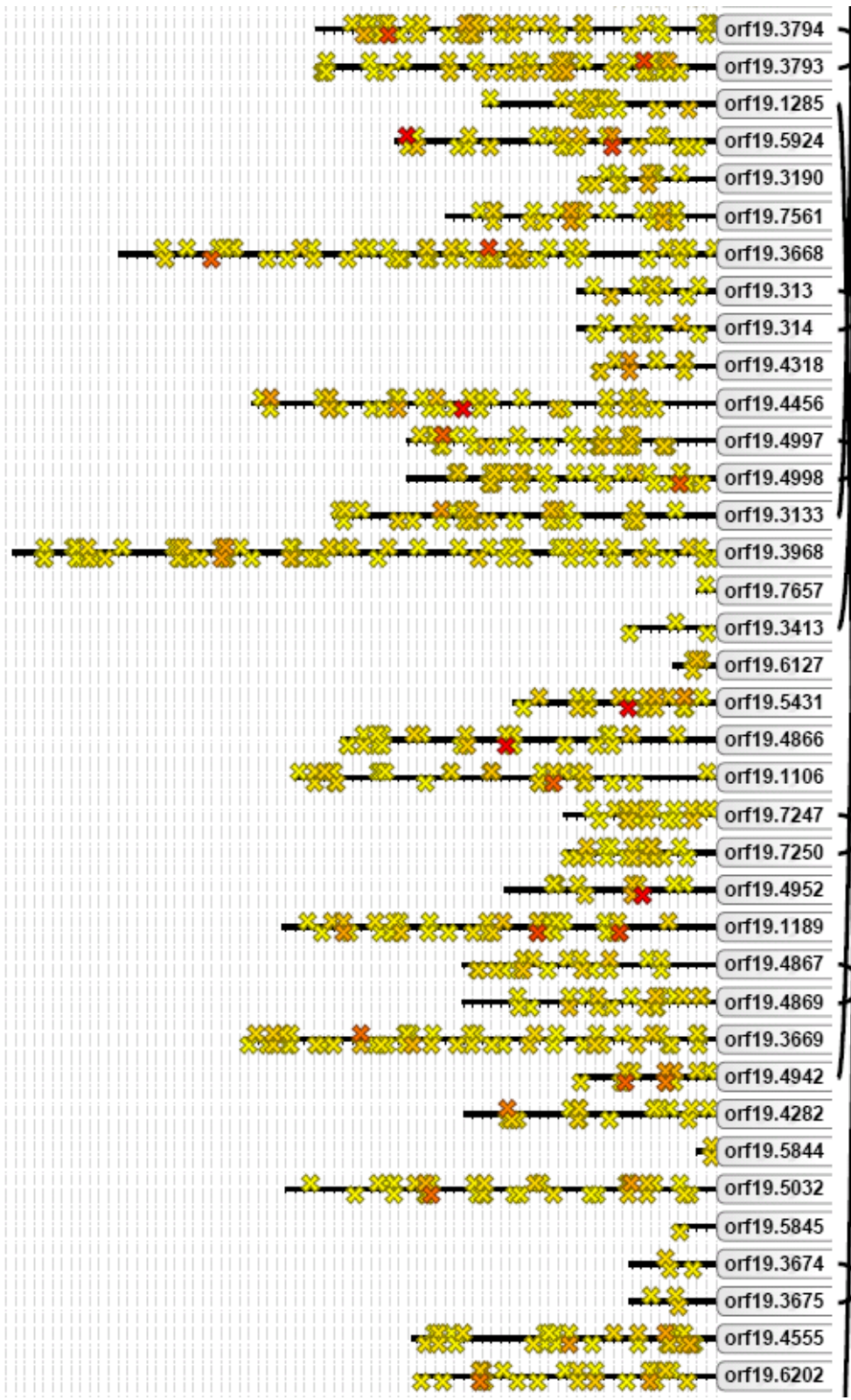


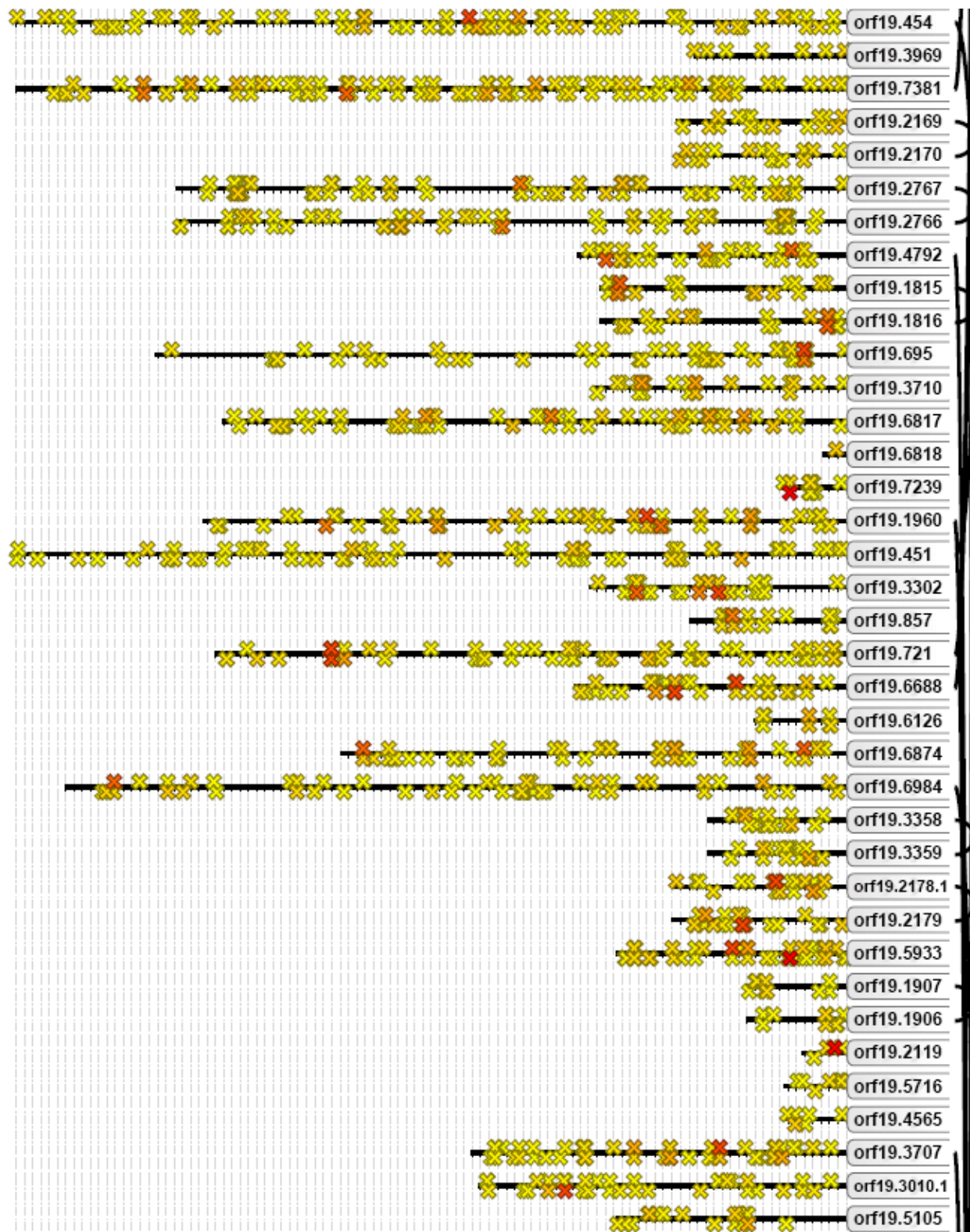
Motif distribution visual summary plots for Efg1 were constructed with MochiView's "compact motif/data/location plot" function using the minimum LOD score cutoffs established from the enrichment plots. A LOD score cutoff of 2.5 was used for the Efg1 motif. Shown are the upstream promoter regions of the direct targets of Efg1. The motifs for Efg1 are indicated by the colored "x," where the increasing color scale from light yellow to red indicates the minimum to maximum LOD score value.

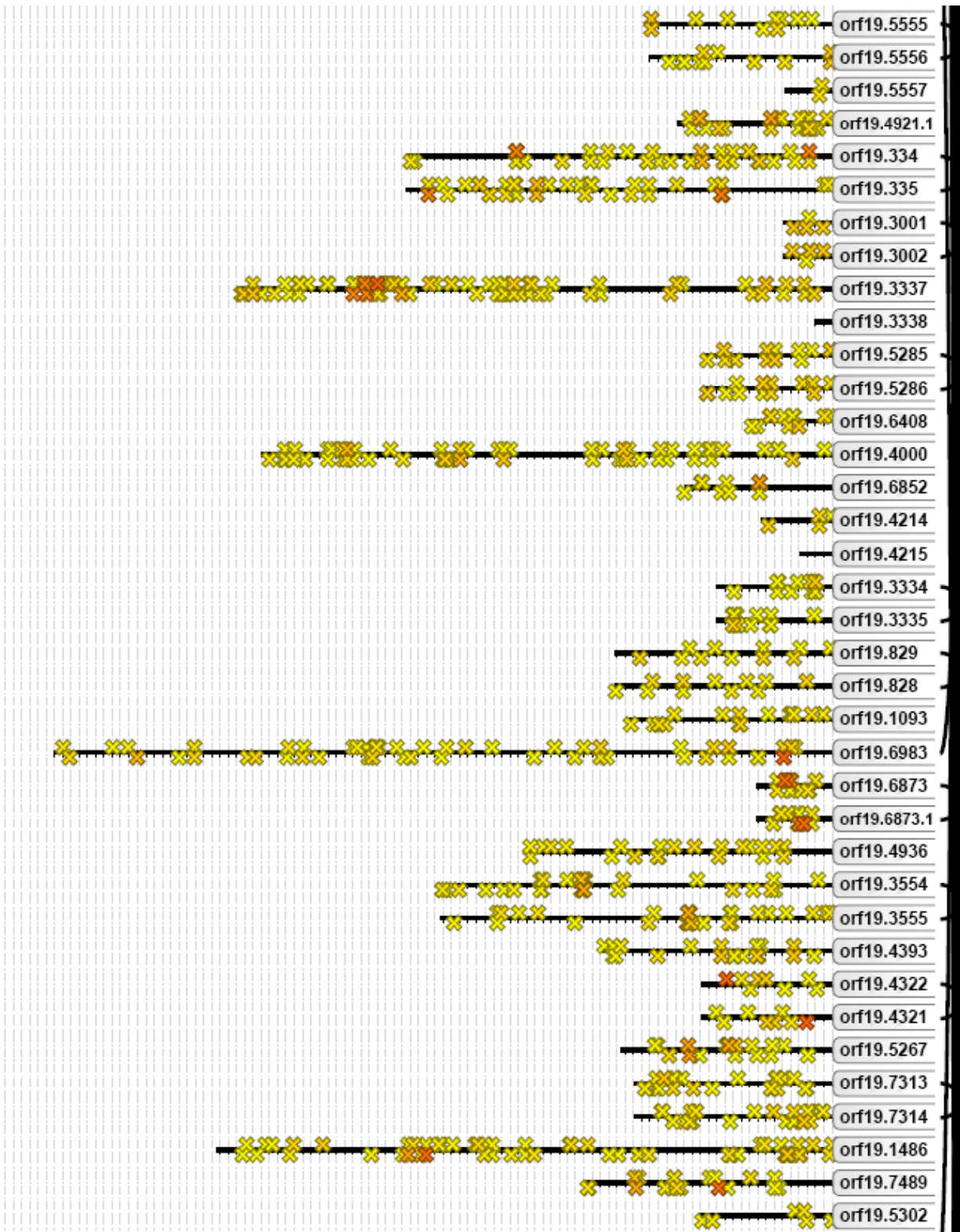


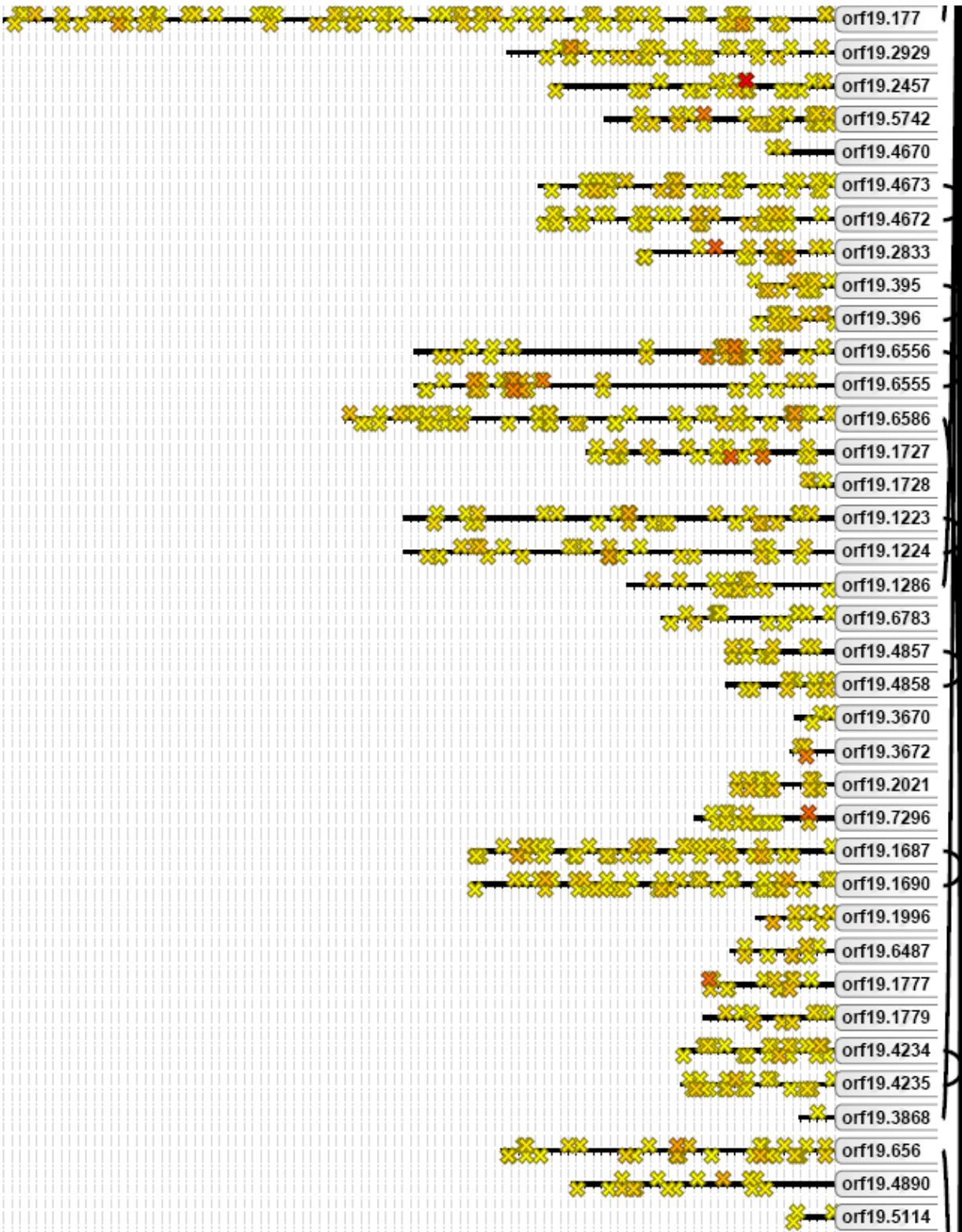


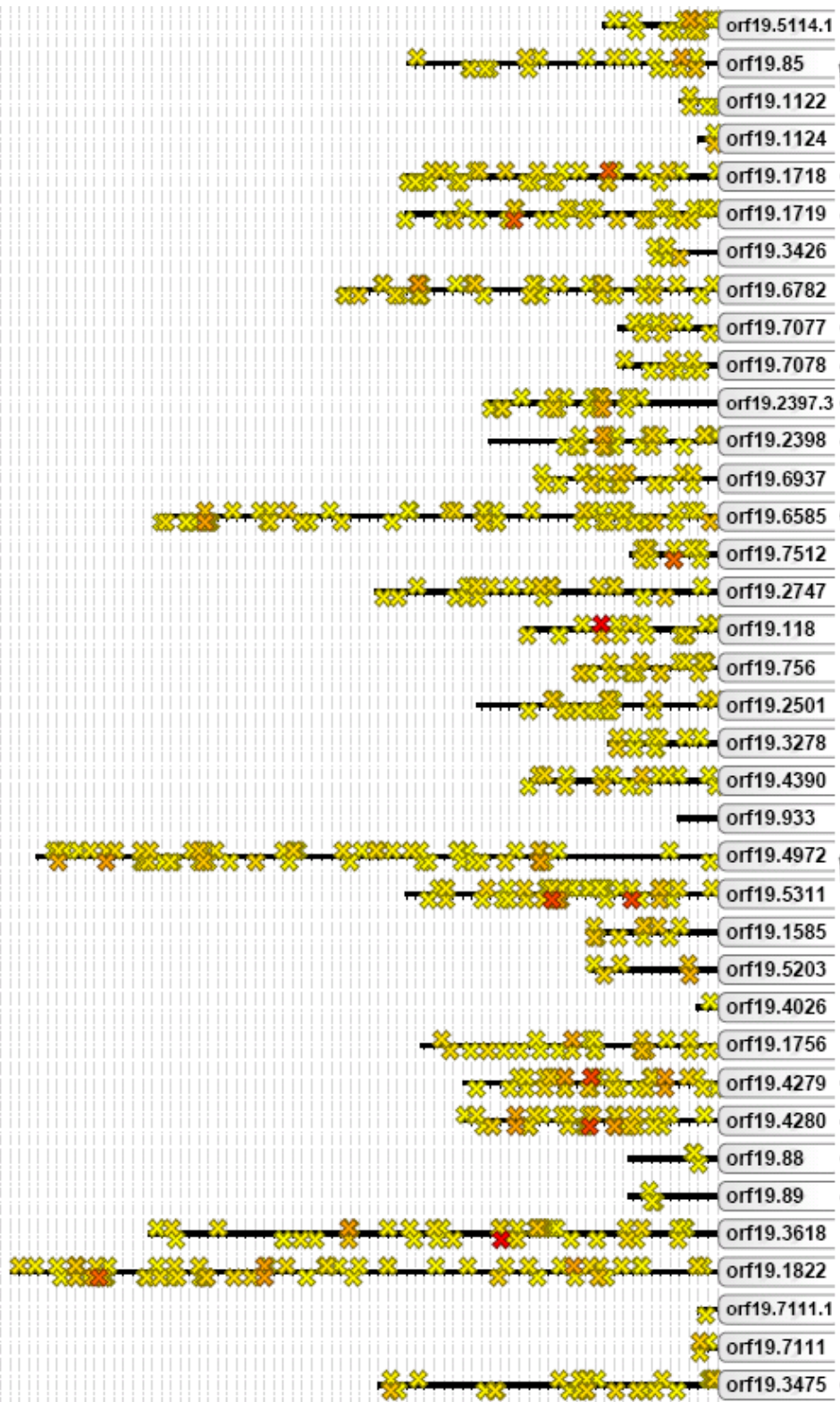


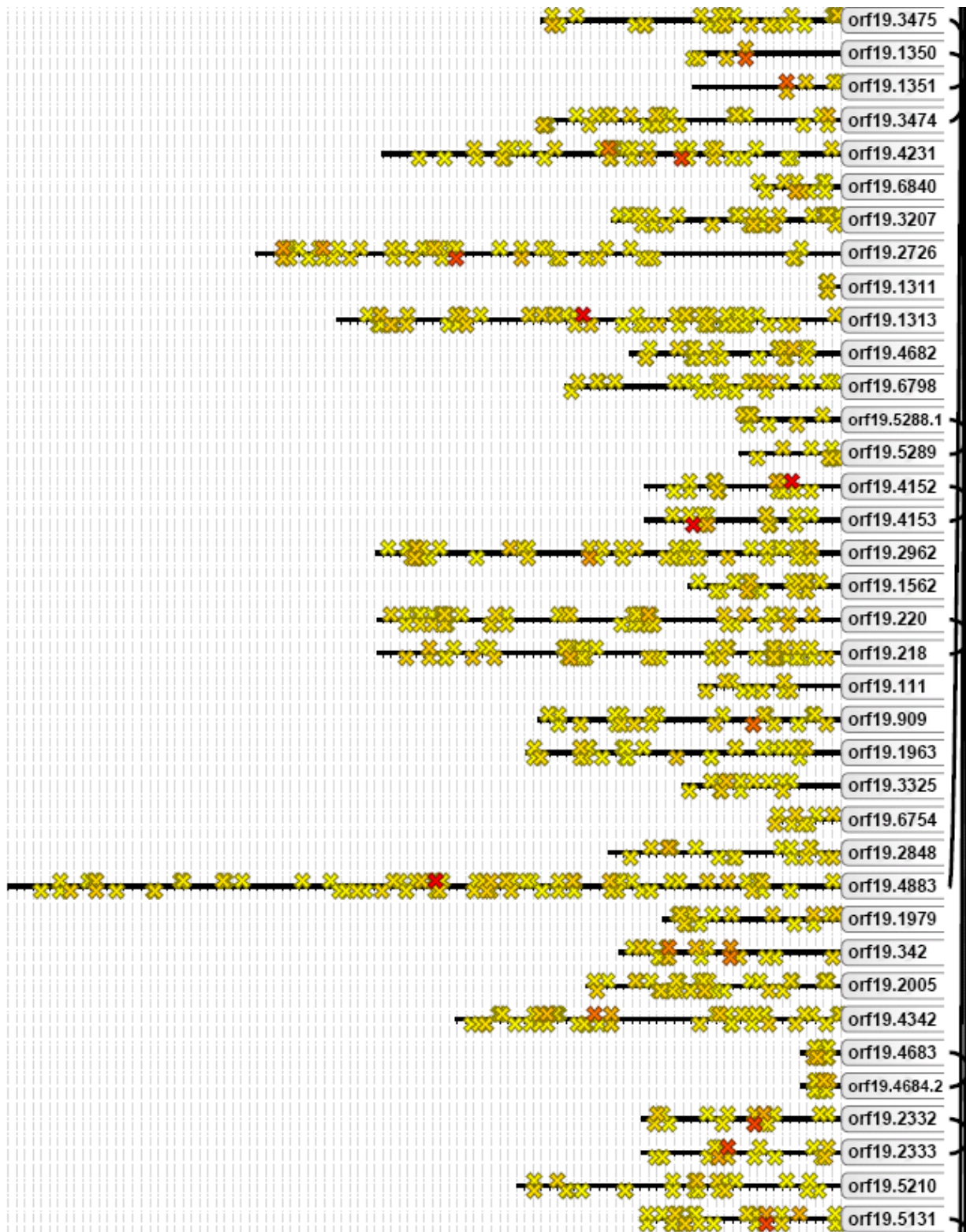


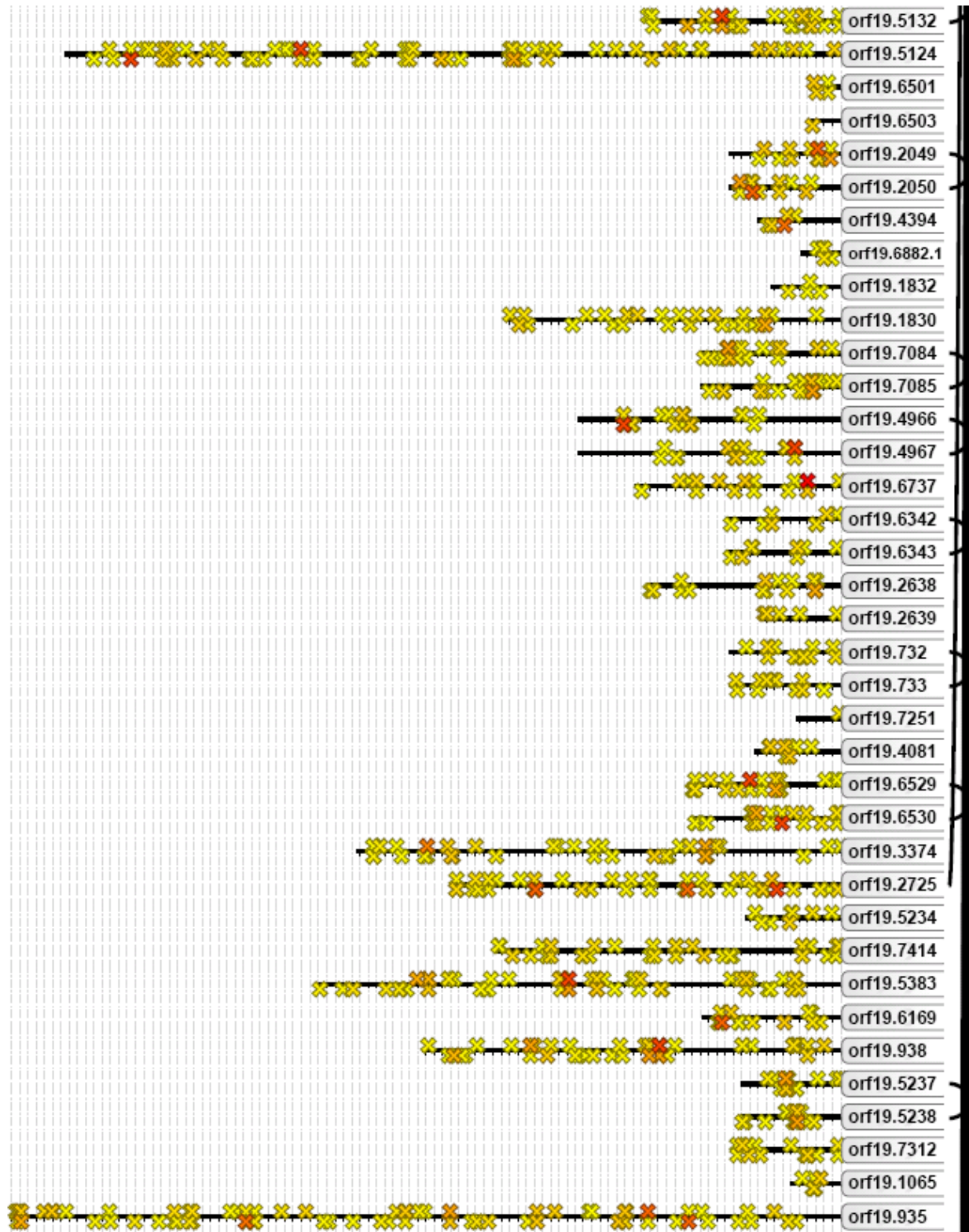


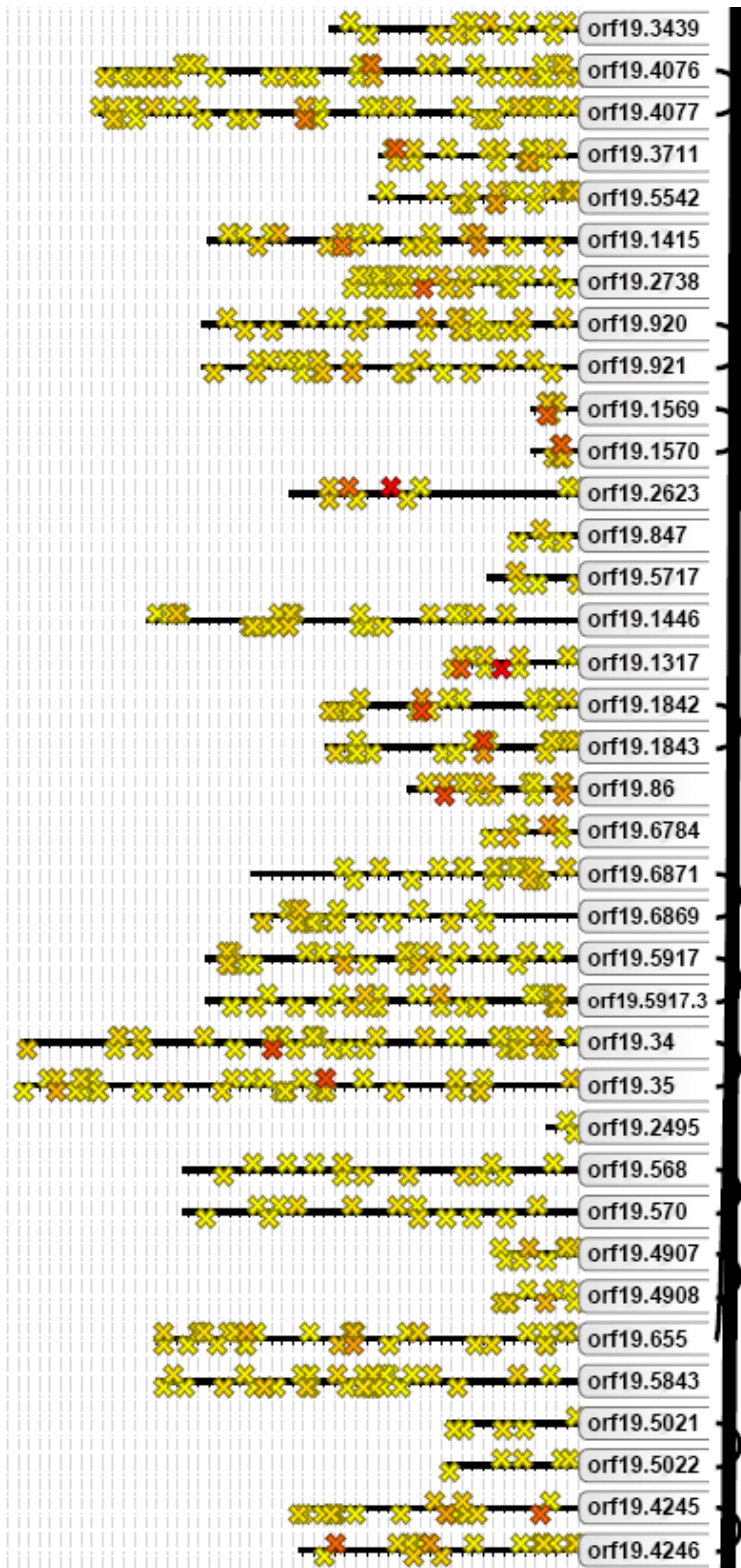


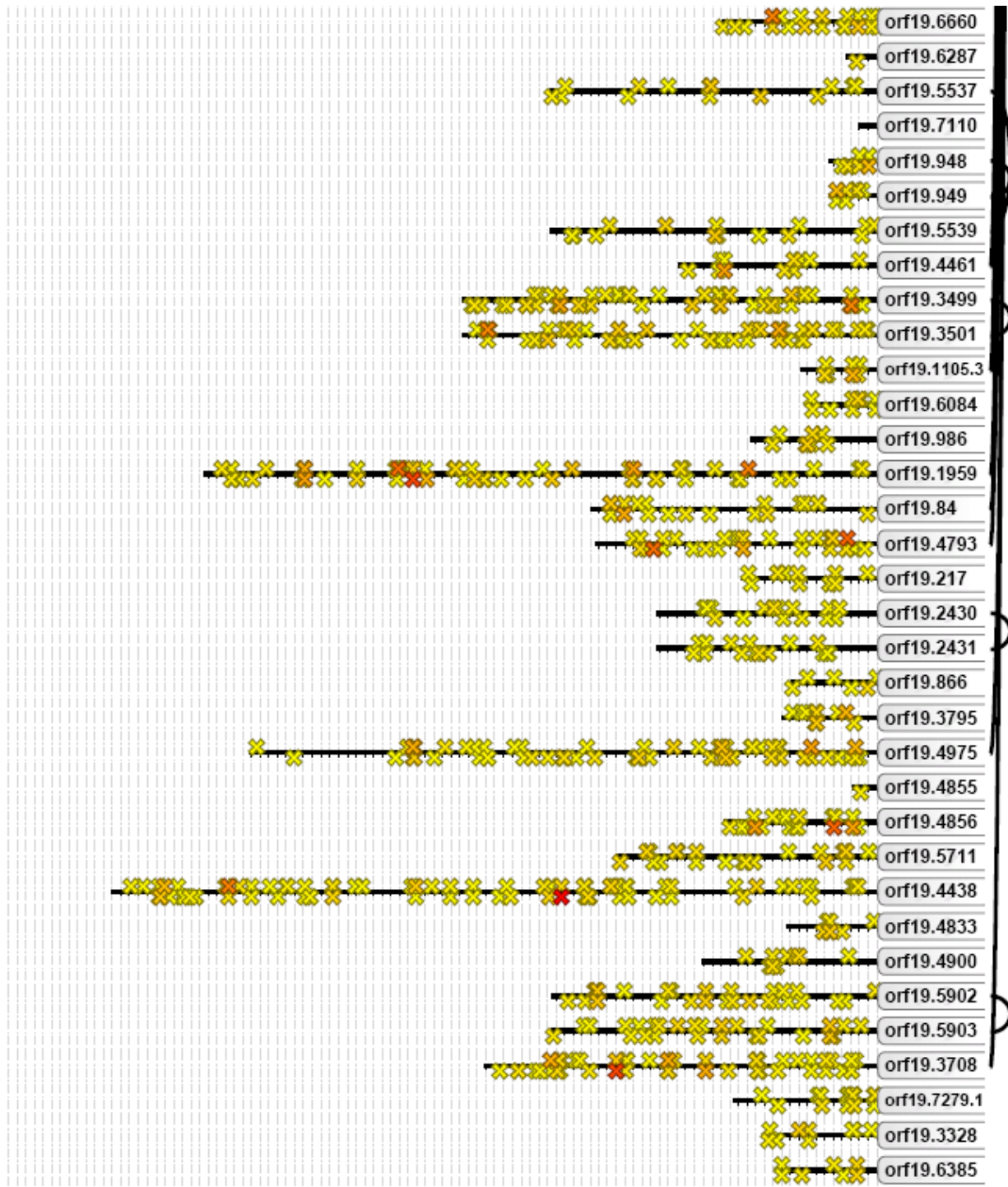










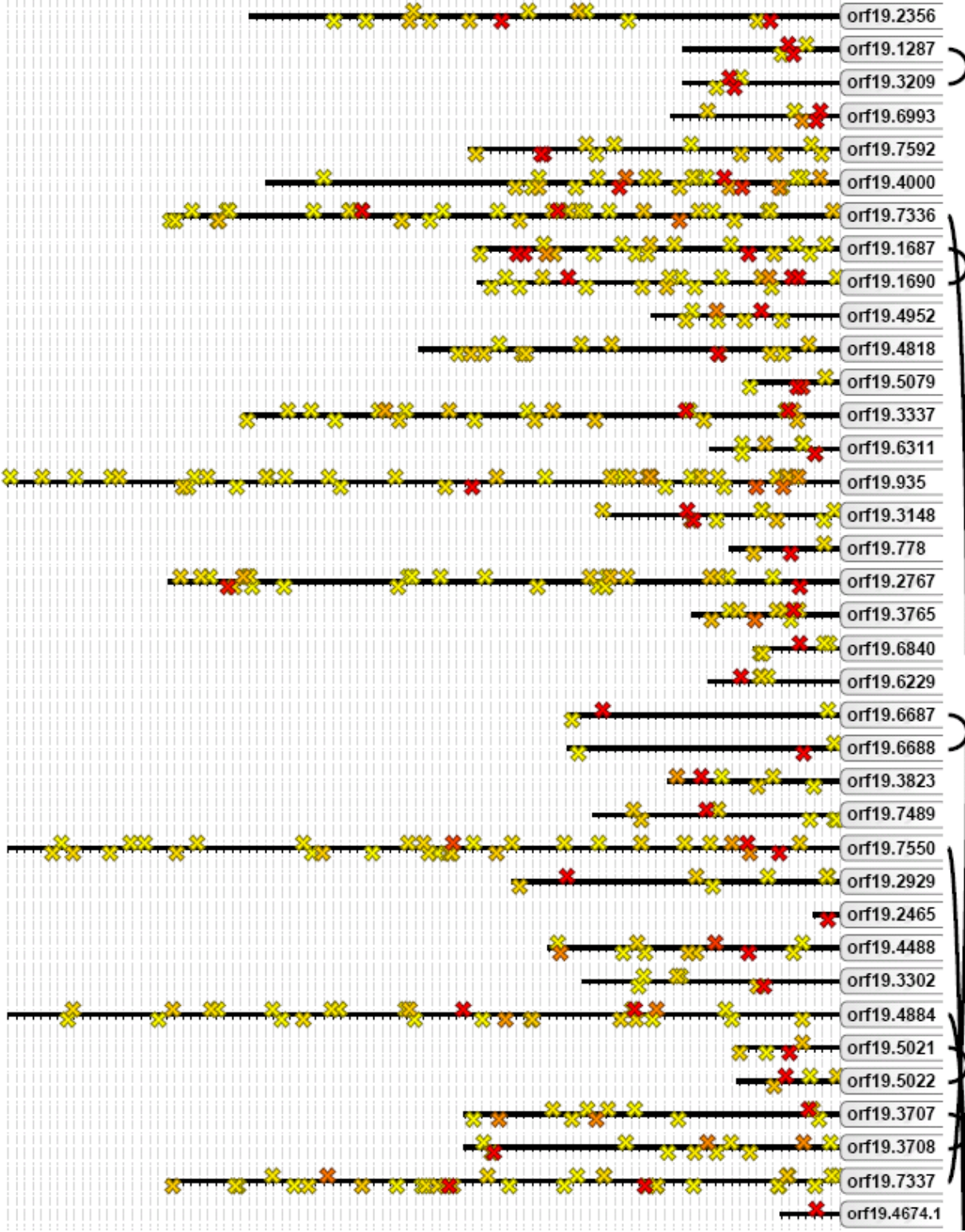


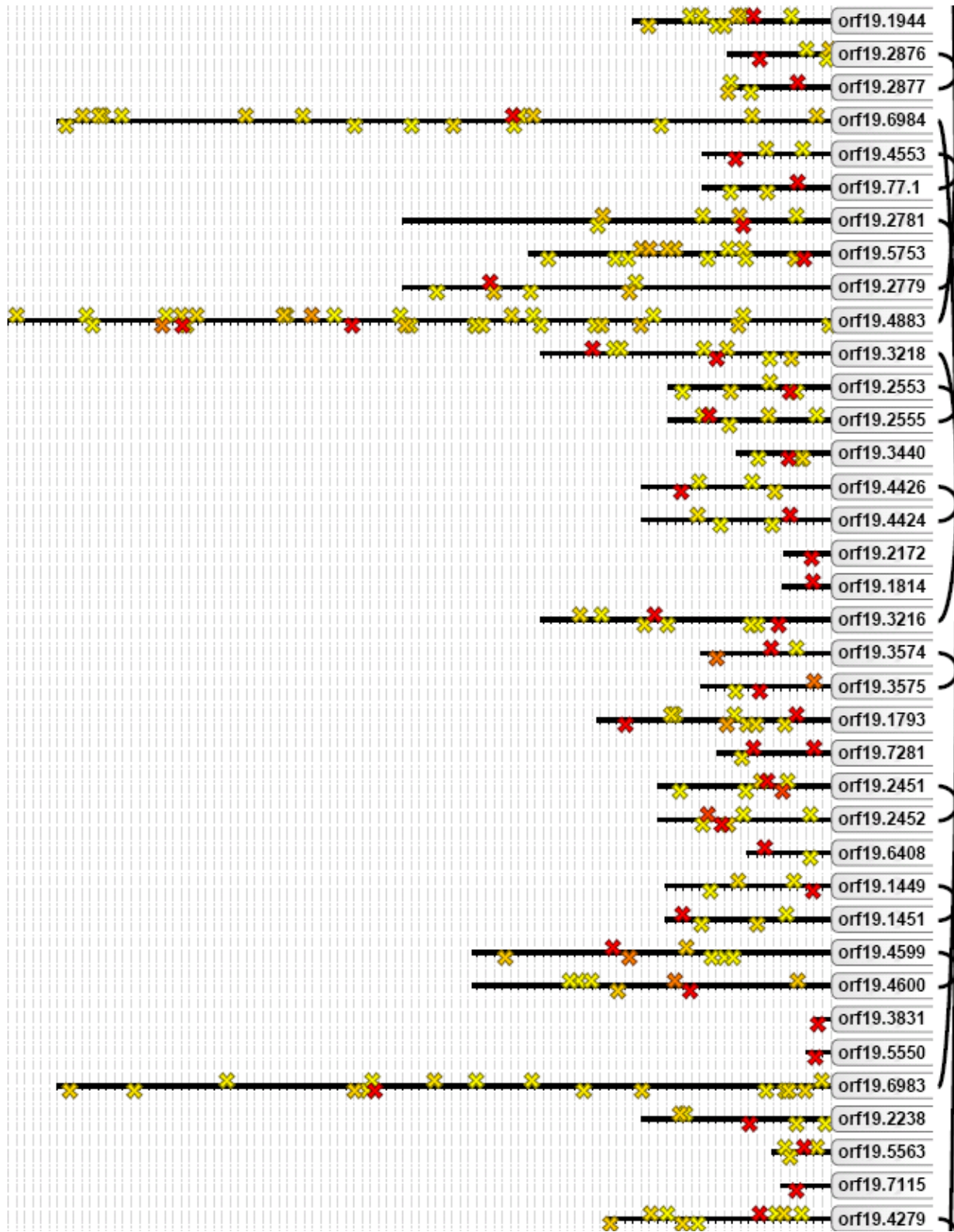
10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000

Efg1 Motif

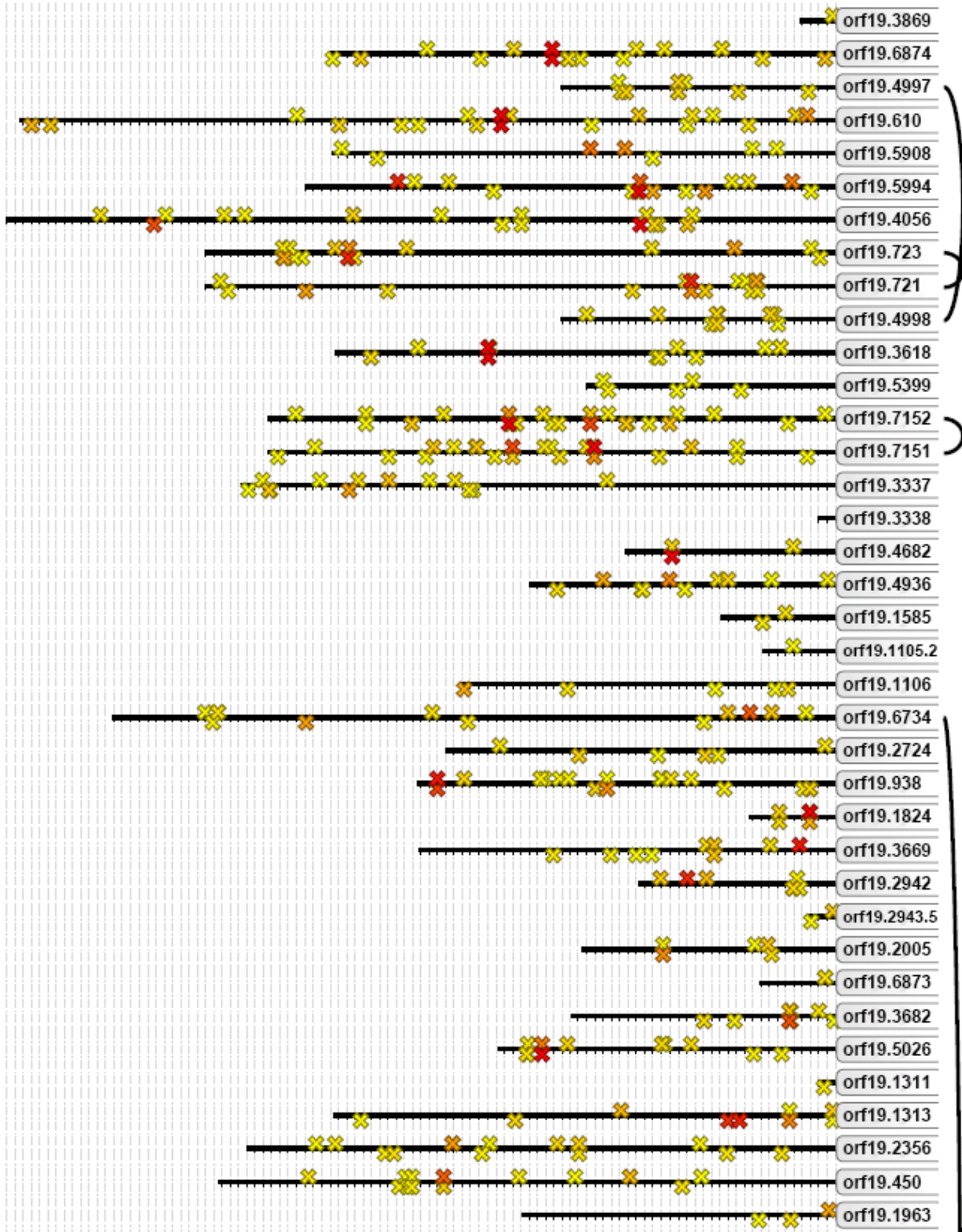


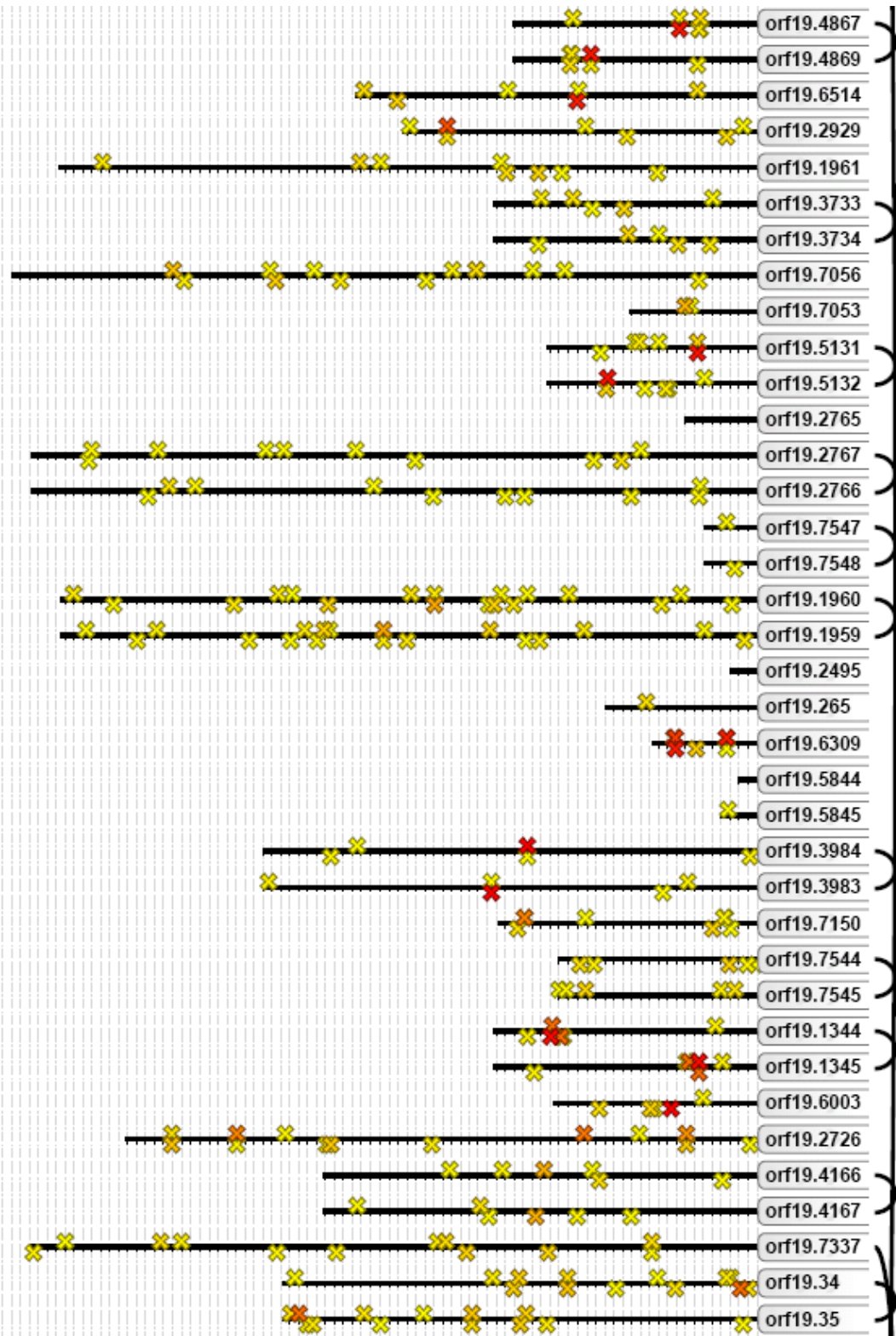
Motif distribution visual summary plots for Ndt80 were constructed with MochiView's "compact motif/data/location plot" function using the minimum LOD score cutoffs established from the enrichment plots. A LOD score cutoff of 3 was used for the Ndt80 motif. Shown are the upstream promoter regions of the direct targets of Ndt80. The motifs for Ndt80 are indicated by the colored "x," where the increasing color scale from light yellow to red indicates the minimum to maximum LOD score value.

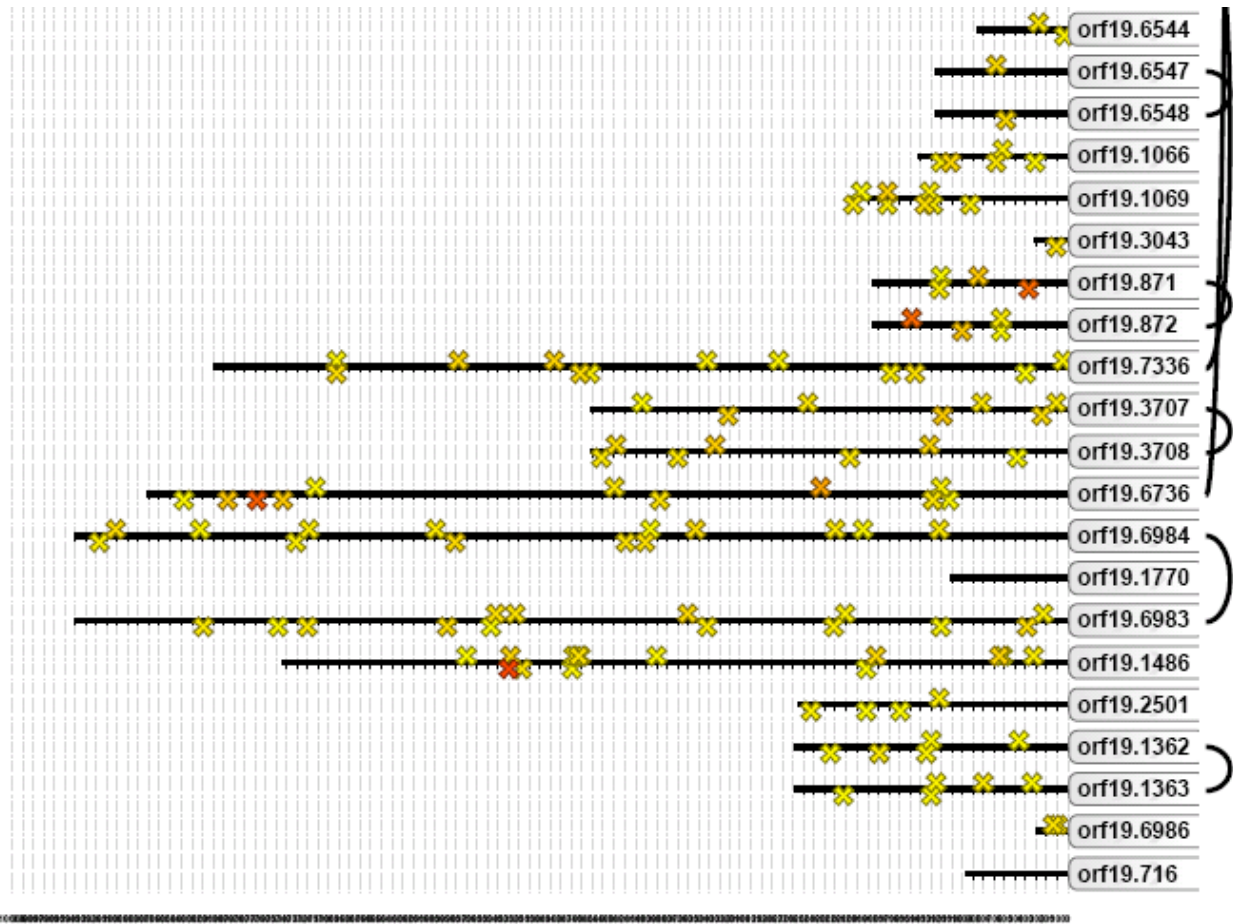




Motif distribution visual summary plots for Rob1 were constructed with MochiView's "compact motif/data/location plot" function using the minimum LOD score cutoffs established from the enrichment plots. A LOD score cutoff of 3 was used for the Rob1 motif. Shown are the upstream promoter regions of the direct targets of Rob1. The motifs for Rob1 are indicated by the colored "x," where the increasing color scale from light yellow to red indicates the minimum to maximum LOD score value.







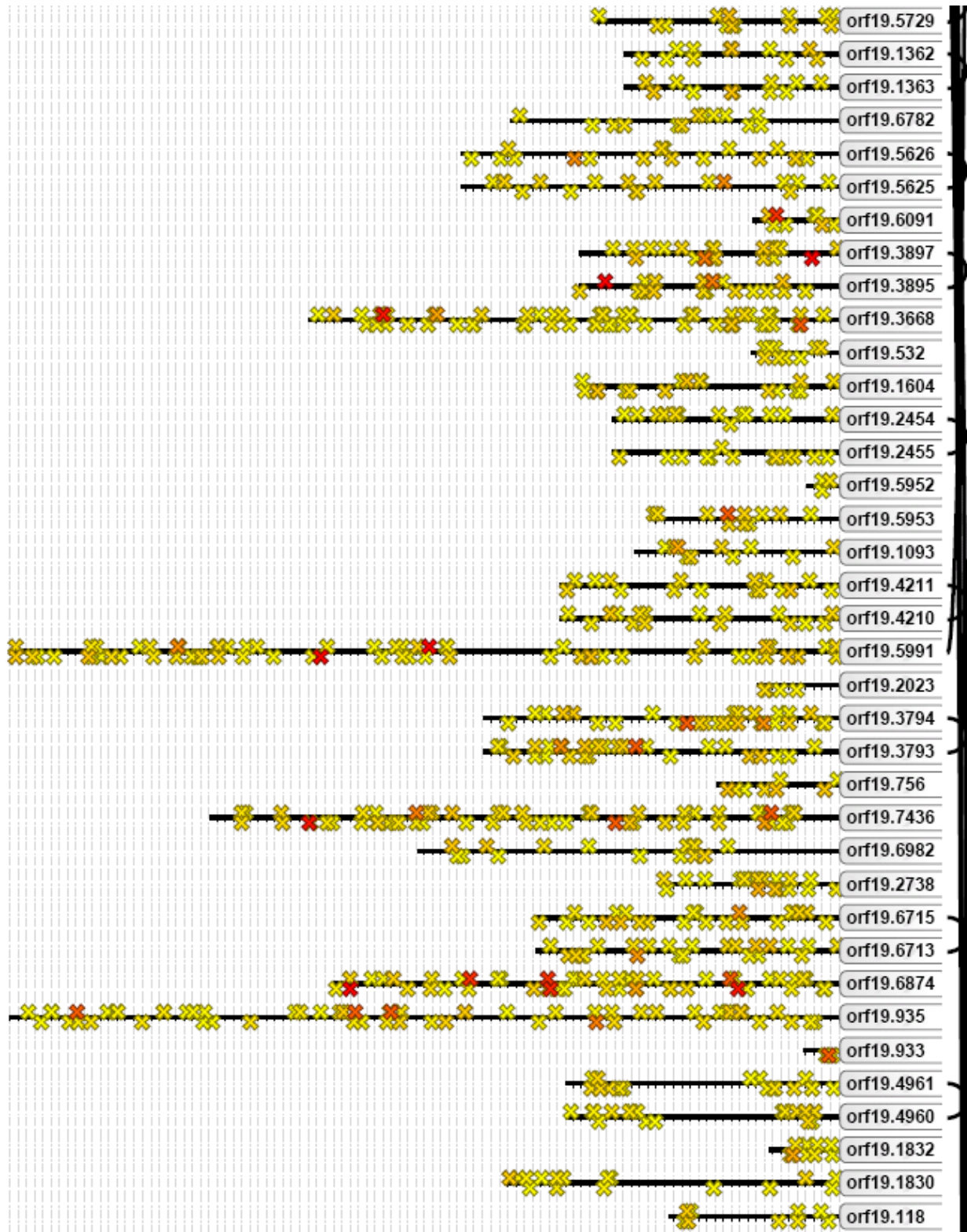
Rob1 Motif

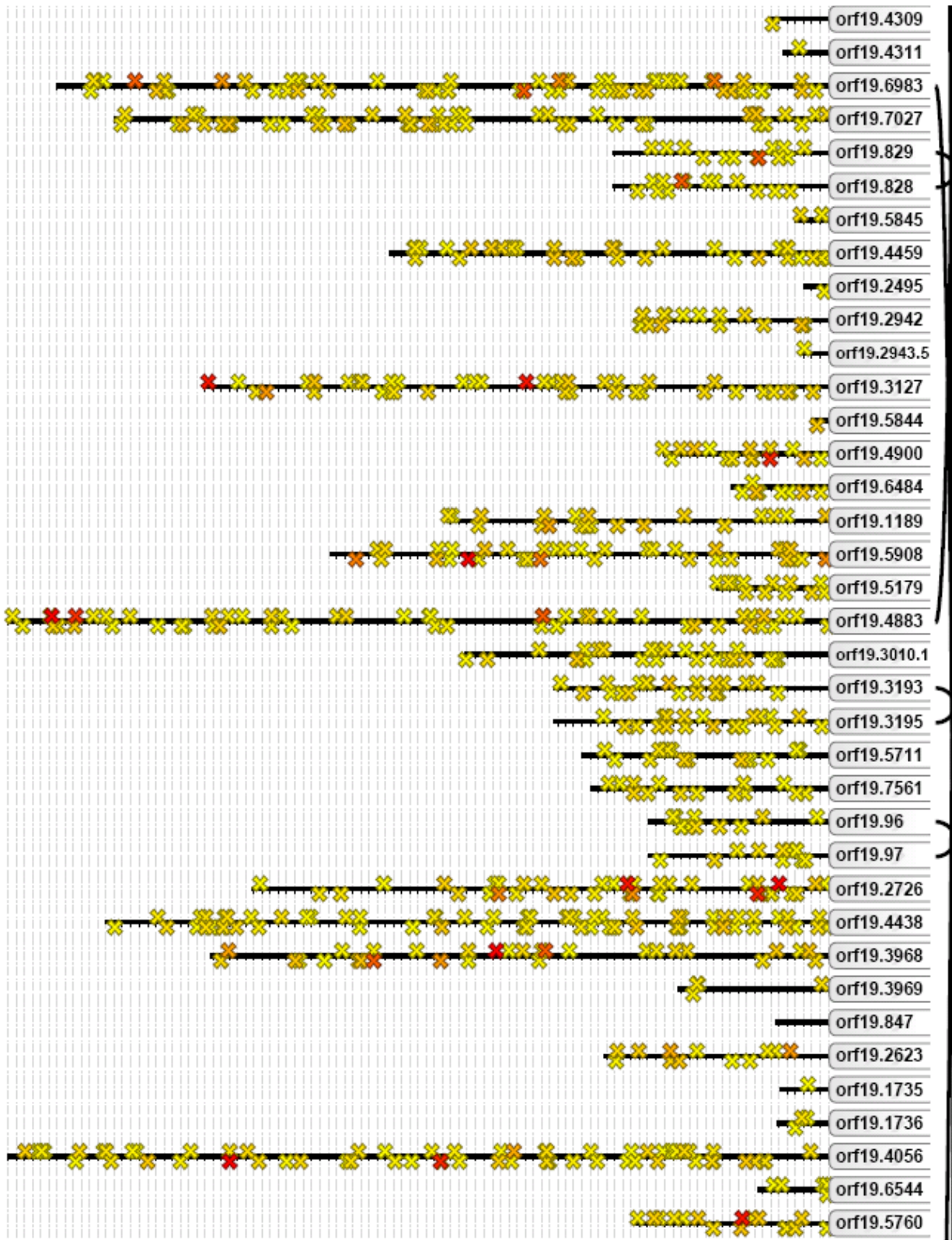


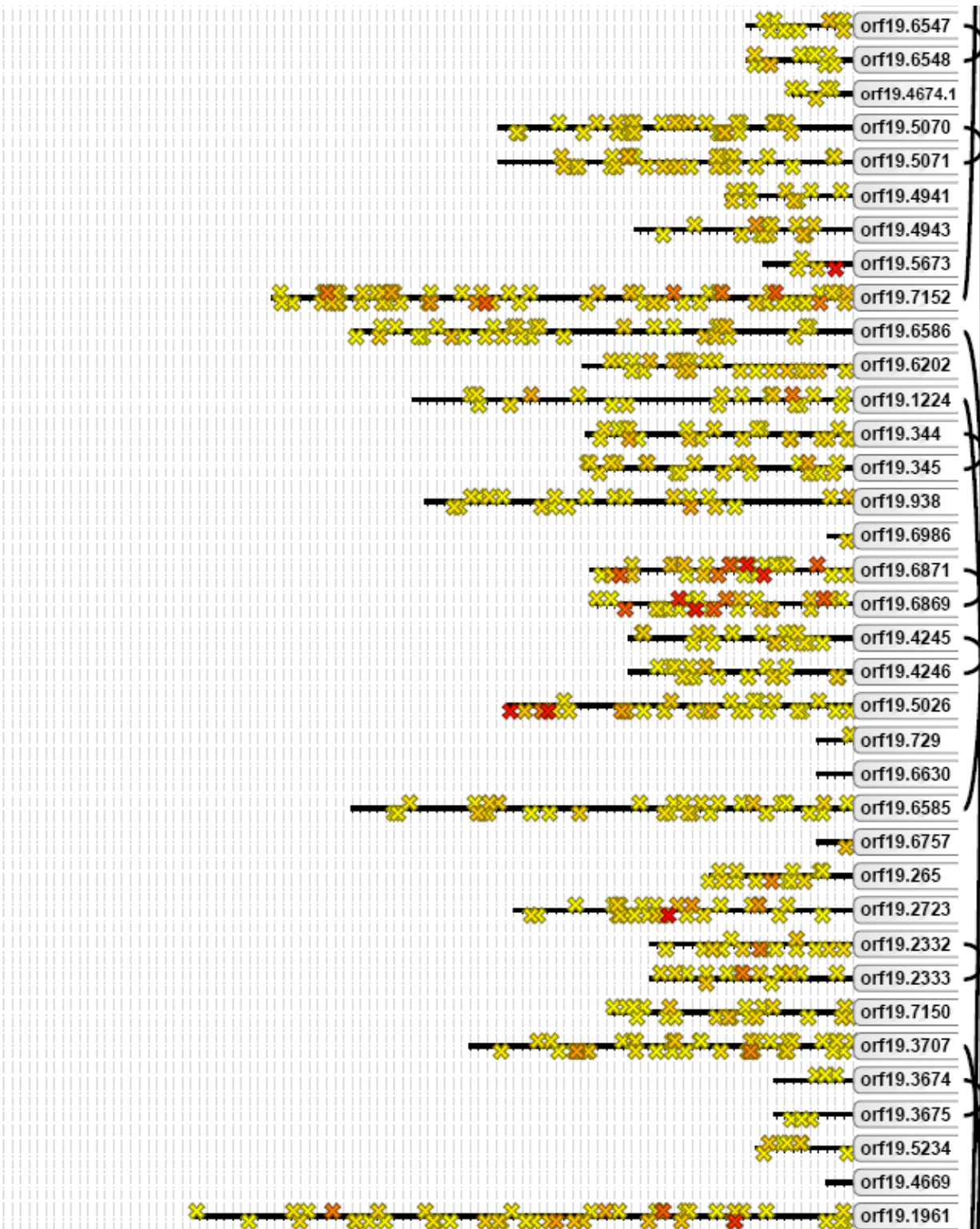
Motif distribution visual summary plots for Brg1 were constructed with MochiView's "compact motif/data/location plot" function using the minimum LOD score cutoffs established from the enrichment plots. A LOD score cutoff of 2.5 was used for the Brg1 motif. Shown are the upstream promoter regions of the direct targets of Brg1. The motifs for Brg1 are indicated by the colored "x," where the increasing color scale from light yellow to red indicates the minimum to maximum LOD score value.

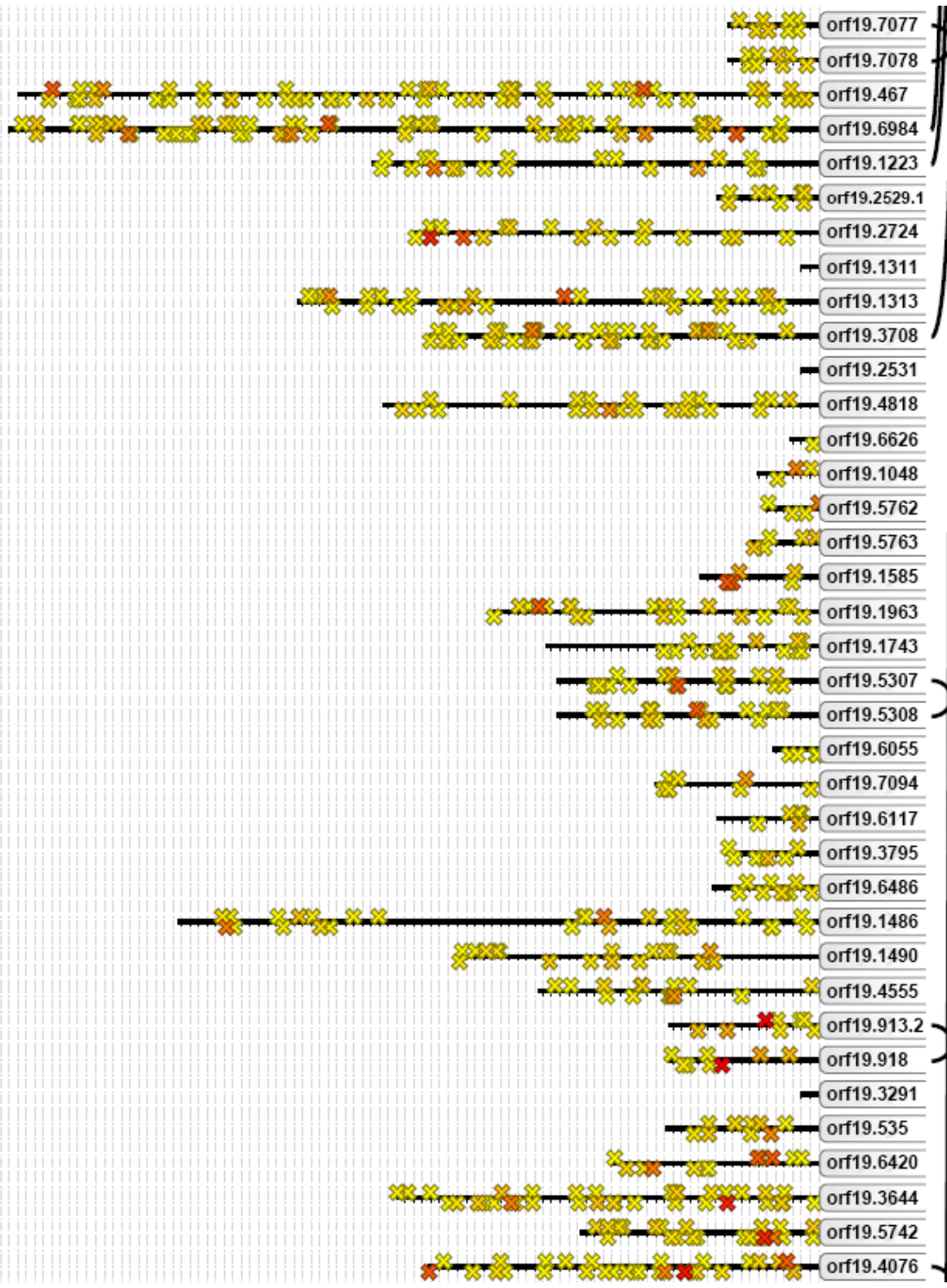


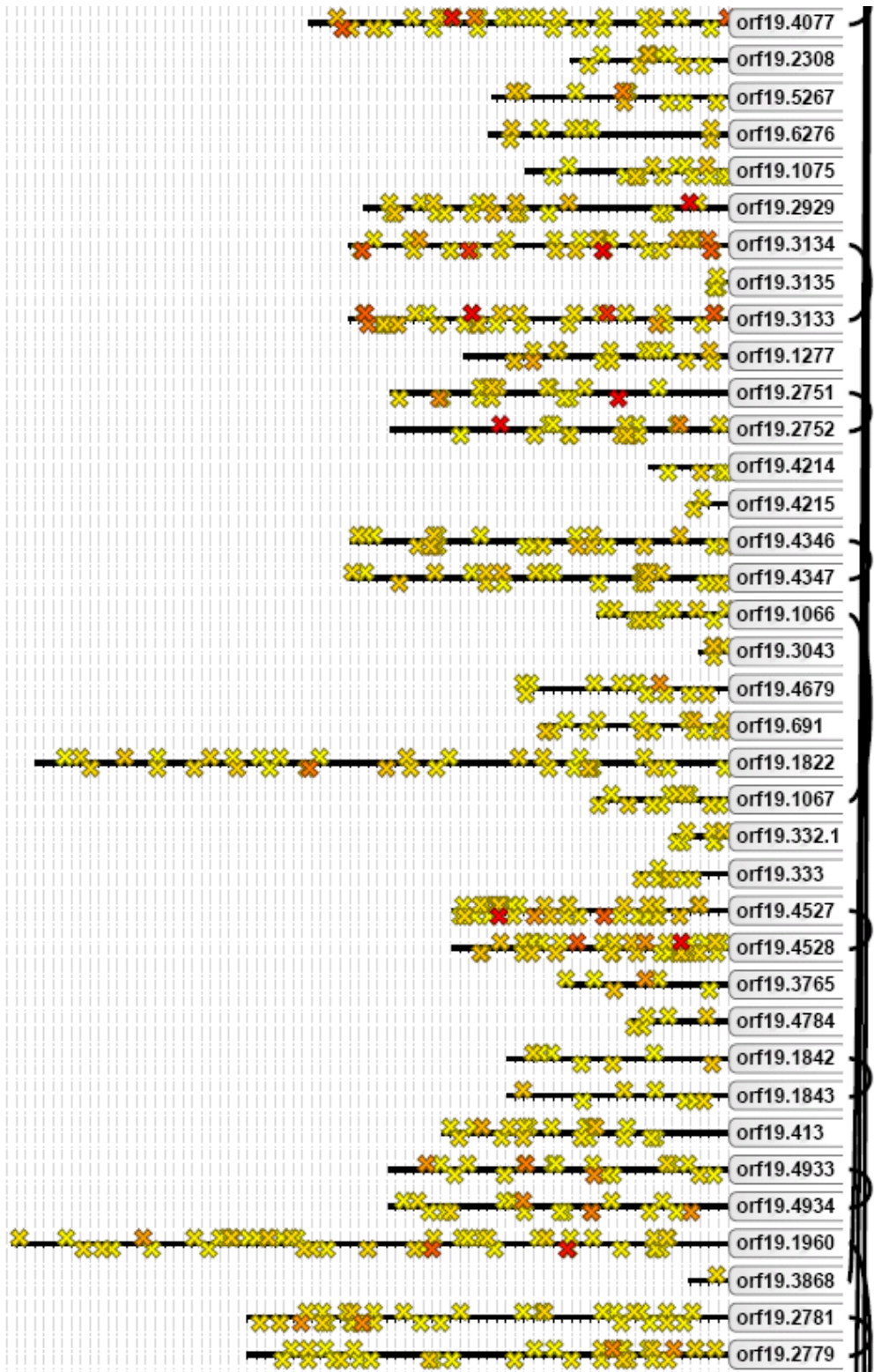


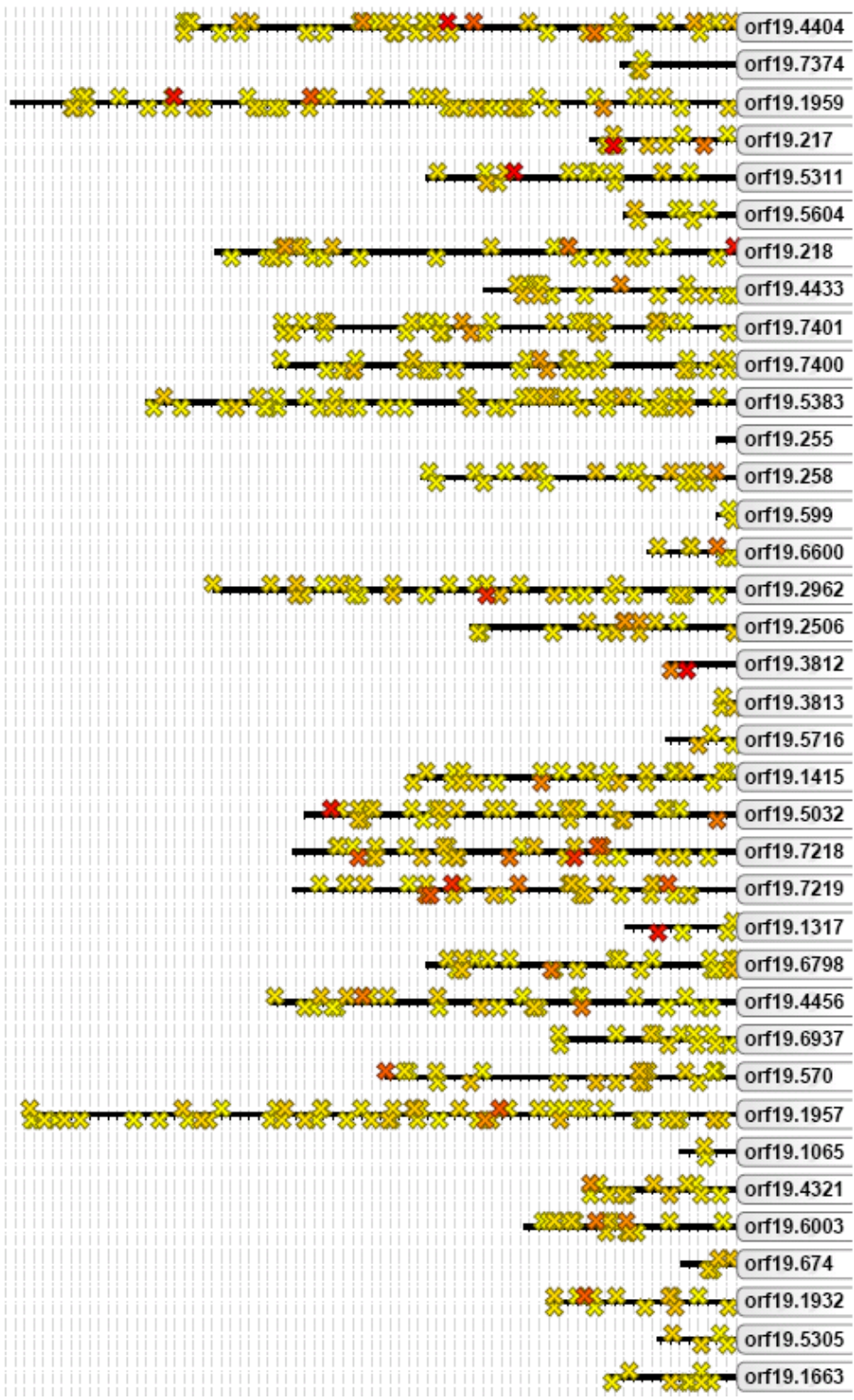


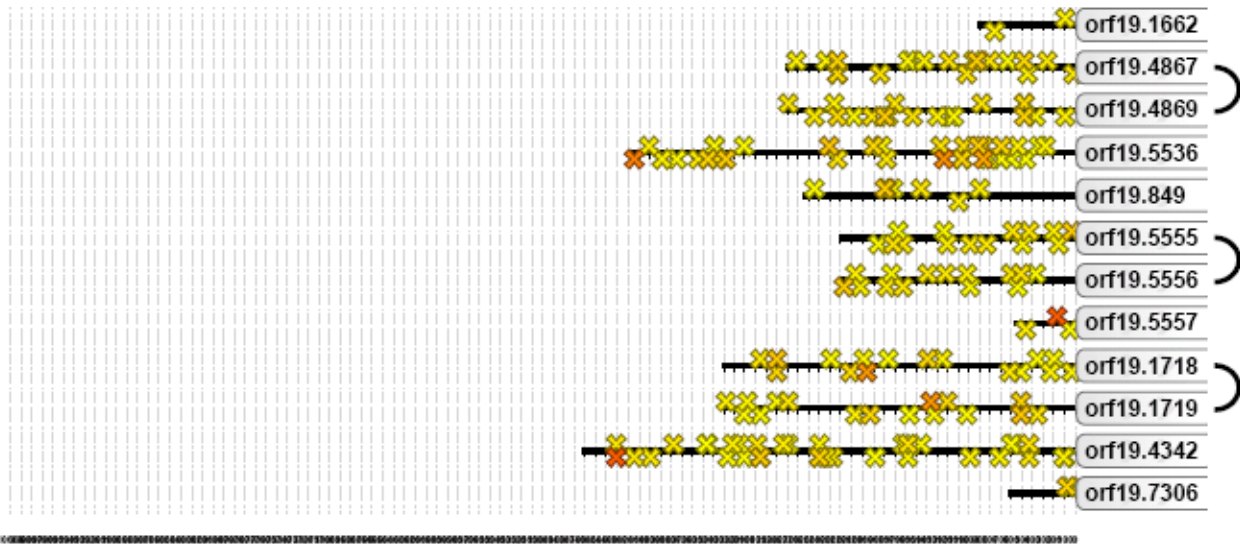












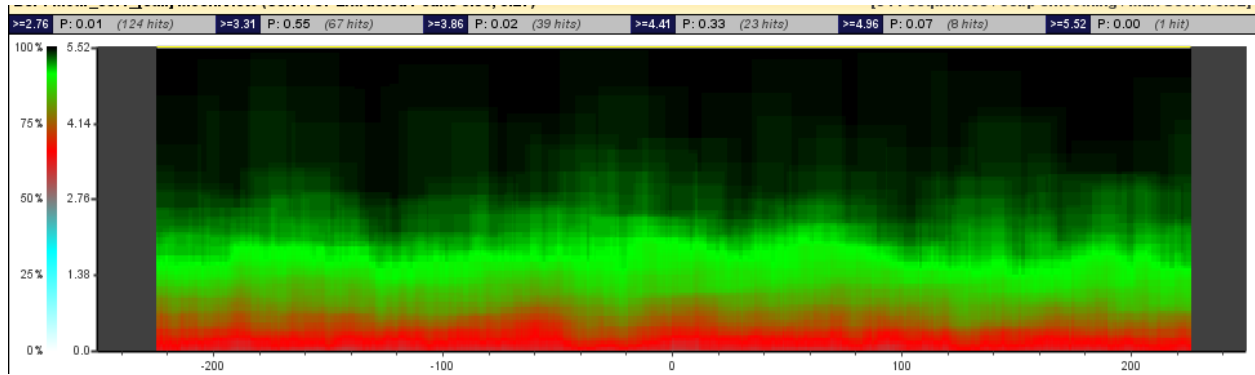
Brg1 Motif



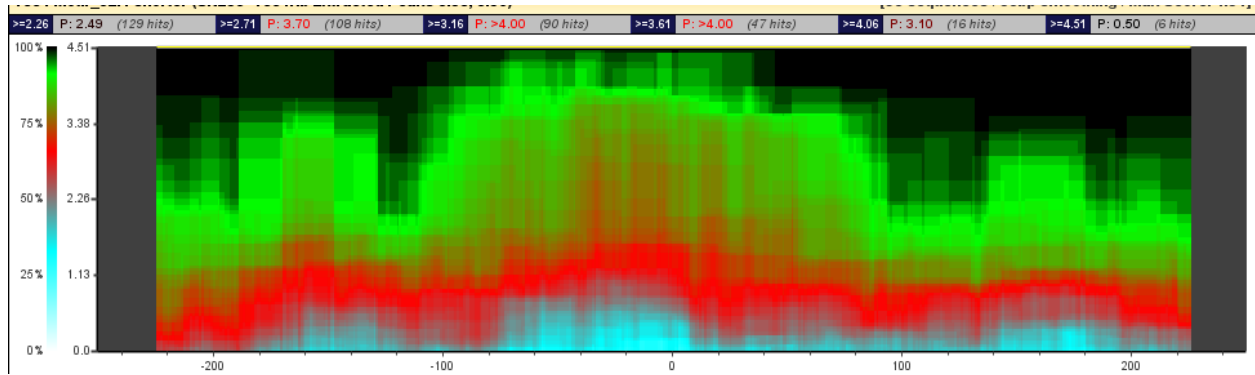
Motif Distribution Relative to Binding Peaks

Motif distribution relative to binding peaks was determined using MochiView's "motif→distribution→relative to locations" function. For each position along the position distribution (x-axis of the plot) and each possible motif score from 0-100% of the maximum score (y-axis of the plot) the percentage of binding peaks that yielded that score or below is expressed on the plot using the indicated color scale. Significant P values are indicated in red. P values are calculated for the motif distributions at 50%, 60%, 70%, 80%, 90%, and 100% of the maximum motif score using a bootstrapped chi-square goodness of fit test (see MochiView manual).

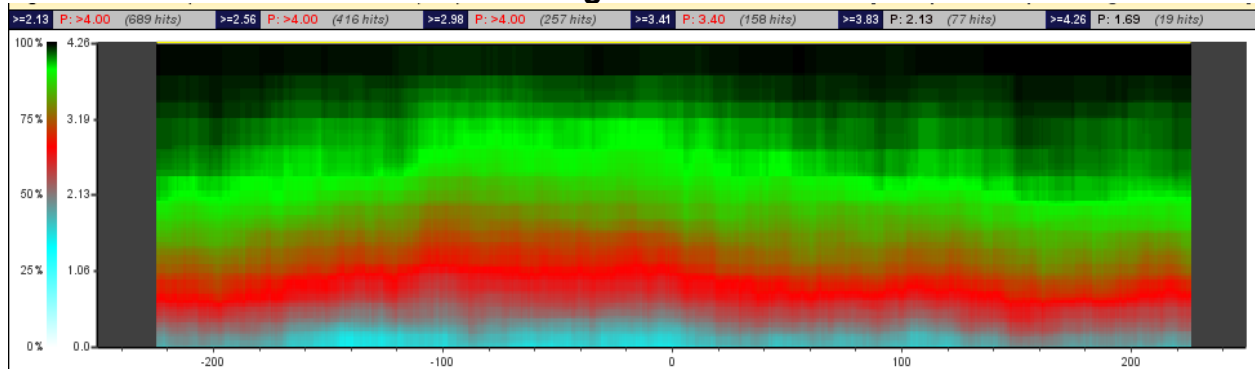
Bcr1 Motif



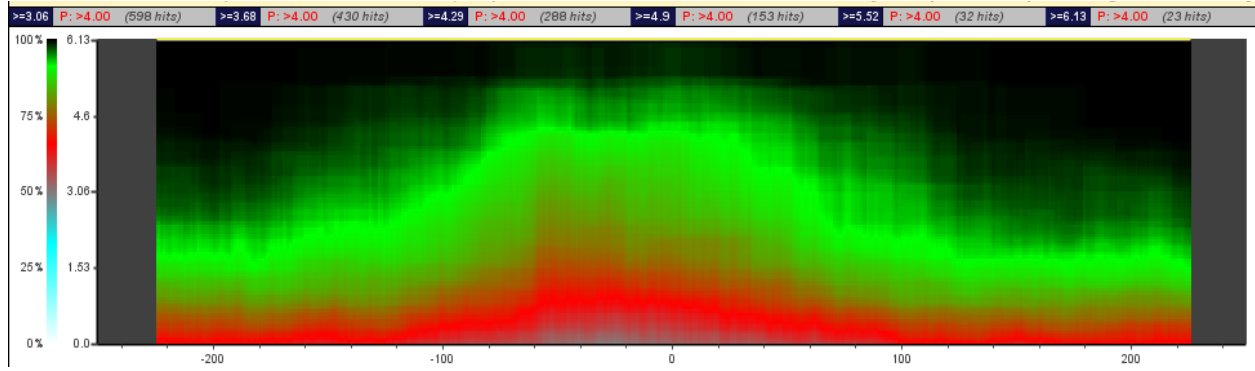
Tec1 Motif



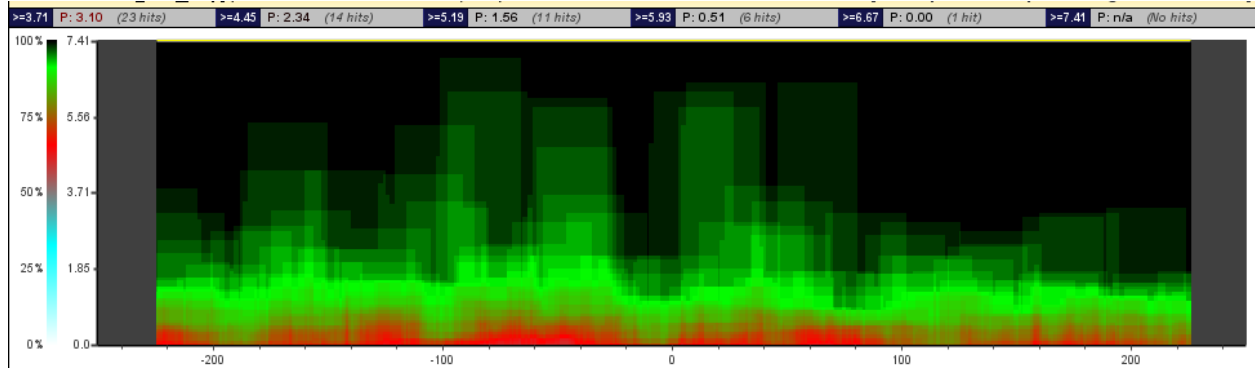
Efg1 Motif



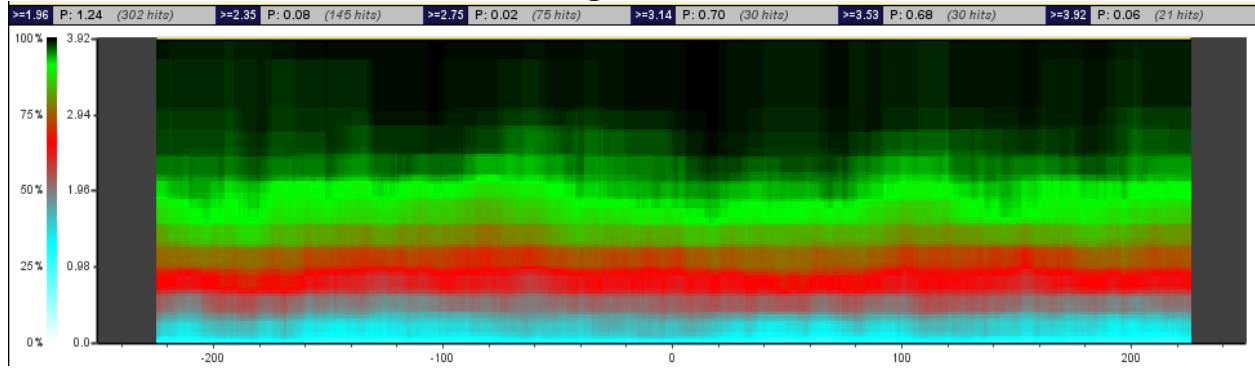
Ndt80 Motif



Rob1 Motif



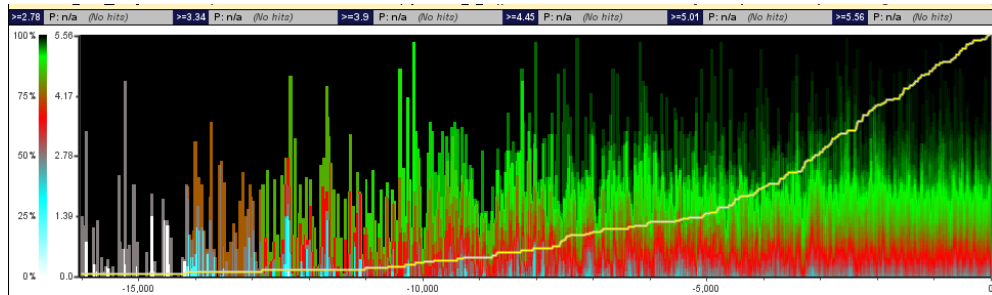
Brg1 Motif



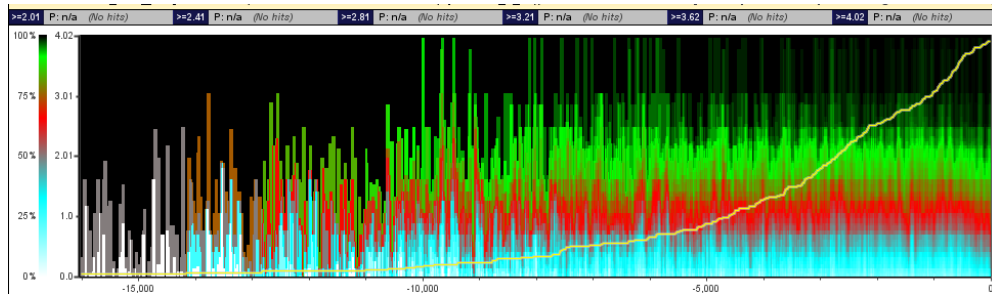
Motif Distribution Relative to Start Site

Motif distribution relative to the start codon was determined using MochiView's "motif→distribution→relative to locations" function. For each position along the position distribution (x-axis of the plot) and each possible motif score from 0-100% of the maximum score (y-axis of the plot) the percentage of binding peaks that yielded that score or below is expressed on the plot using the indicated color scale. The line on the plot reflects the percentage of sequences contributing to the calculation at each x-axis position. Significant *P* values are indicated in red. *P* values are calculated for the motif distributions at 50%, 60%, 70%, 80%, 90%, and 100% of the maximum motif score using a bootstrapped chi-square goodness of fit test (see MochiView manual).

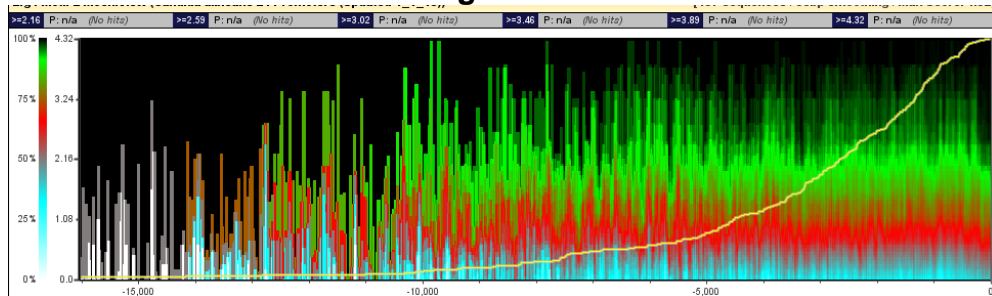
Bcr1 Motif



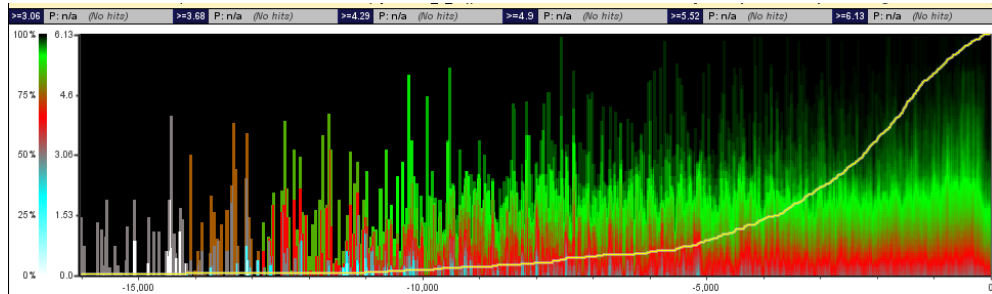
Tec1 Motif



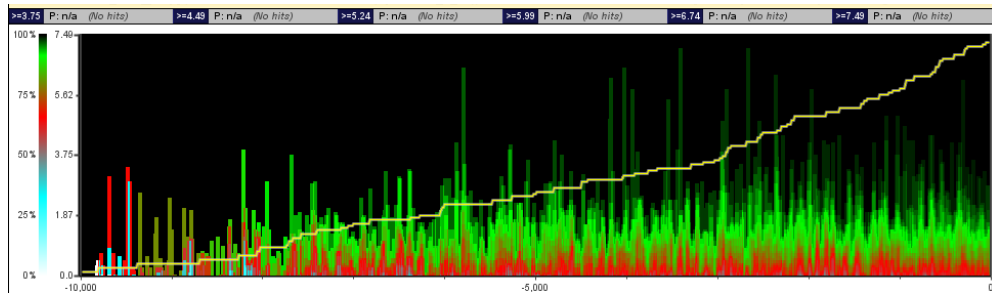
Efg1 Motif



Ndt80 Motif



Rob1 Motif



Brg1 Motif

