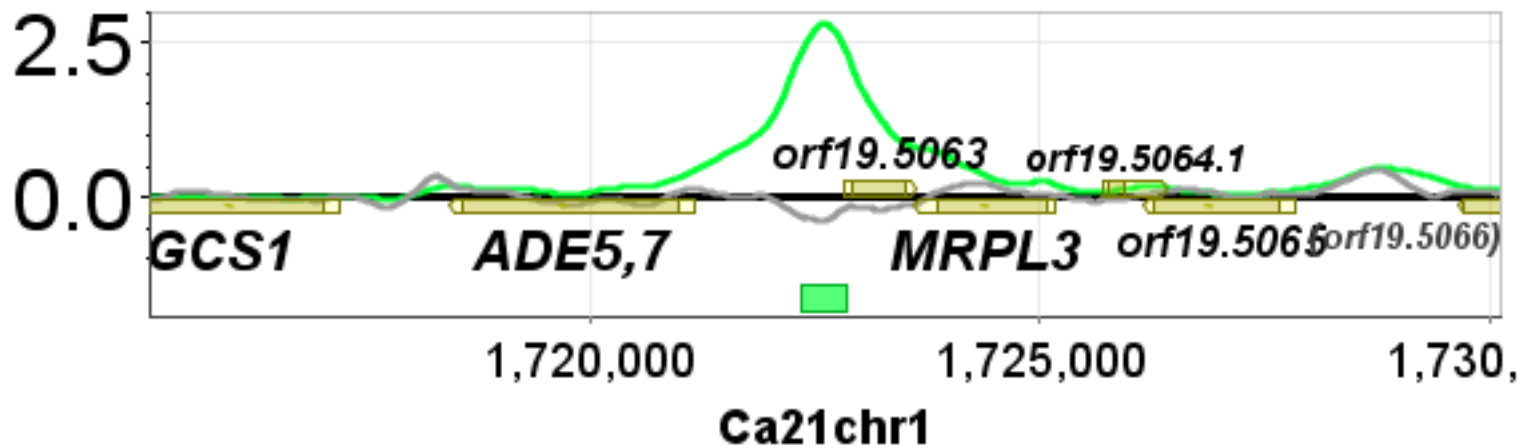


## **Full genome chromatin immunoprecipitation (ChIP-chip) mapping of Czf1 binding sites in white cells.**

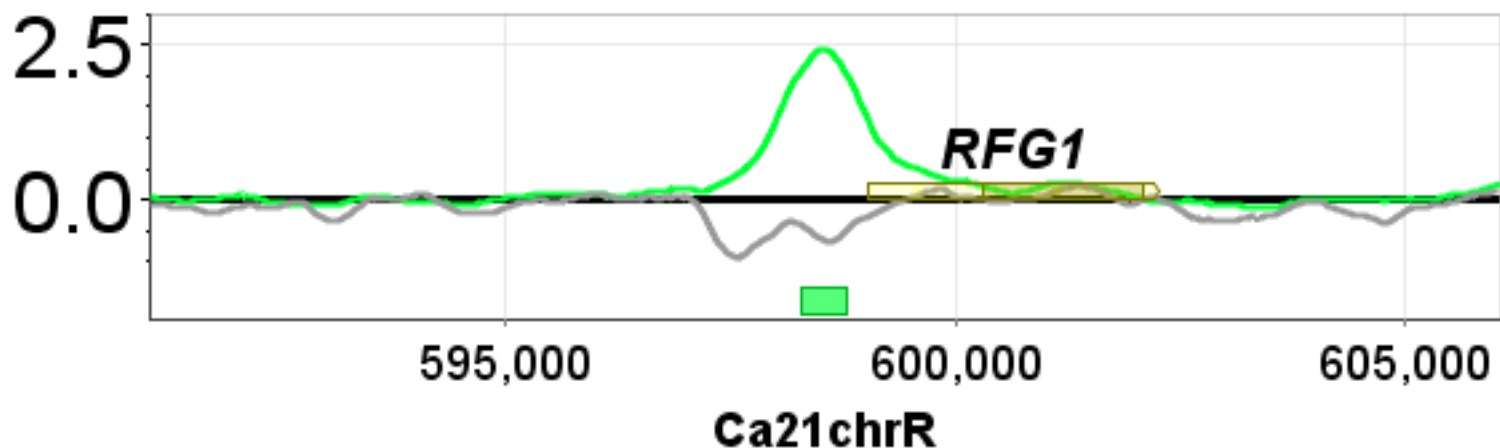
Plots of 15kb regions centered on the set of 39 Czf1 binding sites in white cells.

Smoothed enrichment data for the wild type strain is shown in green, for the *czf1* deletion strain in grey. The 500bp called peaks of Czf1 enrichment are indicated by the green boxes in the lower track in each image. Peaks are arranged in order of decreasing Czf1 enrichment. Enrichment ( $\log_2$ ) is indicated on the y-axis. Chromosomal locations and specific enrichment levels for the peak are indicated in the strip above each panel; when multiple peaks are present the enrichment value corresponds to the peak at the center of the plot. Yellow boxes correspond to genes; 5' or 3' untranslated regions are included as lighter shaded portions of the box. Genes plotted above the bold line read in the sense direction; genes plotted below the line read in the antisense direction. Plots produced using the SnapShot Function in MochiView v1.46 (Homann and Johnson, 2010). This data set contains 38 peaks identified by MochiView as well as one manually annotated binding site in the upstream region of *EFG1*.

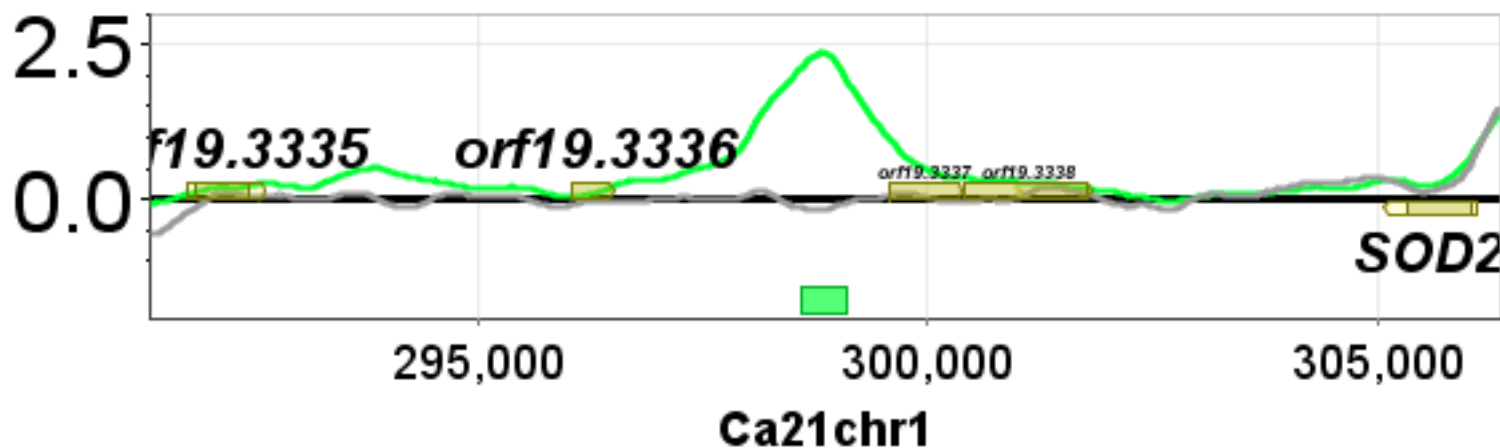
[2.815] Ca21chr1:1715102-1730101 [+] [orf19.5063, ADE5,7, MRPL3, orf19.5064.1, ntar\_159]



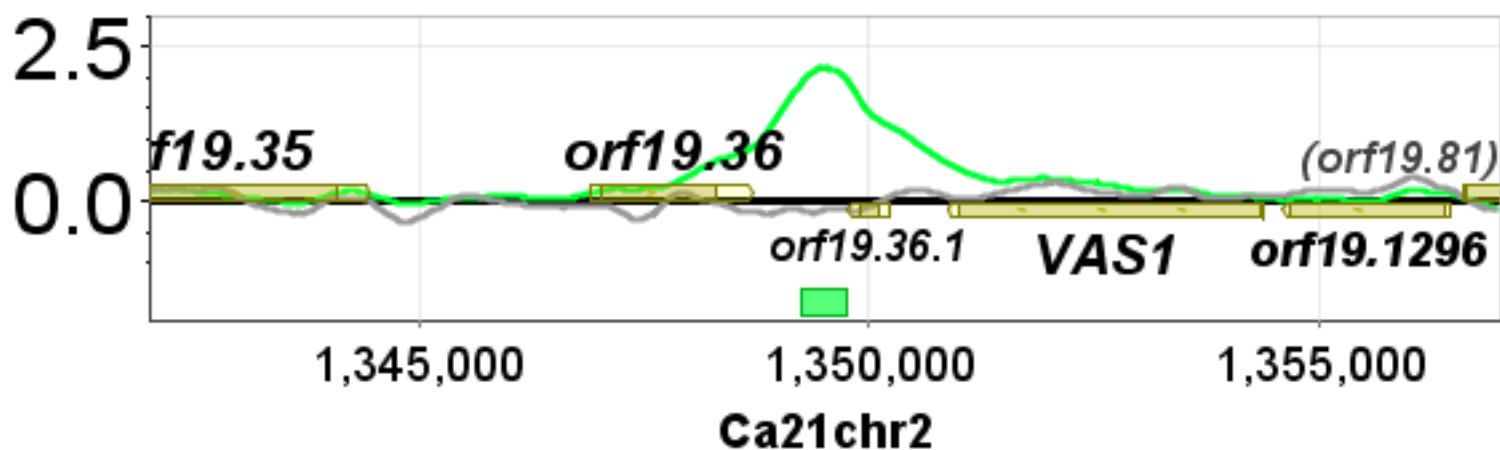
[2.435] Ca21chrR:591039-606038 [+] [RFG1, ntar\_1219]

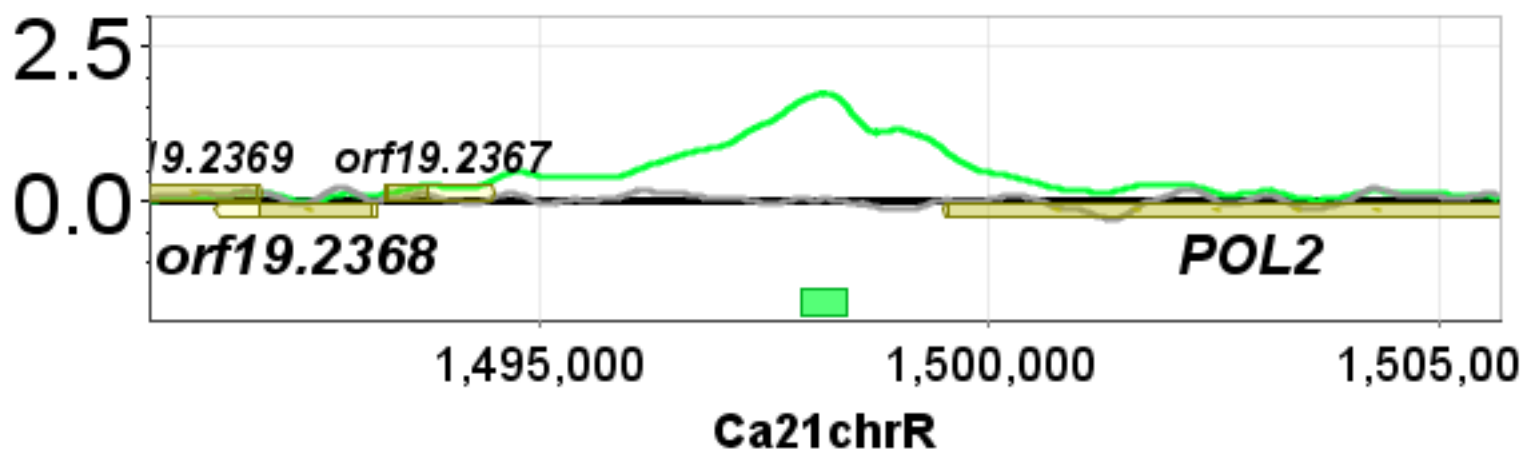
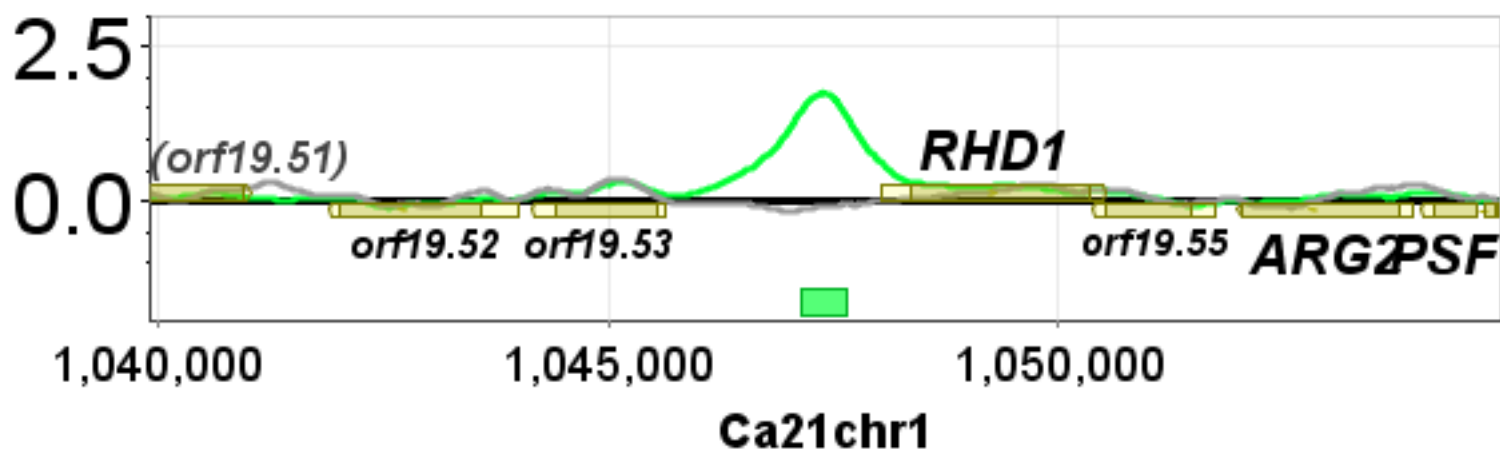
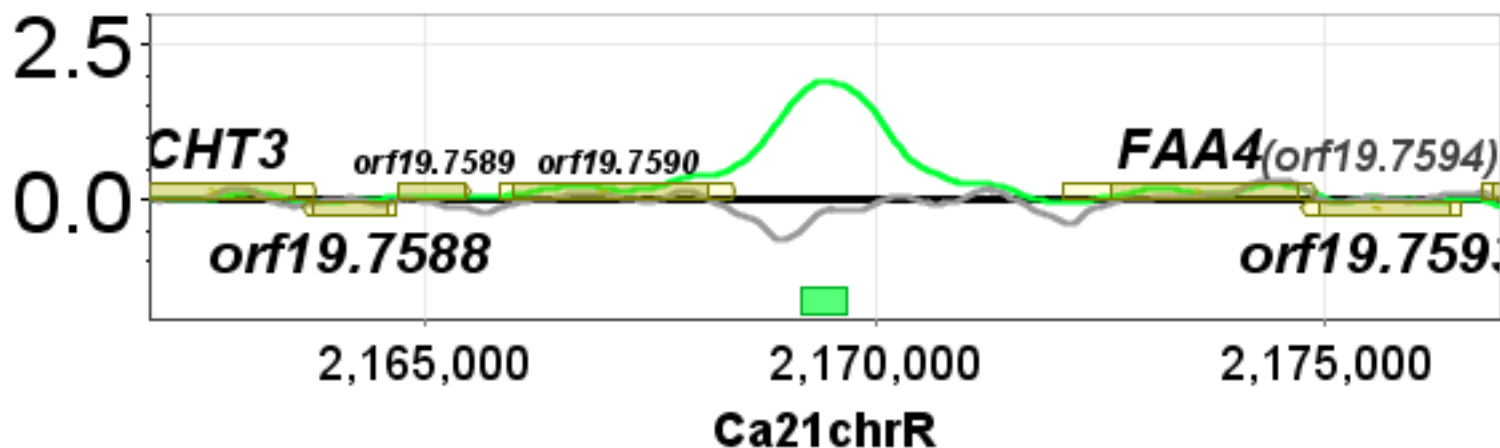
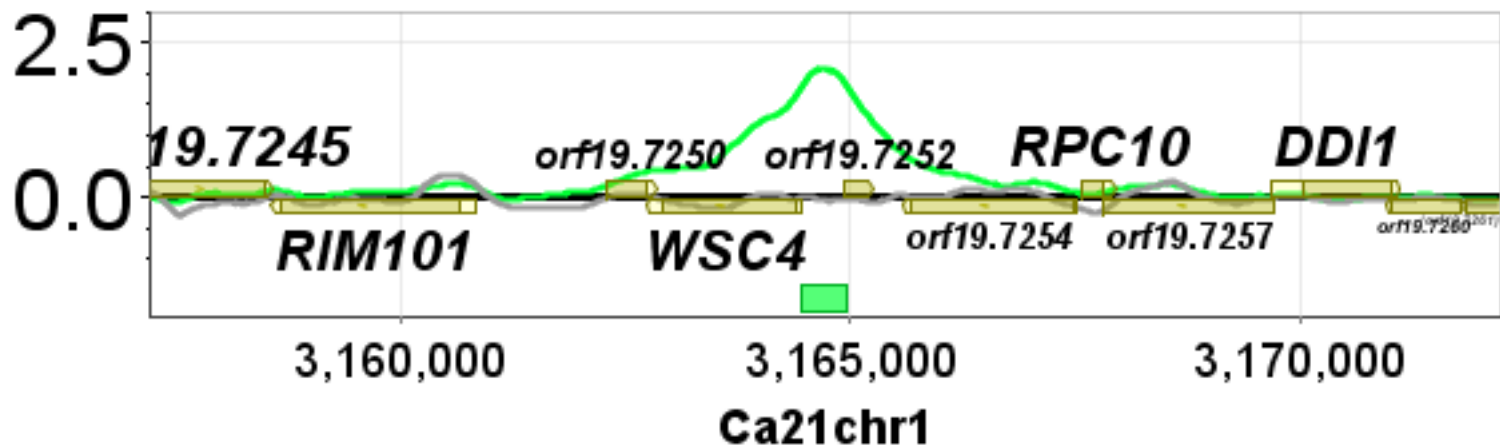


[2.372] Ca21chr1:291349-306348 [+] [orf19.3337, orf19.3338, orf19.3336, orf19.3335, SOD2]

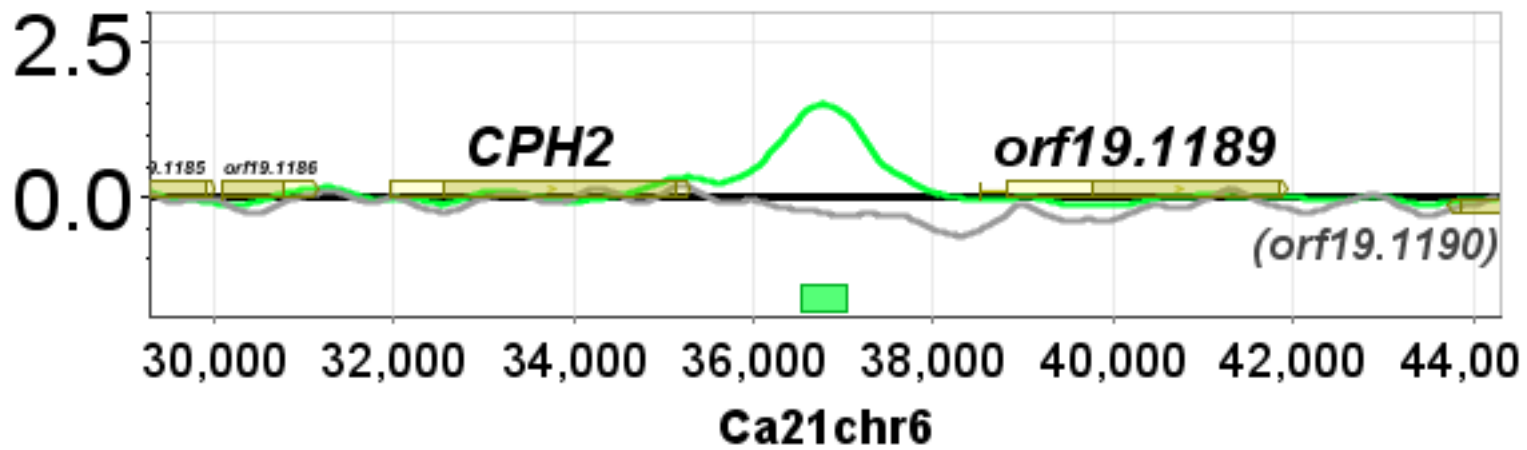


[2.165] Ca21chr2:1342000-1356999 [+] [ntar\_409, orf19.36.1, orf19.36, orf19.35.1, ntar\_408]

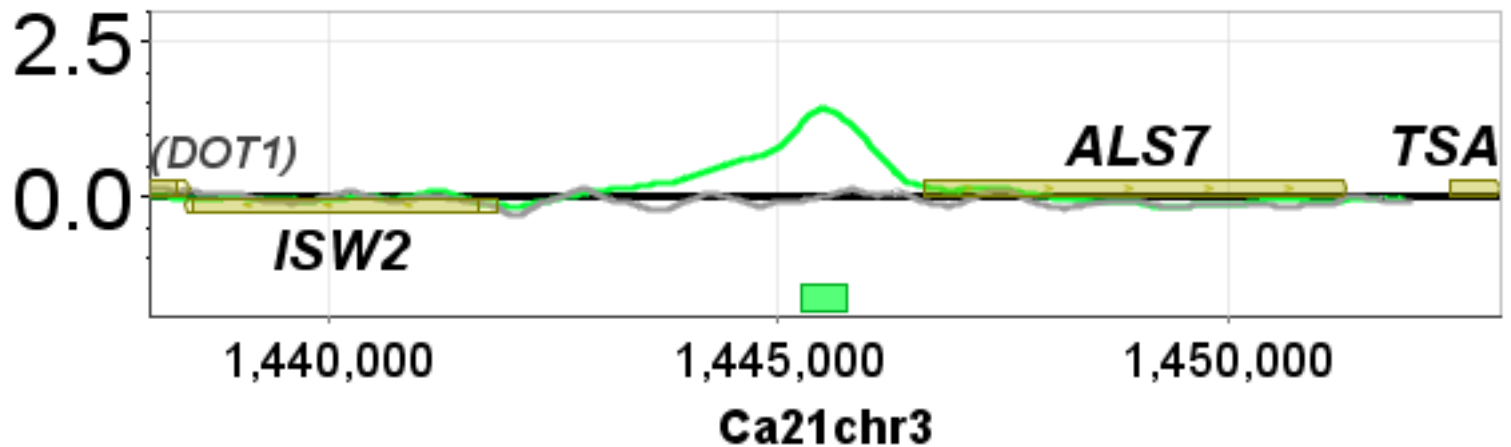




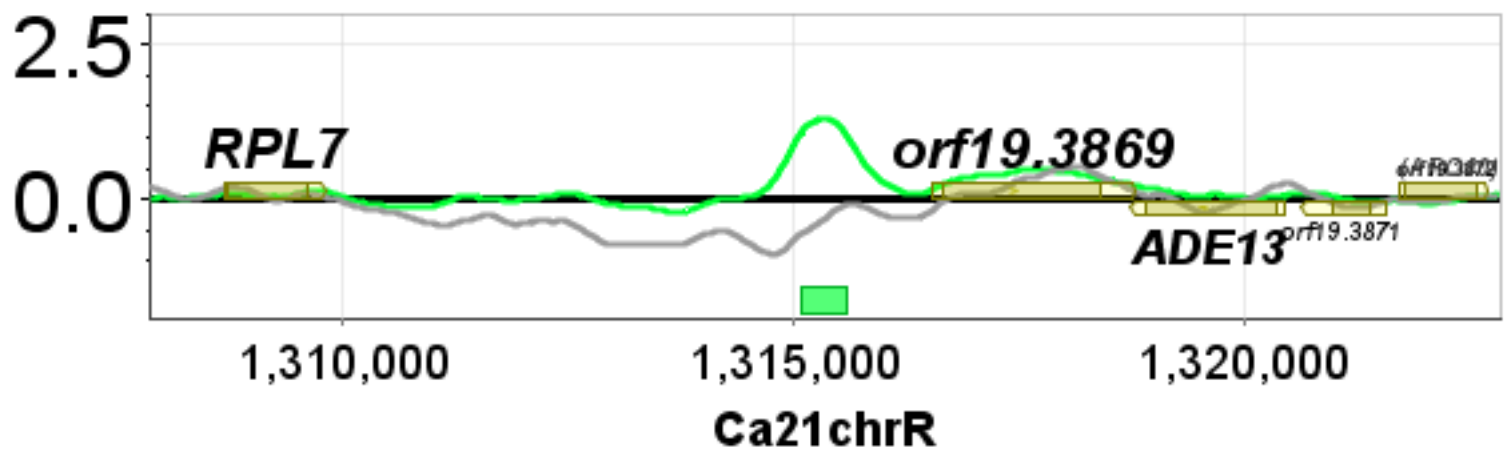
[1.501] Ca21chr6:29286-44285 [+] [ntar\_969, orf19.1189, CPH2, ntar\_968, orf19.1186]



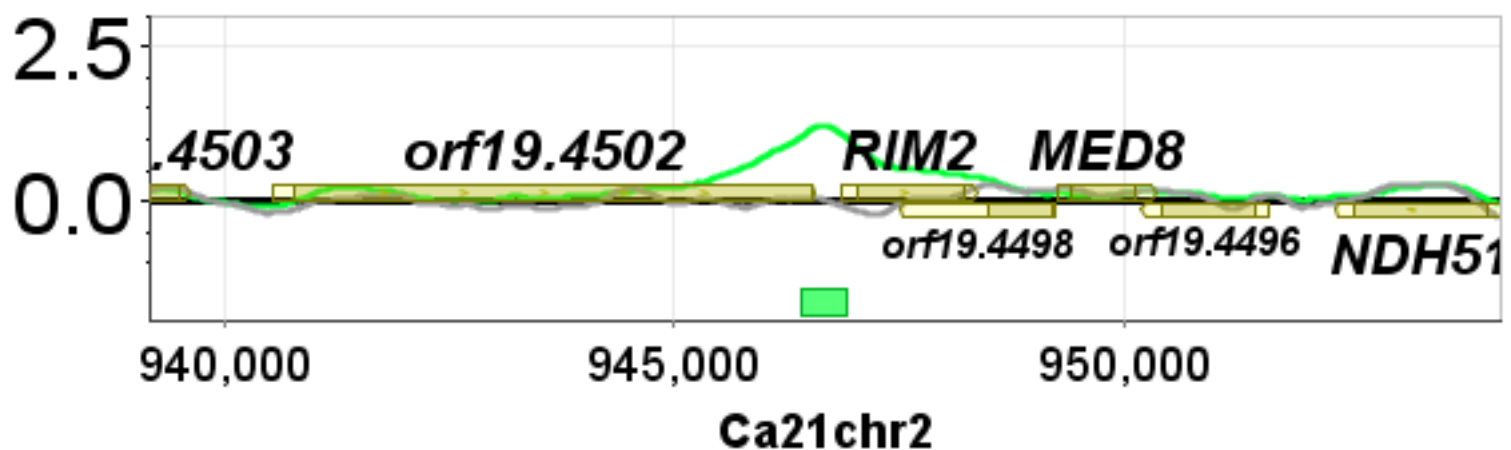
[1.428] Ca21chr3:1438012-1453011 [+] [ALS7, ntar\_656, ISW2, ntar\_657, TSA1B]

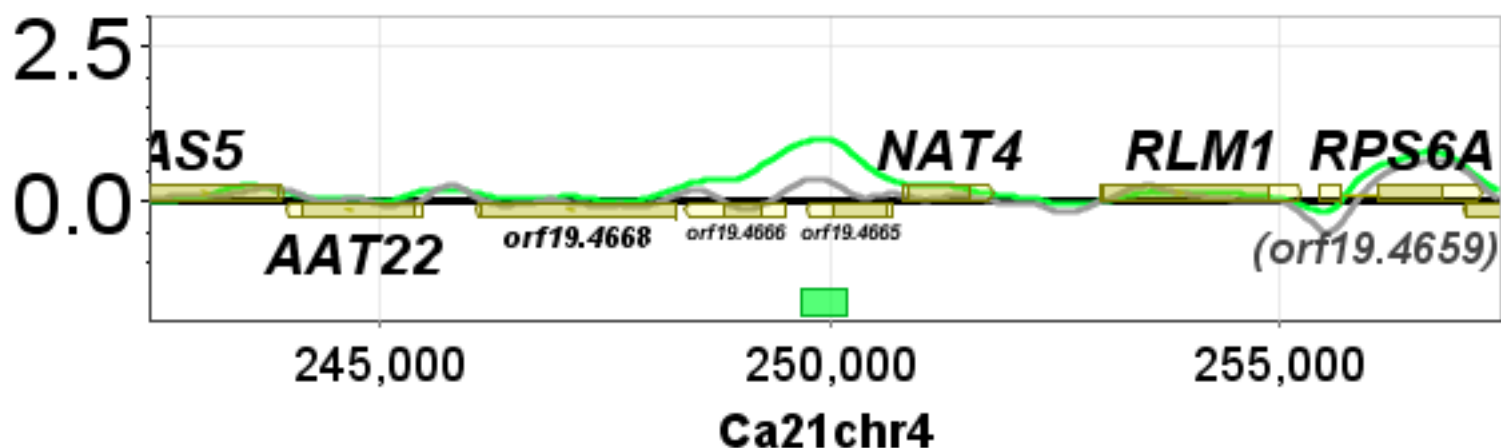
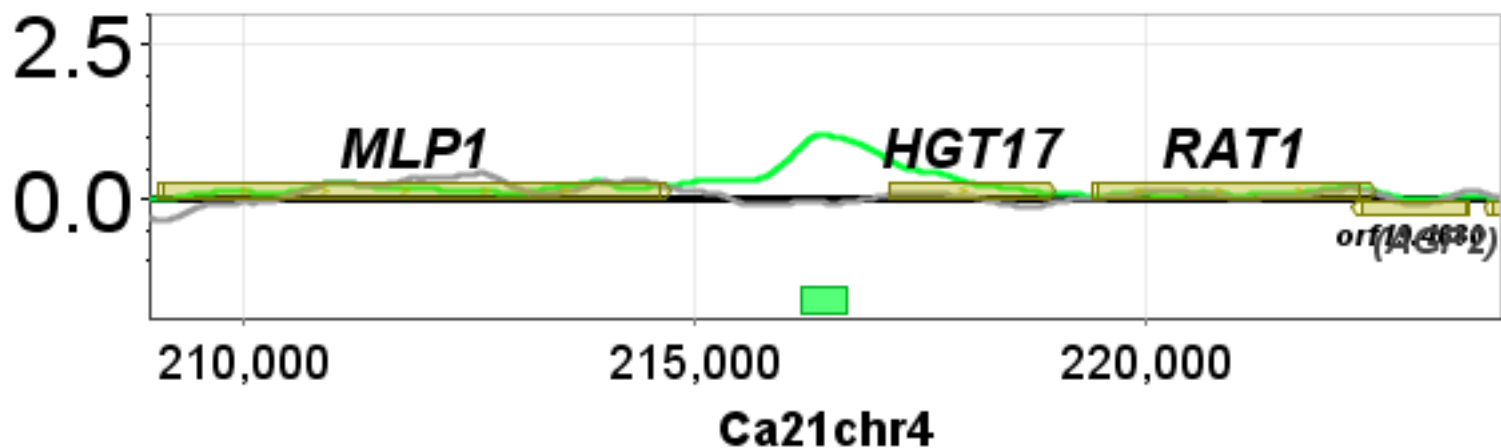
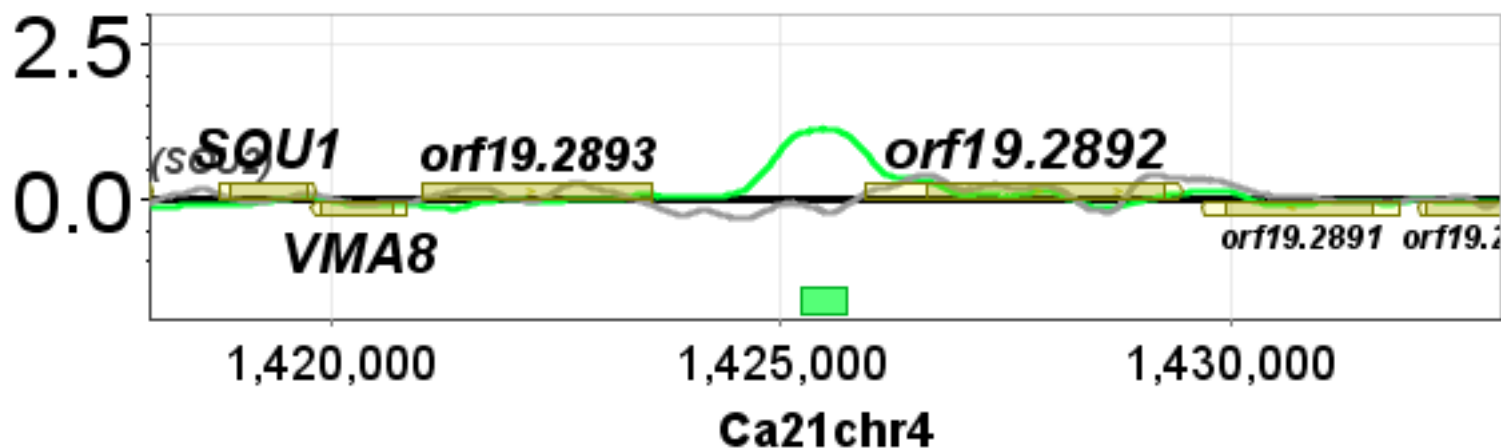
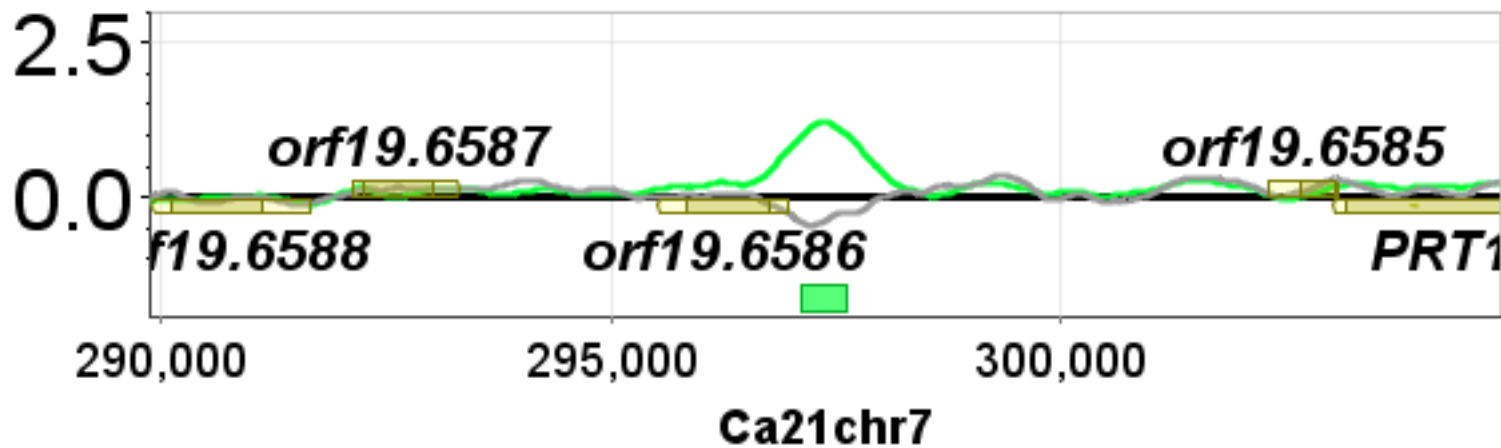


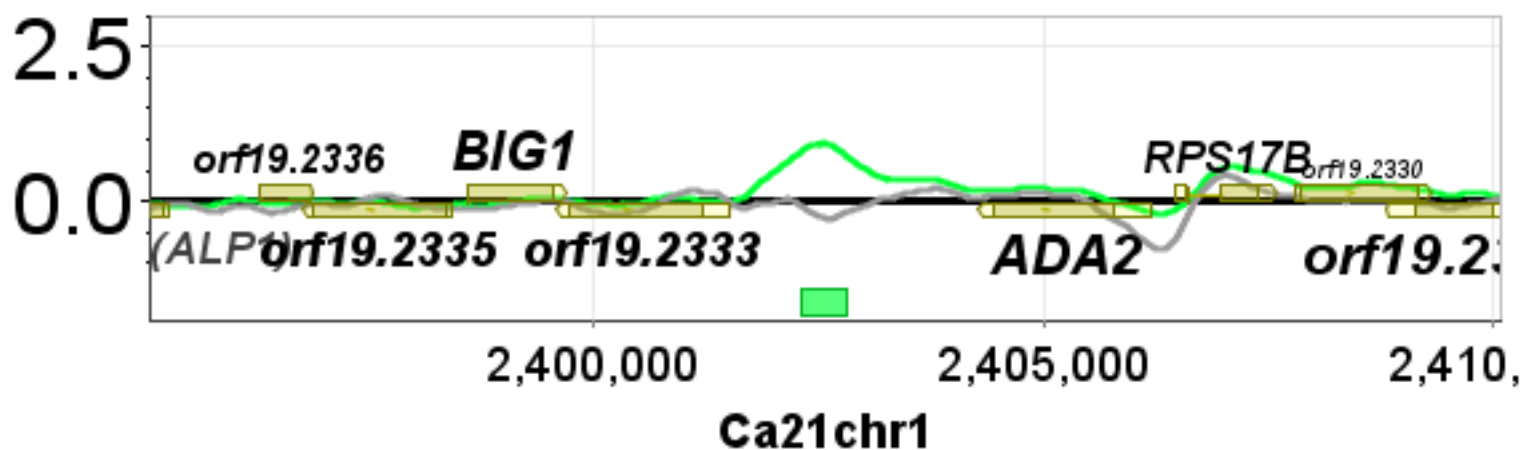
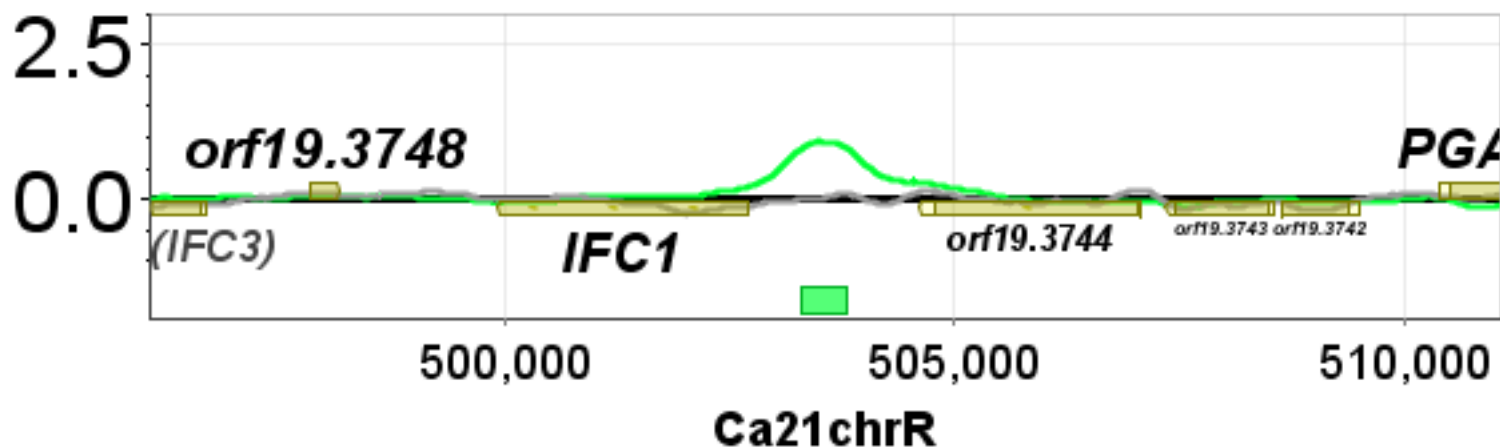
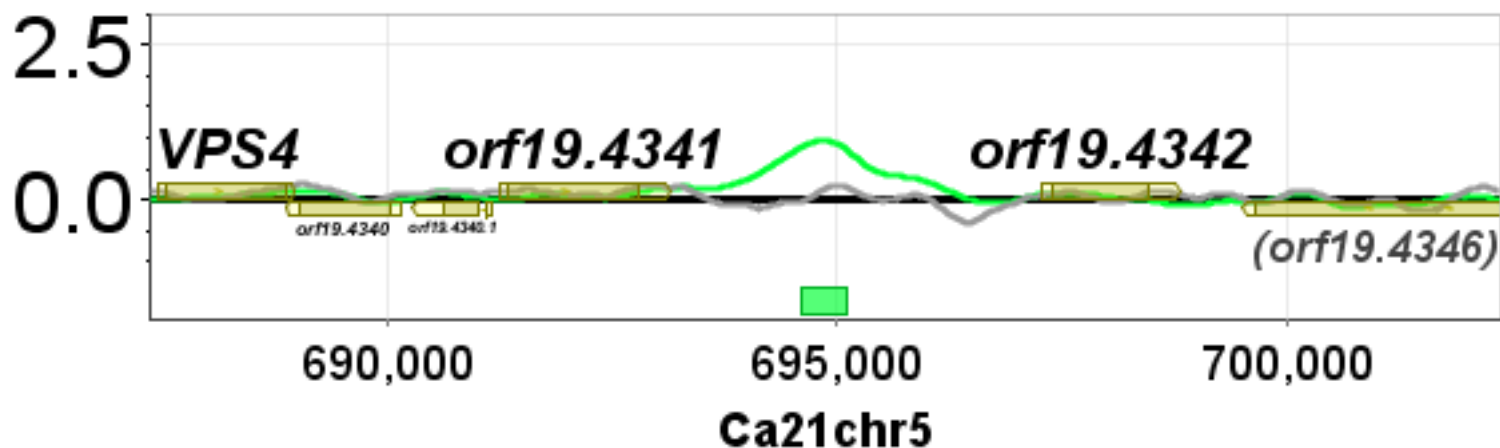
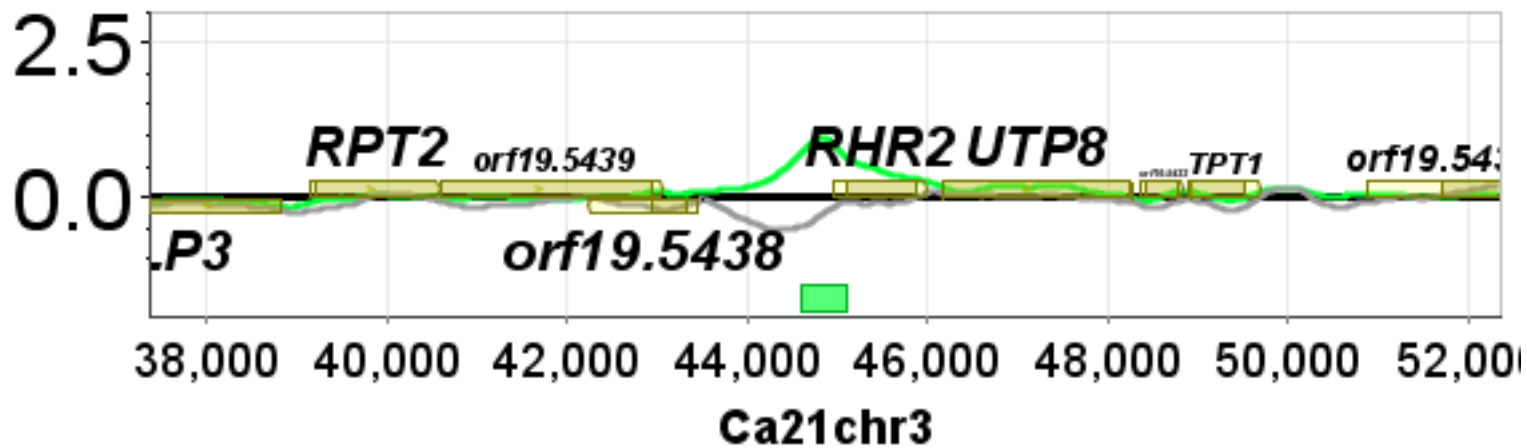
[1.309] Ca21chrR:1307839-1322838 [+] [orf19.3868, orf19.3869, ntar\_1302, ntar\_1301, ADE13]



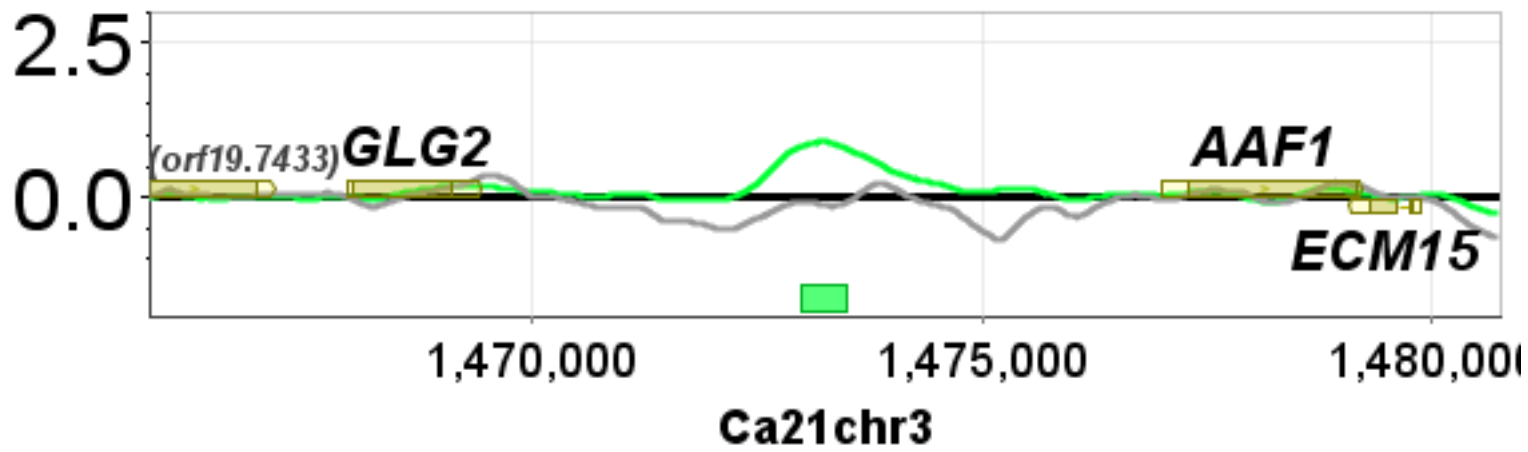
[1.226] Ca21chr2:939162-954161 [+] [RIM2, orf19.4498, MED8, orf19.4496, ntar\_372]



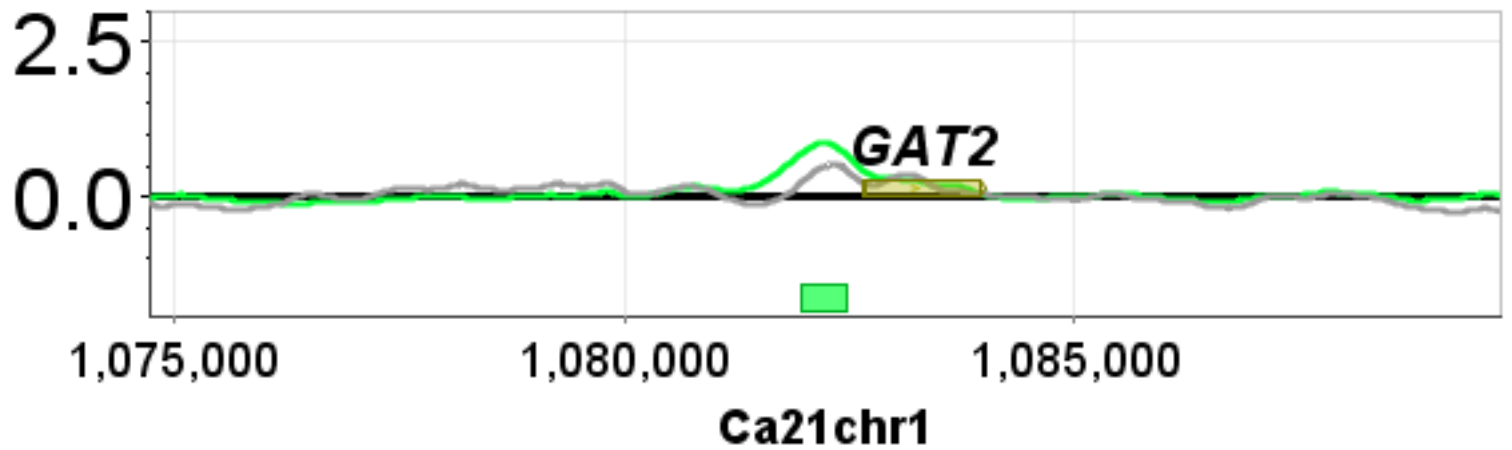




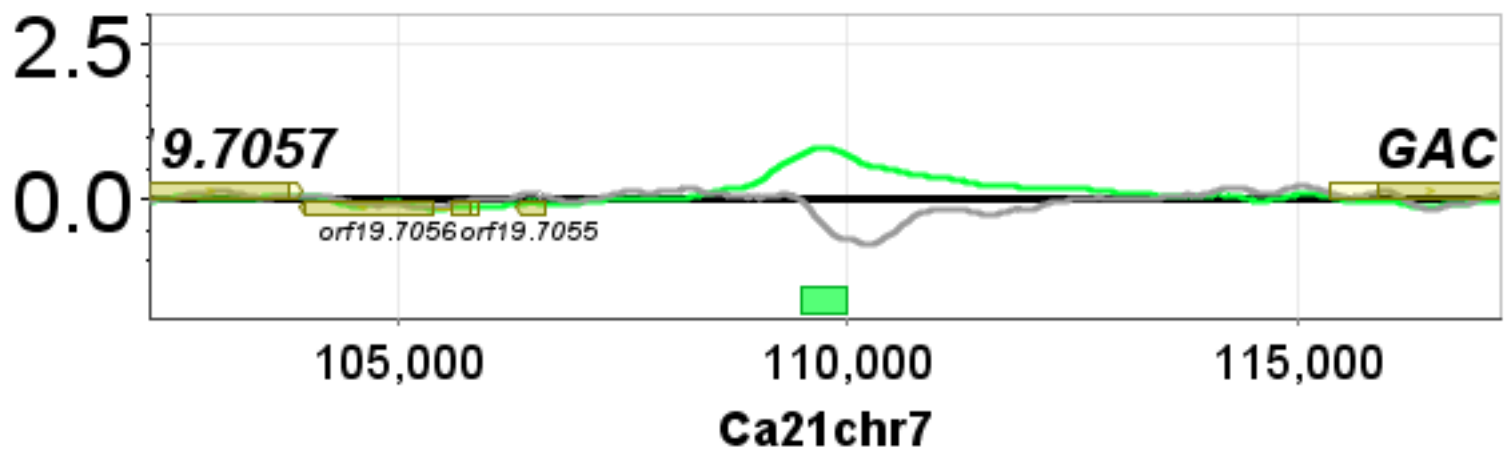
[0.902] Ca21chr3:1465747-1480746 [+] [ntar\_658, ntar\_659, th(gug)3, AAF1, GLG2]



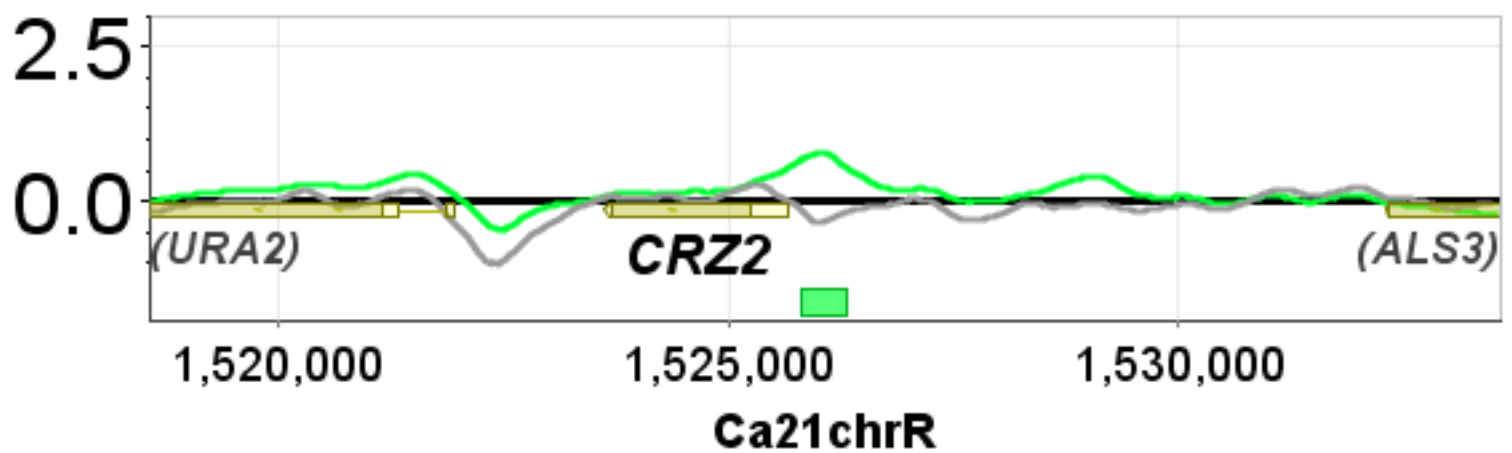
[0.864] Ca21chr1:1074719-1089718 [+] [GAT2, orf19.450, ntar\_104]



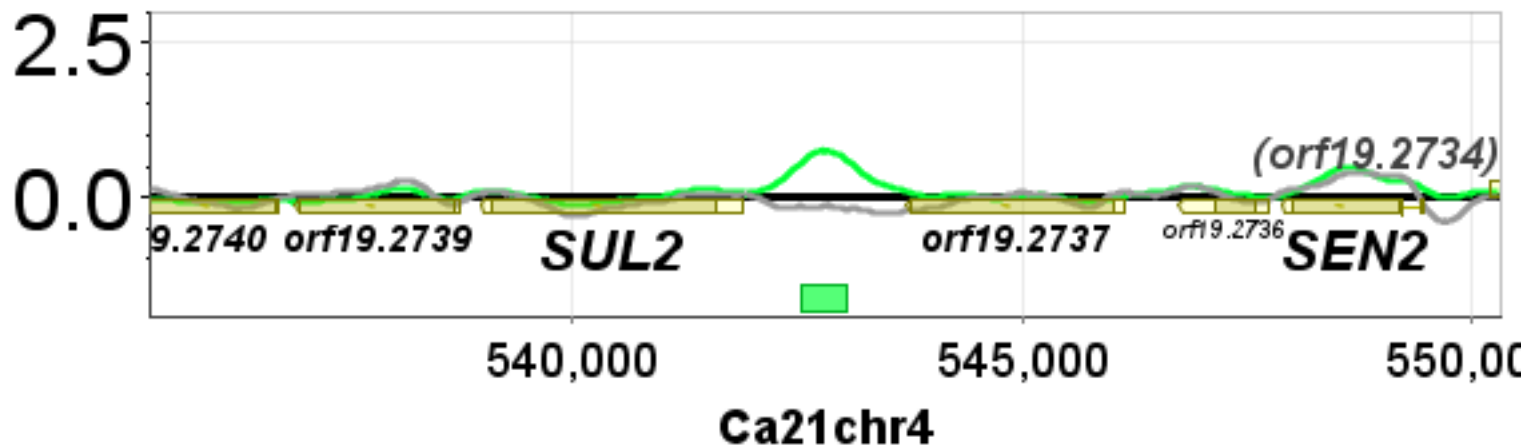
[0.823] Ca21chr7:102241-117240 [+] [ntar\_1413, orf19.7055, orf19.7056, orf19.7054, GAC1]



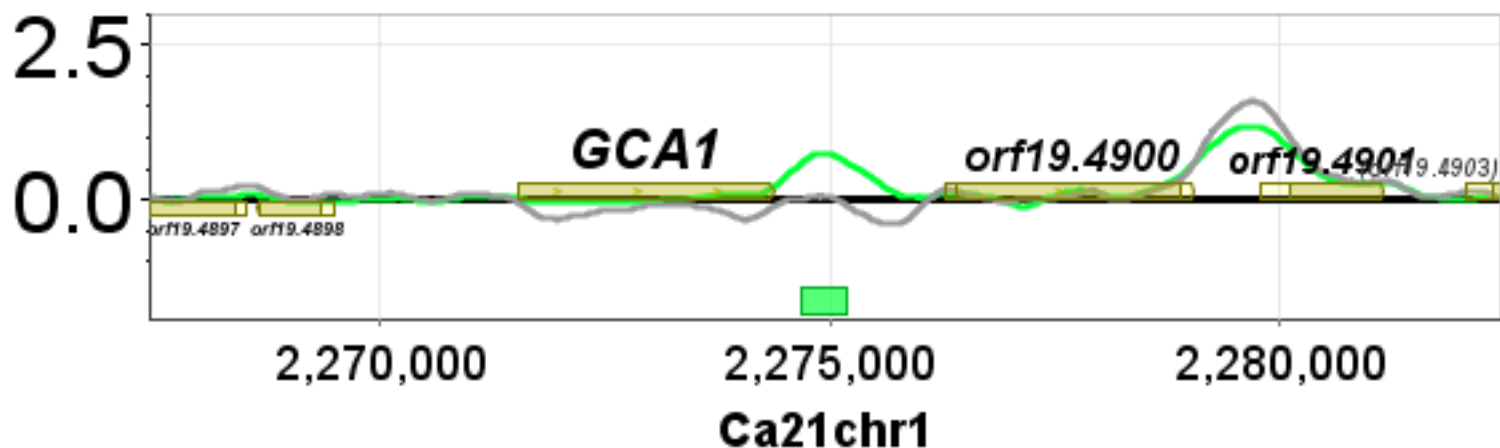
[0.78] Ca21chrR:1518566-1533565 [+] [CRZ2, ntar\_1331, URA2, ALS3]



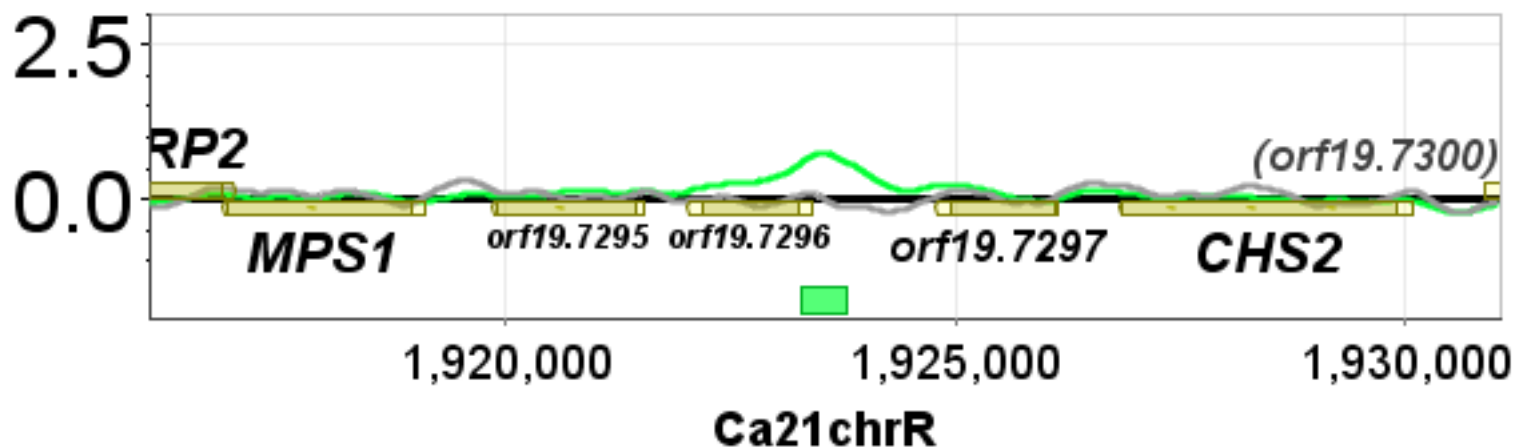
[0.764] Ca21chr4:535297-550296 [+] [SUL2, orf19.2737, ntar\_768, orf19.2739, orf19.2736]



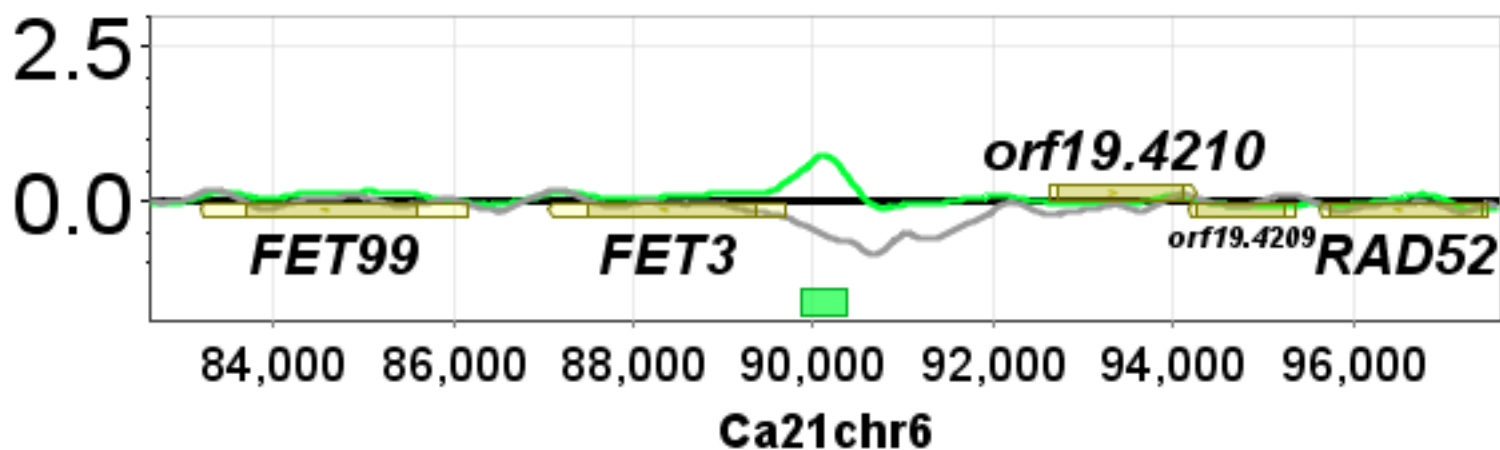
[0.756] Ca21chr1:2267434-2282433 [+] [orf19.4900, ntar\_209, GCA1, ntar\_210, orf19.4901]



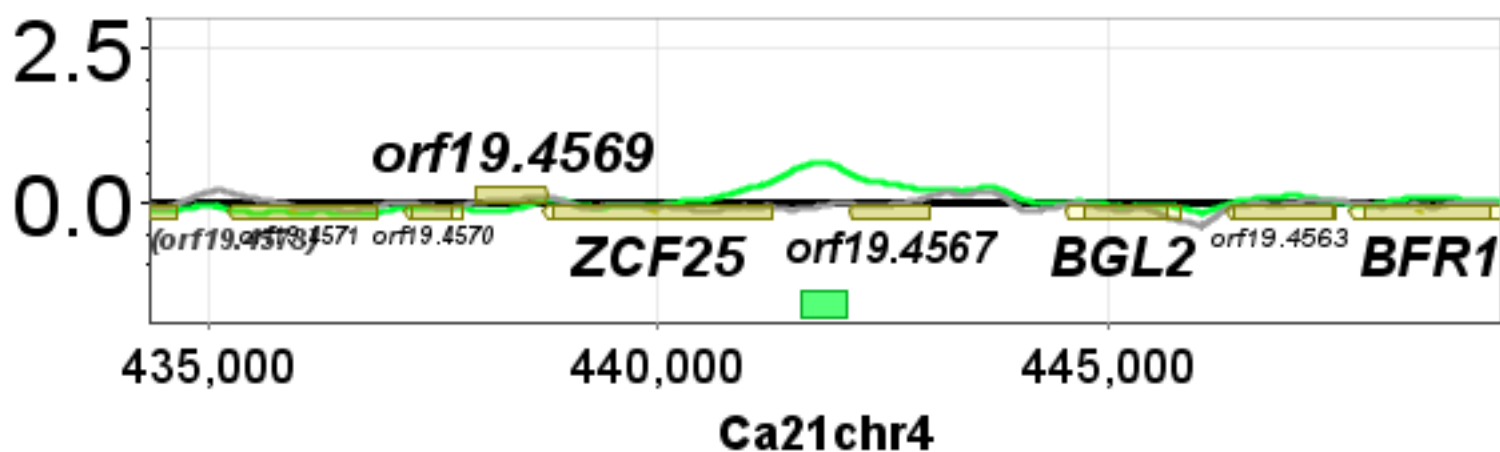
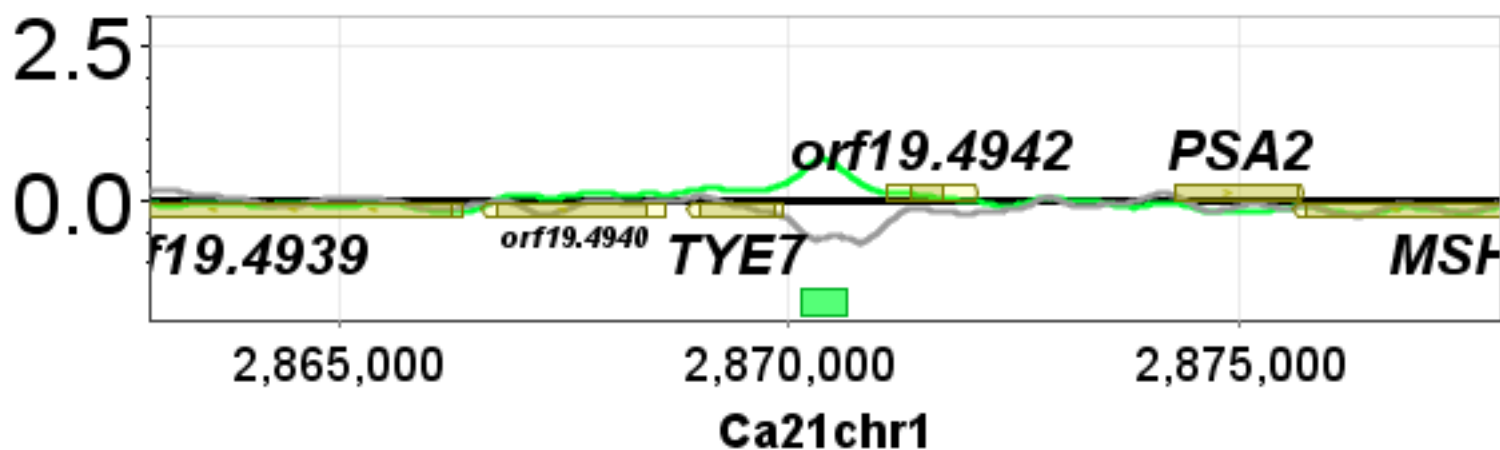
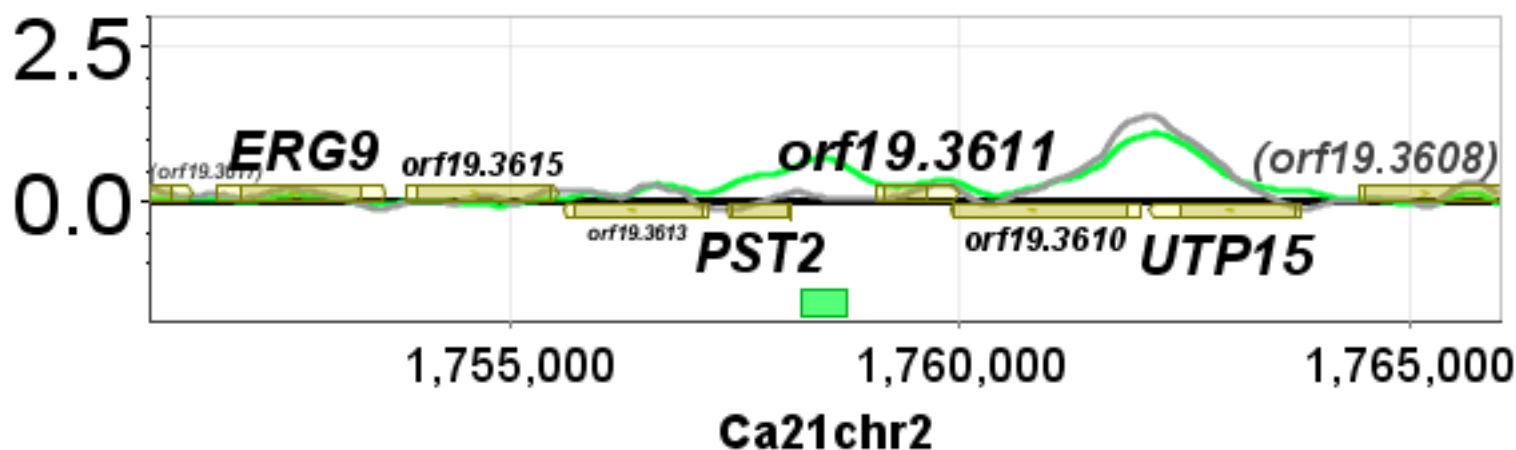
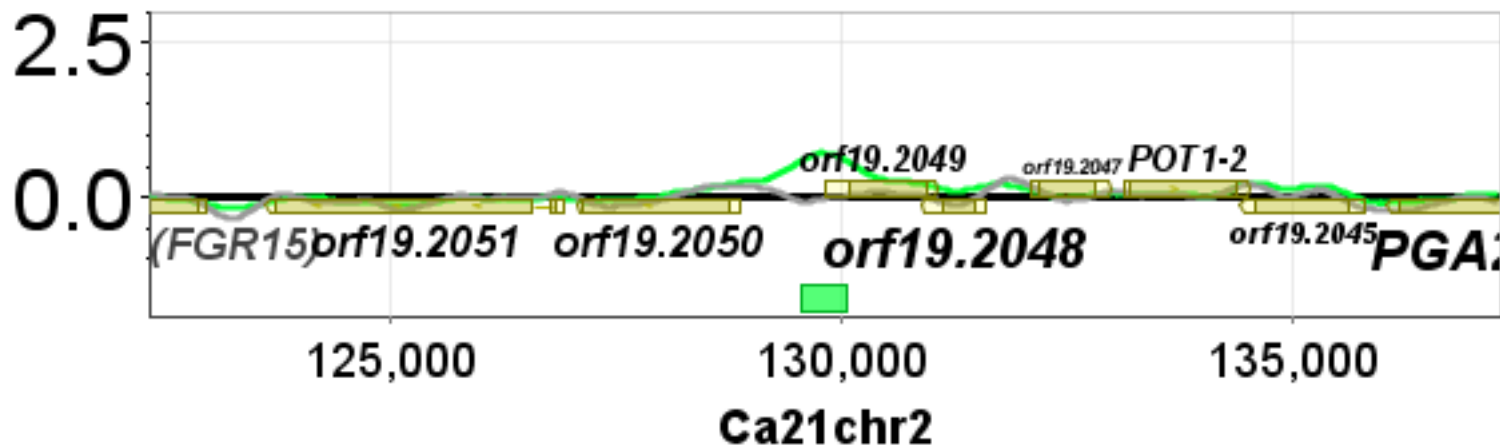
[0.742] Ca21chrR:1916042-1931041 [+] [orf19.7296, ntar\_1370, ntar\_1369, orf19.7295, orf19.7297]

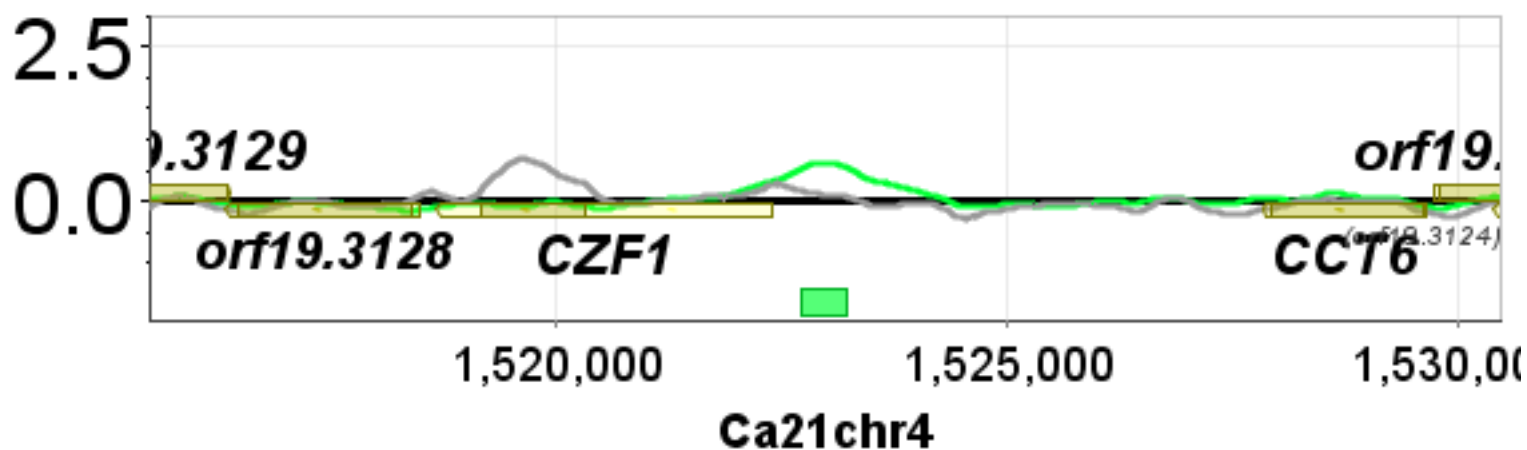
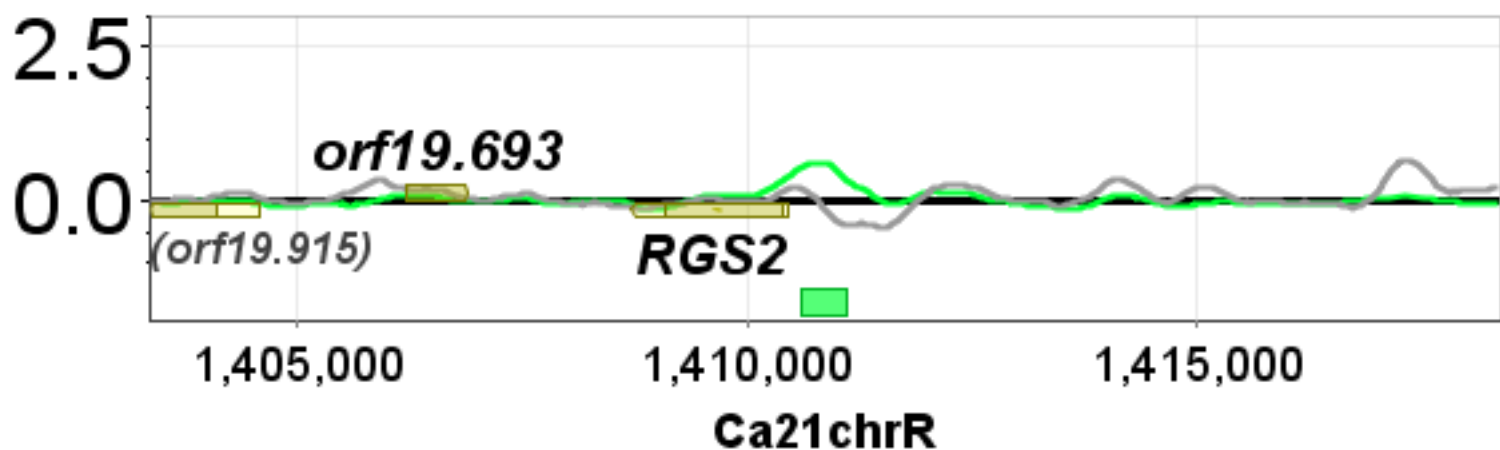
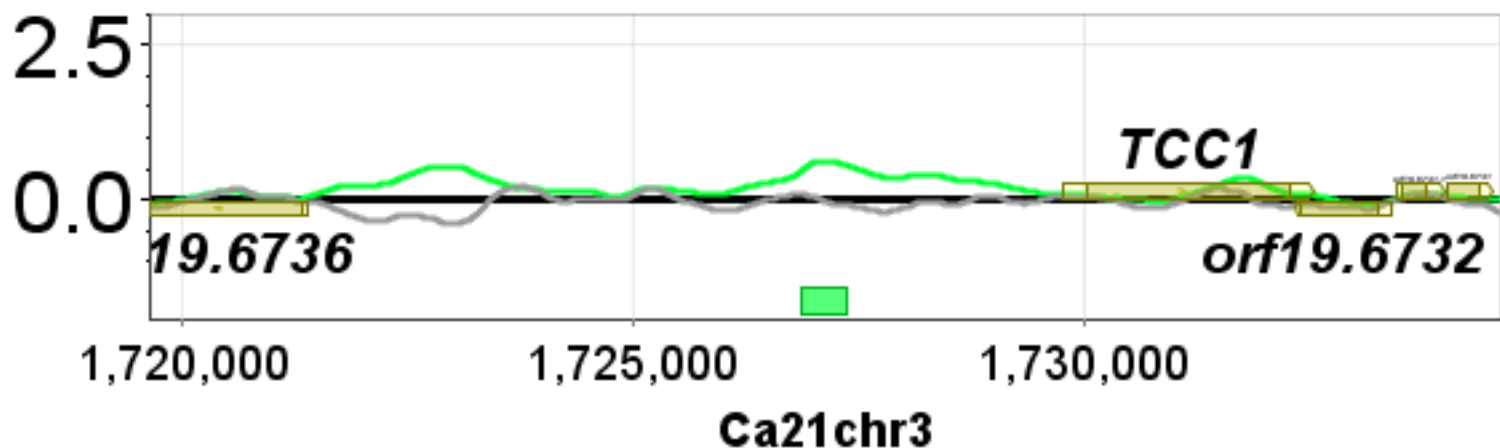
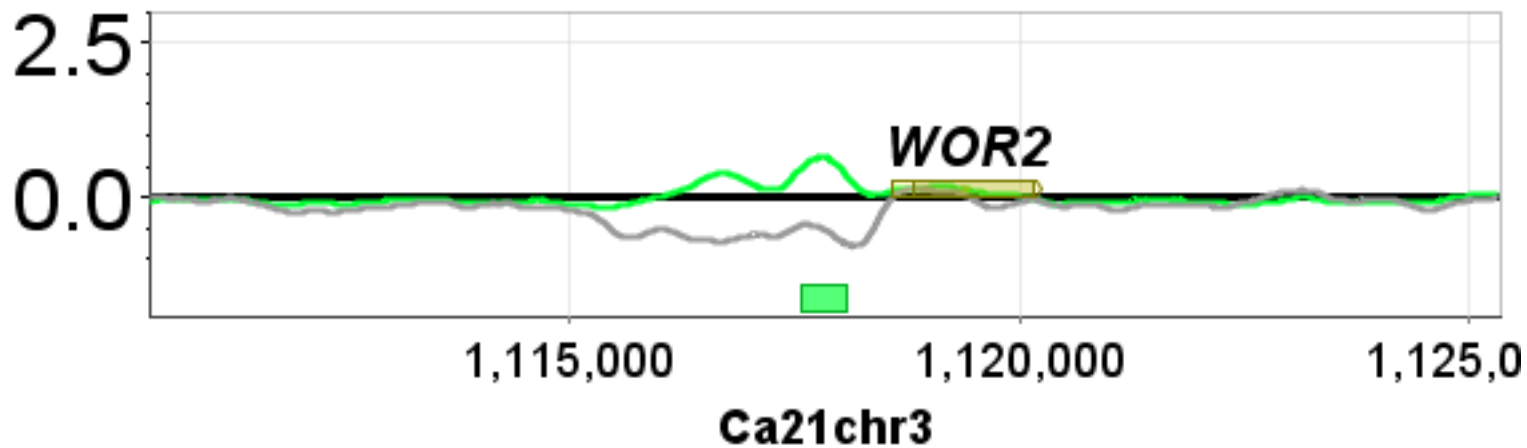


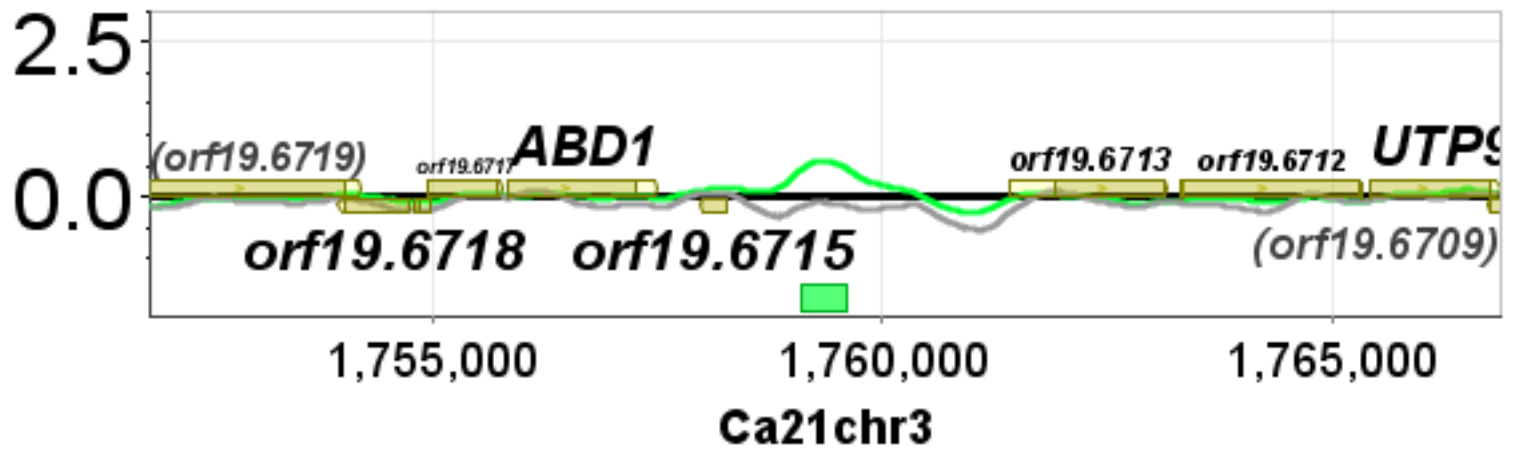
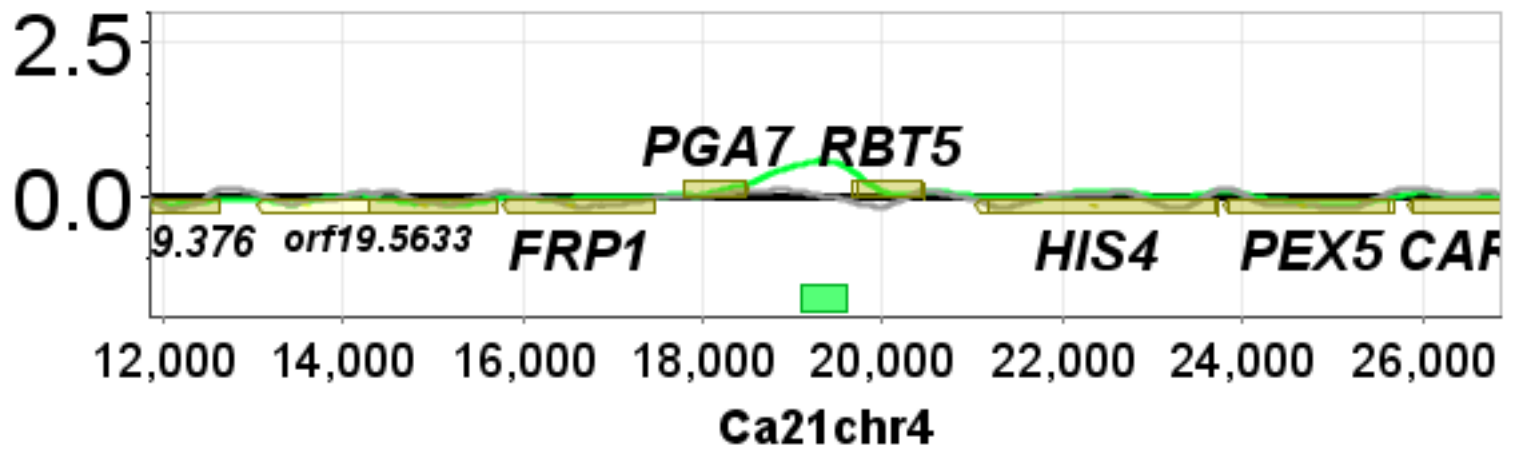
[0.74] Ca21chr6:82620-97619 [+] [ntar\_970, FET3, orf19.4210, FET99, orf19.4209]

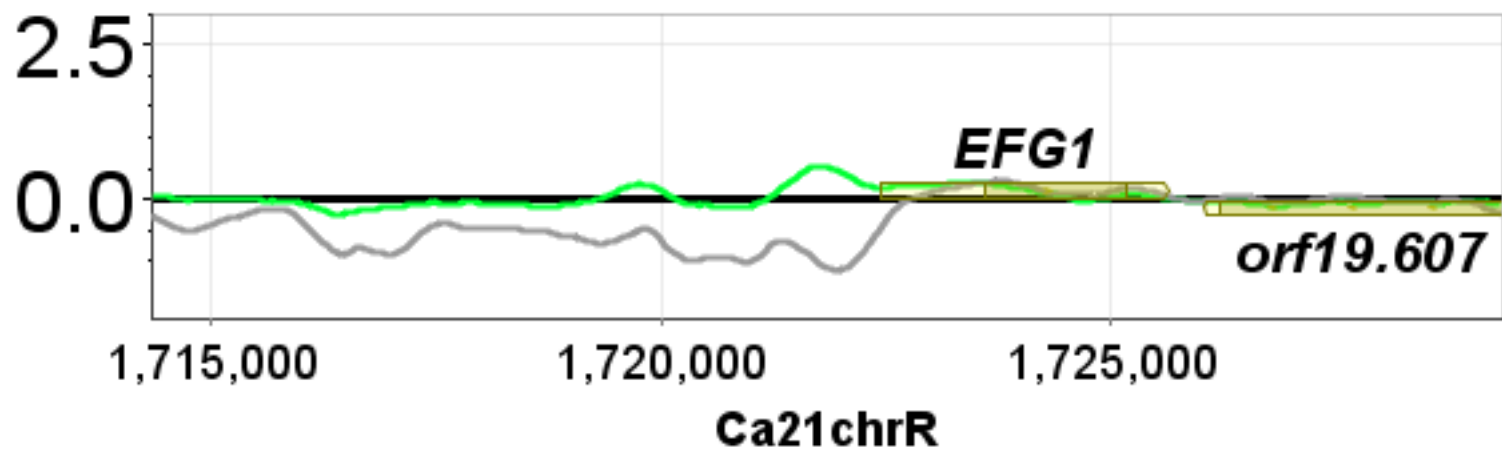










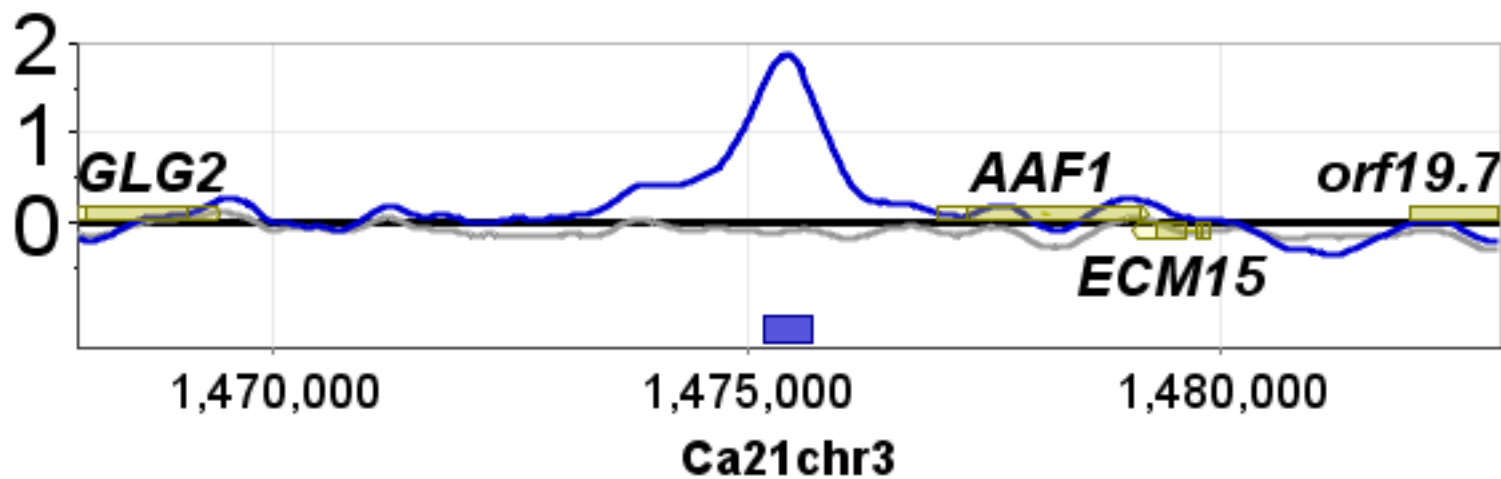


## **Full genome chromatin immunoprecipitation (ChIP-chip) mapping of Efg1 binding sites in white cells.**

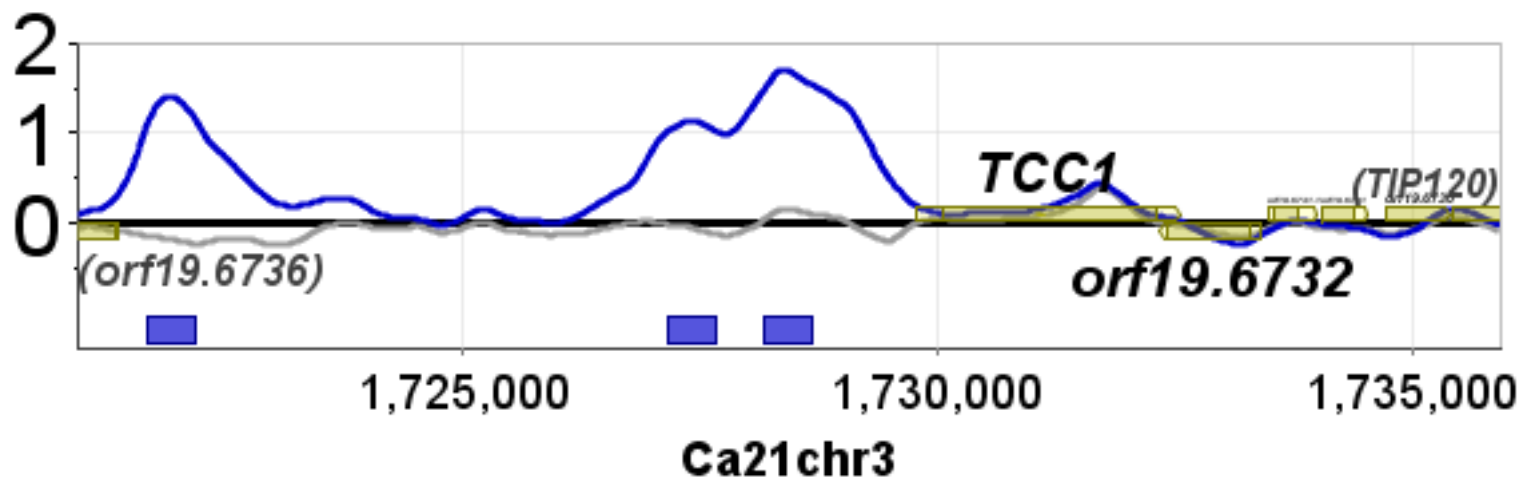
Plots of 15kb regions centered on the set of 58 Efg1 binding sites in white cells.

Smoothed enrichment data for the wild type strain is shown in blue, for the *efg1* deletion strain in grey. The 500bp called peaks of Efg1 enrichment are indicated by the blue boxes in the lower track in each image. Peaks are arranged in order of decreasing Efg1 enrichment. Enrichment ( $\log_2$ ) is indicated on the y-axis. Chromosomal locations and specific enrichment levels for the peak are indicated in the strip above each panel; when multiple peaks are present the enrichment value corresponds to the peak at the center of the plot. Yellow boxes correspond to genes; 5' or 3' untranslated regions are included as lighter shaded portions of the box. Genes plotted above the bold line read in the sense direction; genes plotted below the line read in the antisense direction. Plots produced using the SnapShot Function in MochiView v1.46 (Homann and Johnson, 2010).

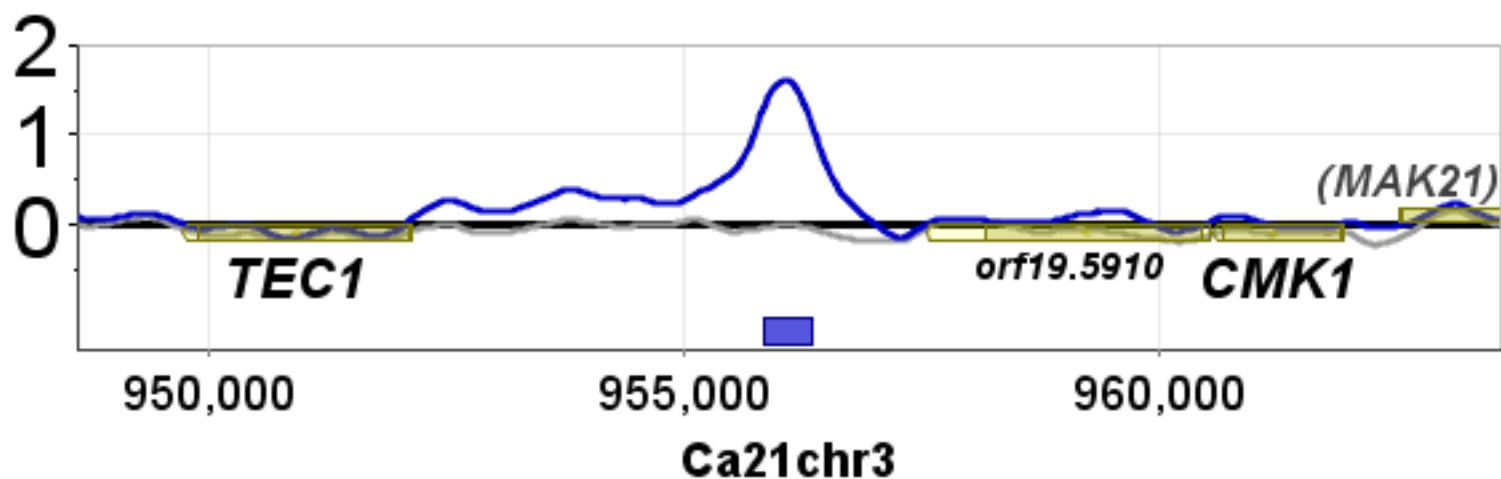
[1.866] Ca21chr3:1467930-1482929 [+] [ntar\_658, ntar\_659, AAF1, ECM15, ntar\_660]



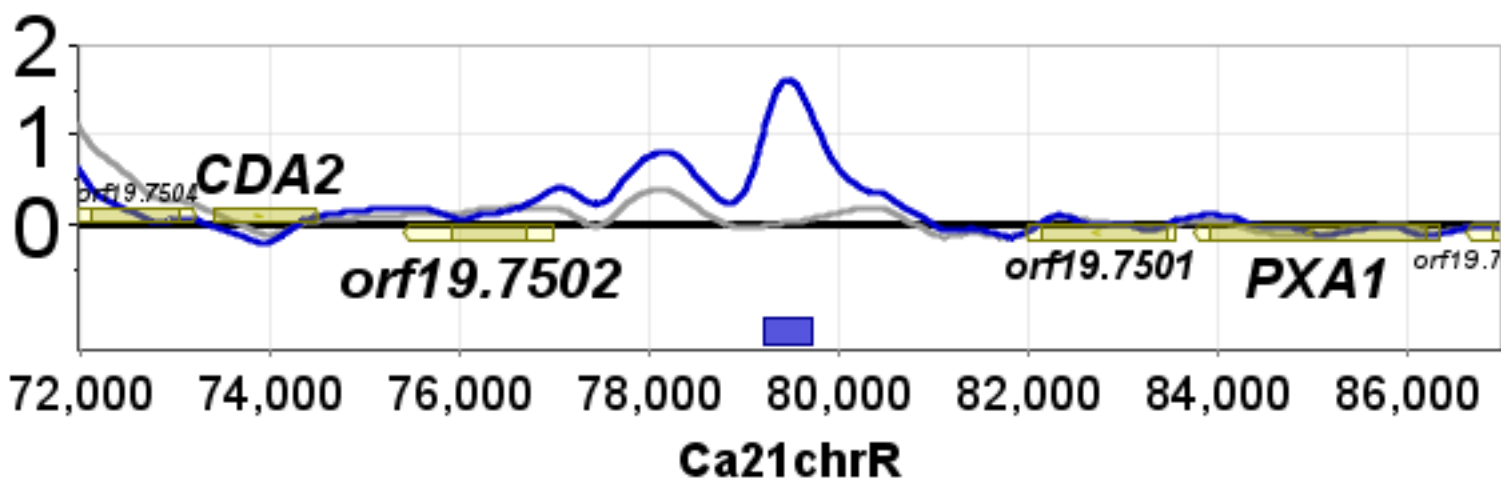
[1.711] Ca21chr3:1720927-1735926 [+] [TCC1, orf19.6732, orf19.6731.1, orf19.6731, ntar\_686]



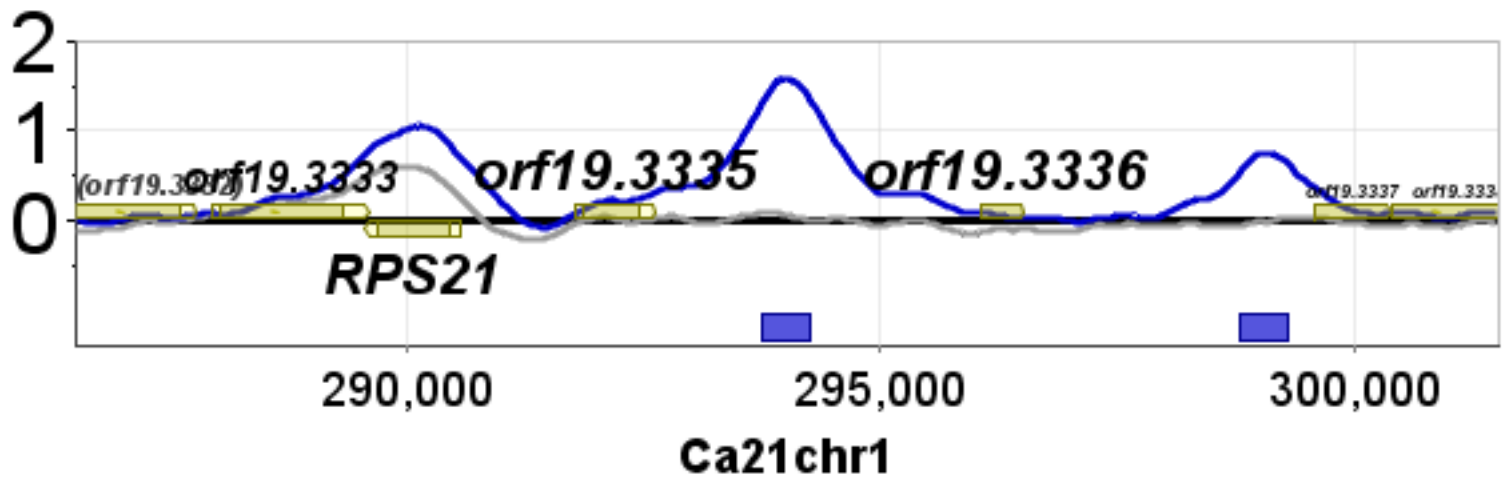
[1.617] Ca21chr3:948602-963601 [+] [TEC1, orf19.5910, CMK1, MAK21]



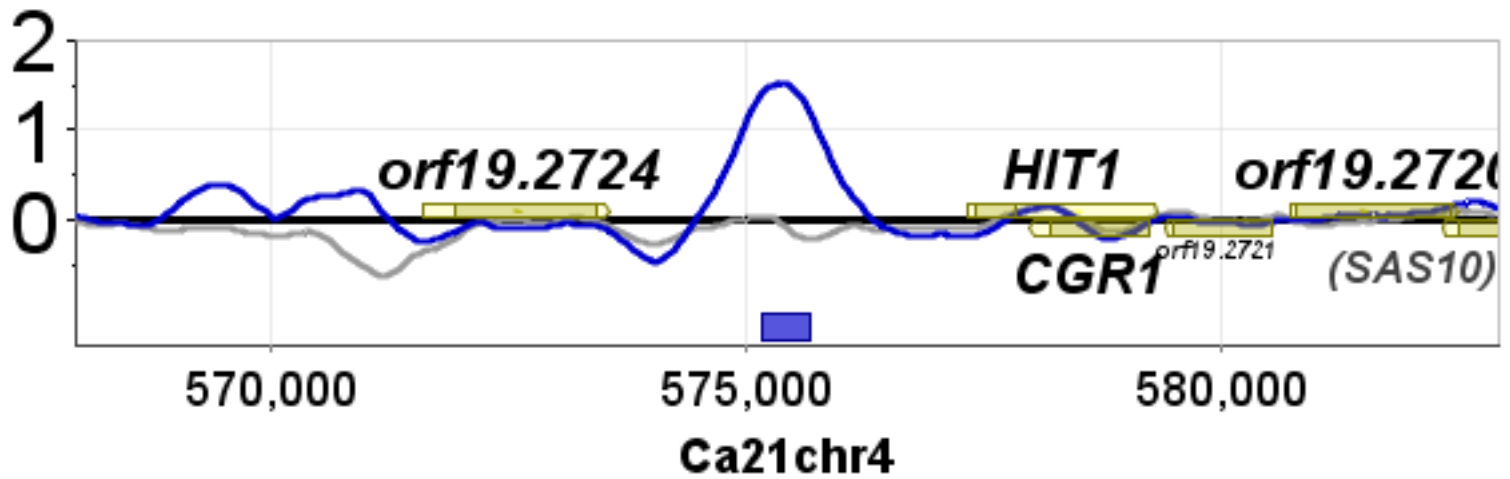
[1.615] Ca21chrR:71967-86966 [+] [orf19.7502, orf19.7501, CDA2, PXA1, orf19.7504]



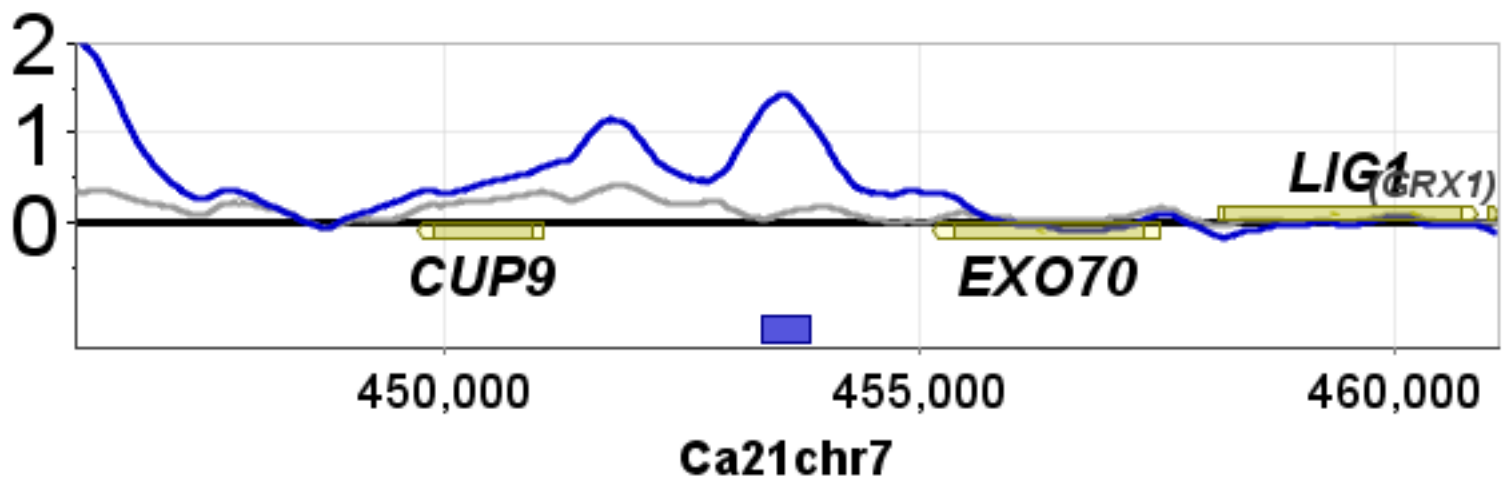
[1.58] Ca21chr1:286508-301507 [+] [orf19.3336, orf19.3335, ntar\_28, RPS21, orf19.3337]



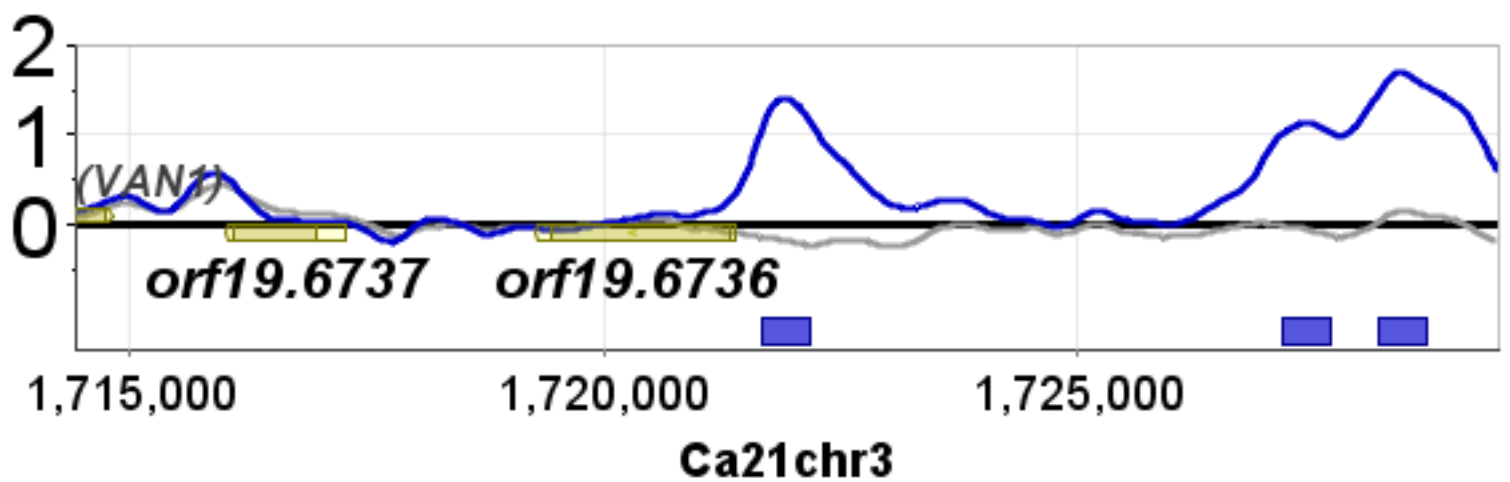
[1.521] Ca21chr4:567920-582919 [+] [ntar\_770, HIT1, orf19.2724, CGR1, orf19.2721]



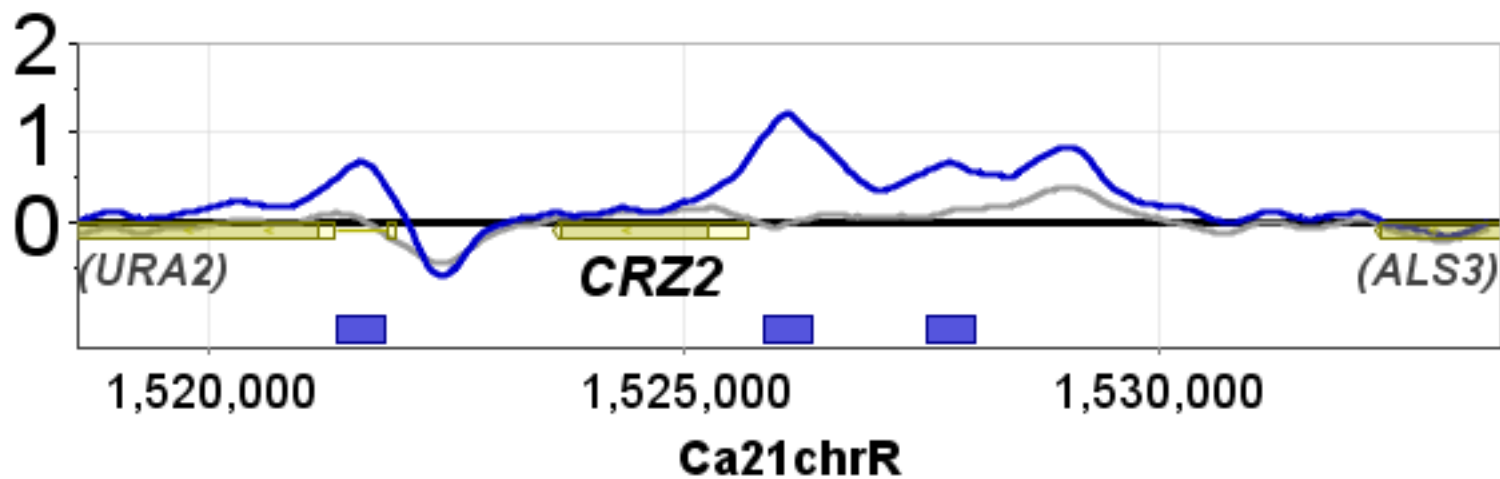
[1.442] Ca21chr7:446097-461096 [+] [CUP9, EXO70, LIG1, GRX1]



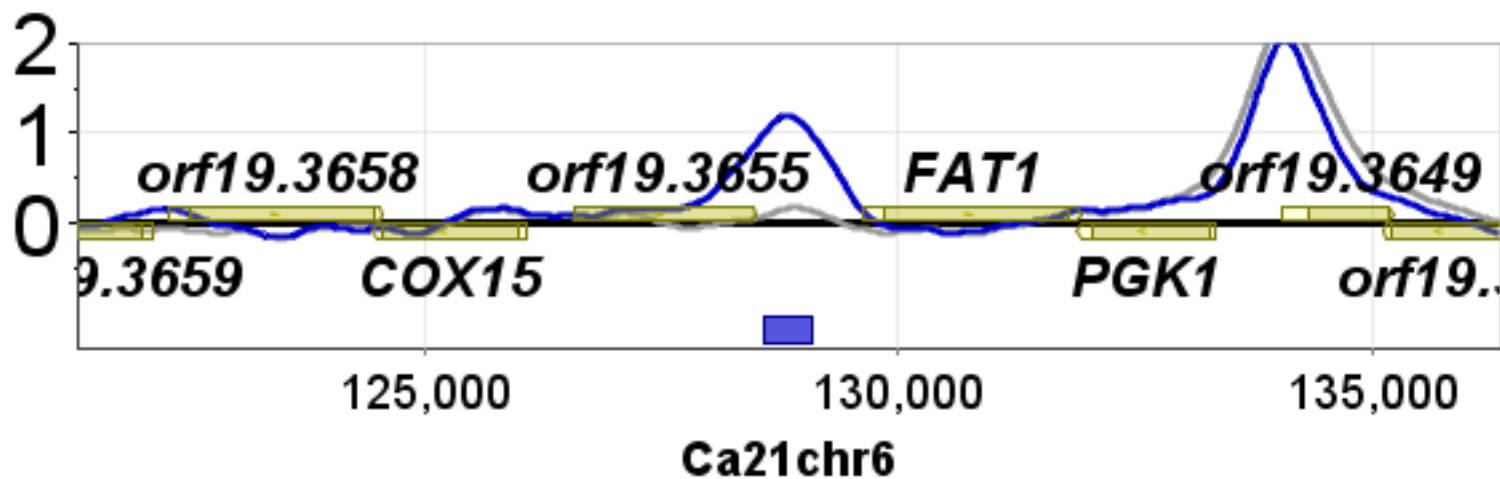
[1.394] Ca21chr3:1714420-1729419 [+] [orf19.6736, ntar\_685, orf19.6737, tf(gaa)5, tr(ucu)5]



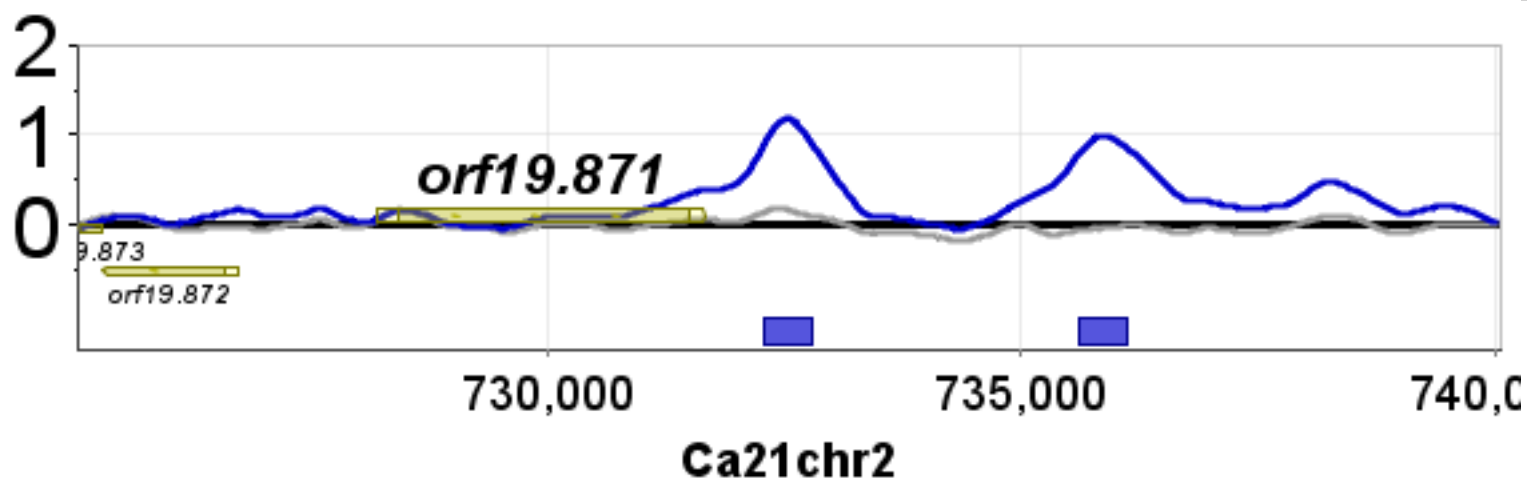
[1.21] Ca21chrR:1518597-1533596 [+] [CRZ2, ntar\_1331, URA2, ALS3]



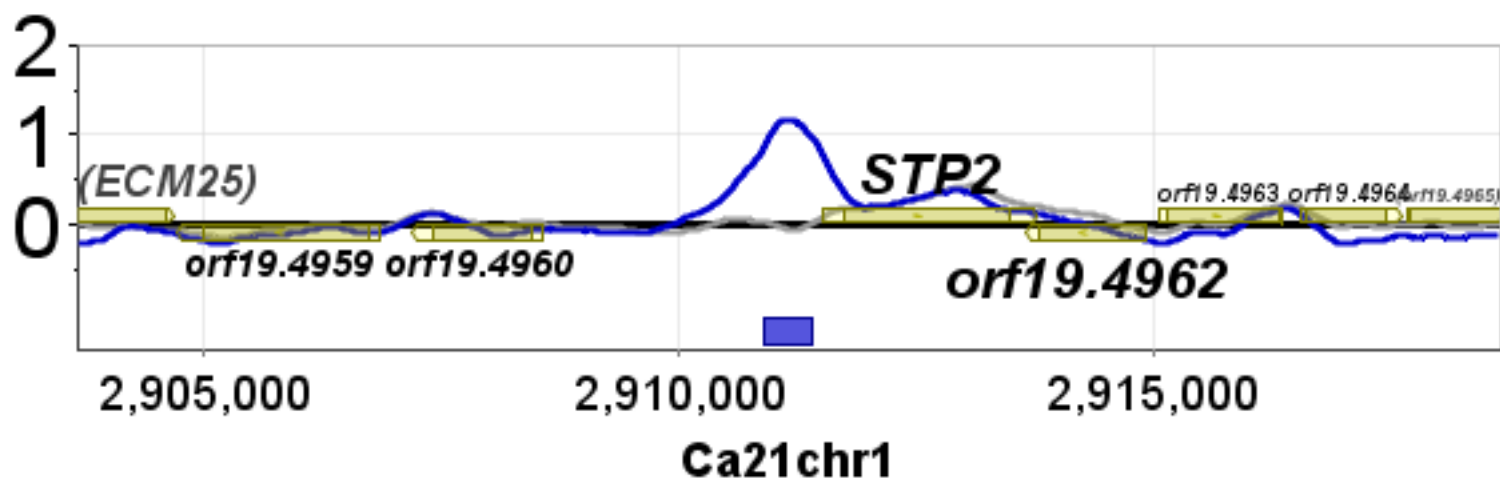
[1.192] Ca21chr6:121338-136337 [+] [Intar\_973, ntar\_972, FAT1, orf19.3655, COX15]



[1.186] Ca21chr2:725040-740039 [+] [ntar\_353, orf19.871, orf19.872, orf19.873]

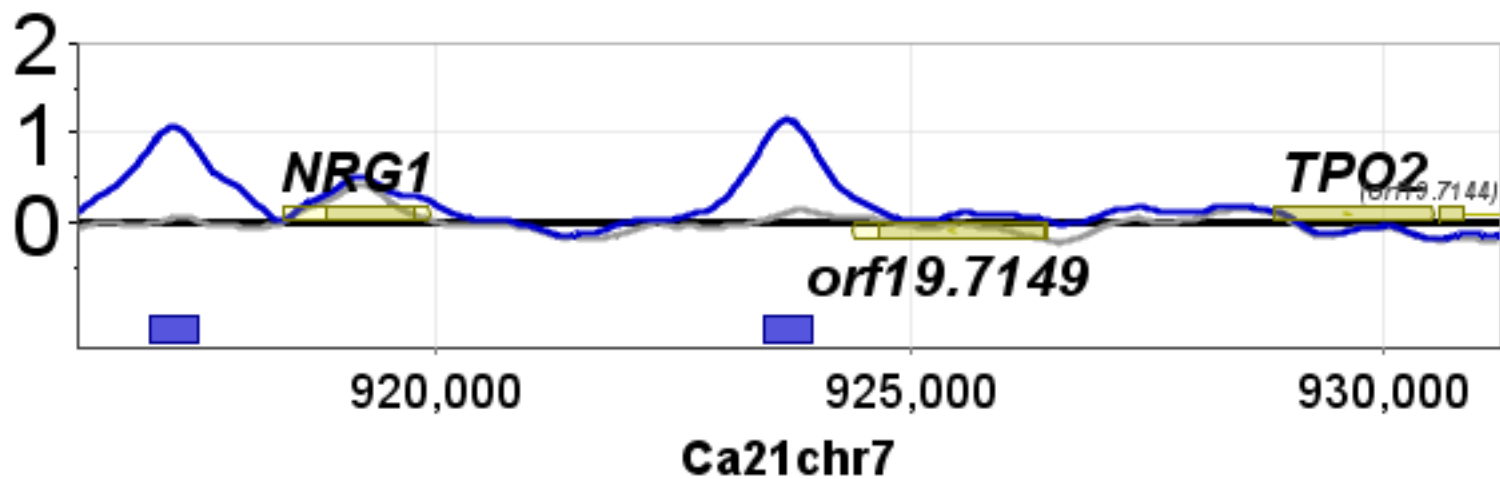


[1.167] Ca21chr1:2903650-2918649 [+] [STP2, ntar\_262, orf19.4960, orf19.4962, orf19.4963]

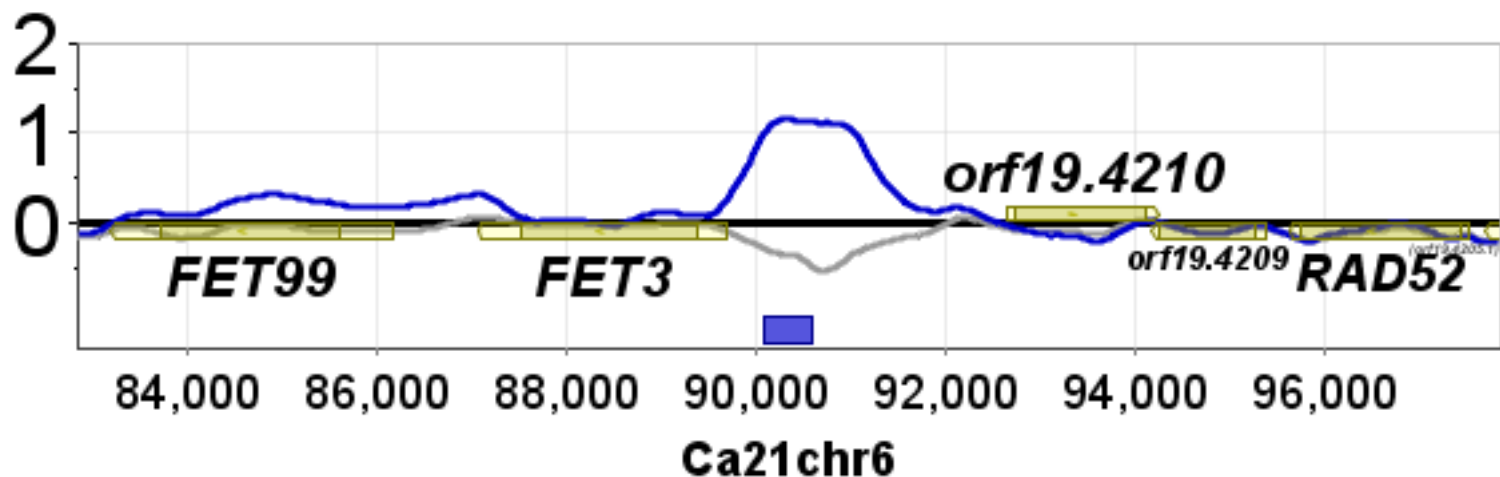




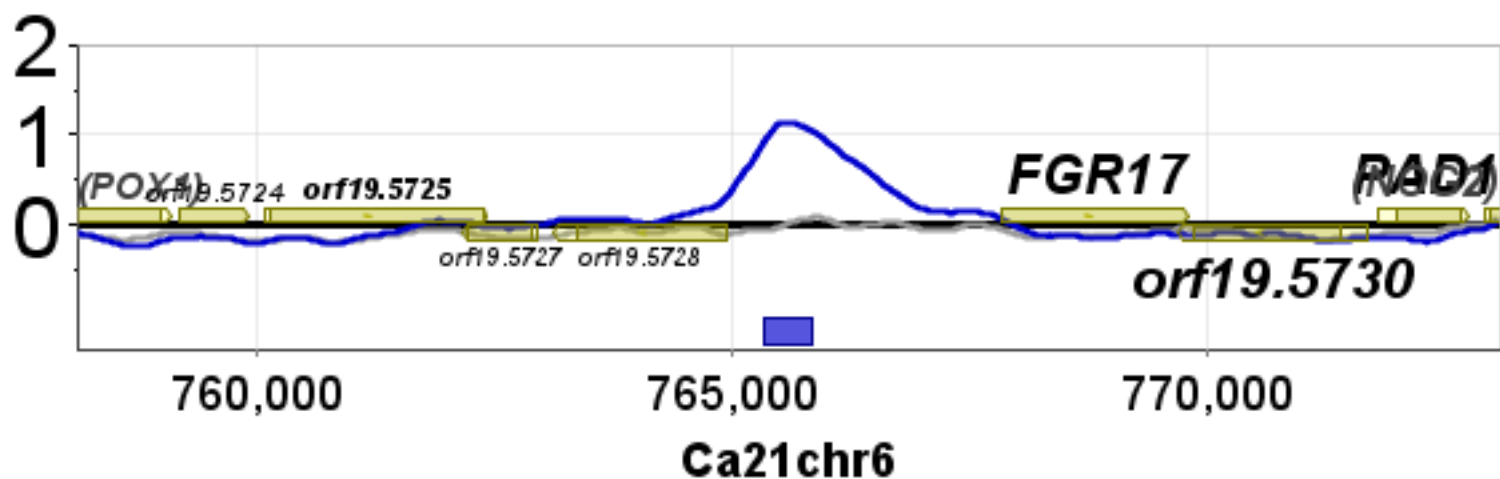
[1.164] Ca21chr7:916211-931210 [+] [orf19.7149, ntar\_1154, TPO2, NRG1, ntar\_1155]



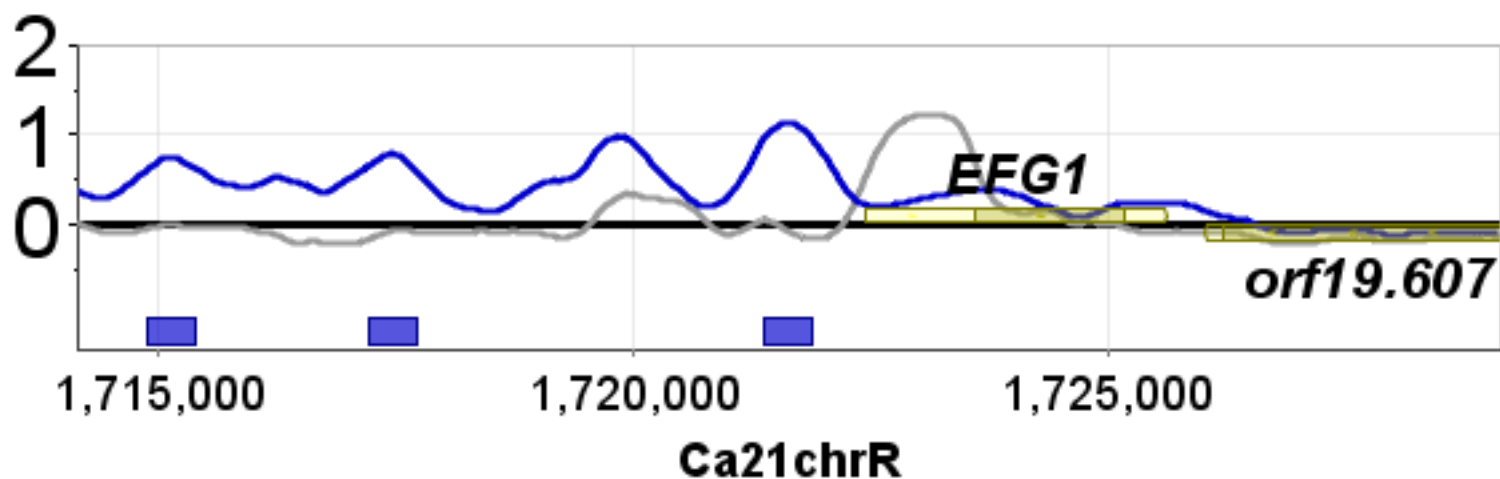
[1.161] Ca21chr6:82830-97829 [+] [ntar\_970, FET3, orf19.4210, FET99, orf19.4209]



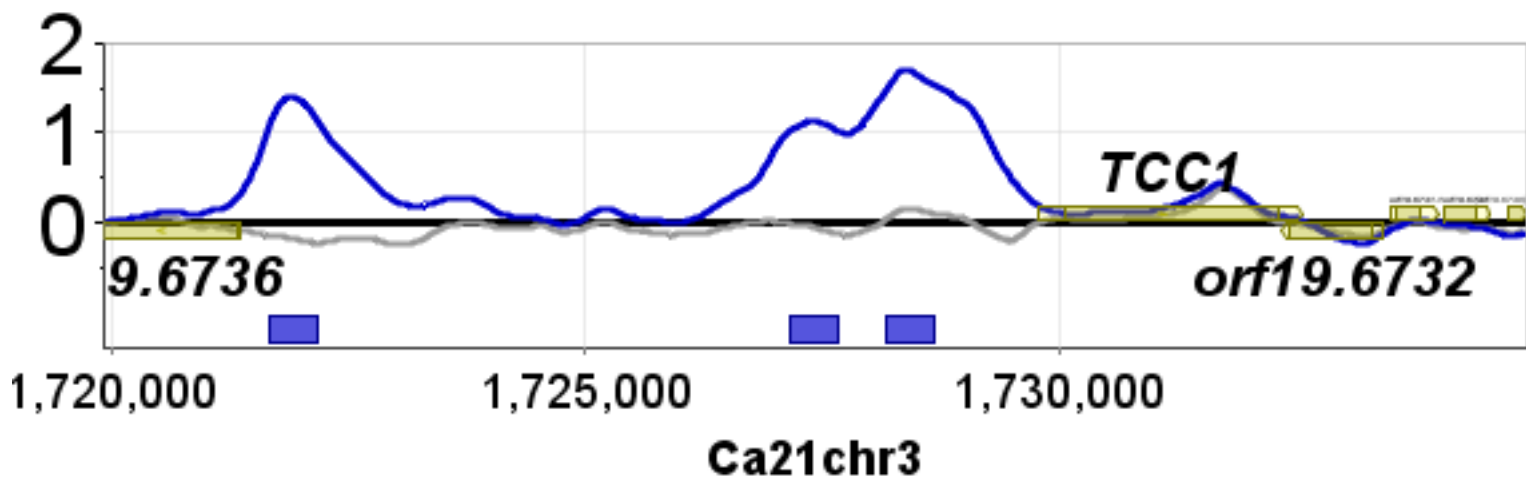
[1.141] Ca21chr6:758090-773089 [+] [orf19.5728, FGR17, orf19.5727, orf19.5725, orf19.5730]



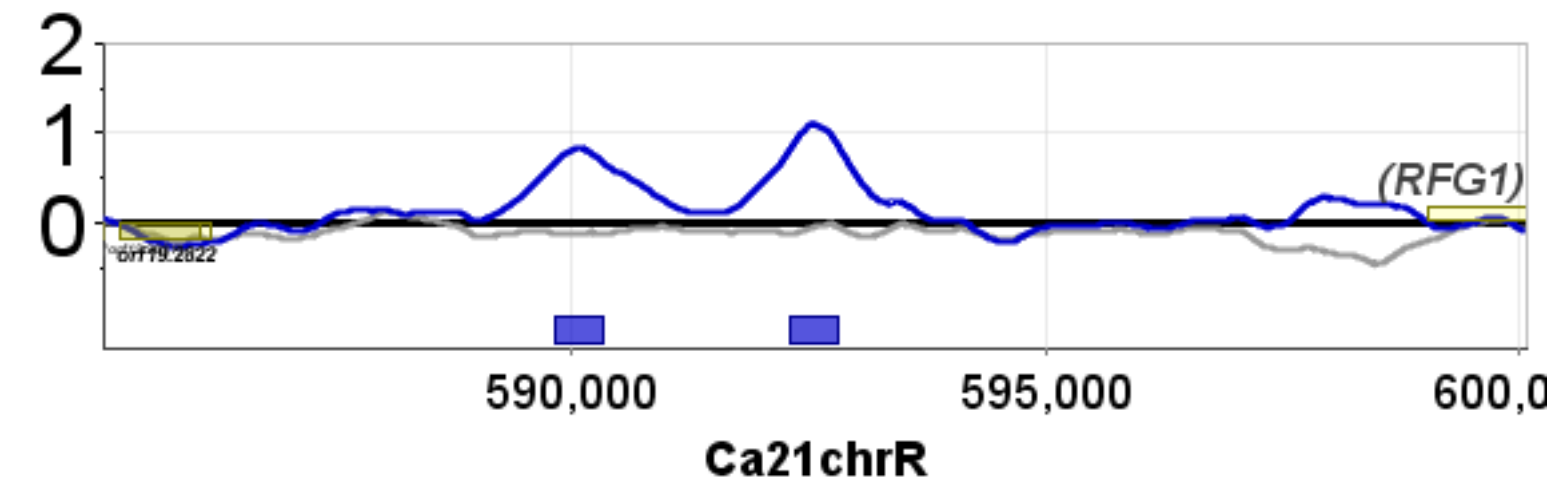
[1.139] Ca21chrR:1714132-1729131 [+] [EFG1, ntar\_1352, ntar\_1353, ntar\_1351, orf19.609]



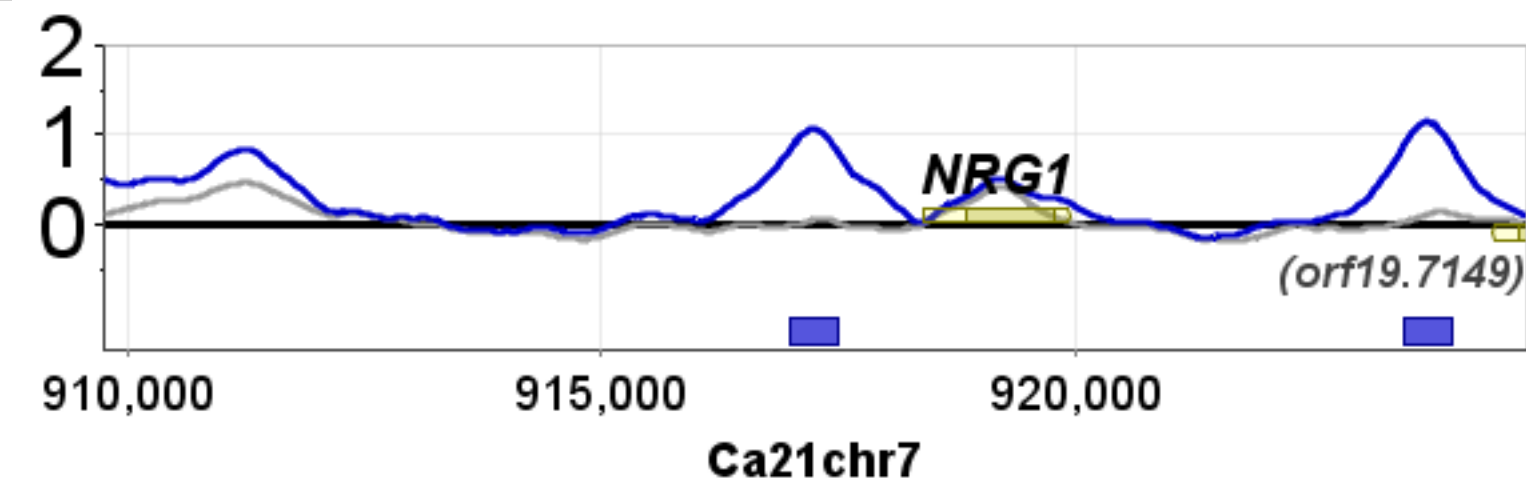
[1.129] Ca21chr3:1719915-1734914 [+] [TCC1, orf19.6732, orf19.6736, orf19.6731.1, orf19.6731]



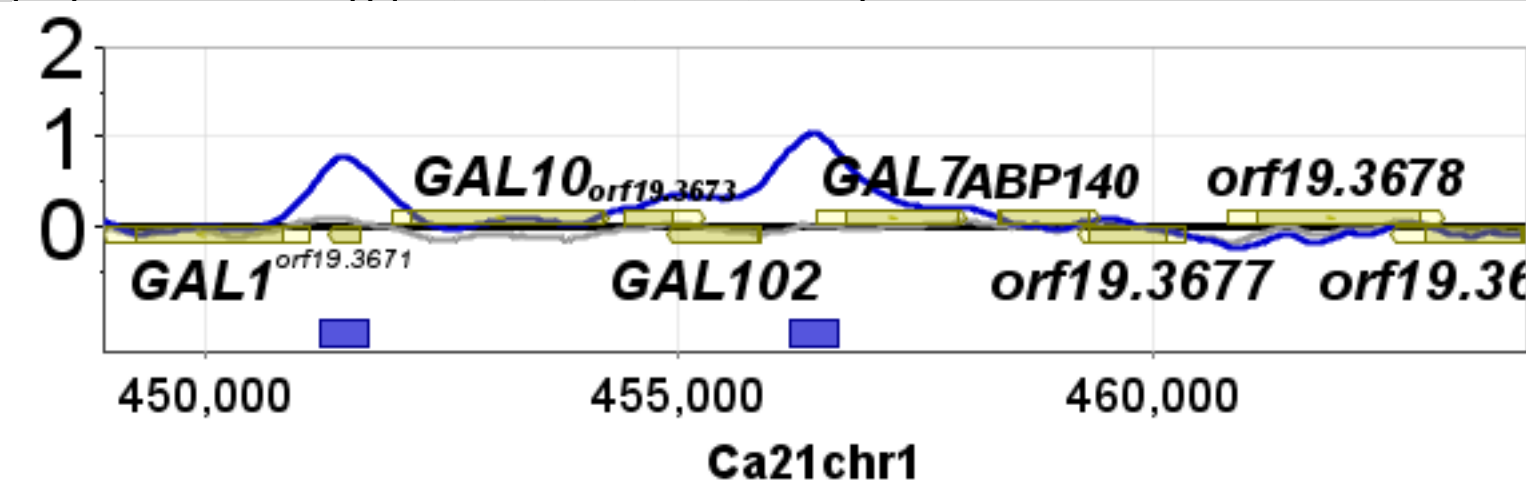
[1.094] Ca21chrR:585064-600063 [+] [orf19.2822, RFG1, orf19.2821]



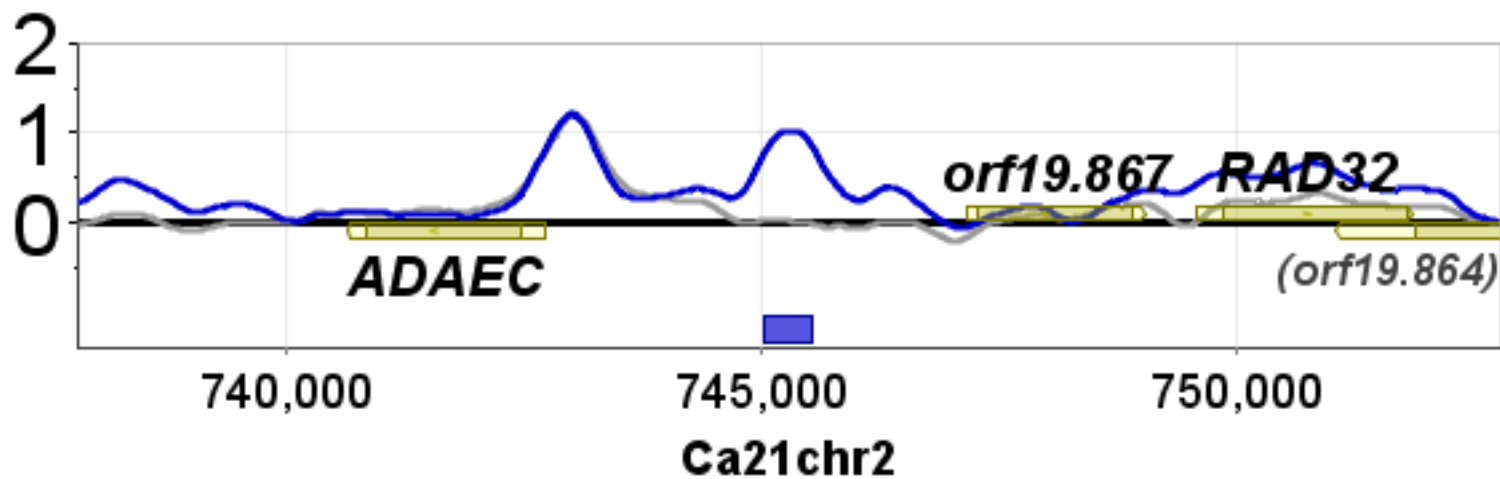
[1.058] Ca21chr7:909738-924737 [+] [NRG1, ntar\_1153, orf19.7151, ntar\_1152, ntar\_1151]



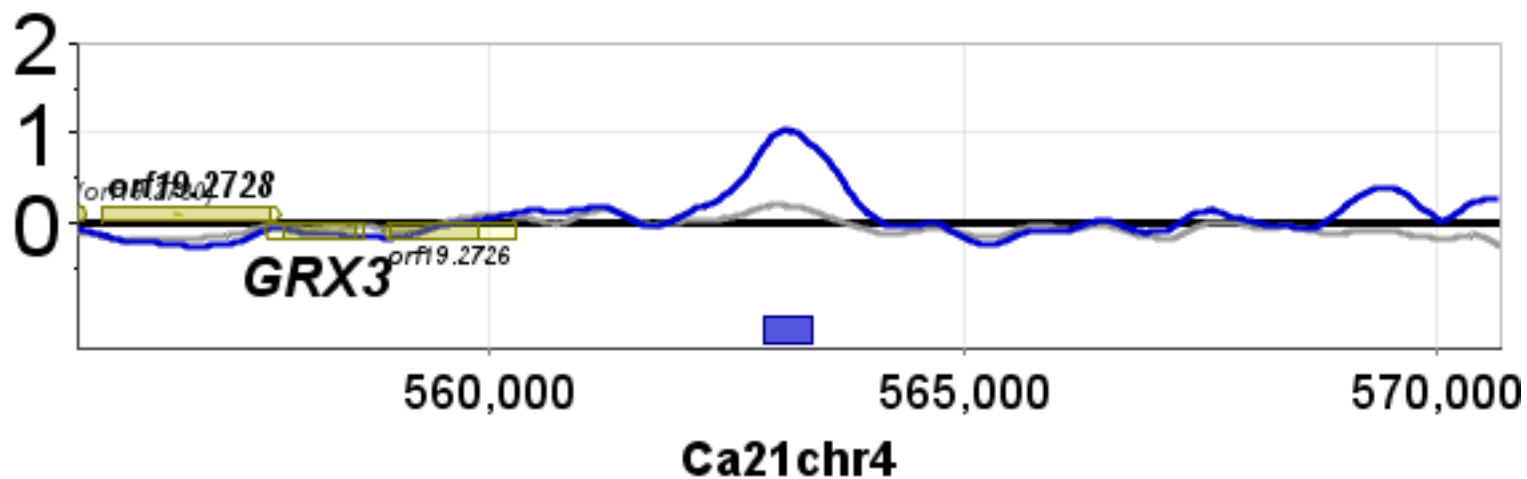
[1.038] Ca21chr1:448928-463927 [+] [GAL7, GAL102, ABP140, orf19.3673, orf19.3677]



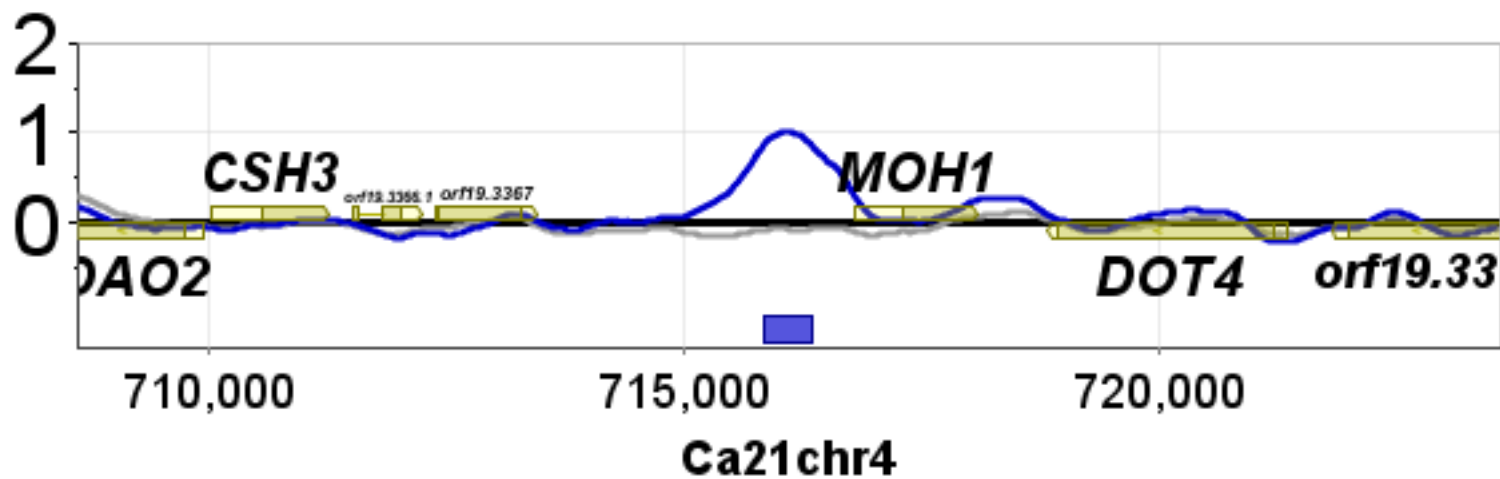
[1.025] Ca21chr2:737779-752778 [+] [orf19.867, ADAEC, RAD32, ntar\_354, orf19.864]



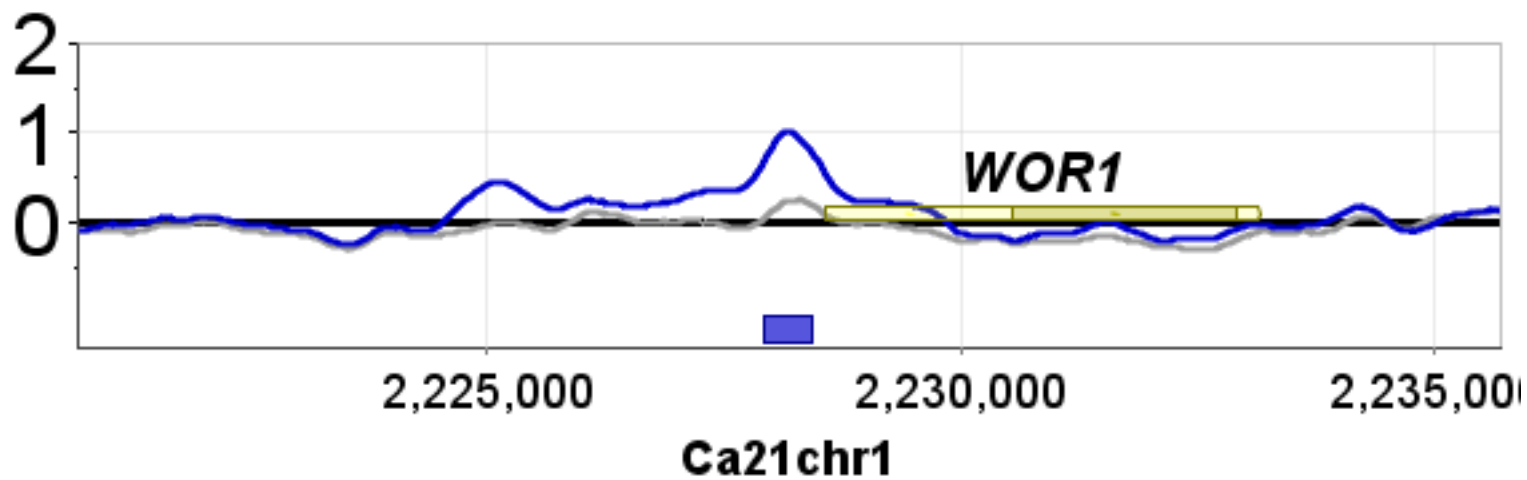
[1.022] Ca21chr4:555654-570653 [+] [orf19.2726, orf19.2725, ntar\_769, GRX3, orf19.2728]



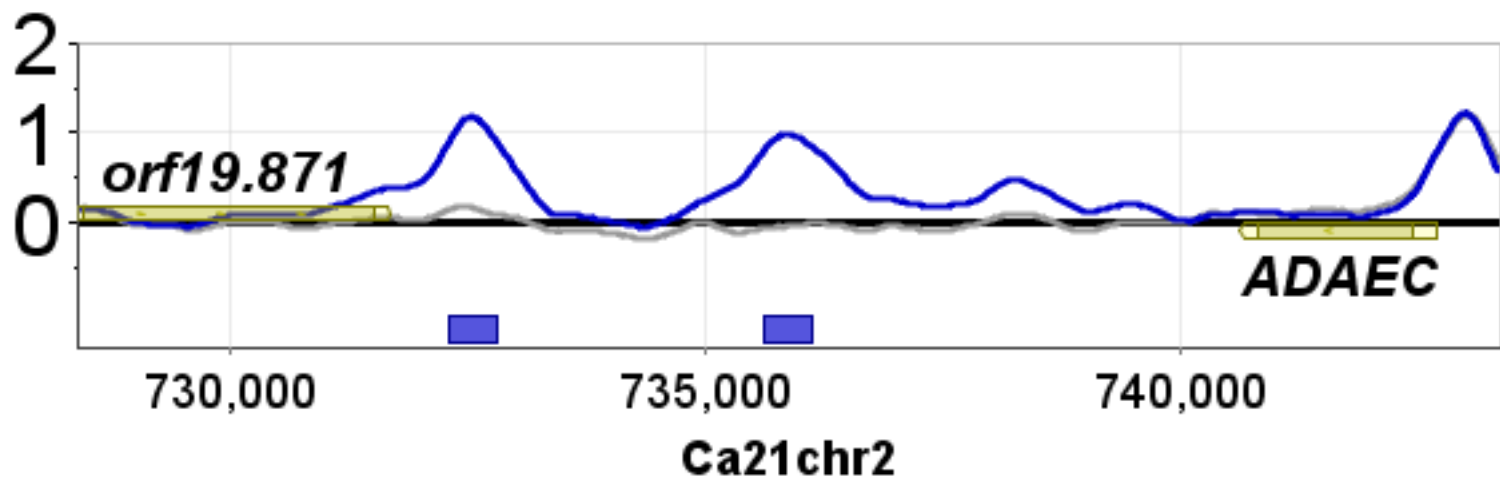
[1.007] Ca21chr4:708600-723599 [+] [MOH1, orf19.3368, orf19.3367, orf19.3366.1, DOT4]



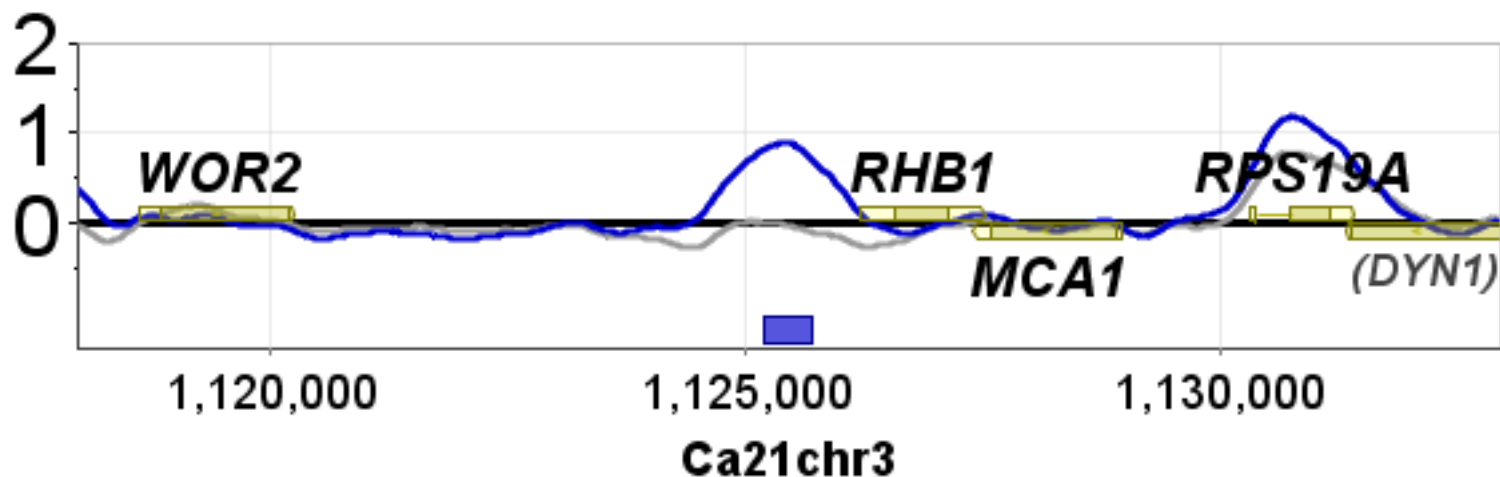
[1.002] Ca21chr1:2220676-2235675 [+] [WOR1, ntar\_207]



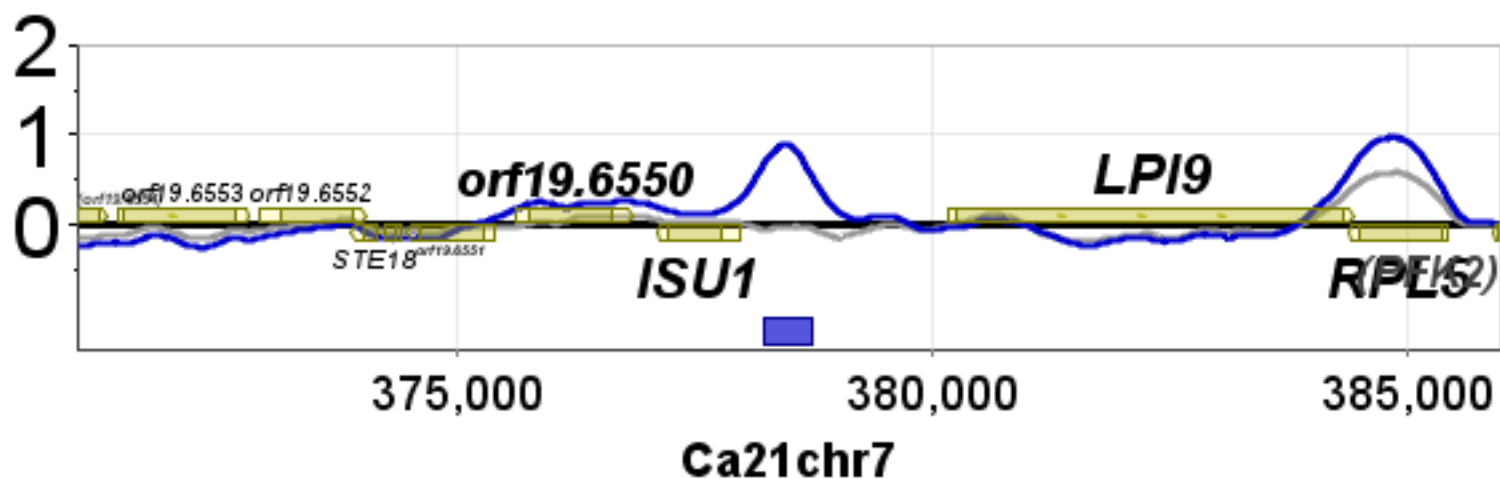
[0.99] Ca21chr2:728369-743368 [+] [ntar\_353, ntar\_354, ADAEC, orf19.871]



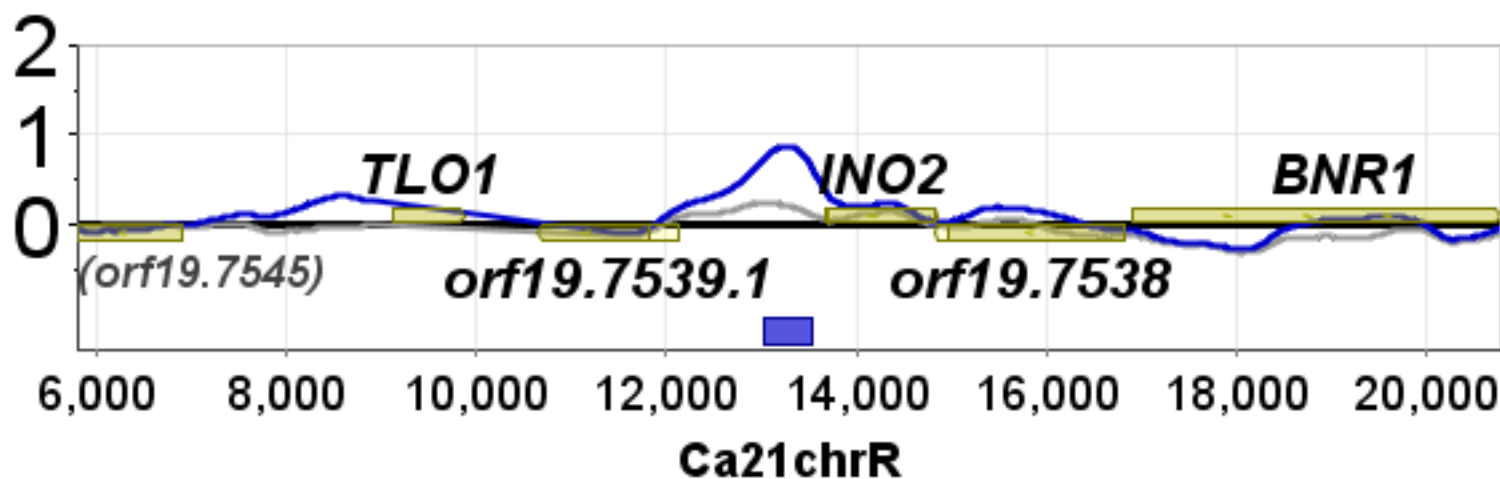
[0.892] Ca21chr3:1117948-1132947 [+] [ntar\_618, RHB1, ntar\_617, ntar\_616, ntar\_615]



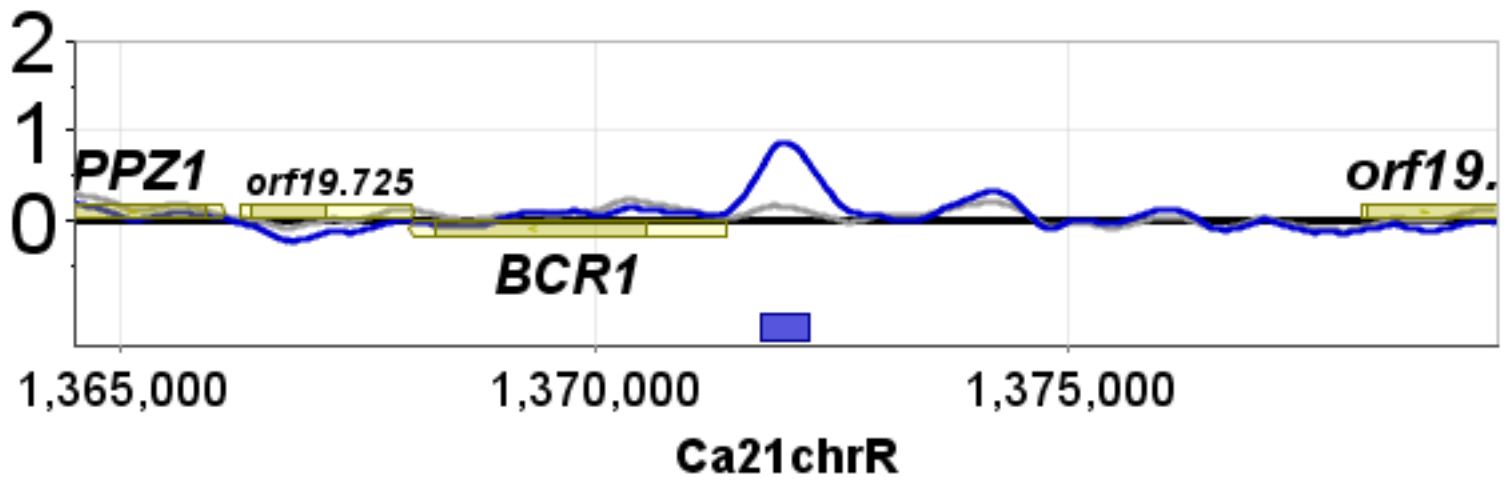
[0.891] Ca21chr7:370979-385978 [+] [ISU1, orf19.6547, ntar\_1096, LPI9, orf19.6550]



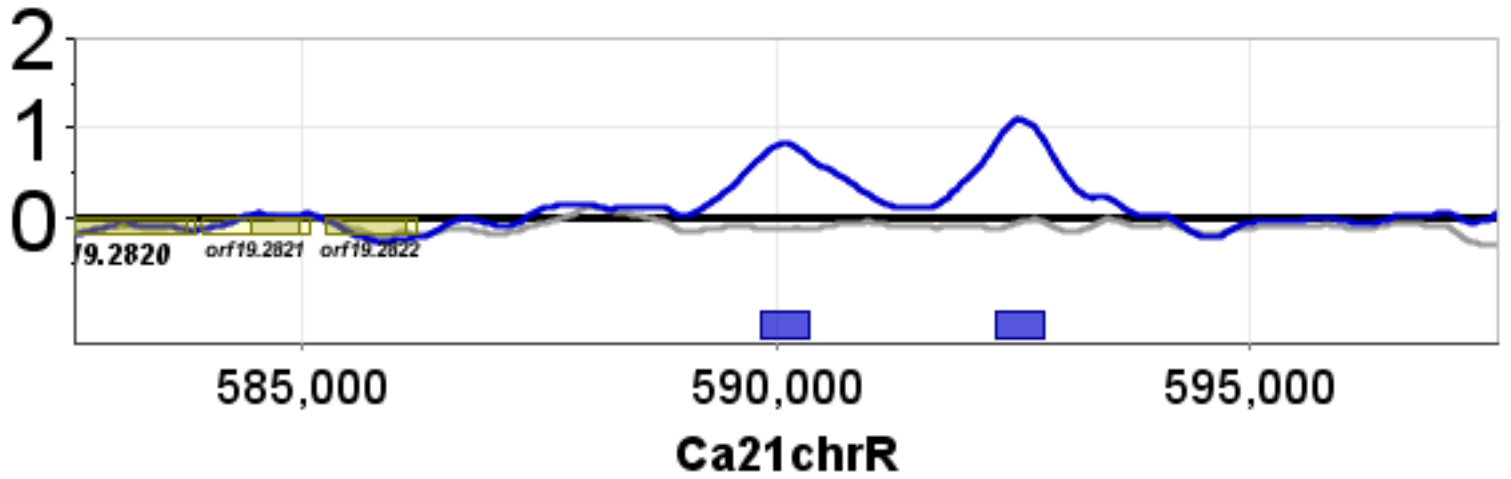
[0.865] Ca21chrR:5782-20781 [+] [INO2, orf19.7539.1, tl(caa)6, orf19.7538, BNR1]



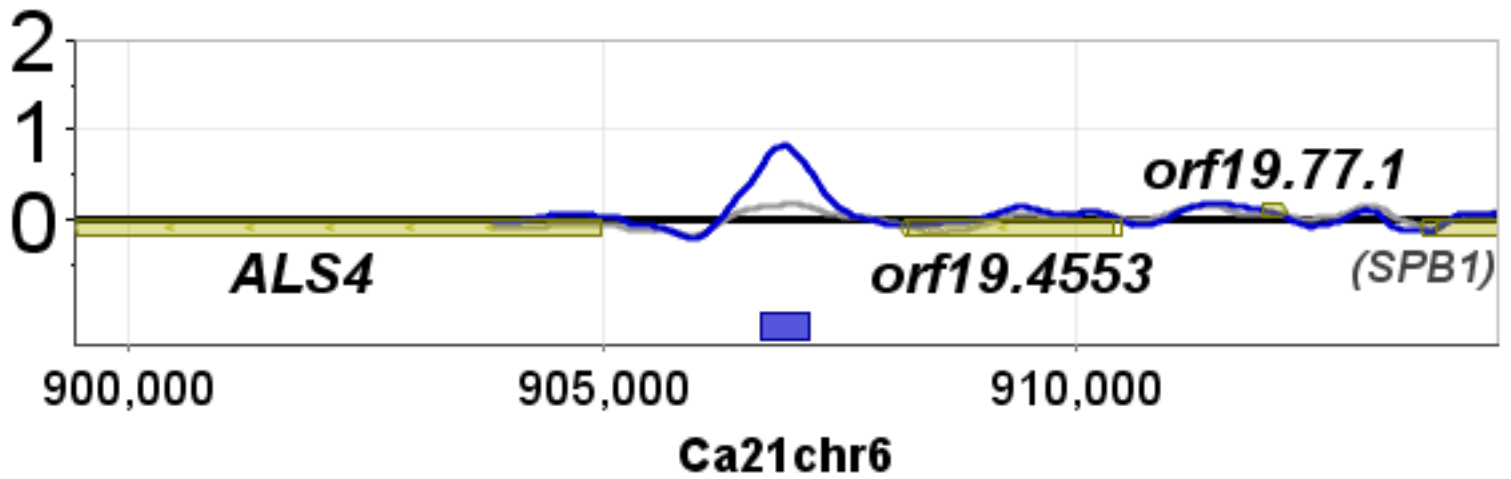
[0.86] Ca21chrR:1364508-1379507 [+] [BCR1, orf19.725, orf19.721, PPZ1]



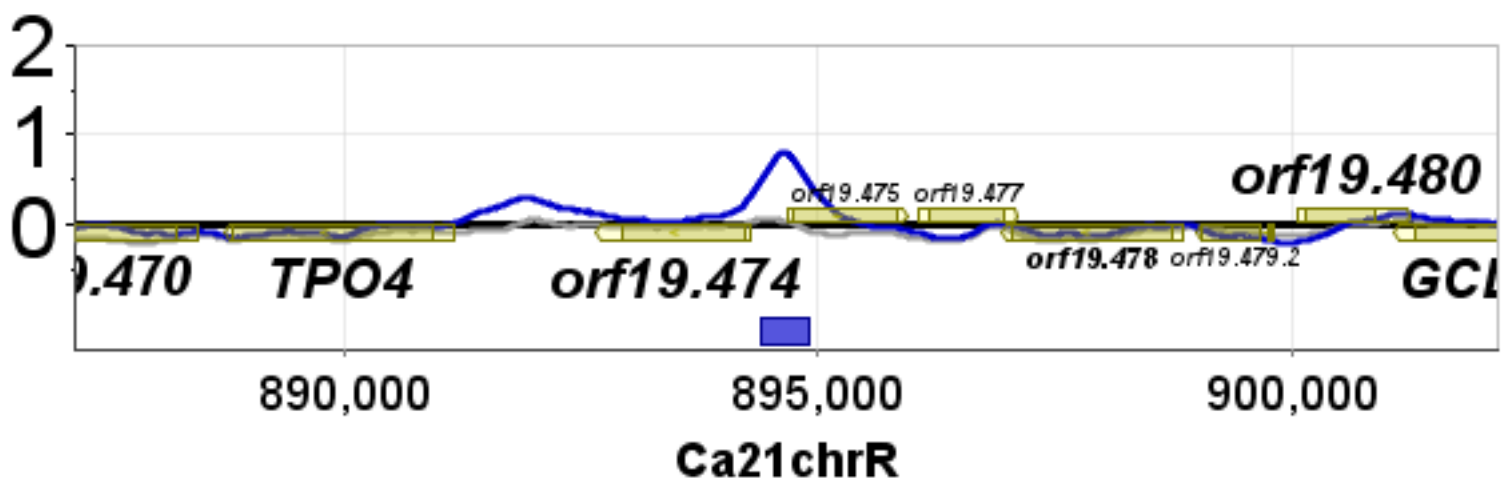
[0.829] Ca21chrR:582592-597591 [+] [orf19.2822, orf19.2821, orf19.2820]



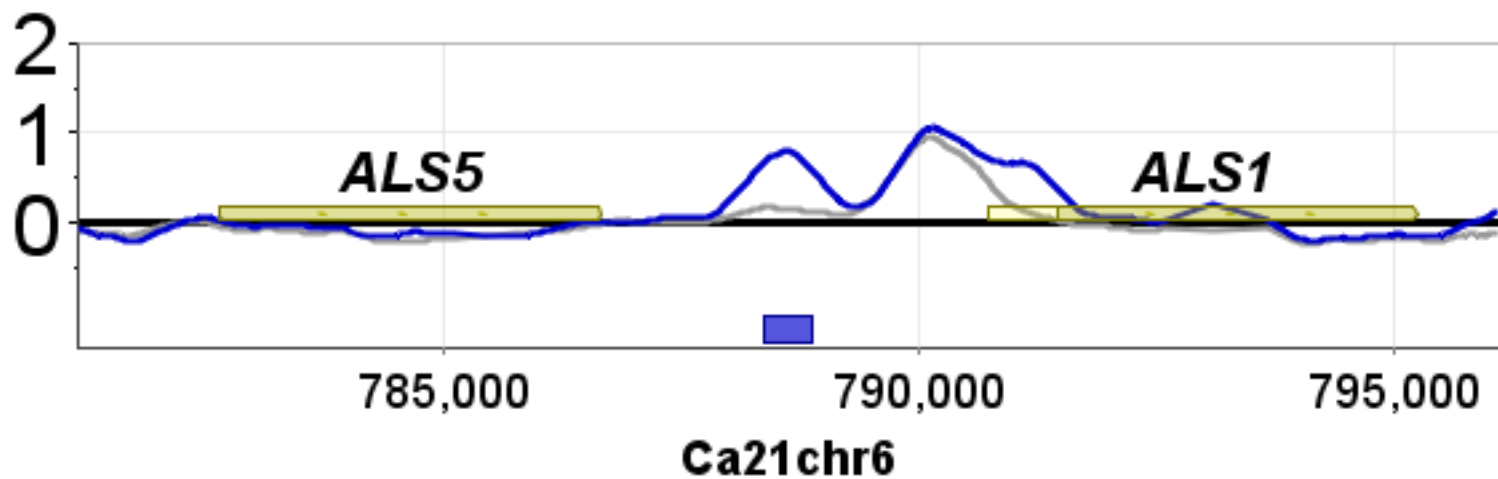
[0.817] Ca21chr6:899422-914421 [+] [ALS4, orf19.4553, ntar\_1042, ntar\_1041, orf19.77.1]



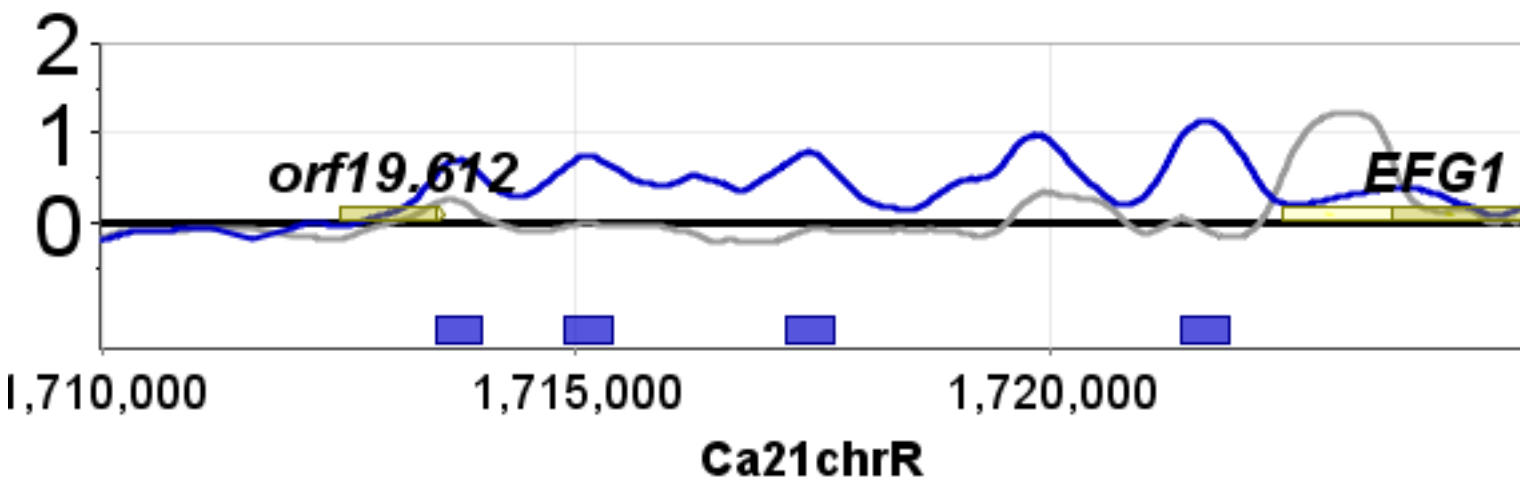
[0.796] Ca21chrR:887157-902156 [+] [orf19.475, orf19.474, orf19.477, TPO4, orf19.478]



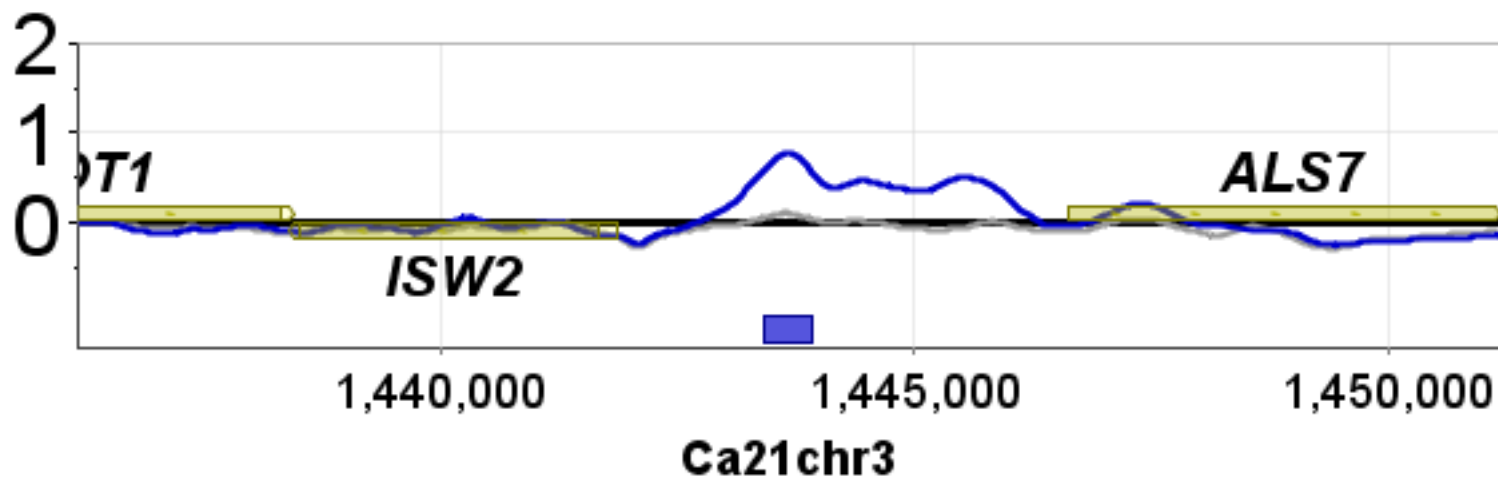
[0.791] Ca21chr6:781117-796116 [+] [ALS1, ALS5, ntar\_1030, ntar\_1029]



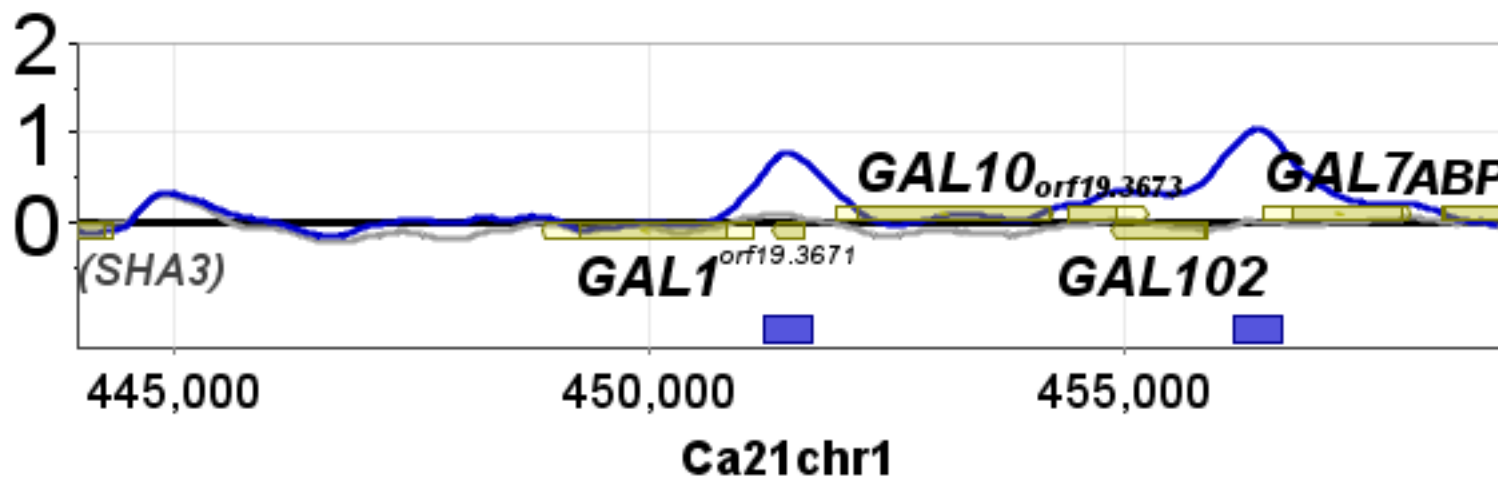
[0.79] Ca21chrR:1709966-1724965 [+] [ntar\_1351, ntar\_1353, ntar\_1352, tq(qcc)1, orf19.612]



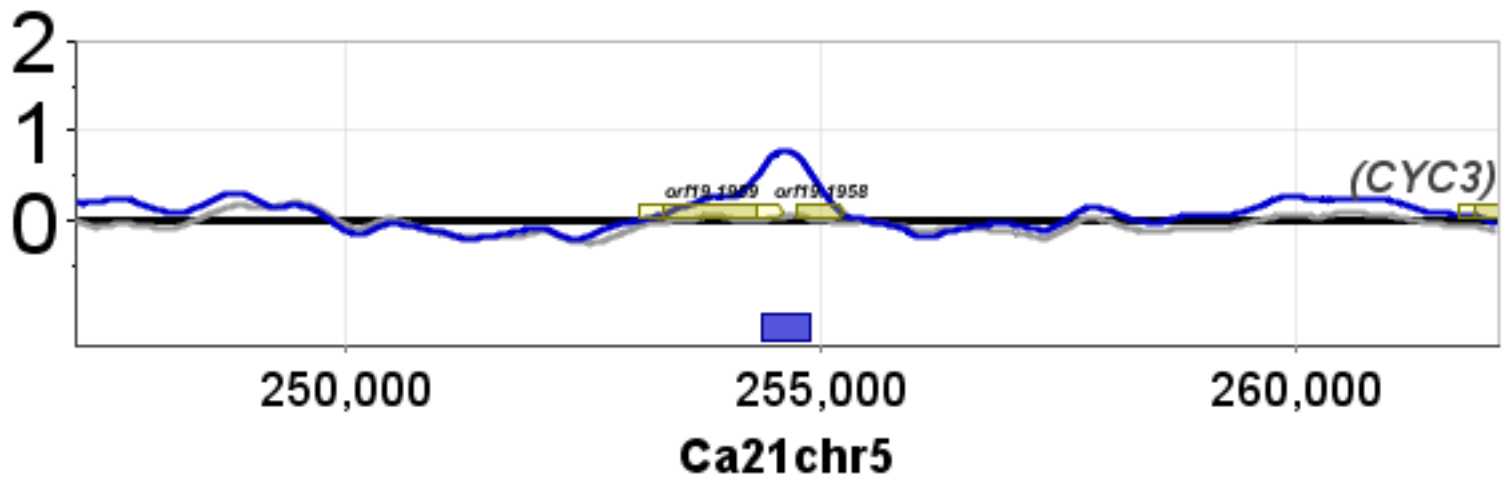
[0.781] Ca21chr3:1436169-1451168 [+] [ntar\_656, ISW2, ALS7, DOT1]



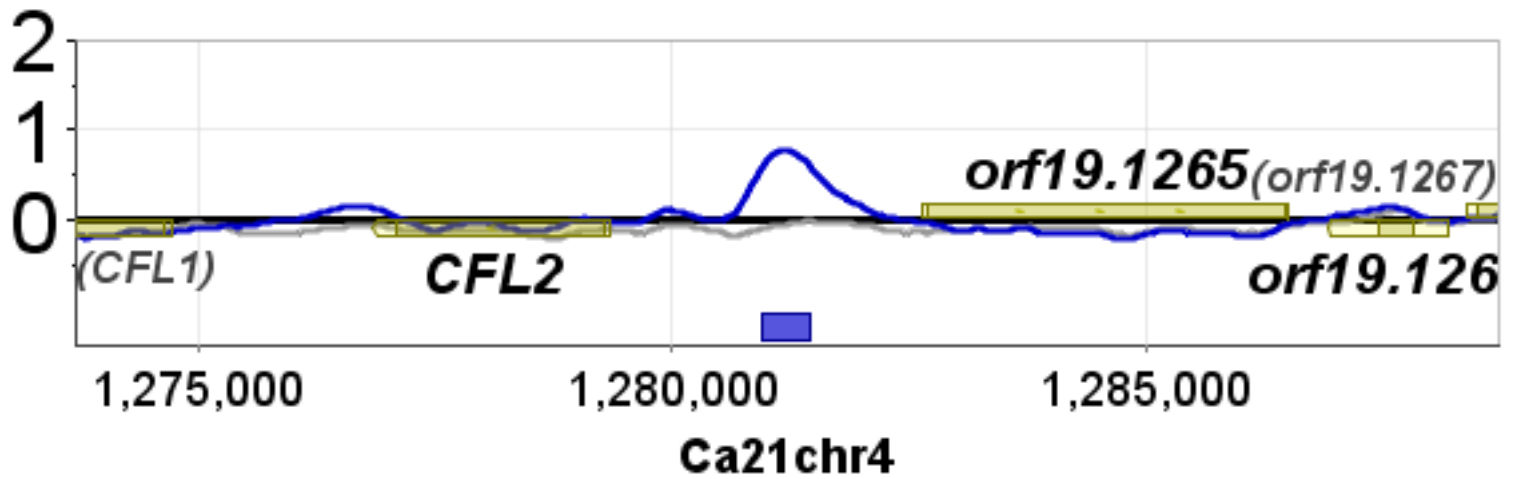
[0.779] Ca21chr1:443967-458966 [+] [orf19.3671, GAL1, GAL10, orf19.3673, ntar\_43]



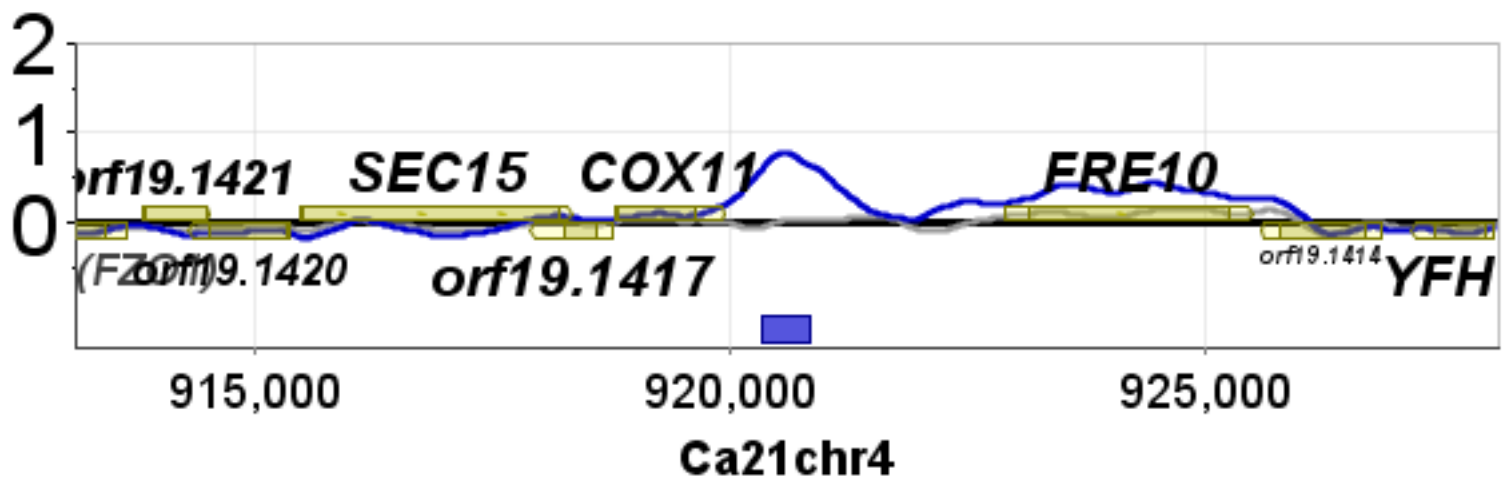
[0.775] Ca21chr5:247139-262138 [+] [orf19.1958, orf19.1959, ntar\_866, ntar\_867, ntar\_864]



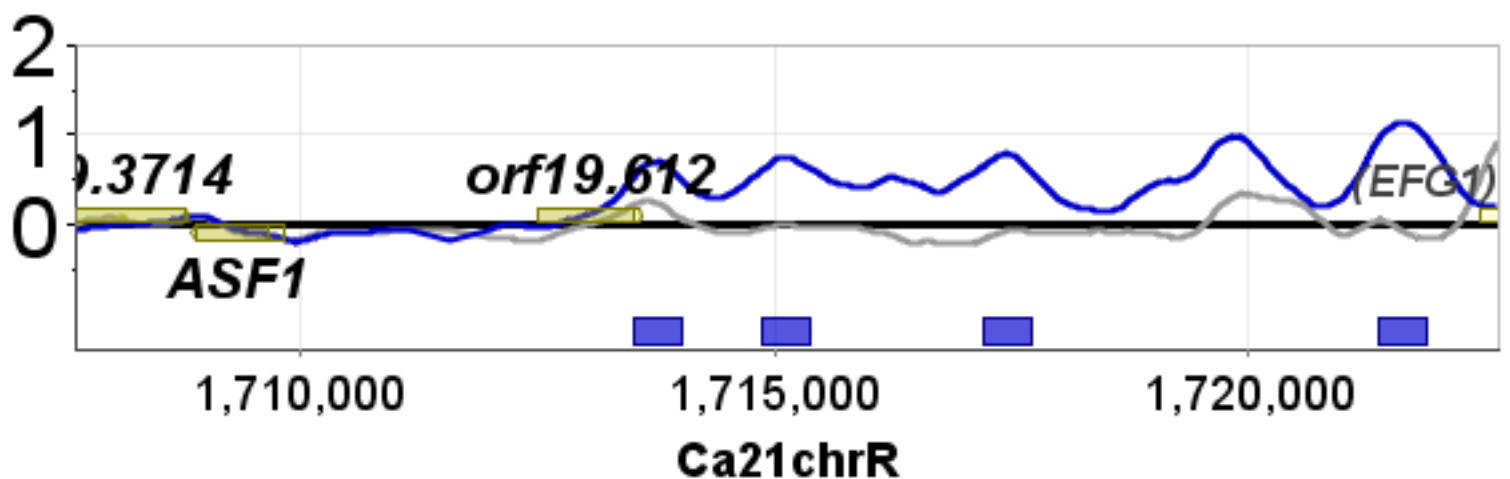
[0.767] Ca21chr4:1273703-1288702 [+] [orf19.1265, CFL2, ntar\_821, ntar\_820, CFL1]



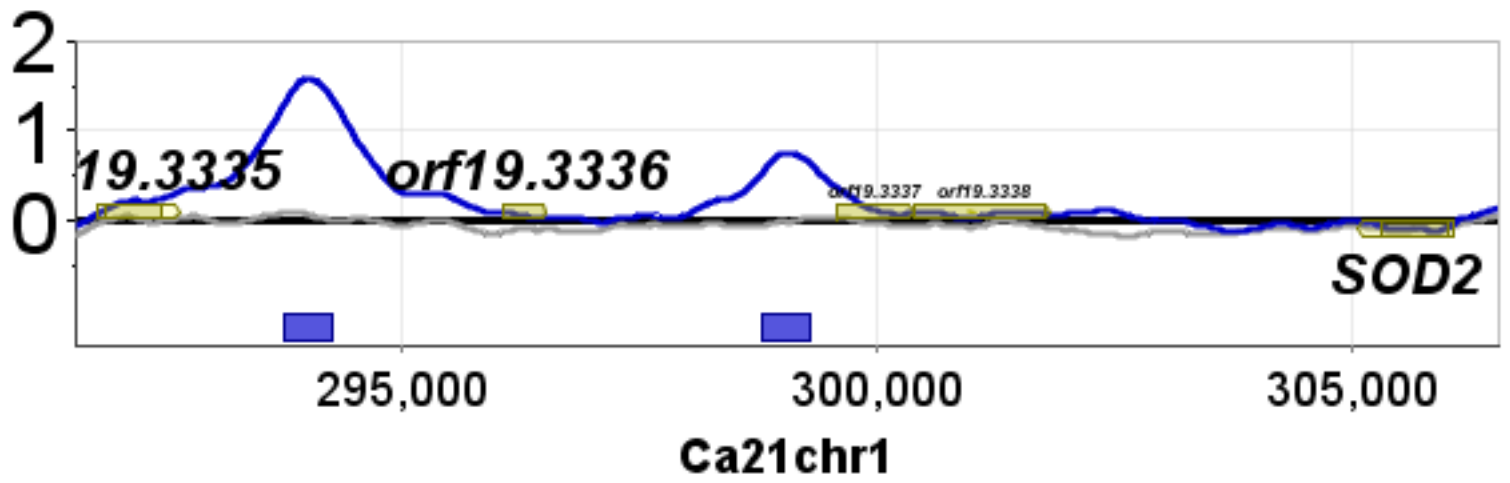
[0.759] Ca21chr4:913087-928086 [+] [ntar\_797, COX11, orf19.1417, FRE10, SEC15]



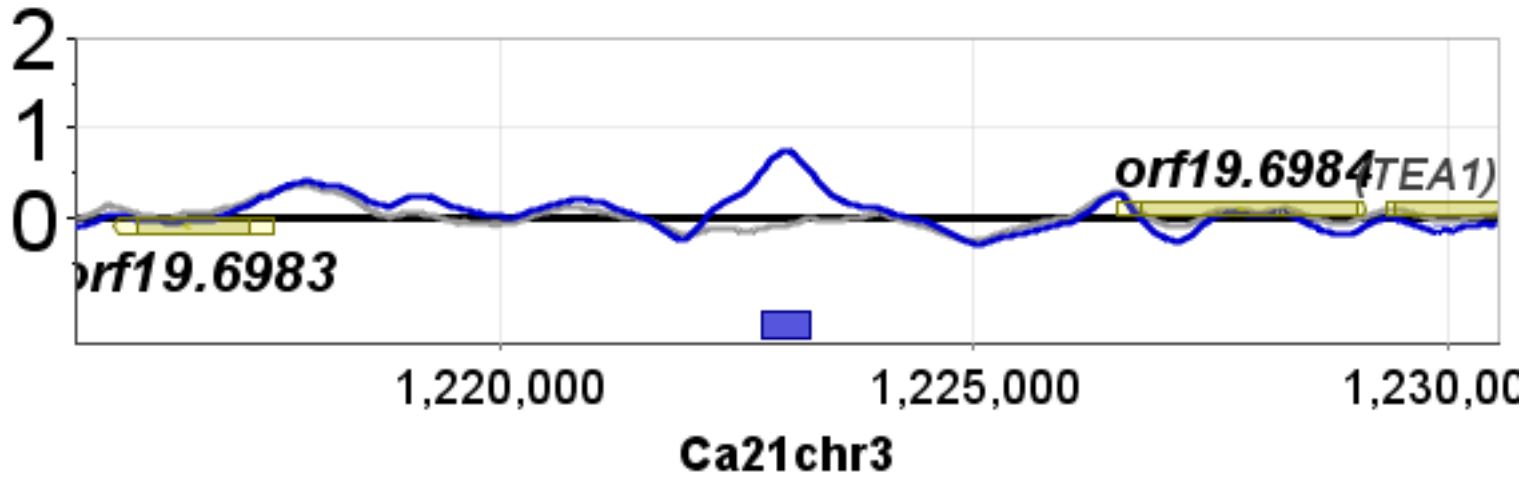
[0.757] Ca21chrR:1707627-1722626 [+] [tg(gcc)1, orf19.612, ntar\_1351, ntar\_1353, ntar\_1352]



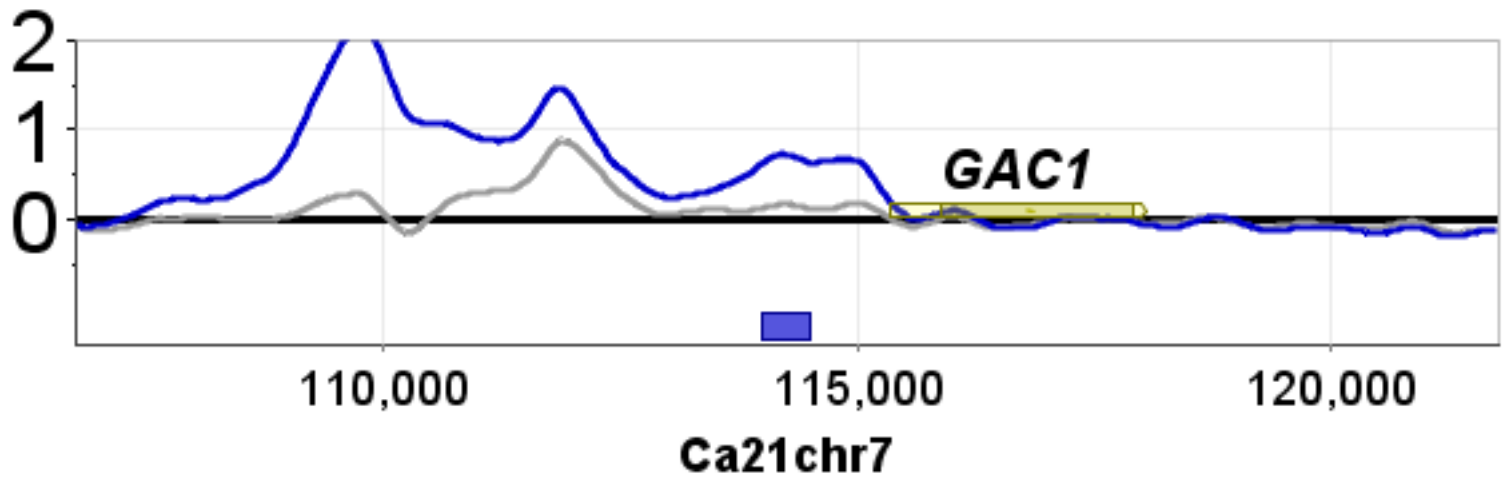
[0.751] Ca21chr1:291541-306540 [+] [orf19.3337, orf19.3338, orf19.3336, SOD2, orf19.3335]



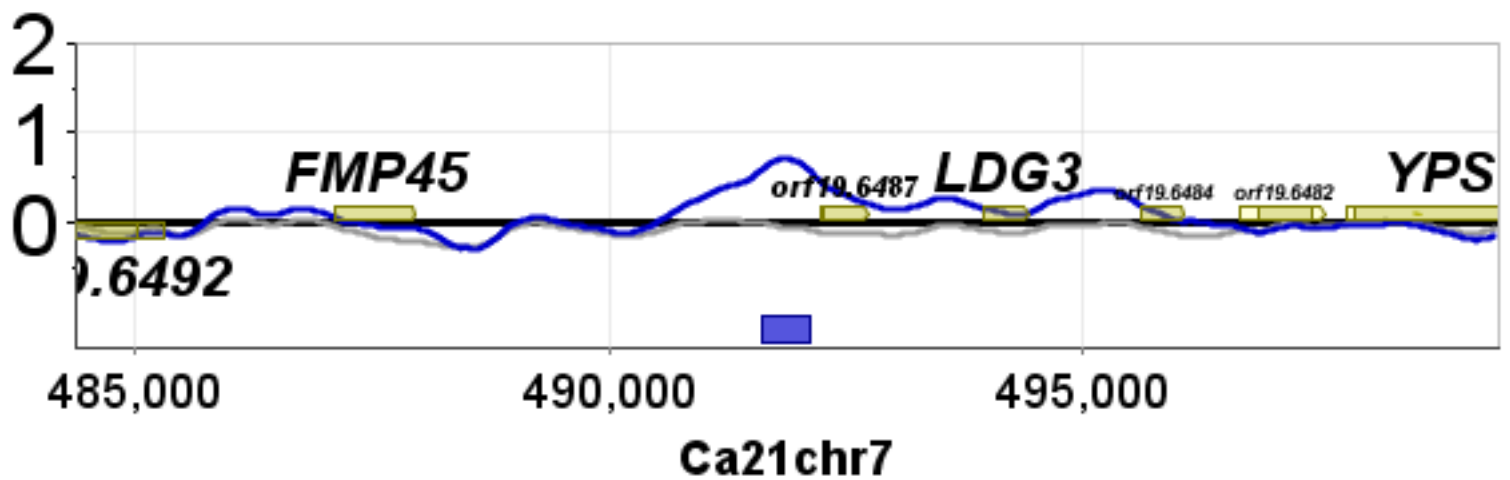
[0.74] Ca21chr3:1215524-1230523 [+] [ntar\_633, orf19.6984, orf19.6983, TEA1, ntar\_632]



[0.724] Ca21chr7:106753-121752 [+] [orf19.7054, GAC1, ntar\_1413, ntar\_1056, ntar\_1057]

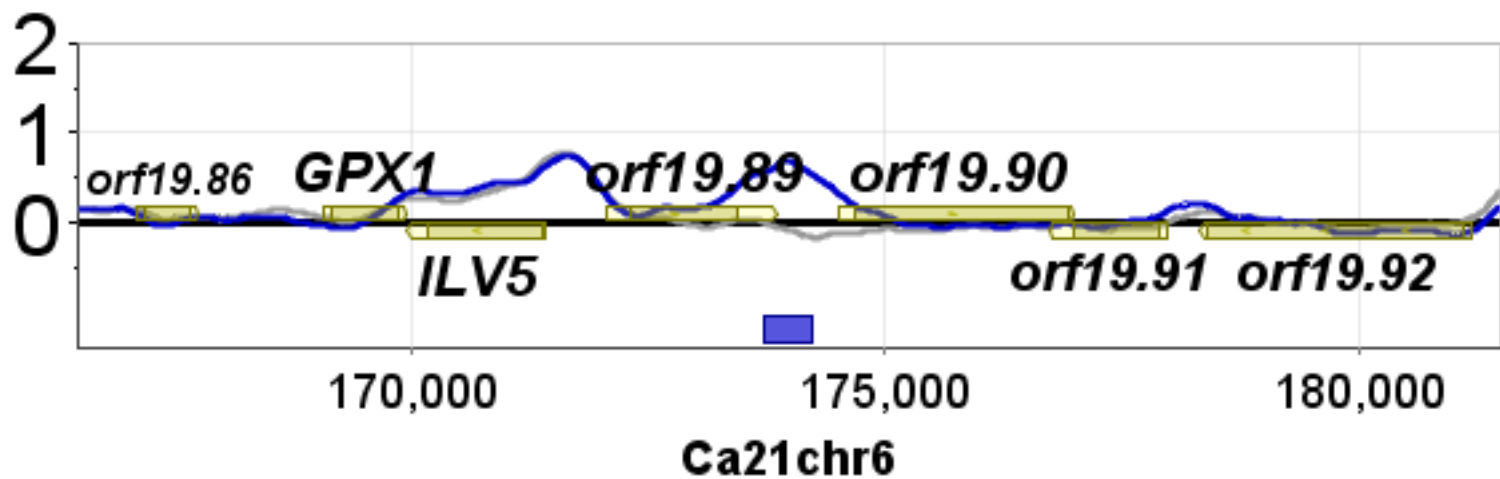


[0.714] Ca21chr7:484367-499366 [+] [orf19.6487, LDG3, orf19.6488, orf19.6484, FMP45]

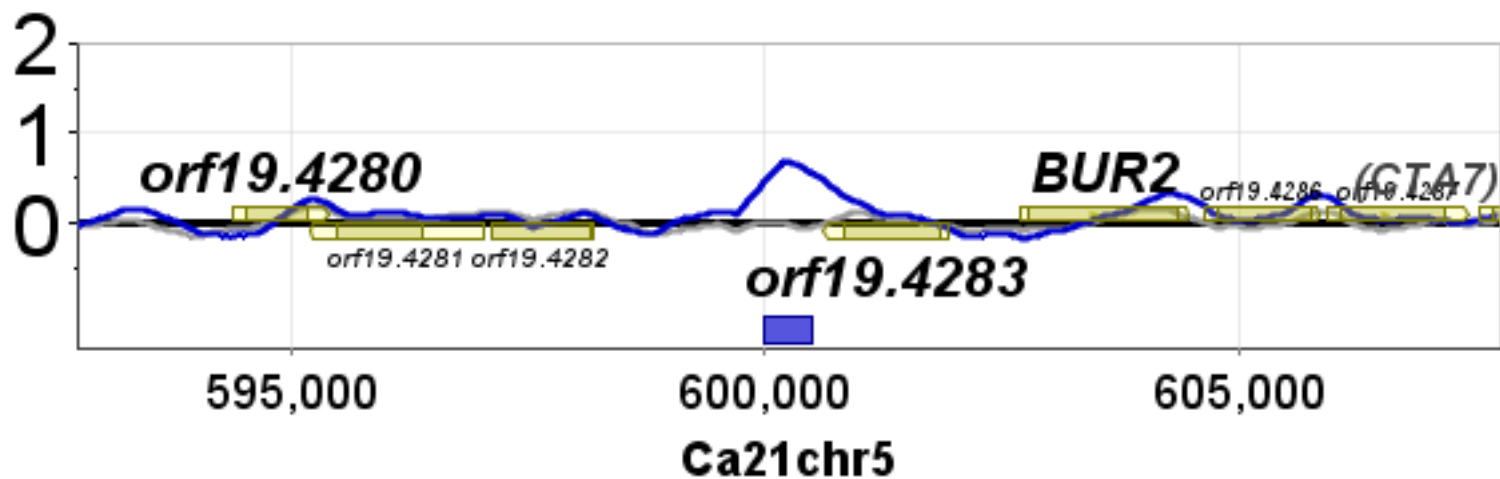




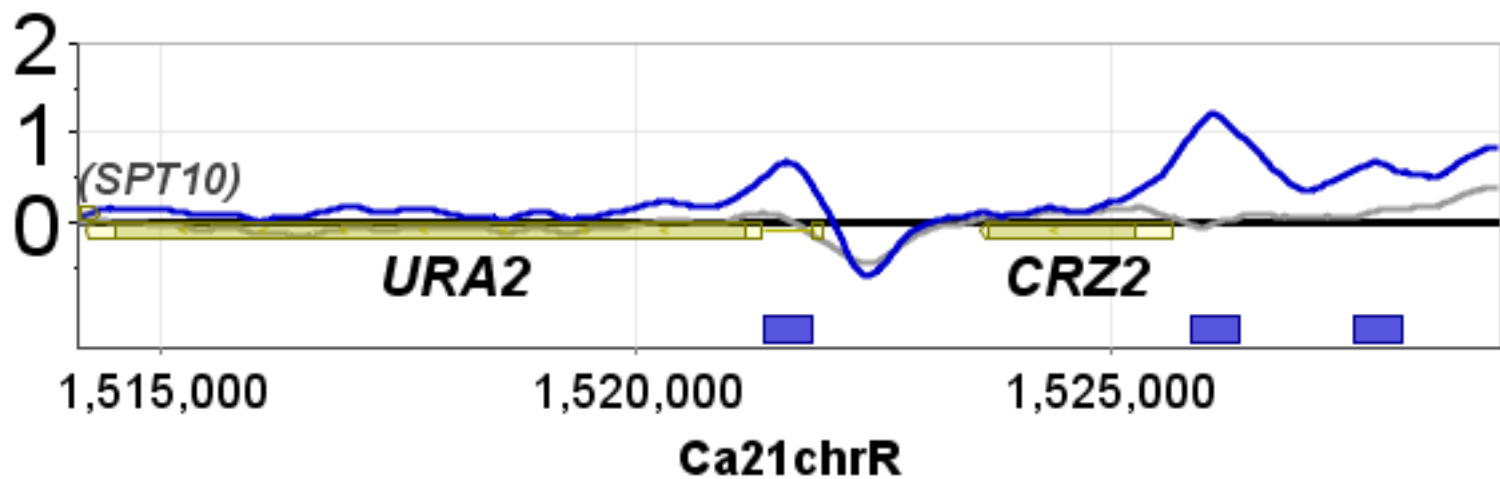
[0.684] Ca21chr6:166477-181476 [+] [orf19.89, orf19.89, ILV5, orf19.91, ntar\_976]



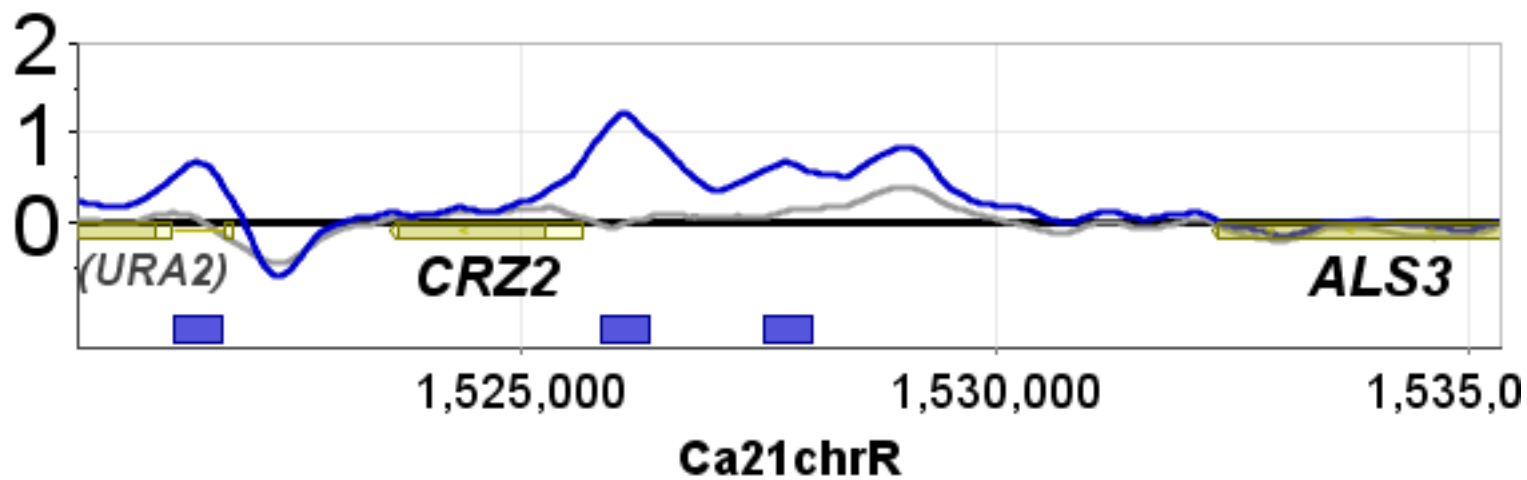
[0.679] Ca21chr5:592749-607748 [+] [ntar\_902, ntar\_901, orf19.4283, orf19.4282, BUR2]



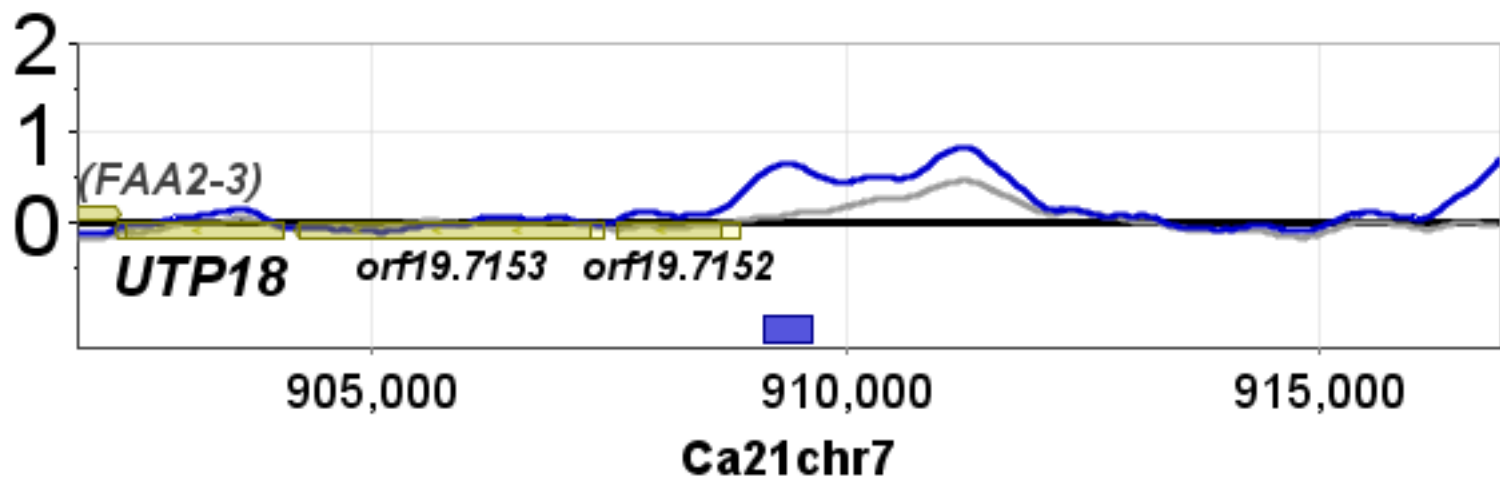
[0.673] Ca21chrR:1514101-1529100 [+] [URA2, CRZ2, SPT10]



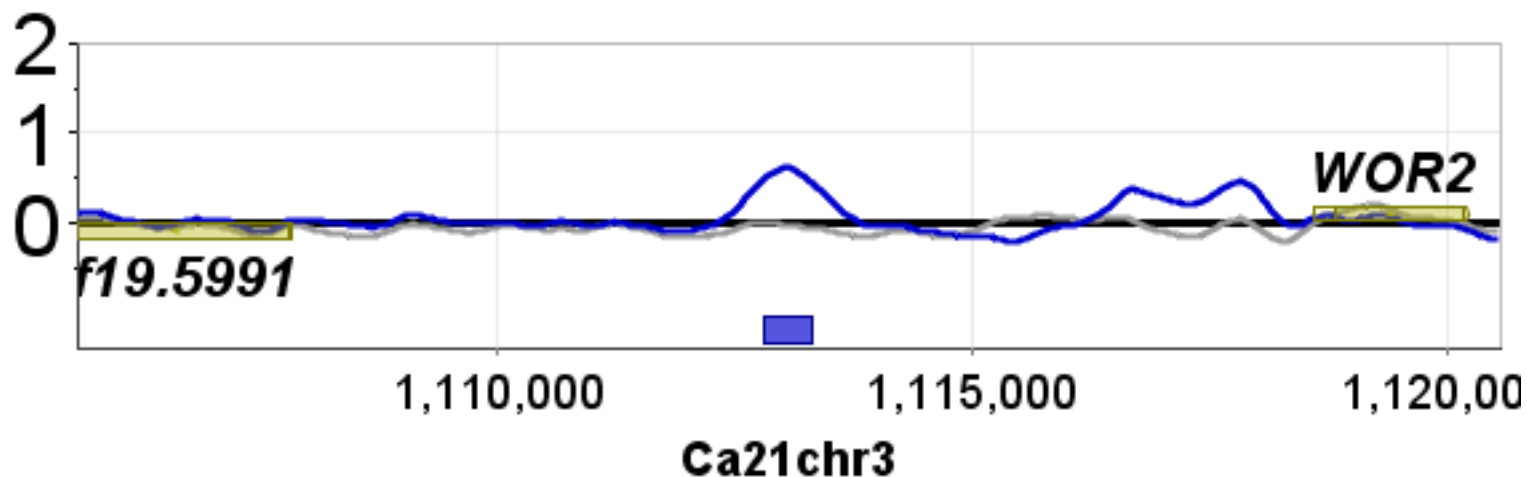
[0.672] Ca21chrR:1520318-1535317 [+] [ntar\_1331, CRZ2, URA2, ALS3]



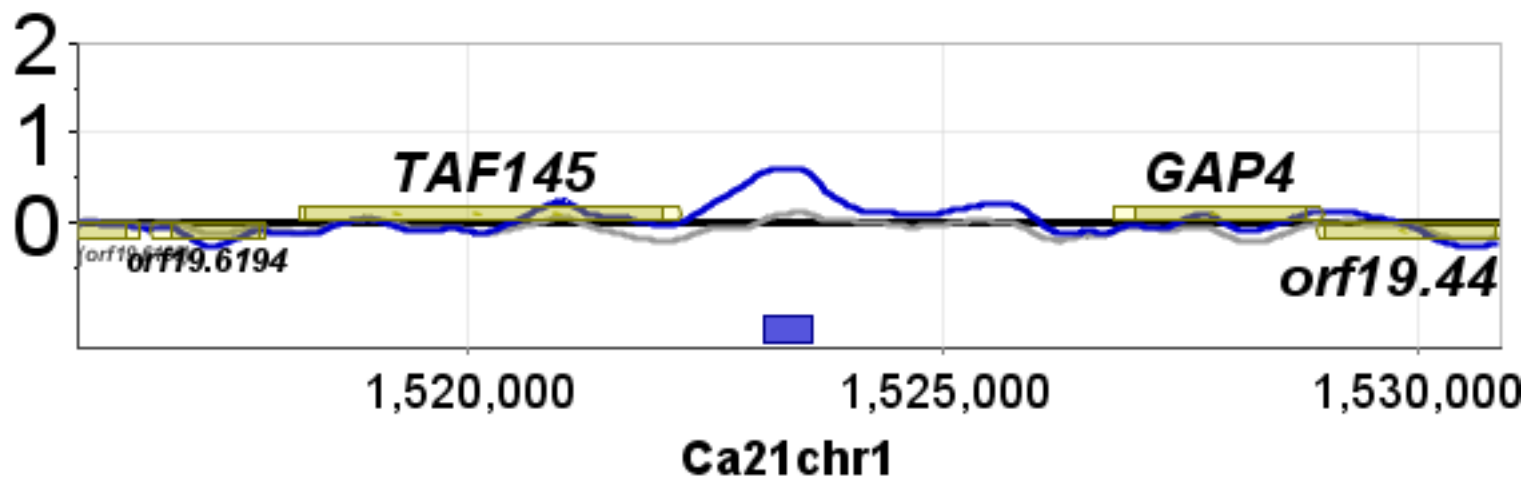
[0.662] Ca21chr7:901888-916887 [+] [orf19.7152, orf19.7153, ntar\_1151, UTP18, ntar\_1152]



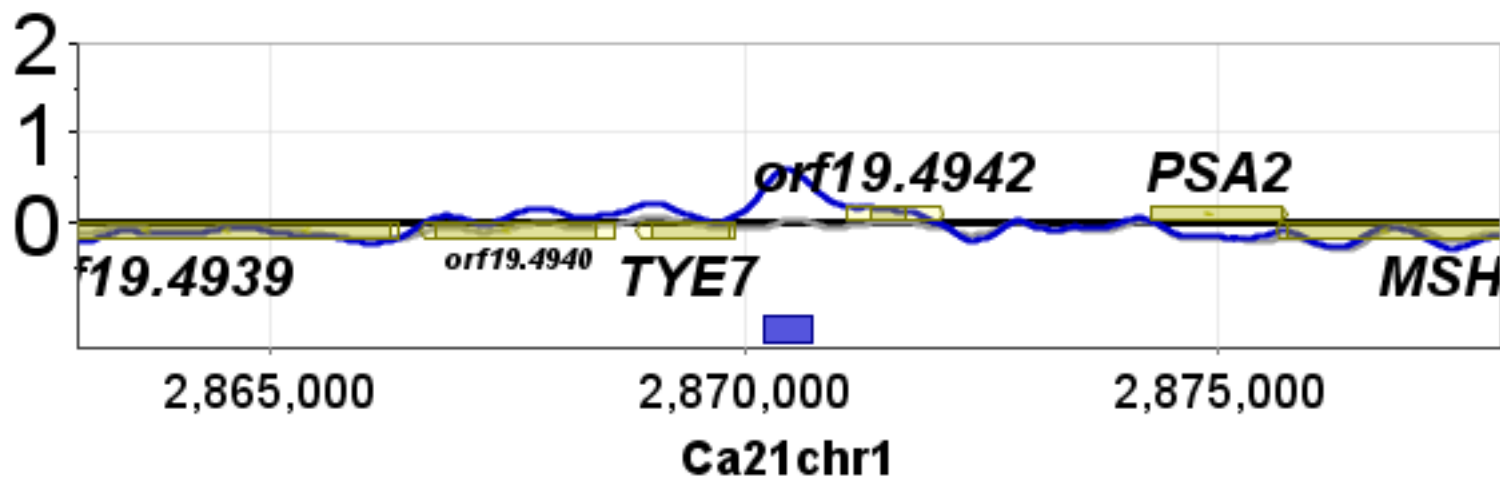
[0.61] Ca21chr3:1105562-1120561 [+] [ntar\_613, orf19.5991, WOR2]

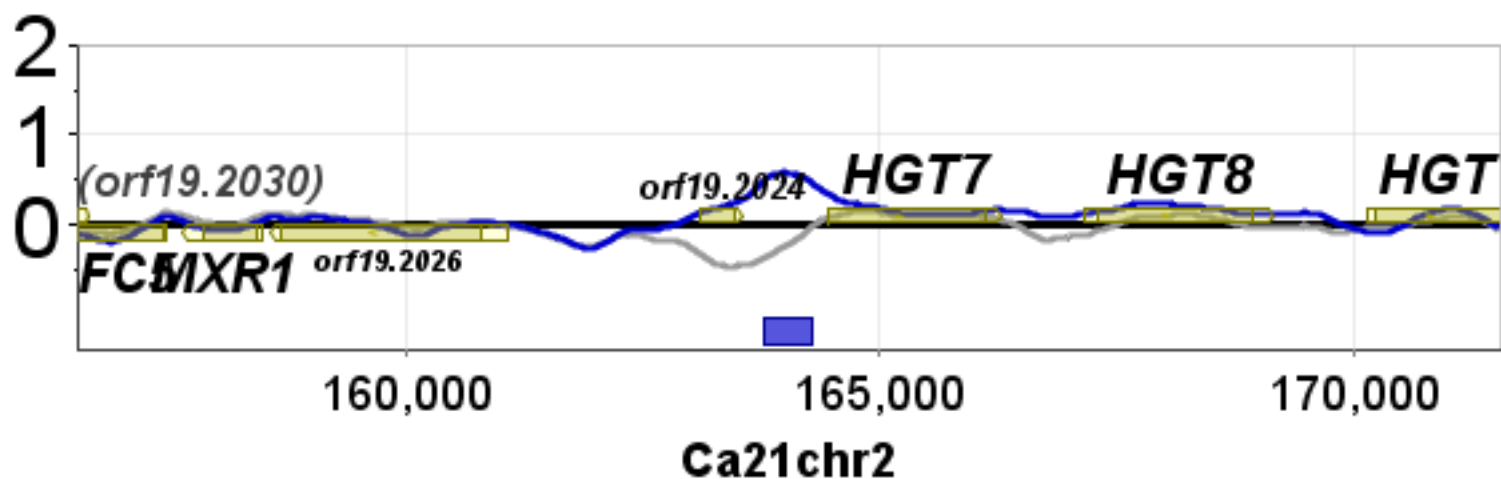
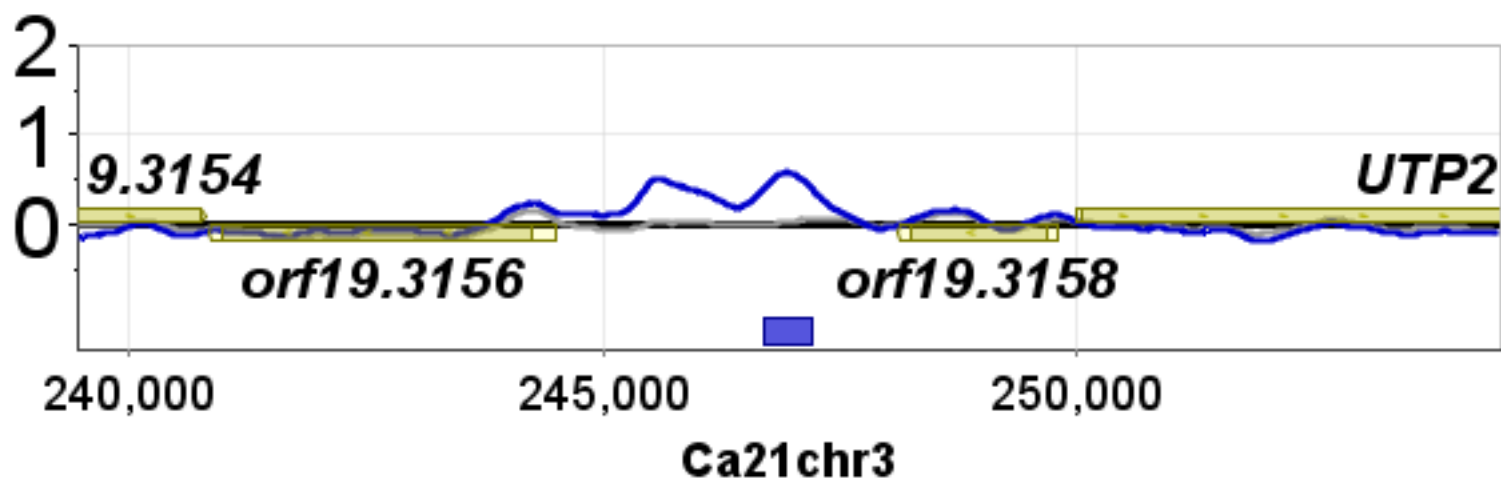
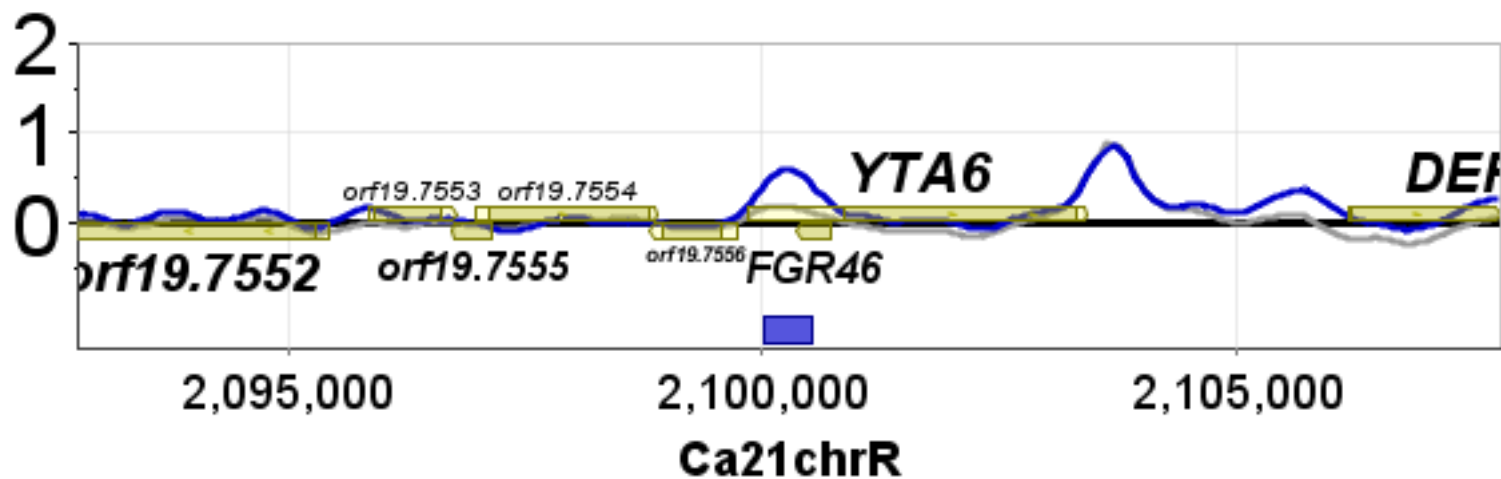
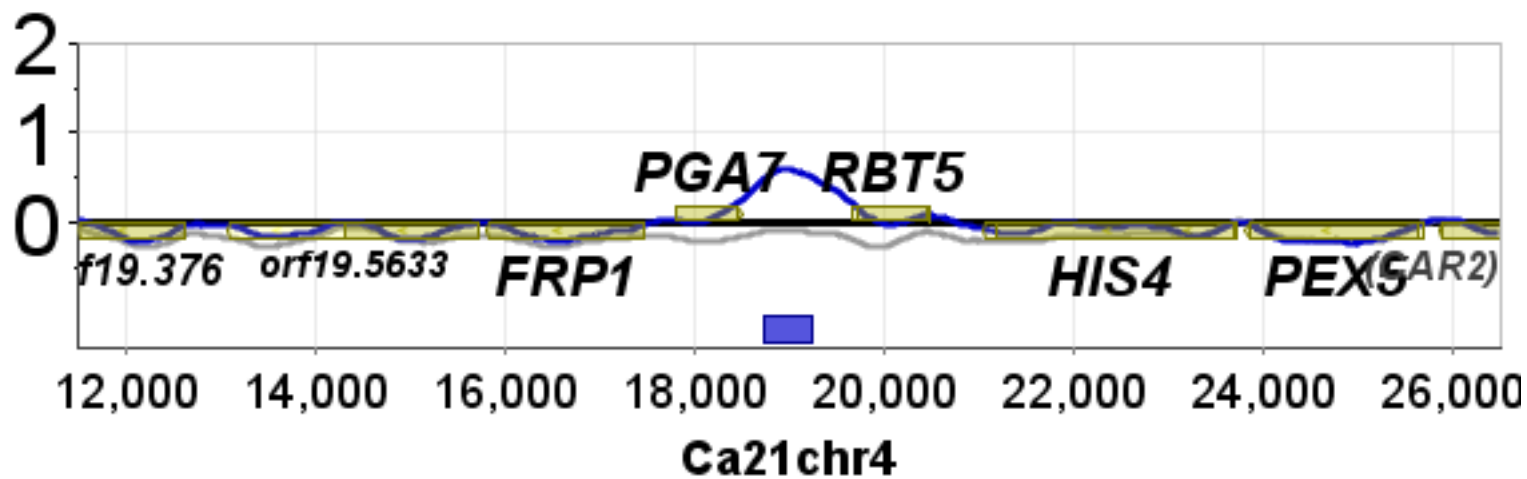


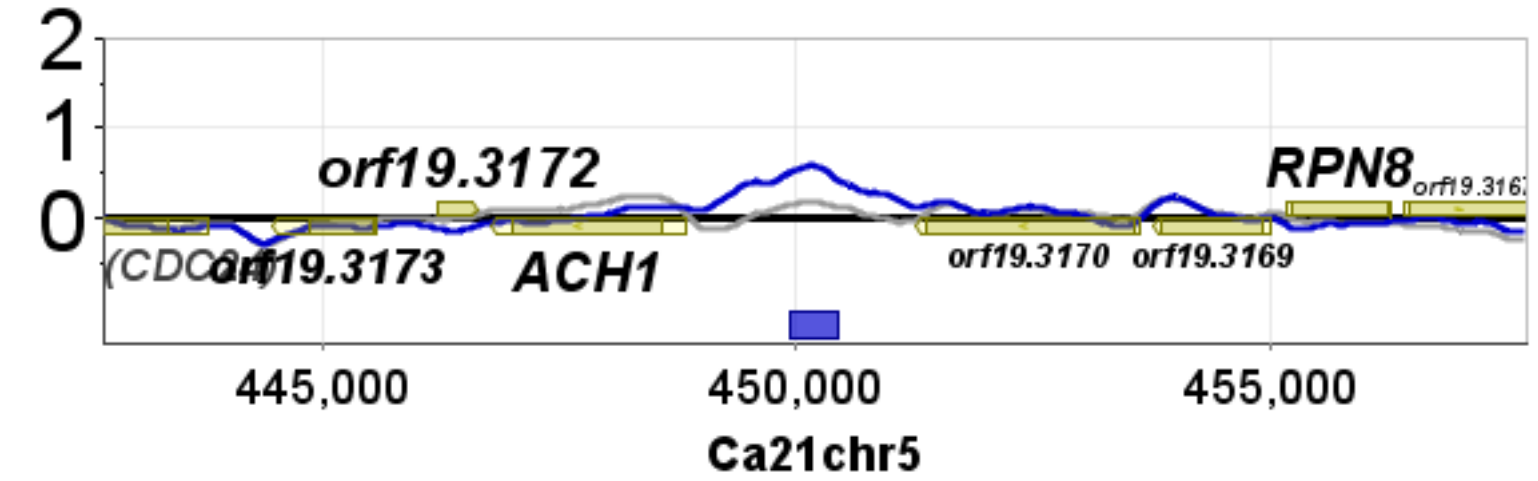
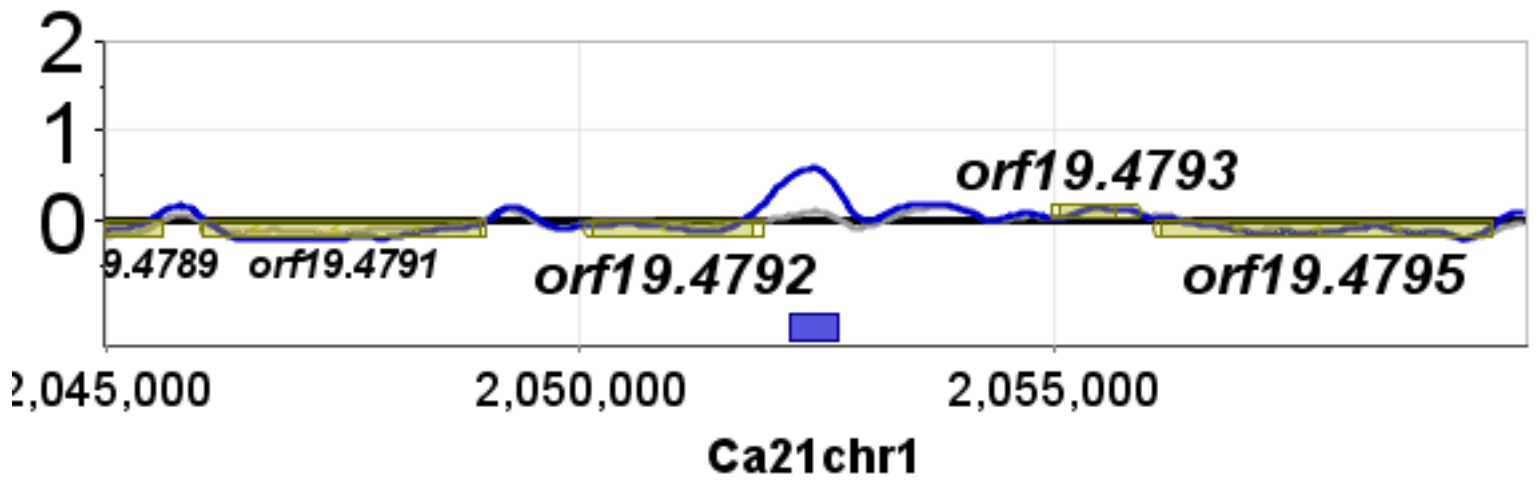
[0.601] Ca21chr1:1515864-1530863 [+] [GAP4, TAF145, orf19.6194, ntar\_136, orf19.6195]



[0.59] Ca21chr1:2862962-2877961 [+] [TYE7, orf19.4942, orf19.4940, PSA2, orf19.4939]





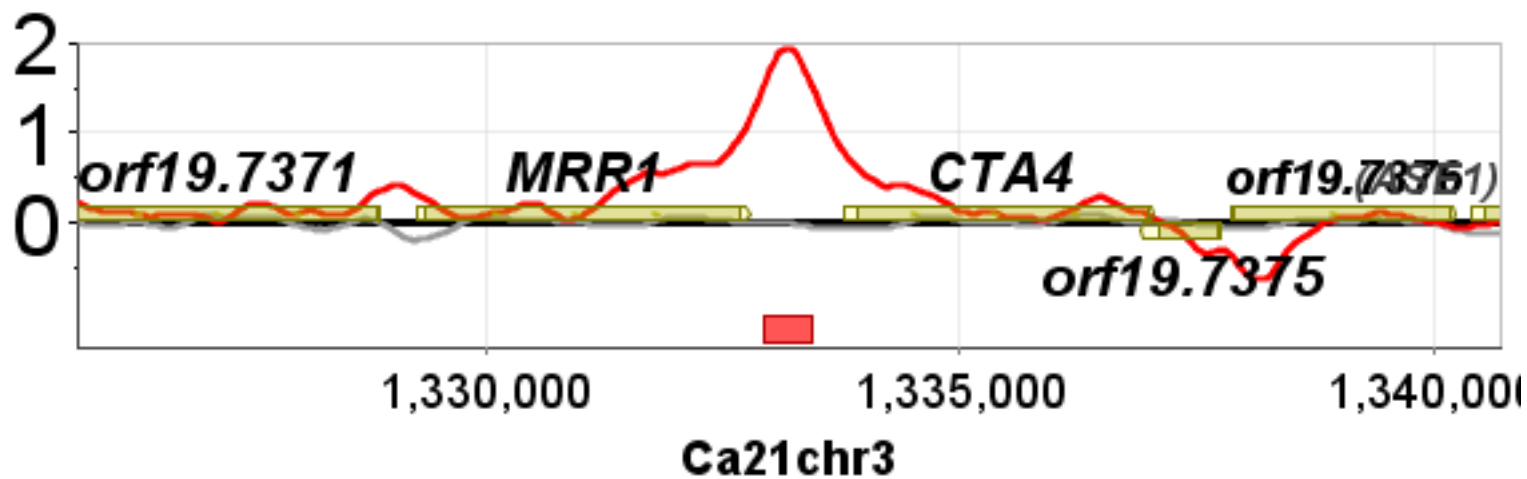


## **Full genome chromatin immunoprecipitation (ChIP-chip) mapping of Ahr1 binding sites in white cells.**

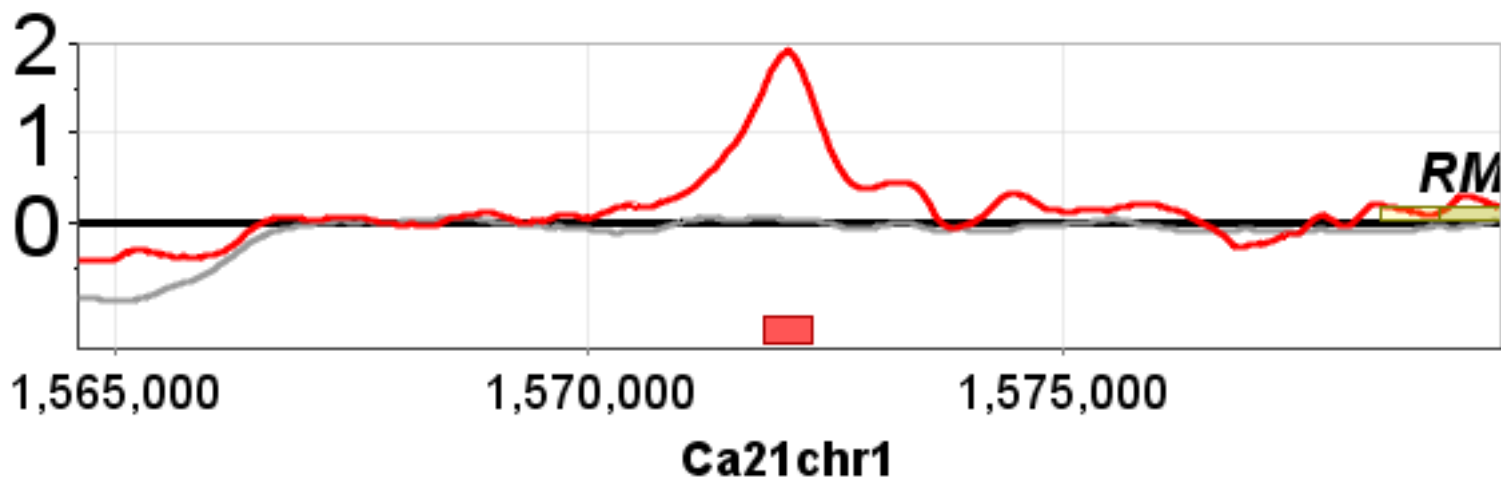
Plots of 15kb regions centered on the set of 79 Ahr1 binding sites in white cells.

Smoothed enrichment data for the Ahr1-myc strain is shown in red, for the untagged control strain in grey. The 500bp called peaks of Ahr1 enrichment are indicated by the red boxes in the lower track in each image. Peaks are arranged in order of decreasing Ahr1 enrichment. Enrichment ( $\log_2$ ) is indicated on the y-axis. Chromosomal locations and specific enrichment levels for the peak are indicated in the strip above each panel; when multiple peaks are present the enrichment value corresponds to the peak at the center of the plot. Yellow boxes correspond to genes; 5' or 3' untranslated regions are included as lighter shaded portions of the box. Genes plotted above the bold line read in the sense direction; genes plotted below the line read in the antisense direction. Plots produced using the SnapShot Function in MochiView v1.46 (Homann and Johnson, 2010).

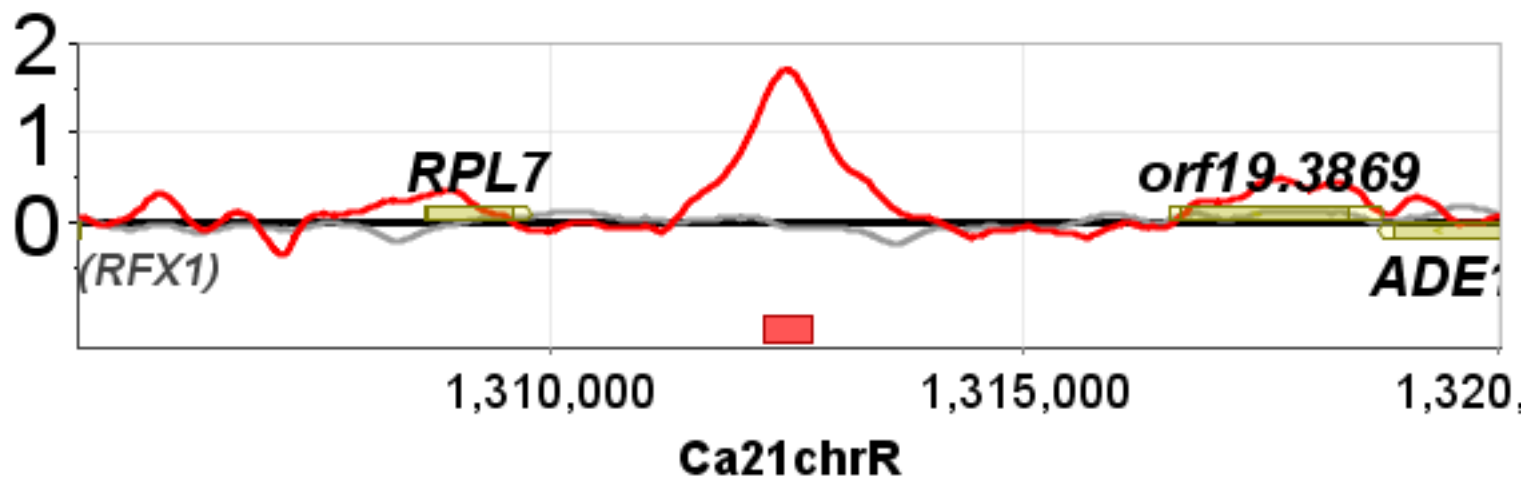
[1.933] Ca21chr3:1325694-1340693 [+] [ntar\_647, ntar\_648, CTA4, MRR1, orf19.7375]



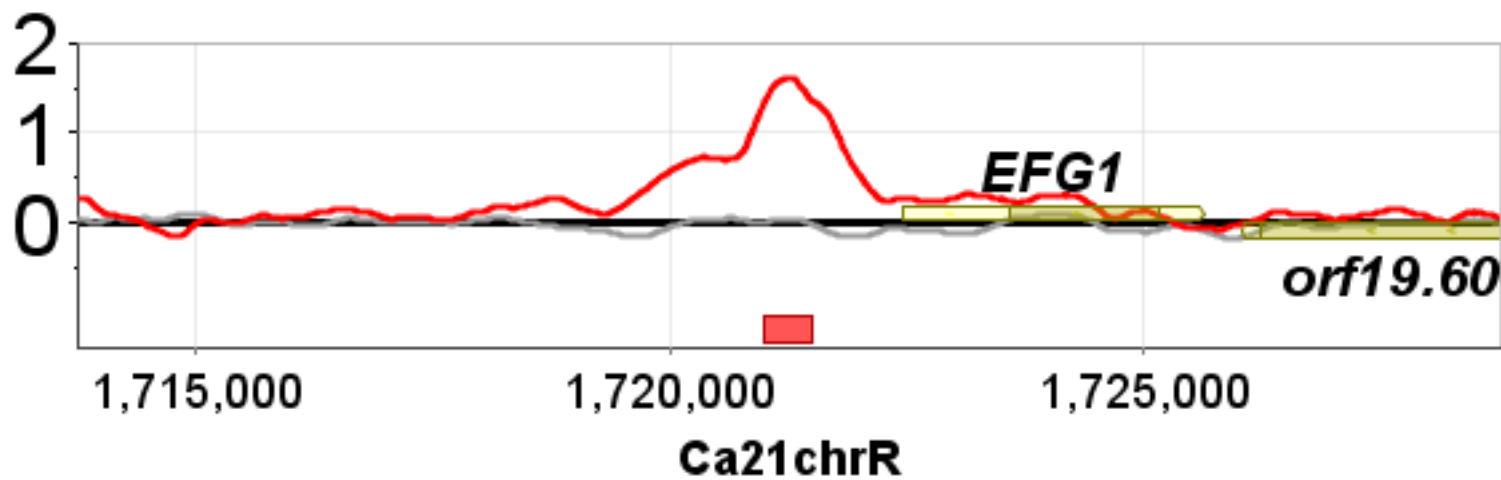
[1.924] Ca21chr1:1564602-1579601 [+] [ntar\_139, ntar\_138, ntar\_140, t(aag)2, RME1]



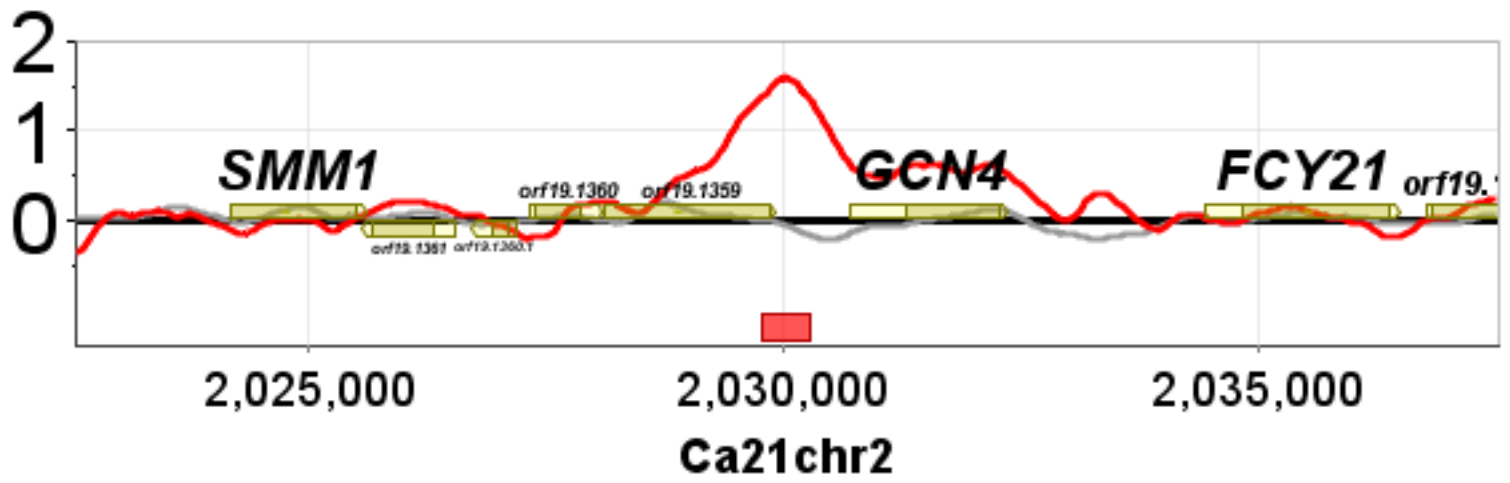
[1.713] Ca21chrR:1305011-1320010 [+] [ntar\_1302, ntar\_1301, ntar\_1300, orf19.3868, RPL7]



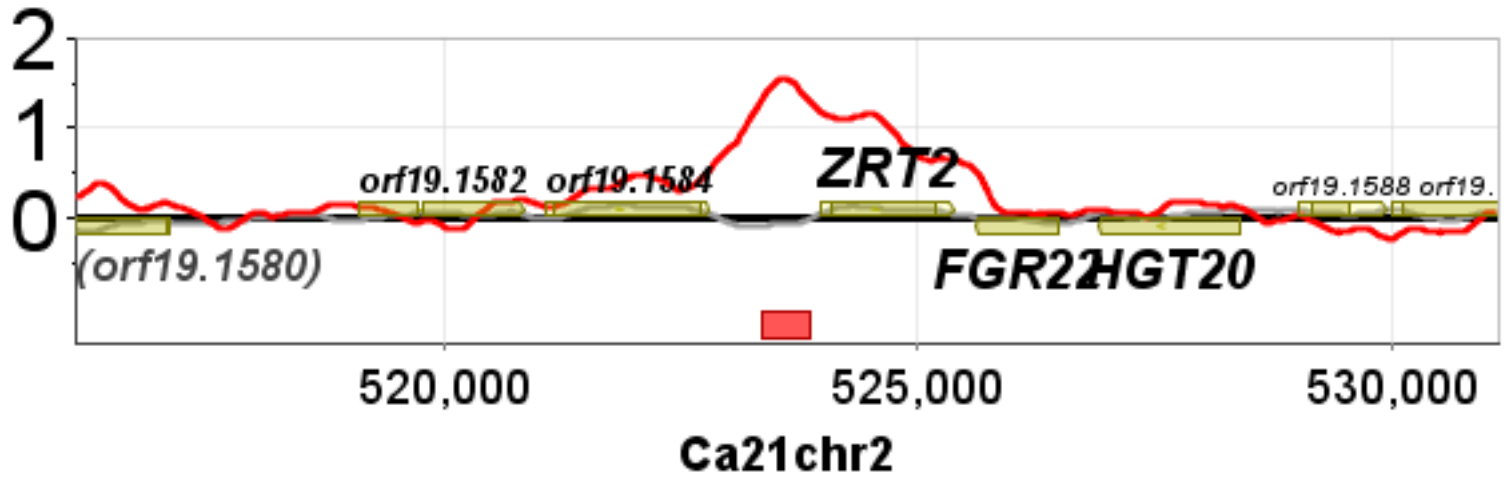
[1.611] Ca21chrR:1713745-1728744 [+] [EFG1, ntar\_1352, ntar\_1353, ntar\_1351, orf19.609]



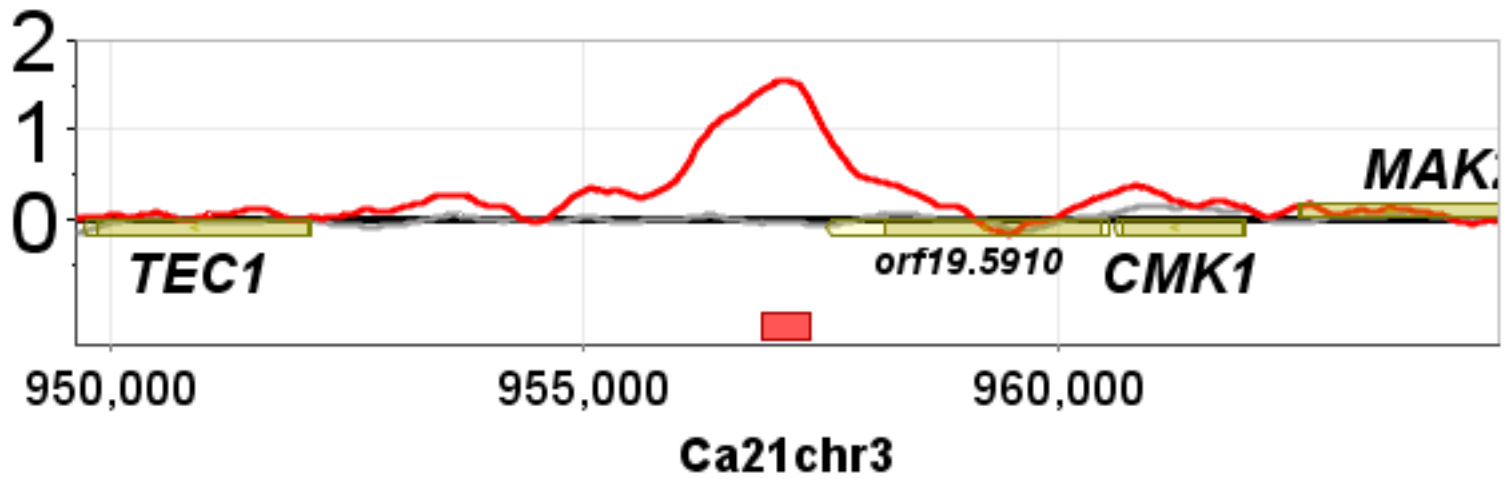
[1.593] Ca21chr2:2022532-2037531 [+] [ntar\_486, GCN4, orf19.1359, orf19.1360, ntar\_488]



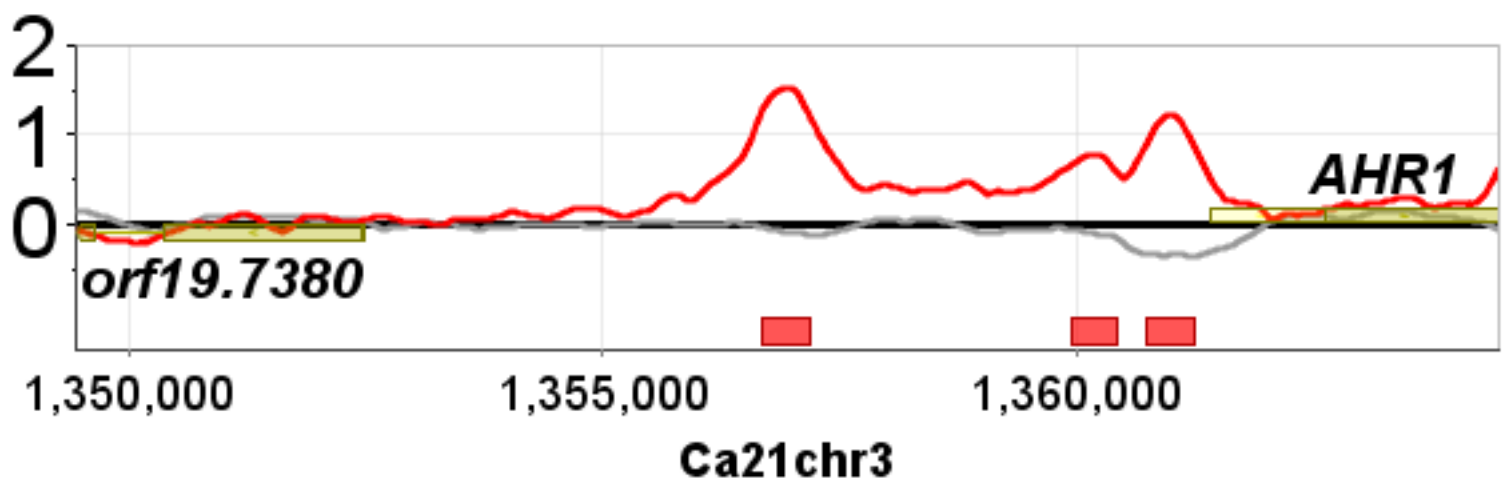
[1.556] Ca21chr2:516109-531108 [+] [ntar\_335, ZRT2, ntar\_334, orf19.1584, ntar\_333]



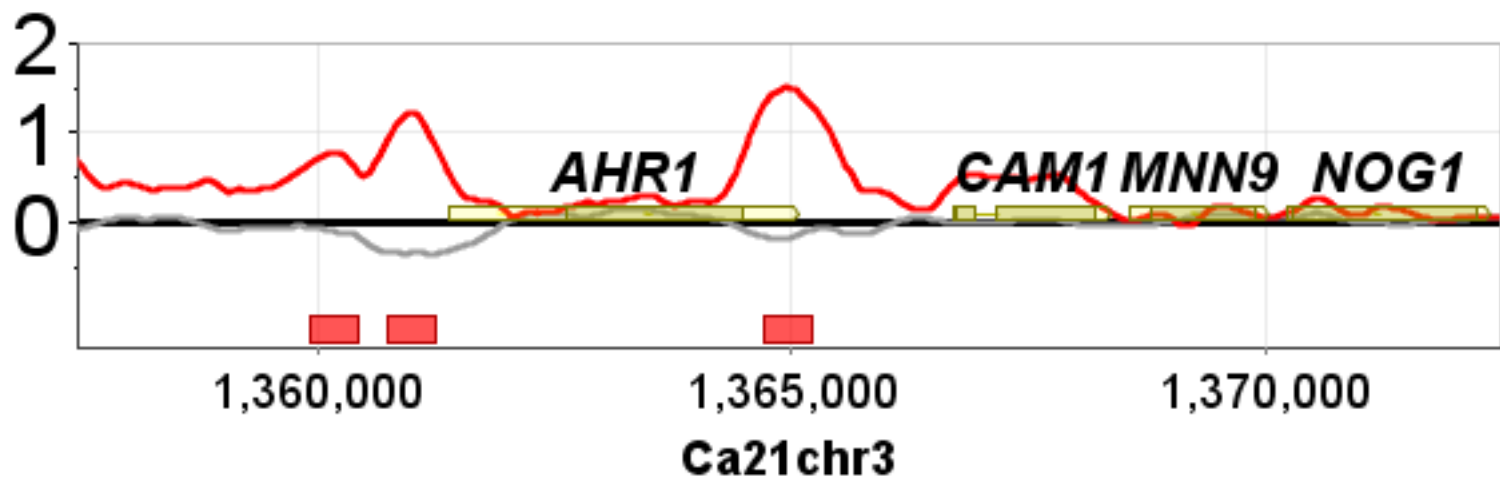
[1.551] Ca21chr3:949629-964628 [+] [orf19.5910, CMK1, TEC1, MAK21]



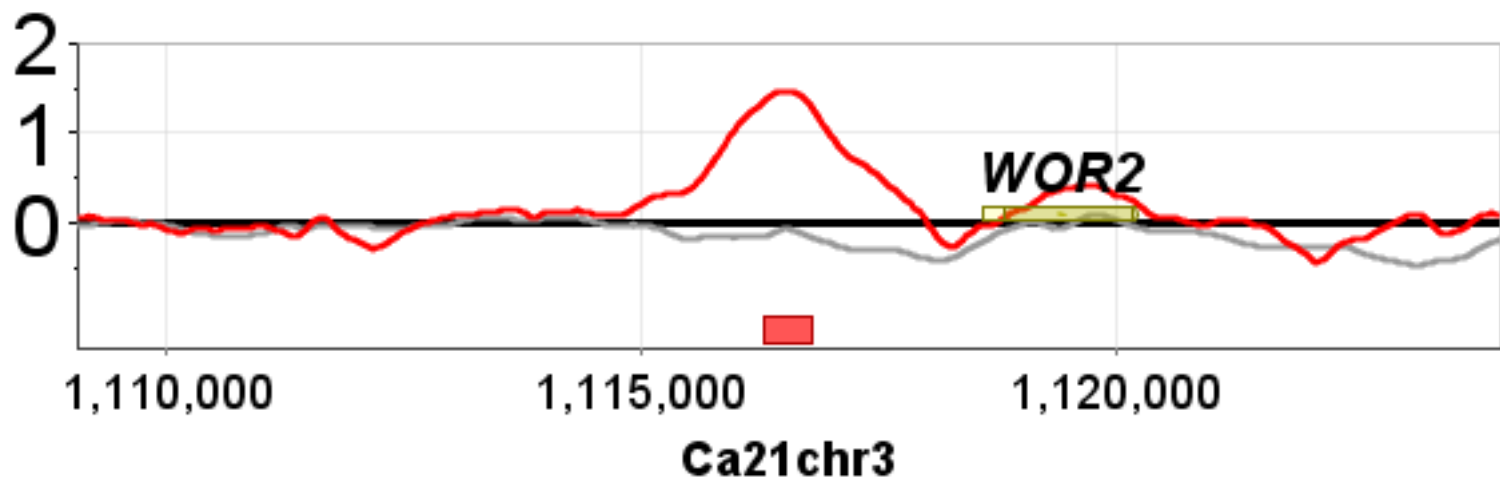
[1.513] Ca21chr3:1349435-1364434 [+] [orf19.7380, orf19.7381]



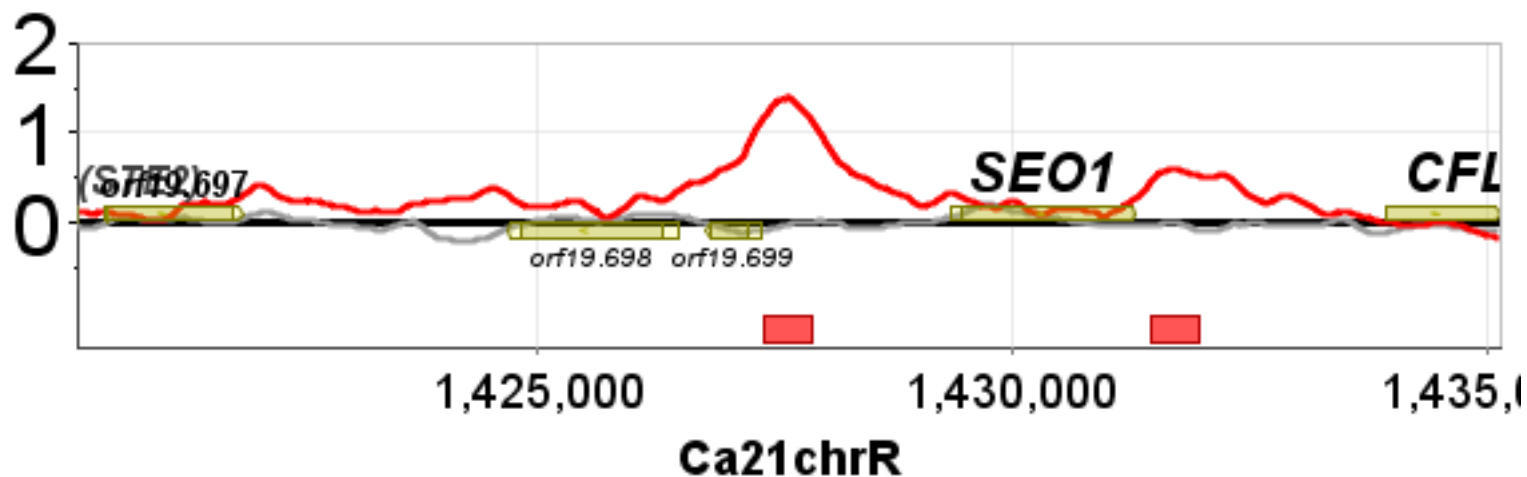
[1.509] Ca21chr3:1357464-1372463 [+] [CAM1, orf19.7381, MNN9, NOG1]



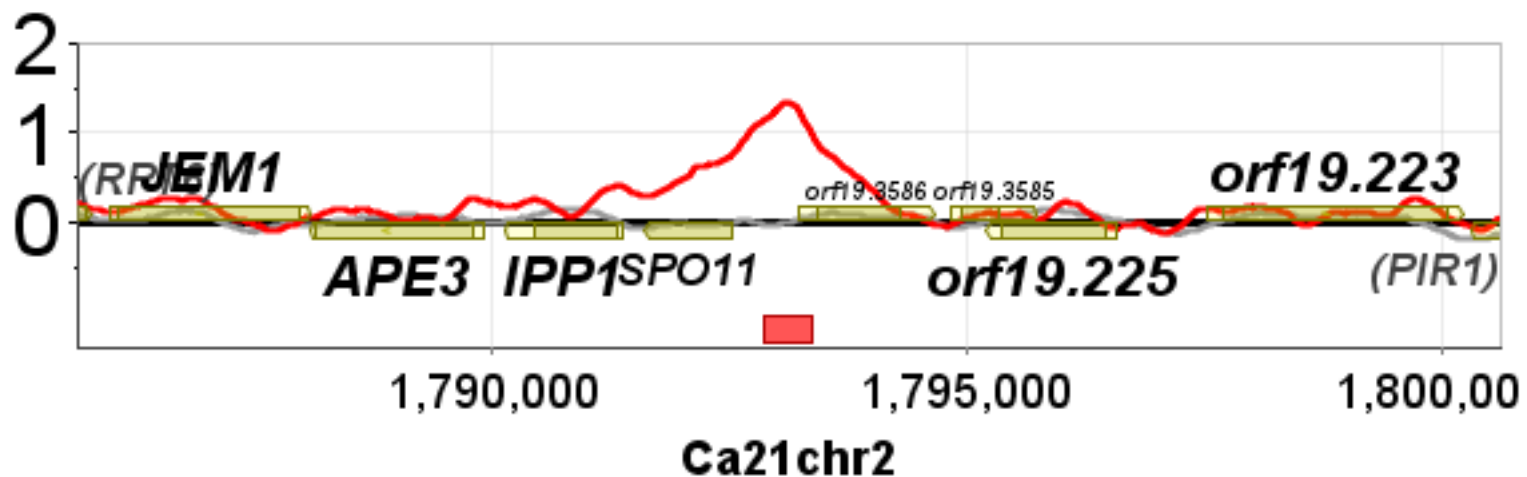
[1.46] Ca21chr3:1109050-1124049 [+] [WOR2, ntar\_614, ntar\_615, ntar\_616, ntar\_617]



[1.386] Ca21chrR:1420138-1435137 [+] [orf19.699, ntar\_1319, orf19.698, ntar\_1320, SEO1]

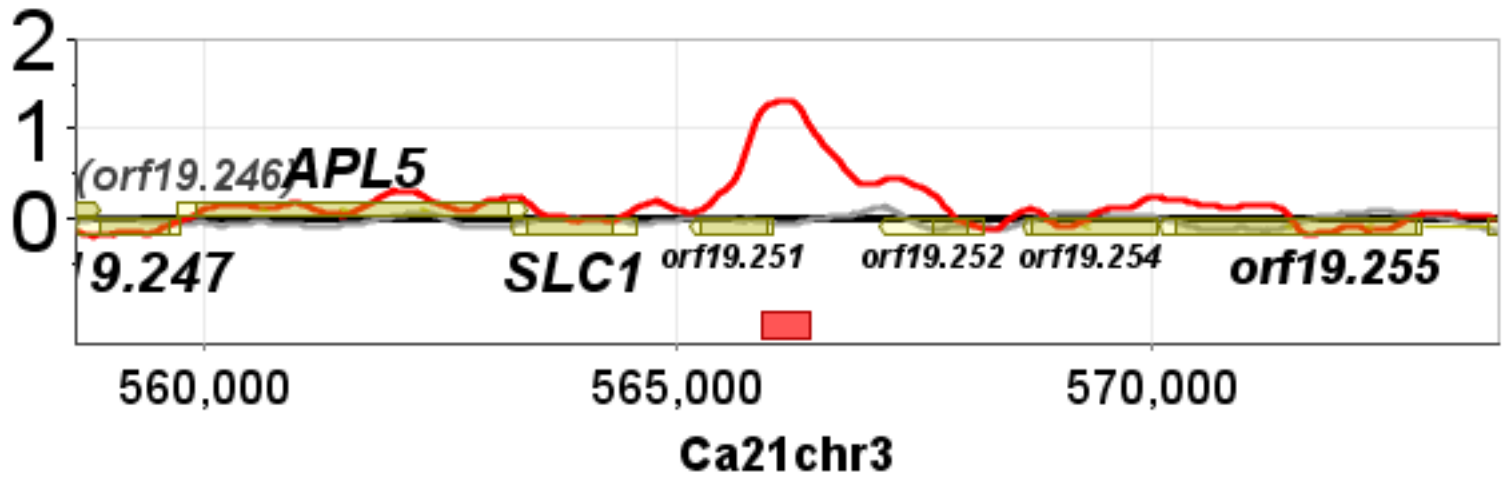


[1.337] Ca21chr2:1785616-1800615 [+] [orf19.3586, SPO11, orf19.3585, IPP1, APE3]

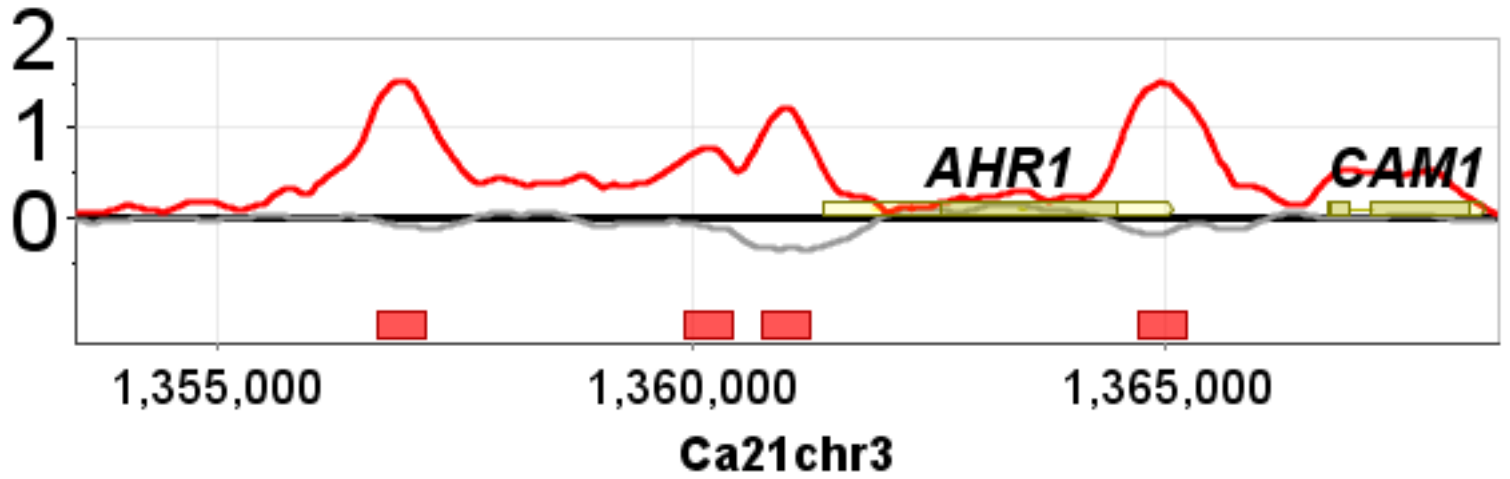




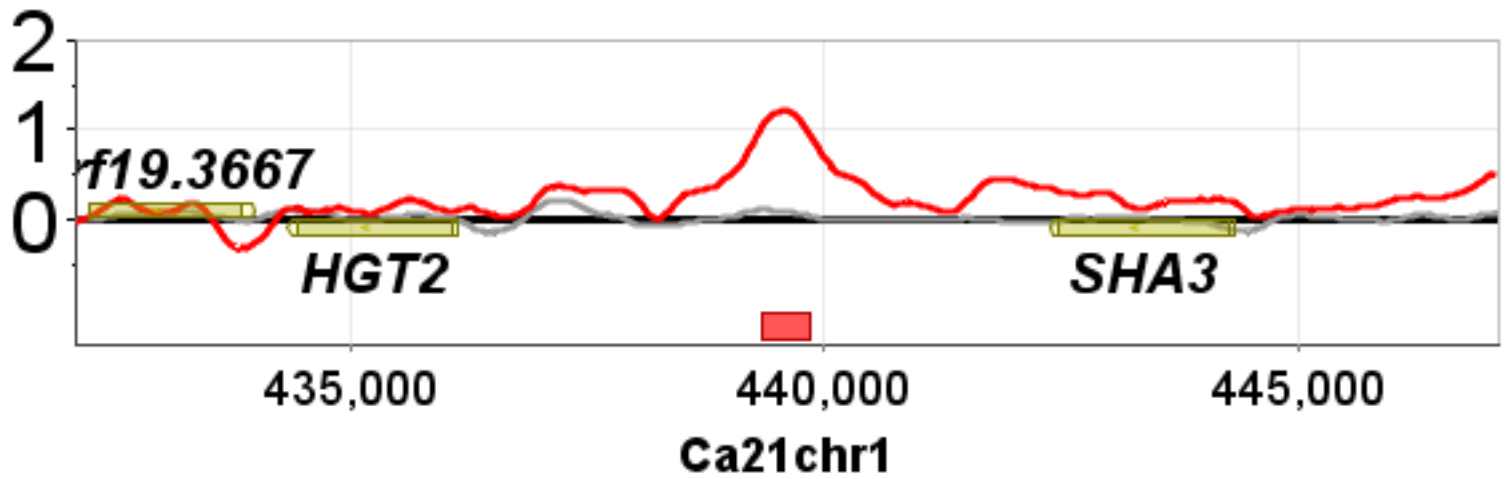
[1.323] Ca21chr3:558643-573642 [+] [orf19.251, ntar\_572, SLC1, orf19.252, orf19.254]



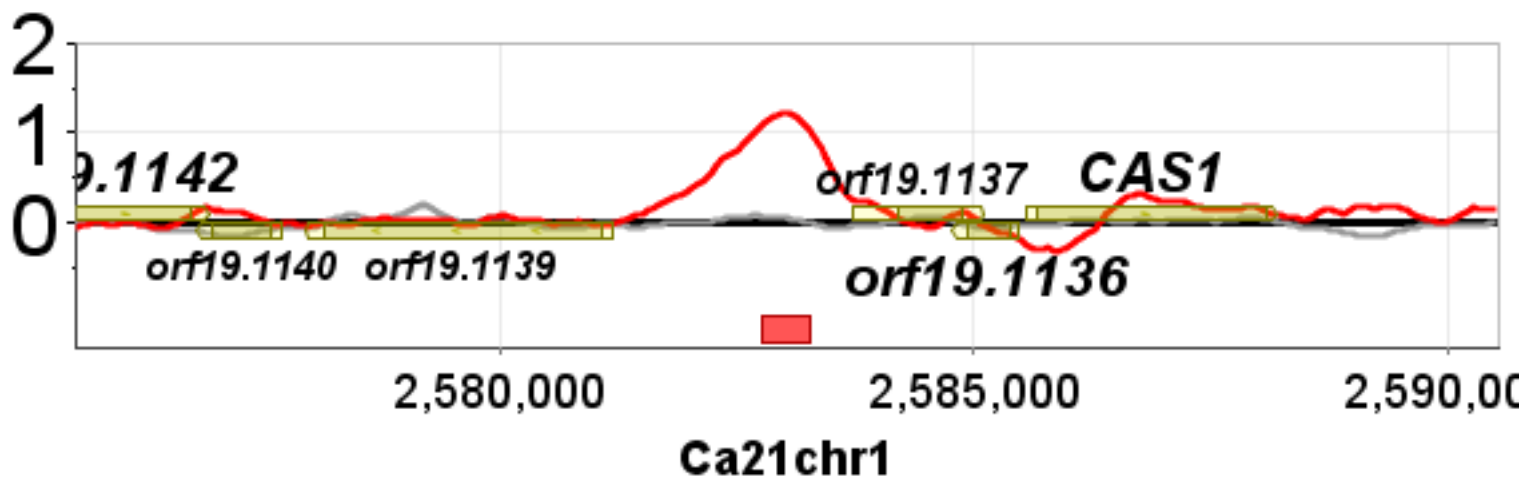
[1.229] Ca21chr3:1353496-1368495 [+] [orf19.7381, CAM1]



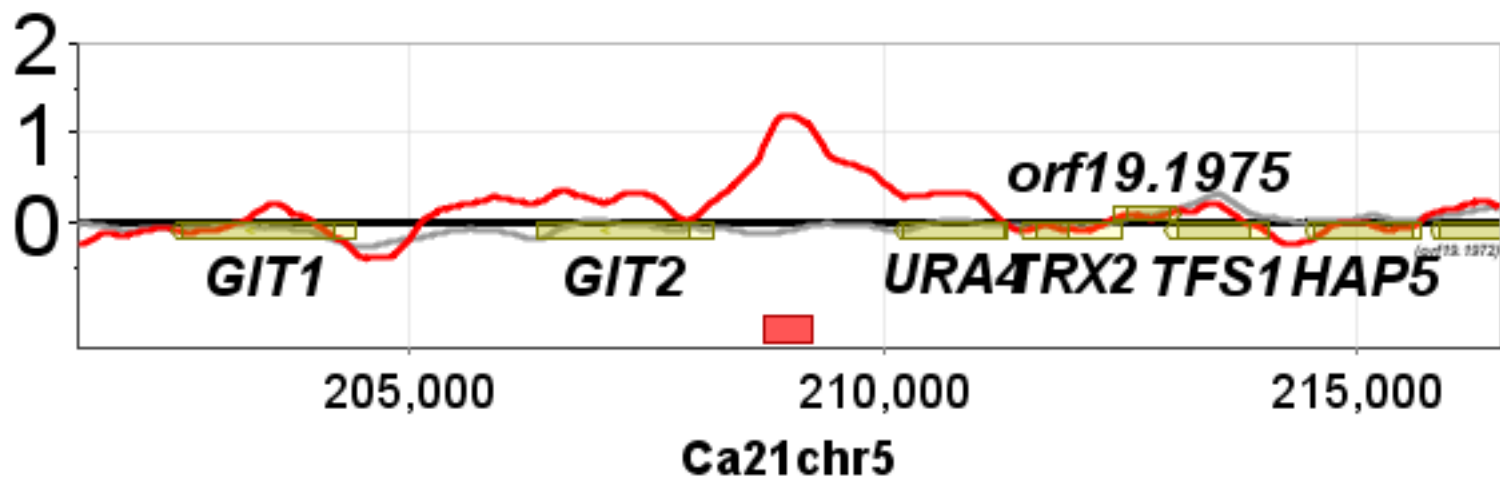
[1.219] Ca21chr1:432099-447098 [+] [HGT2, ntar\_41, SHA3, ntar\_40, ntar\_42]



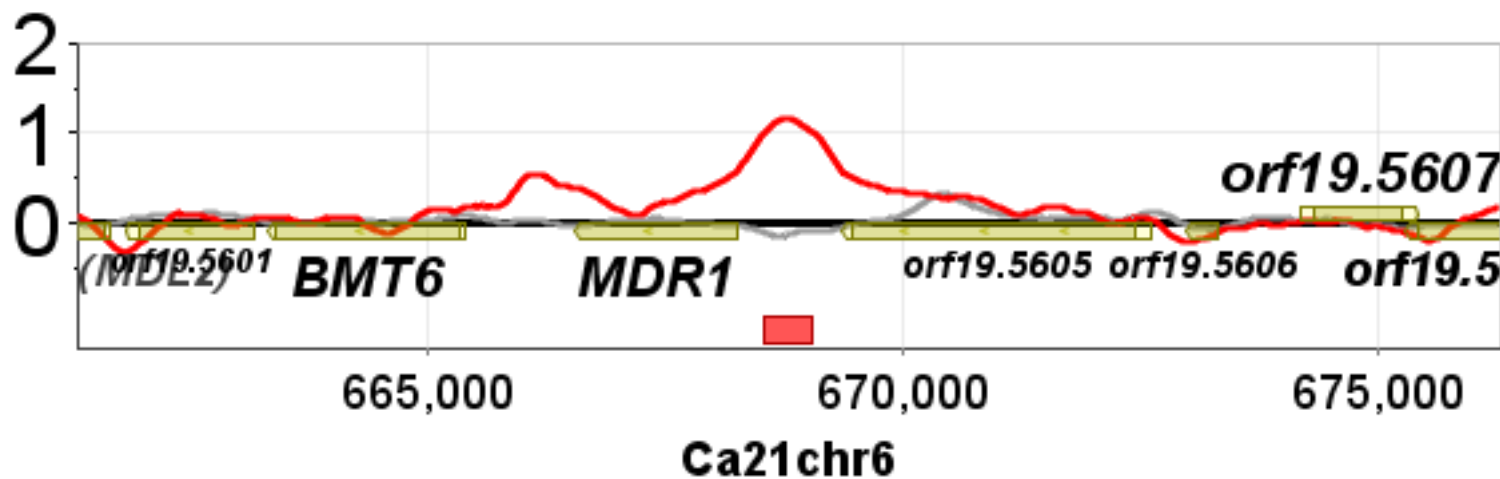
[1.215] Ca21chr1:2575520-2590519 [+] [orf19.1137, orf19.1139, orf19.1136, CAS1, orf19.1140]



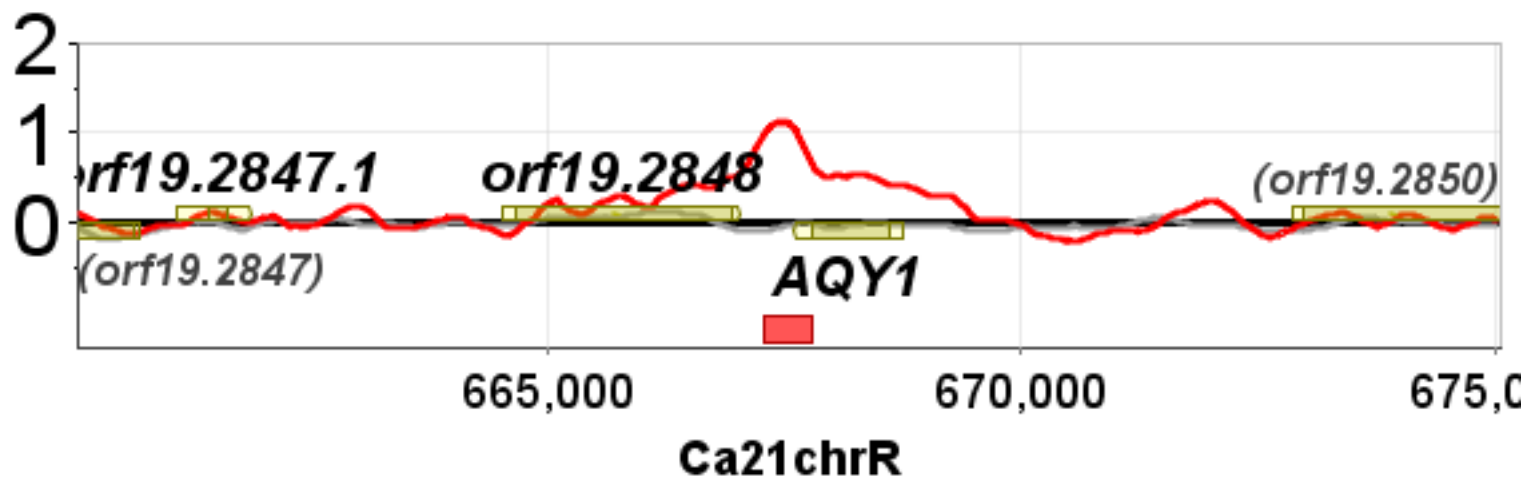
[1.188] Ca21chr5:201500-216499 [+] [GIT2, URA4, orf19.1975, TRX2, GIT1]



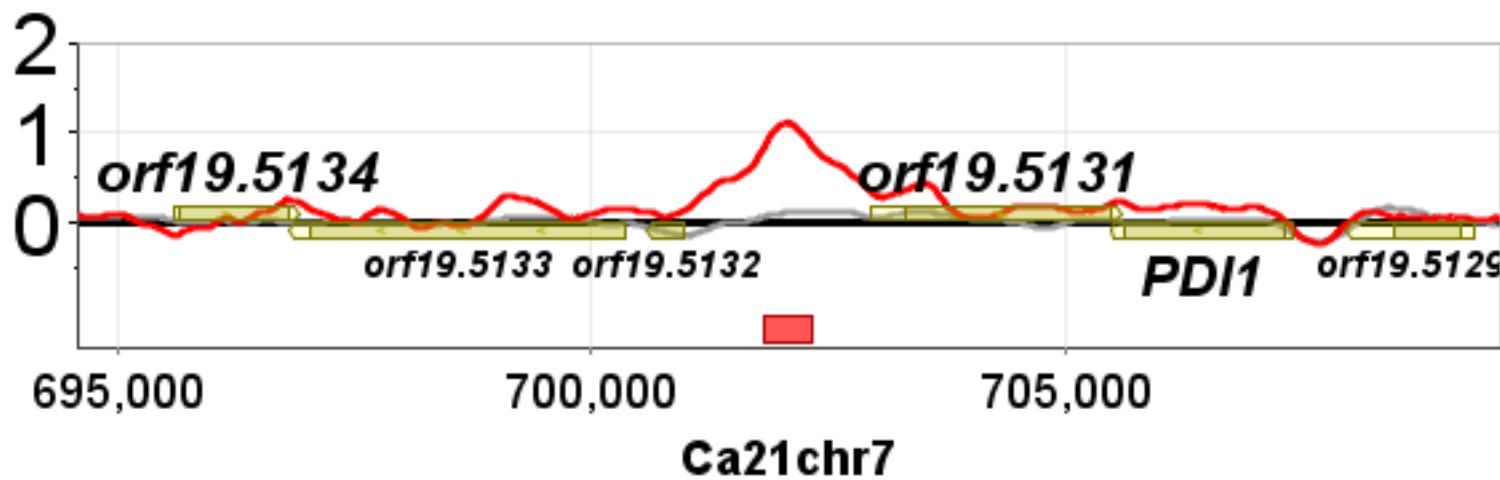
[1.174] Ca21chr6:661287-676286 [+] [Intar\_1017, MDR1, BMT6, orf19.5605, orf19.5606]



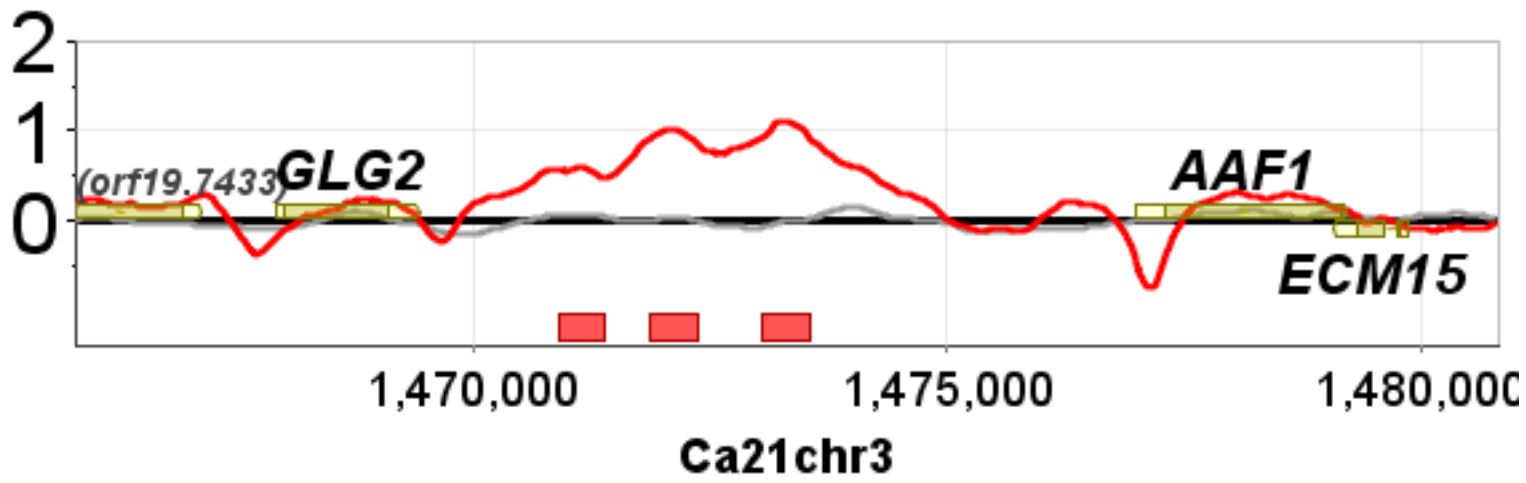
[1.12] Ca21chrR:660043-675042 [+] [AQY1, orf19.2848, orf19.2850, orf19.2847.1, orf19.2847]



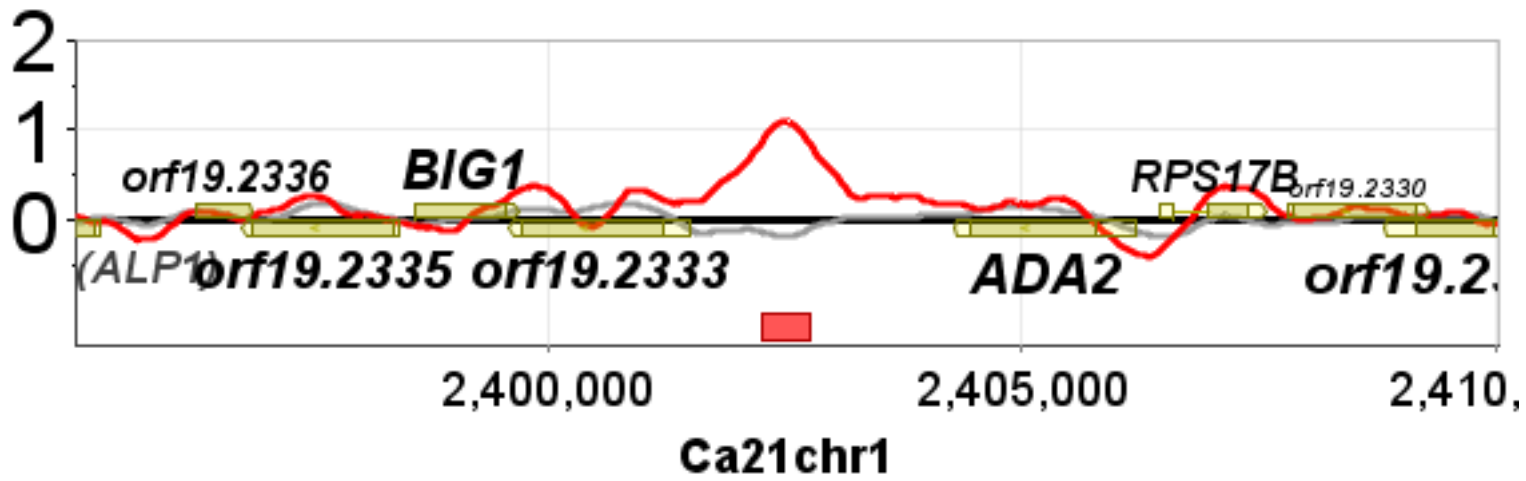
[1.118] Ca21chr7:694578-709577 [+] [Intar\_1132, orf19.5131, orf19.5132, orf19.5133, PDI1]



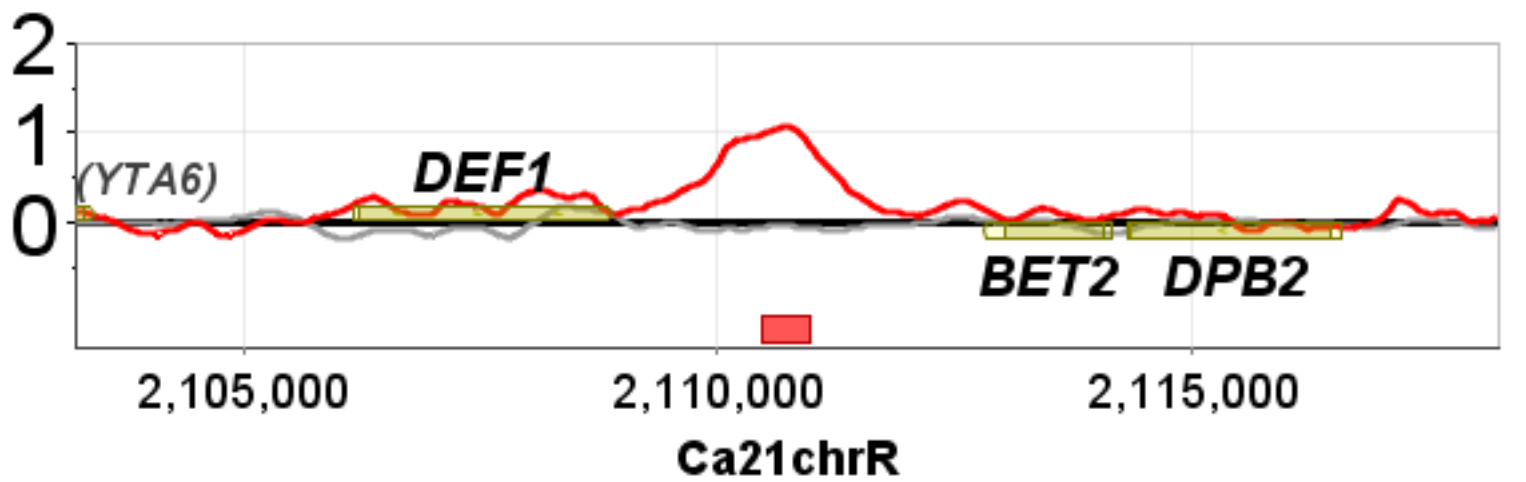
[1.107] Ca21chr3:1465806-1480805 [+] [ntar\_658, ntar\_659, th(gug)3, AAF1, GLG2]



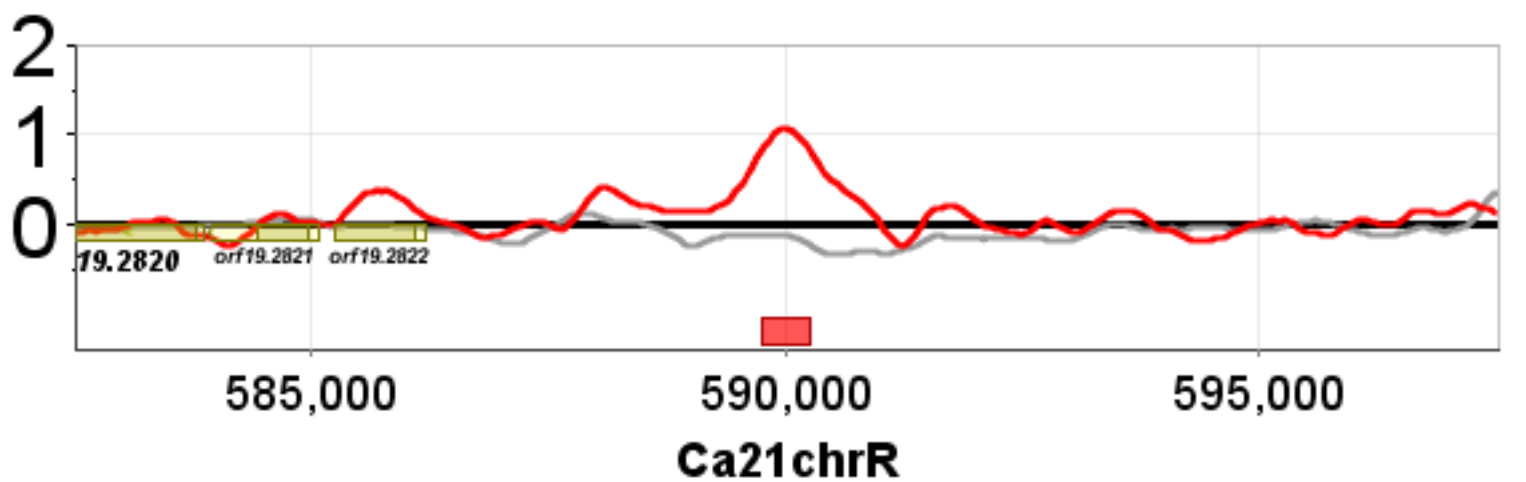
[1.095] Ca21chr1:2395016-2410015 [+] [orf19.2333, orf19.2332, ADA2, BIG1, RPS17B]



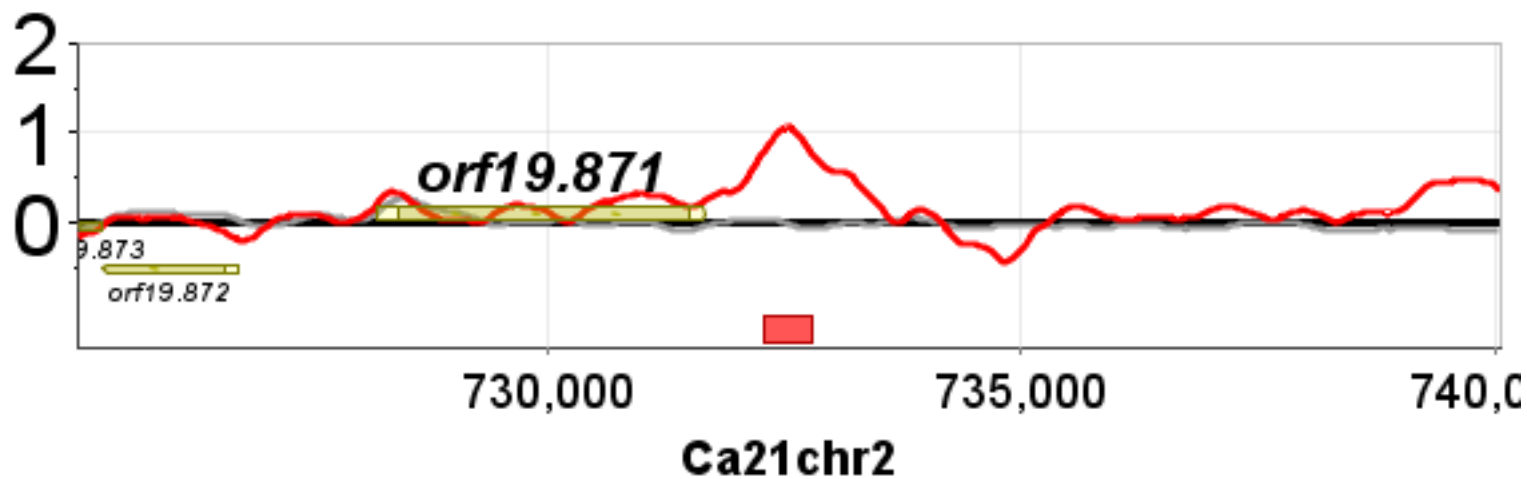
[1.075] Ca21chrR:2103220-2118219 [+] [BET2, DEF1, DPB2, YTA6]



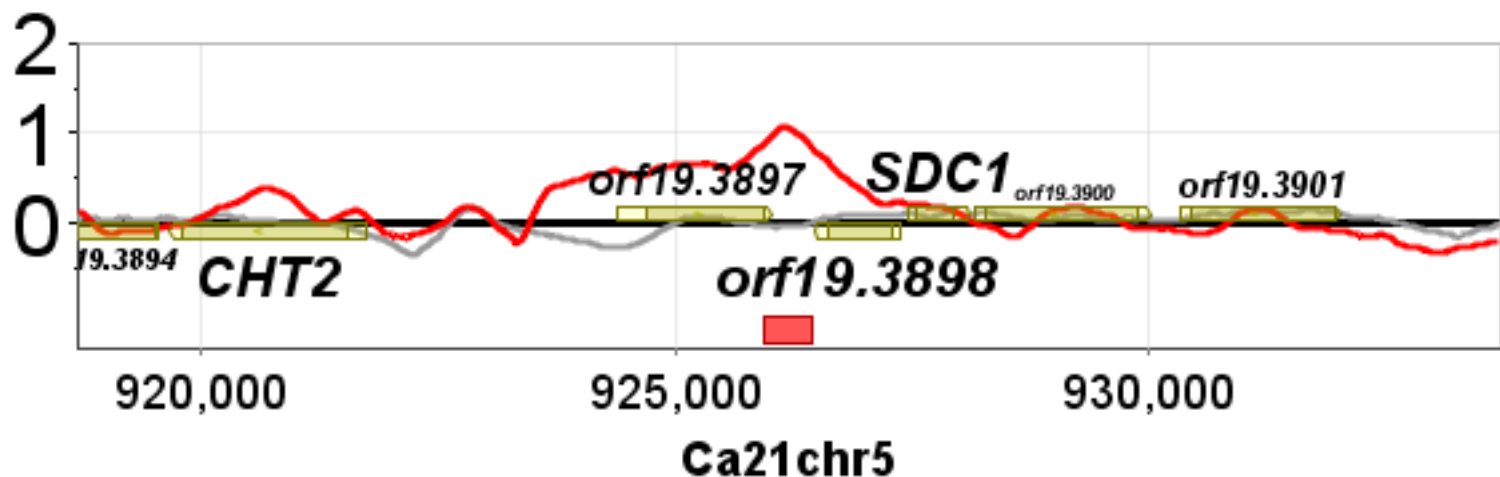
[1.071] Ca21chrR:582510-597509 [+] [orf19.2822, orf19.2821, orf19.2820]



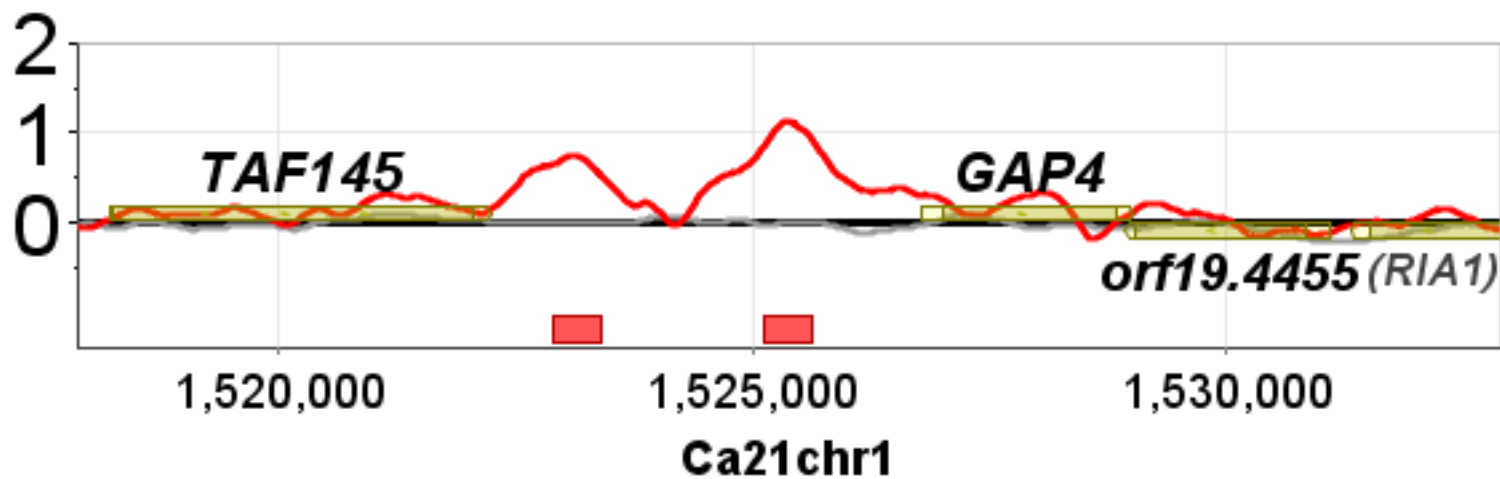
[1.067] Ca21chr2:725040-740039 [+] [ntar\_353, orf19.871, orf19.872, orf19.873]



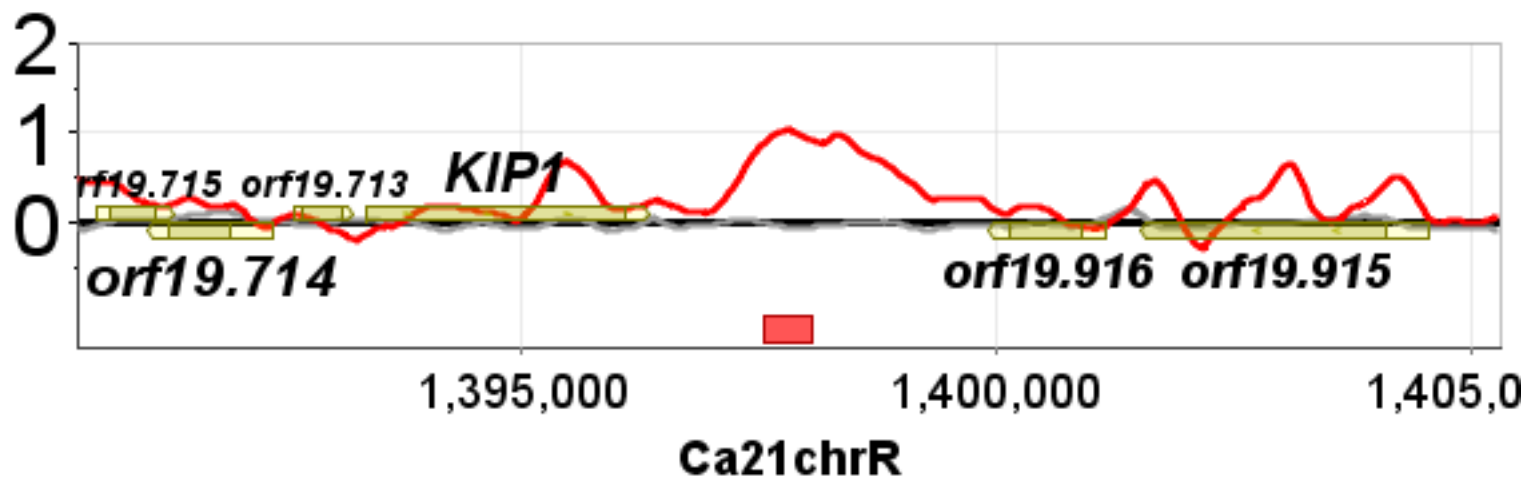
[1.064] Ca21chr5:918690-933689 [+] [ntar\_941, orf19.3898, SDC1, orf19.3897, orf19.3900]



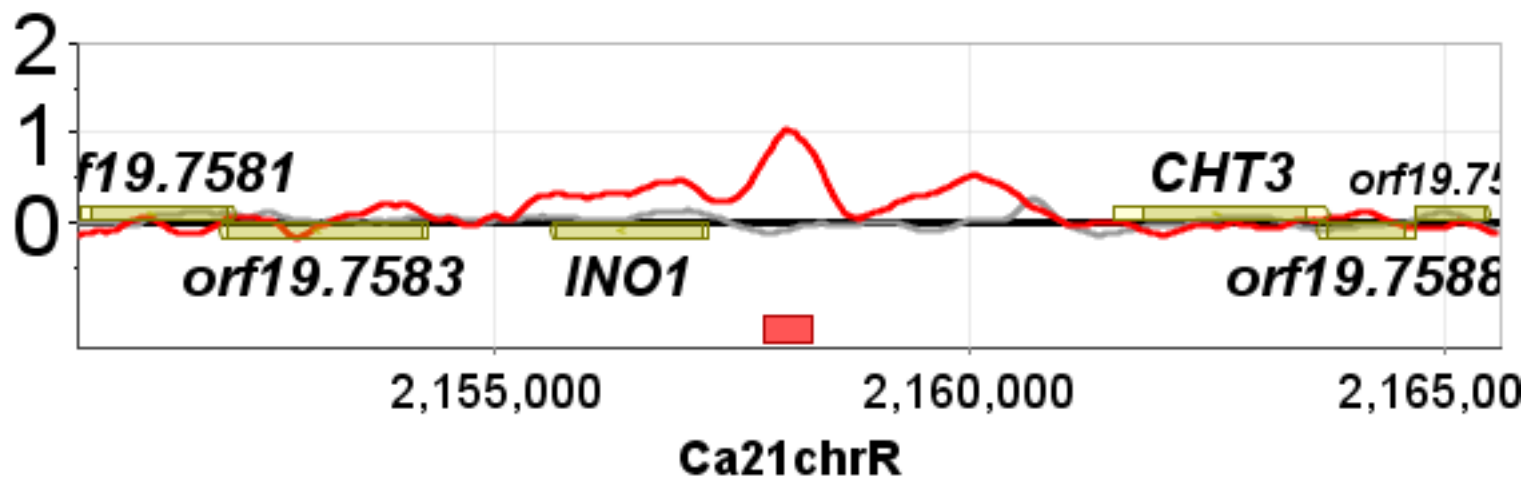
[1.059] Ca21chr1:1517875-1532874 [+] [GAP4, orf19.4455, TAF145, RIA1]



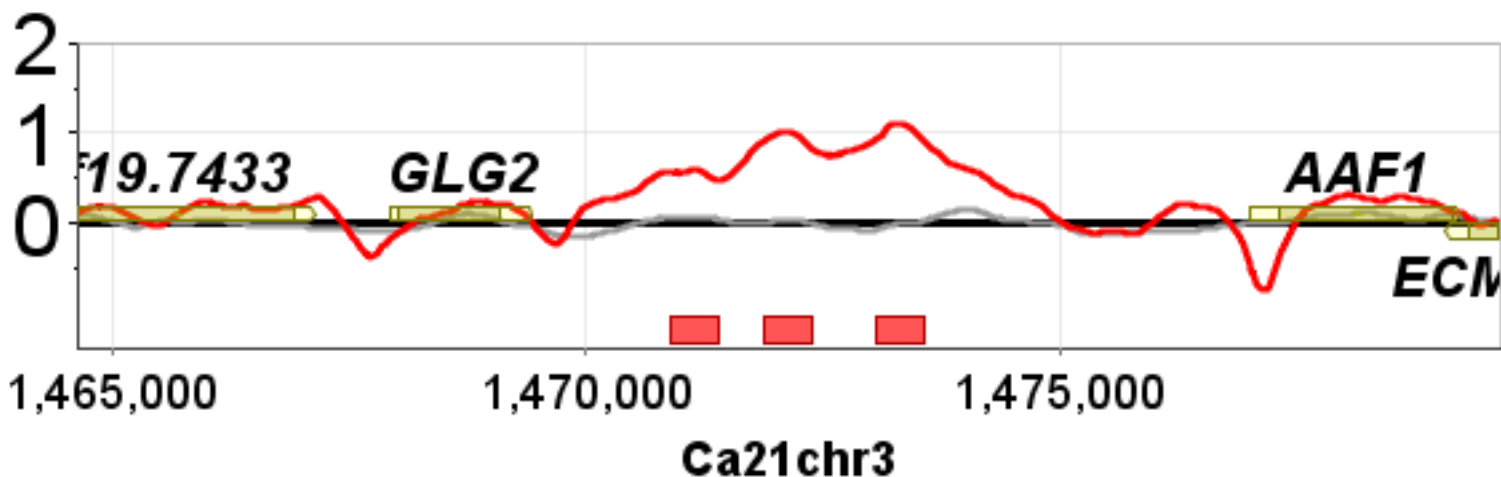
[1.035] Ca21chrR:1390308-1405307 [+] [ntar\_1308, orf19.916, KIP1, orf19.713, orf19.714]



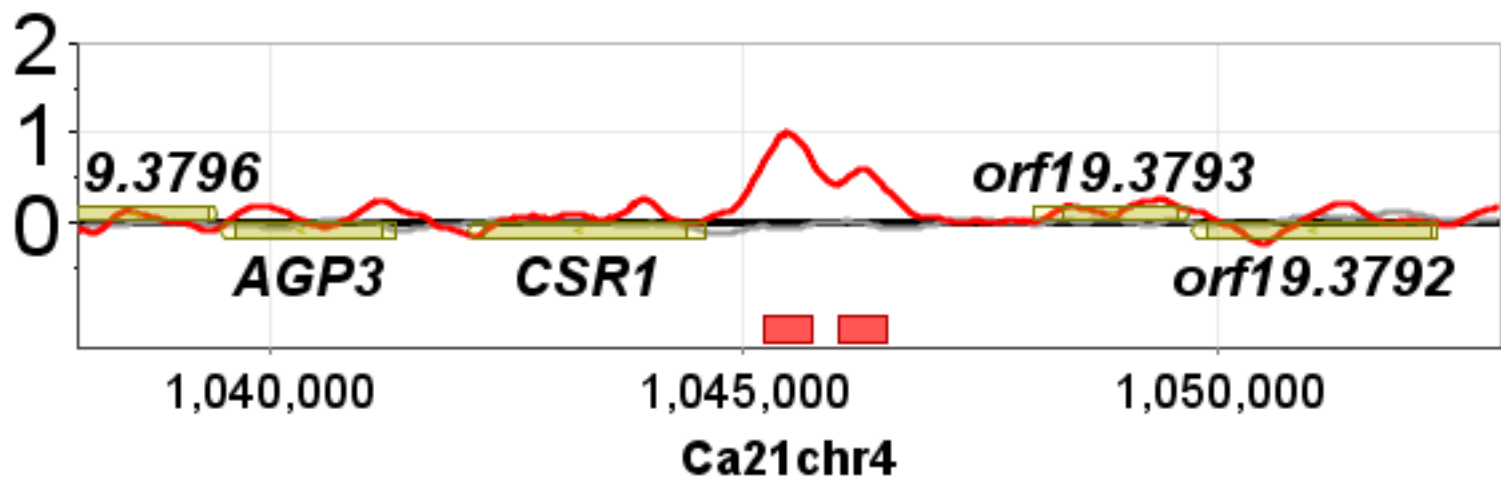
[1.023] Ca21chrR:2150588-2165587 [+] [INO1, ntar\_1403, CHT3, orf19.7583, orf19.7588]



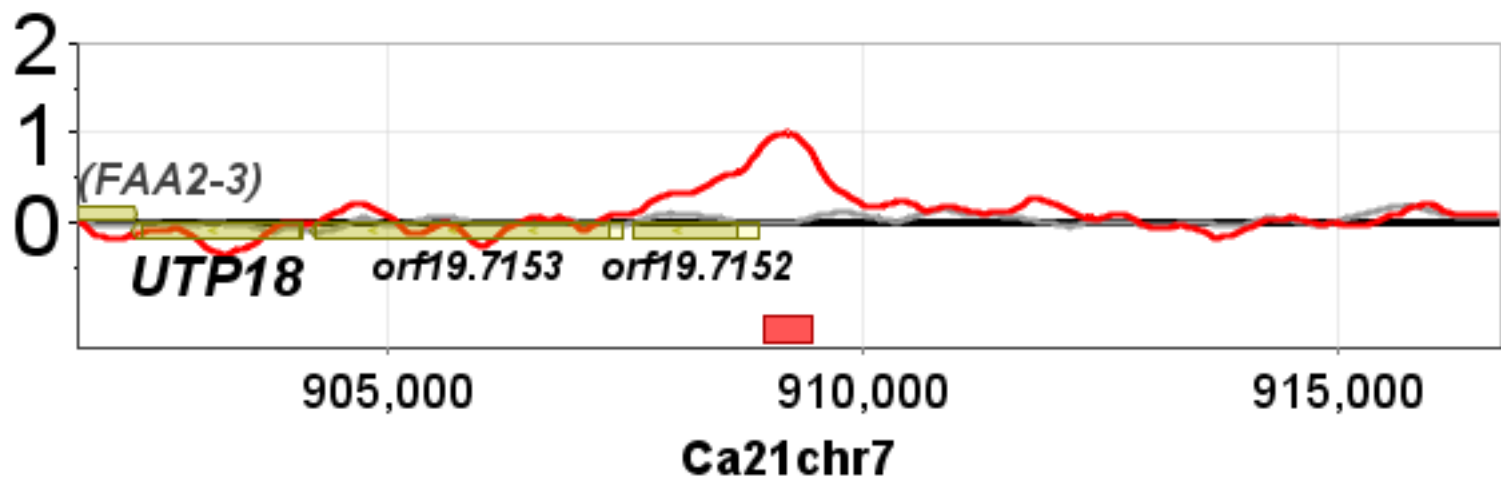
[1.016] Ca21chr3:1464631-1479630 [+] [th(quq)3, GLG2, ntar\_658, ntar\_659, AAF1]



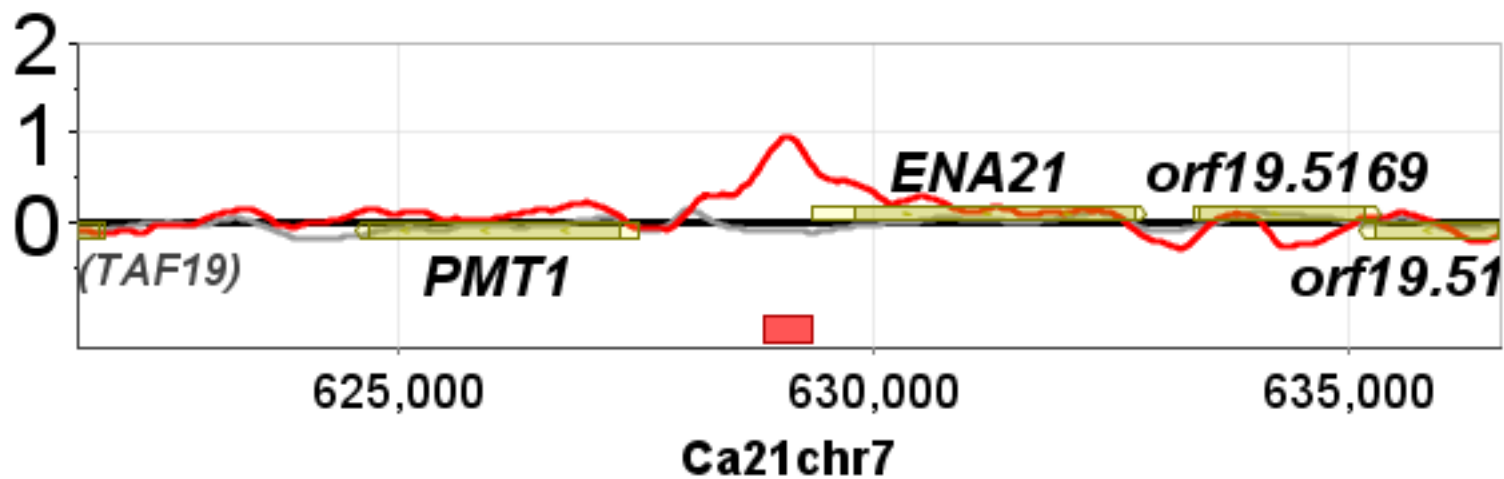
[0.993] Ca21chr4:1037968-1052967 [+] [CSR1, orf19.3793, AGP3, orf19.3792, orf19.3796]



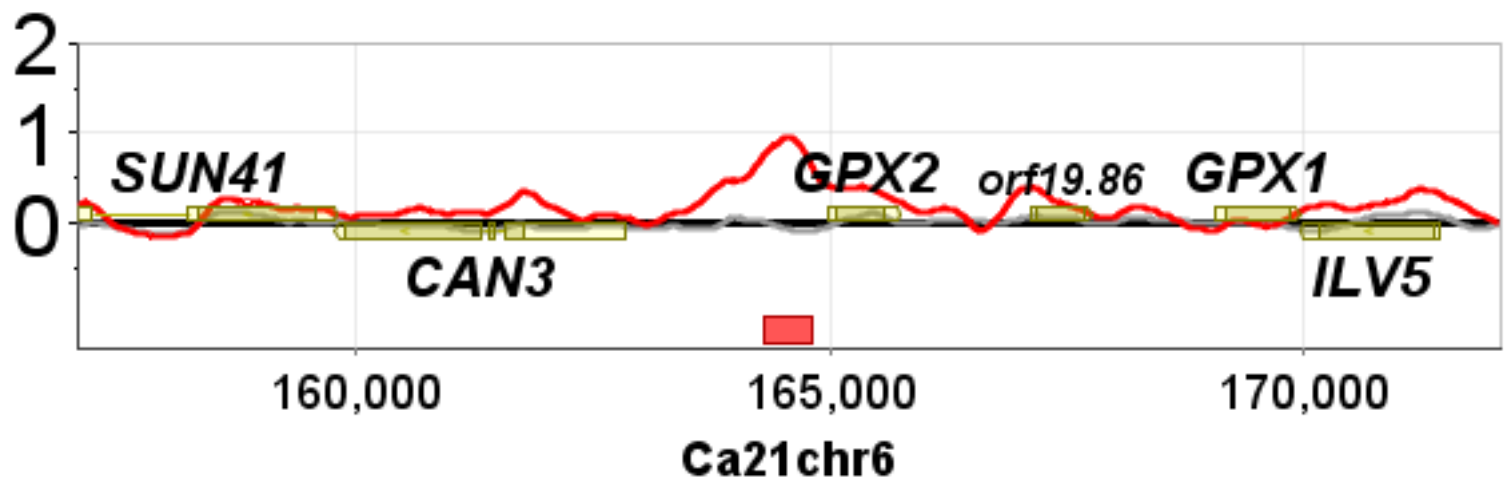
[0.992] Ca21chr7:901710-916709 [+] [orf19.7152, orf19.7153, ntar\_1151, UTP18, ntar\_1152]



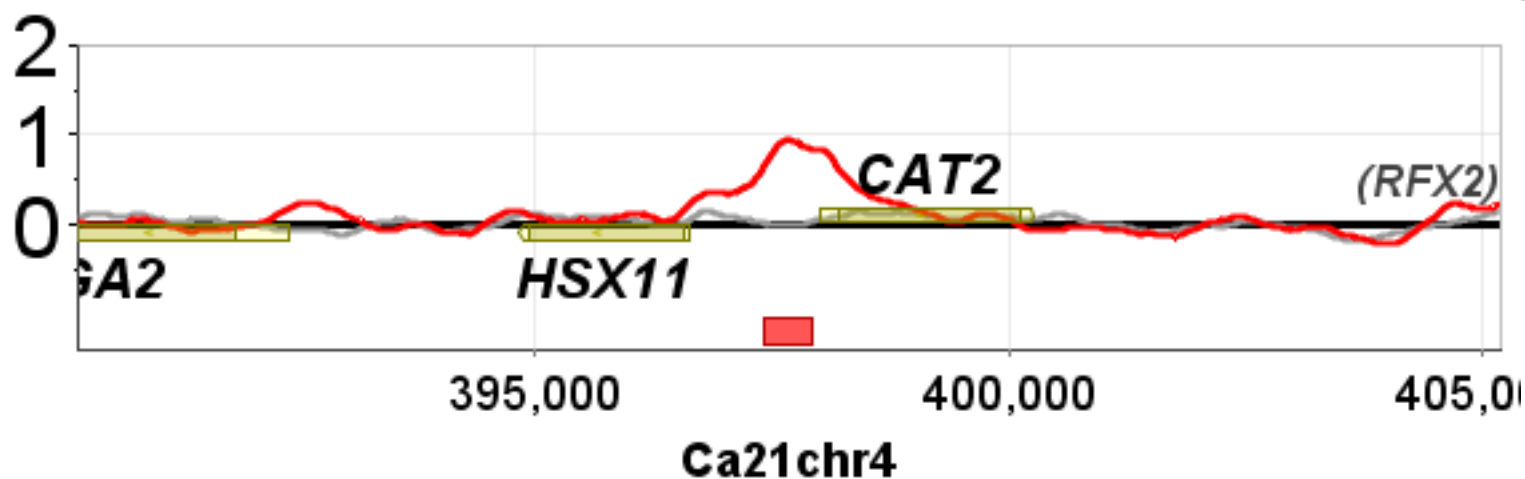
[0.966] Ca21chr7:621600-636599 [+] [ENA21, PMT1, orf19.5169, LIP9, TAF19]



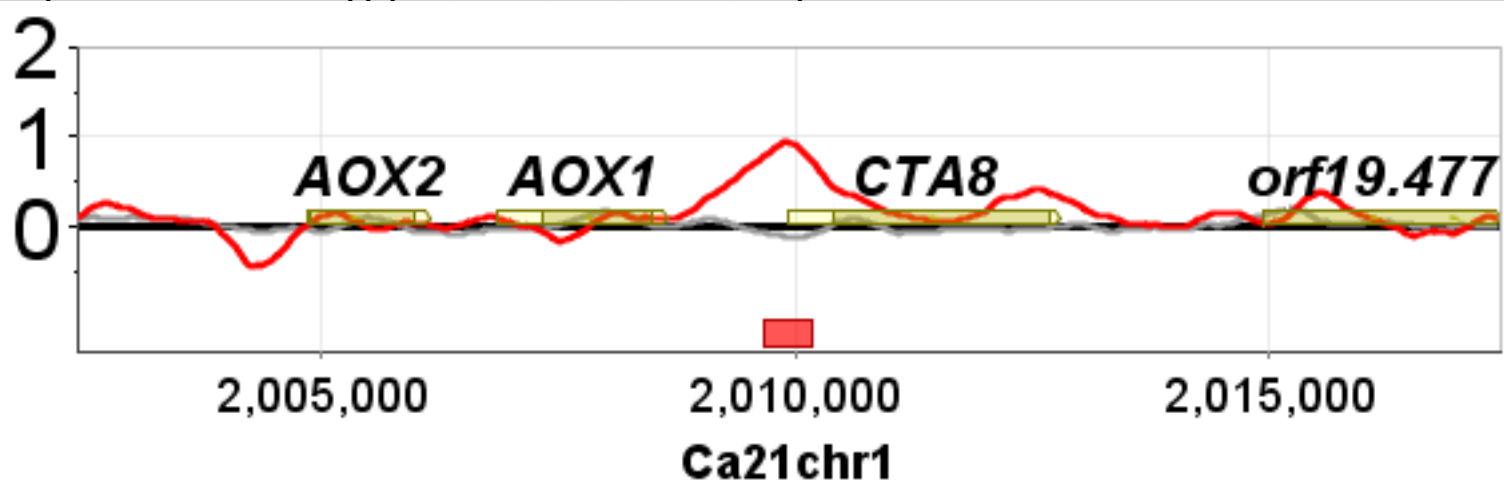
[0.954] Ca21chr6:157062-172061 [+] [GPX2, CAN3, orf19.86, ntar\_974, GPX1]



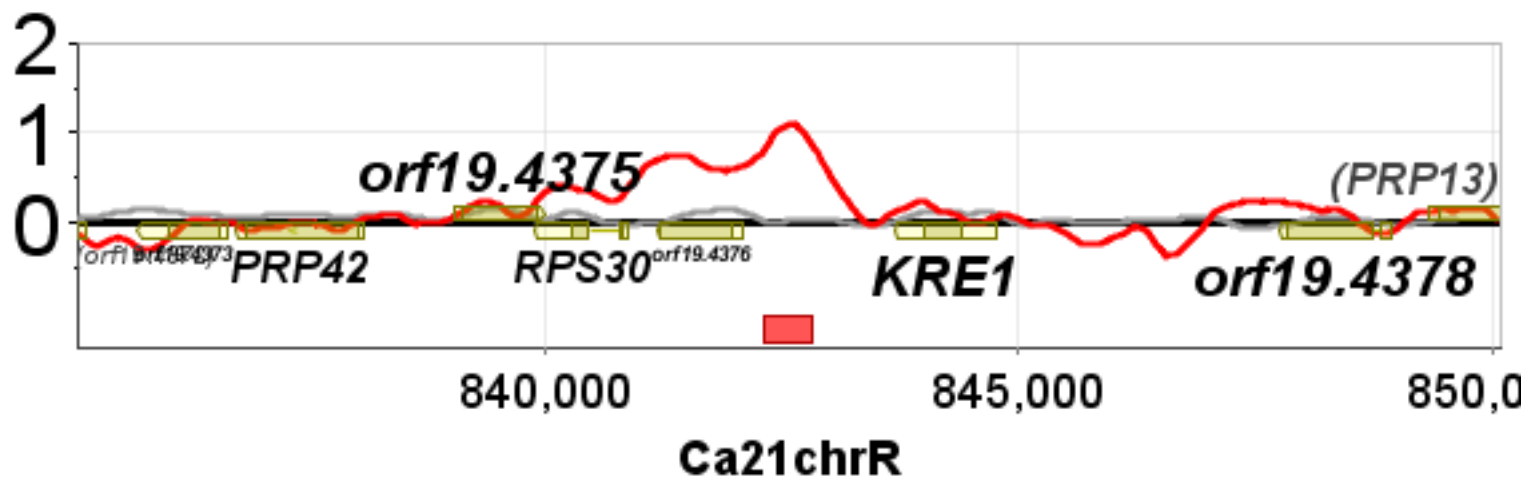
[0.942] Ca21chr4:390171-405170 [+] [CAT2, HSX11, RGA2, RFX2]



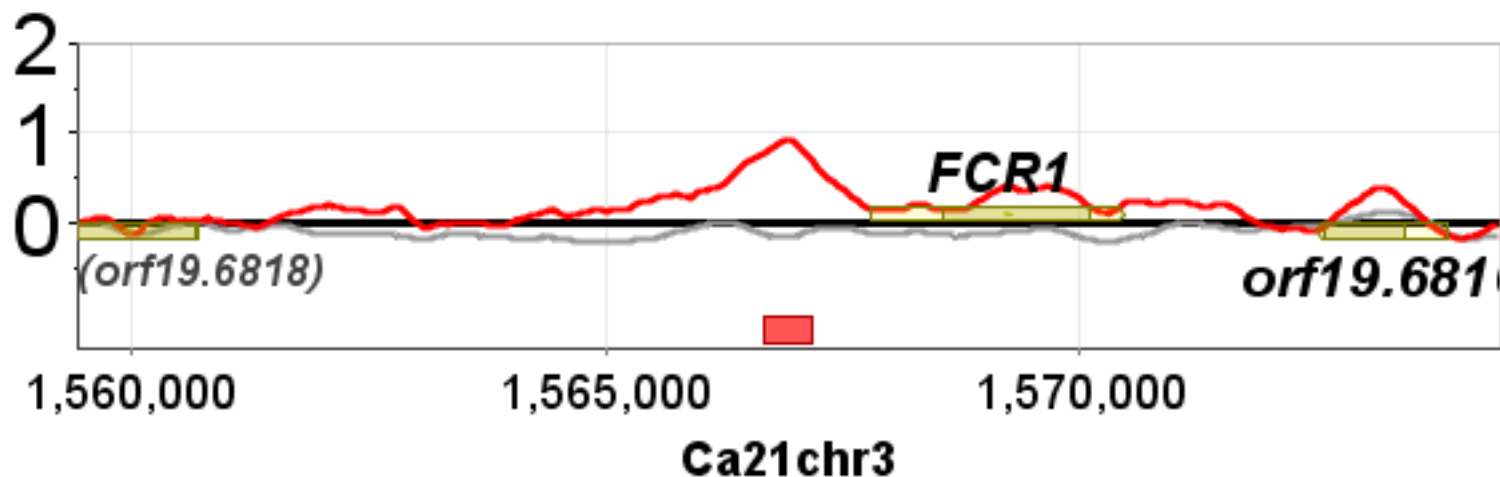
[0.937] Ca21chr1:2002422-2017421 [+] [CTA8, ntar\_191, AOX1, orf19.4776, AOX2]



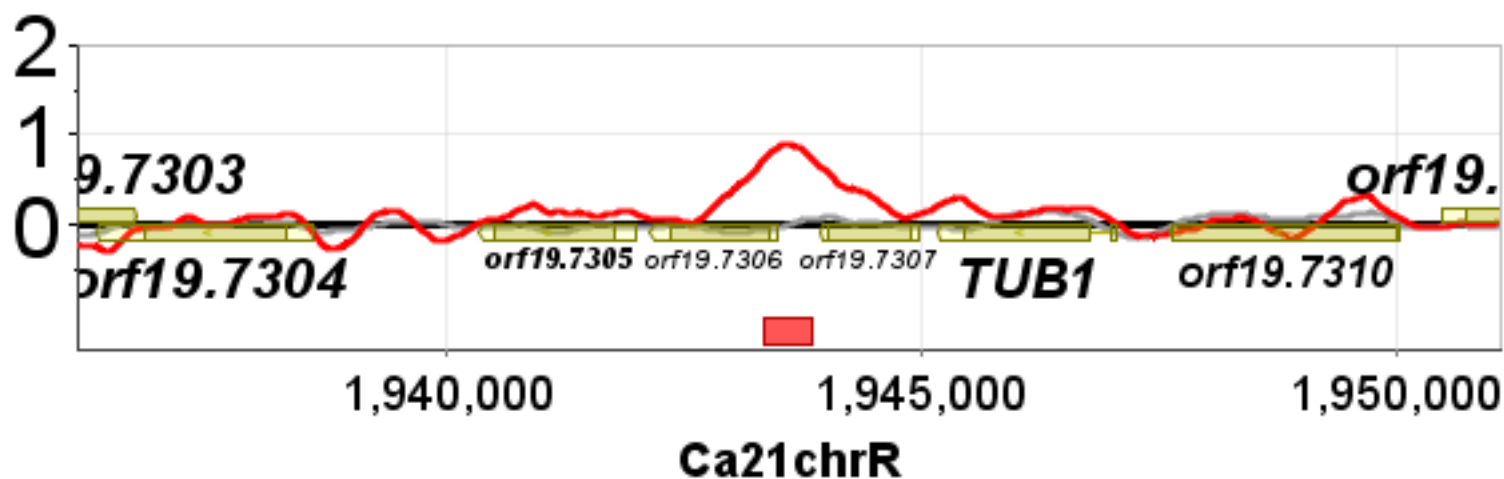
[0.937] Ca21chrR:835075-850074 [+] [orf19.4376, ntar\_1252, RPS30, KRE1, orf19.4375]



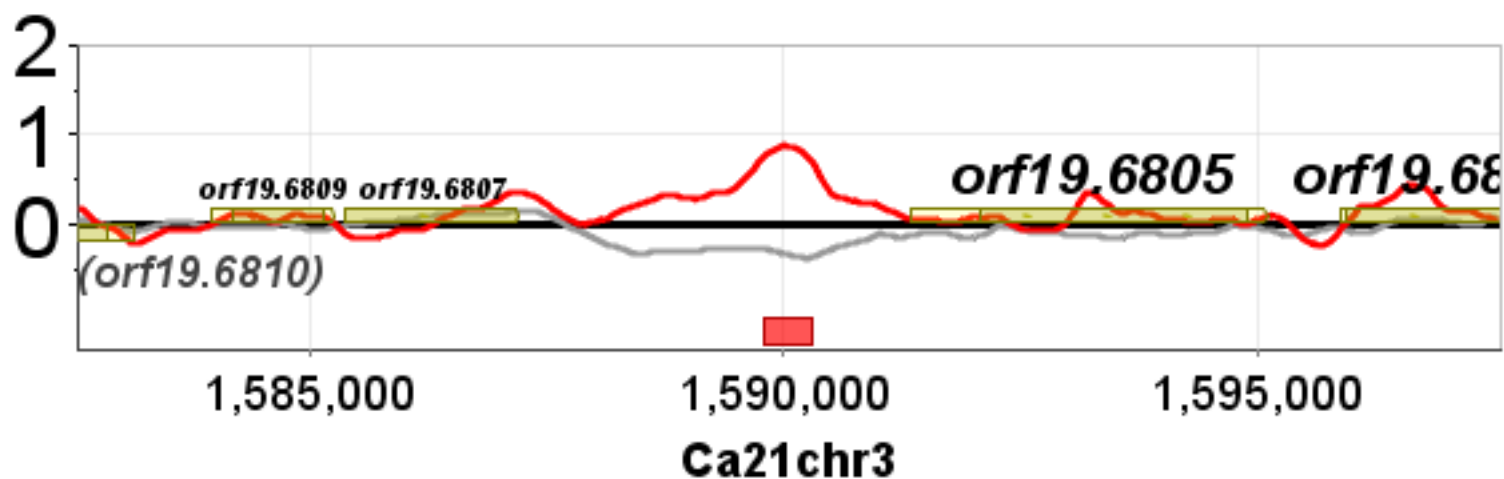
[0.927] Ca21chr3:1559426-1574425 [+] [FCR1, ntar\_663, tw(cca)2, orf19.6818, orf19.6816]



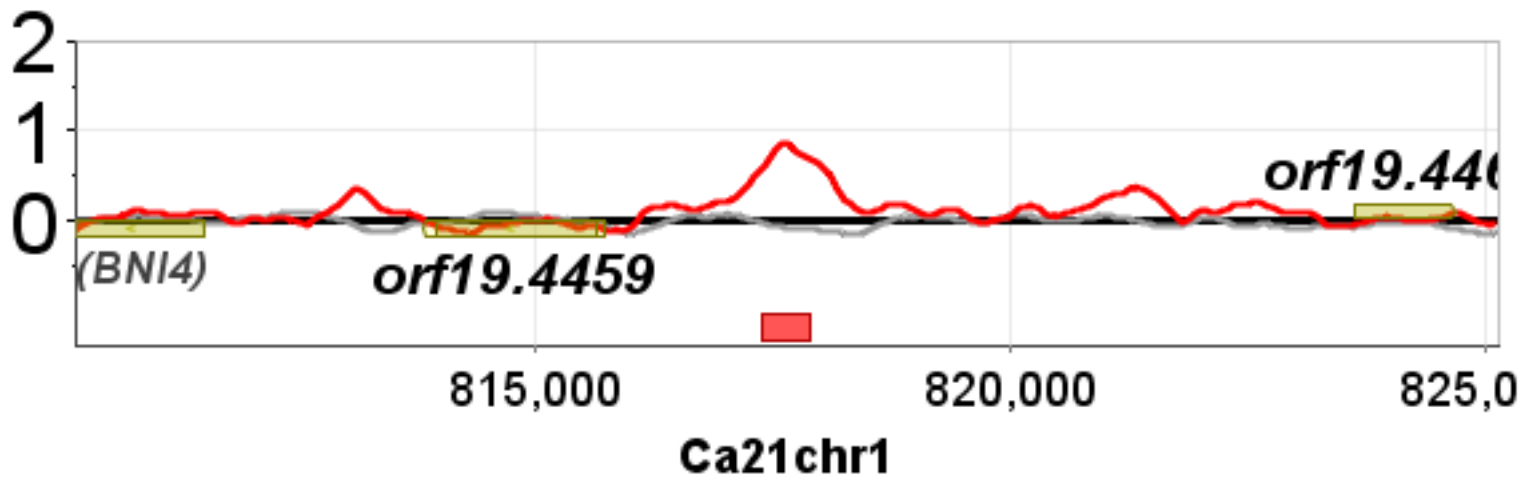
[0.89] Ca21chrR:1936094-1951093 [+] [orf19.7306, orf19.7307, orf19.7305, TUB1, ntar\_1374]



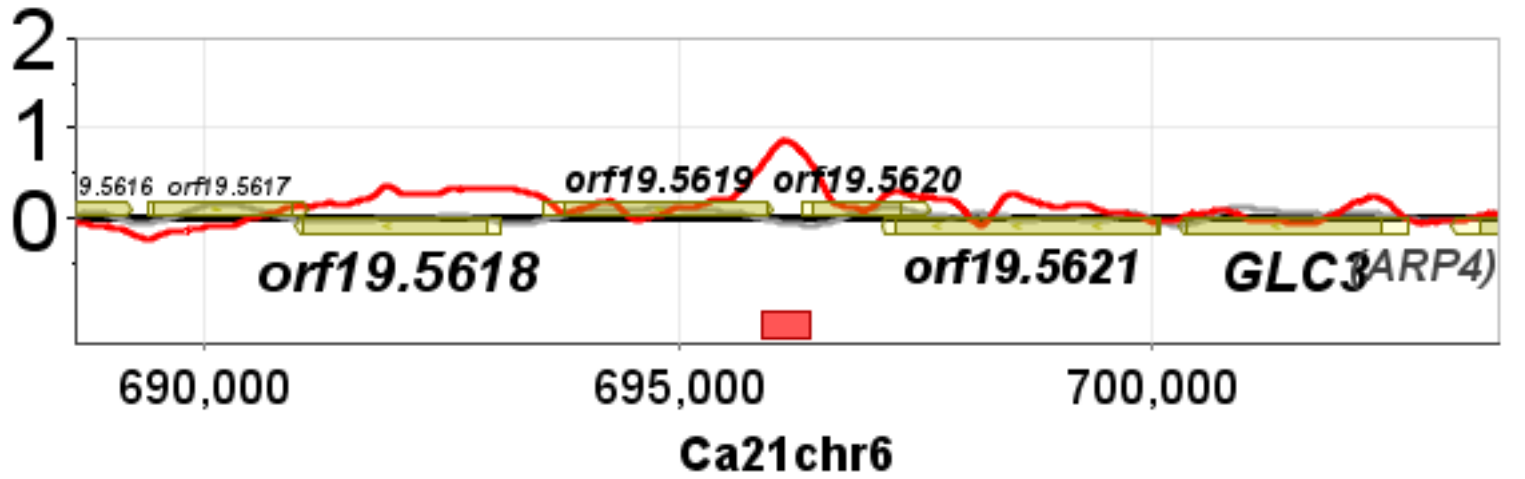
[0.881] Ca21chr3:1582549-1597548 [+] [ntar\_667, orf19.6805, ntar\_666, ntar\_665, orf19.6807]



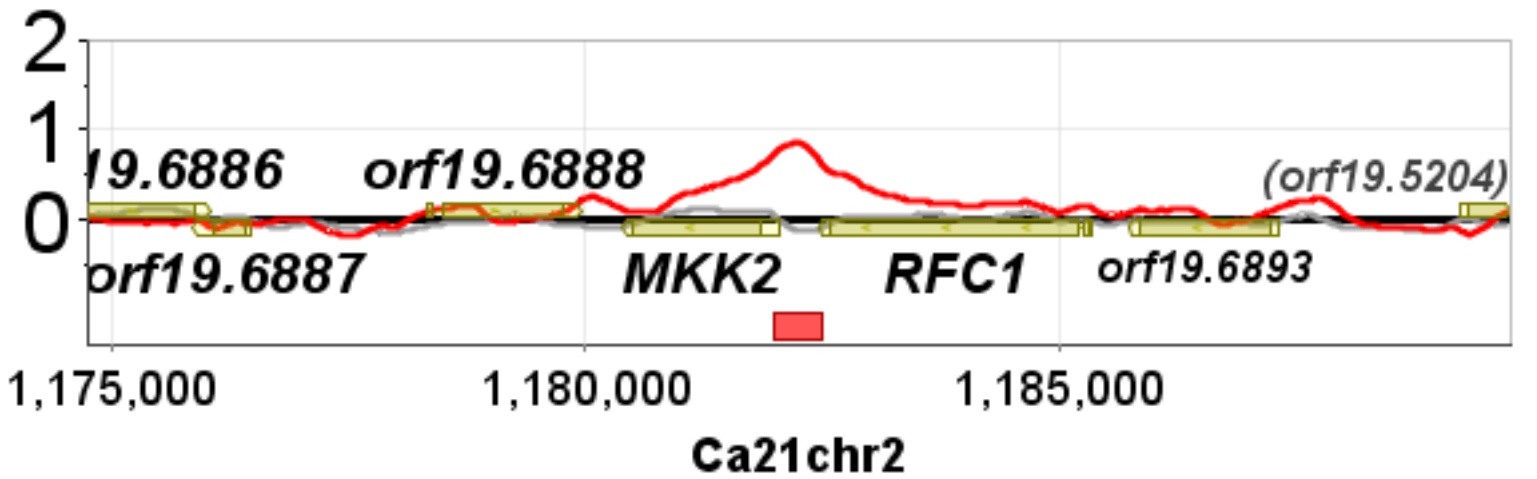
[0.864] Ca21chr1:810135-825134 [+] [orf19.4459, orf19.4461, ntar\_81, ntar\_80, ntar\_79]



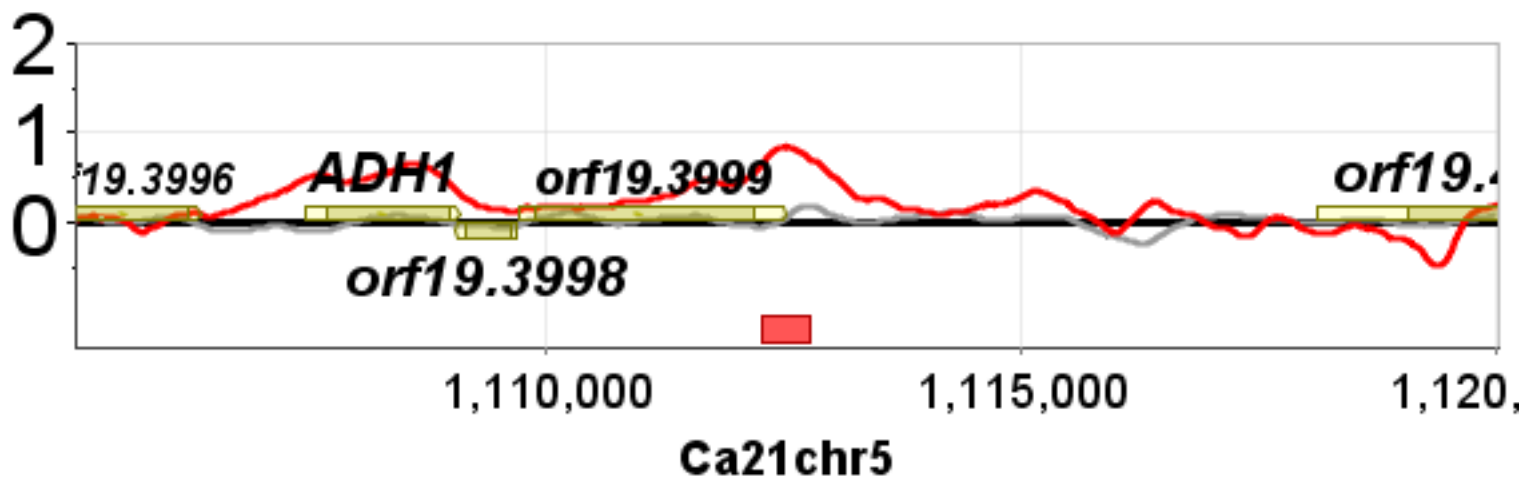
[0.859] Ca21chr6:688637-703636 [+] [orf19.5620, ntar\_1021, ntar\_1020, orf19.5619, orf19.5618]



[0.854] Ca21chr2:1174745-1189744 [+] [MKK2, RFC1, orf19.6888, orf19.6893, orf19.6887]

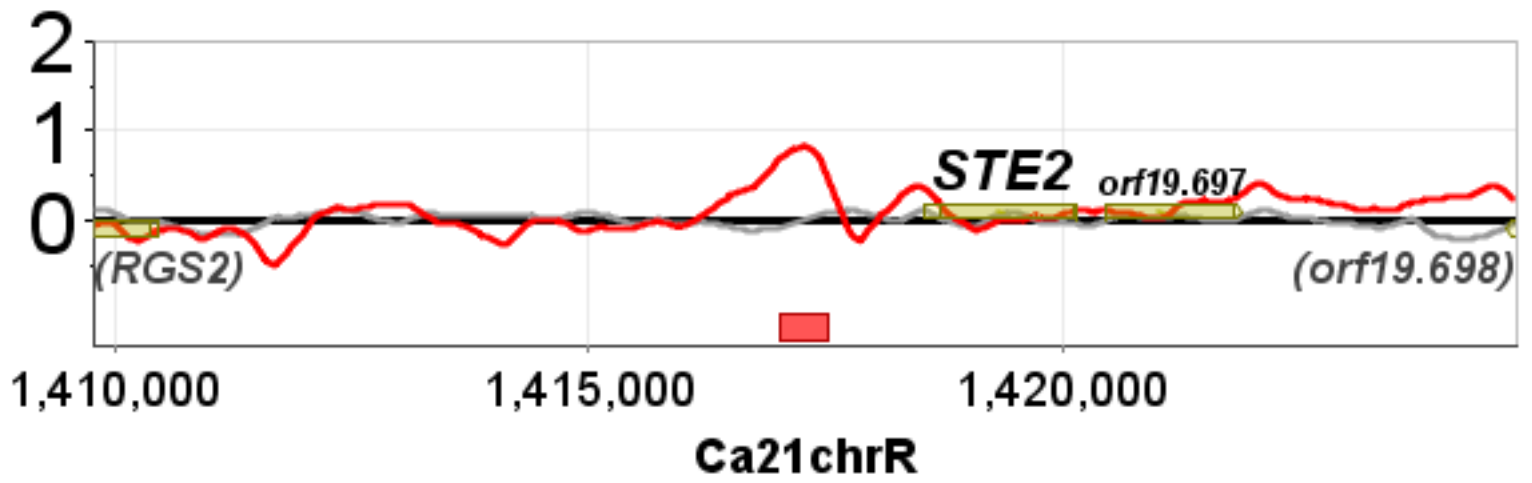


[0.853] Ca21chr5:1105022-1120021 [+] [orf19.3999, orf19.3998, ADH1, orf19.4000, ntar\_963]

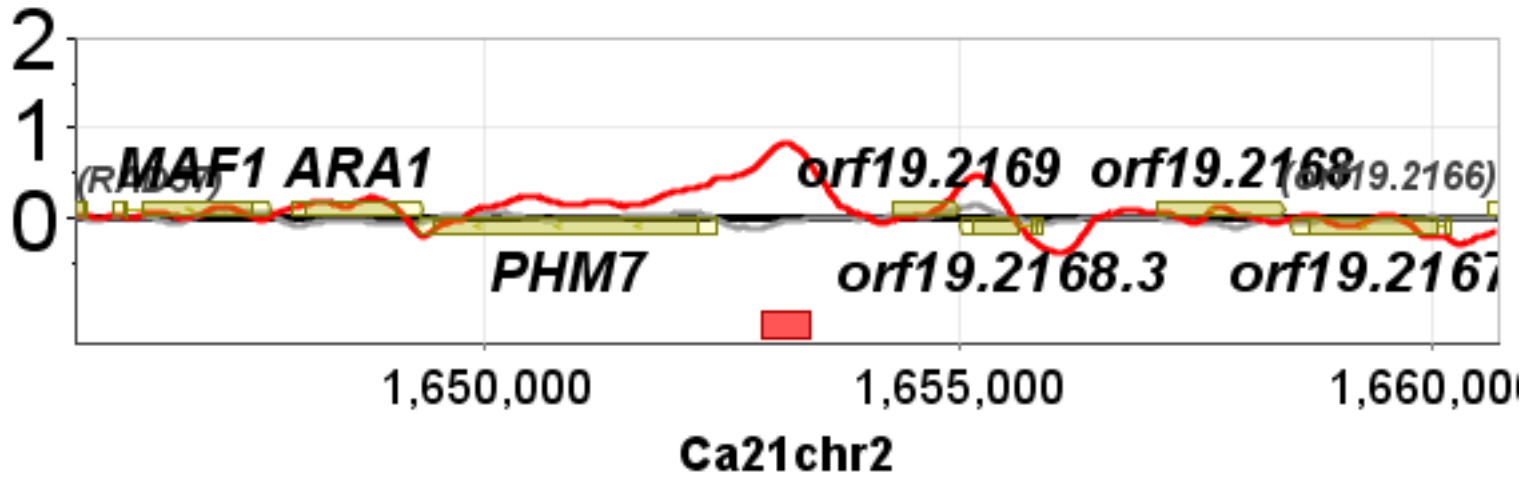




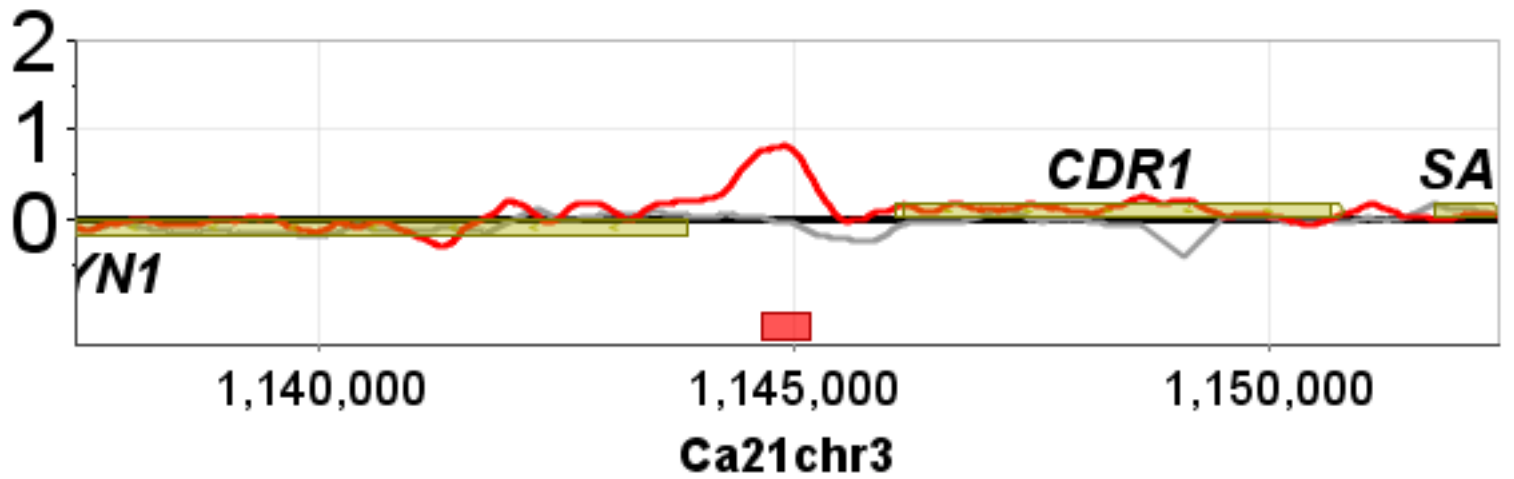
[0.84] Ca21chrR:1409775-1424774 [+] [ntar\_1315, ntar\_1313, STE2, ntar\_1314, ntar\_1312]



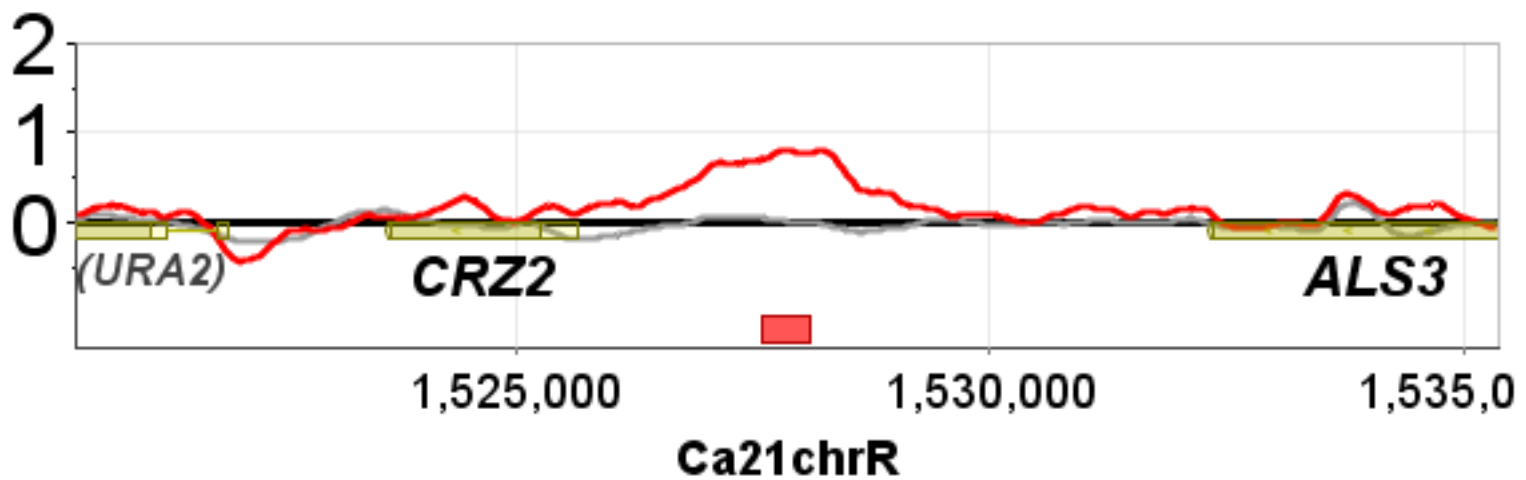
[0.83] Ca21chr2:1645676-1660675 [+] [PHM7, orf19.2169, orf19.2168.3, ntar\_438, orf19.2168]



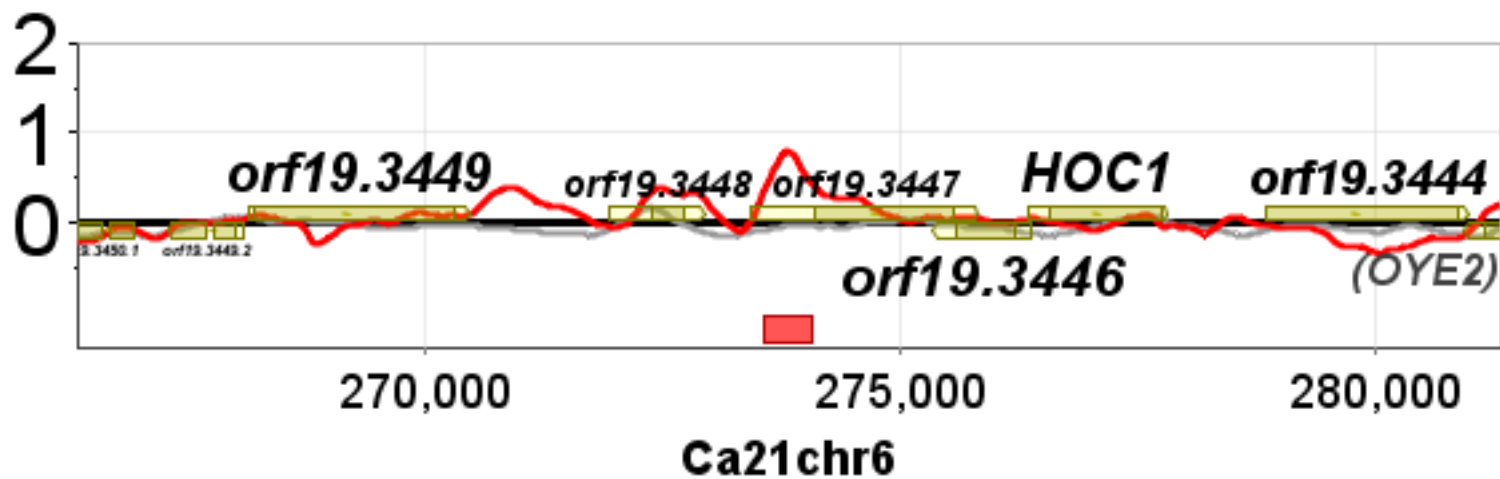
[0.82] Ca21chr3:1137419-1152418 [+] [DYN1, CDR1, SAP3, ntar\_620]



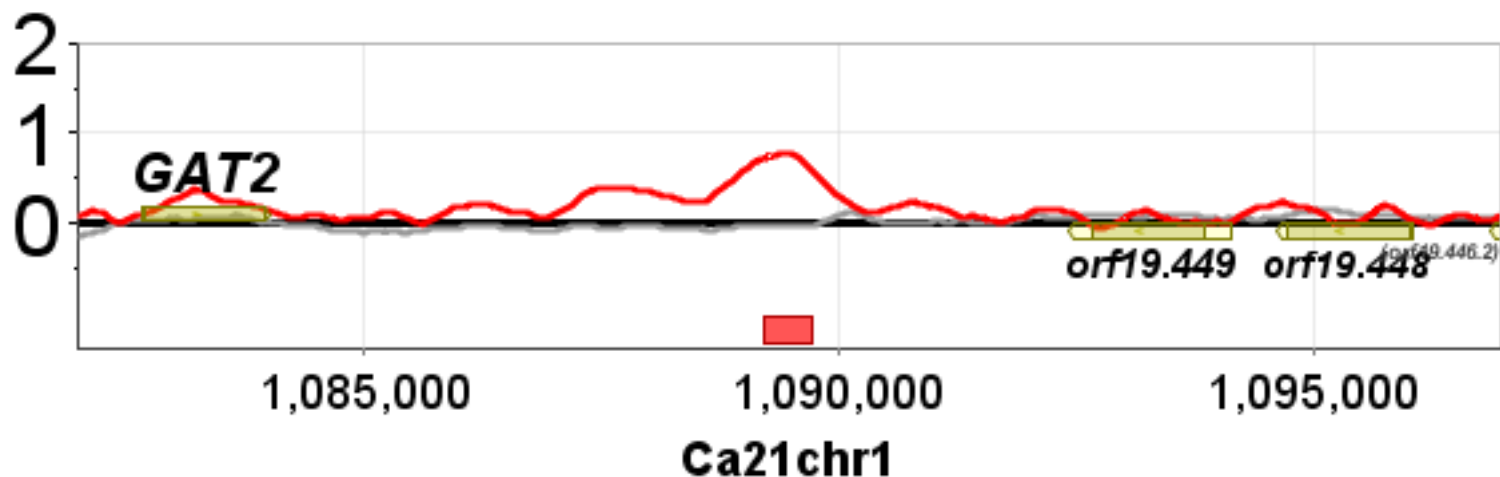
[0.799] Ca21chrR:1520356-1535355 [+] [ntar\_1331, CRZ2, URA2, ALS3]



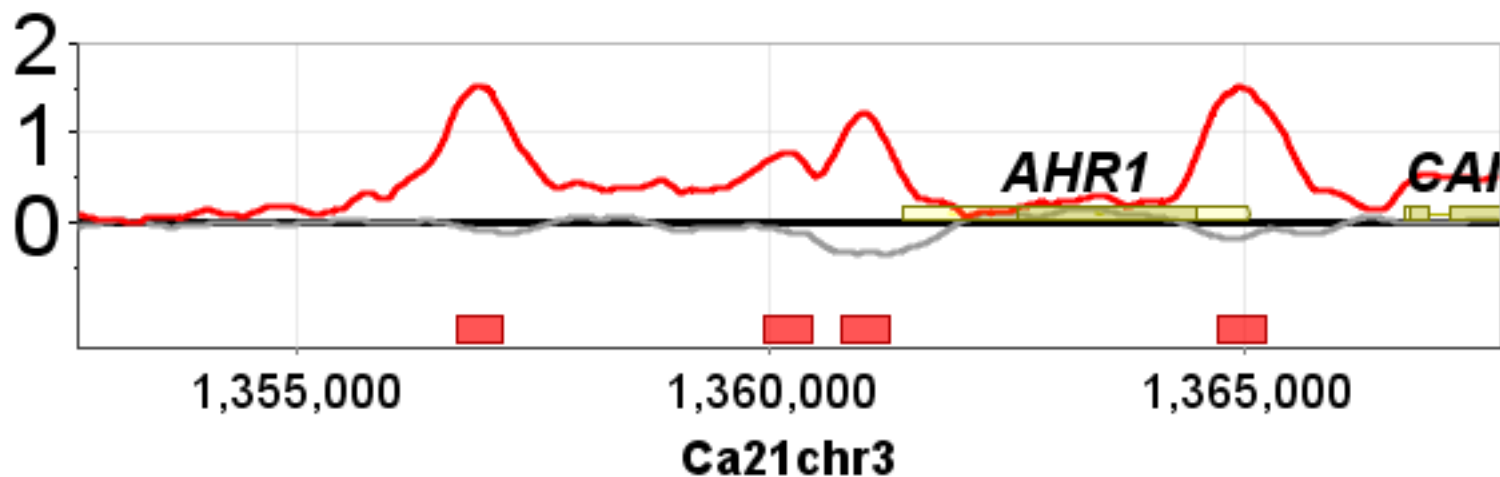
[0.794] Ca21chr6:266321-281320 [+] [ntar\_982, orf19.3447, ntar\_983, orf19.3448, HOC1]



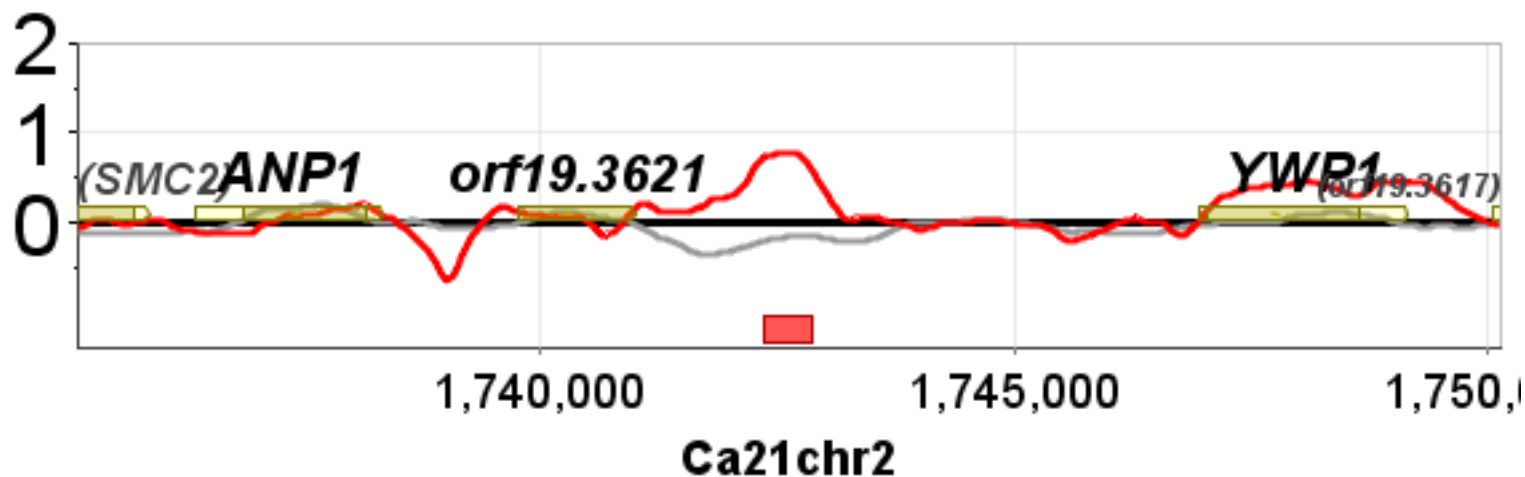
[0.783] Ca21chr1:1081966-1096965 [+] [ntar\_104, orf19.450, orf19.449, orf19.448, GAT2]



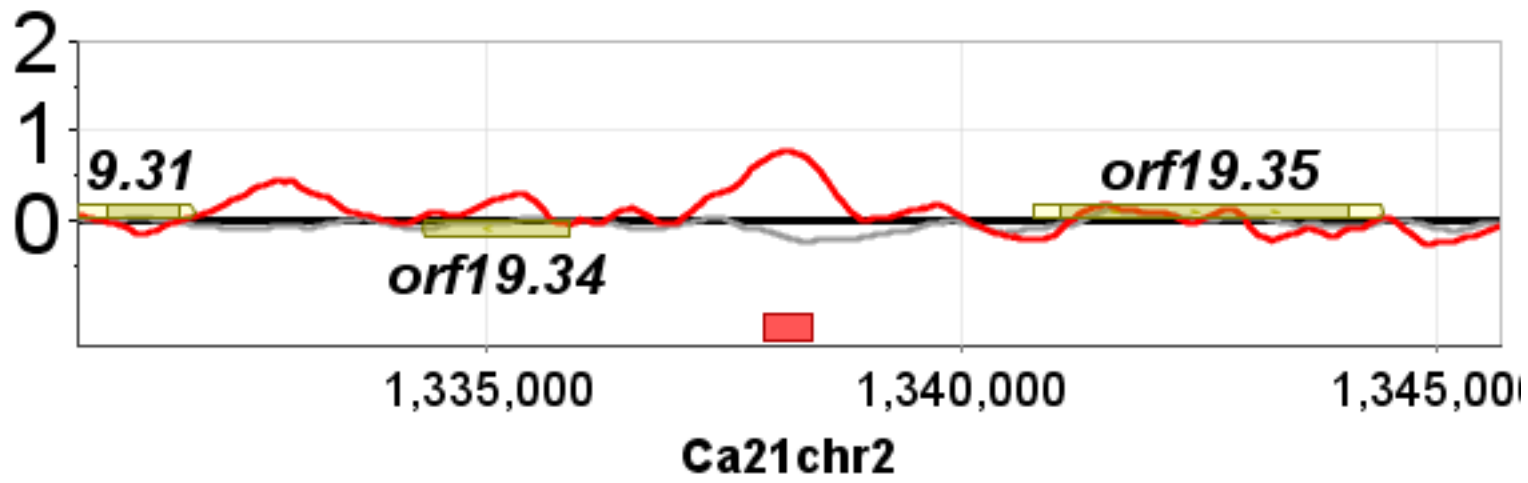
[0.777] Ca21chr3:1352688-1367687 [+] [orf19.7381, CAM1]



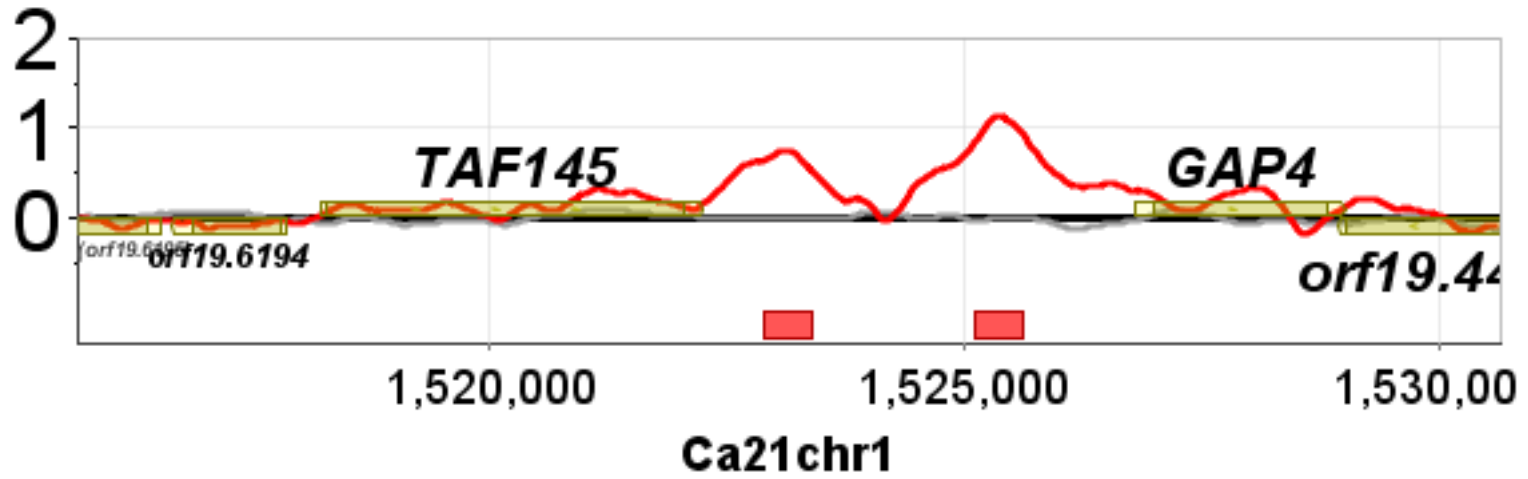
[0.776] Ca21chr2:1735119-1750118 [+] [ntar\_446, ntar\_447, ntar\_445, ntar\_448, ntar\_450]



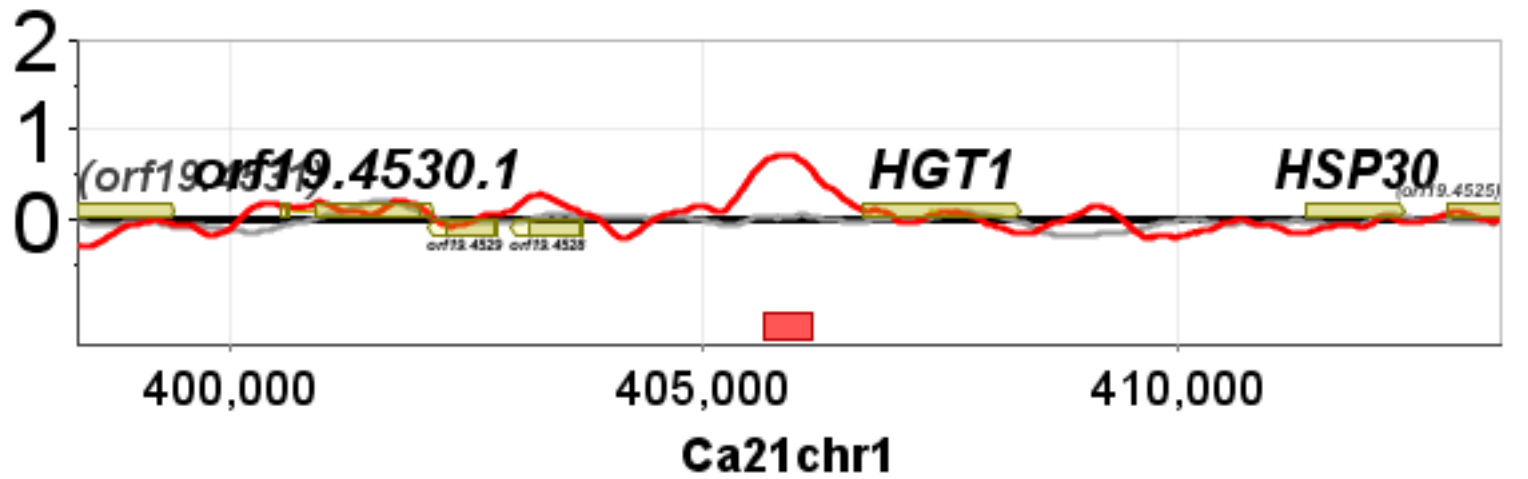
[0.766] Ca21chr2:1330672-1345671 [+] [ntar\_406, orf19.34, orf19.35, ntar\_405, ntar\_404]



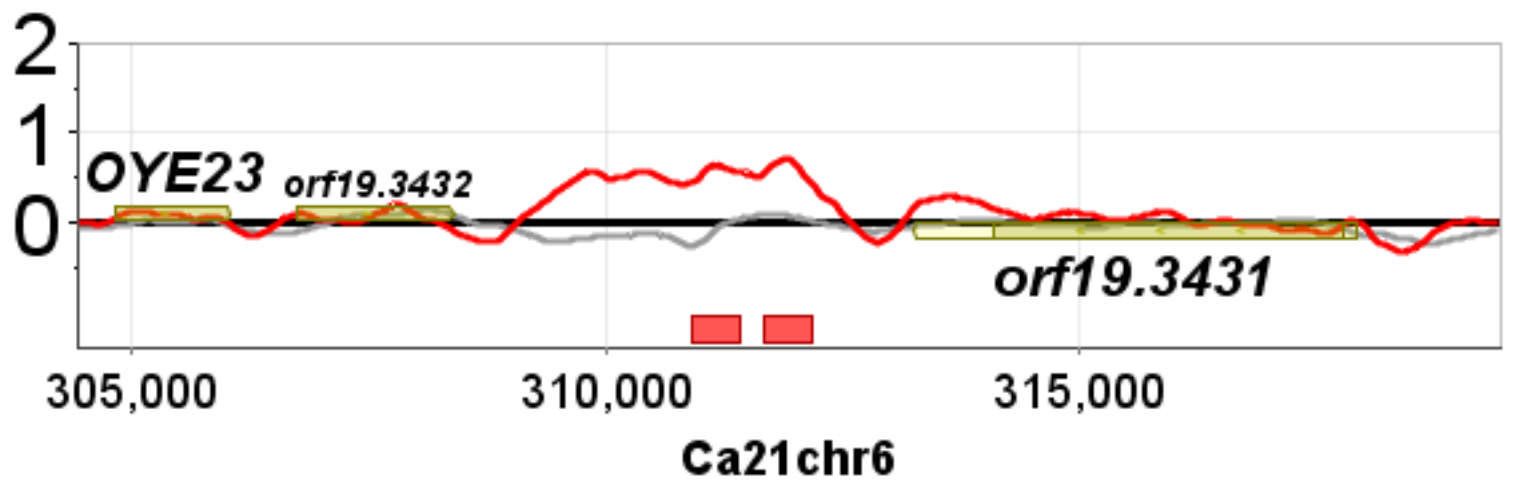
[0.753] Ca21chr1:1515644-1530643 [+] [GAP4, TAF145, orf19.6194, ntar\_136, orf19.6195]



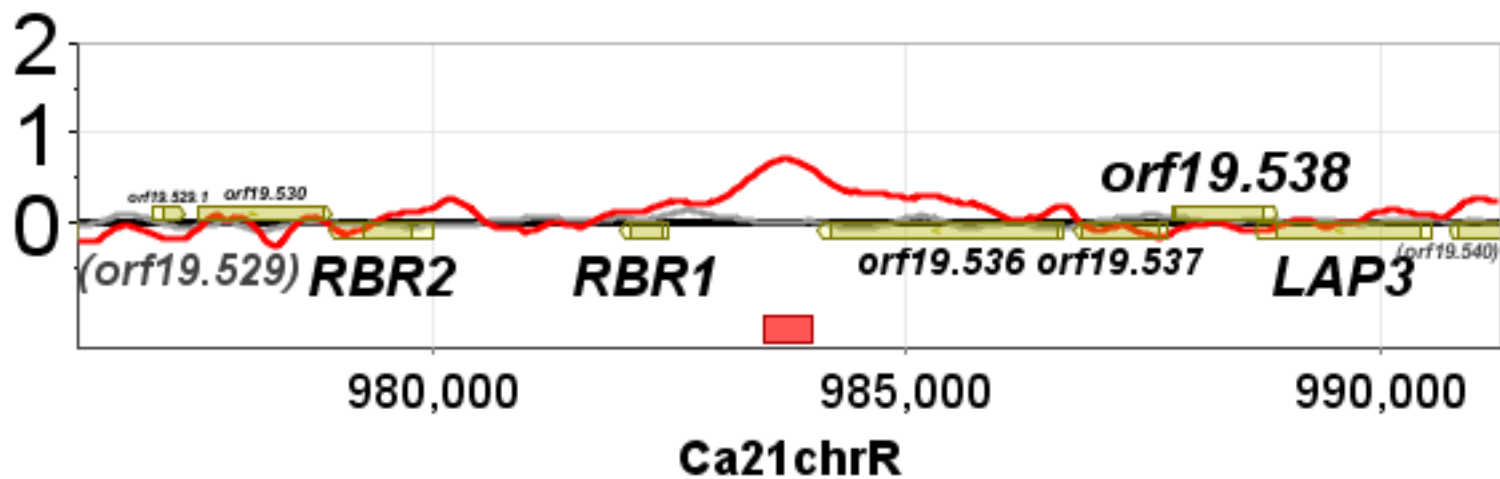
[0.715] Ca21chr1:398393-413392 [+] [ntar\_36, HGT1, ntar\_37, ntar\_35, orf19.4528]



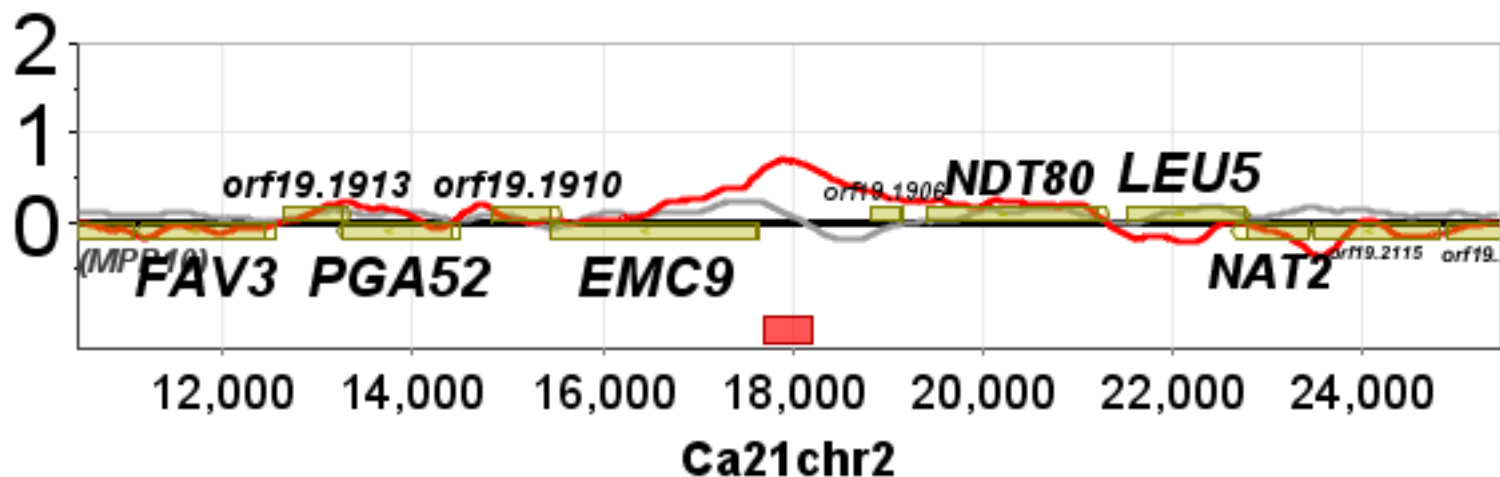
[0.713] Ca21chr6:304425-319424 [+] [ntar\_990, ntar\_989, ntar\_988, orf19.3432, orf19.3431]



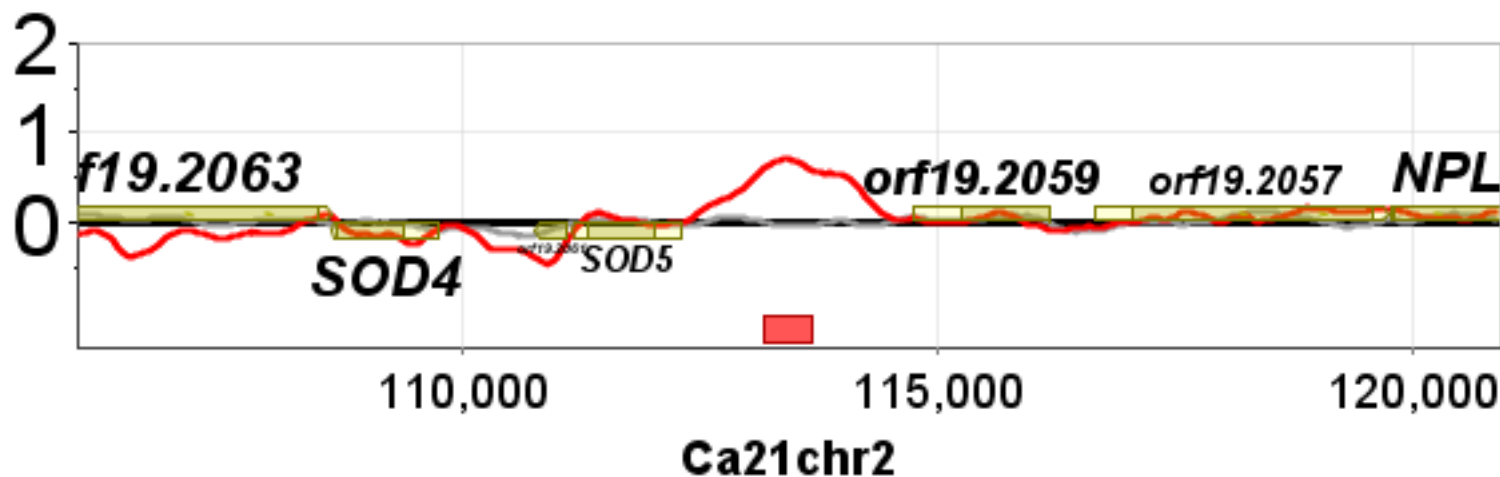
[0.708] Ca21chrR:976257-991256 [+] [RBR1, orf19.536, orf19.533, RBR2, orf19.537]



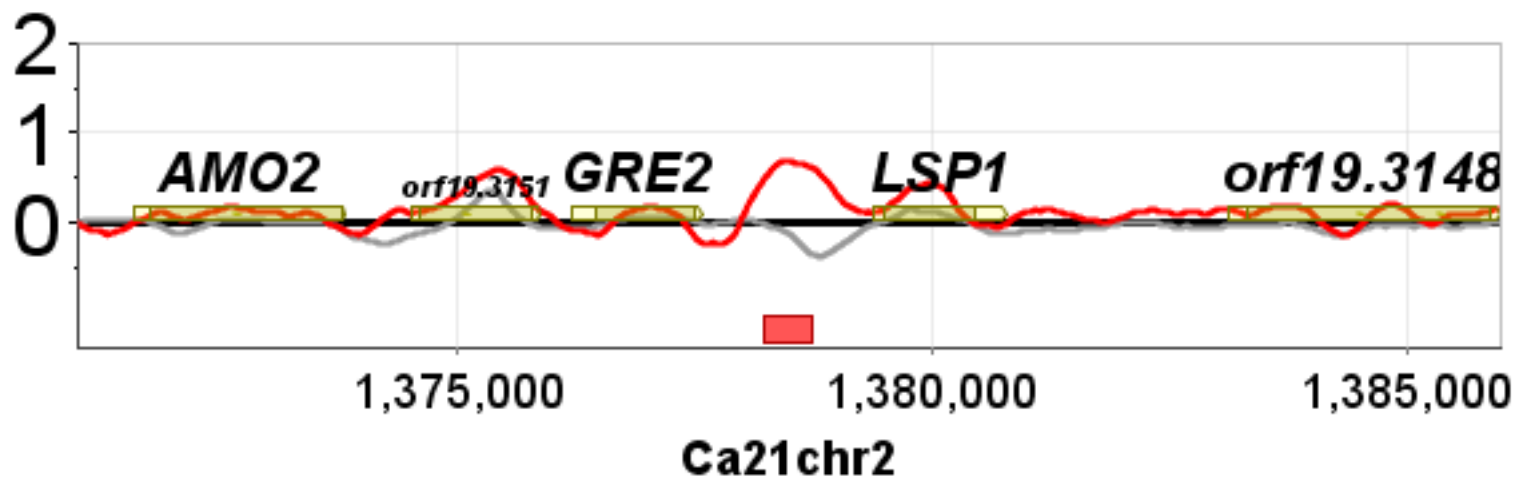
[0.703] Ca21chr2:10455-25454 [+] [EMC9, ntar\_288, orf19.1906, NDT80, orf19.1910]



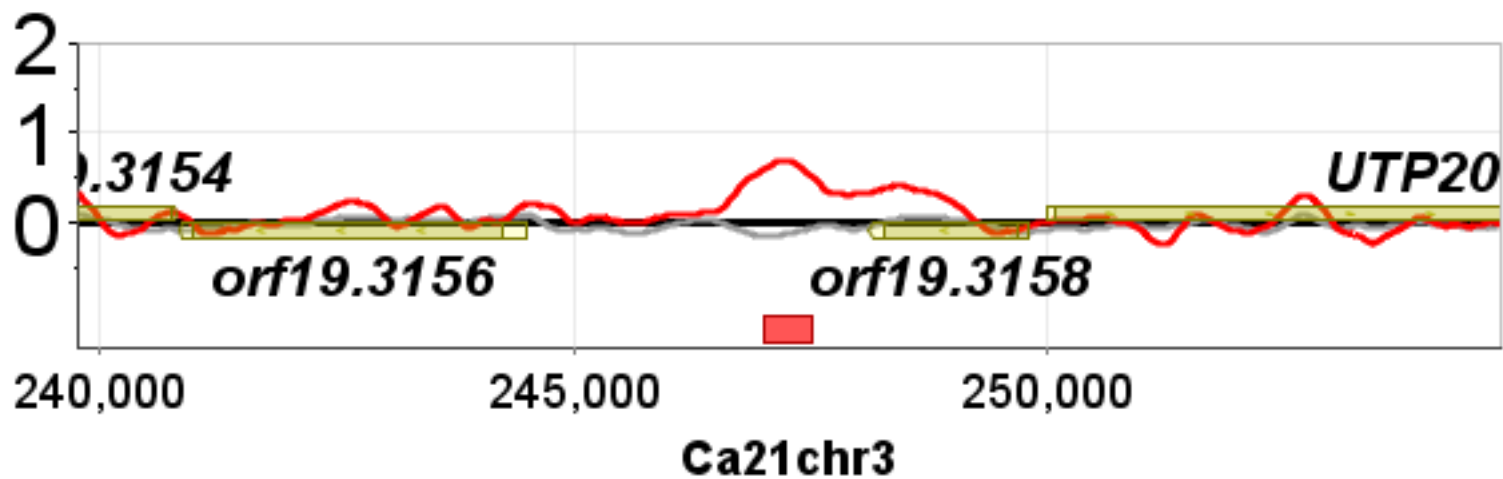
[0.699] Ca21chr2:105929-120928 [+] [SOD5, orf19.2059, orf19.2061, orf19.2057, ntar\_293]



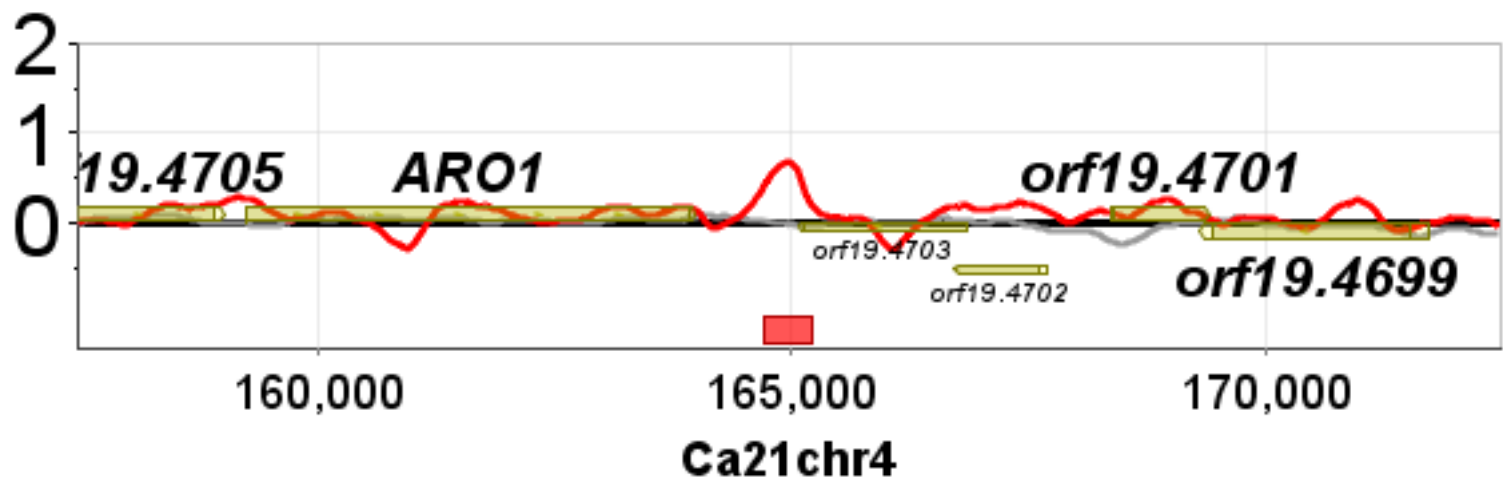
[0.696] Ca21chr2:1370984-1385983 [+] [ntar\_421, ntar\_422, LSP1, GRE2, ntar\_420]



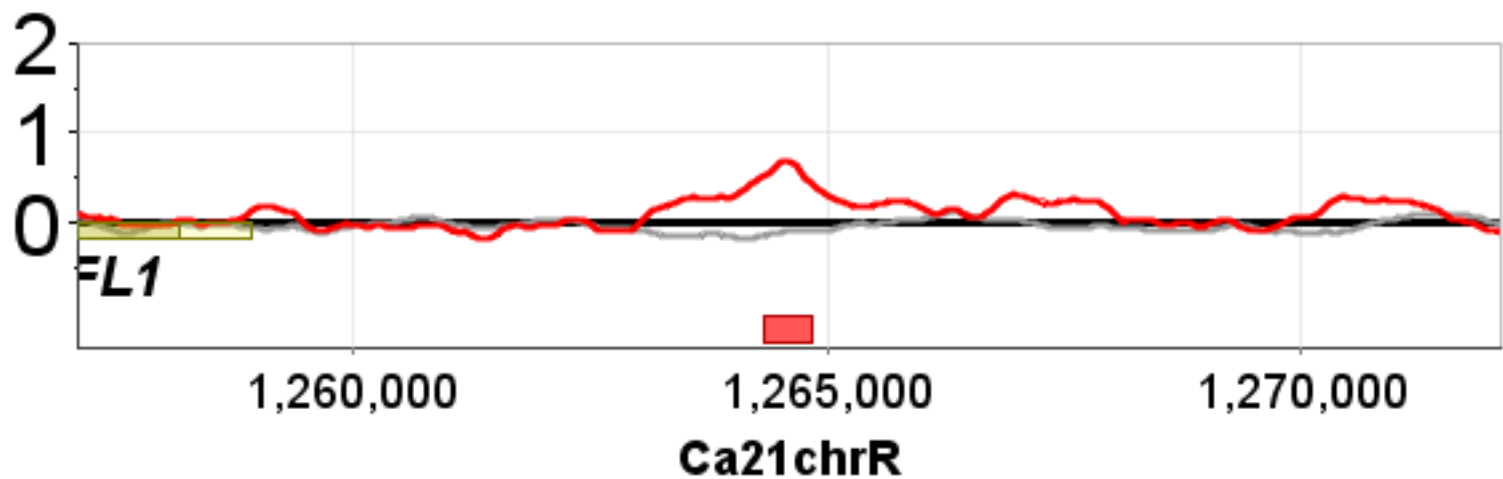
[0.694] Ca21chr3:239757-254756 [+] [ntar\_543, ntar\_544, orf19.3158, UTP20, orf19.3156]



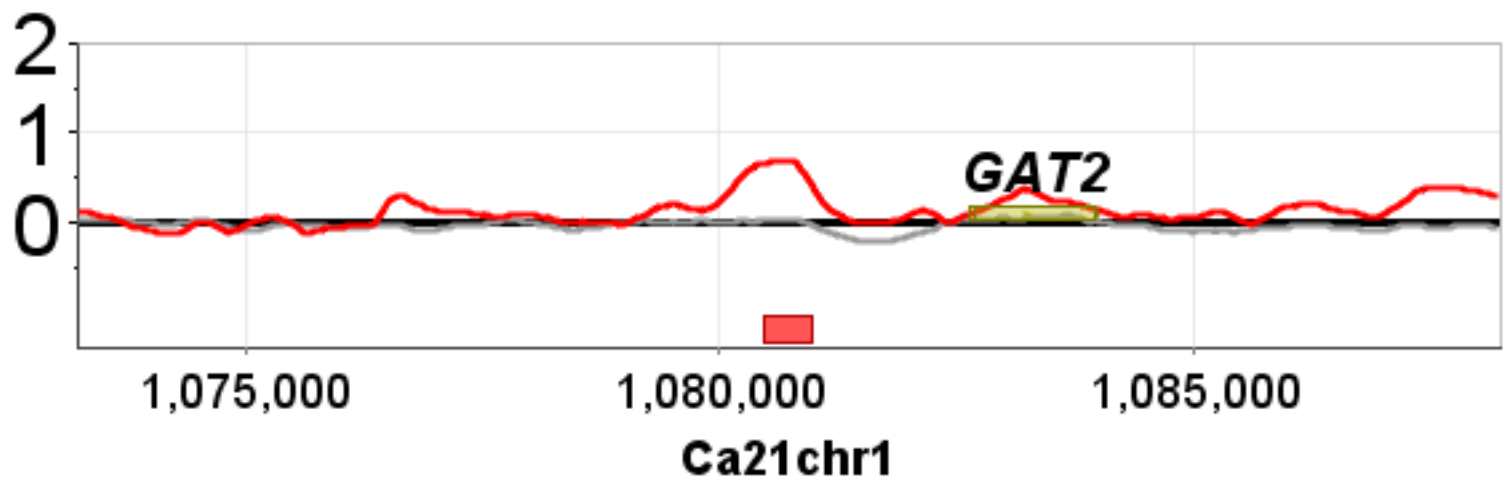
[0.693] Ca21chr4:157460-172459 [+] [ntar\_720, ntar\_721, tq(acc)5, orf19.4703, orf19.4702]



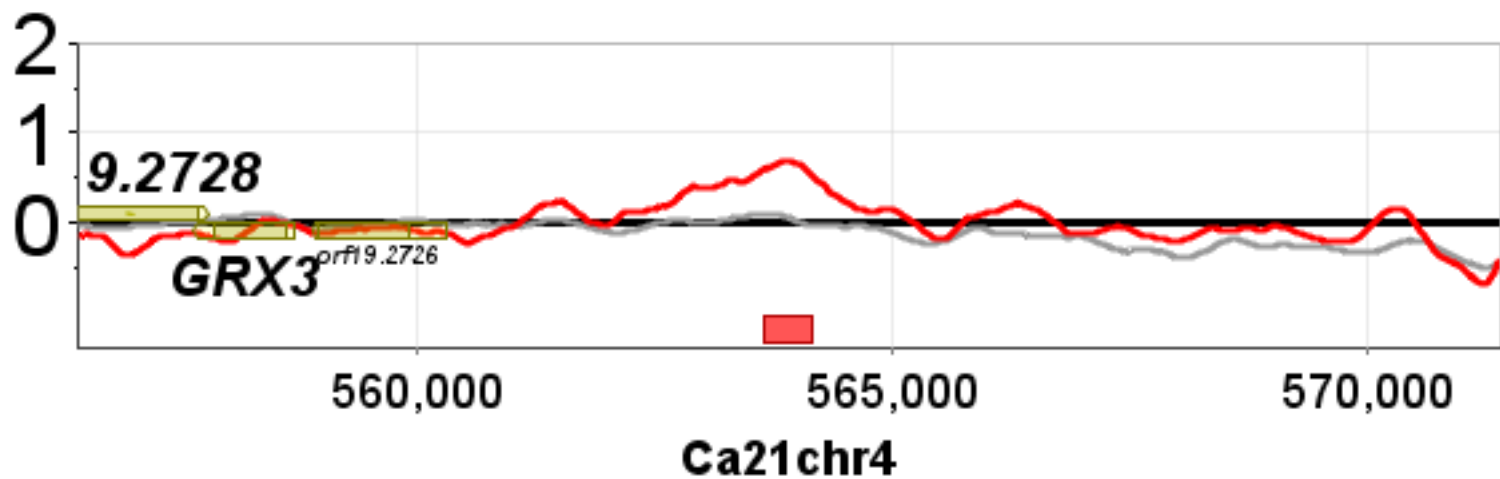
[0.691] Ca21chrR:1257090-1272089 [+] [ntar\_1292, ntar\_1291, SFL1]



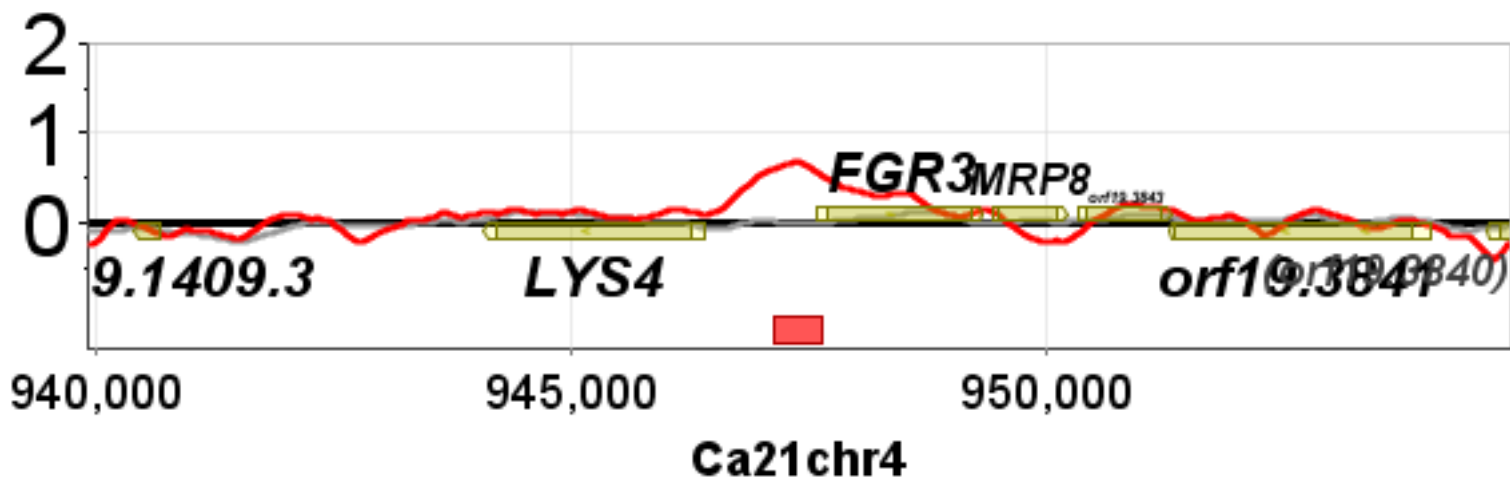
[0.688] Ca21chr1:1073222-1088221 [+] [GAT2, orf19.450]



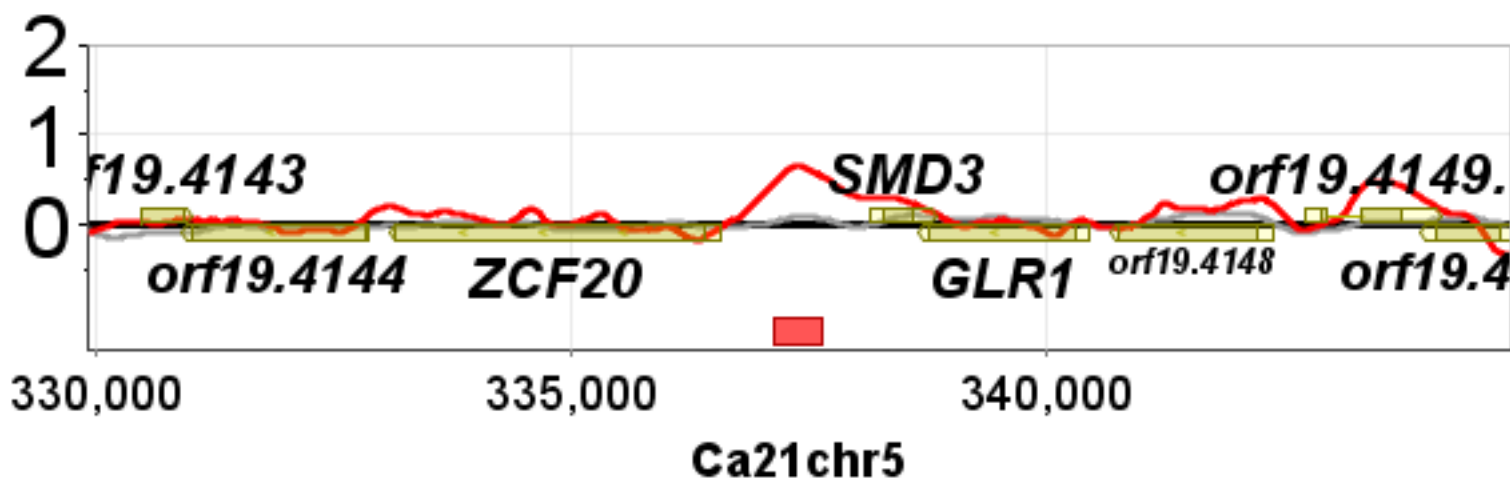
[0.675] Ca21chr4:556406-571405 [+] [orf19.2725, orf19.2726, ntar\_769, GRX3, orf19.2728]



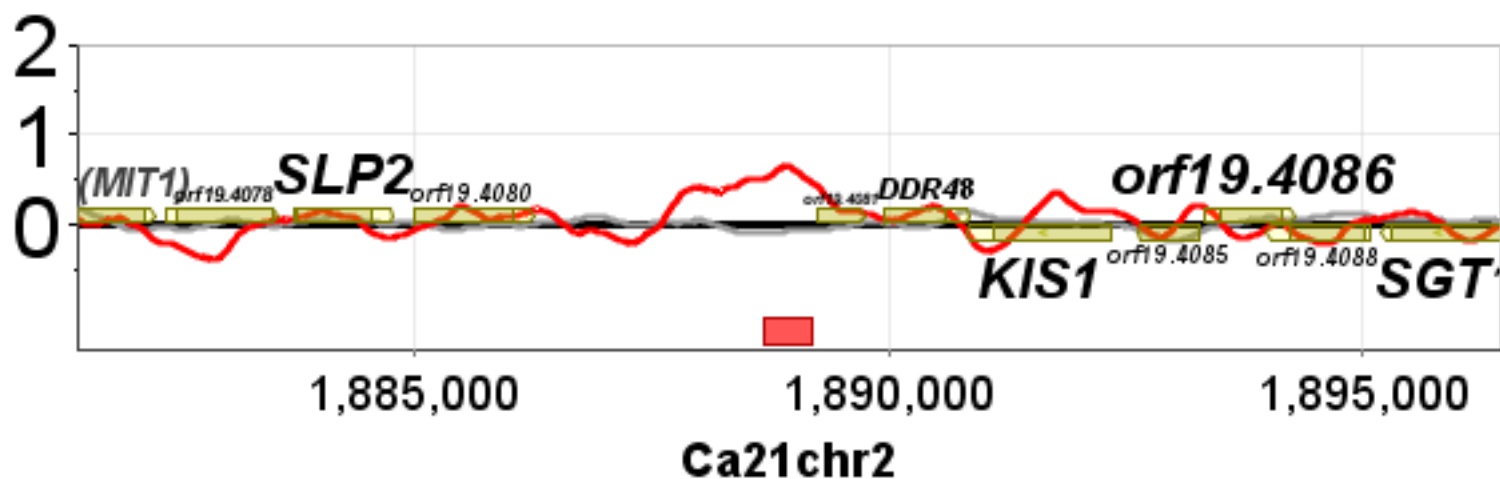
[0.667] Ca21chr4:939889-954888 [+] [FGR3, LYS4, ntar\_799, MRP8, orf19.3843]



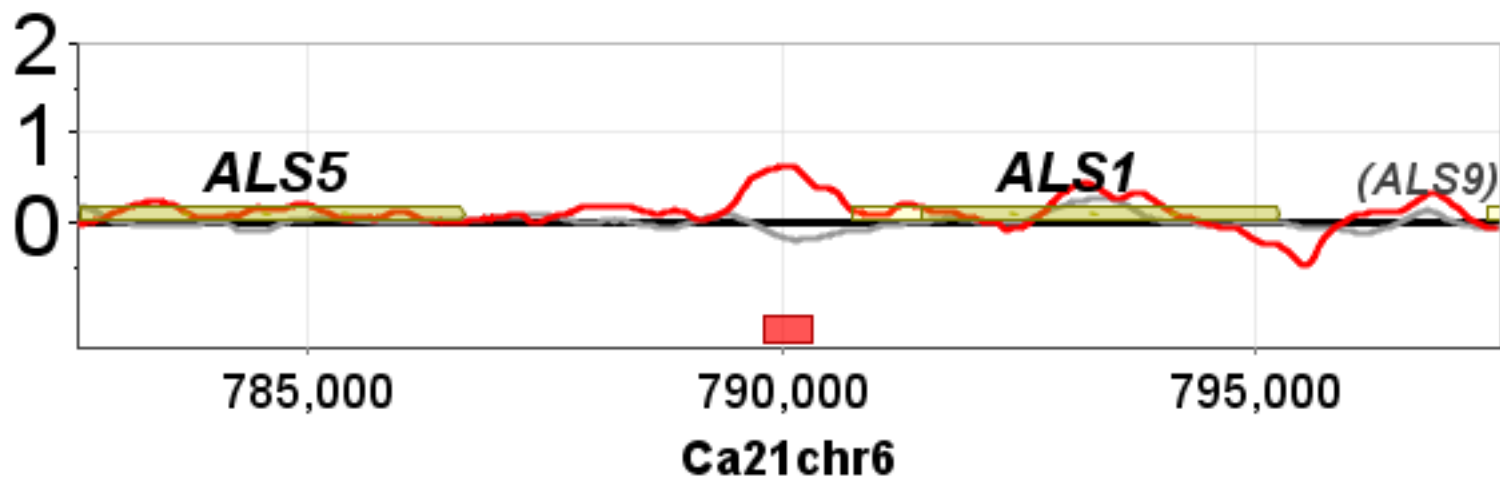
[0.656] Ca21chr5:329897-344896 [+] [ntar\_873, SMD3, ZCF20, GLR1, orf19.4144]



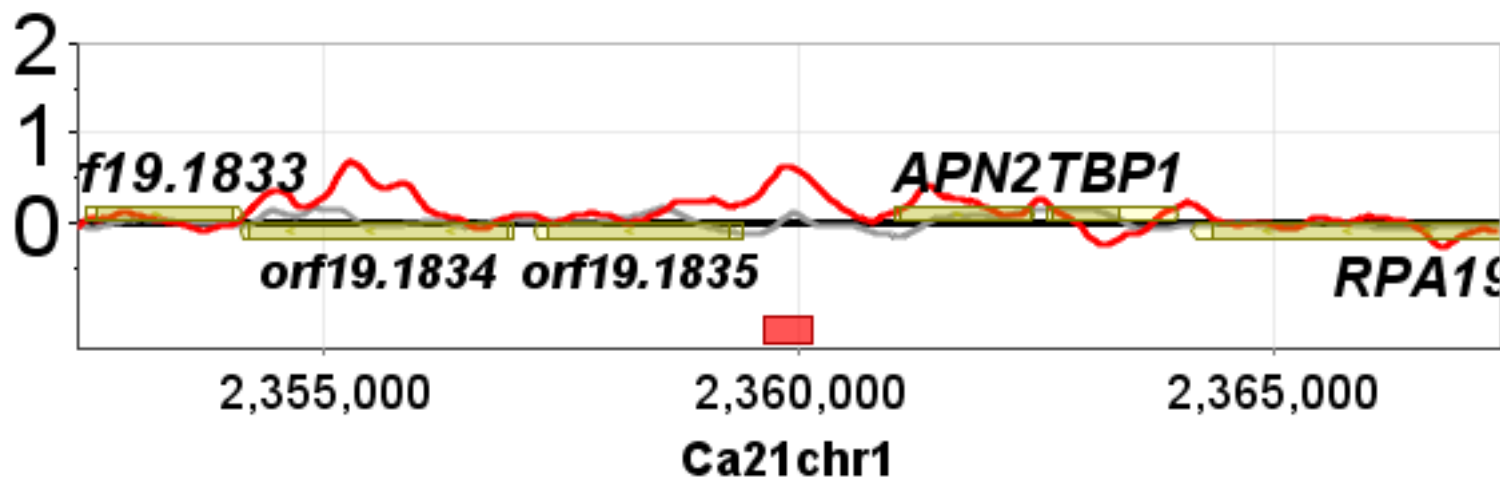
[0.652] Ca21chr2:1881443-1896442 [+] [orf19.4081, tp(ugg)2, DDR48, ntar\_472, ntar\_1415]



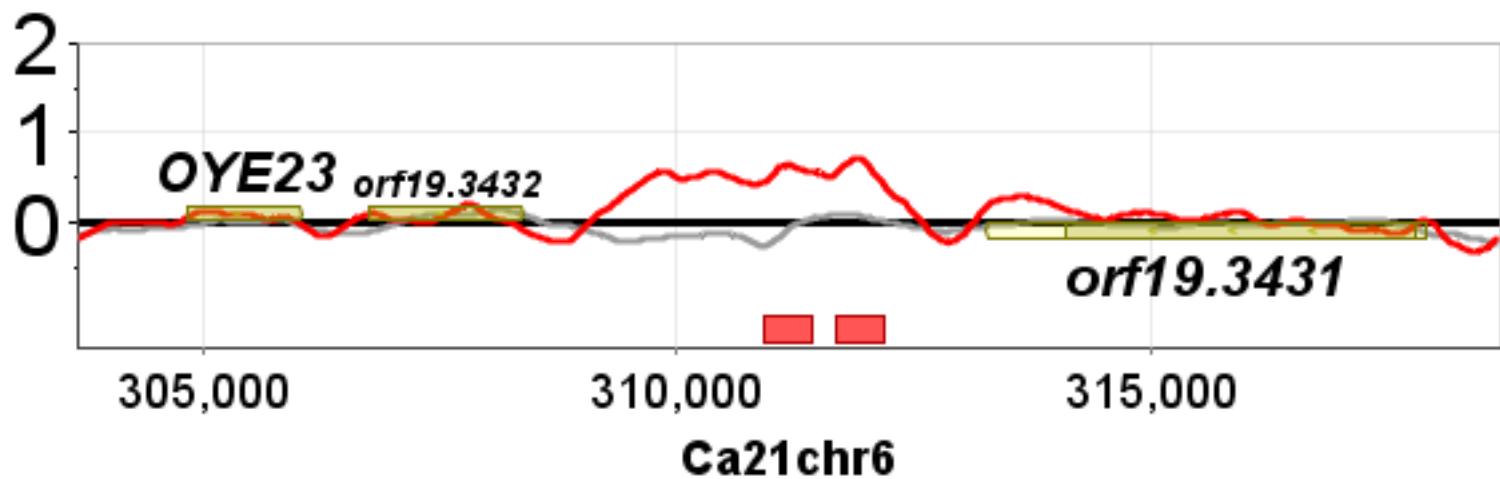
[0.637] Ca21chr6:782569-797568 [+] [ALS1, ALS9, ALS5]



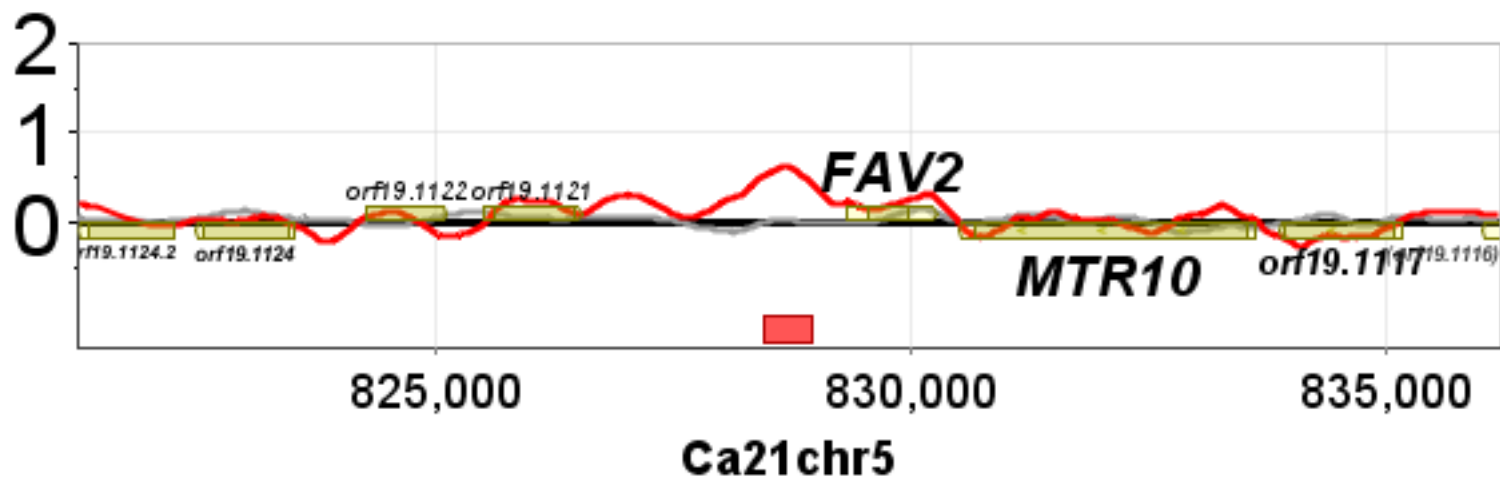
[0.633] Ca21chr1:2352385-2367384 [+] [orf19.1835, APN2, ntar\_224, TBP1, orf19.1834]



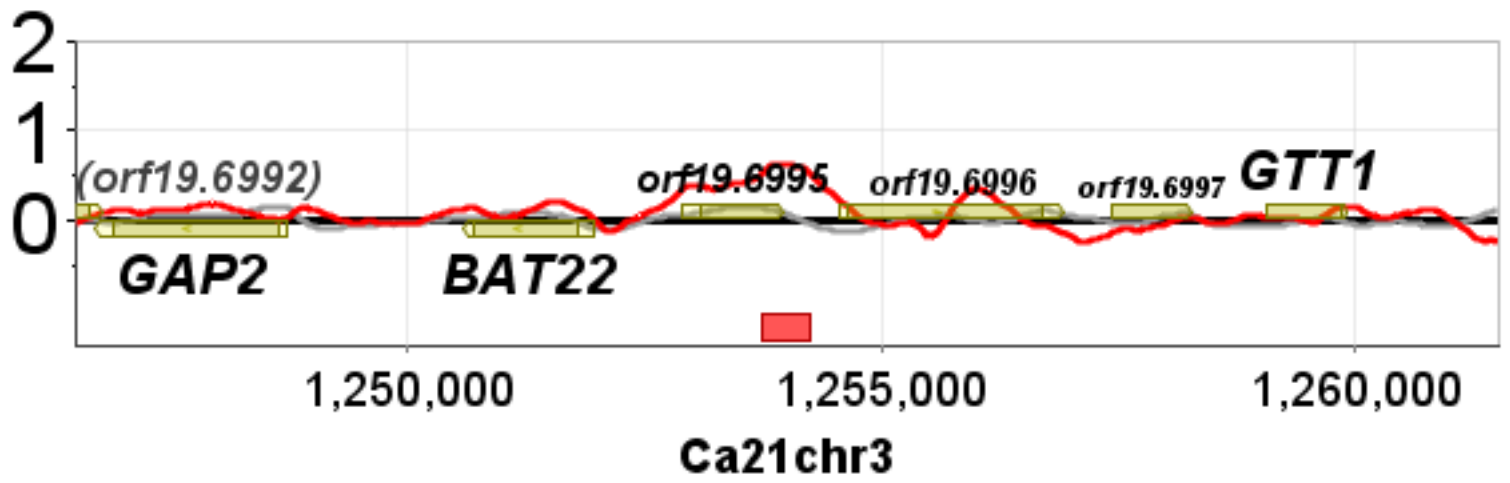
[0.633] Ca21chr6:303672-318671 [+] [ntar\_989, ntar\_990, ntar\_988, orf19.3432, OYE23]



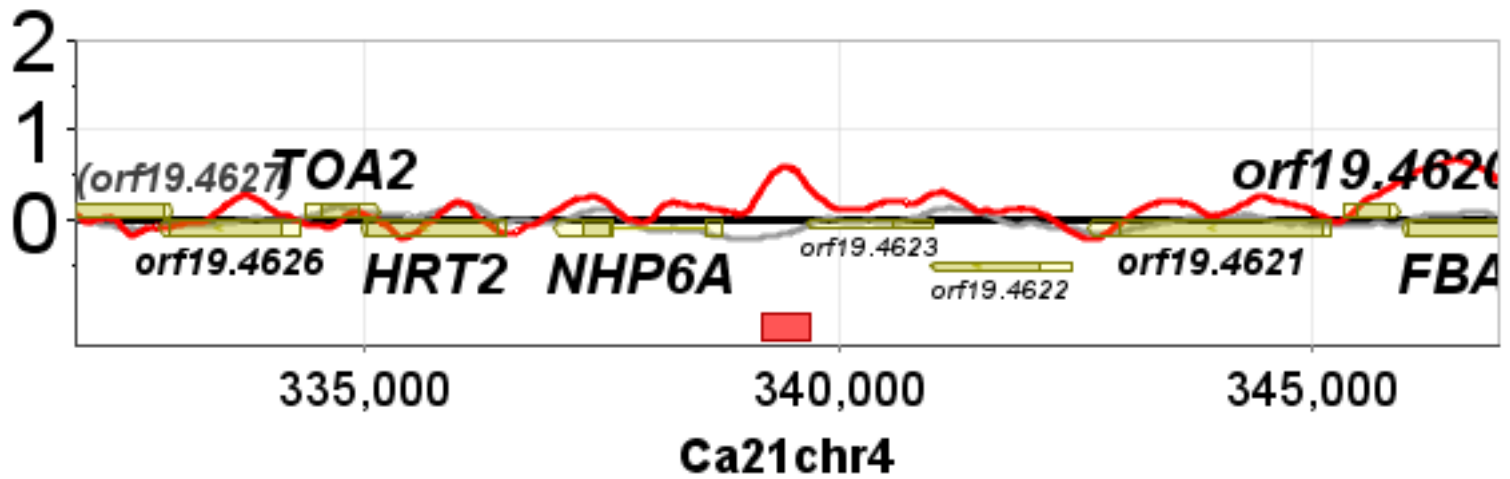
[0.621] Ca21chr5:821206-836205 [+] [FAV2, orf19.1121, orf19.1122, orf19.1123, MTR10]



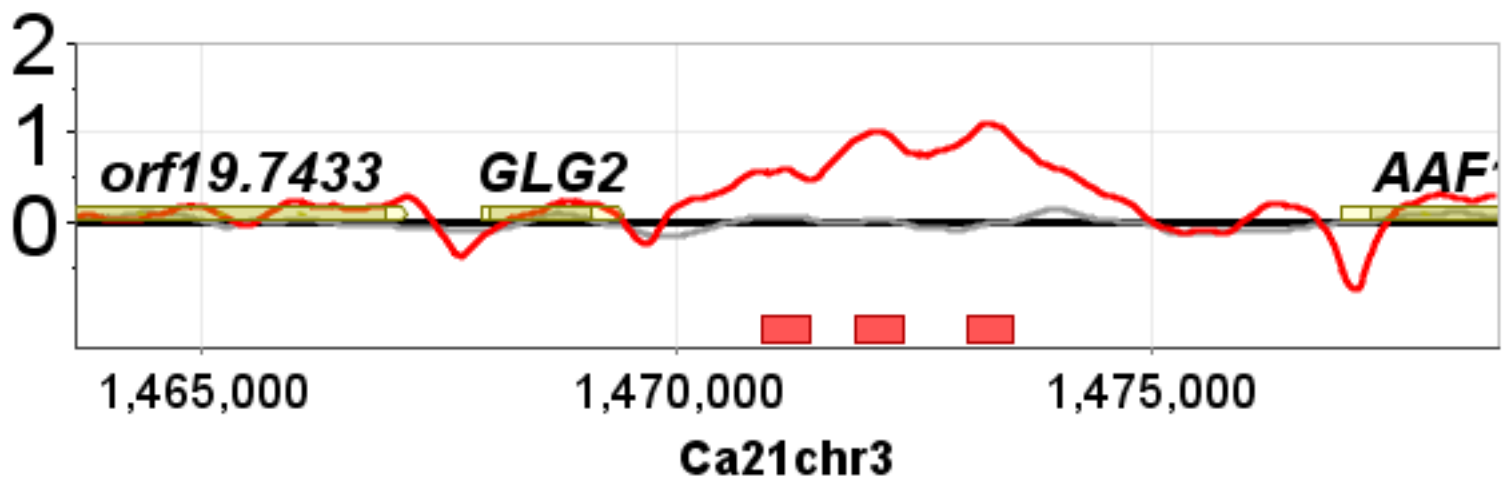
[0.611] Ca21chr3:1246495-1261494 [+] [orf19.6996, orf19.6995, BAT22, orf19.6997, GTT1]



[0.6] Ca21chr4:331950-346949 [+] [Intar\_745, ntar\_744, NHP6A, orf19.4623, HRT2]



[0.593] Ca21chr3:1463654-1478653 [+] [th(gug)3, GLG2, ntar\_658, ntar\_659, AAF1]



[0.59] Ca21chr1:1776171-1791170 [+] [BUL1, ntar\_170, orf19.5093, orf19.5092, orf19.5095]

