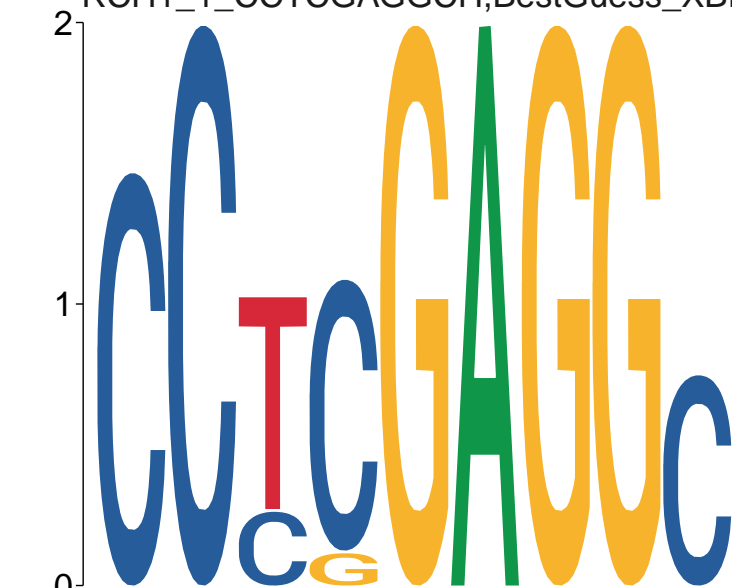
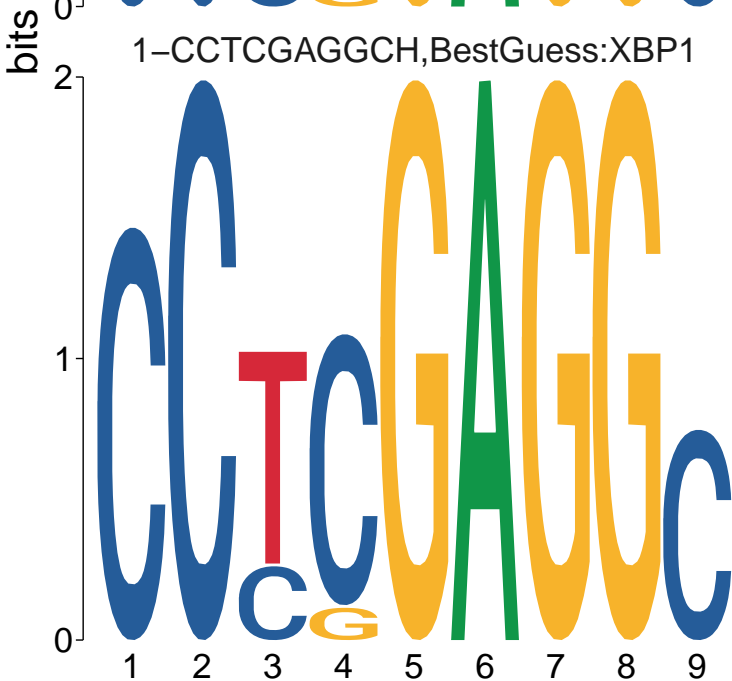


RCH1_1_CCTCGAGGCH,BestGuess_XBP



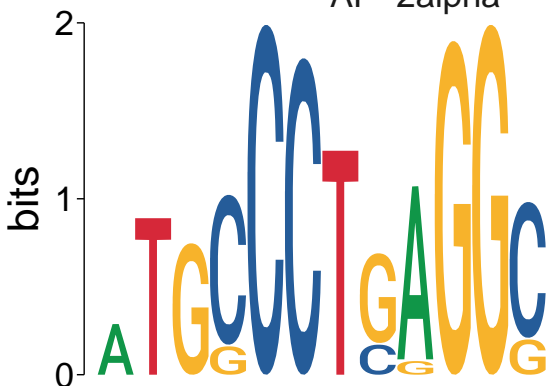
1-CCTCGAGGCH,BestGuess:XBP1



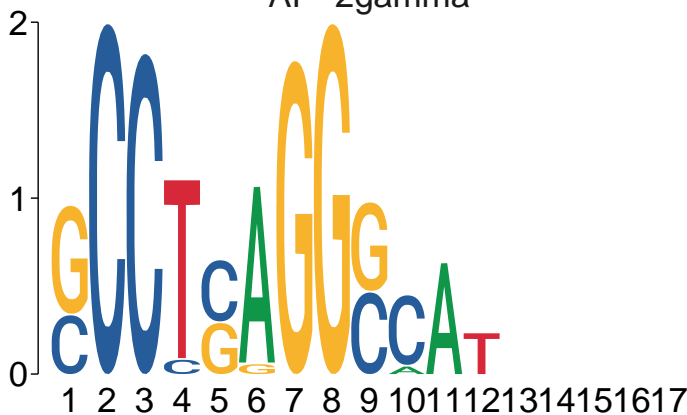
ARCH2_AP_2gamma_AP_2alpha



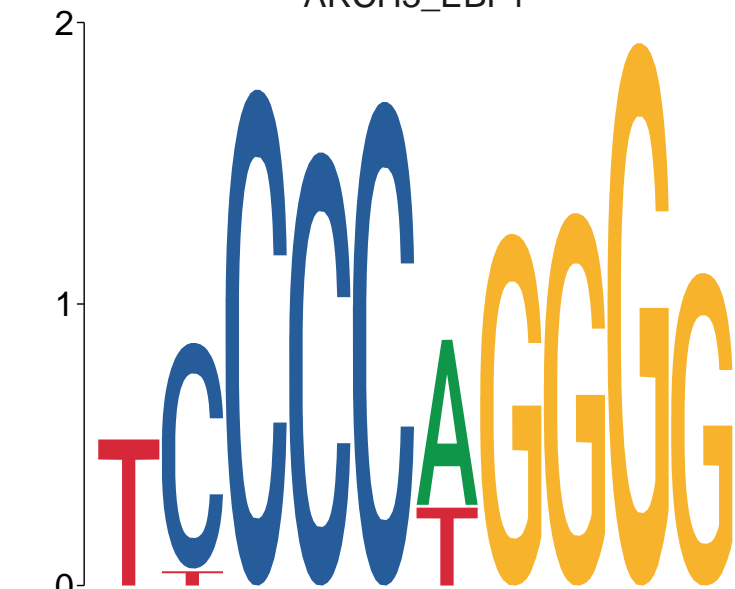
AP-2alpha



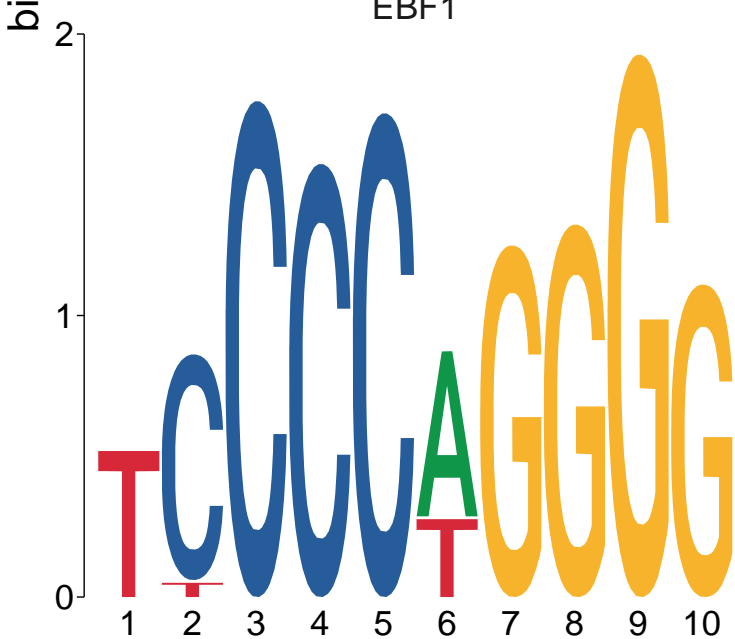
AP-2gamma



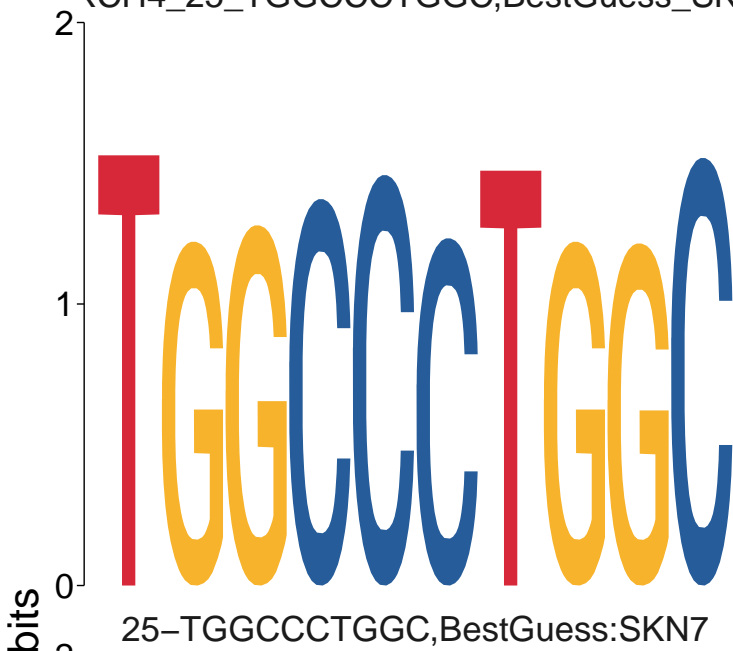
ARCH3_EBF1



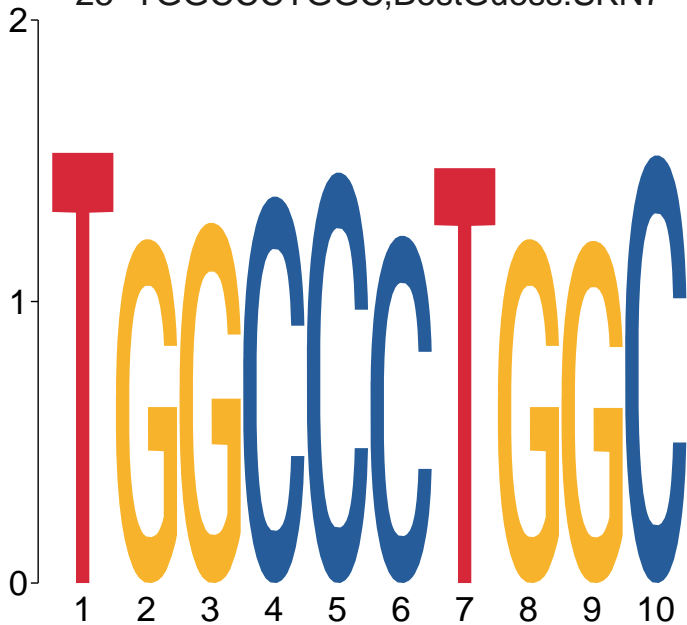
EBF1



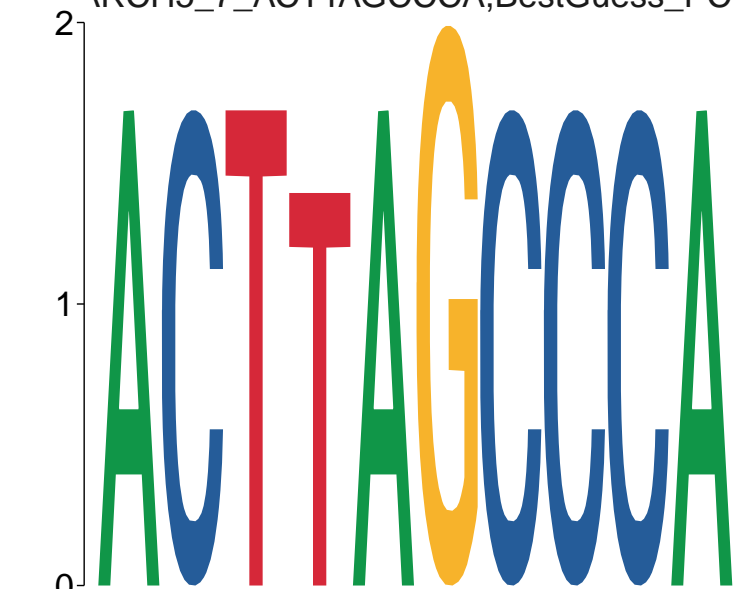
RCH4_25_TGGCCCTGGC,BestGuess_SKI



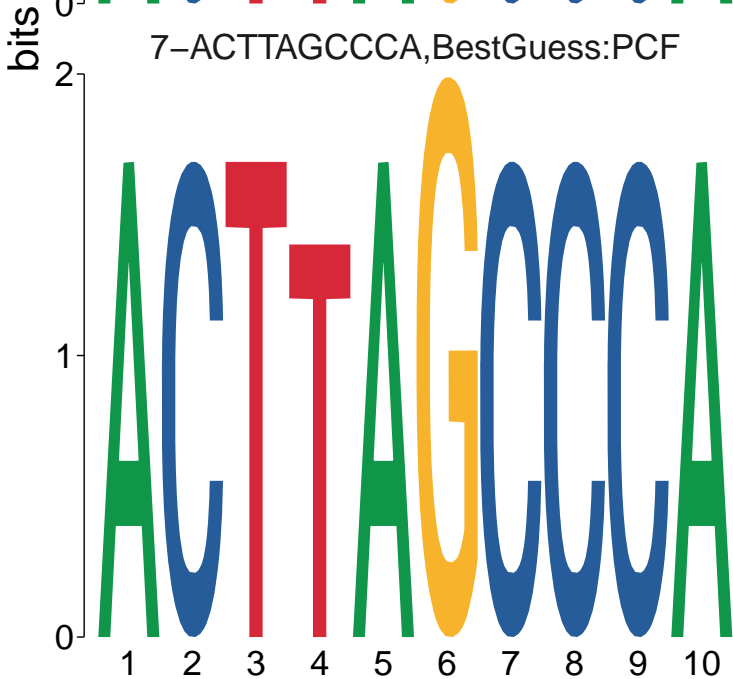
25-TGGCCCTGGC,BestGuess:SKN7



ARCH5_7_ACTTAGCCCA,BestGuess_PCF



7-ACTTAGCCCA,BestGuess:PCF



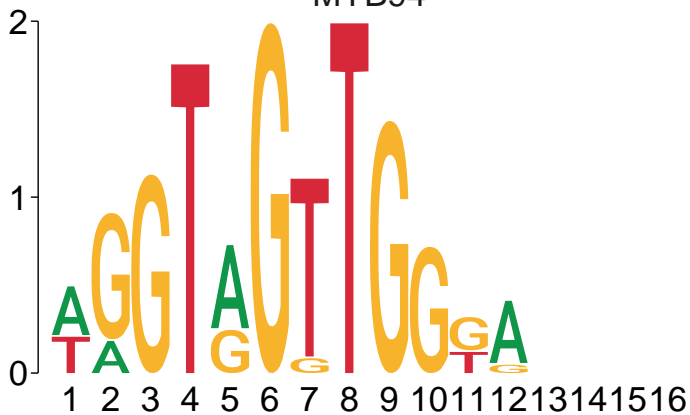
ARCH6_MYB94_MYB30



MYB30



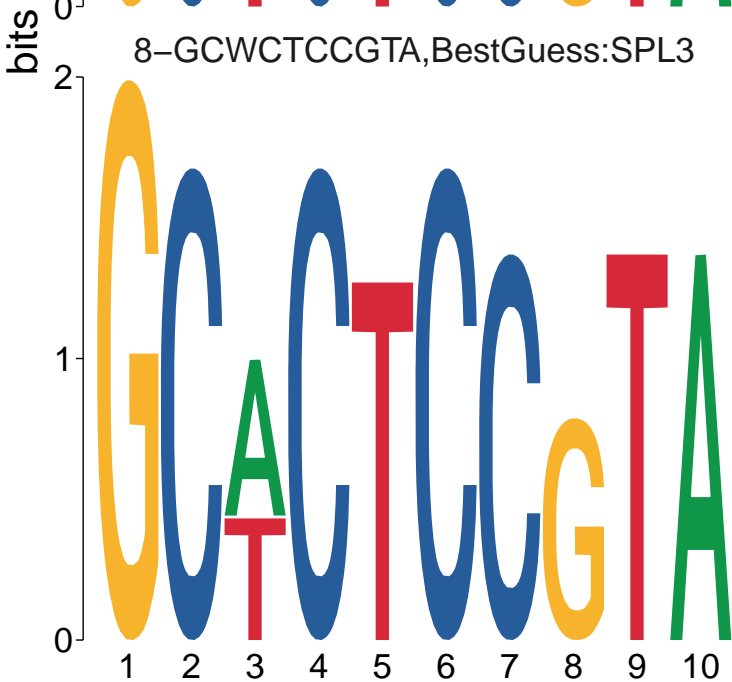
MYB94



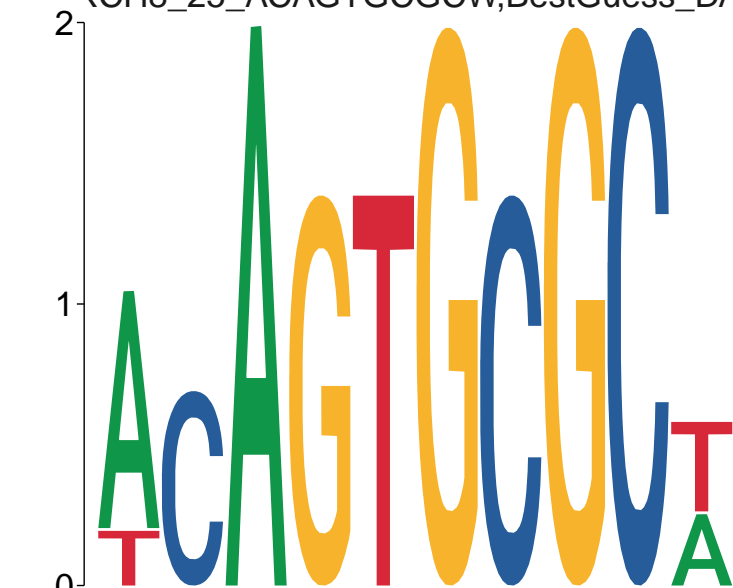
RCH7_8_GCWCTCCGTA,BestGuess_SPL



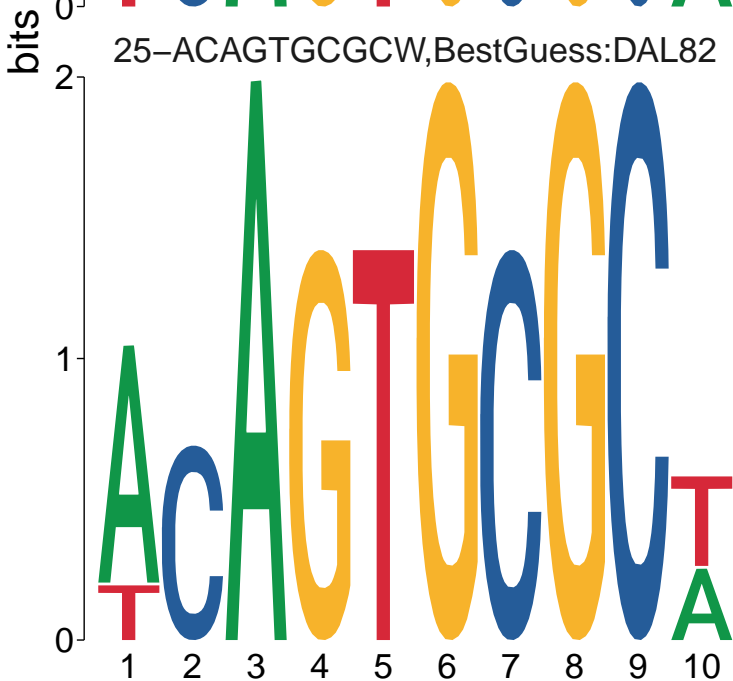
8-GCWCTCCGTA,BestGuess:SPL3



RCH8_25_ACAGTGCGCW,BestGuess_DAI



25-ACAGTGCGCW,BestGuess:DAL82

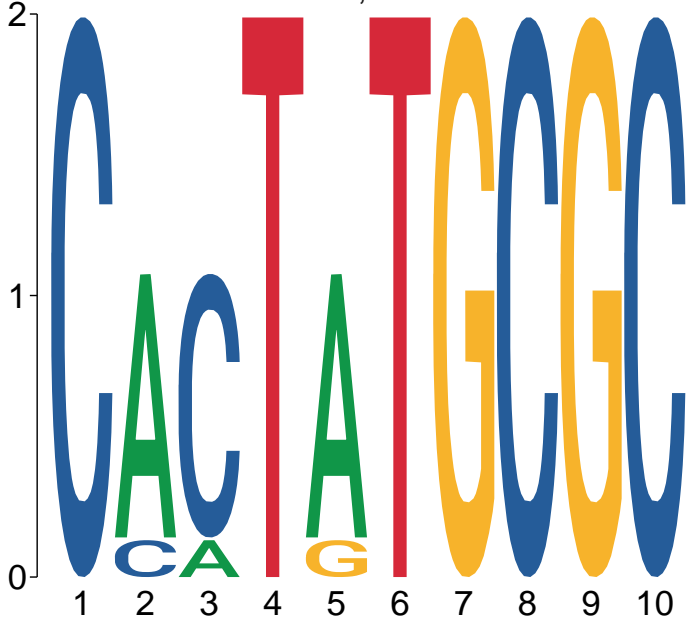


RCH9_3_CACTATGCGC,BestGuess_DAL8

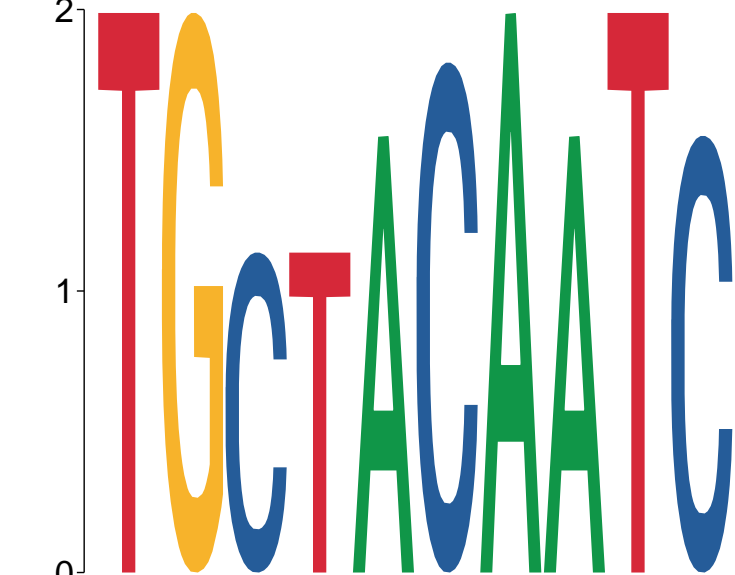
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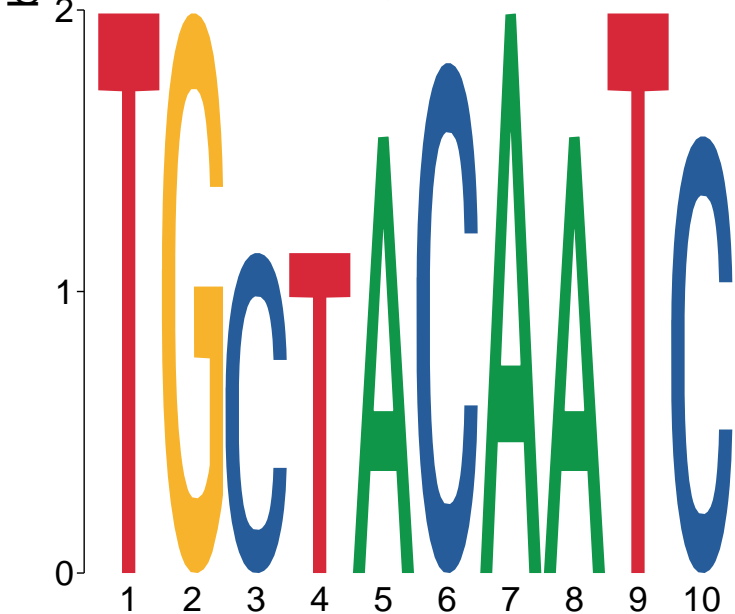
3-CACTATGCGC,BestGuess:DAL82



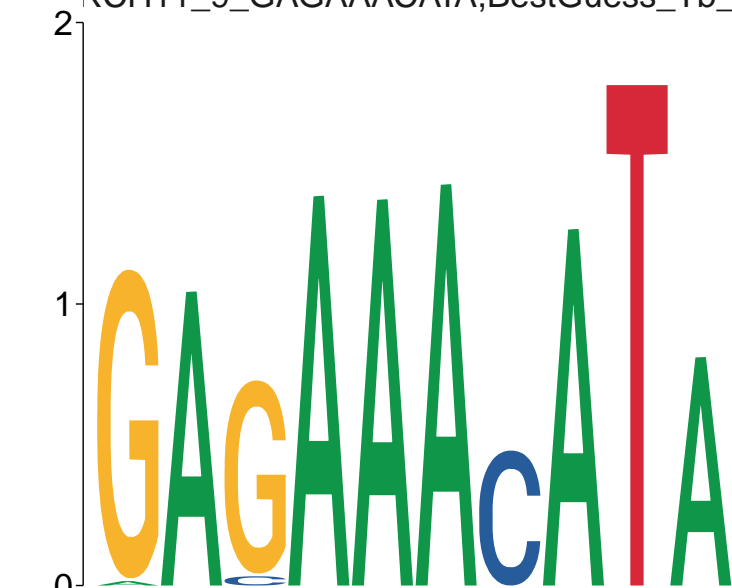
9-TGCTACAATC, BestGuess_DMR'



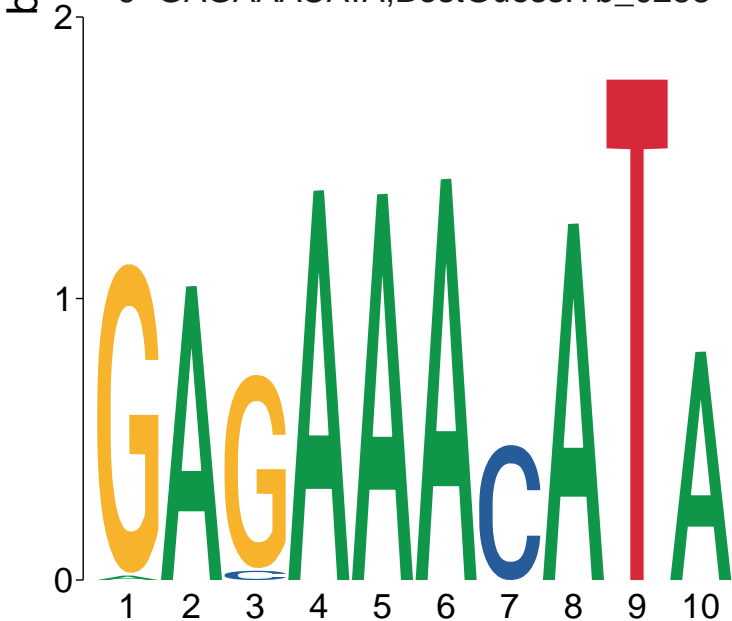
9-TGCTACAATC, BestGuess:DMRTA2



RCH11_9_GAGAAACATA,BestGuess_Tb_C



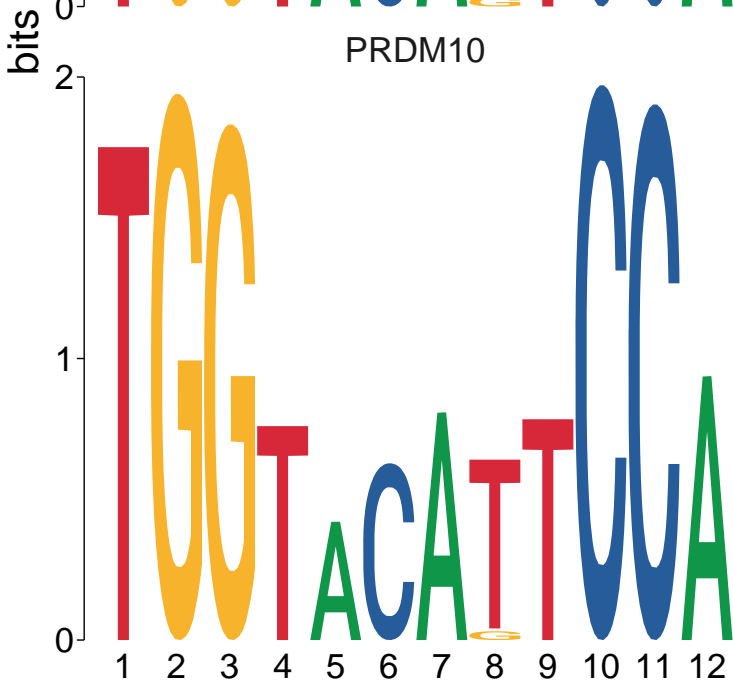
9-GAGAAACATA,BestGuess:Tb_0253



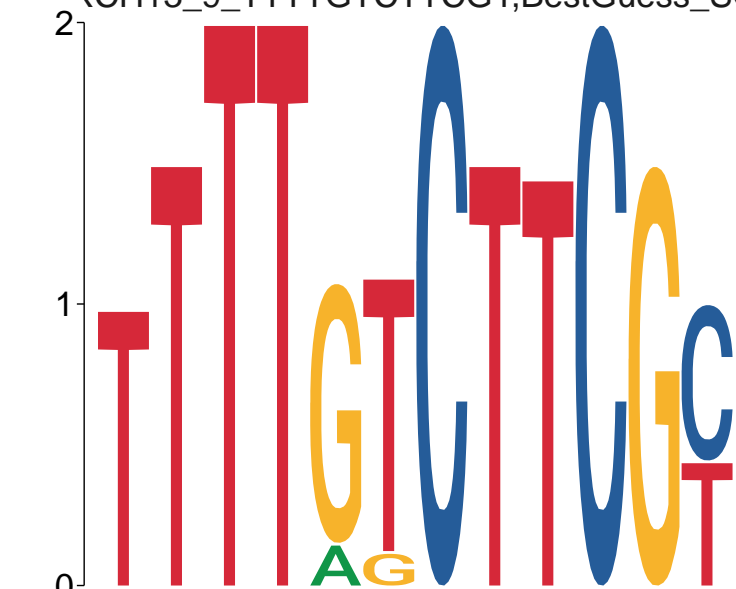
ARCH12_PRDM10



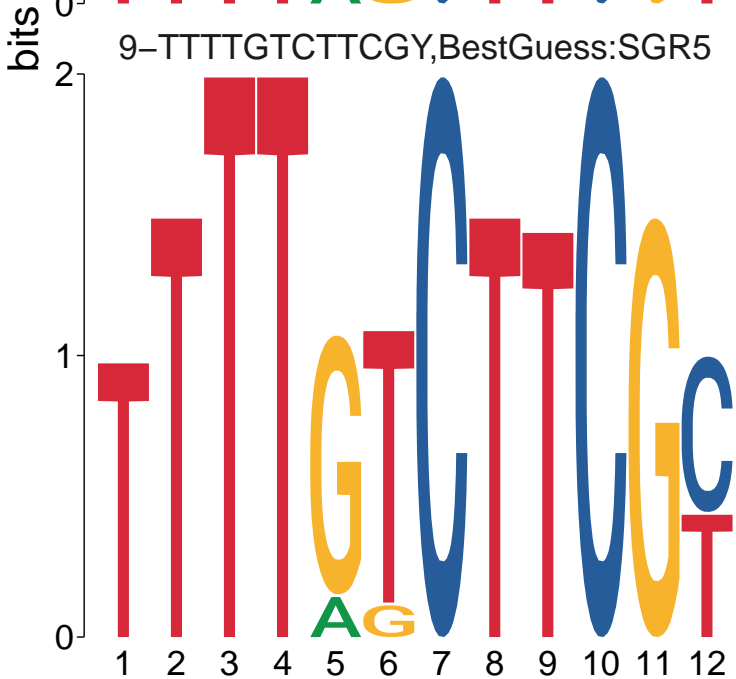
PRDM10



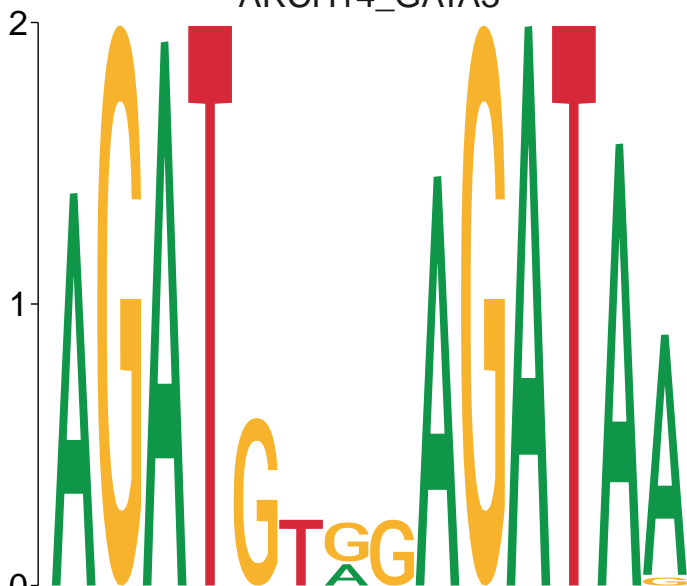
CH13_9_TTTTGTCTTCGY,BestGuess_SC



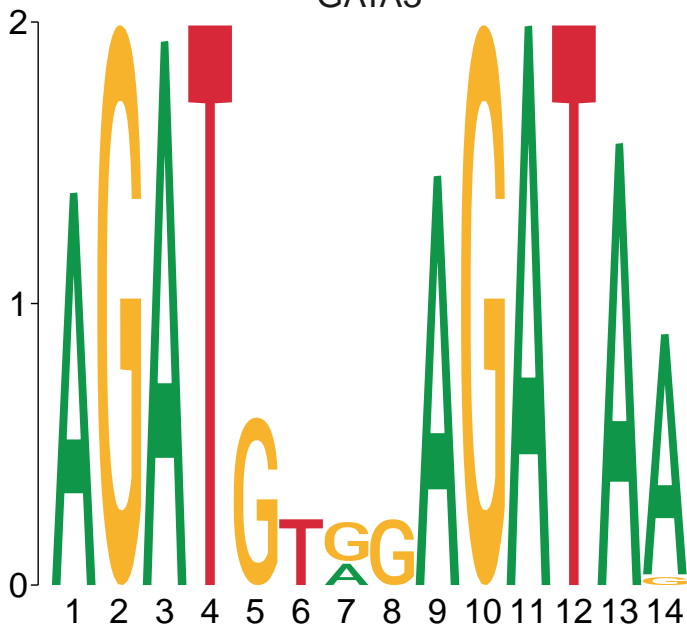
9-TTTTGTCTTCGY,BestGuess:SGR5



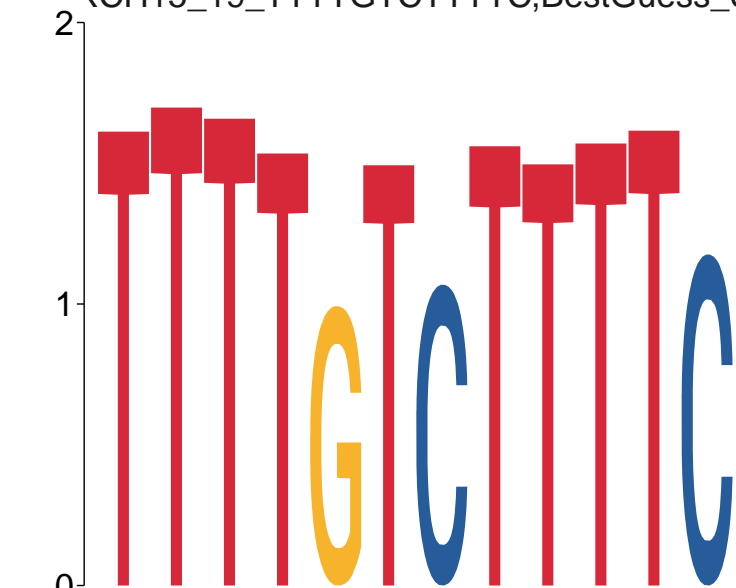
ARCH14_GATA3



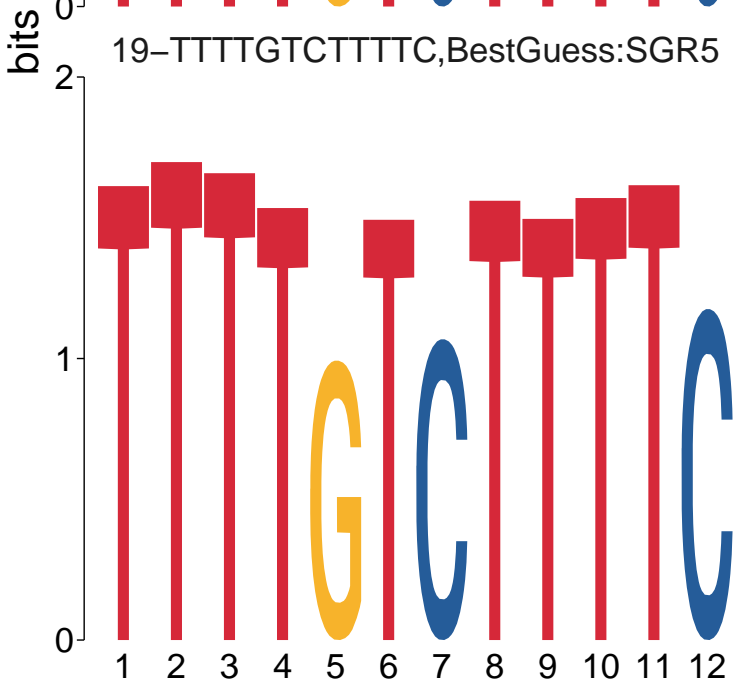
GATA3

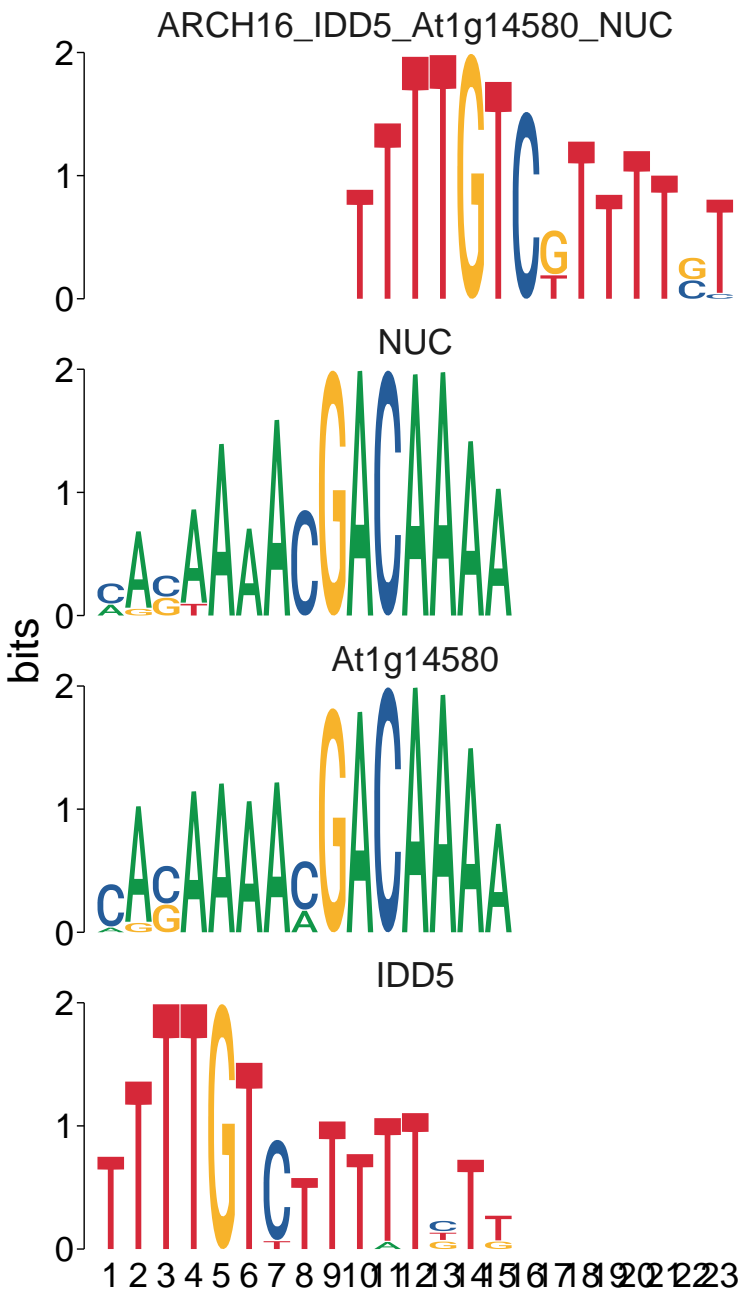


RCH15_19_TTTTGTCTTTTC,BestGuess_S

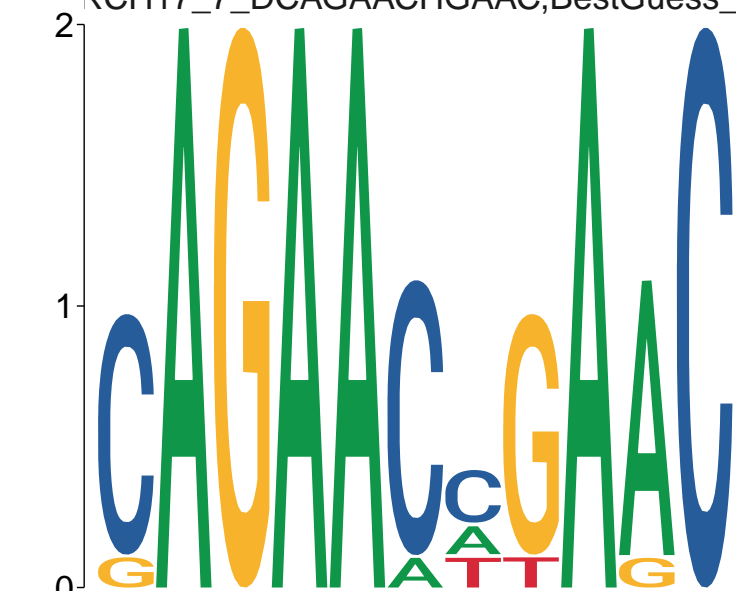


19-TTTTGTCTTTTC,BestGuess:SGR5

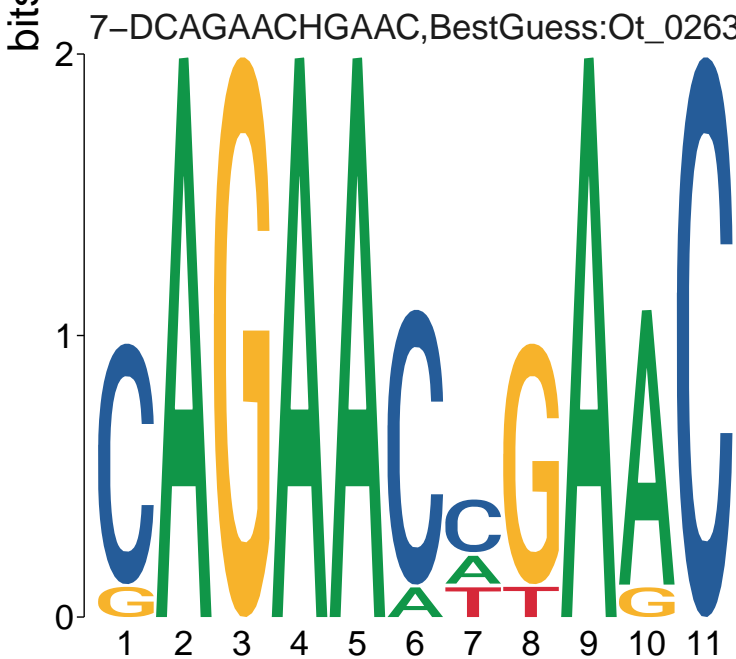




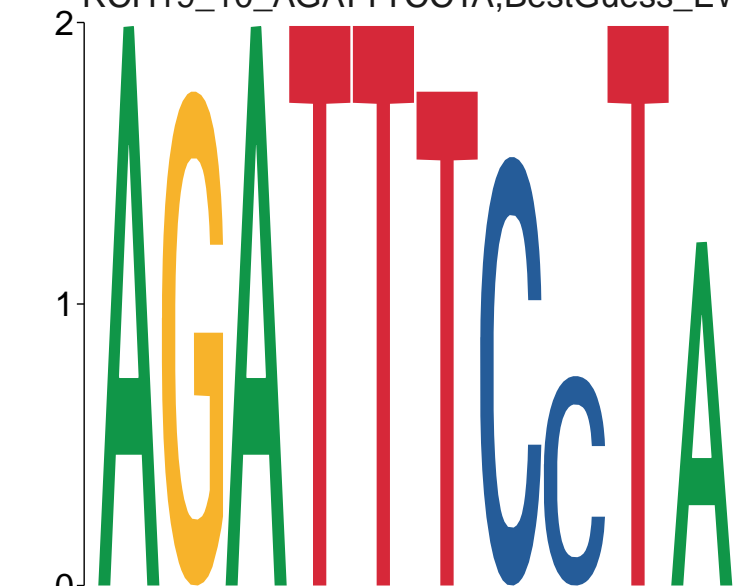
RCH17_7_DCAGAACHGAAC,BestGuess_C



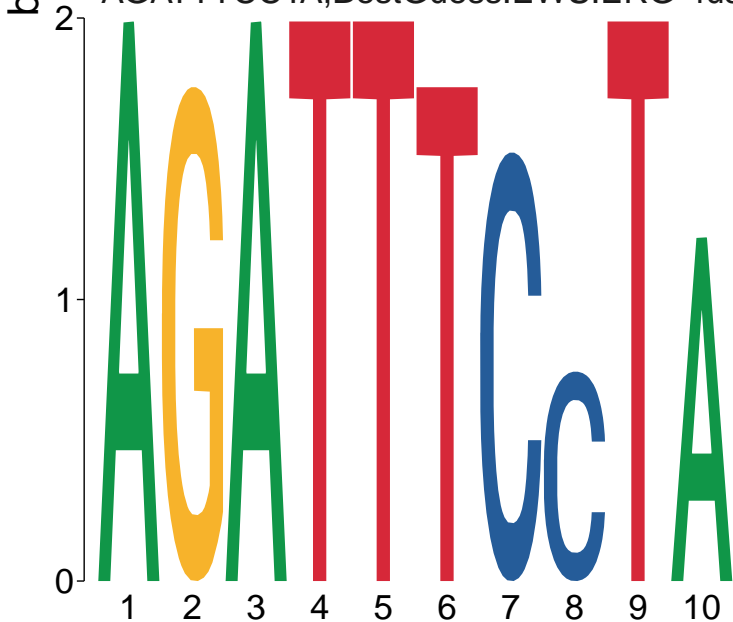
7-DCAGAACHGAAC,BestGuess:Ot_0263



RCH19_10_AGATTTTCCTA,BestGuess_EW



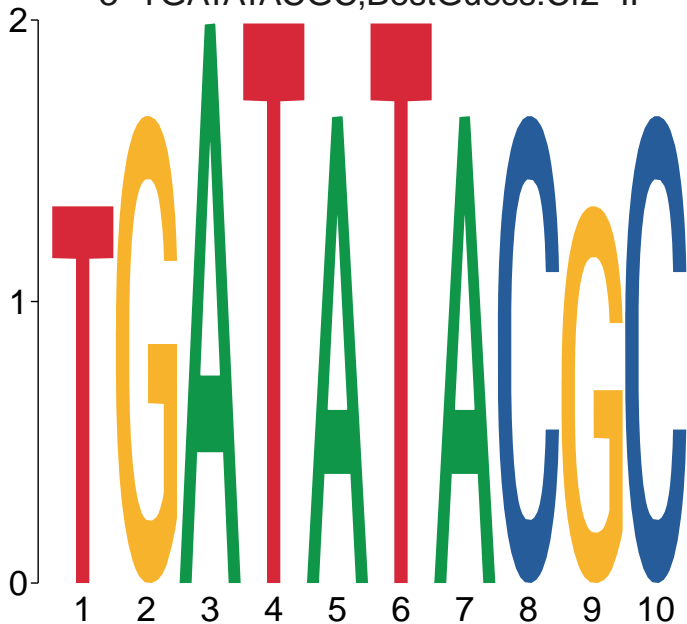
-AGATTTTCCTA,BestGuess:EWS:ERG-fusi



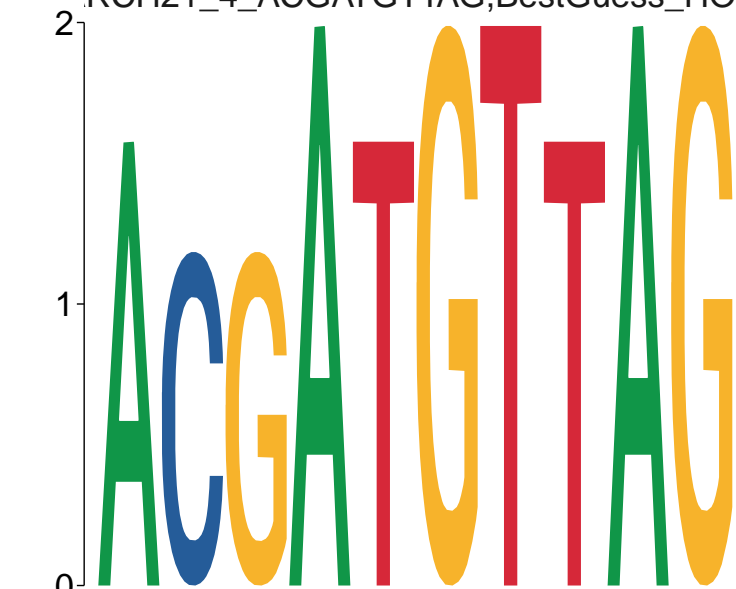
1-RCH20_3_TGATATACGC,BestGuess_Cf2_



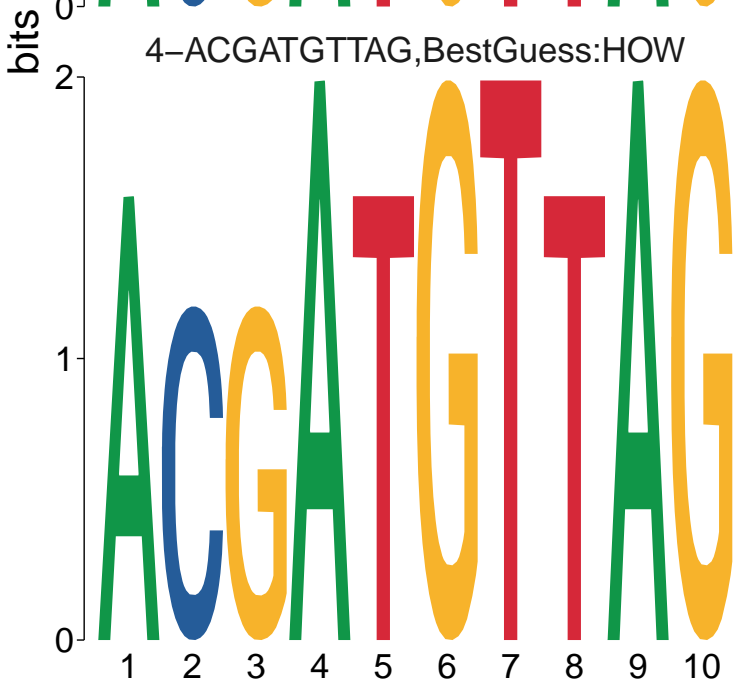
3-TGATATACGC,BestGuess:Cf2-II



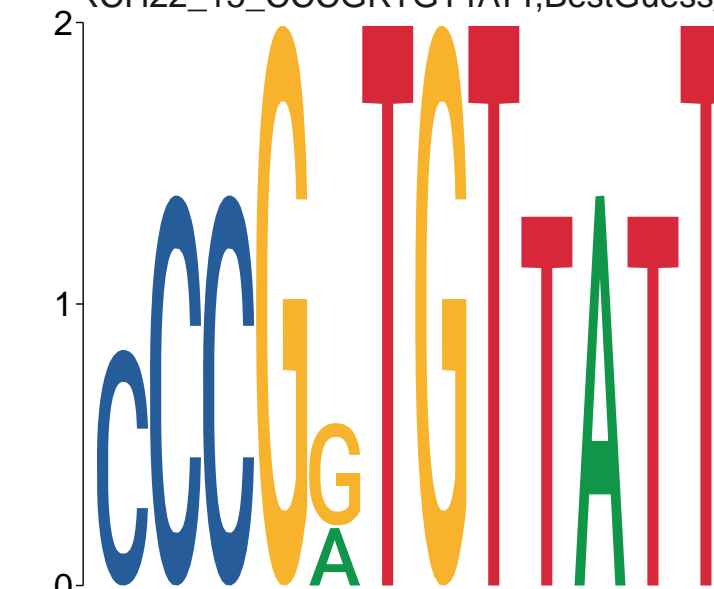
RCH21_4_ACGATGTTAG,BestGuess_HOV



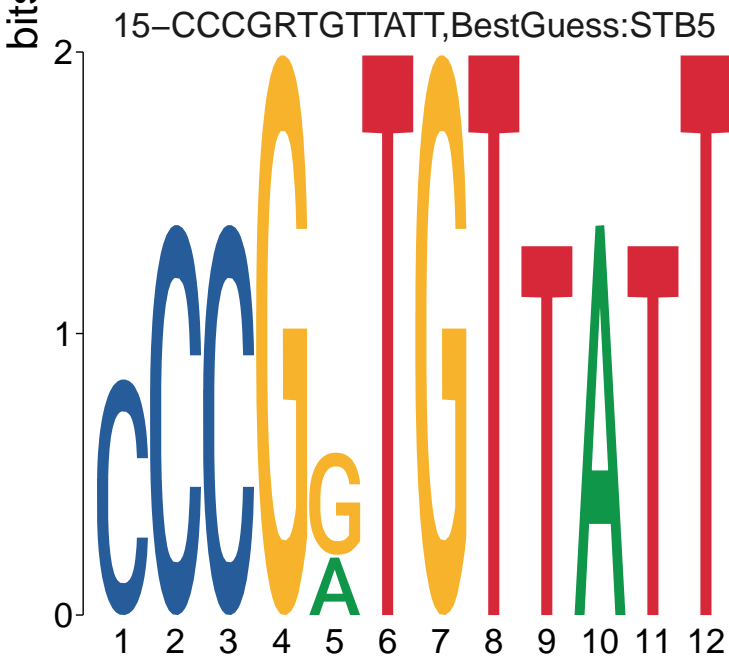
4-ACGATGTTAG,BestGuess:HOW



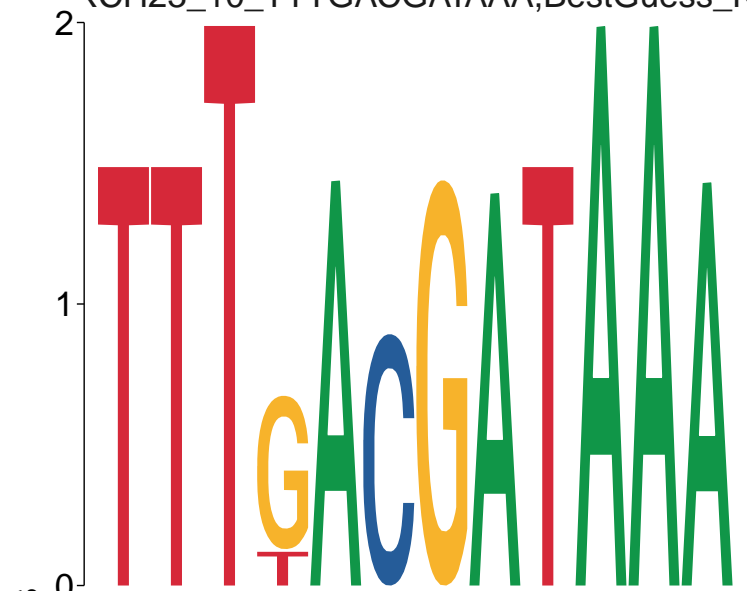
RCH22_15_CCCGRTGTTATT,BestGuess_S



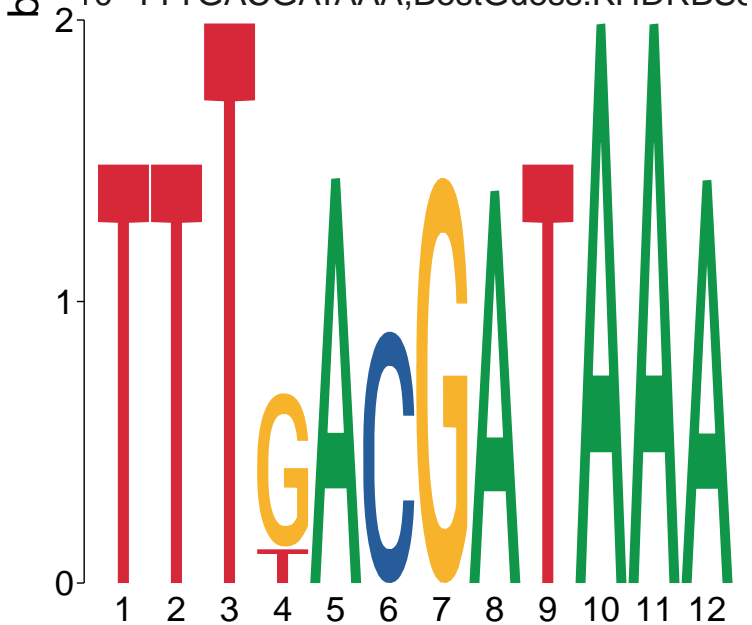
15-CCCGRTGTTATT,BestGuess:STB5



RCH23_10_TTTGACGATAAA,BestGuess_k



10-TTTGACGATAAA,BestGuess:KHDRBS3



RCH24_18_ACAACGAAAAAT,BestGuess_F

2

1

0

bits

ACGAAAAAT,BestGuess:PB0032.1_IRC9C

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ARCH25_IDD4_SGR5_At5g66730_IDD7



IDD7



At5g66730

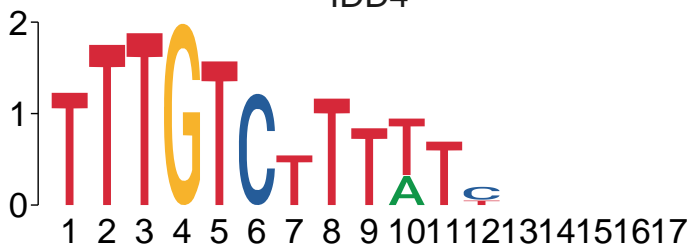
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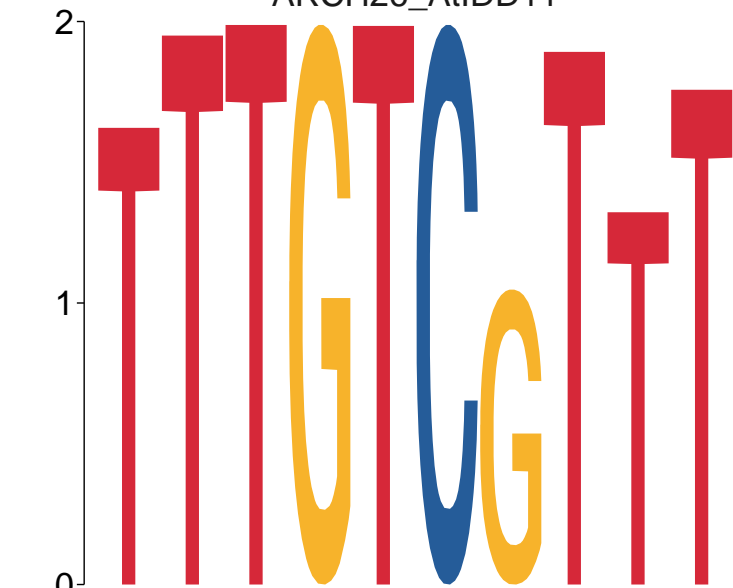
SGR5



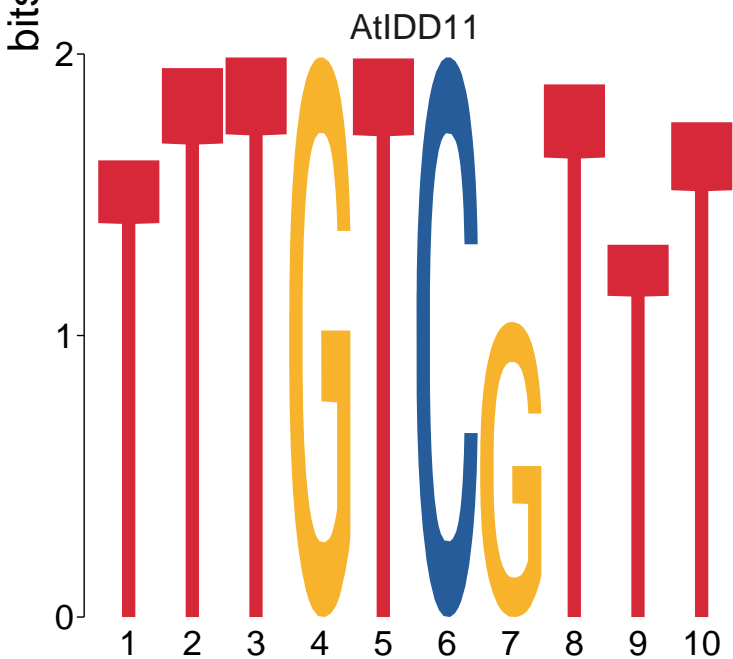
IDD4



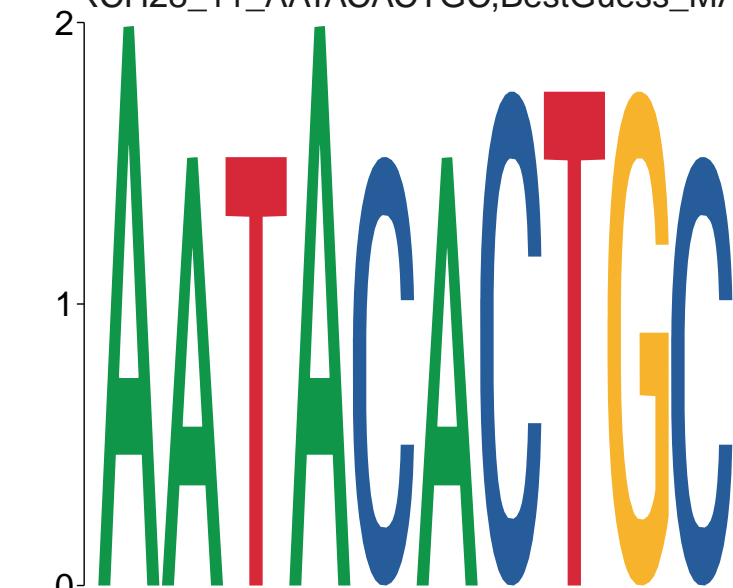
ARCH26_AtIDD11



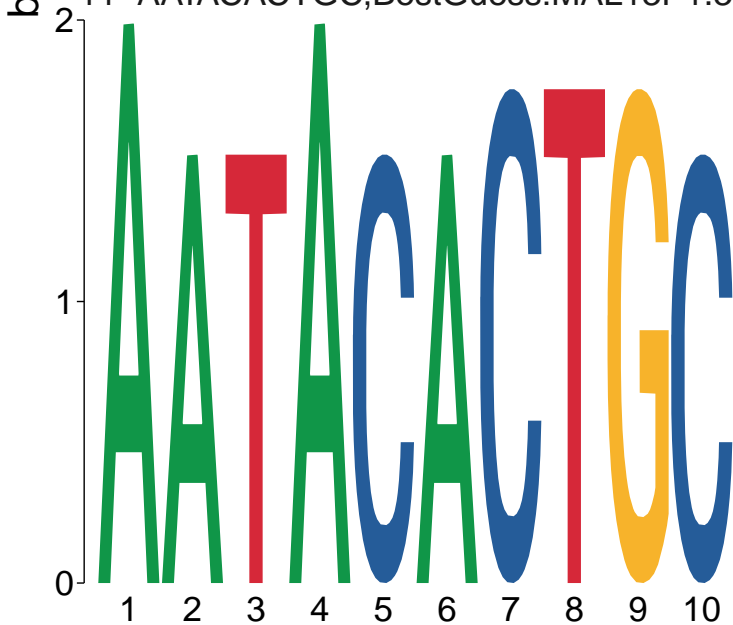
AtIDD11



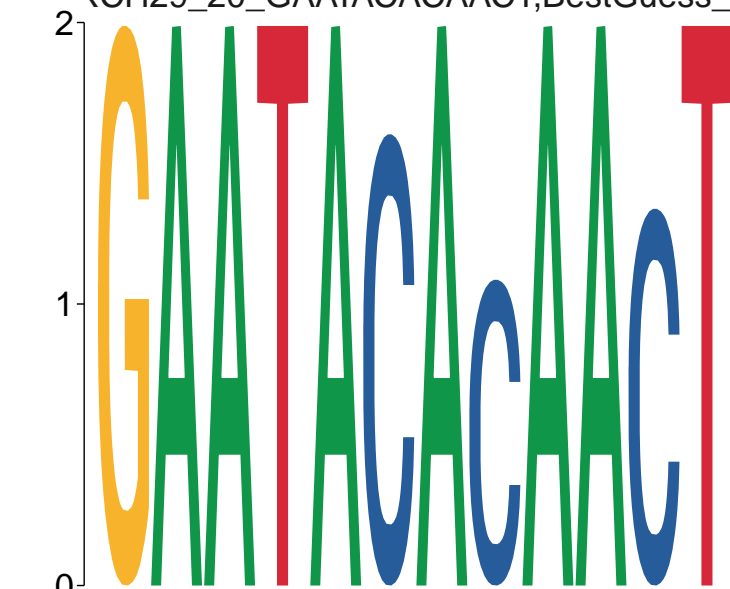
RCH28_11_AATACACTGC,BestGuess_MAI



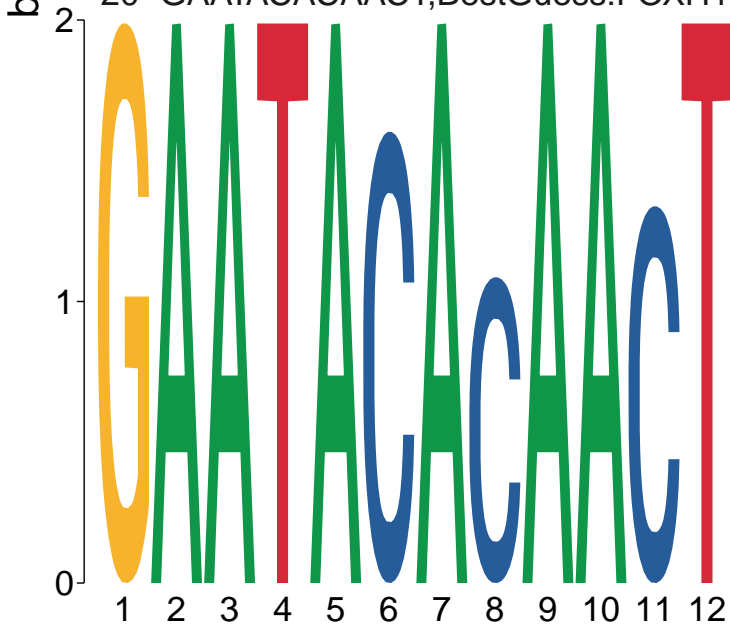
11-AATACACTGC,BestGuess:MAL13P1.35



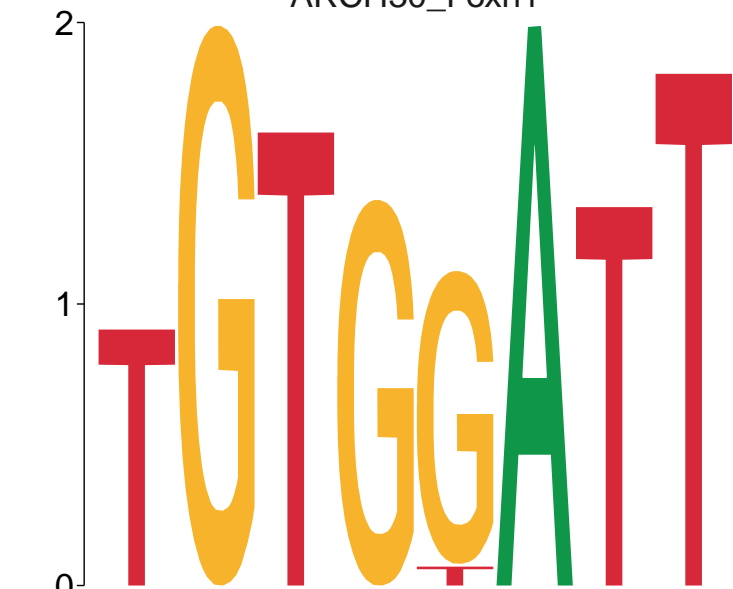
RCH29_20_GAATACACAACACT, BestGuess_F



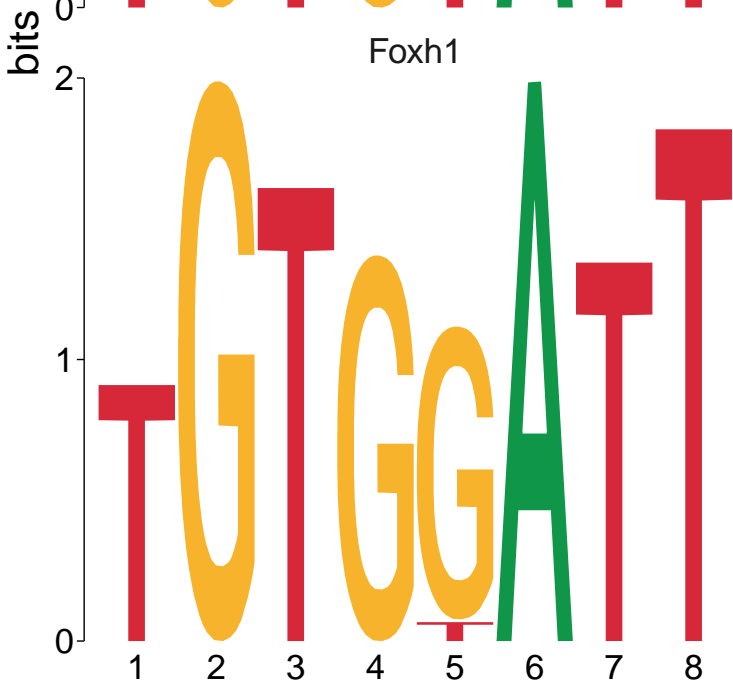
20-GAATACACAACACT, BestGuess:FOXH1



ARCH30_Foxh1



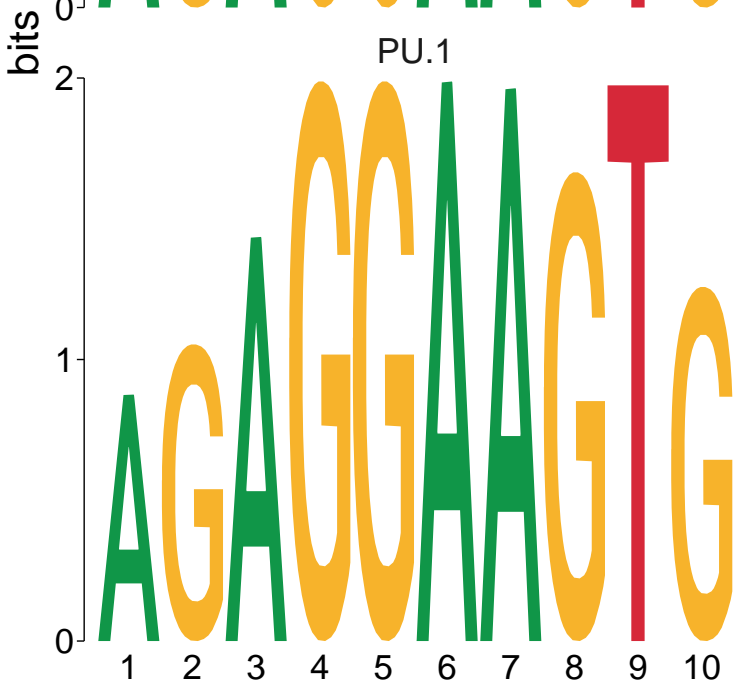
Foxh1

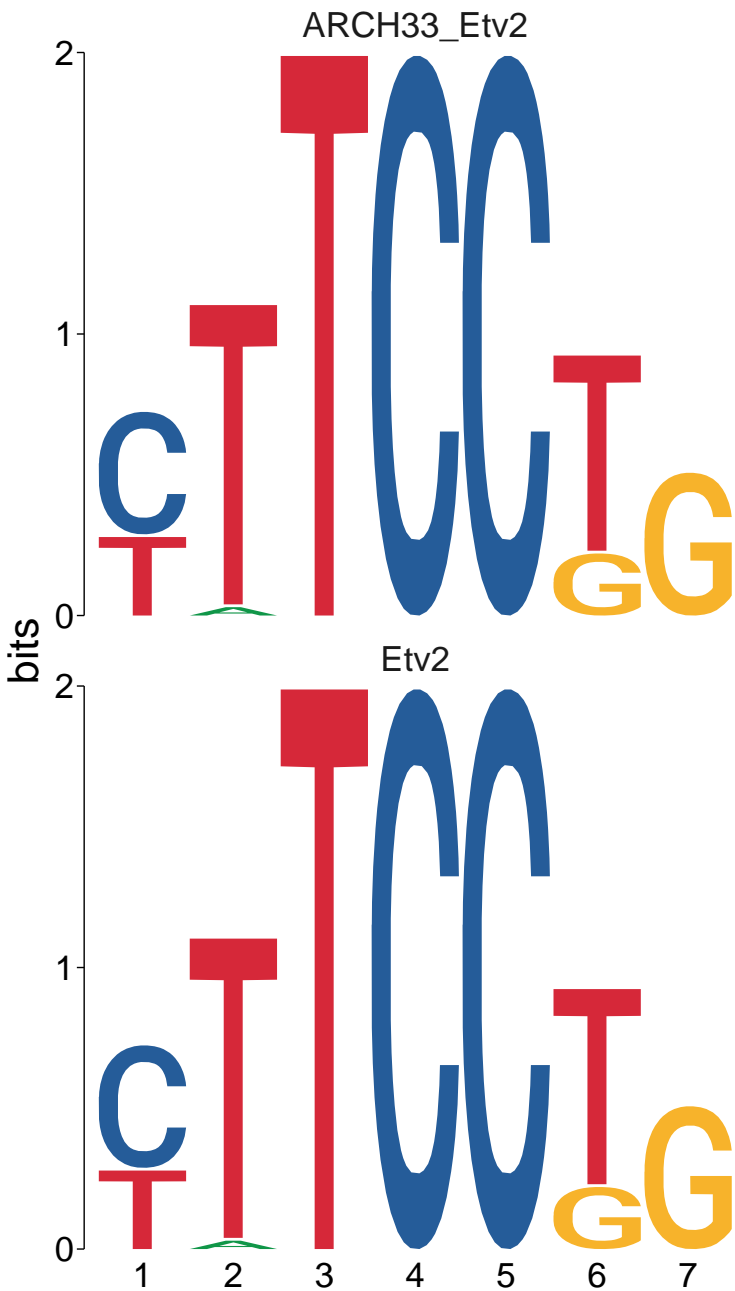


ARCH32_PU.1

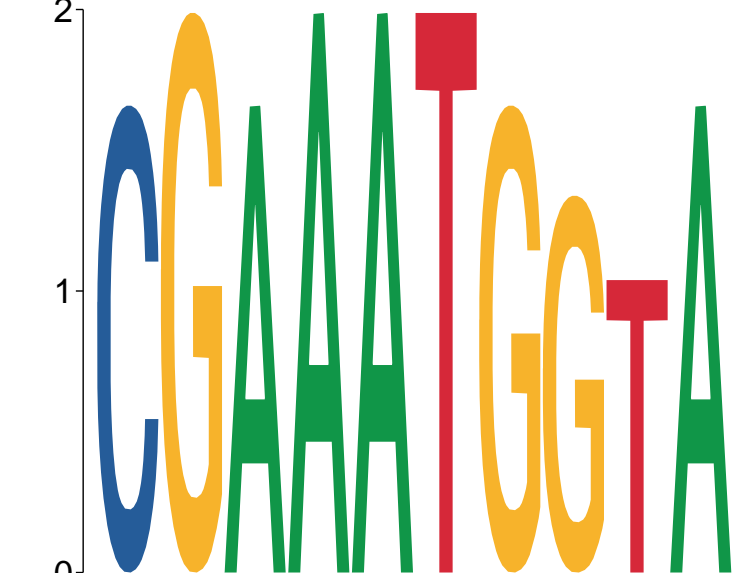


PU.1

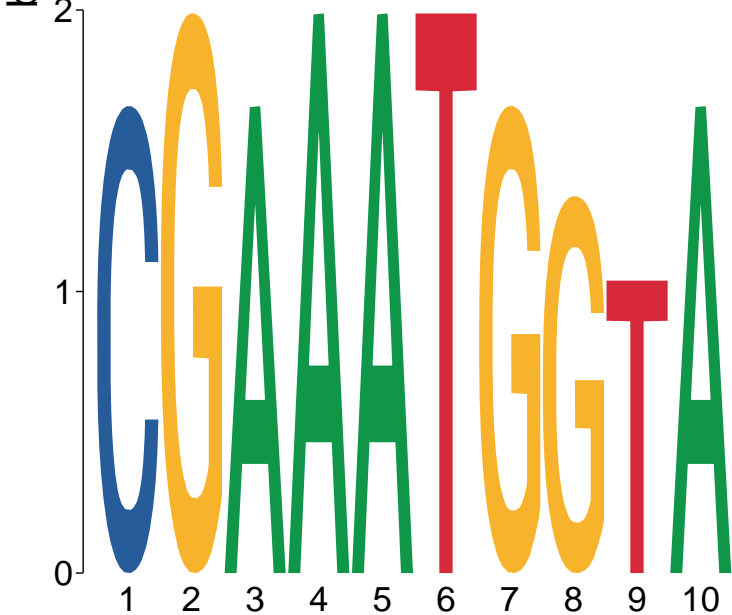




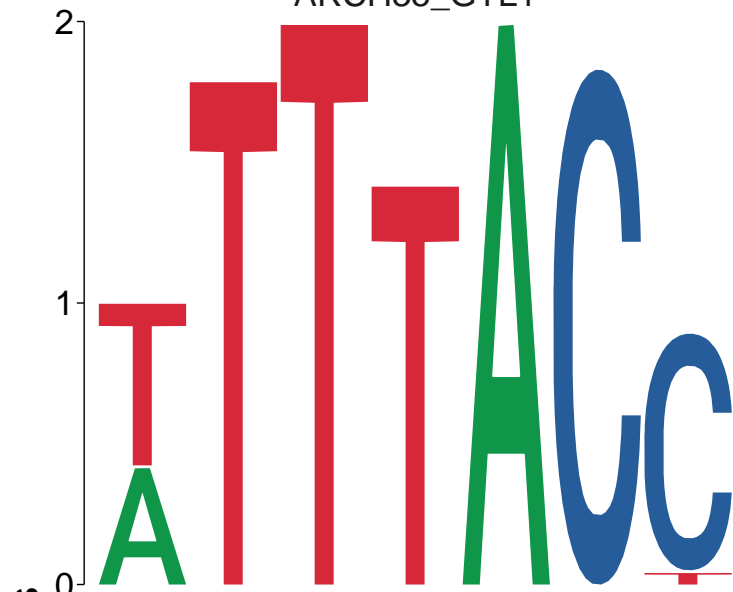
RCH34_12_CGAAATGGTA,BestGuess_AT2



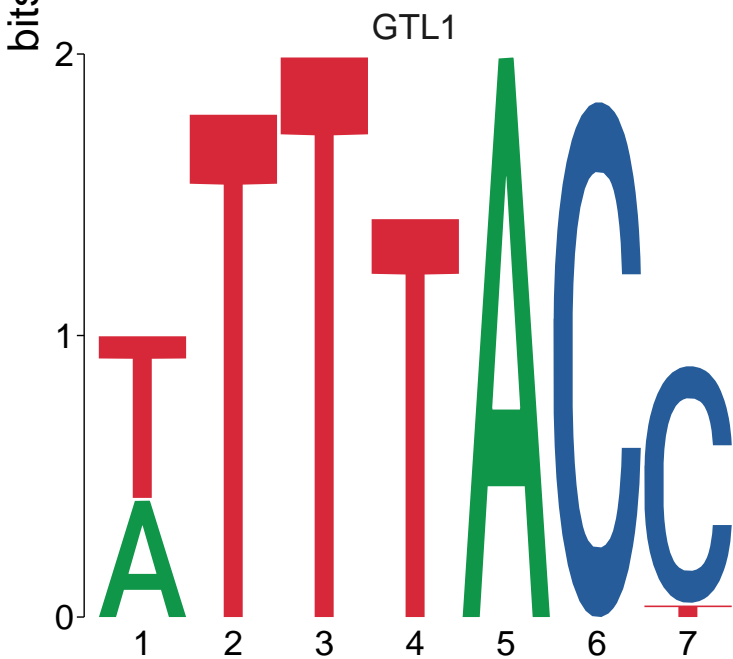
12-CGAAATGGTA,BestGuess:AT2G31460



ARCH35_GTL1



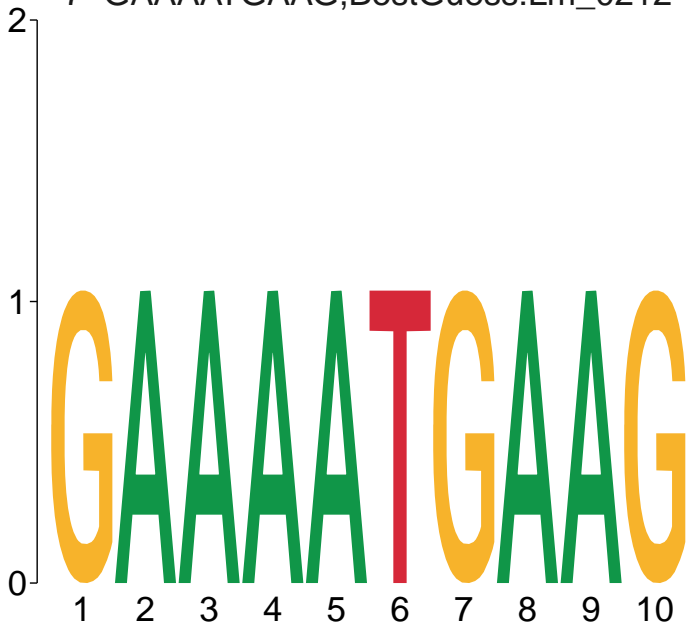
GTL1



RCH36_7_GAAAATGAAG,BestGuess_Lm_0212



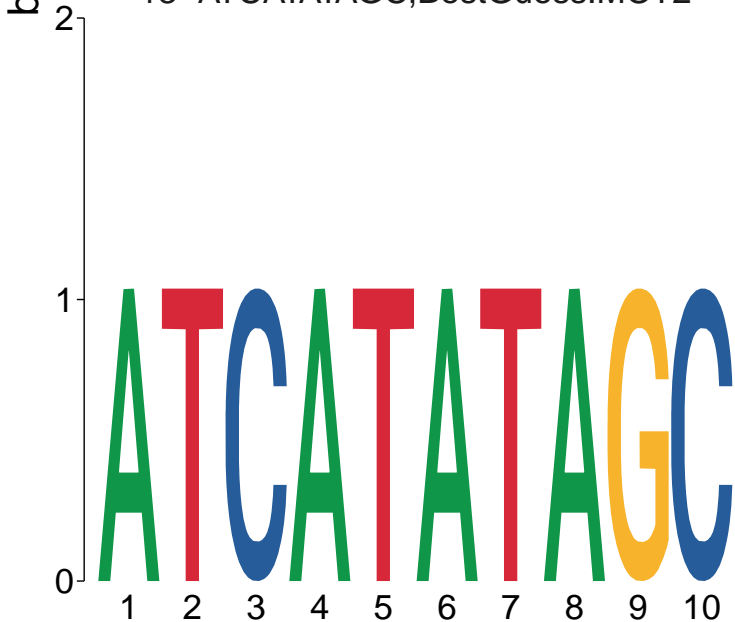
7-GAAAATGAAG,BestGuess:Lm_0212



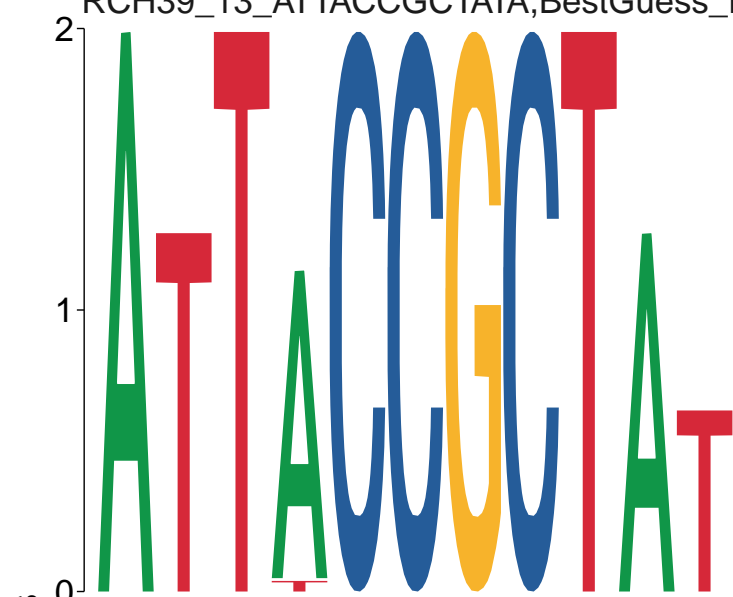
RCH37_13_ATCATATAGC,BestGuess_MOT



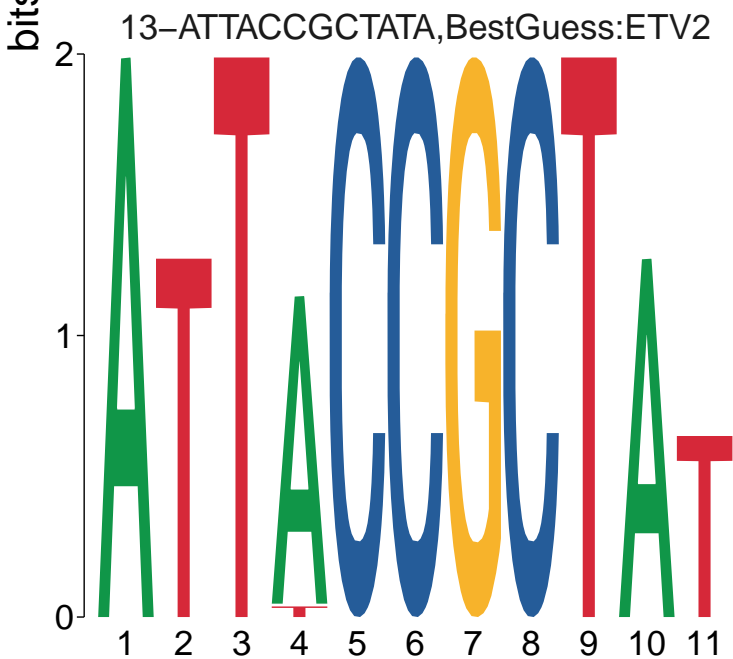
13-ATCATATAGC,BestGuess:MOT2



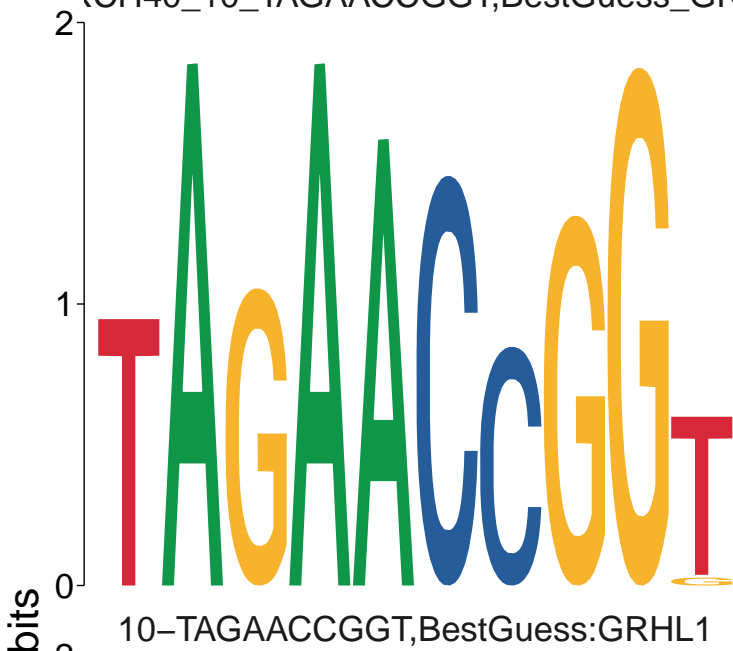
RCH39_13_ATTACCGCTATA,BestGuess_E



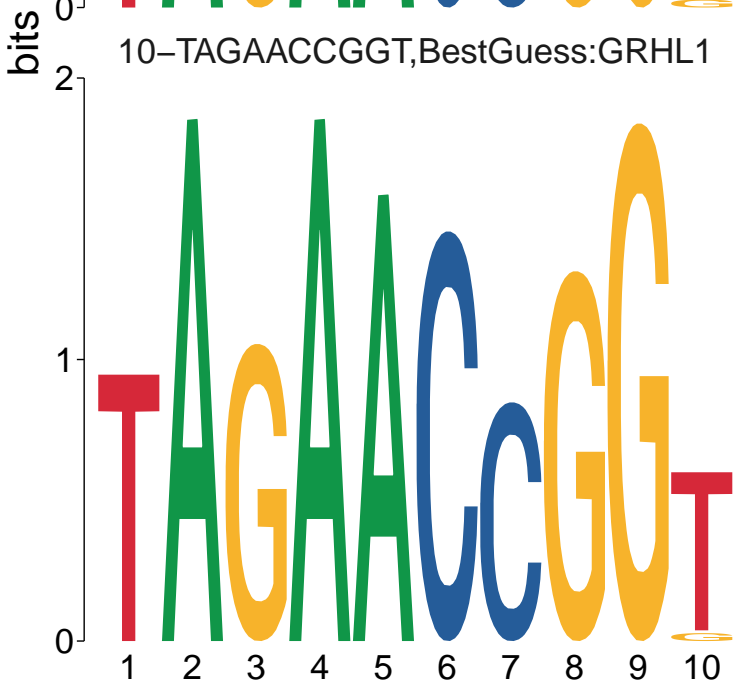
13-ATTACCGCTATA,BestGuess:ETV2



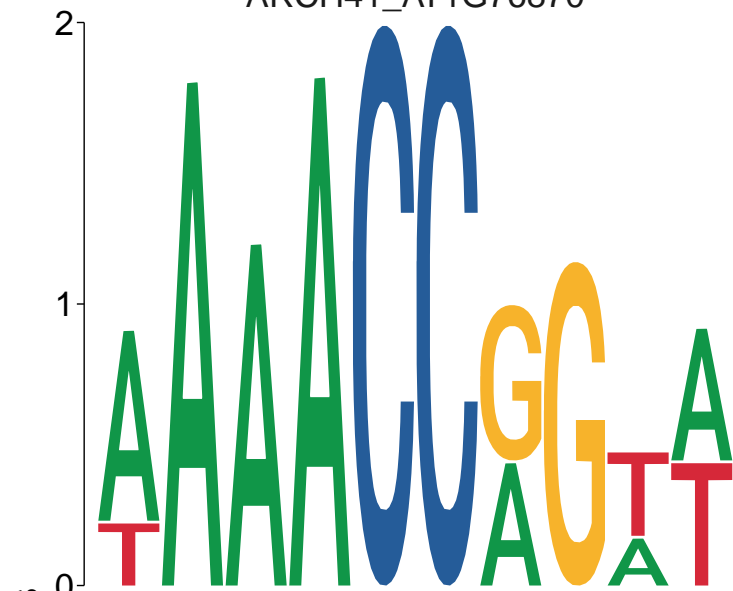
CH40_10_TAGAACCGGT,BestGuess_GRI



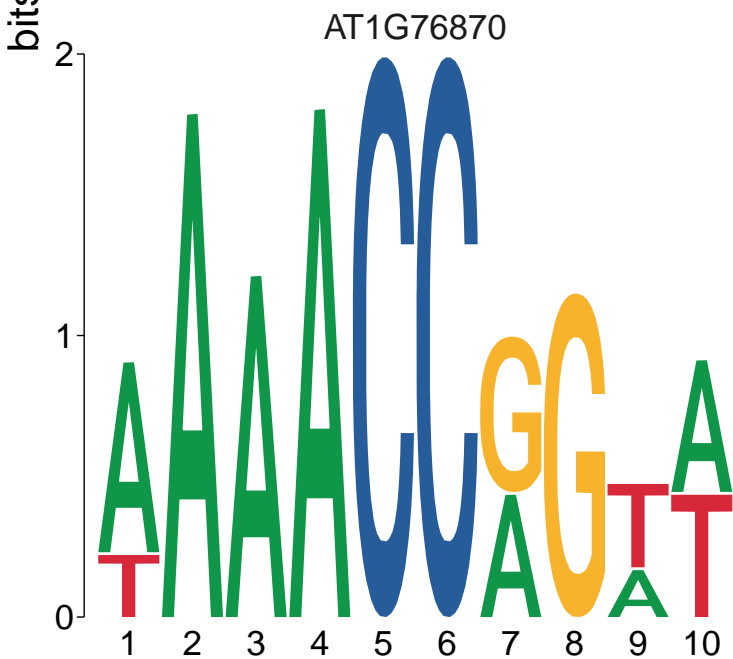
10-TAGAACCGGT,BestGuess:GRHL1



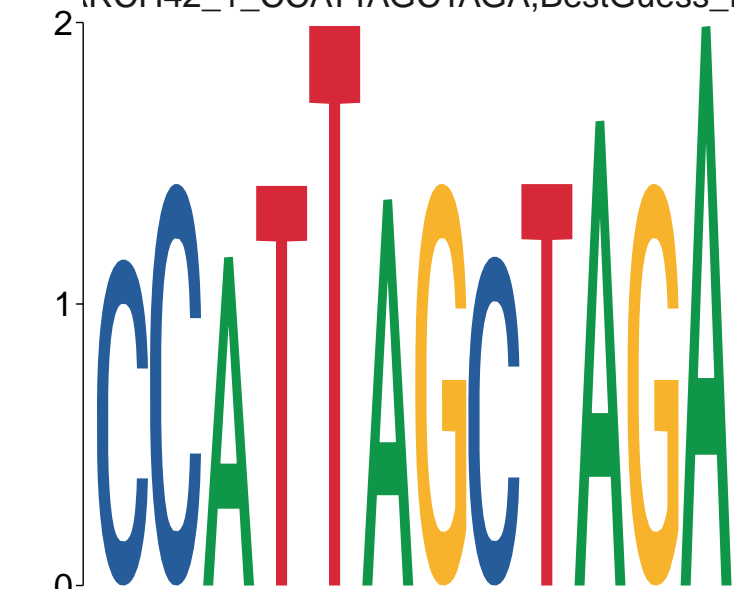
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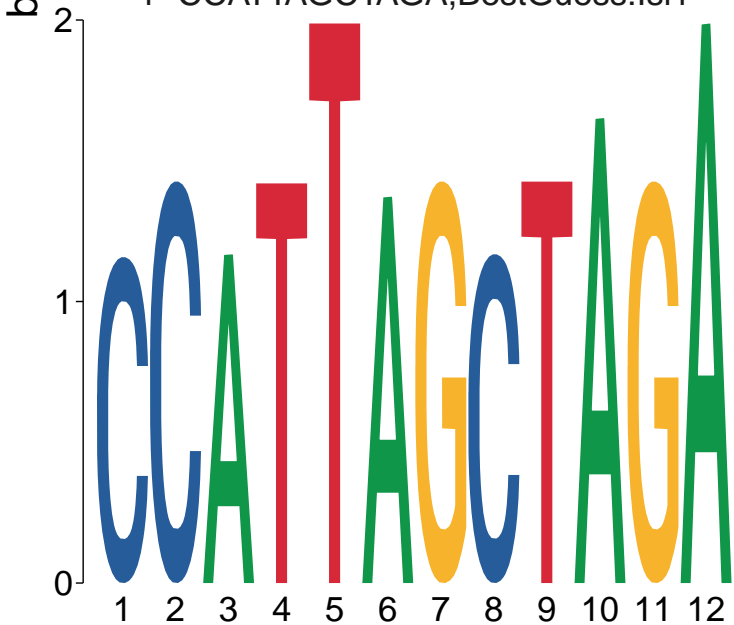
AT1G76870



RCH42_1_CCATTAGCTAGA,BestGuess_Is



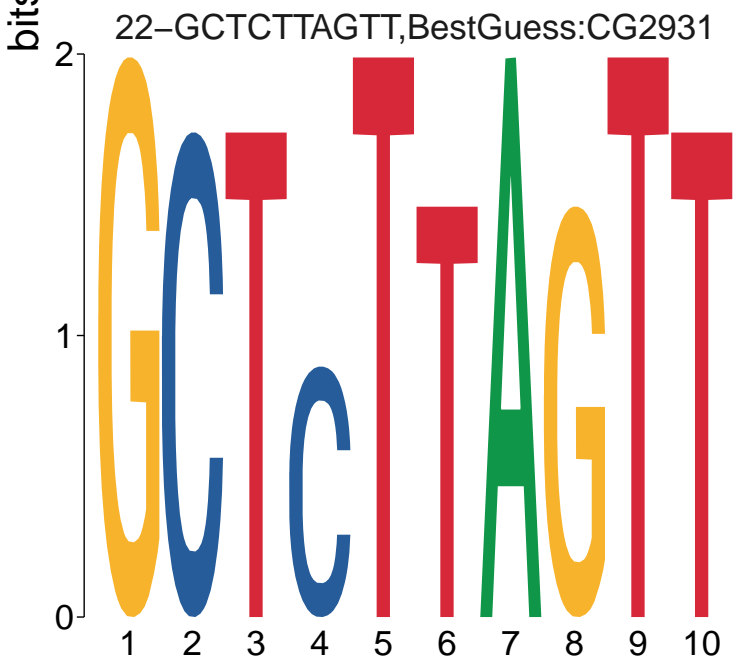
1-CCATTAGCTAGA,BestGuess:Is1



RCH43_22_GCTCTTAGTT,BestGuess_CG2

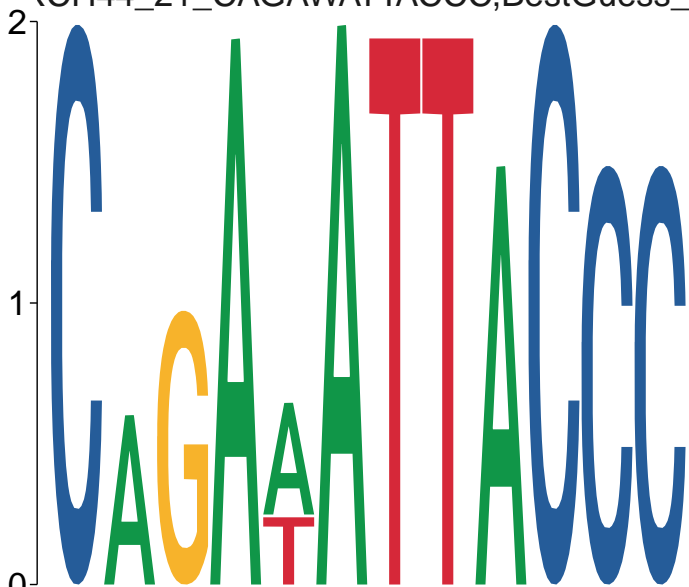


22-GCTCTTAGTT,BestGuess:CG2931

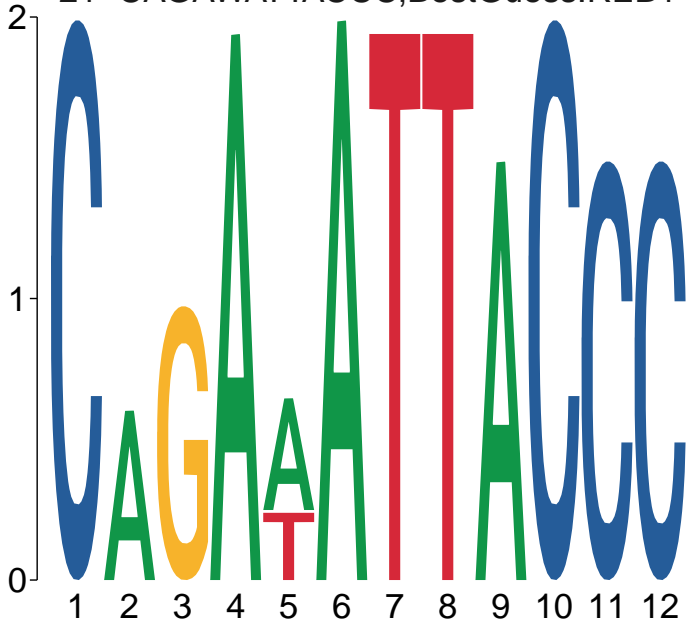


CH44_21_CAGAWATTACCC,BestGuess_F

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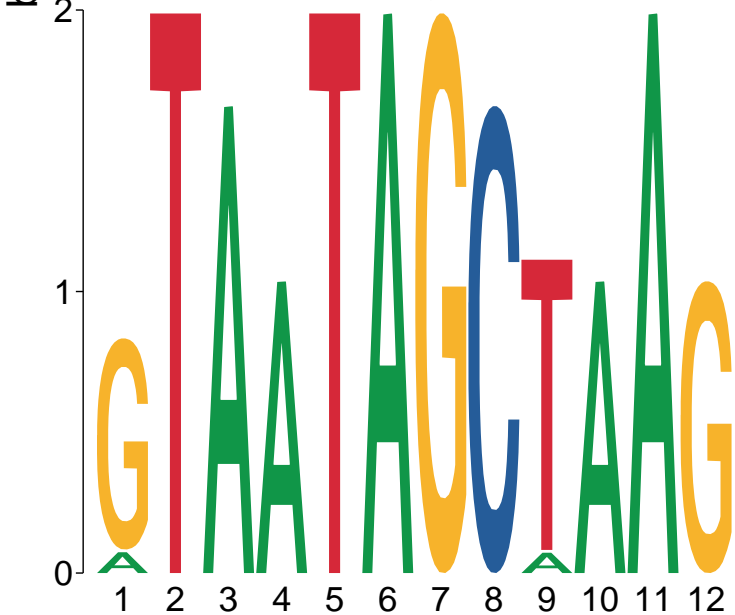
21-CAGAWATTACCC,BestGuess:REB1



ARCH45_1_GTAATAGCTAAG,BestGuess_b

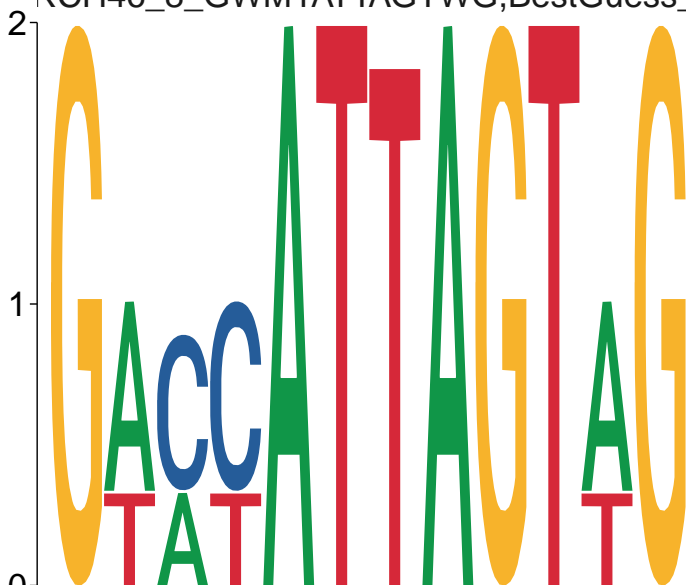


1-GTAATAGCTAAG,BestGuess:br-Z2

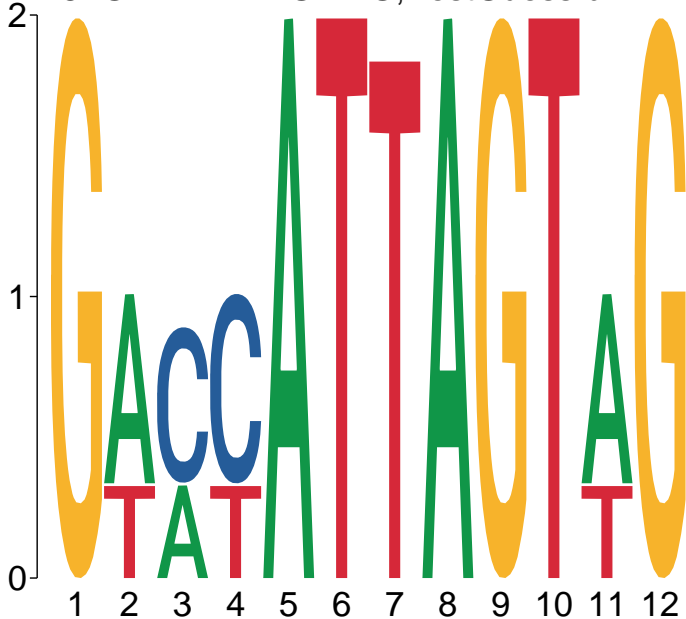


RCH46_8_GWMYATTAGTWG,BestGuess_1

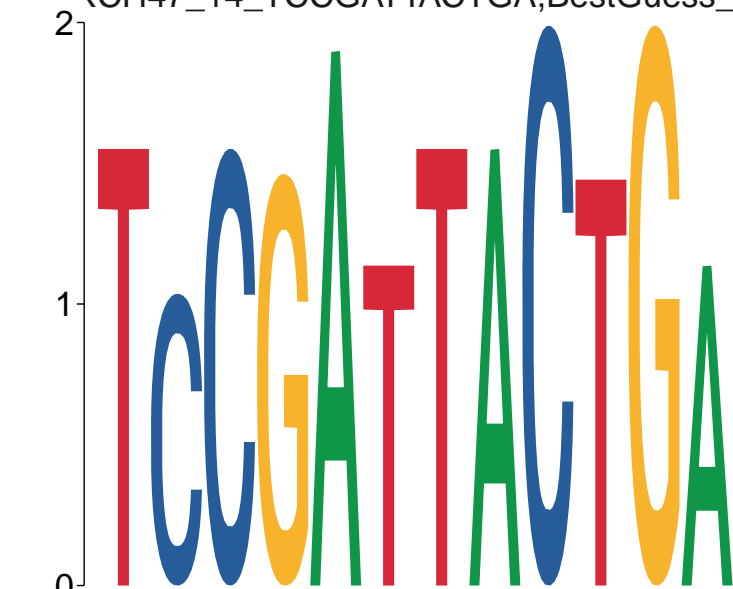
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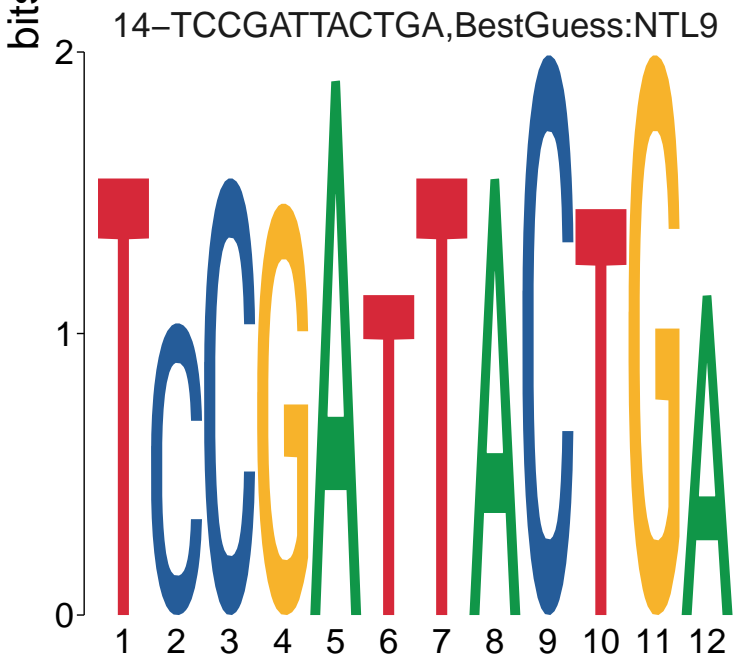
8-GWMYATTAGTWG,BestGuess:br-Z4



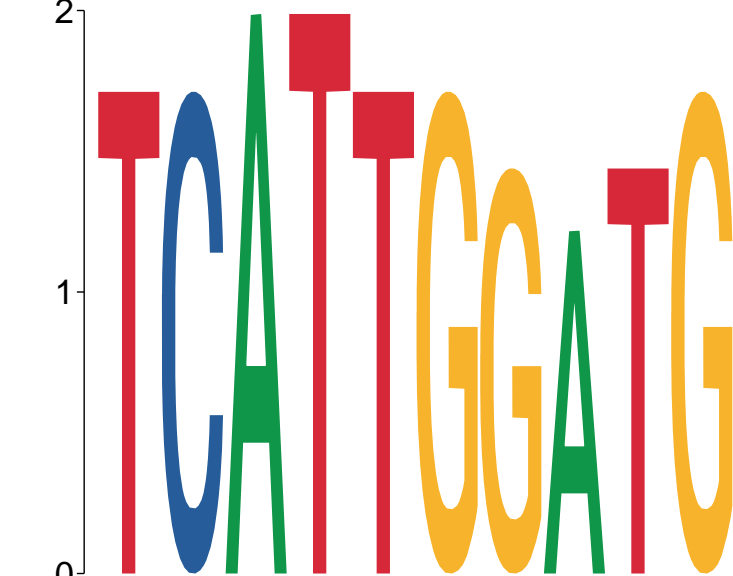
RCH47_14_TCCGATTACTGA,BestGuess_1



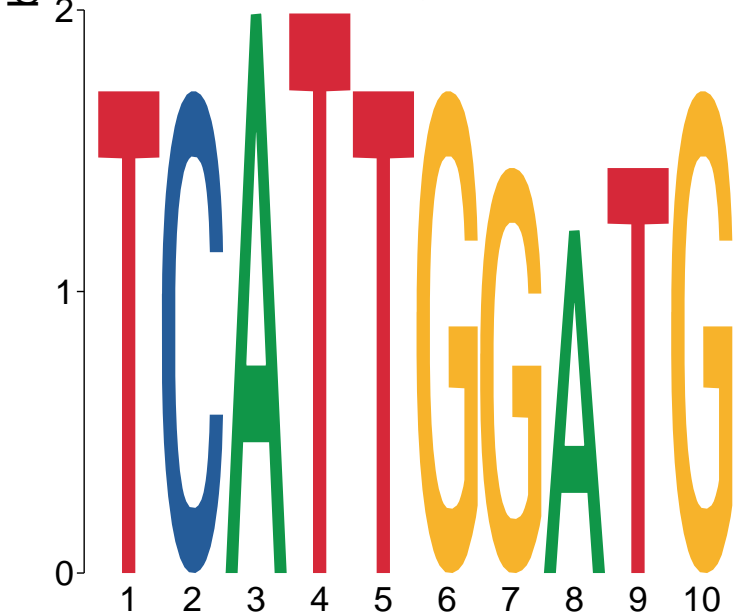
14-TCCGATTACTGA,BestGuess:NTL9



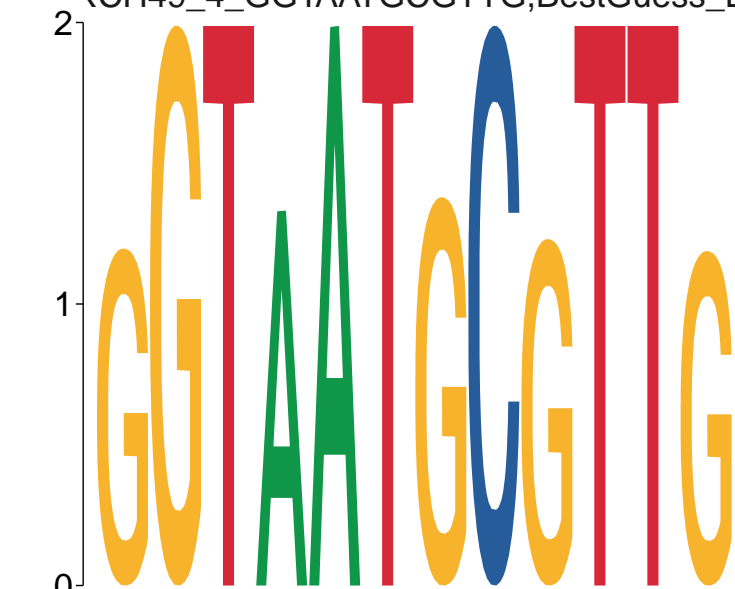
RCH48_15_TCATTGGATG,BestGuess_HAF



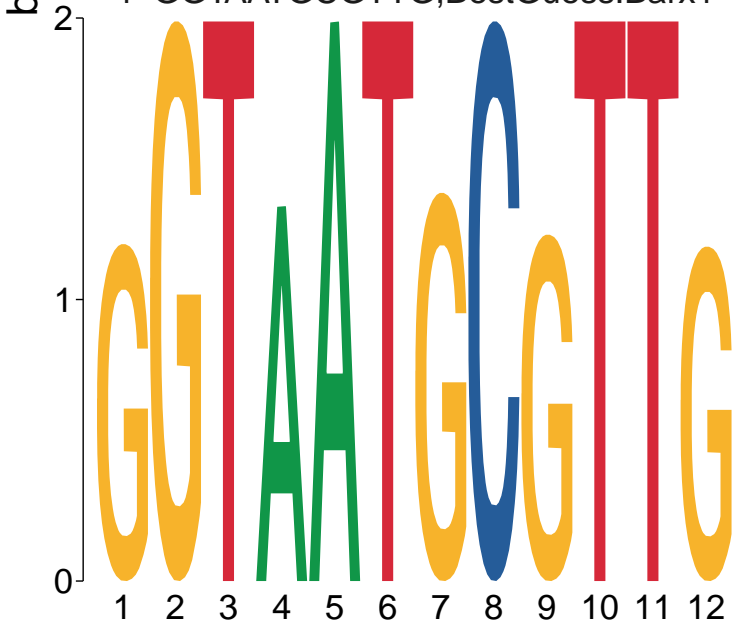
15-TCATTGGATG,BestGuess:HAP2



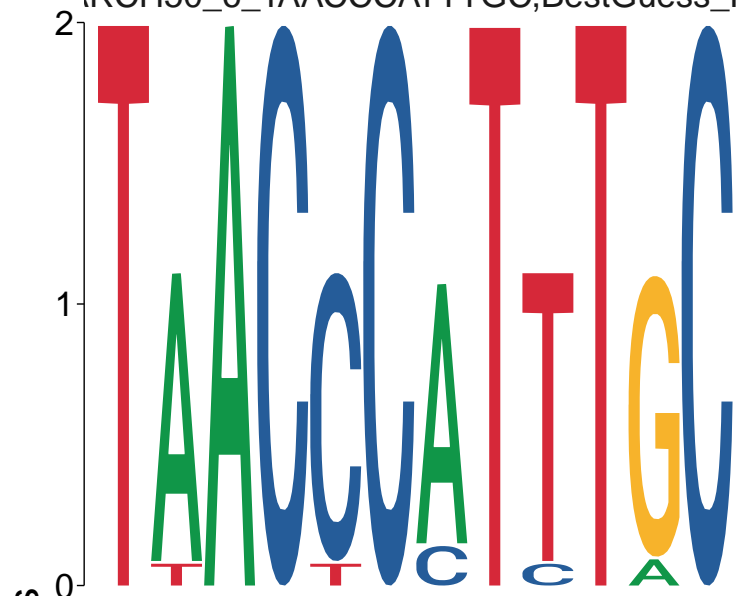
RCH49_4_GGTAATGCGTTG,BestGuess_B



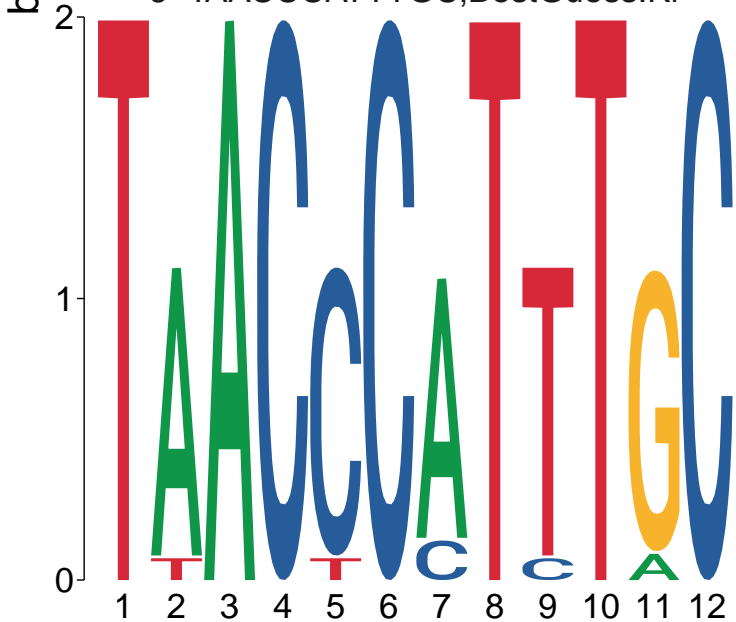
4-GGTAATGCGTTG,BestGuess:Barx1



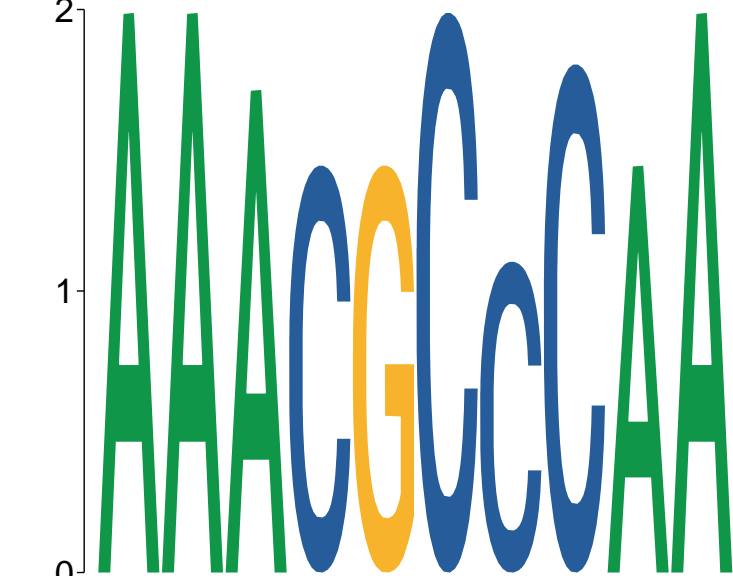
RCH50_6_TAACCCATTTC, BestGuess_K



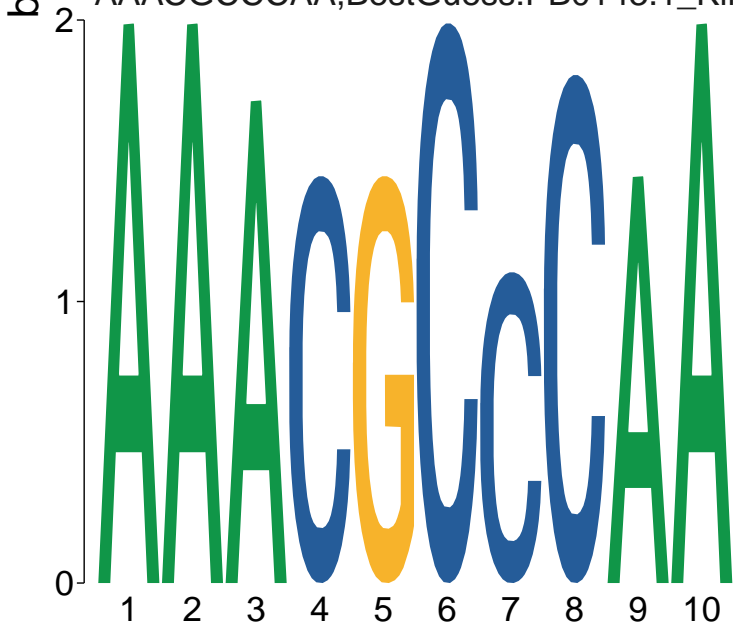
6-TAACCCATTTC, BestGuess:Kr



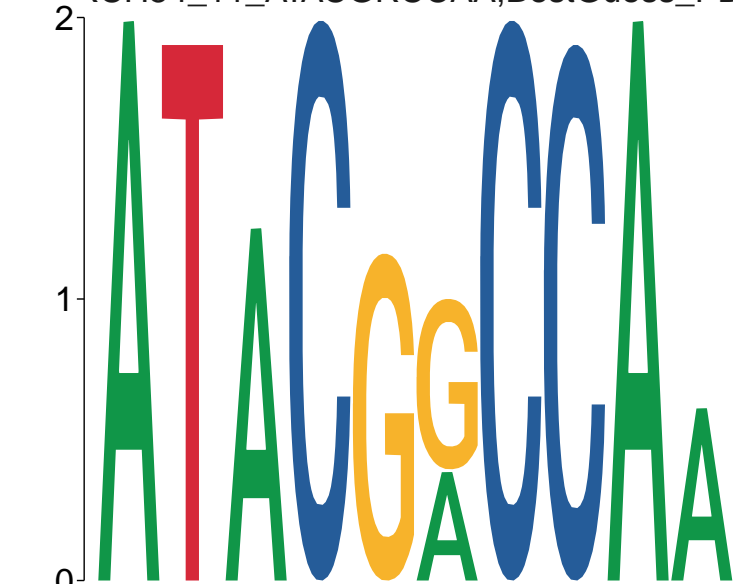
CH53_13_AAACGCCCAA,BestGuess_PB



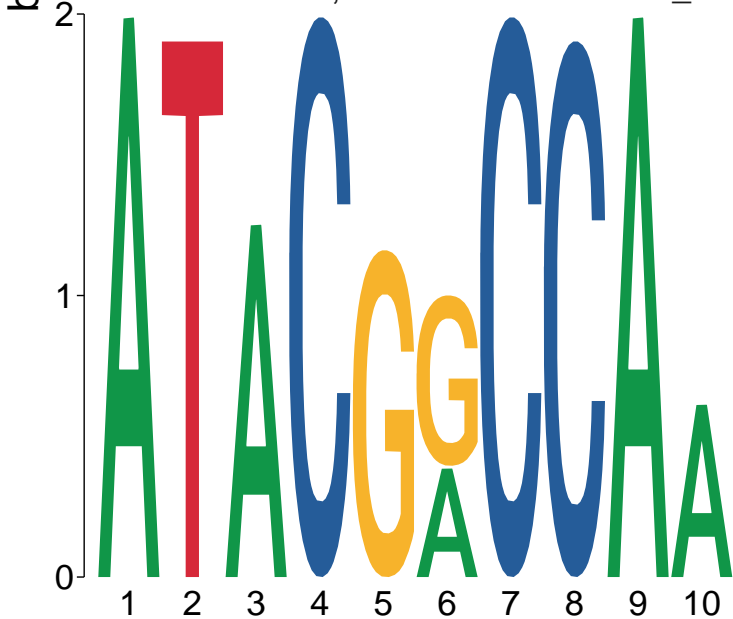
-AAACGCCCAA,BestGuess:PB0143.1_Klf7



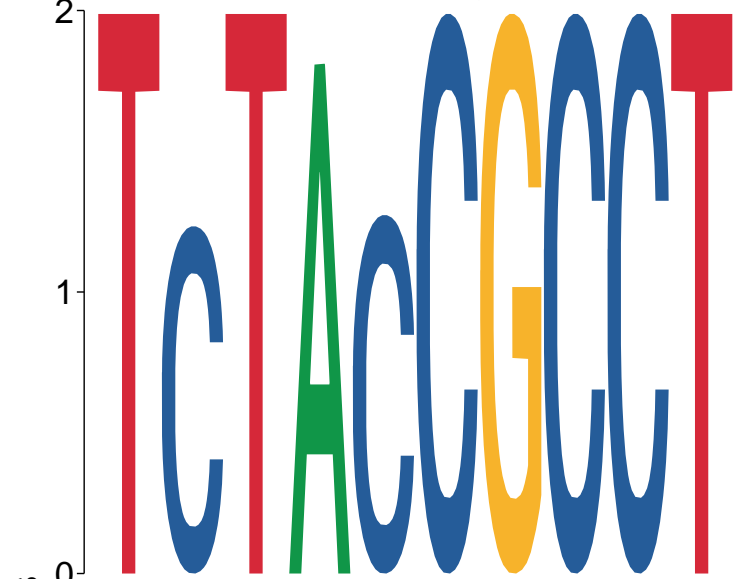
RCH54_11_ATACGRCCAA,BestGuess_PB(



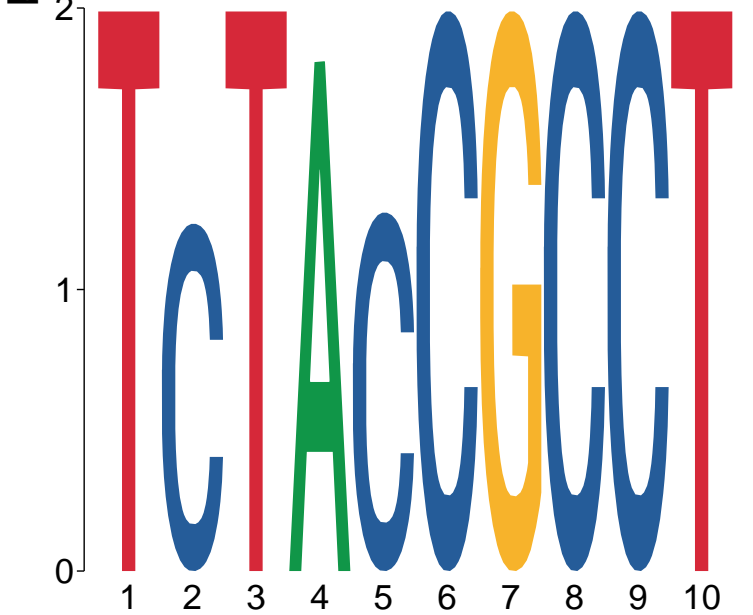
-ATACGRCCAA,BestGuess:PB0143.1_Klf7



RCH55_6_TCTACCGCCT,BestGuess_AT3C



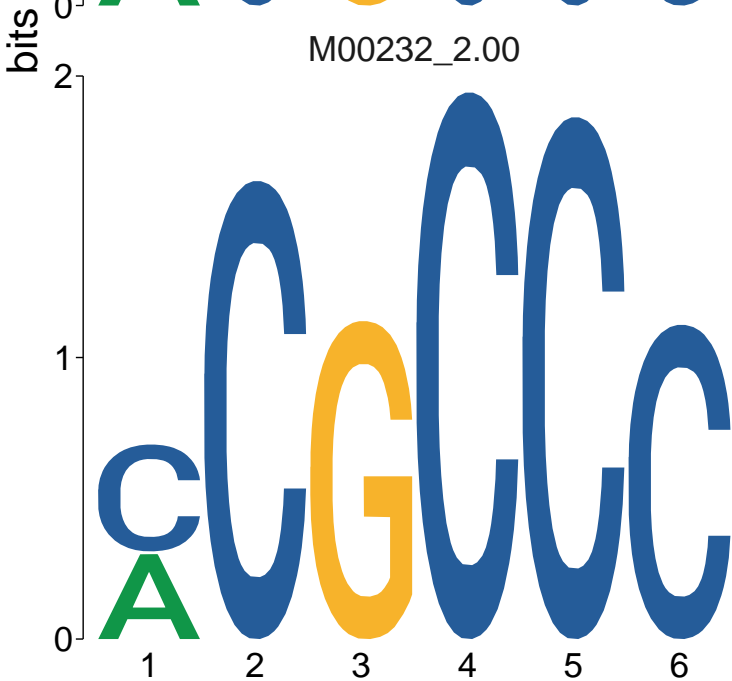
6-TCTACCGCCT,BestGuess:AT3G57600



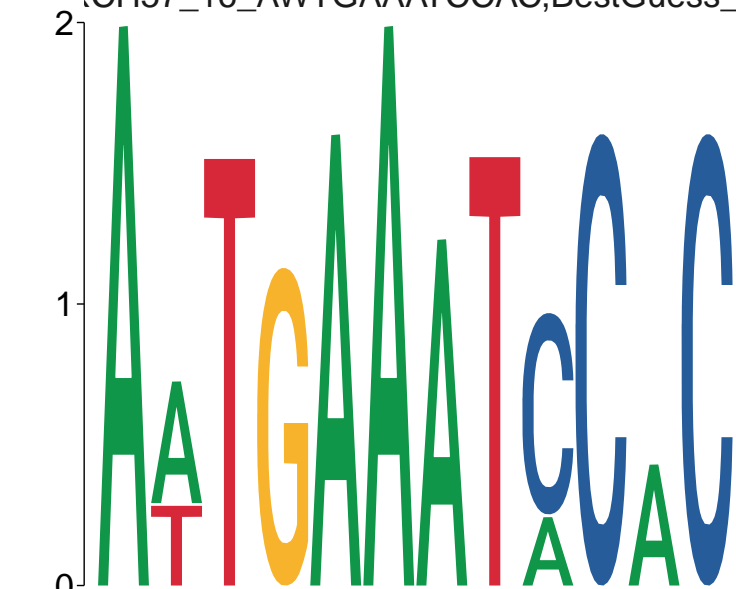
ARCH56_zf-C2H2



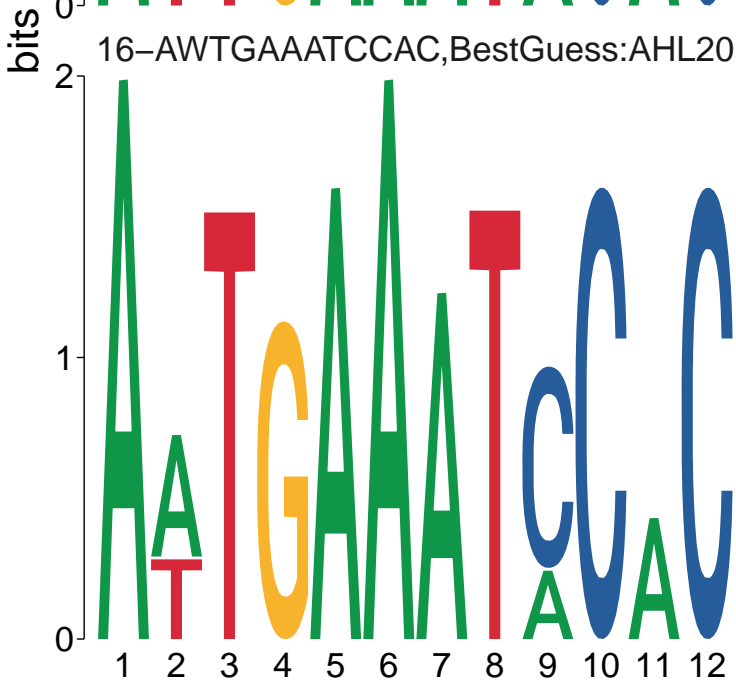
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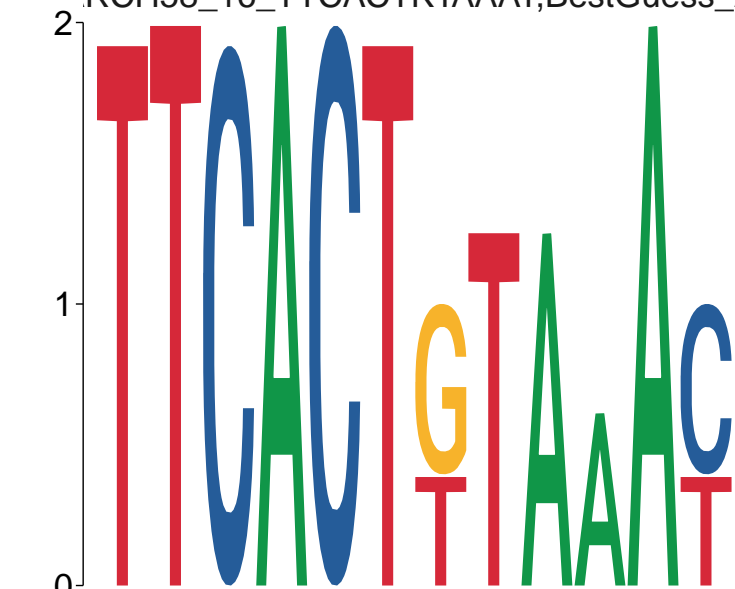
CH57_16_AWTGAAATCCAC,BestGuess_1



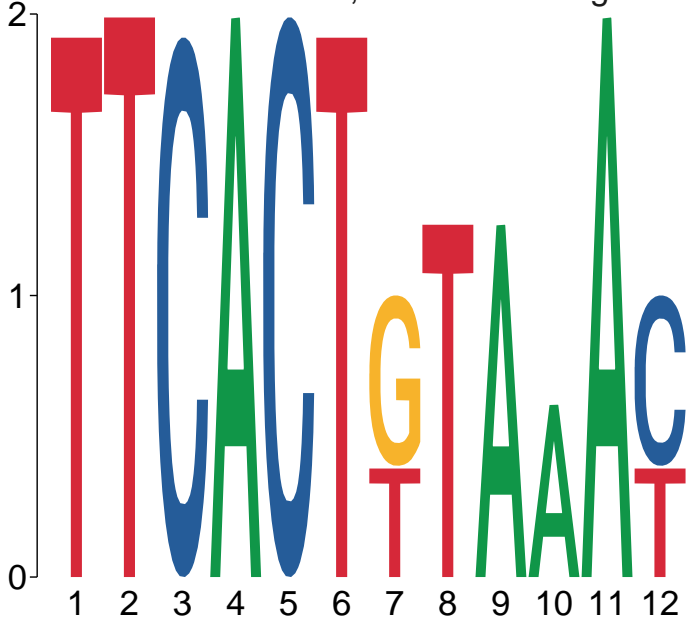
16-AWTGAAATCCAC,BestGuess: AHL20



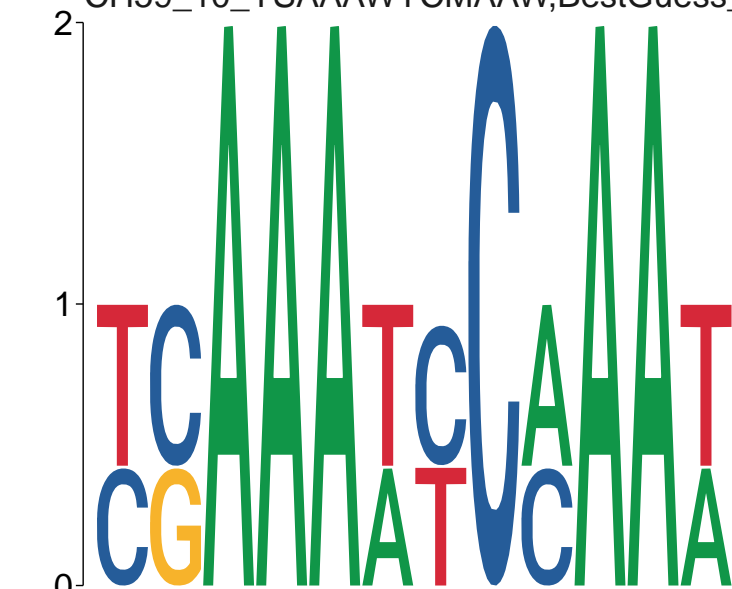
RCH58_16_TTCACTKTAAAY,BestGuess_1



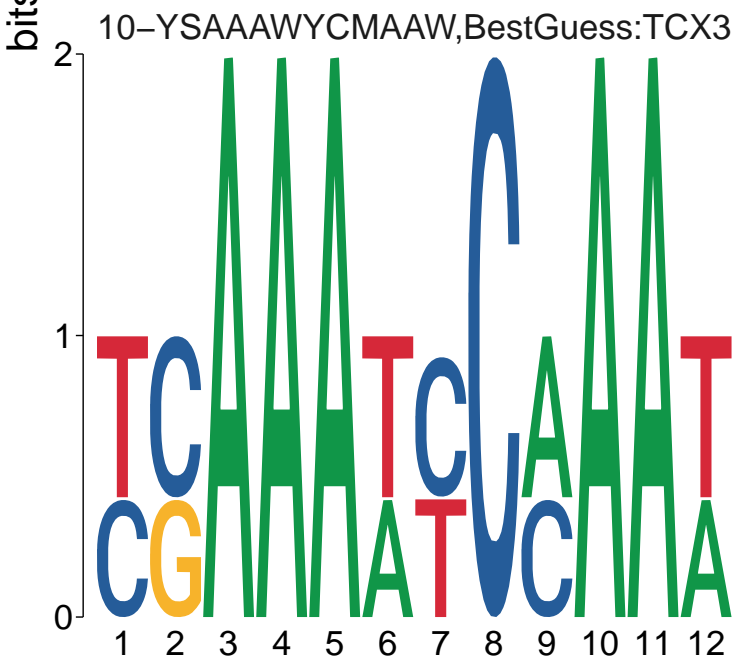
16-TTCACTKTAAAY,BestGuess:At5g0439C



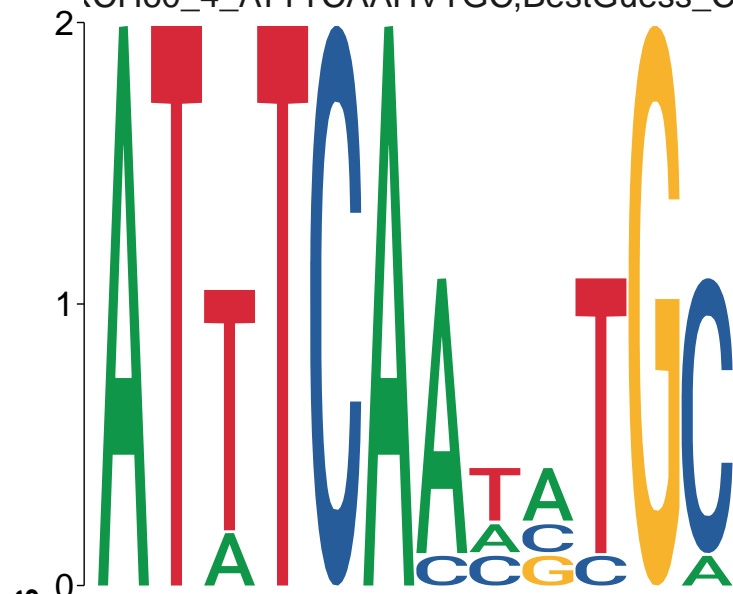
CH59_10_YSAAAWYCMAAW,BestGuess_



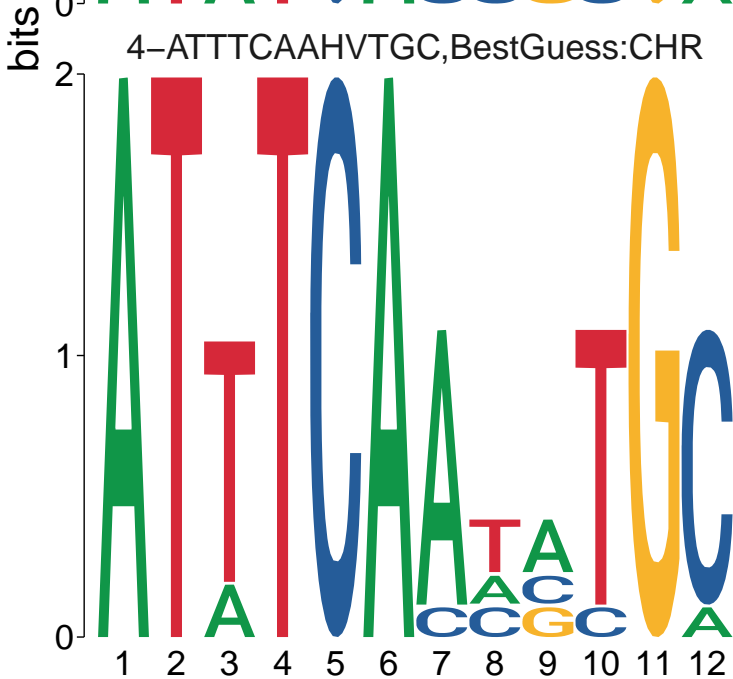
10-YSAAAWYCMAAW,BestGuess:TCX3



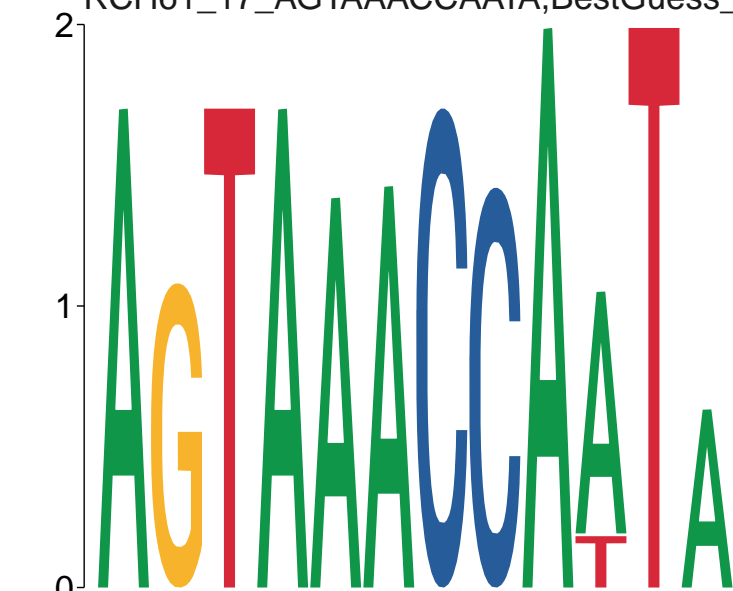
CH60_4_ATTTCAAHVTGC,BestGuess_Cf



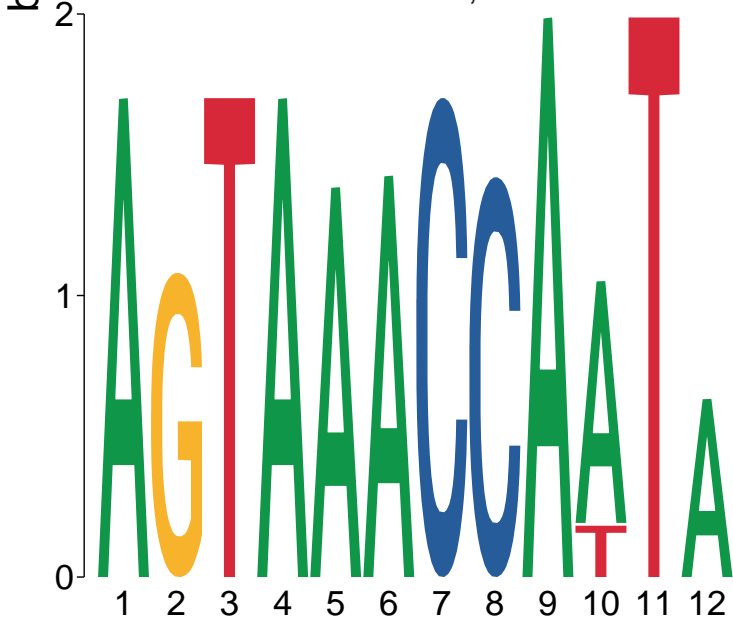
4-ATTTCAAHVTGC,BestGuess:CHR



RCH61_17_AGTAACCAATA,BestGuess_k



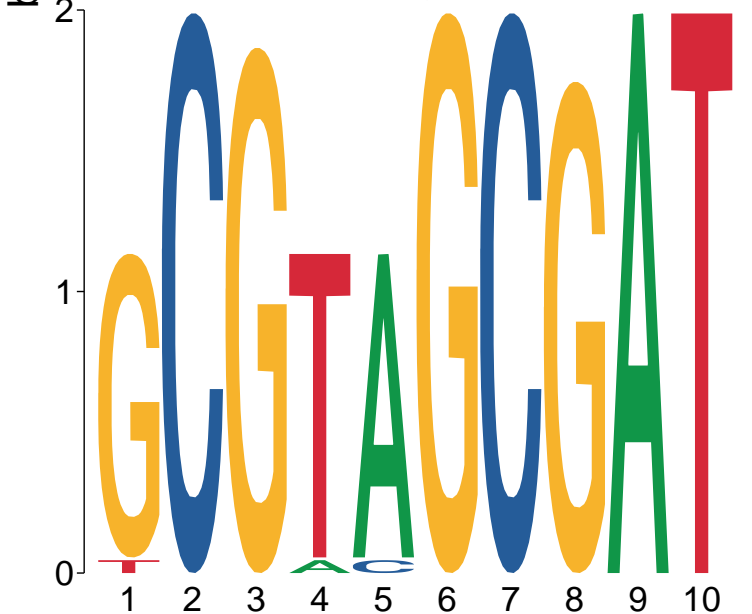
17-AGTAACCAATA,BestGuess:br



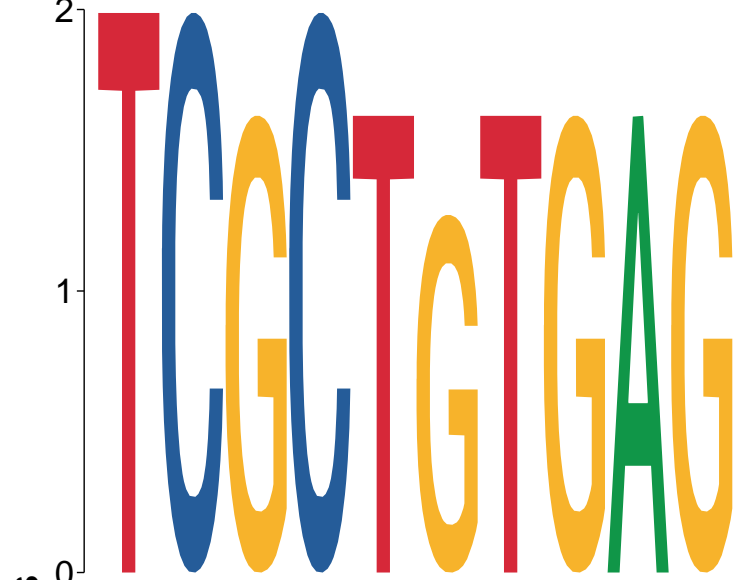
RCH63_17_GCGTAGCGAT,BestGuess_STE



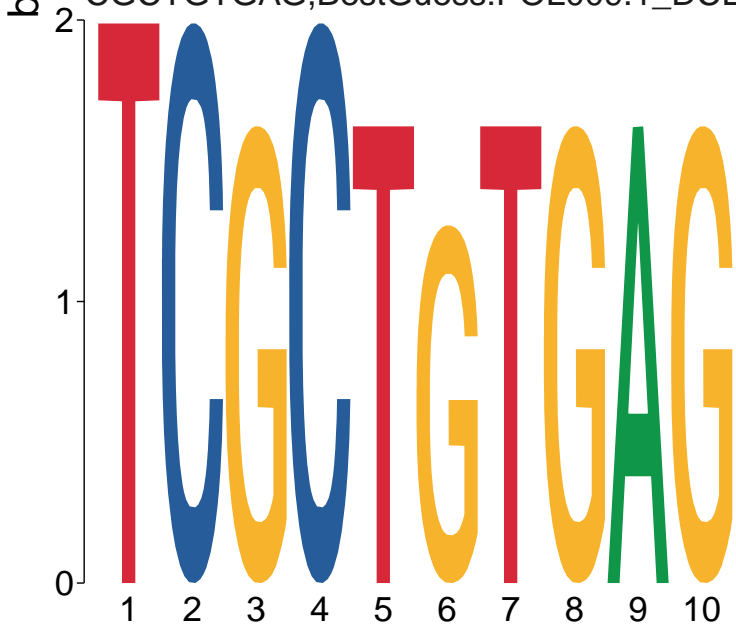
17-GCGTAGCGAT,BestGuess:STB4



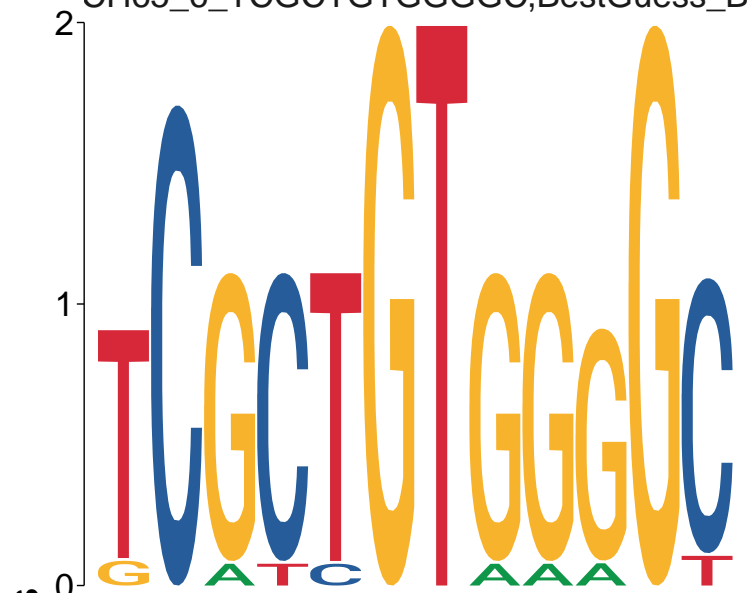
CH64_10_TCGCTGTGAG,BestGuess_PO



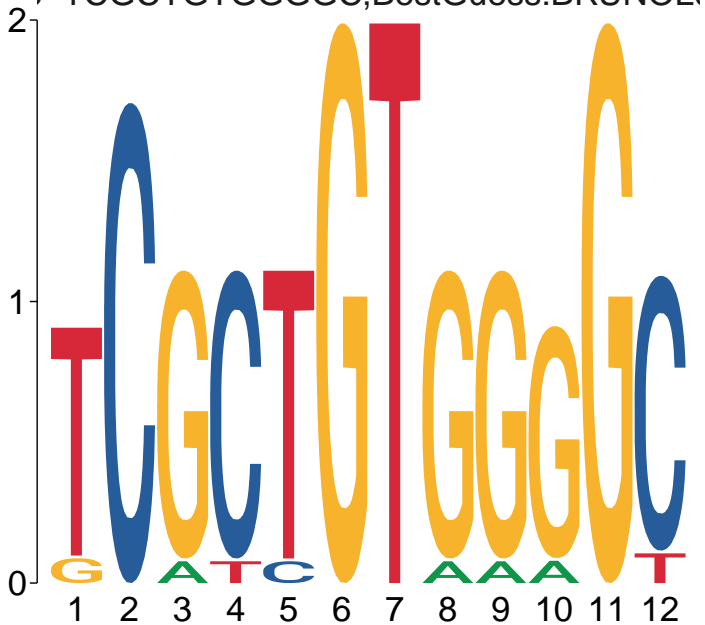
CGCTGTGAG,BestGuess:POL009.1_DCE.



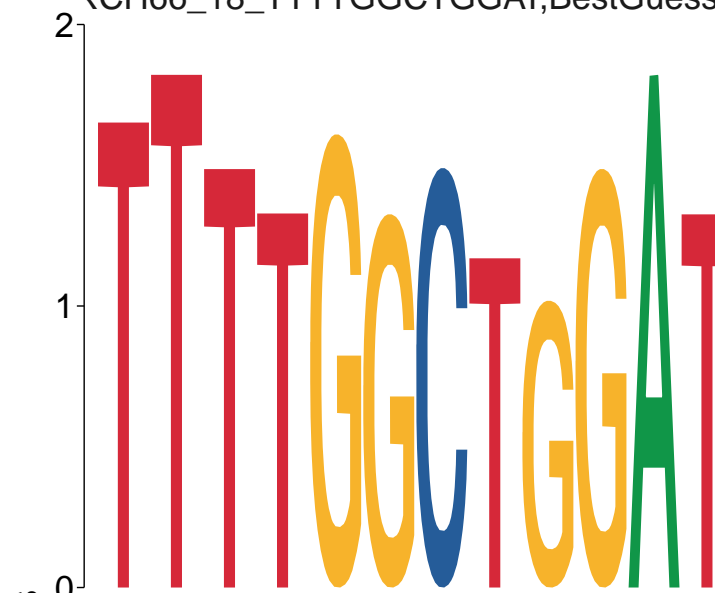
CH65_6_TCGCTGTGGGGGC, BestGuess_B



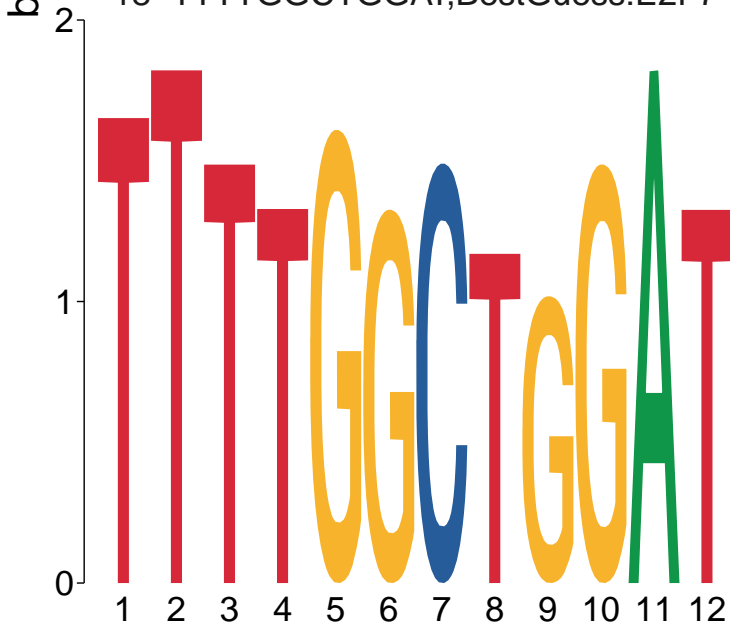
CH65_6_TCGCTGTGGGGGC, BestGuess:BRUNOL



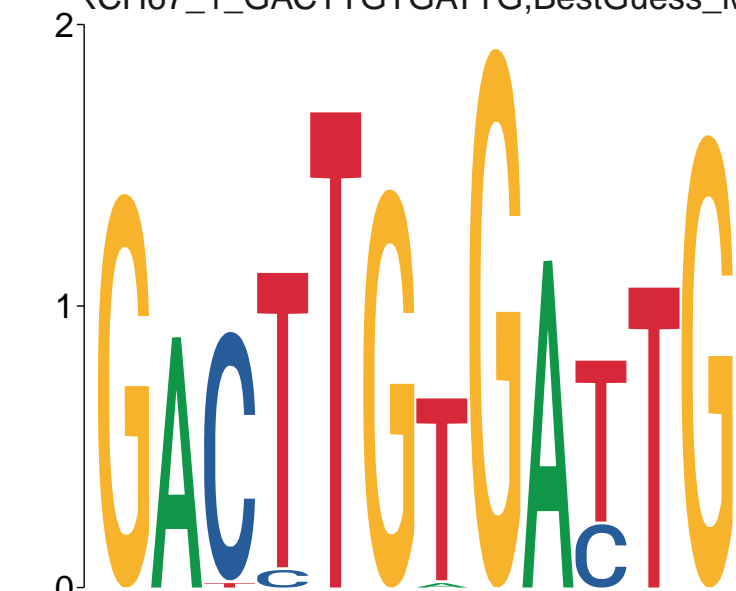
RCH66_18_TTTTGGCTGGAT,BestGuess_E



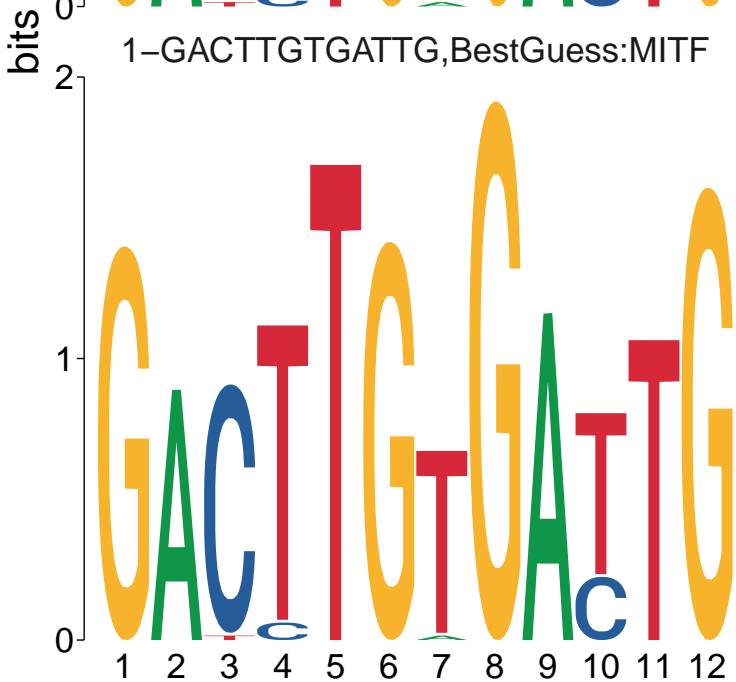
18-TTTTGGCTGGAT,BestGuess:E2F7



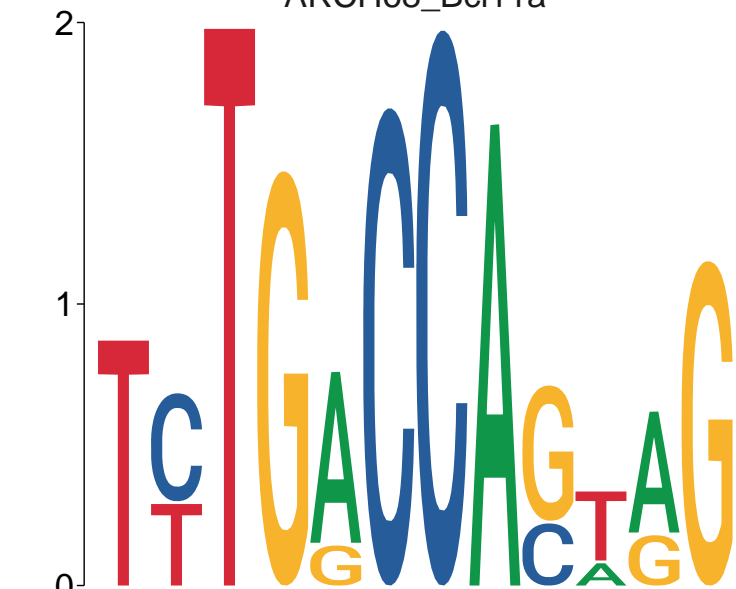
RCH67_1_GACTTGTGATTG,BestGuess_M



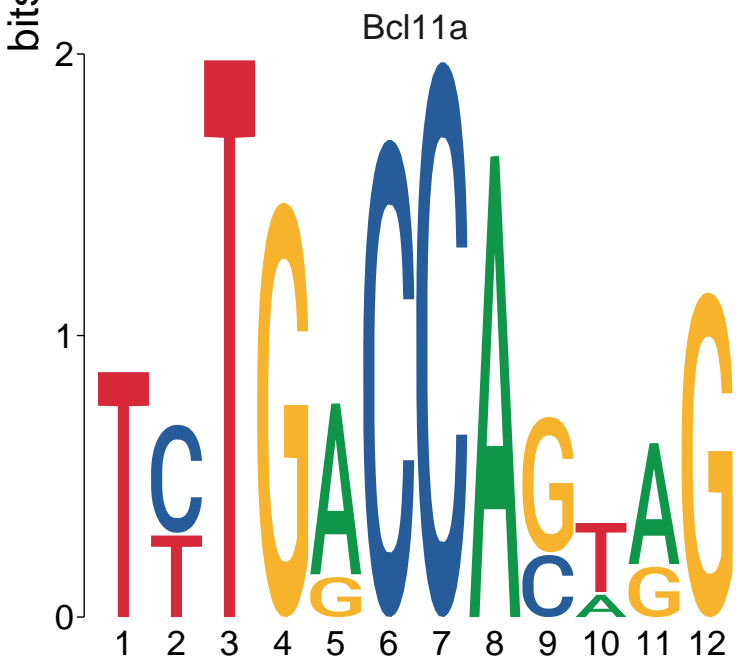
1-GACTTGTGATTG,BestGuess:MITF



ARCH68_Bcl11a



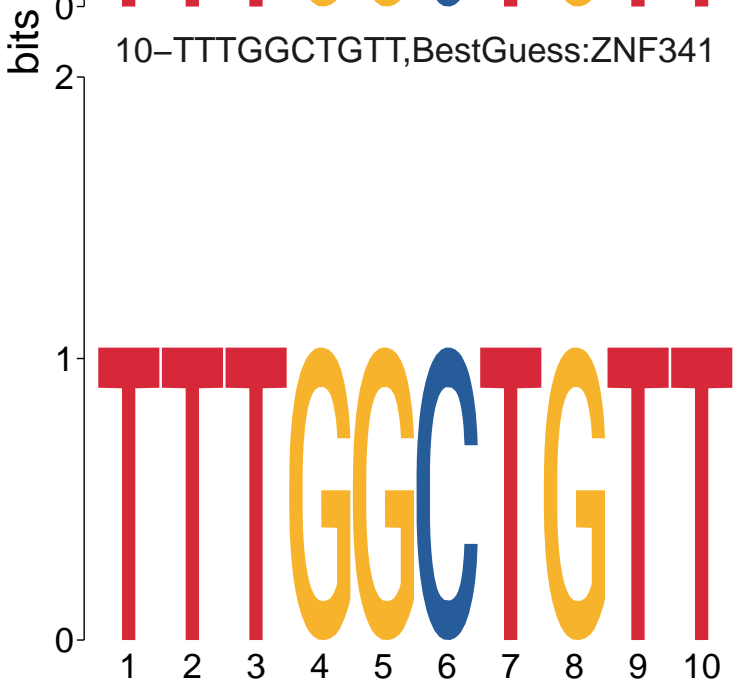
Bcl11a



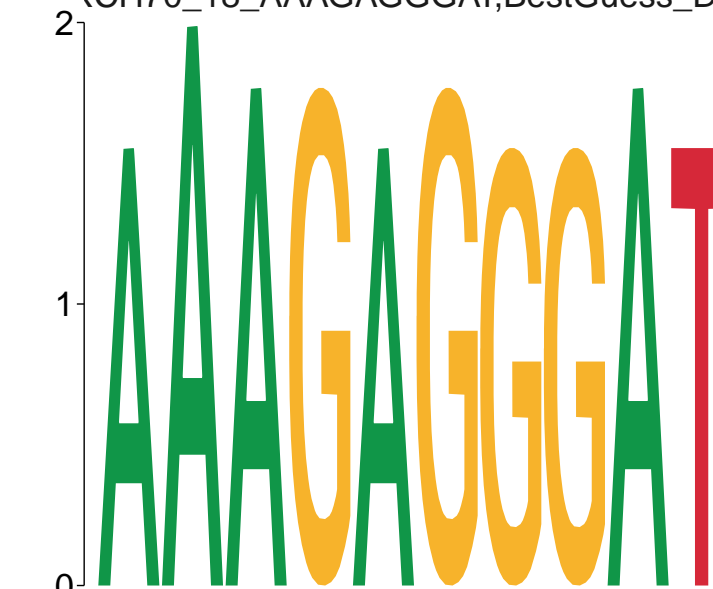
RCH69_10_TTTGGCTGTT,BestGuess_ZNF



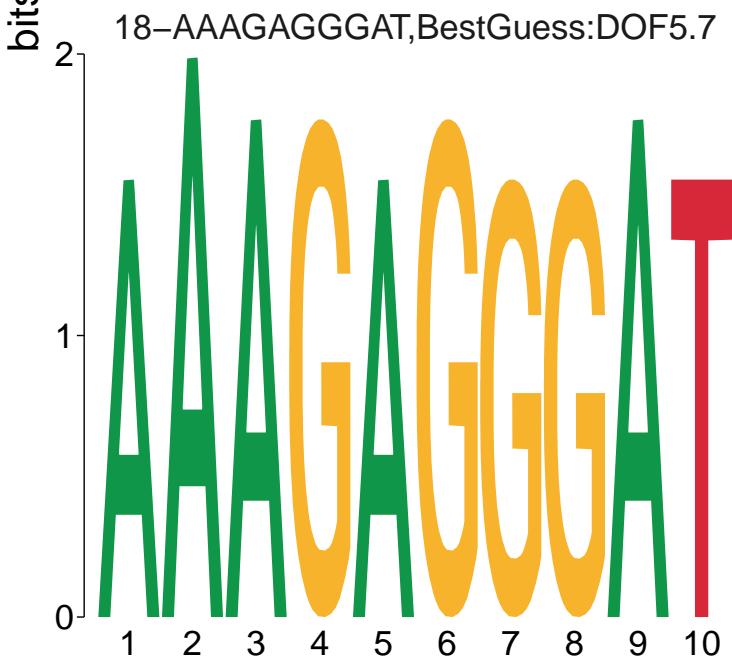
10-TTTGGCTGTT,BestGuess:ZNF341



CH70_18_AAAGAGGGAT,BestGuess_DO



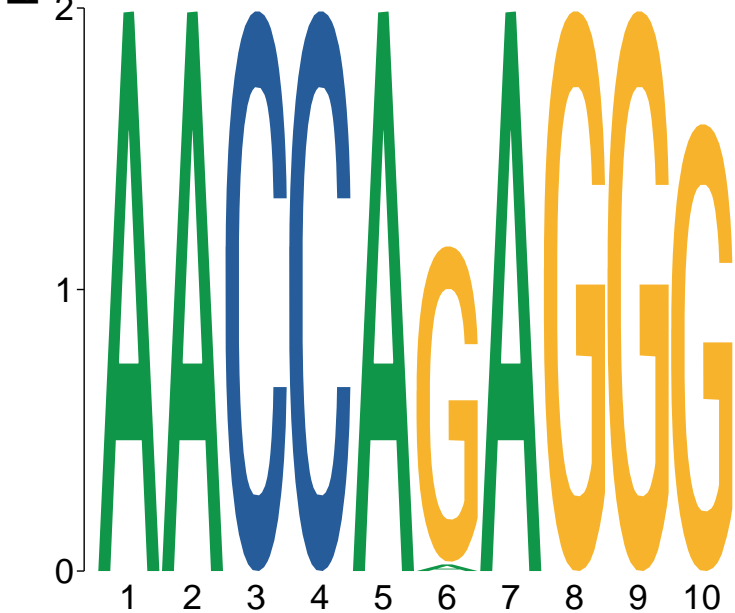
18-AAAGAGGGAT,BestGuess:DOF5.7



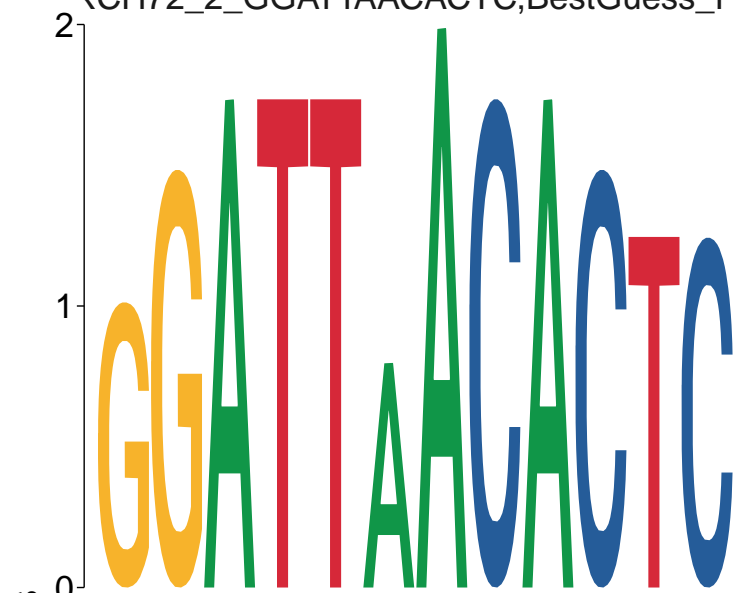
RCH71_4_AACCAGAGGG,BestGuess_REF



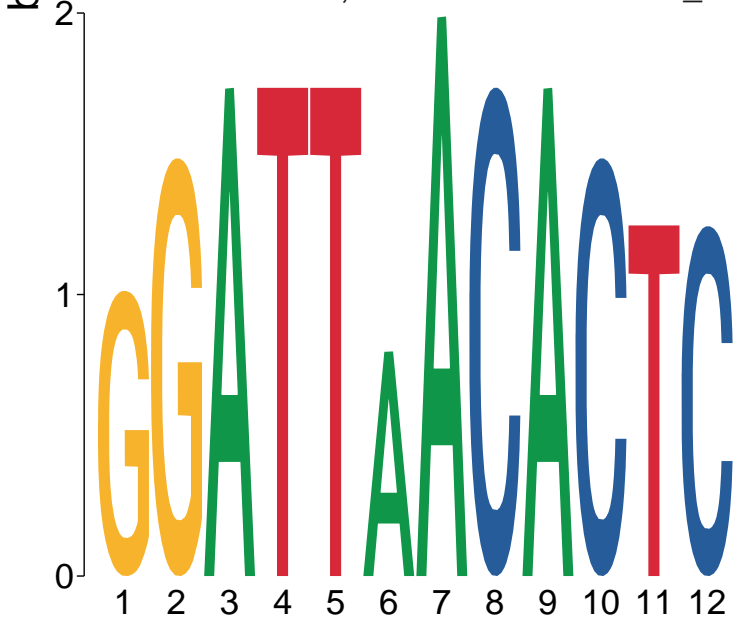
4-AACCAGAGGG,BestGuess:REF6



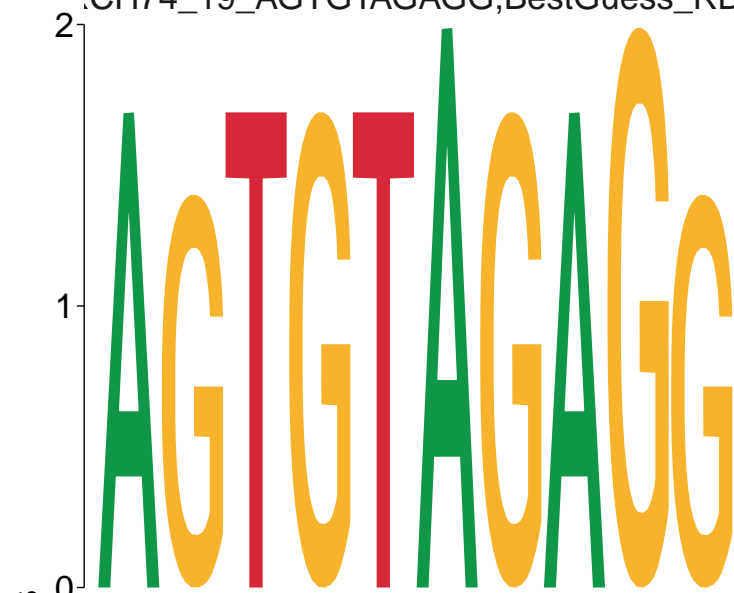
RCH72_2_GGATTAACACTC,BestGuess_Pf



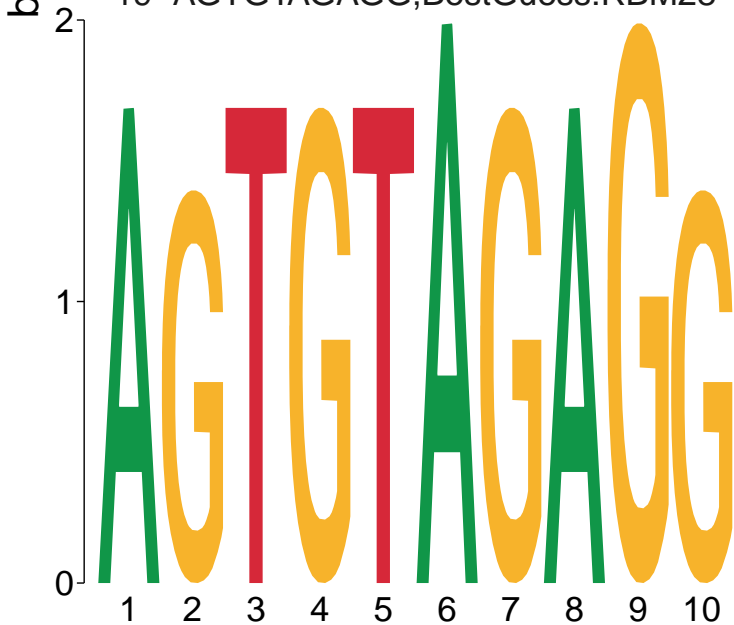
GGATTAACACTC,BestGuess:PH0123.1_Ob



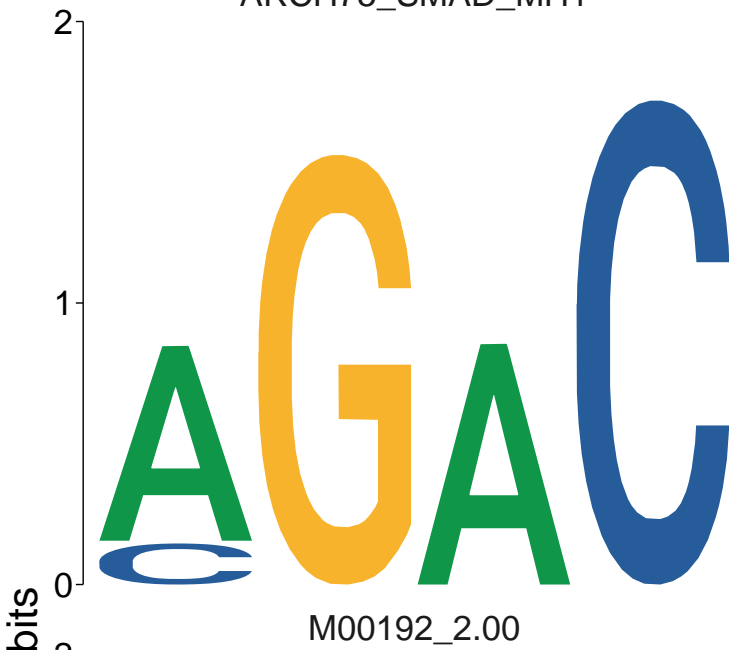
CH74_19_AGTGTAGAGG,BestGuess_RBI



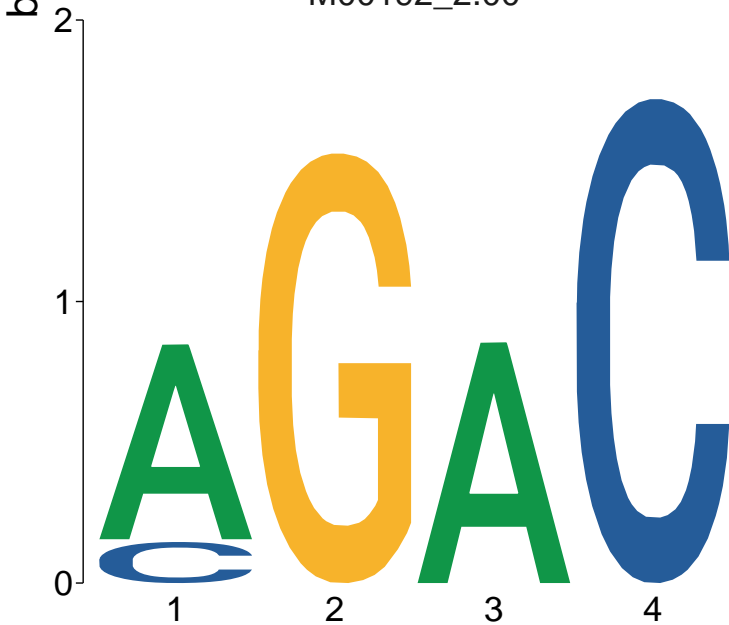
19-AGTGTAGAGG,BestGuess:RBM28



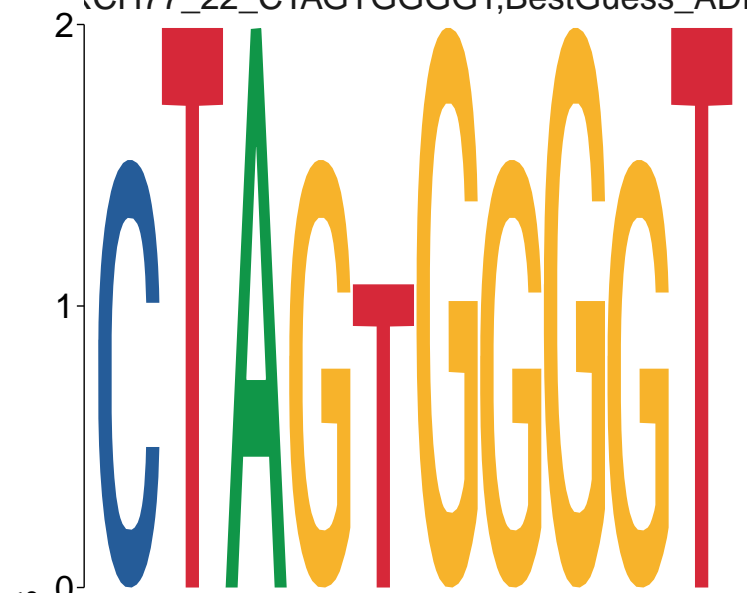
ARCH75_SMAD_MH1



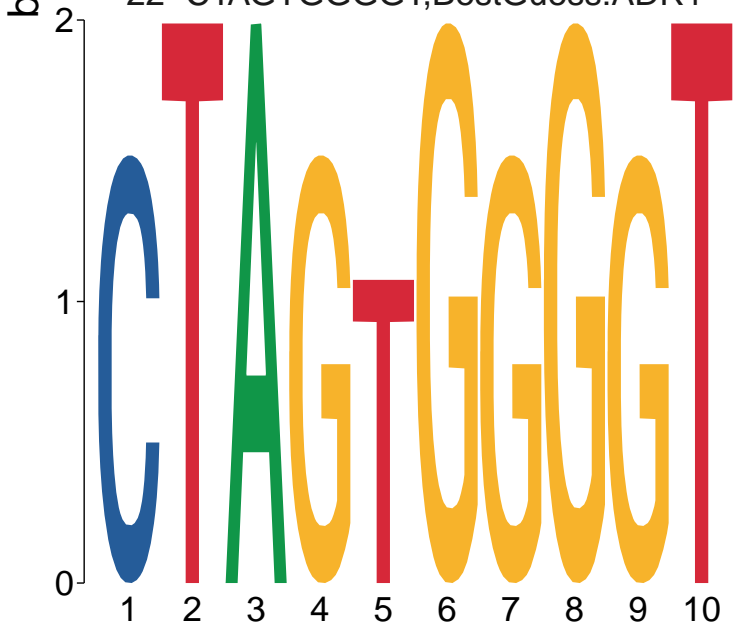
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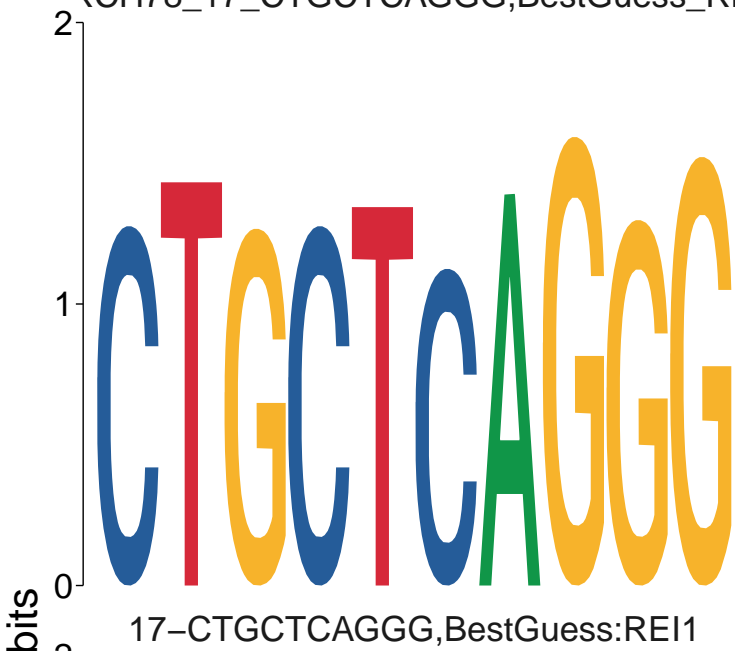
CH77_22_CTAGTGGGGGT,BestGuess_ADI



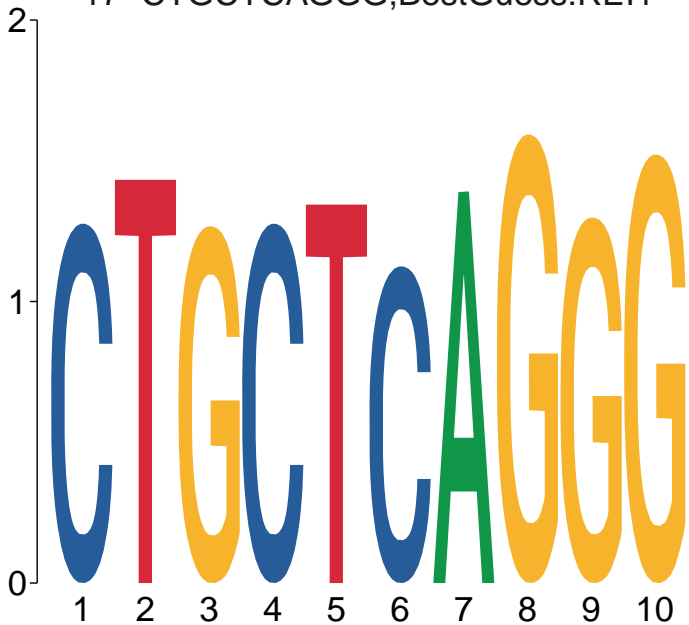
22-CTAGTGGGGGT,BestGuess:ADR1



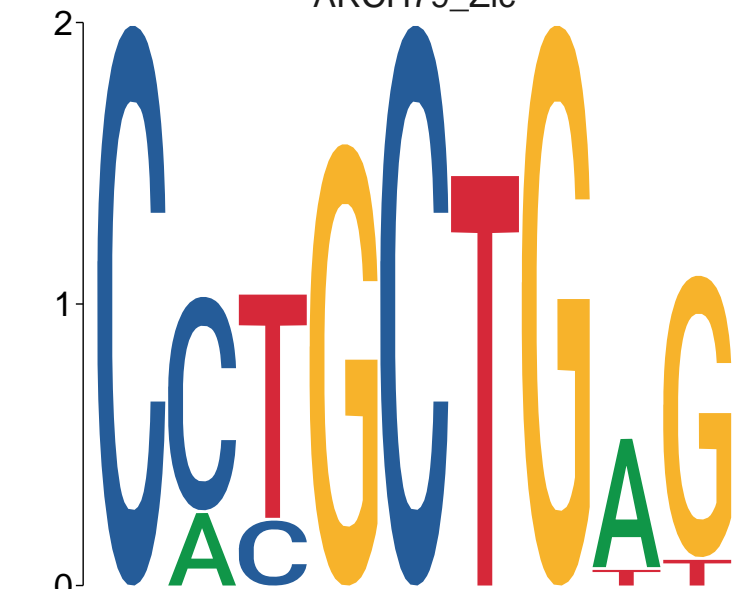
CH78_17_CTGCTCAGGG,BestGuess_RE



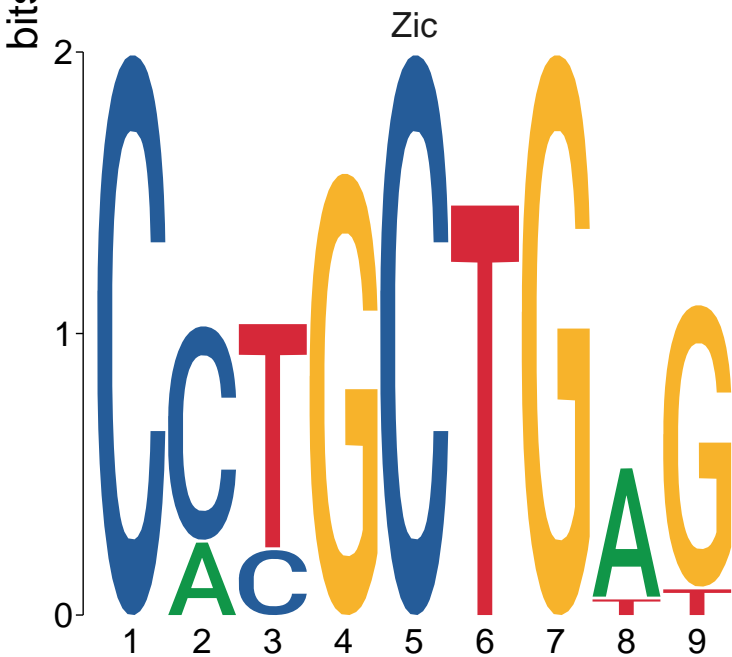
17-CTGCTCAGGG,BestGuess:REI1



ARCH79_Zic



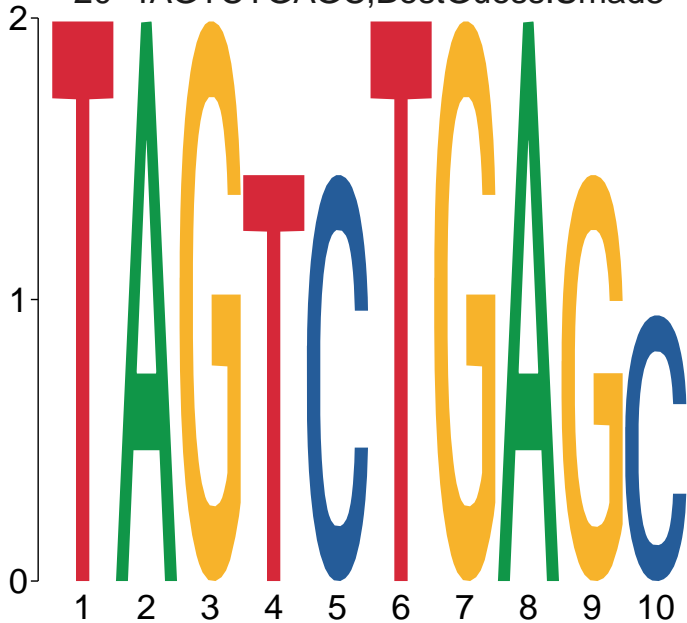
Zic



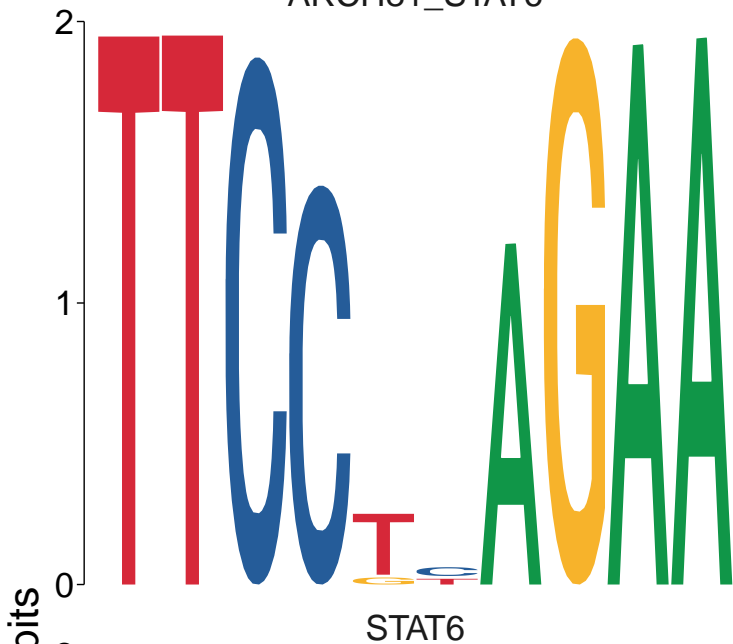
20-CH80_20_TAGTCTGAGC,BestGuess_Sm



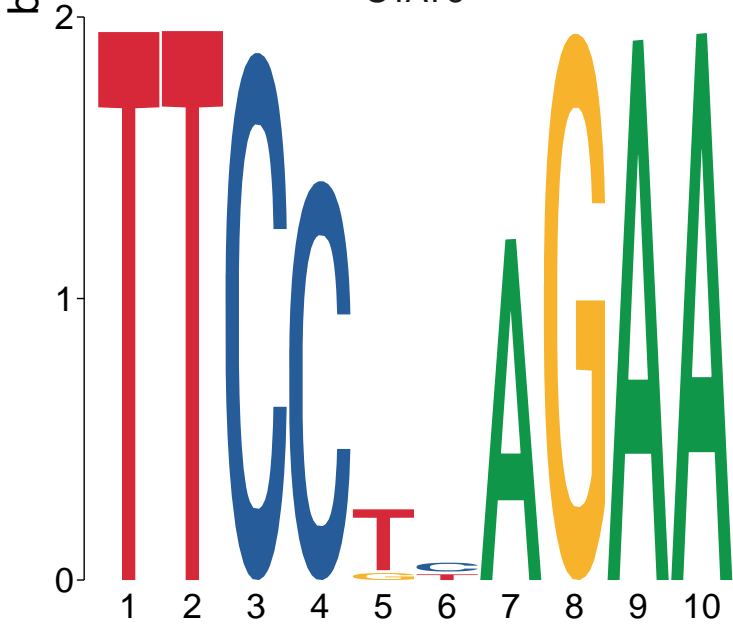
20-TAGTCTGAGC,BestGuess:Smad3



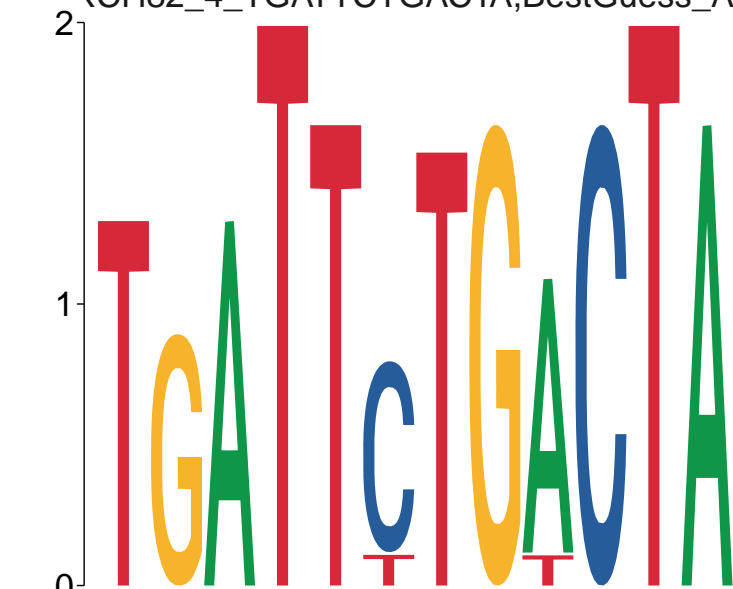
ARCH81_STAT6



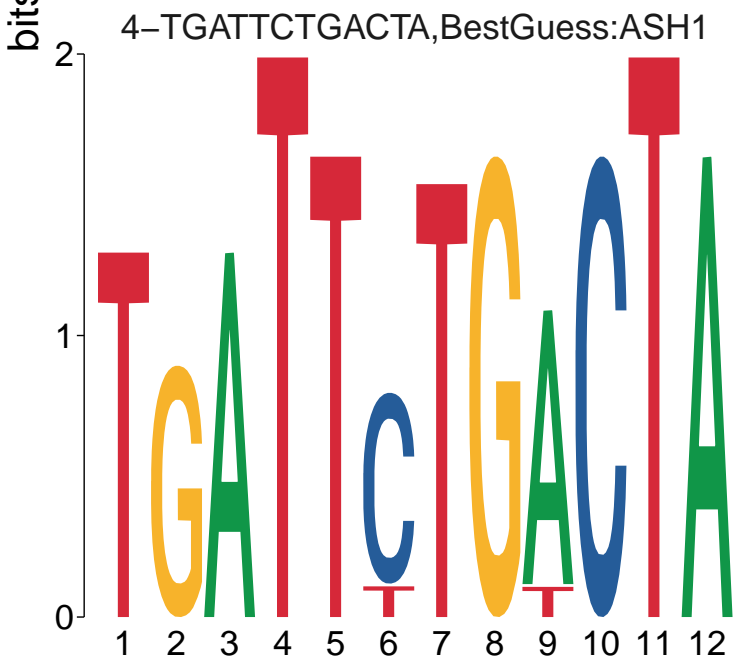
STAT6



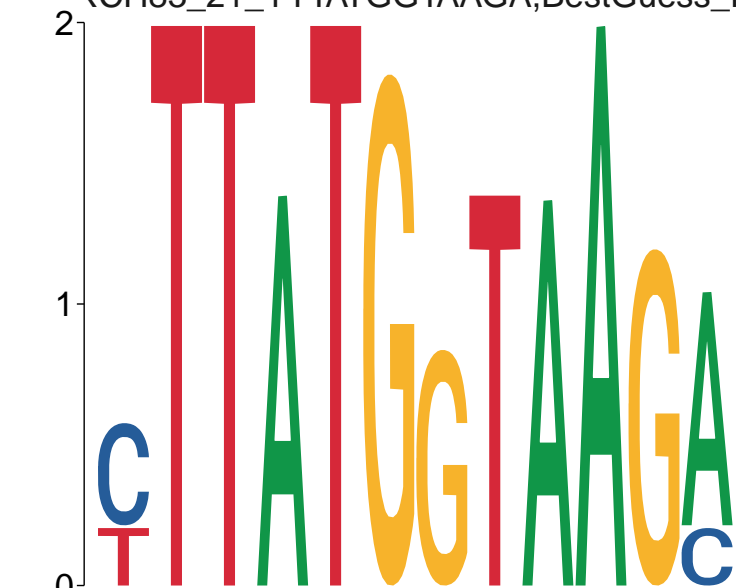
RCH82_4_TGATTCTGACTA,BestGuess_AS



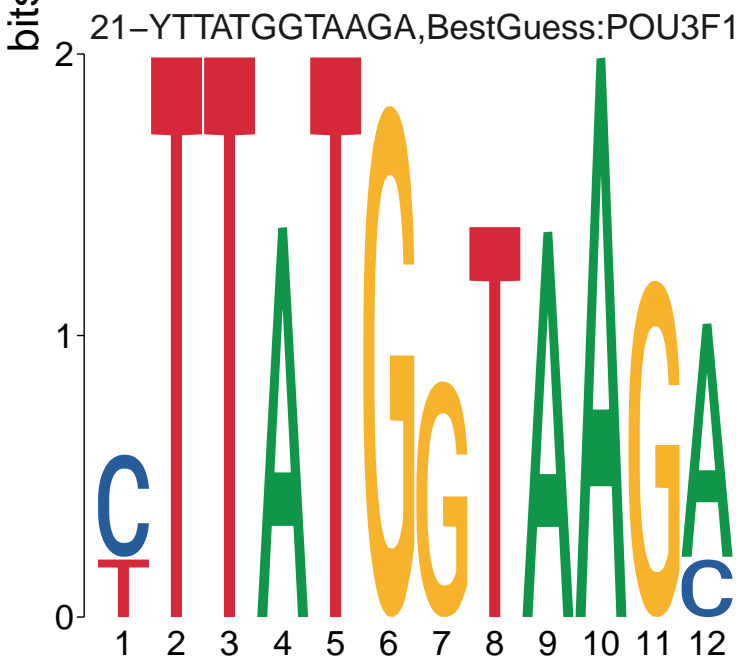
4-TGATTCTGACTA,BestGuess:ASH1



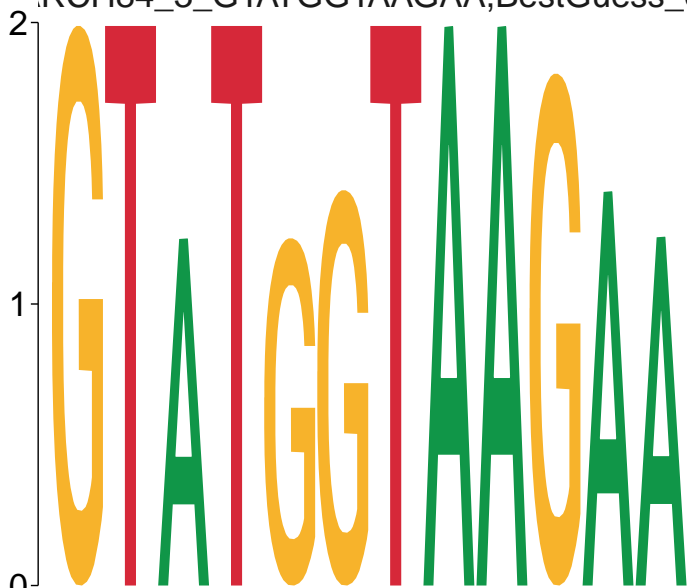
RCH83_21_YTTATGGTAAGA,BestGuess_F



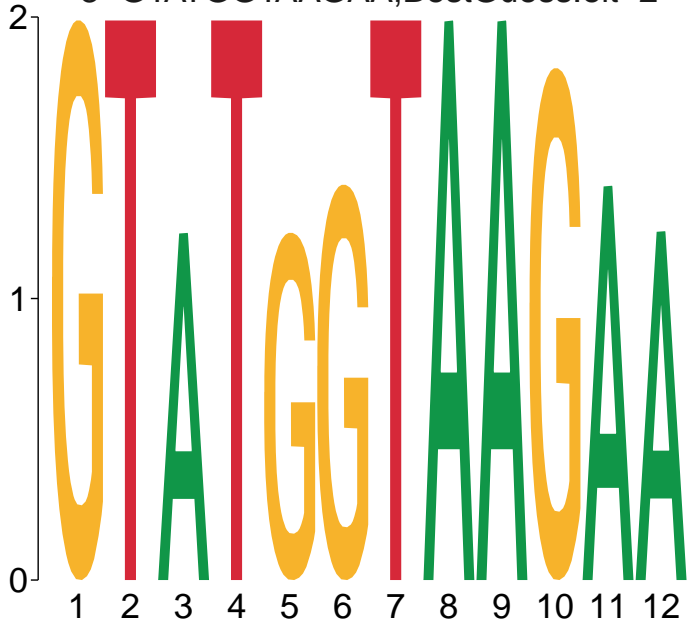
21-YTTATGGTAAGA,BestGuess:POU3F1



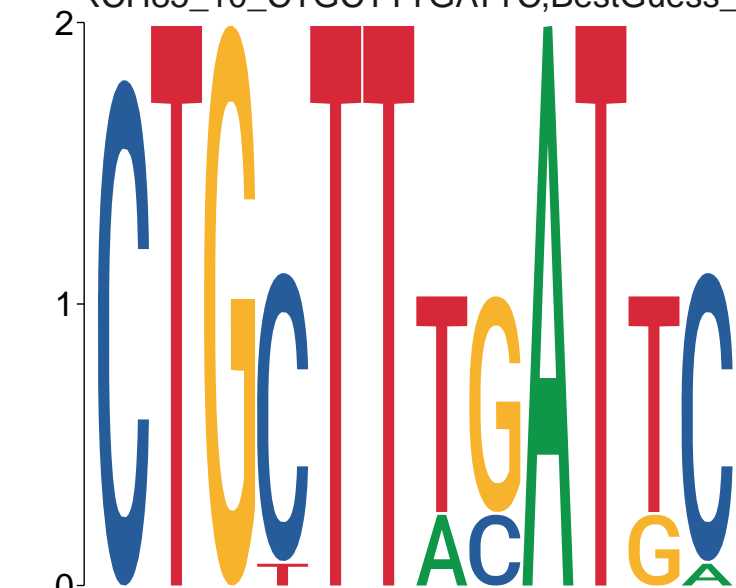
RCH84_3_GTATGGTAAGAA,BestGuess_e



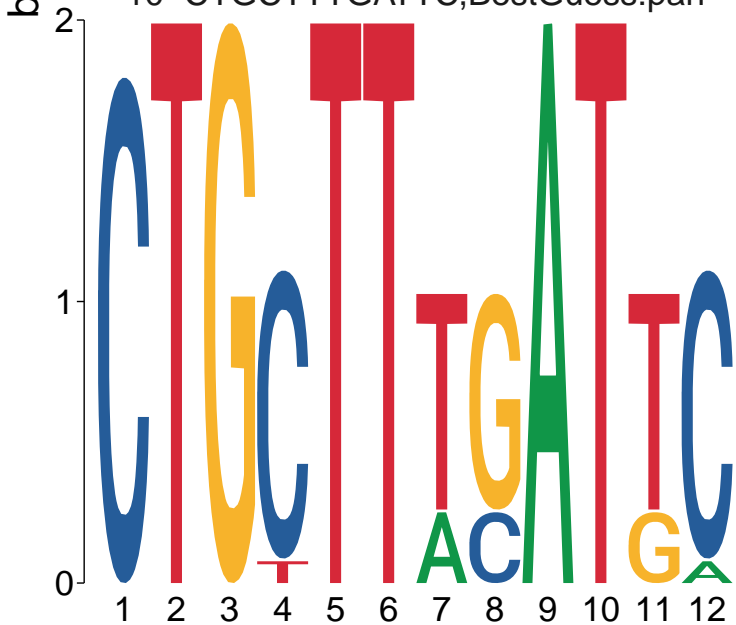
3-GTATGGTAAGAA,BestGuess:elt-2



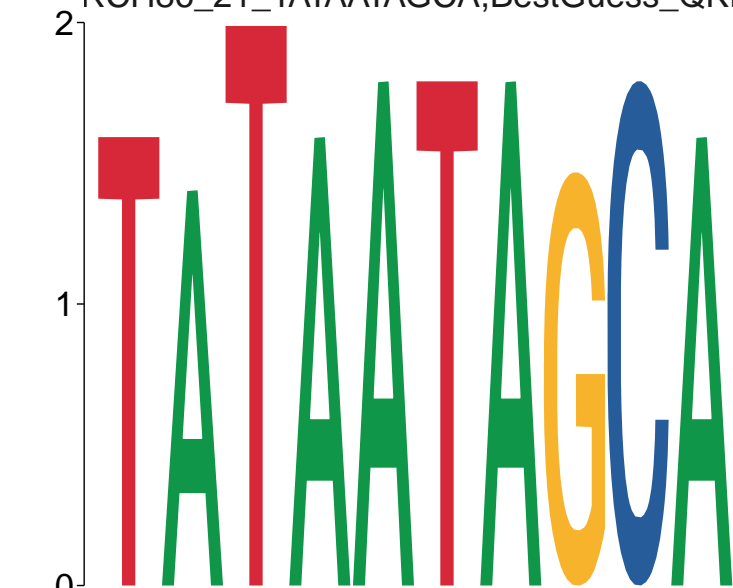
RCH85_10_CTGCTTTGATTC,BestGuess_1



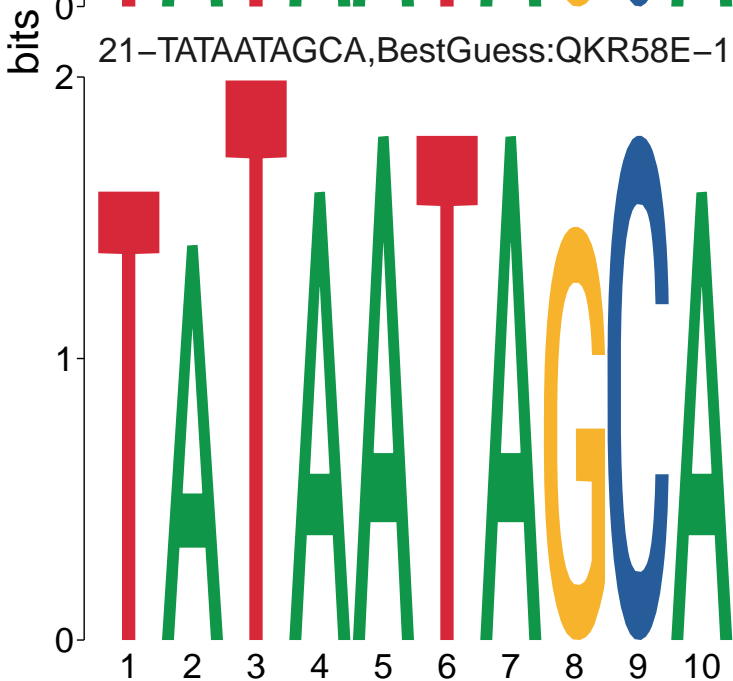
10-CTGCTTTGATTC,BestGuess:pan



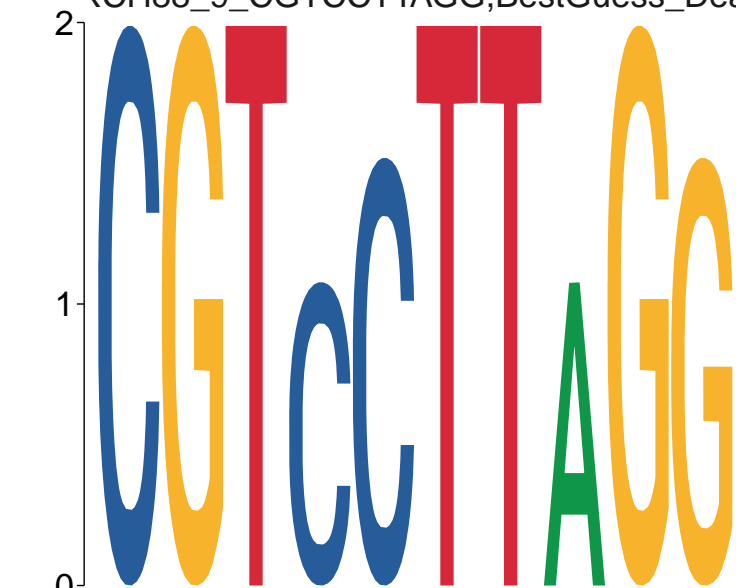
RCH86_21_TATAATAGCA,BestGuess_QKR



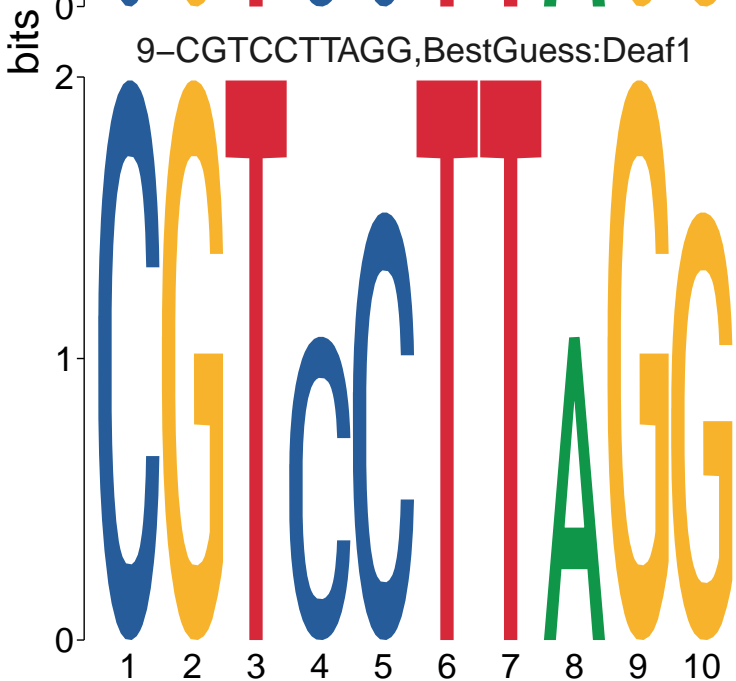
21-TATAATAGCA,BestGuess:QKR58E-1

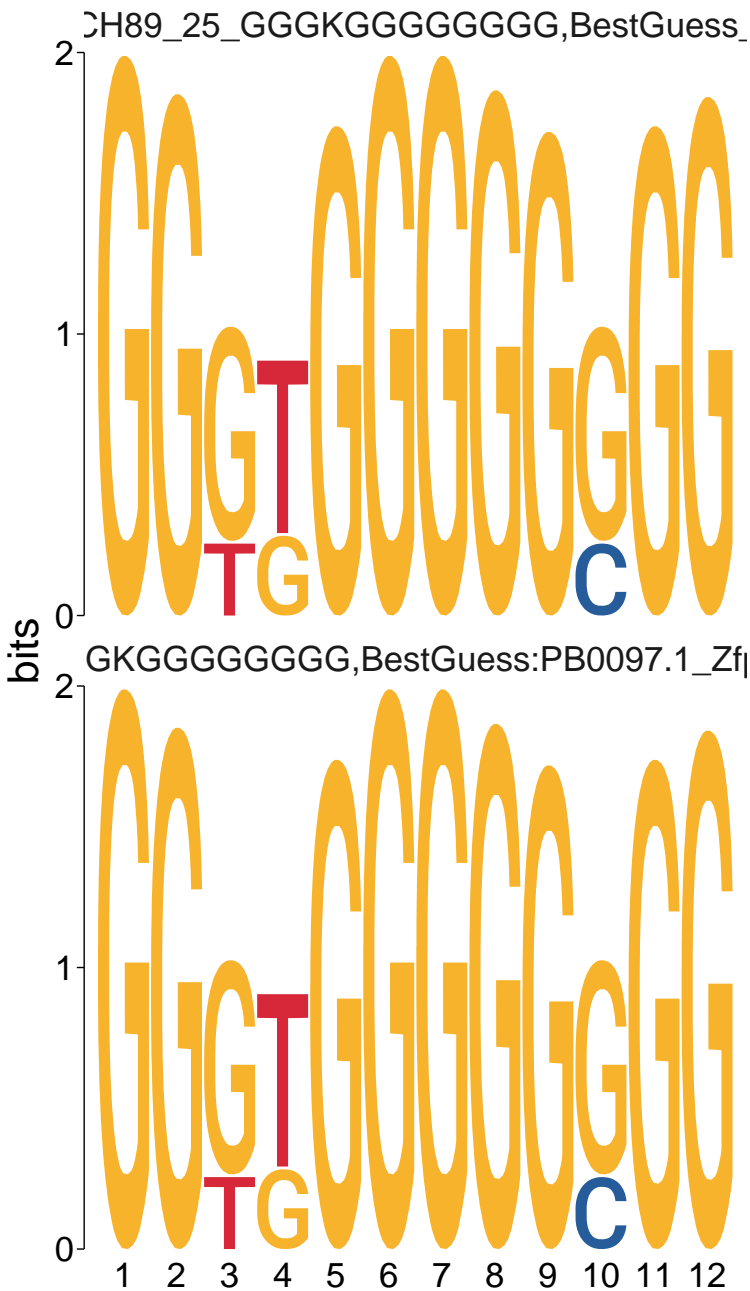


RCH88_9_CGTCCTTAGG,BestGuess_Deaf

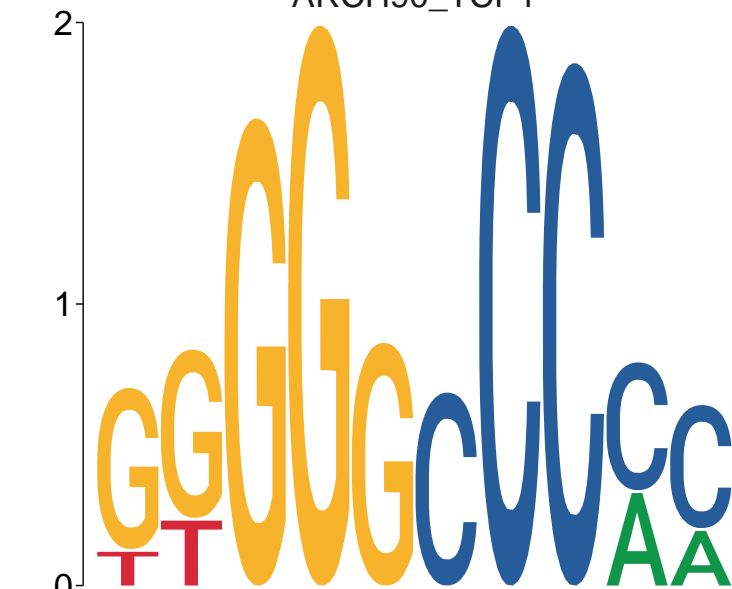


9-CGTCCTTAGG,BestGuess:Deaf1

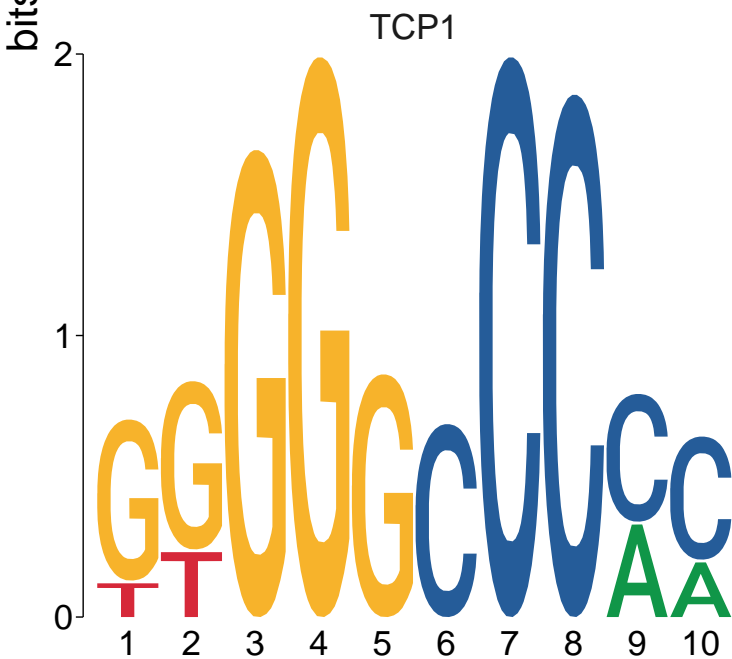




ARCH90_TCP1



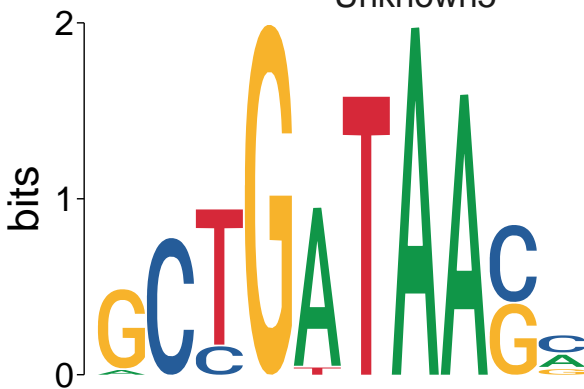
TCP1



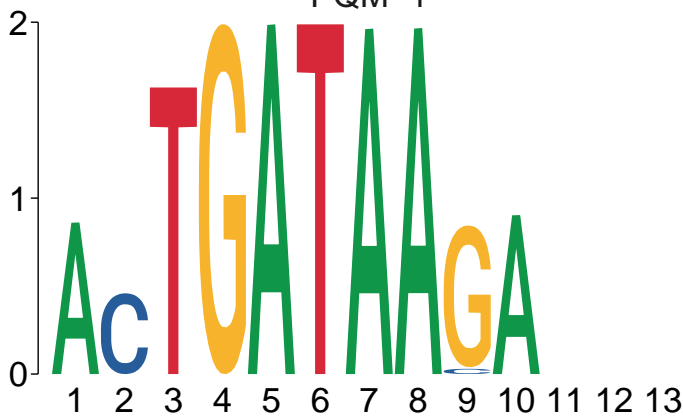
ARCH91_PQM_1_Unknown5



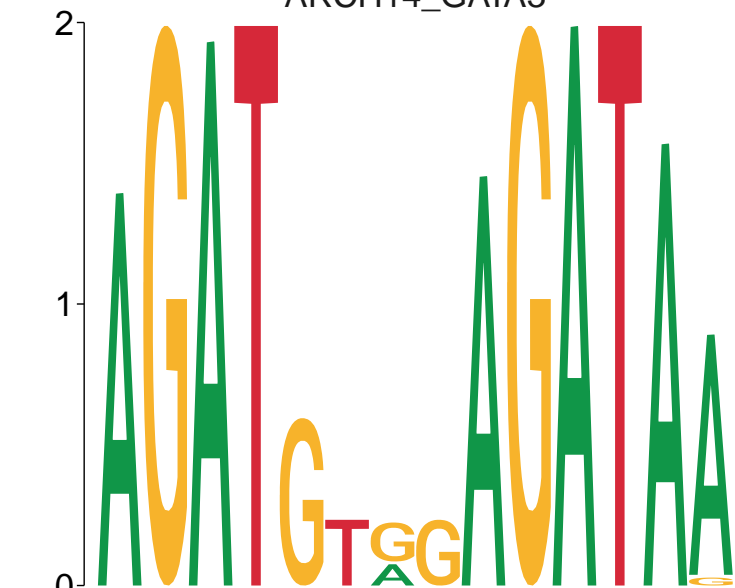
Unknown5



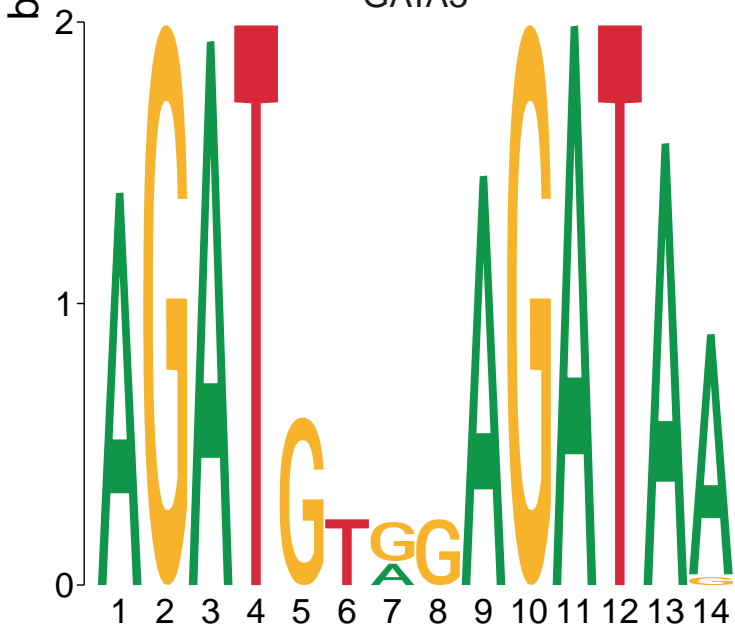
PQM-1



ARCH14_GATA3



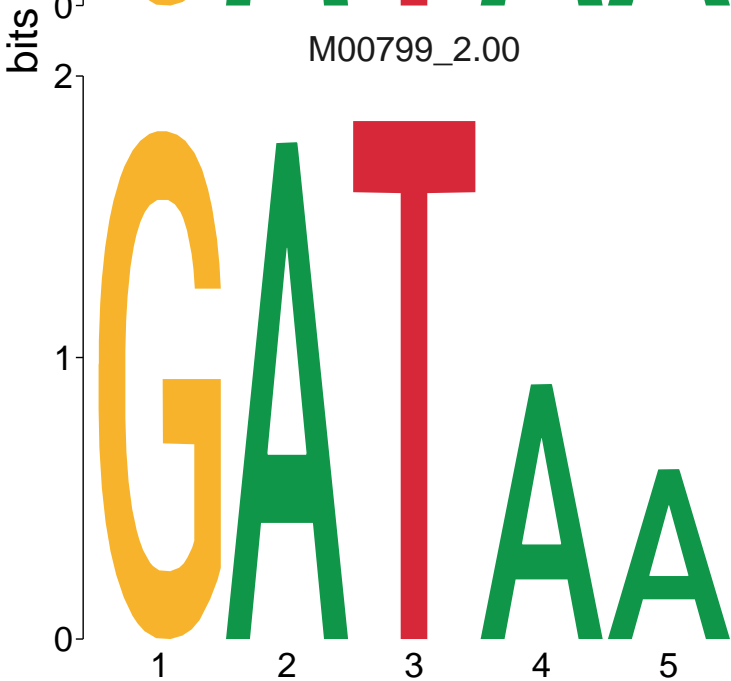
GATA3



ARCH93_GATA



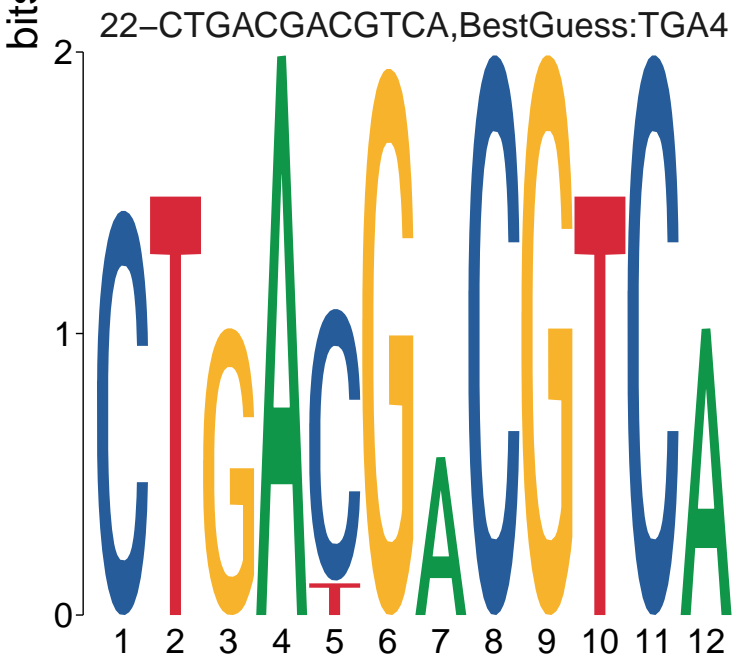
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CH96_22_CTGACGACGTCA,BestGuess_



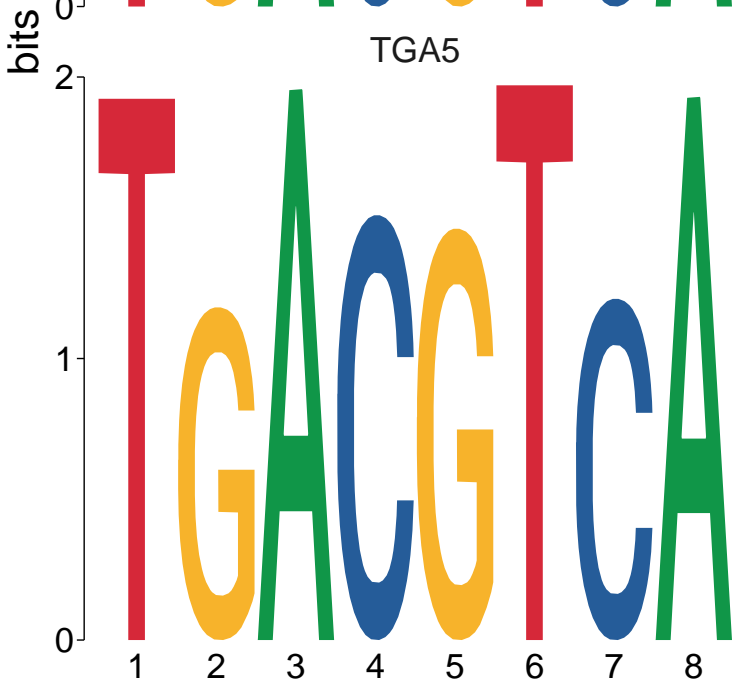
22-CTGACGACGTCA,BestGuess:TGA4



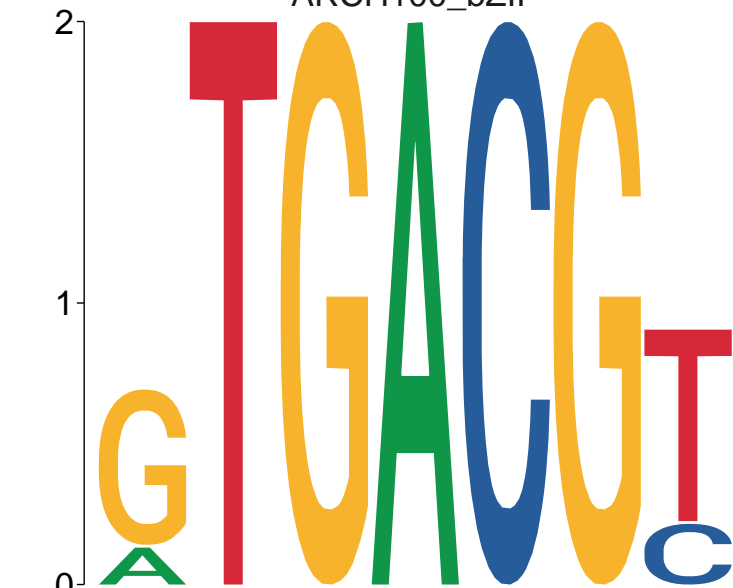
ARCH99_TGA5



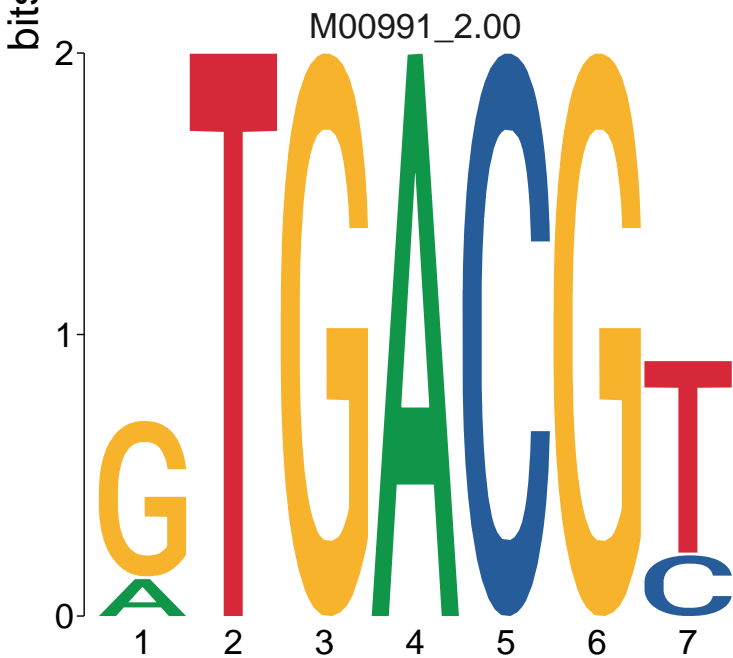
TGA5



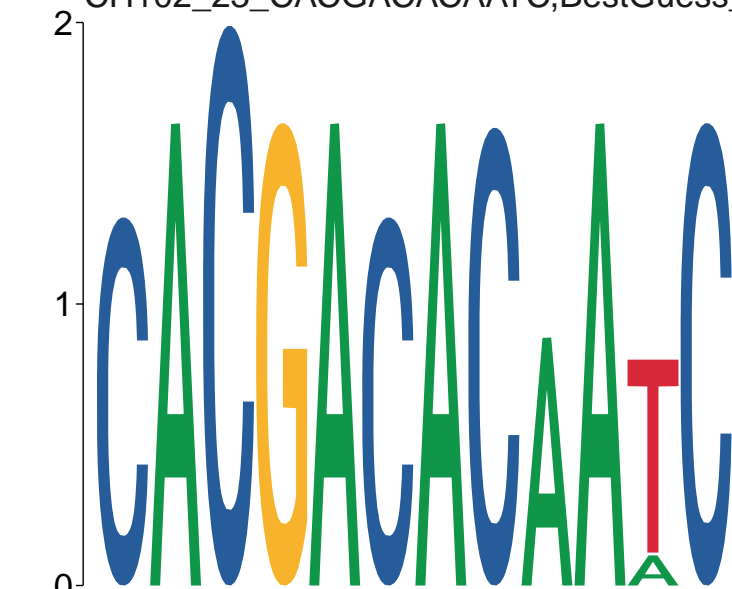
ARCH100_bZIP



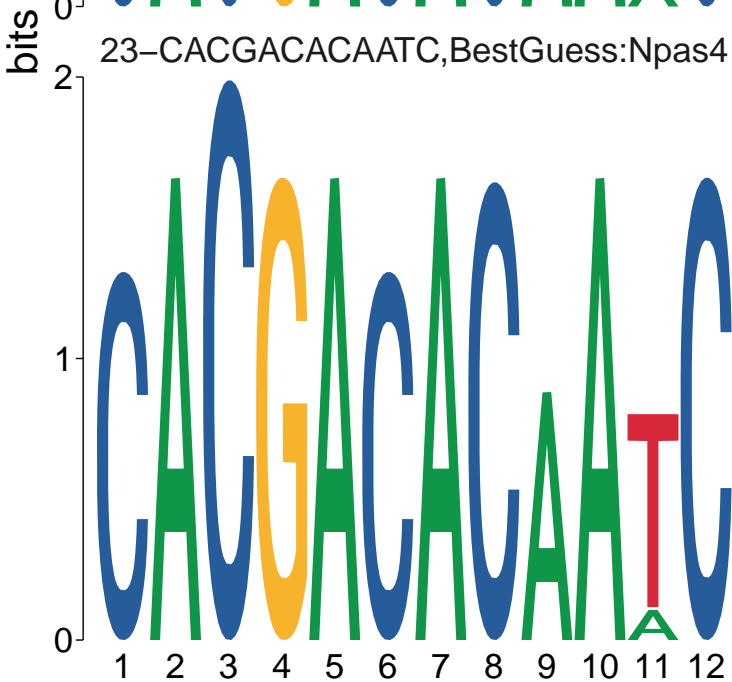
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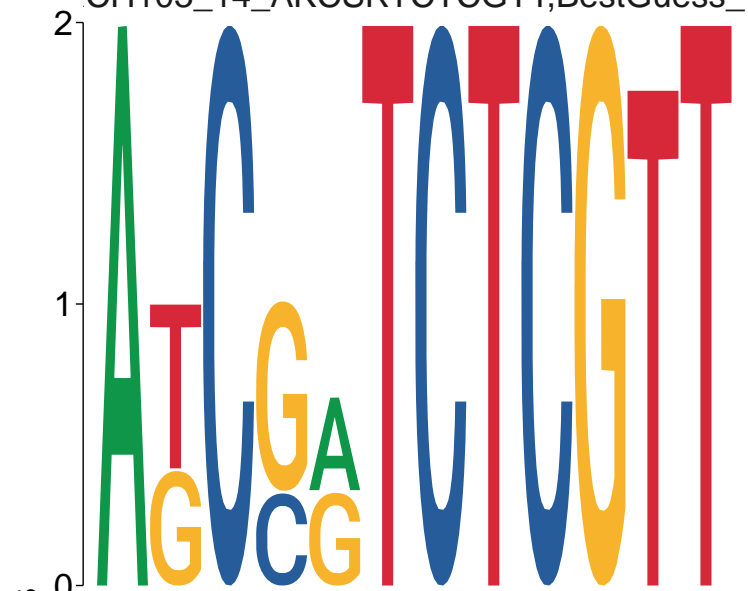
CH102_23_CACGACACAATC,BestGuess_



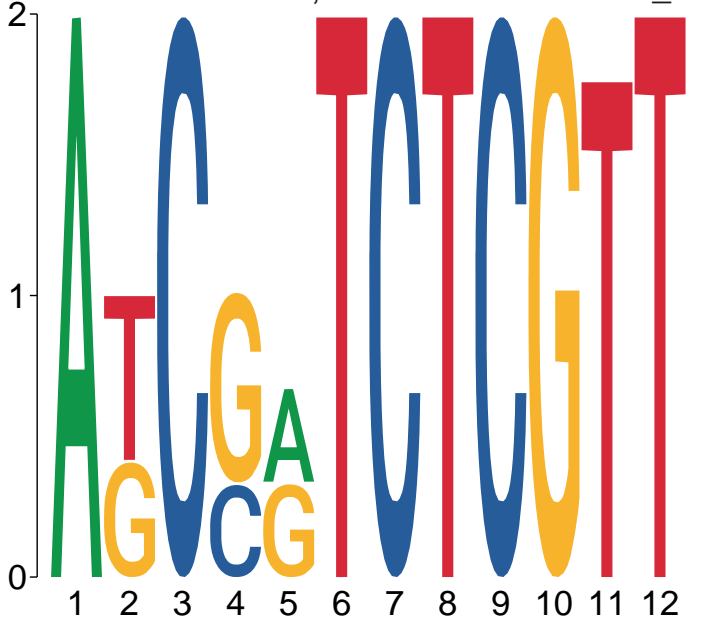
23-CACGACACAATC,BestGuess:Npas4



CH103_14_AKCSRTCTCGTT,BestGuess_



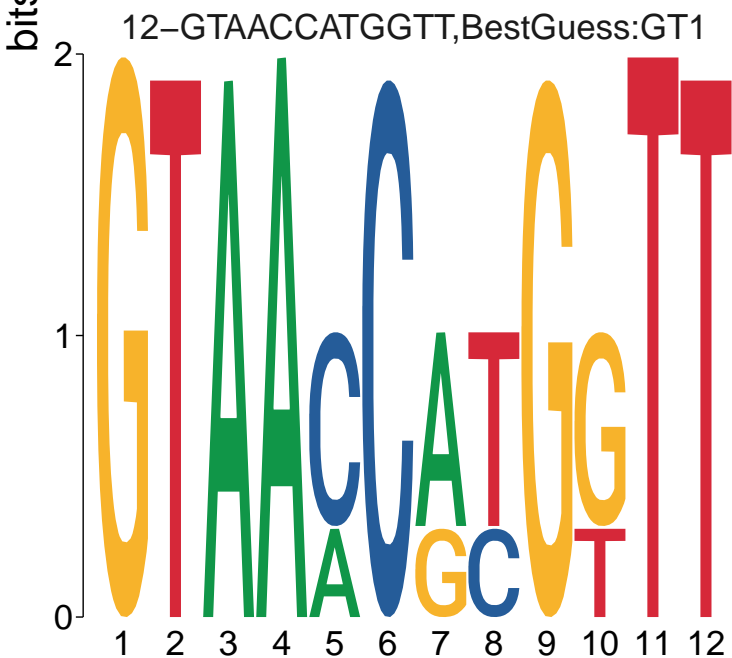
AKCSRTCTCGTT,BestGuess:PB0140.1_Irf



CH104_12_GTAACCATGGTT,BestGuess_1

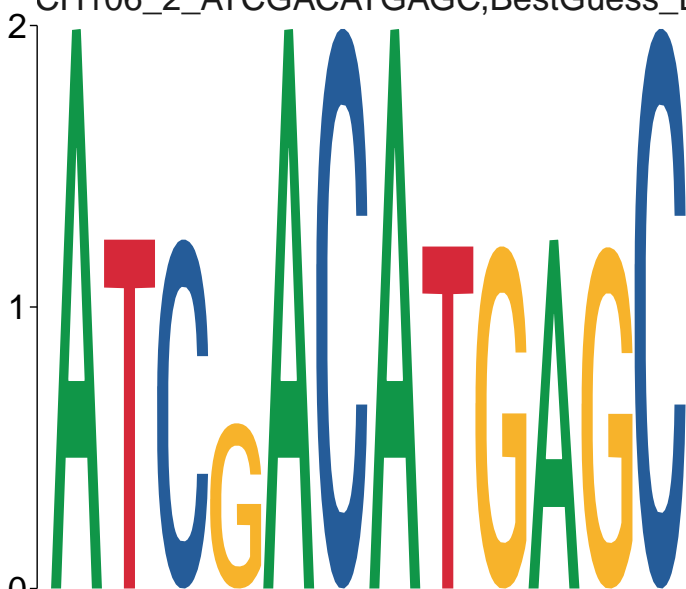


12-GTAACCATGGTT,BestGuess:GT1

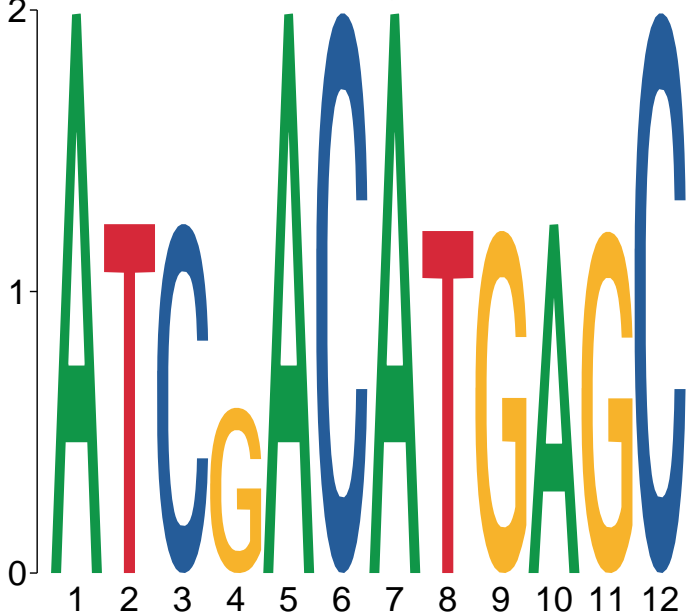


CH106_2_ATCGACATGAGC,BestGuess_D

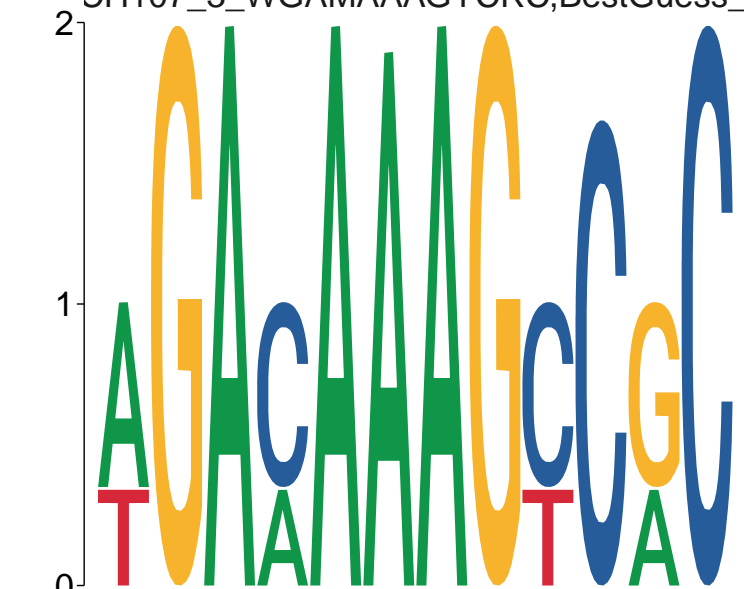
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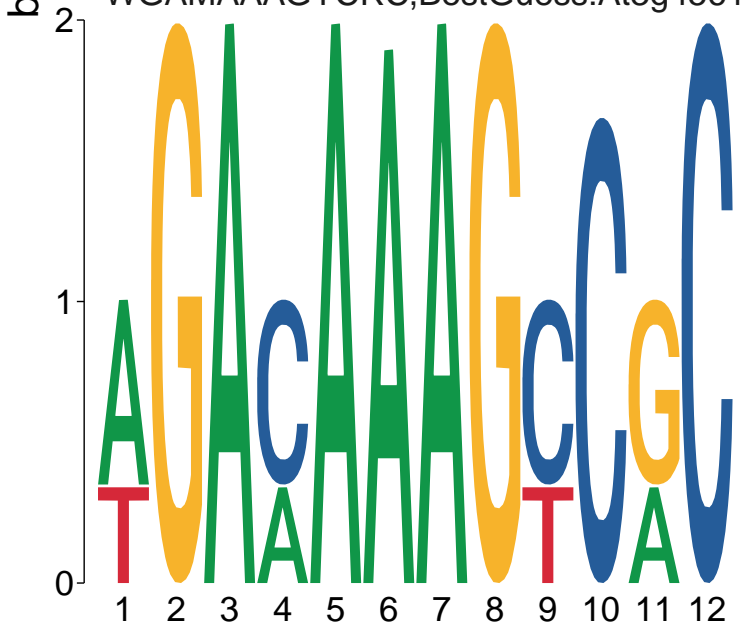
2-ATCGACATGAGC,BestGuess:DDF2



CH107_3_WGAMAAAGYCRC,BestGuess_



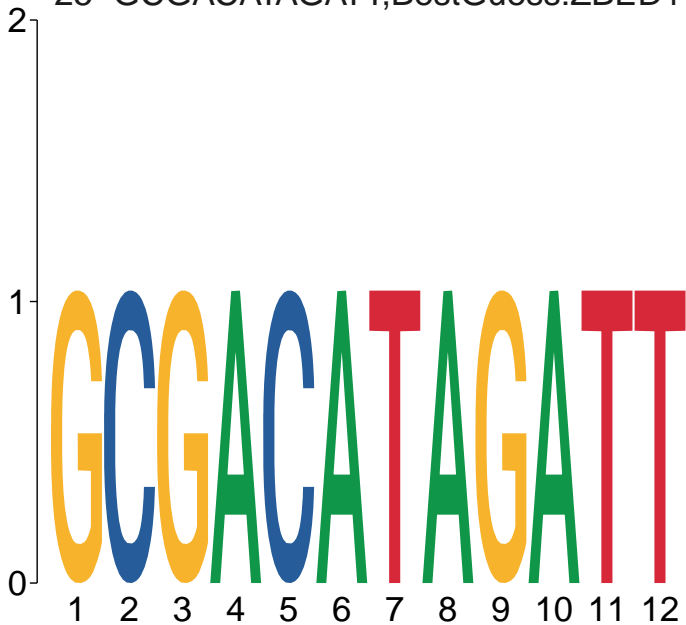
-WGAMAAAGYCRC,BestGuess:At3g4561



CH108_25_GCGACATAGATT,BestGuess_



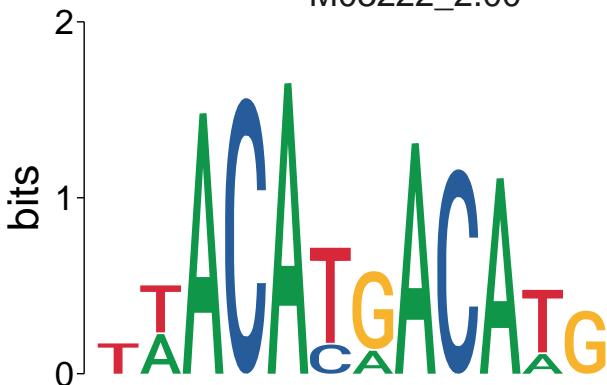
25-GCGACATAGATT,BestGuess:ZBED1



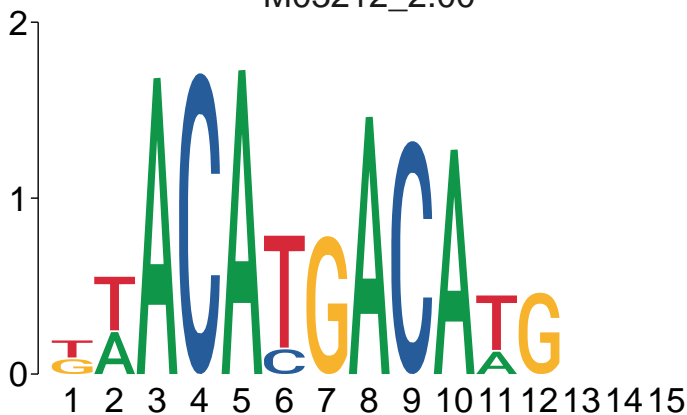
ARCH111_Homeodomains



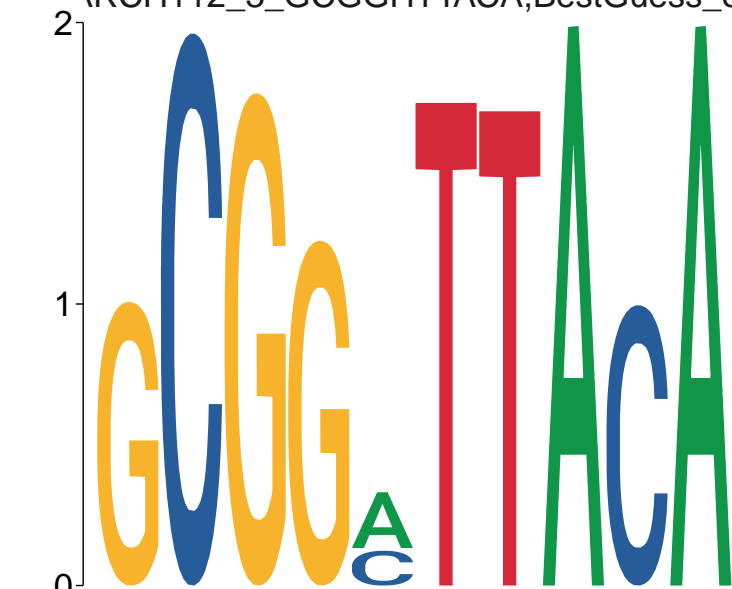
M03222_2.00



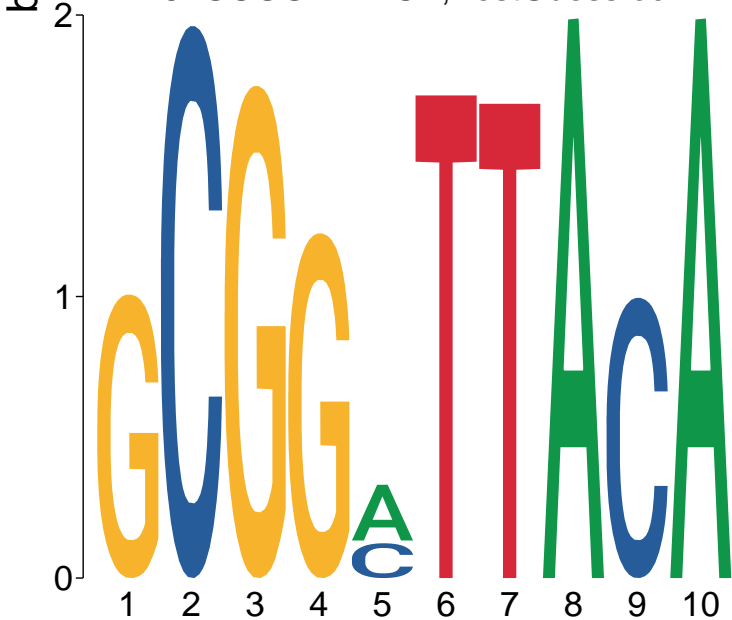
M03212_2.00



ARCH112_3_GCGGHTTACA,BestGuess_oc



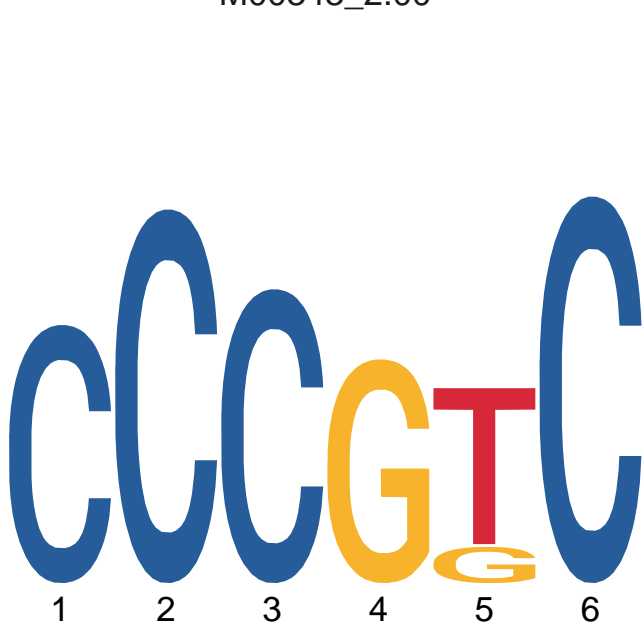
3-GCGGHTTACA,BestGuess:oc



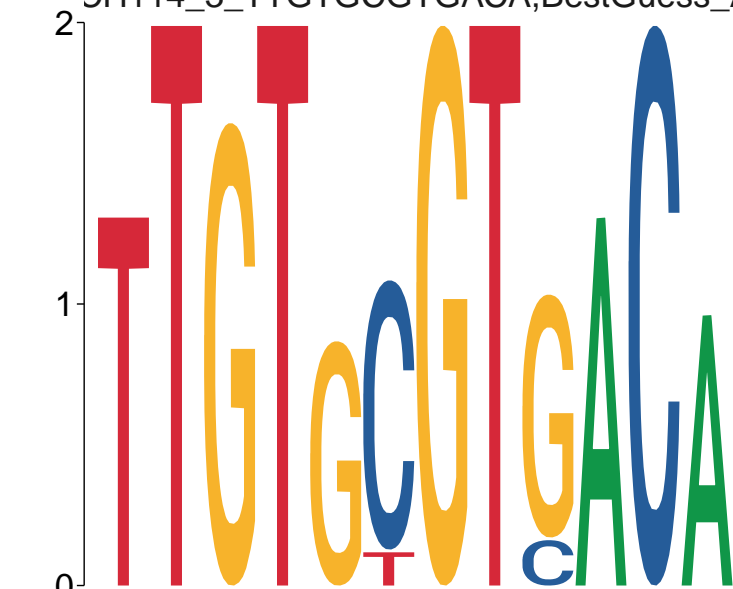
RCH113_Nvec_v1g168908_Nvec_v1g2395:



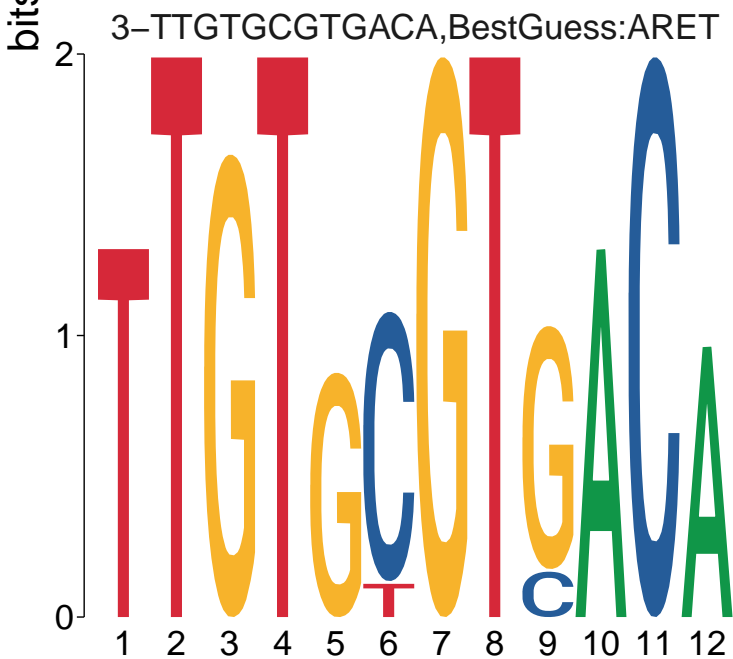
M00343_2.00



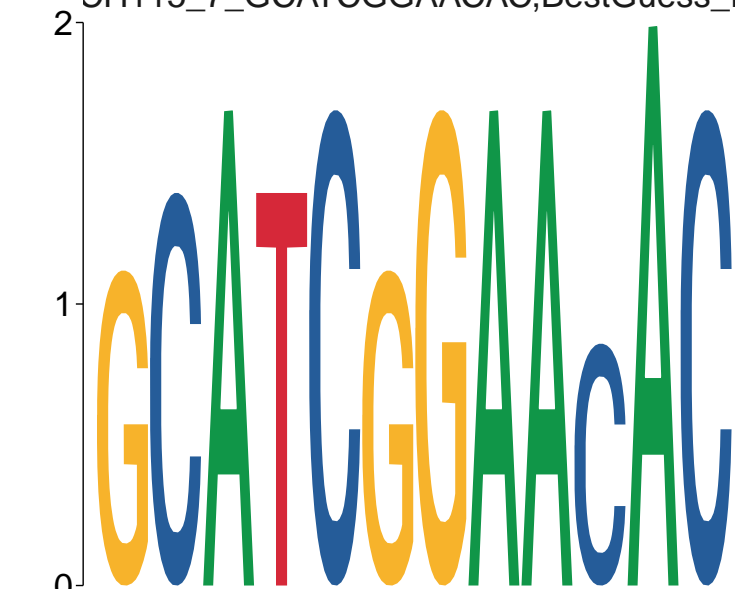
CH114_3_TTGTGCGTGACA,BestGuess_A



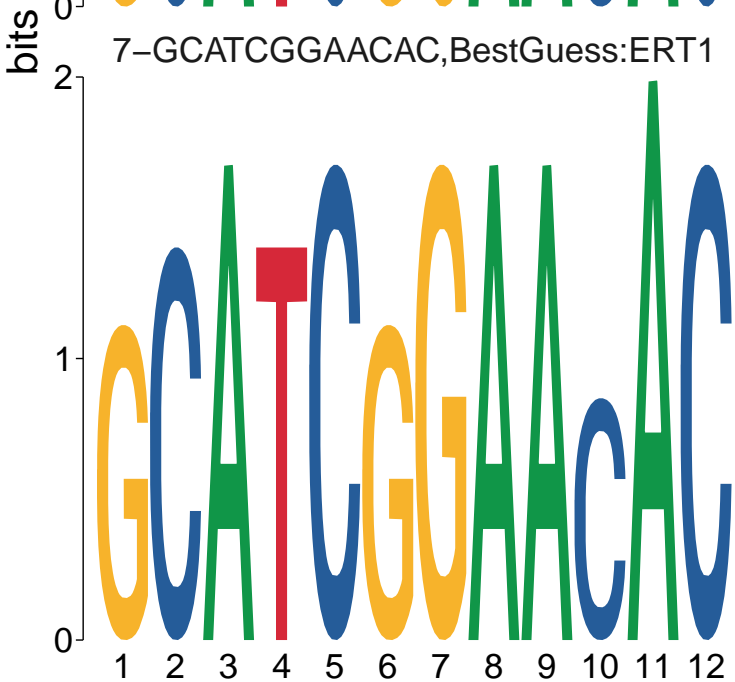
3-TTGTGCGTGACA,BestGuess:ARET



CH115_7_GCATCGGAACAC,BestGuess_E



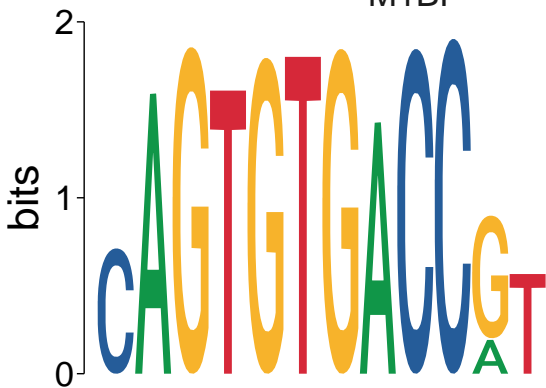
7-GCATCGGAACAC,BestGuess:ERT1



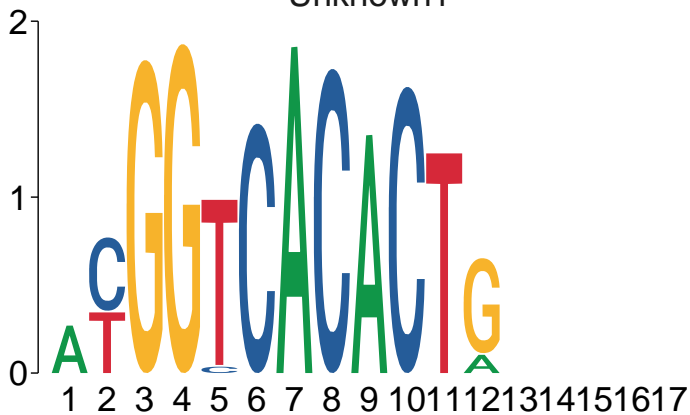
ARCH116_Unknown1_M1BP



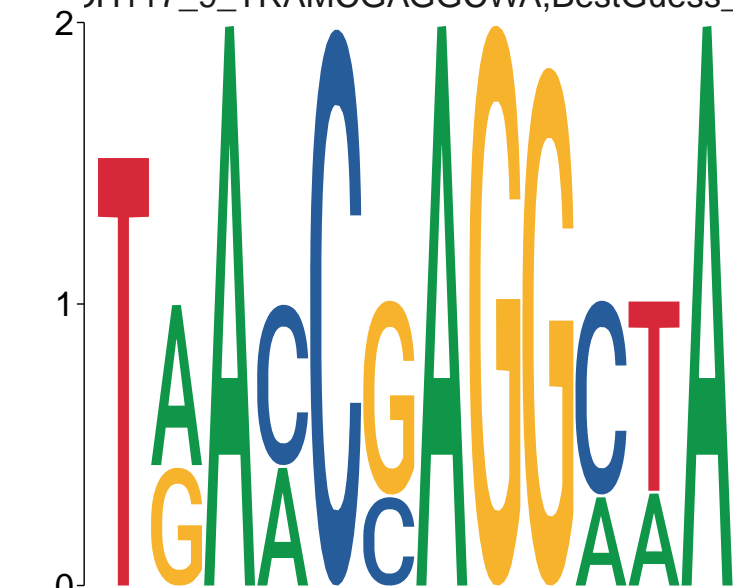
M1BP



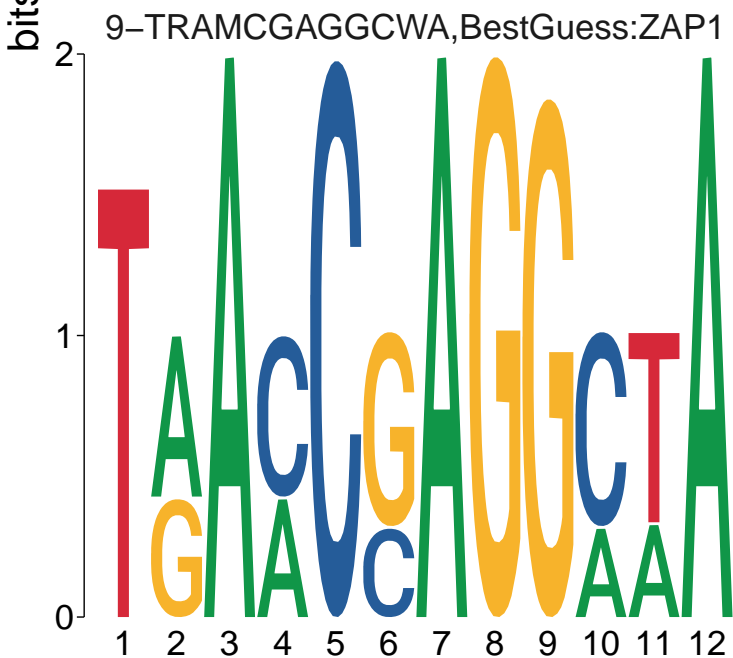
Unknown1



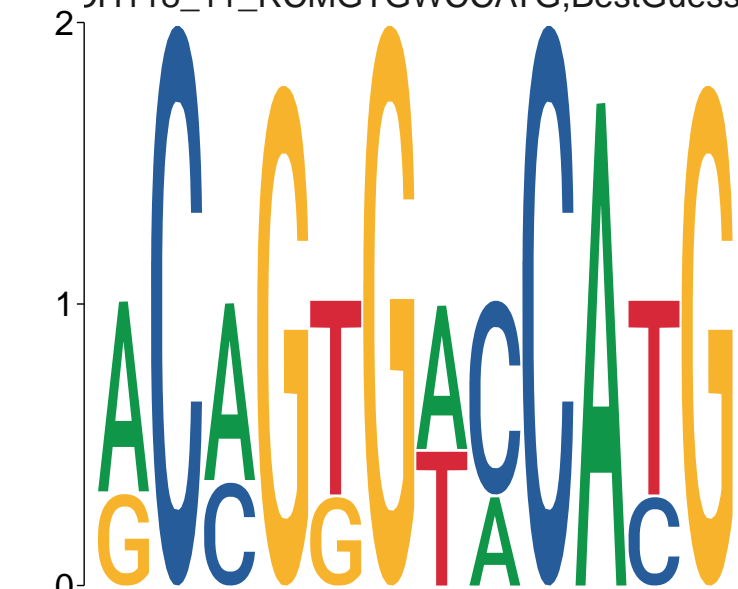
CH117_9-TRAMCGAGGCWA,BestGuess_ZAP1



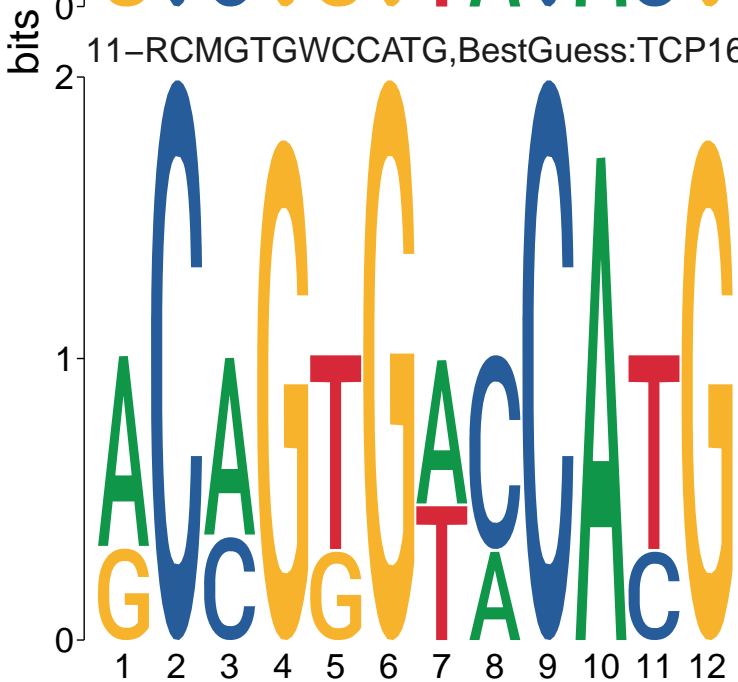
9-TRAMCGAGGCWA,BestGuess:ZAP1



CH118_11_RCMGTGWCCATG,BestGuess_



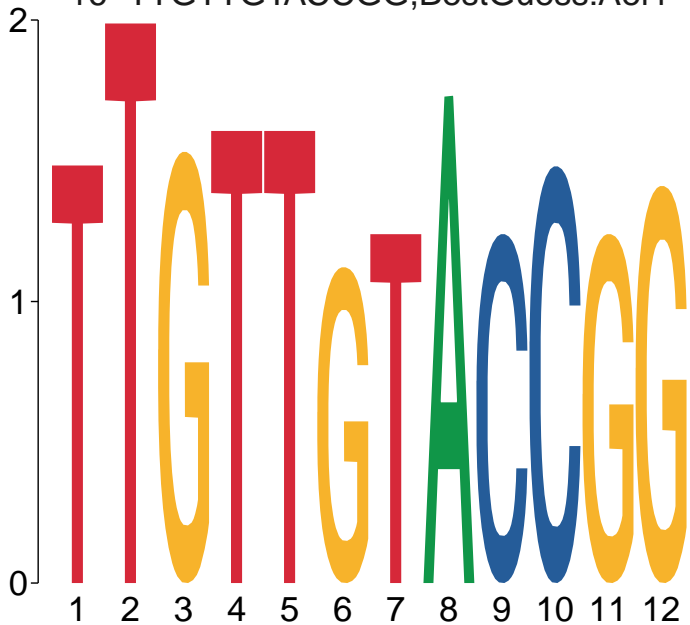
11-RCMGTGWCCATG,BestGuess:TCP16



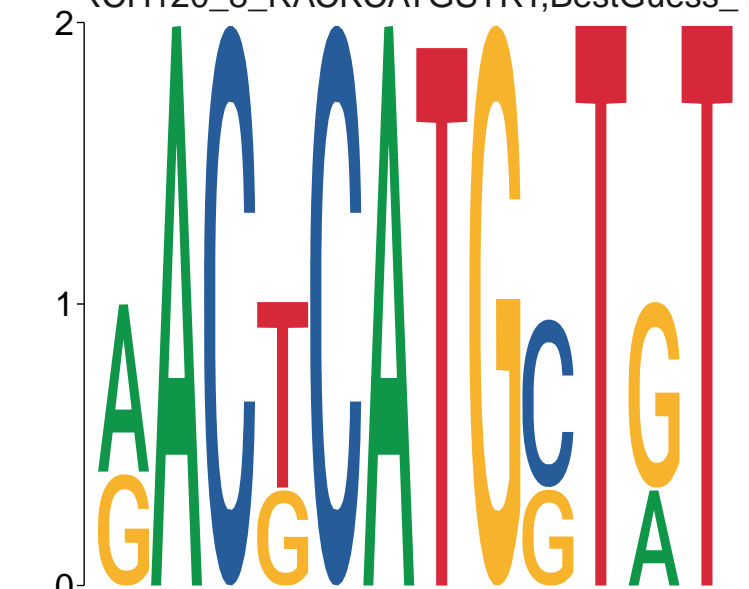
CH119_16_TTGTTGTACCGG,BestGuess_



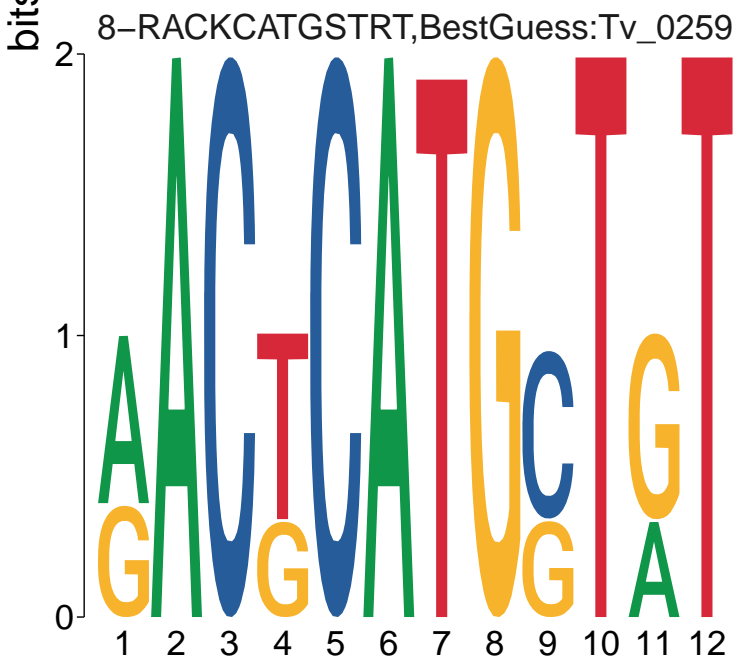
16-TTGTTGTACCGG,BestGuess:Aef1



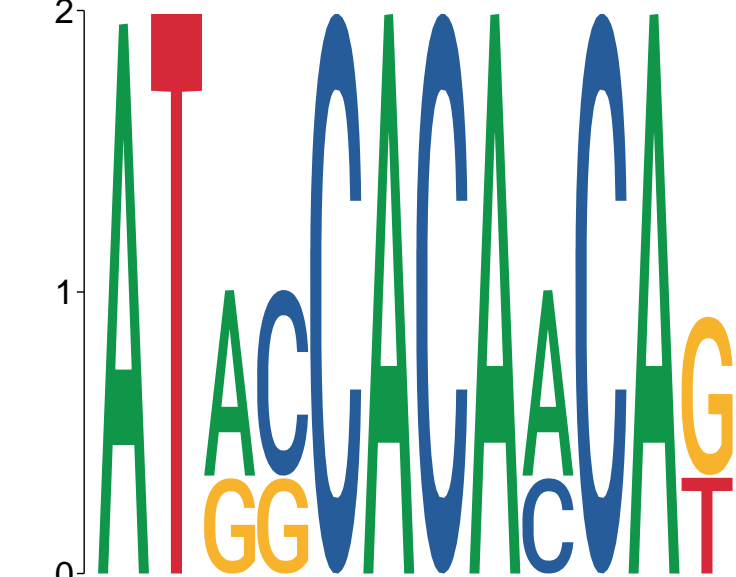
RCH120_8_RACKCATGSTRT,BestGuess_7



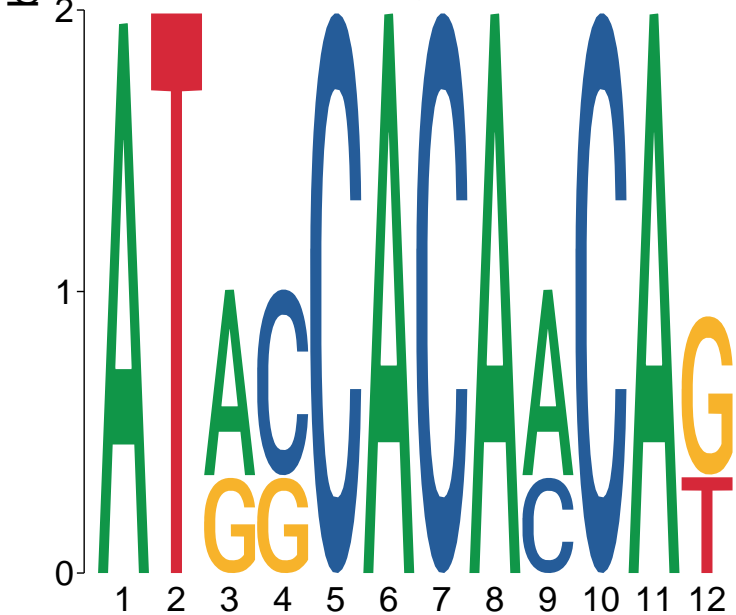
8-RACKCATGSTRT,BestGuess:Tv_0259



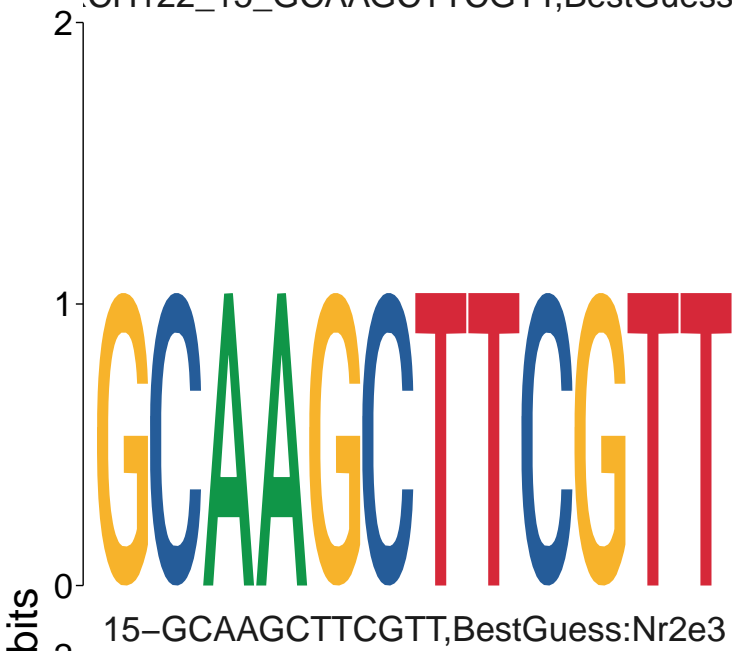
CH121_1_ATRSCACAMCAK,BestGuess_U



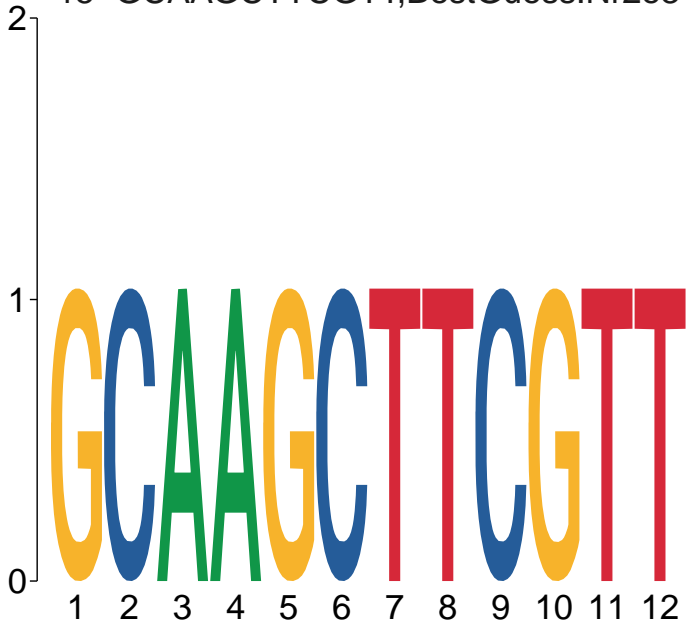
1-ATRSCACAMCAK,BestGuess:UNC-75



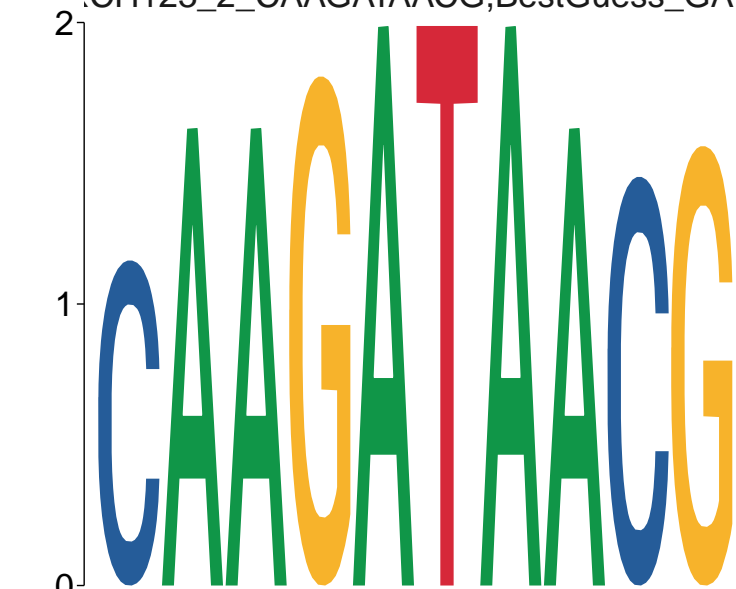
CH122_15_GCAAGCTTCGTT,BestGuess_



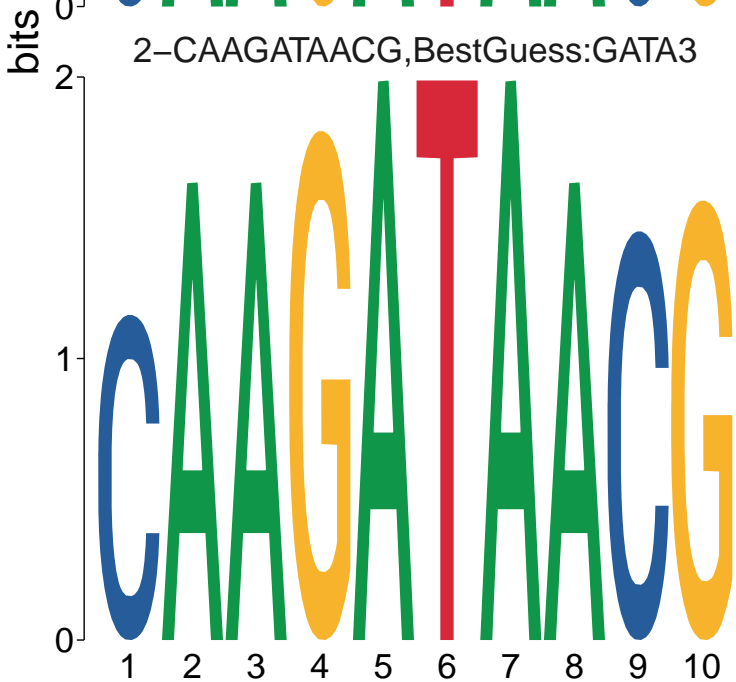
15-GCAAGCTTCGTT,BestGuess:Nr2e3



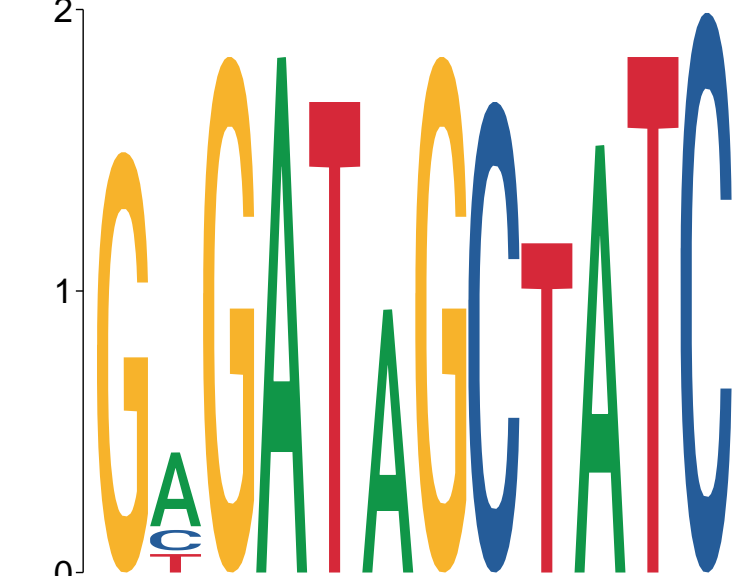
CH123_2_CAAGATAACG,BestGuess_GAT



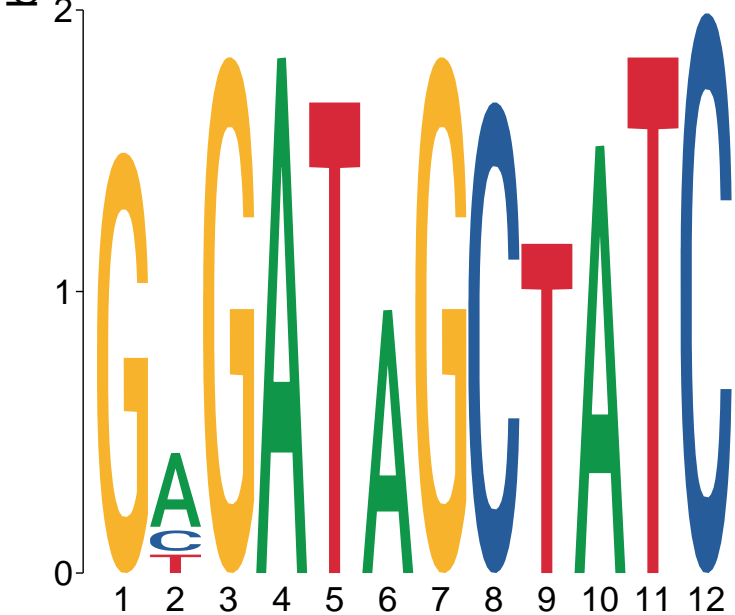
2-CAAGATAACG,BestGuess:GATA3



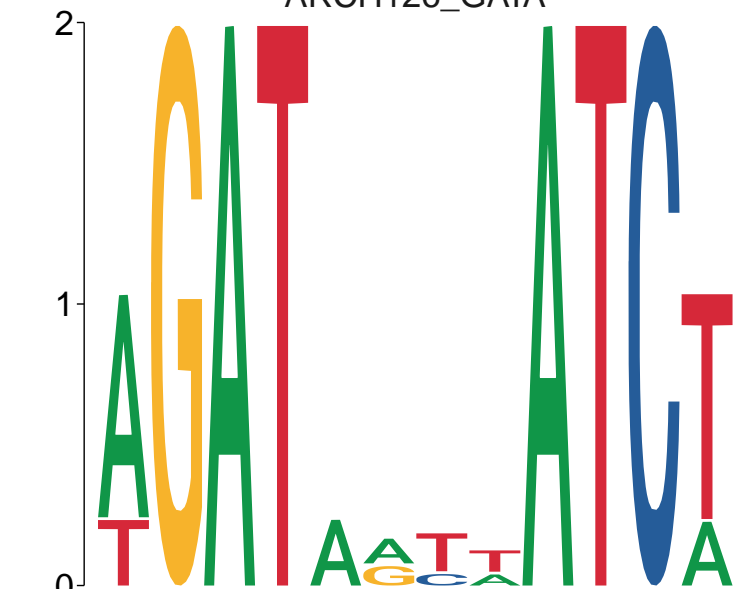
CH125_6_GHGATAGCTATC,BestGuess_G



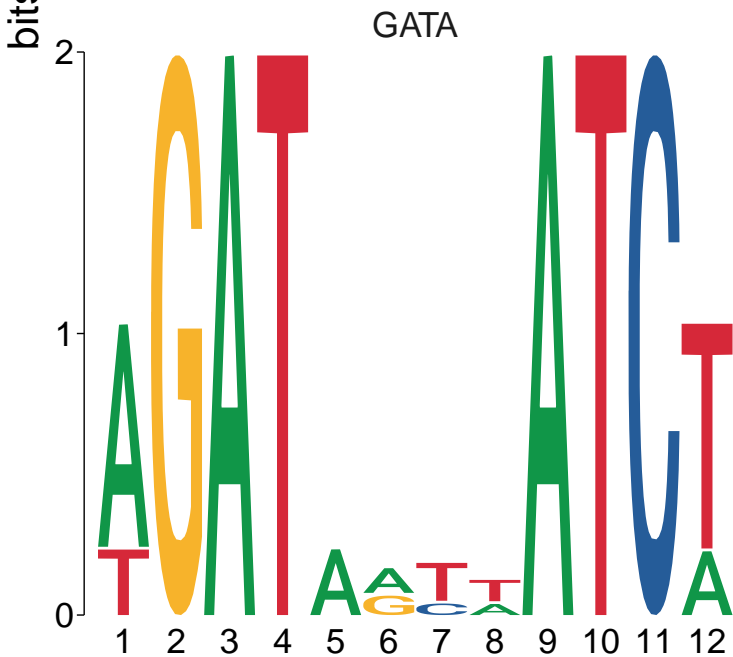
6-GHGATAGCTATC,BestGuess:GATA



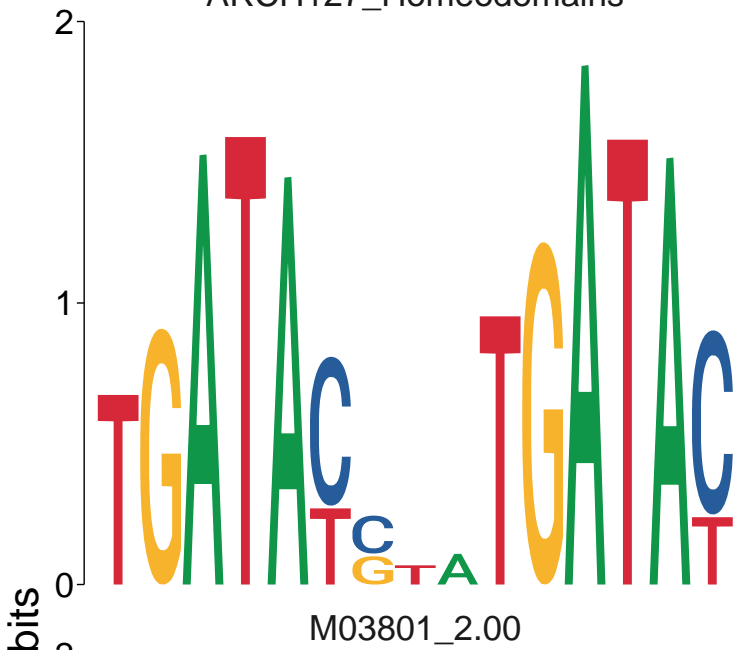
ARCH126_GATA



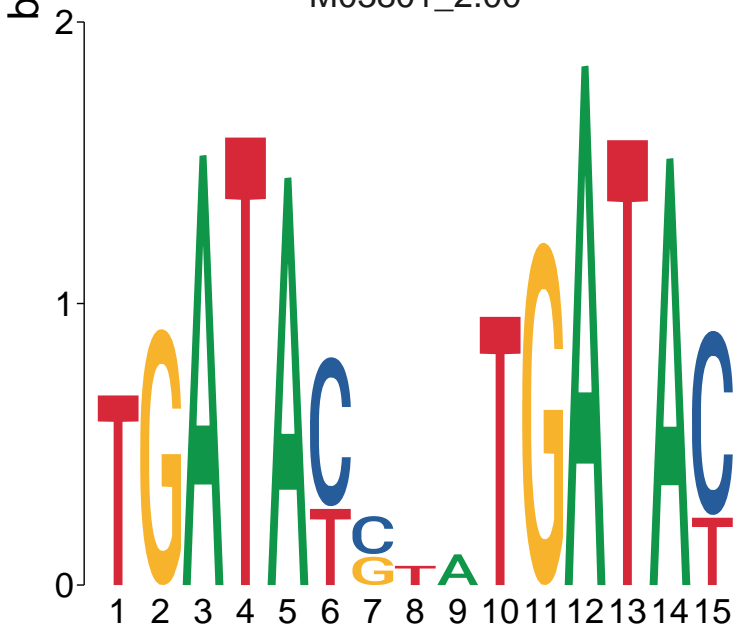
GATA



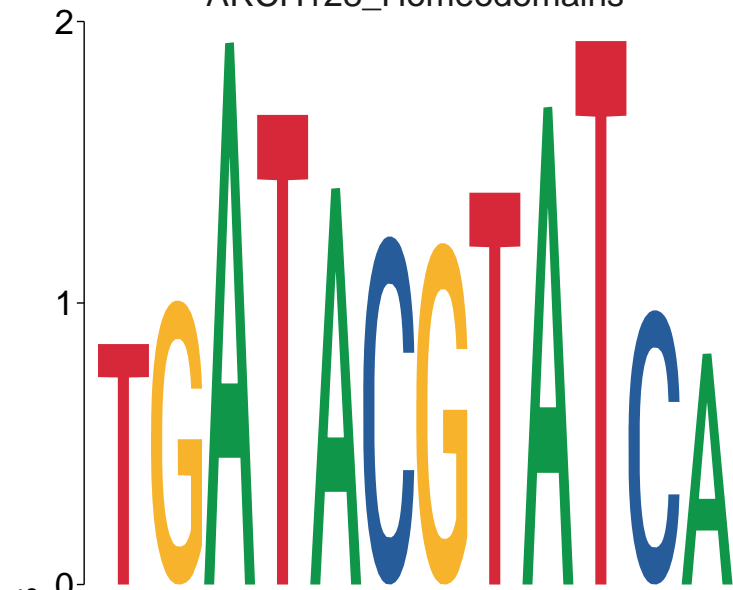
ARCH127_Homeodomains



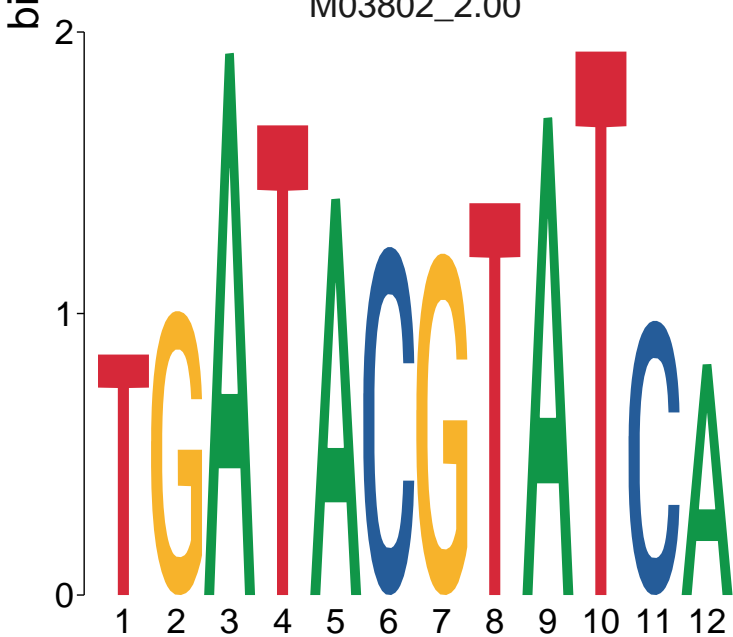
M03801_2.00



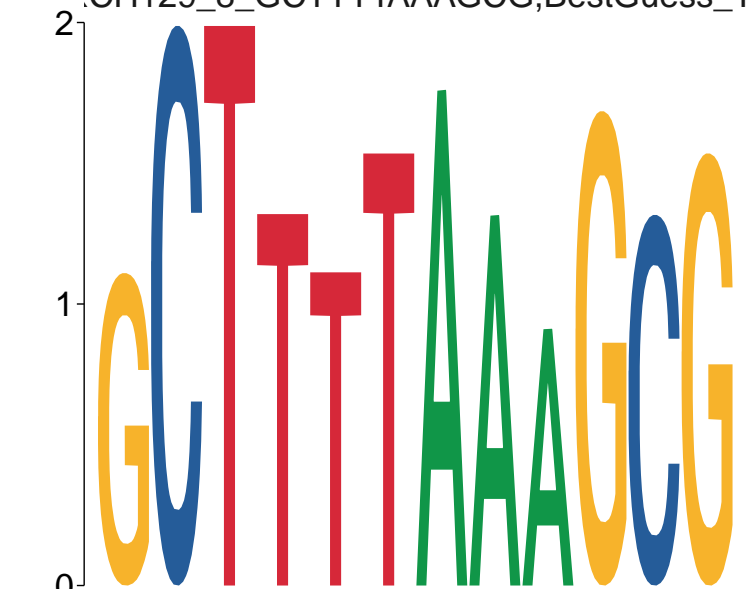
ARCH128_Homeodomains



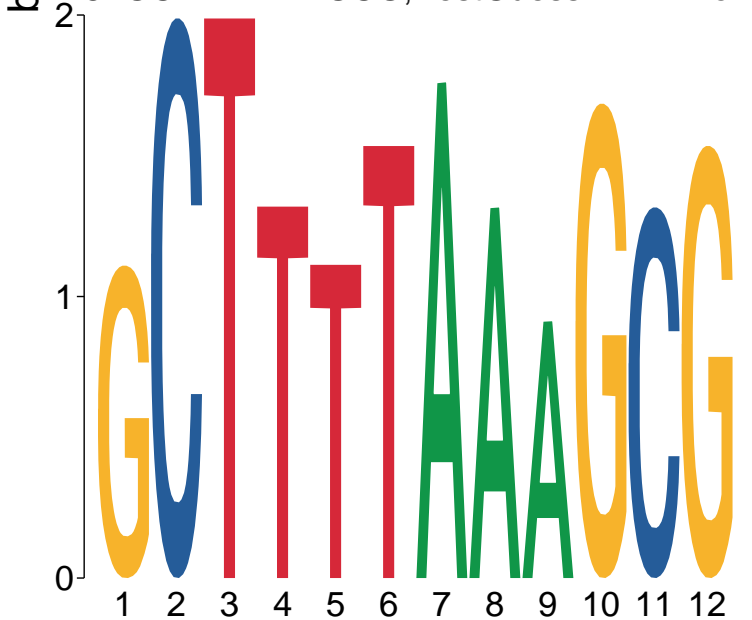
M03802_2.00



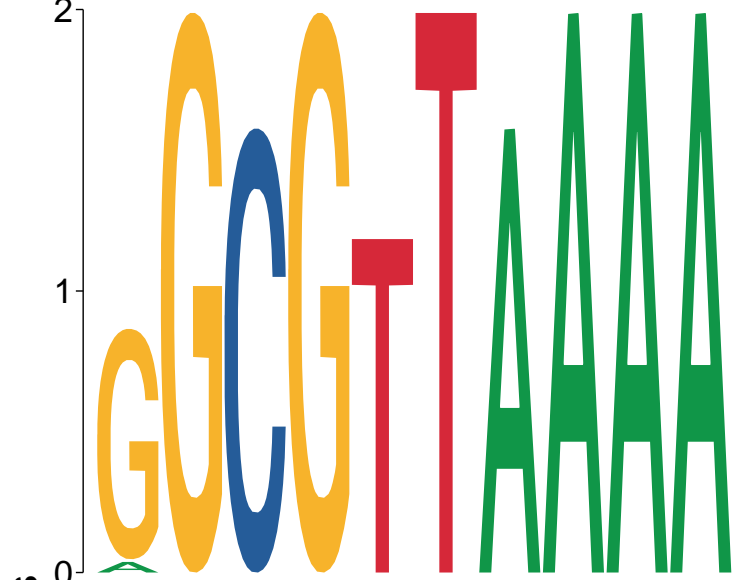
CH129_8_GCTTTTAAAGCG,BestGuess_T



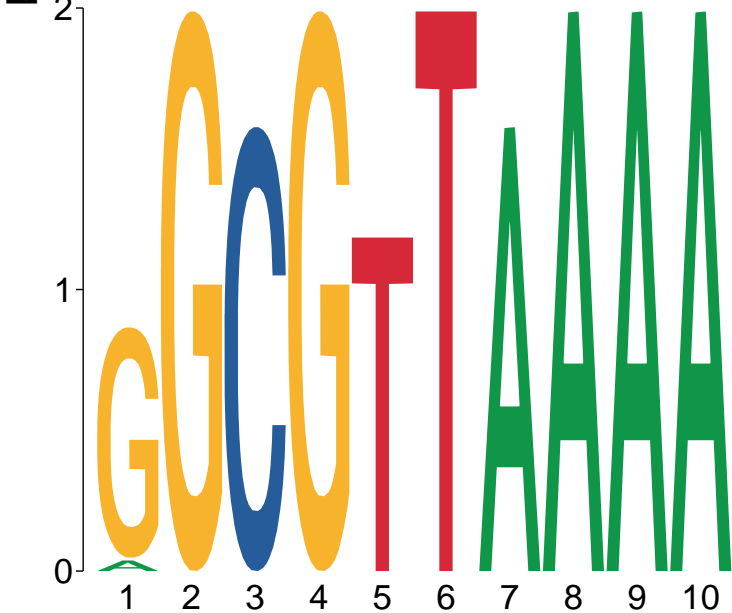
8-GCTTTTAAAGCG,BestGuess:TATA-Box



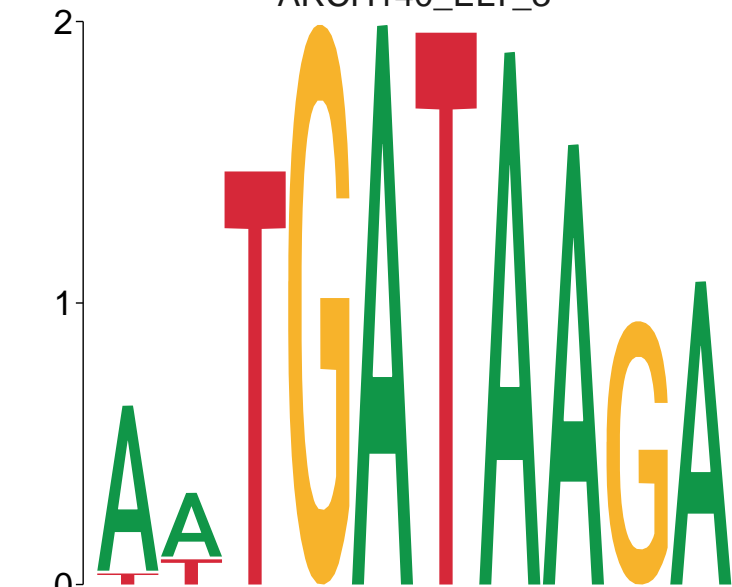
5-CH130_5_GGCGTTAAAA,BestGuess_DE



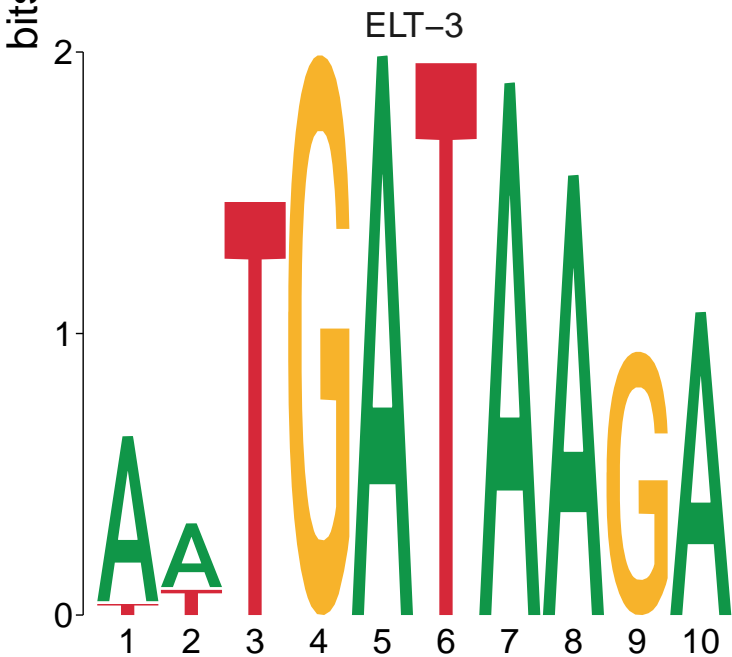
5-GGCGTTAAAA,BestGuess:DEL2



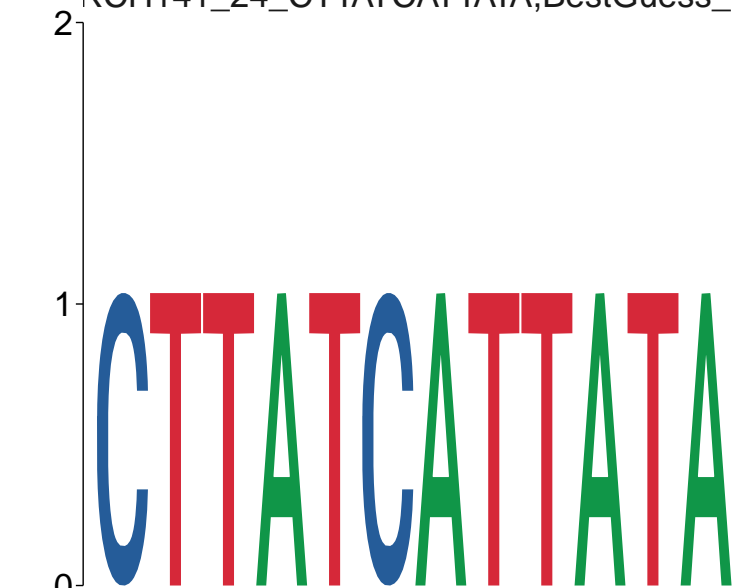
ARCH140_ELT_3



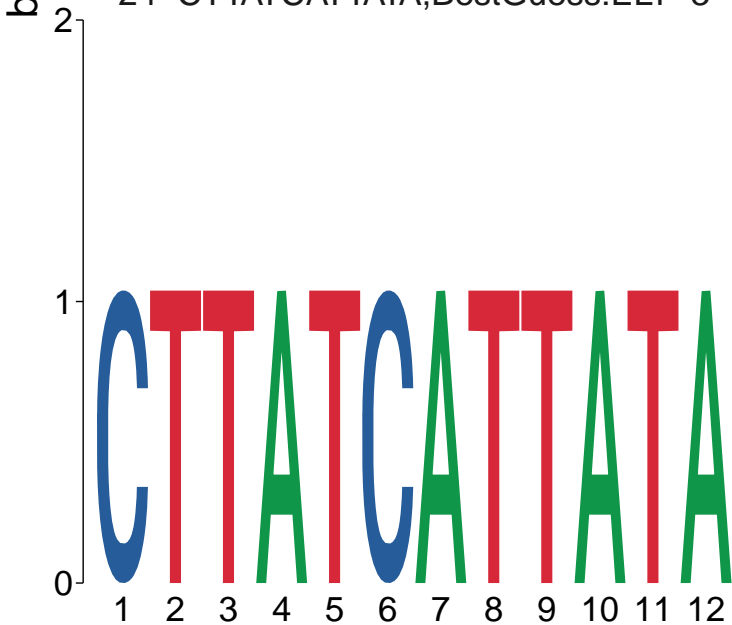
ELT-3



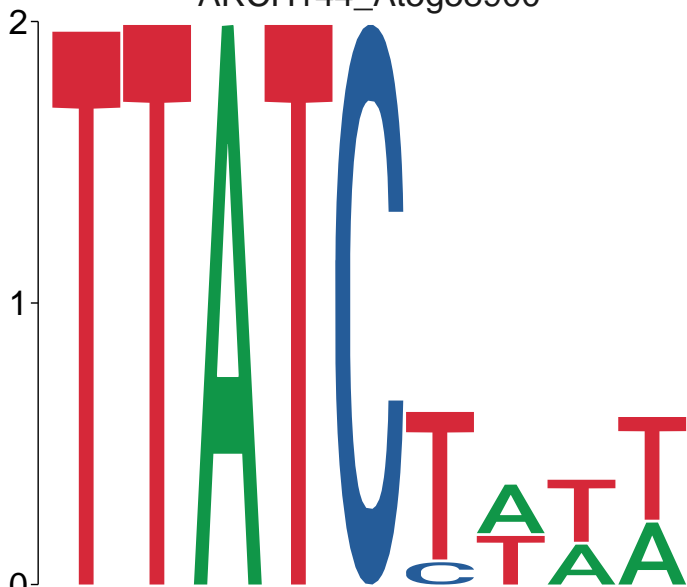
RCH141_24_CTTATCATTATA,BestGuess_E



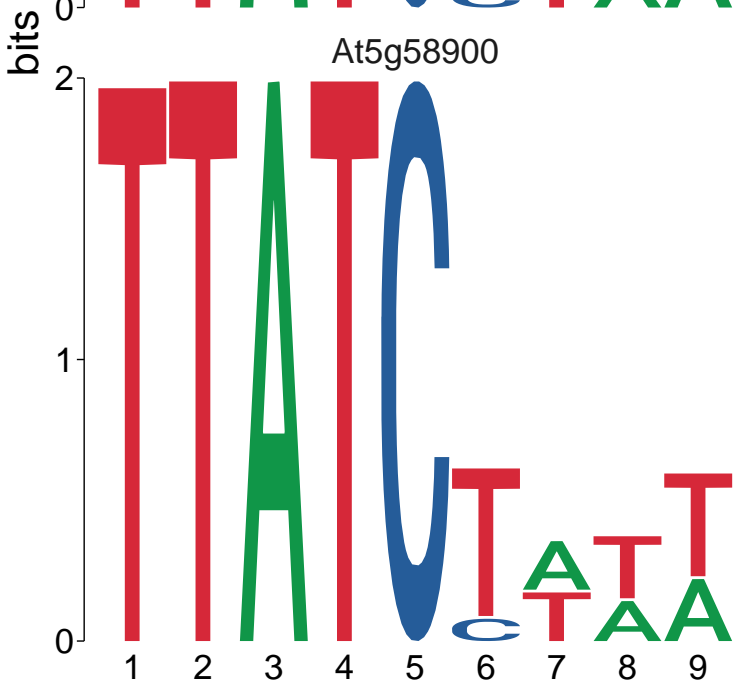
24-CTTATCATTATA,BestGuess:ELT-3



ARCH144_At5g58900



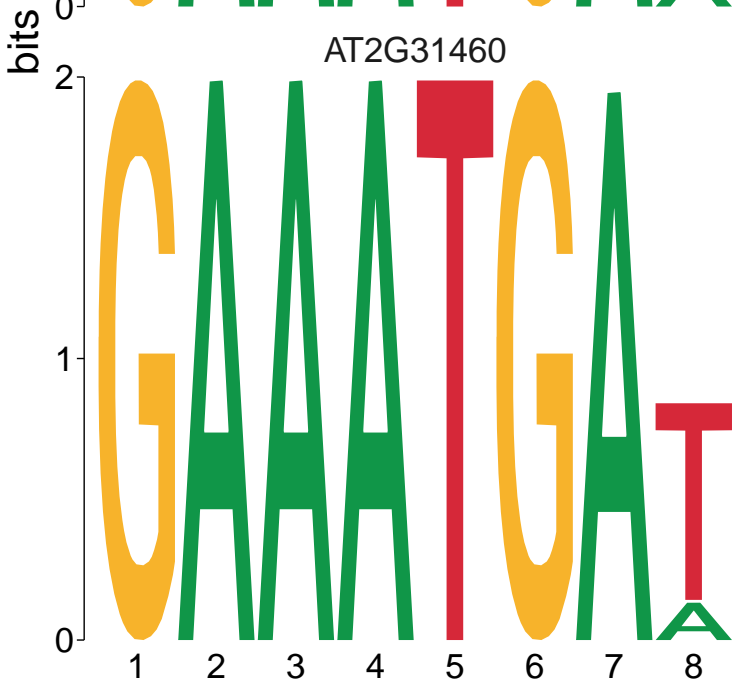
At5g58900



ARCH145_AT2G31460



AT2G31460



RCH146_24_TATCTATCTTAT,BestGuess_G

2

1

0

bits

24-TATCTATCTTAT,BestGuess:GLN3

2

1

0

1

2

3

4

5

6

7

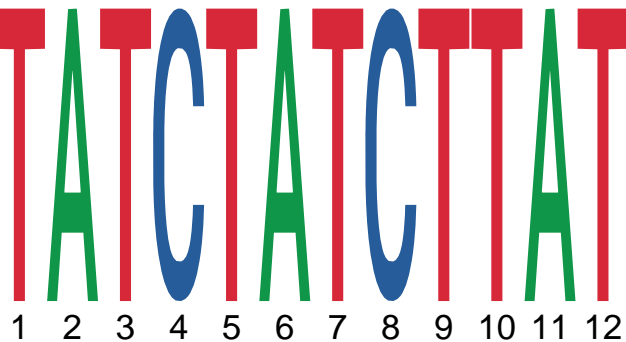
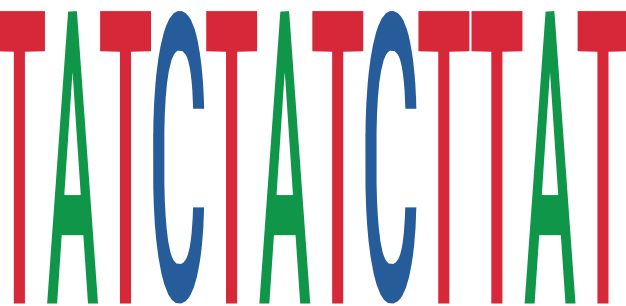
8

9

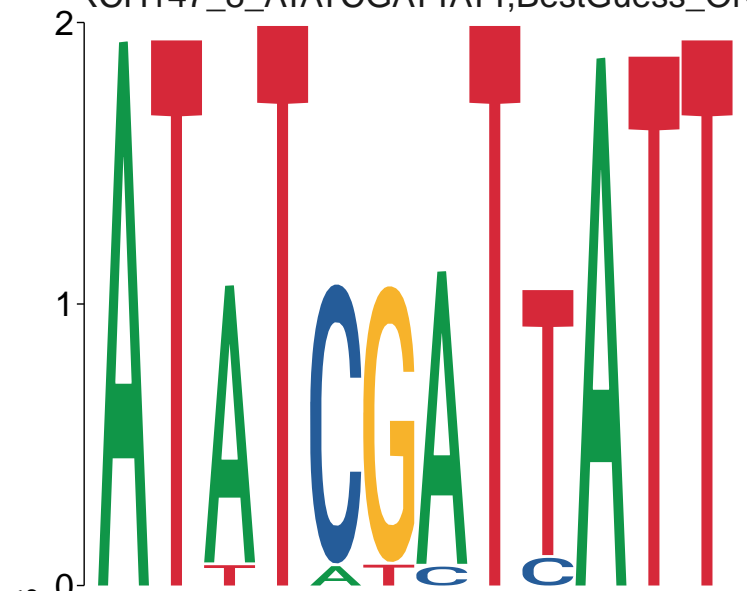
10

11

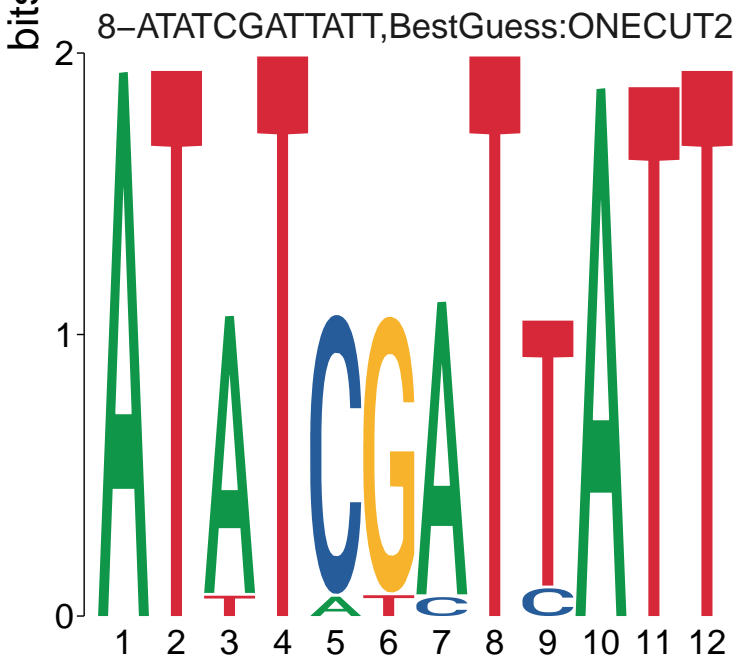
12



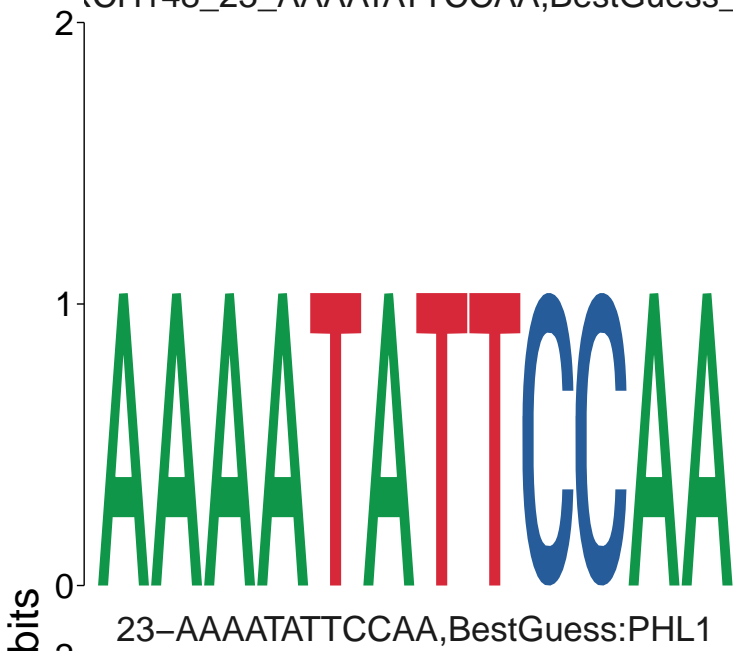
RCH147_8_ATATCGATTATT,BestGuess_ON



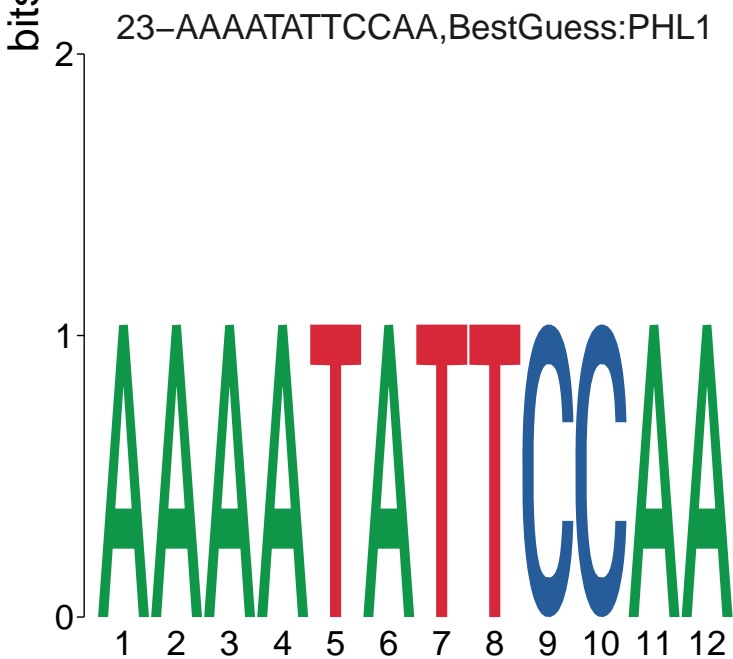
8-ATATCGATTATT,BestGuess:ONECUT2



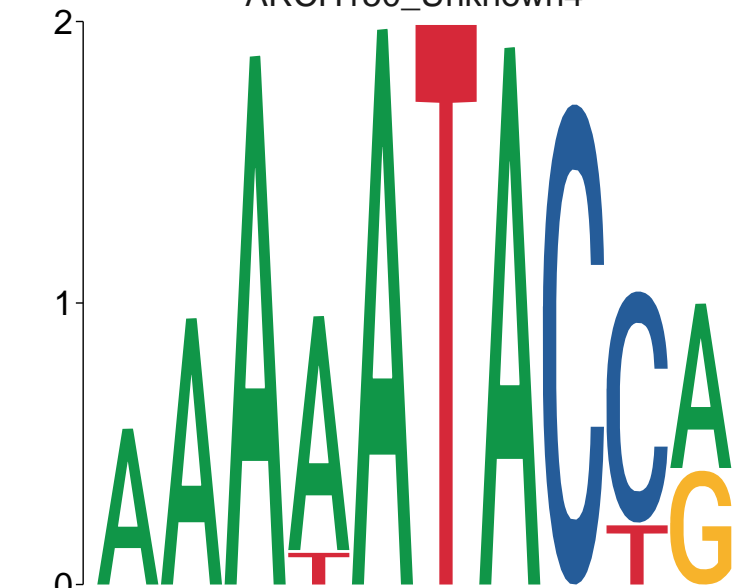
CH148_23_AAAATATTCCAA,BestGuess_f



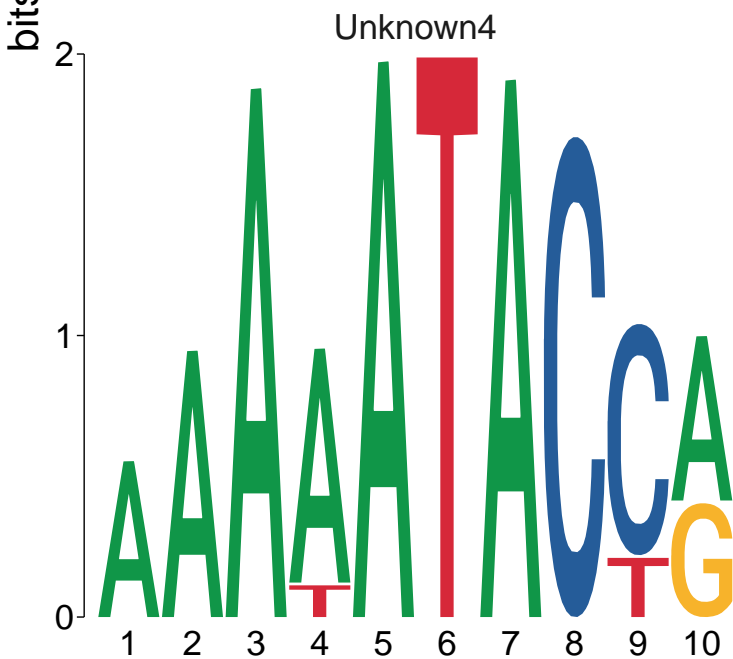
23-AAAATATTCCAA,BestGuess:PHL1



ARCH150_Unknown4



Unknown4



RCH151_12_TAAATATGTTBH,BestGuess_

2

1

0

bits

12-TAAATATGTTBH,BestGuess:At3g09600

2

1

0

1

2

3

4

5

6

7

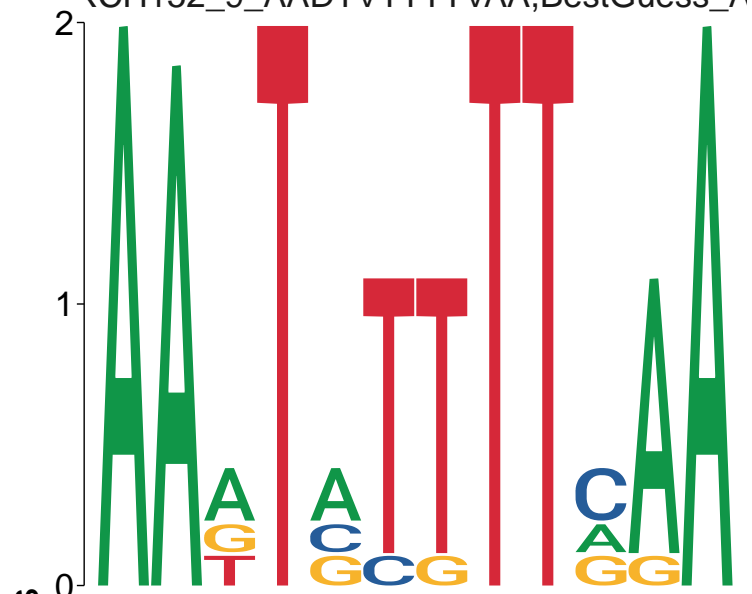
8

9

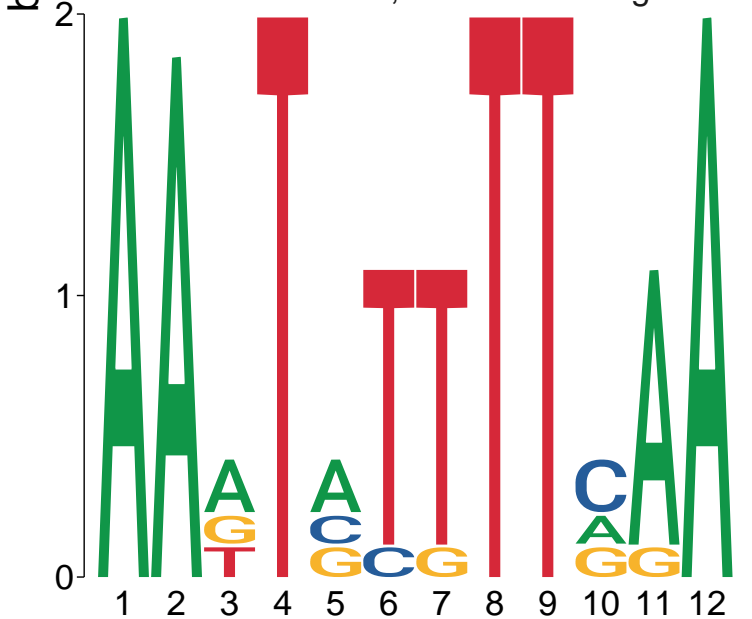
10



RCH152_9_AADTVTTTTVAA,BestGuess_A



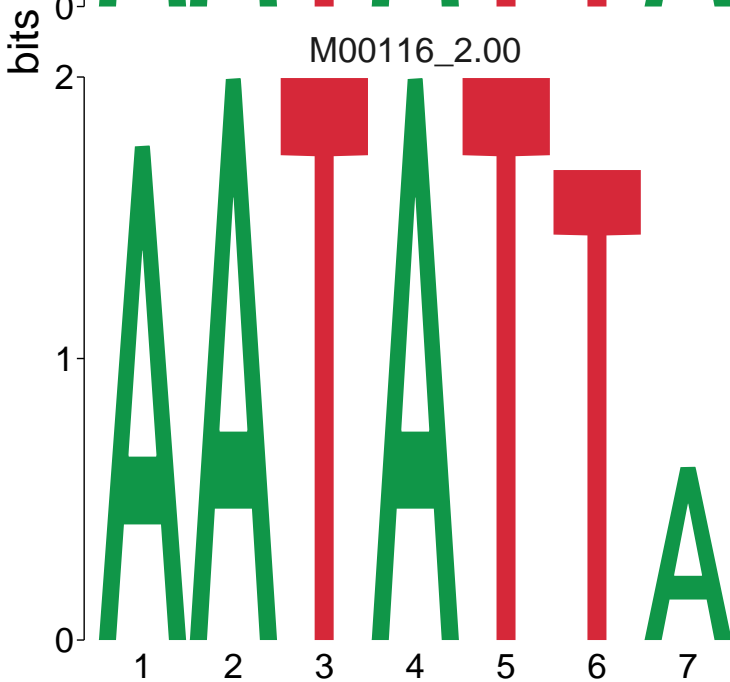
9-AADTVTTTTVAA,BestGuess:At2g41835



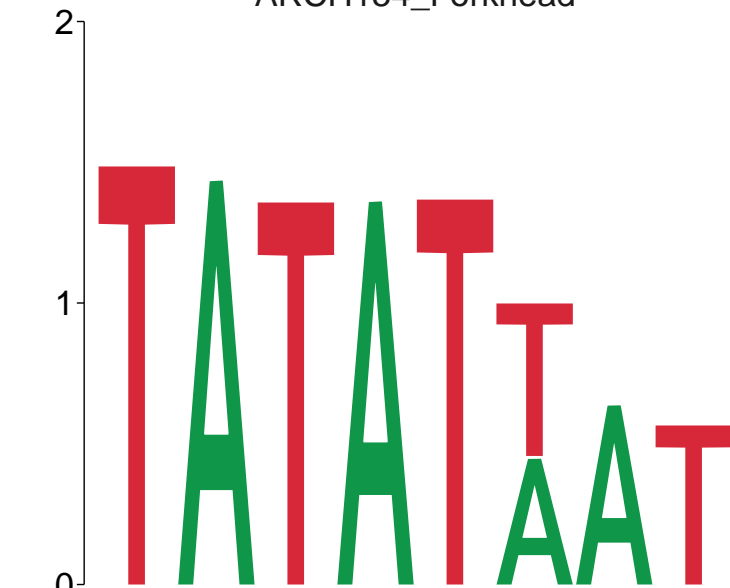
ARCH153_ARID_BRIGHT



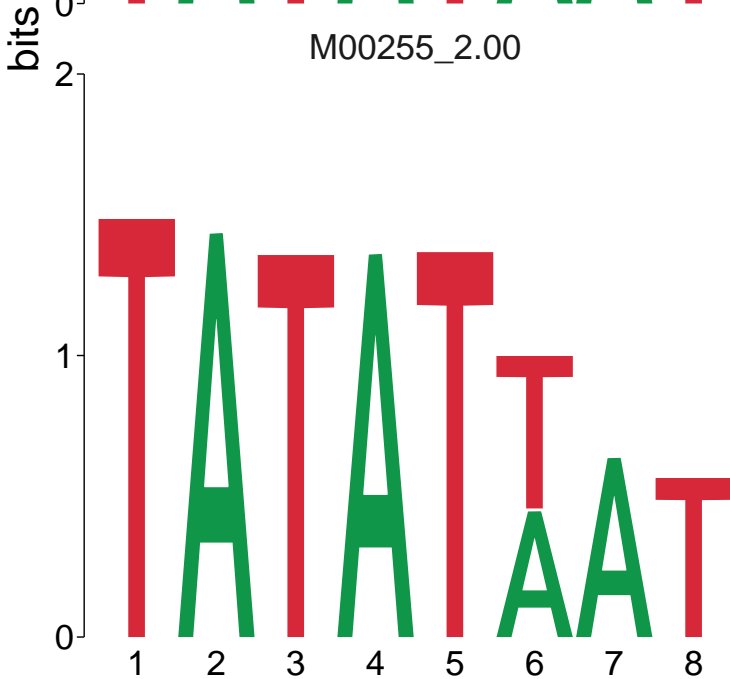
M00116_2.00



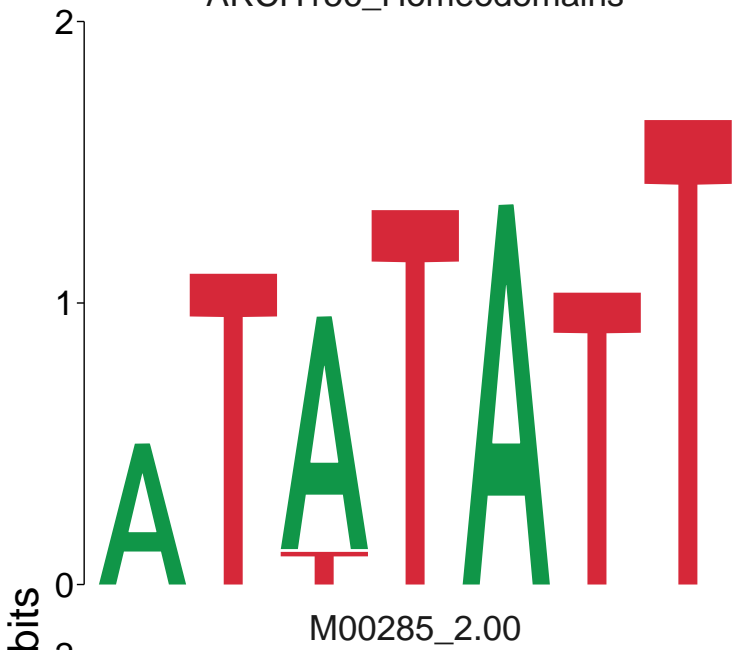
ARCH154_Forkhead



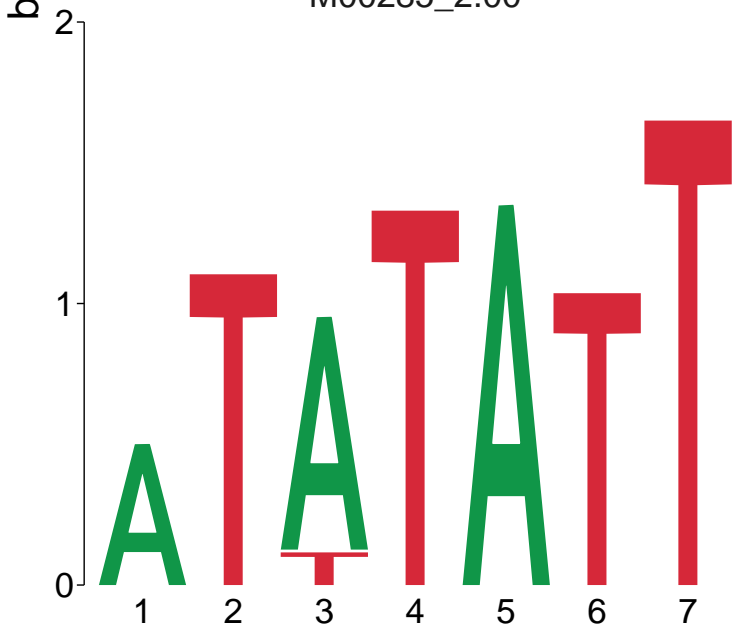
M00255_2.00



ARCH156_Homeodomains



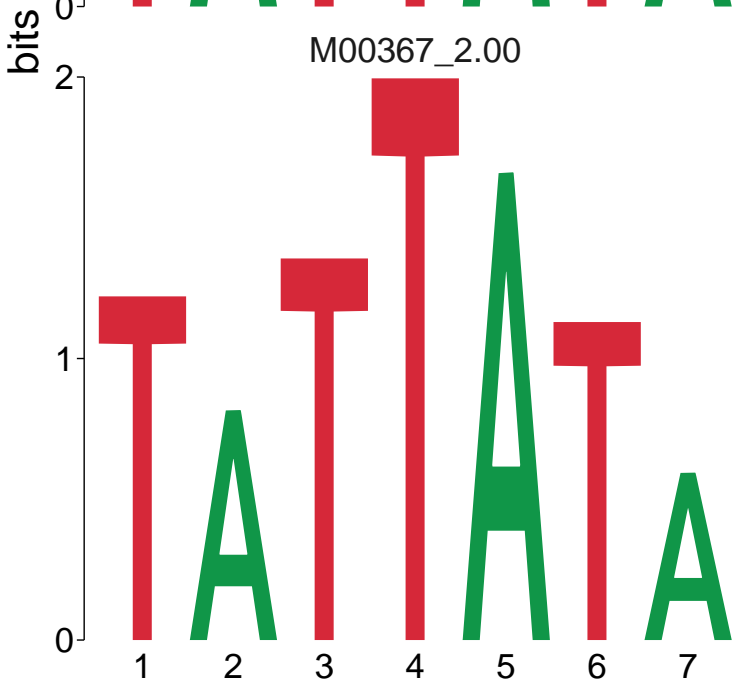
M00285_2.00



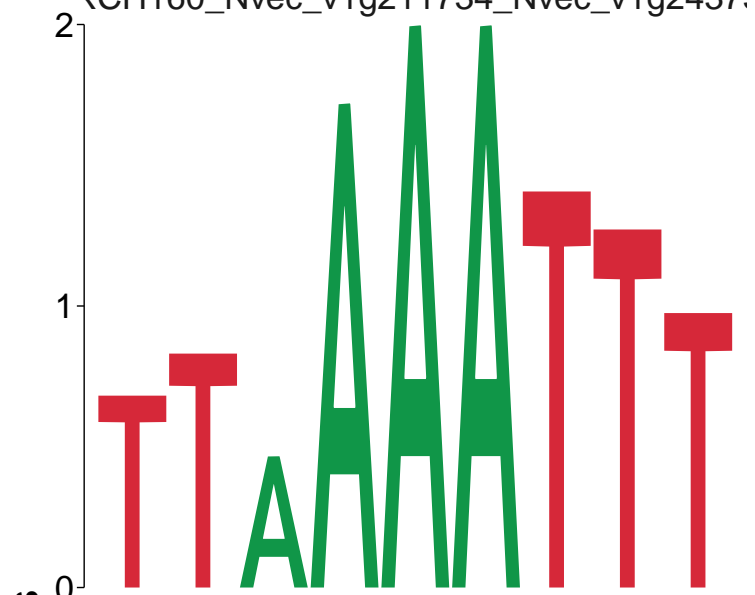
ARCH158_zf-C4_Nuclear_receptors



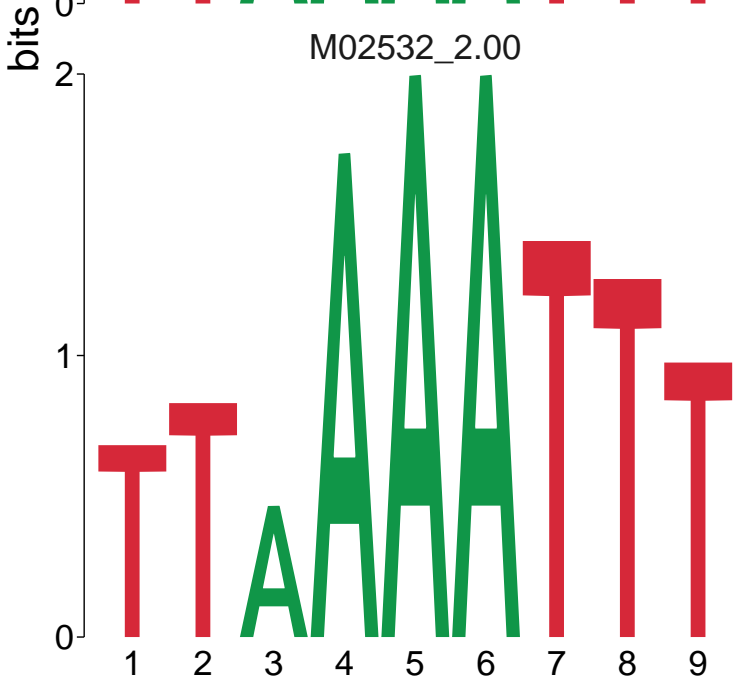
M00367_2.00



RCH160_Nvec_v1g211734_Nvec_v1g2437:



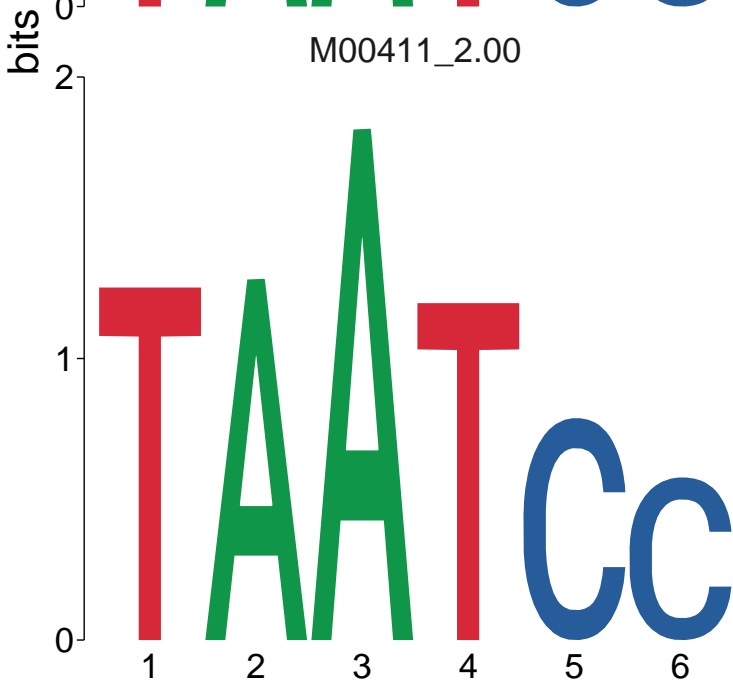
M02532_2.00



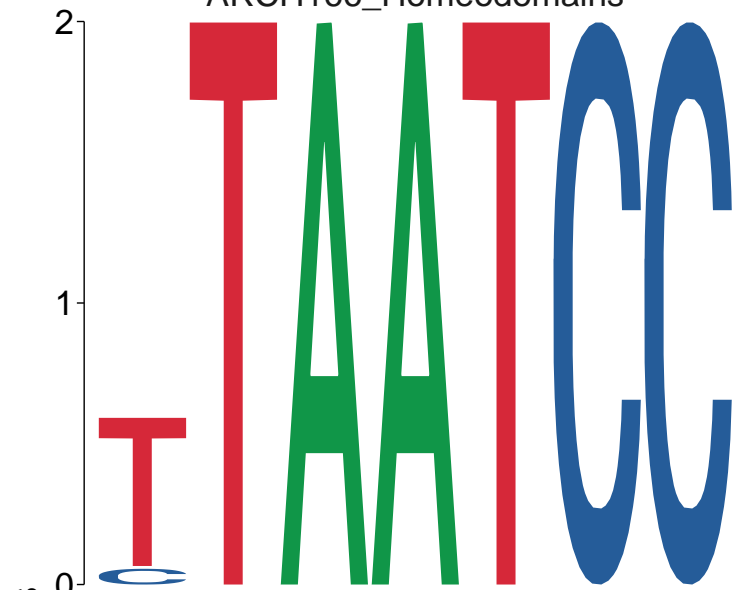
ARCH165_Homeodomains



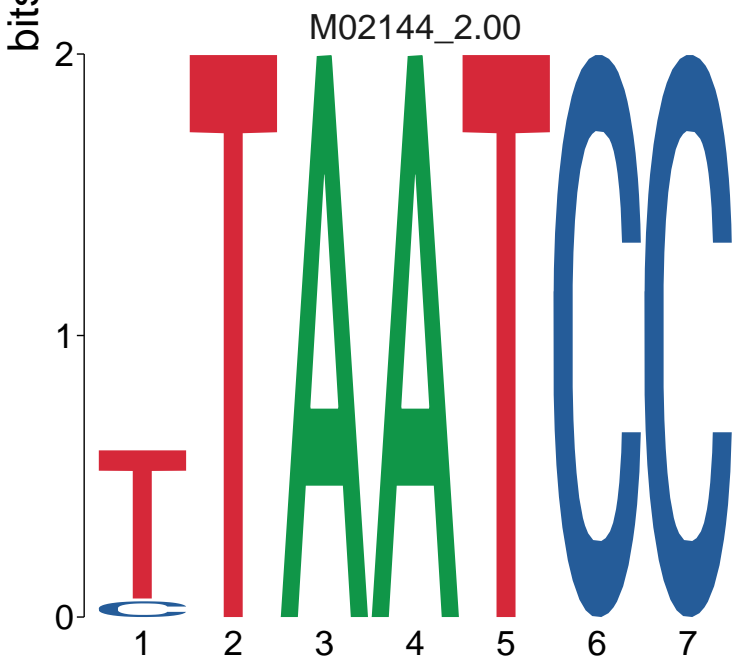
M00411_2.00



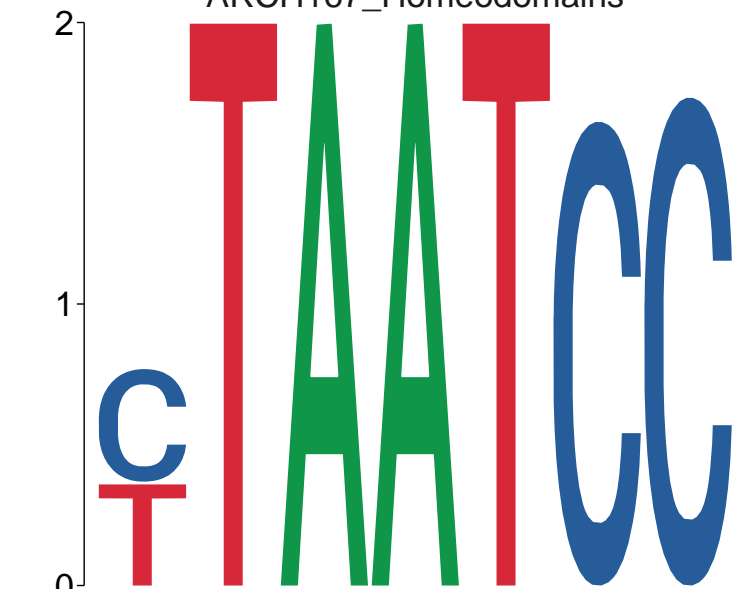
ARCH166_Homeodomains



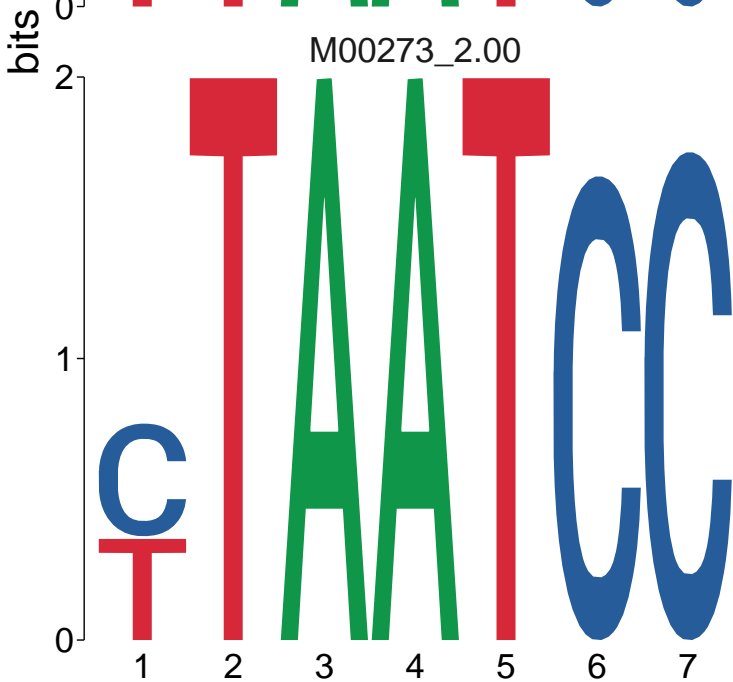
M02144_2.00



ARCH167_Homeodomains



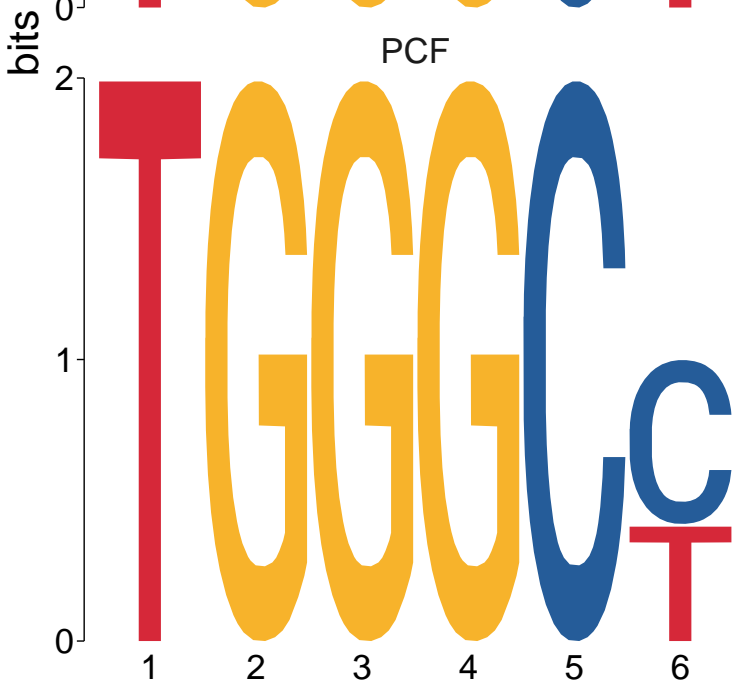
M00273_2.00



ARCH168_PCF



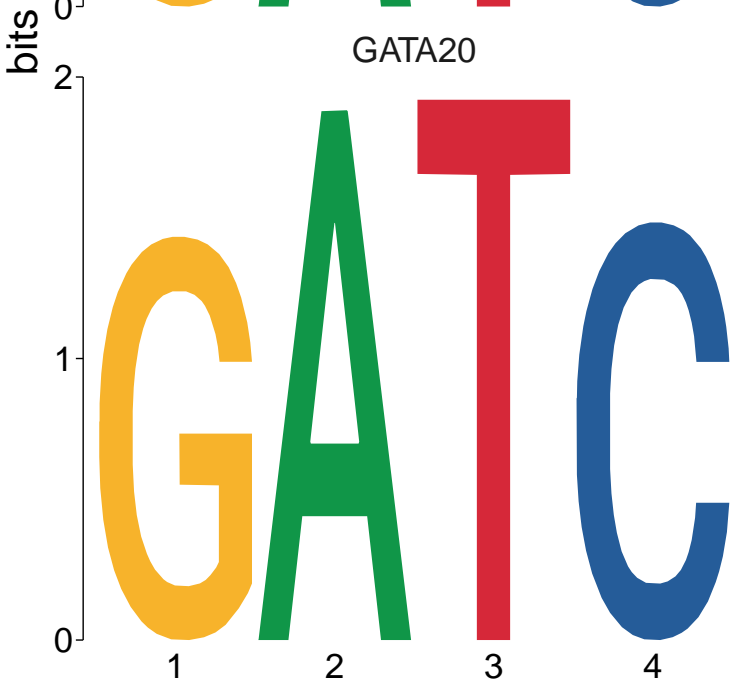
PCF



ARCH171_GATA20



GATA20



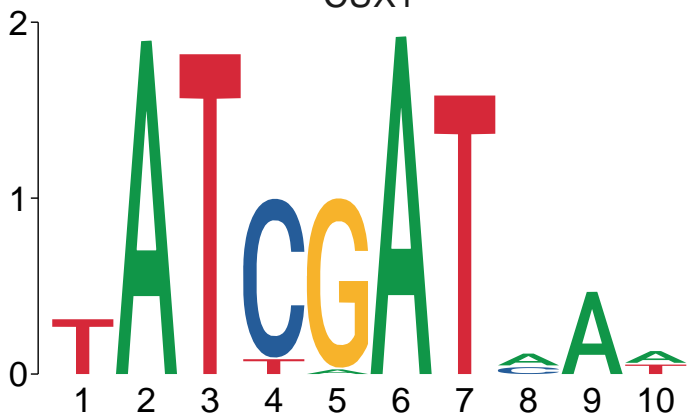
RCH172_CUX1_16_WCTATCGATA,BestGu



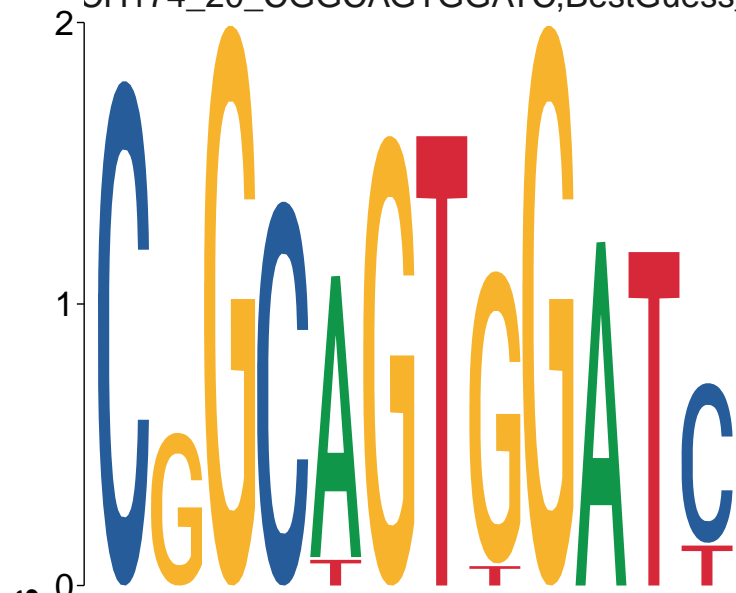
16-WCTATCGATA,BestGuess:Dref [RC]



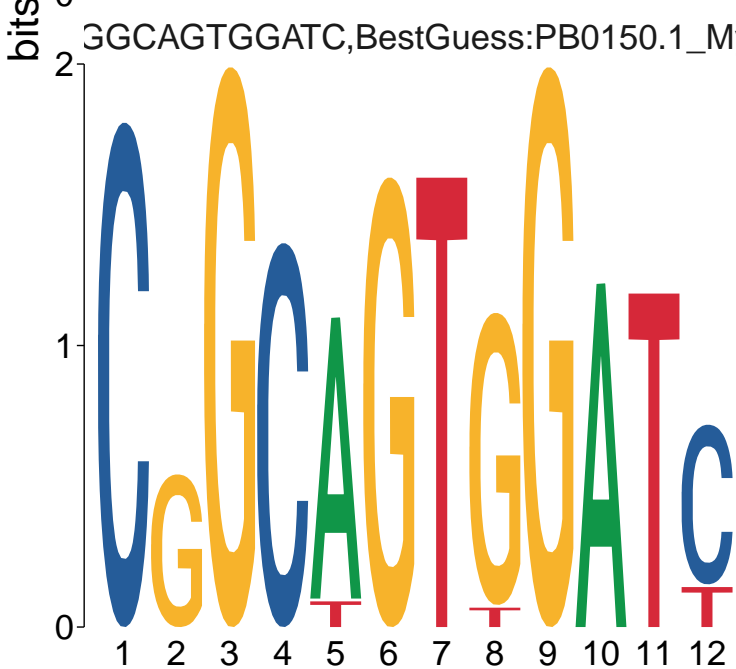
CUX1



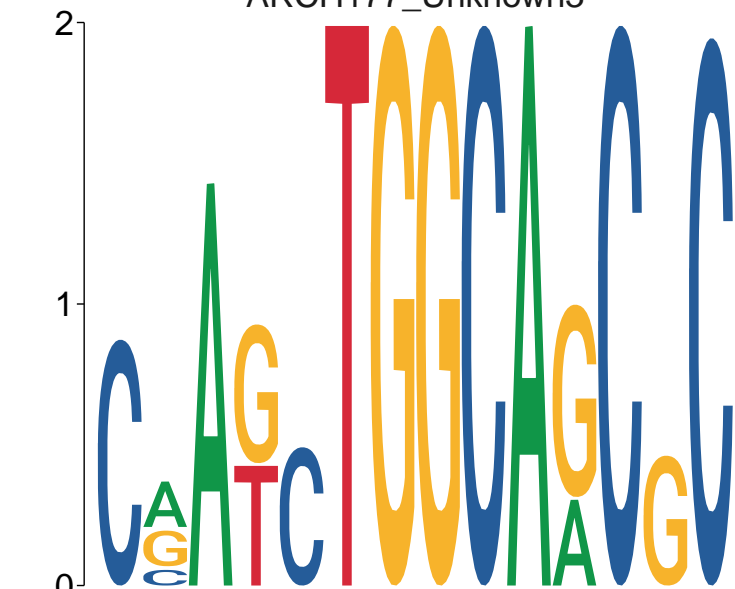
CH174_20_CGGCAGTGGATC,BestGuess_



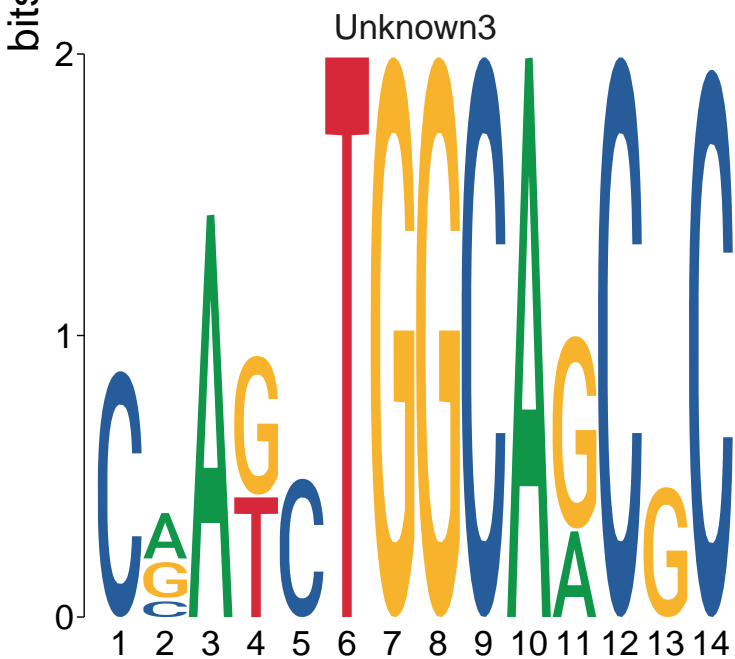
GGCAGTGGATC,BestGuess:PB0150.1_My



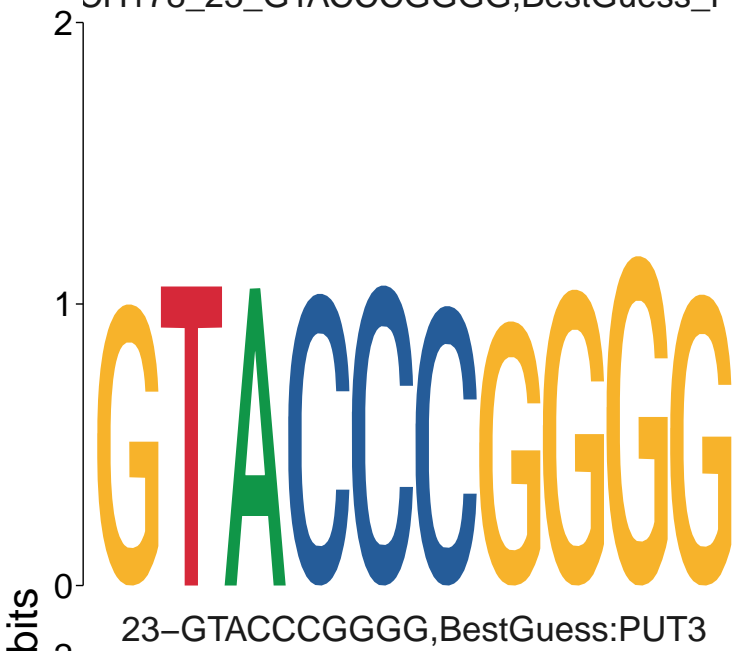
ARCH177_Unknown3



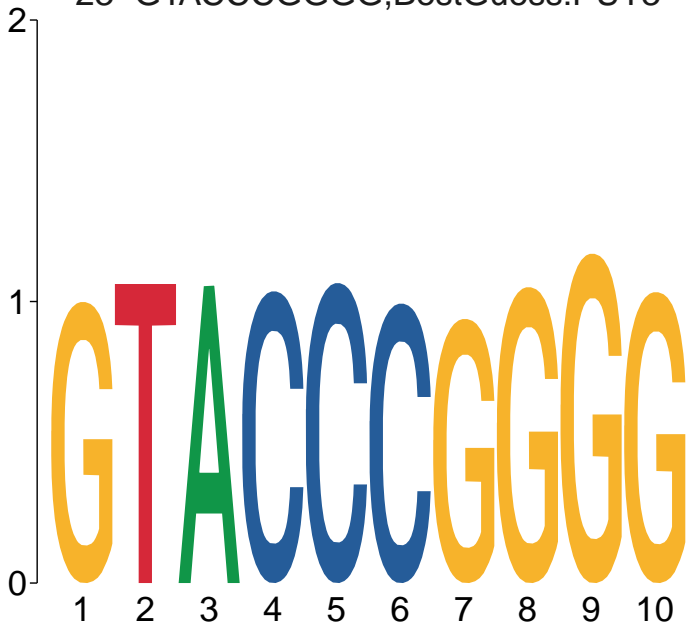
Unknown3



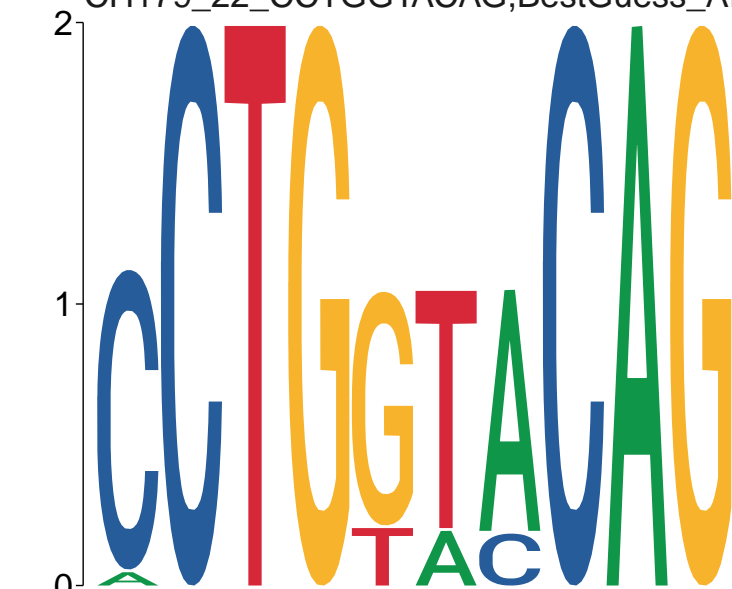
CH178_23_GTACCCGGGG, BestGuess_PL



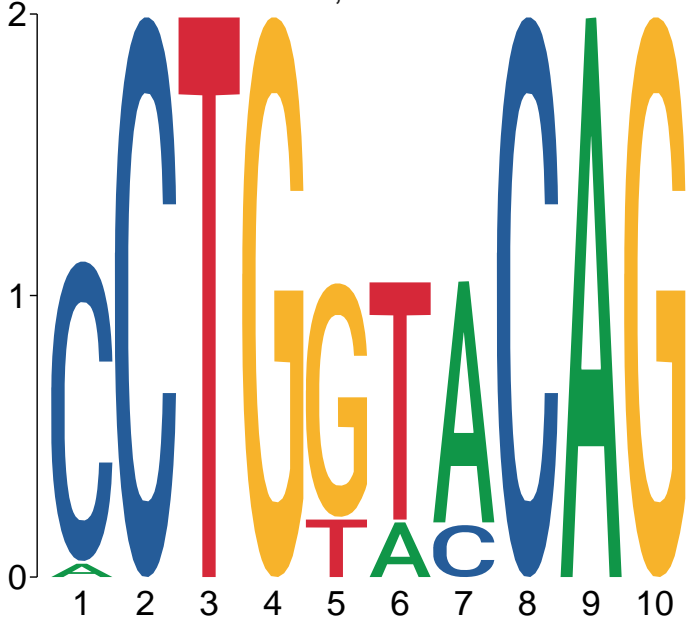
23-GTACCCGGGG, BestGuess:PUT3



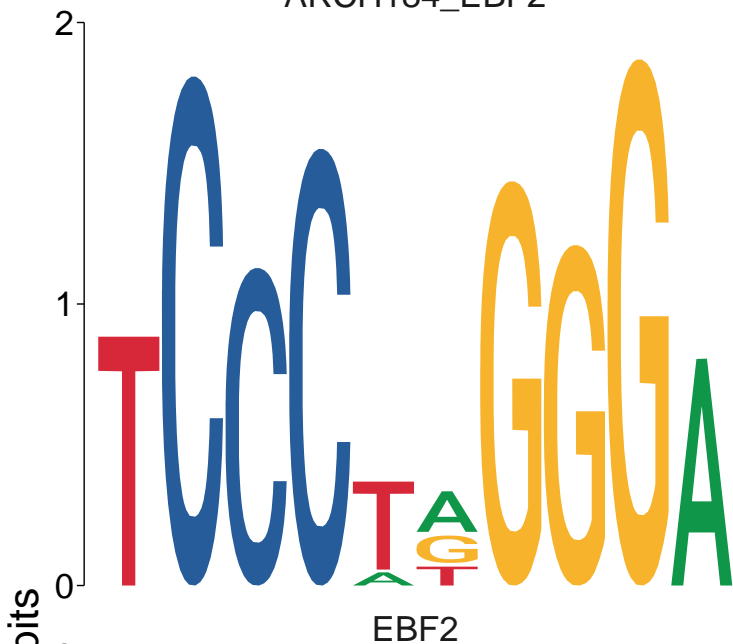
CH179_22_CCTGGTACAG,BestGuess_AR



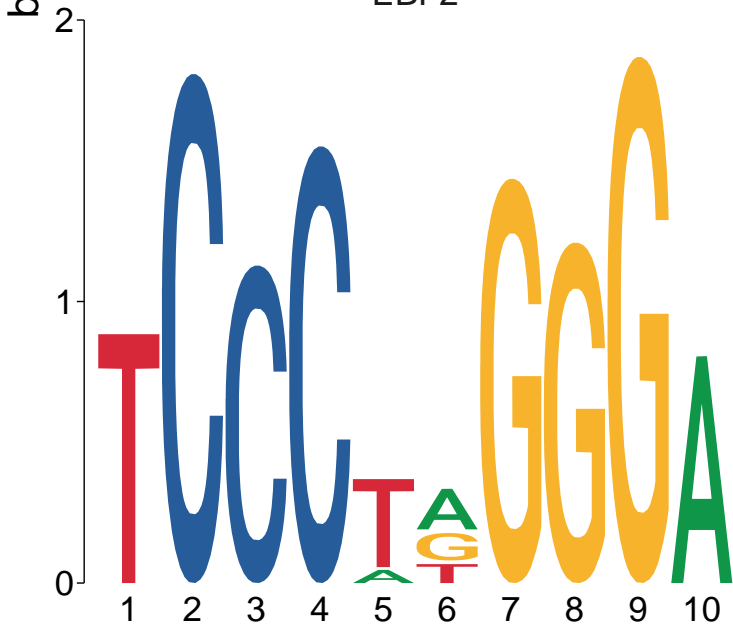
22-CCTGGTACAG,BestGuess:AR-halfsite



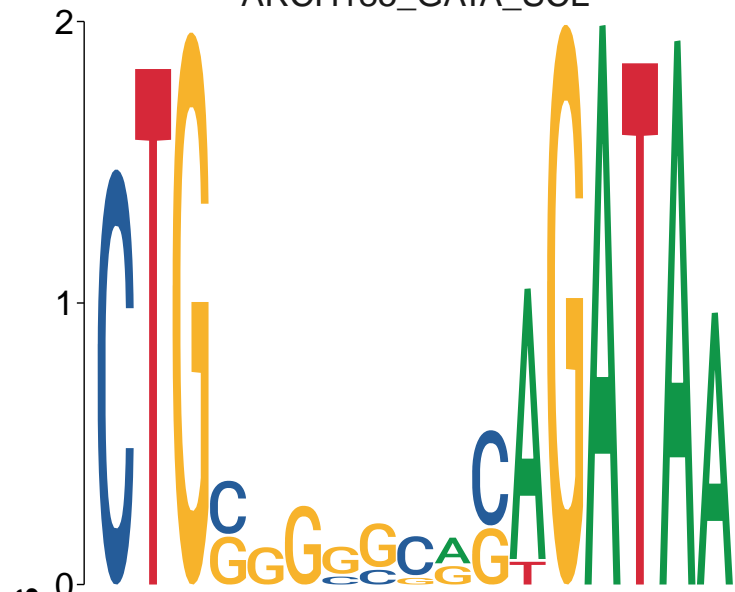
ARCH184_EBF2



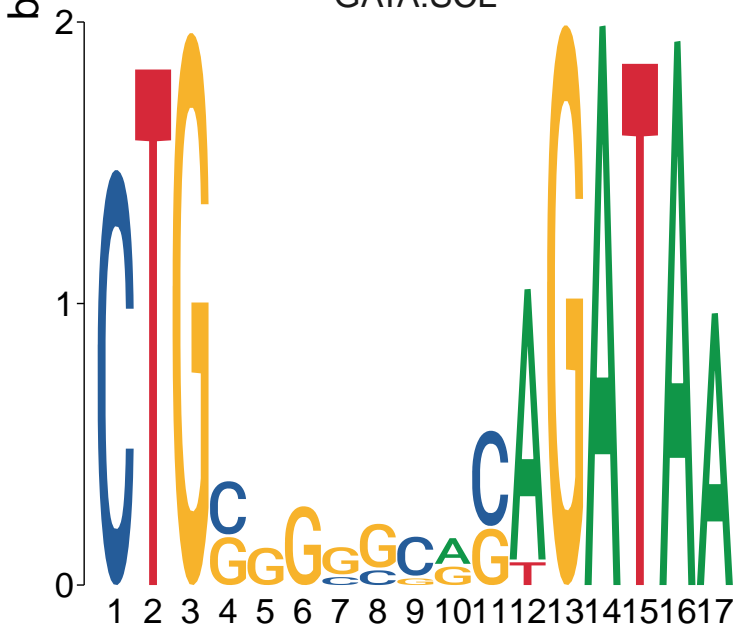
EBF2



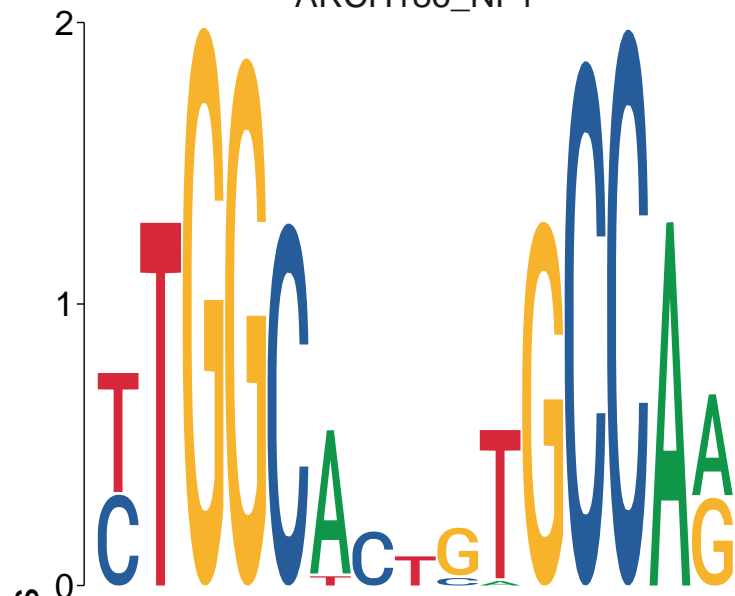
ARCH185_GATA_SCL



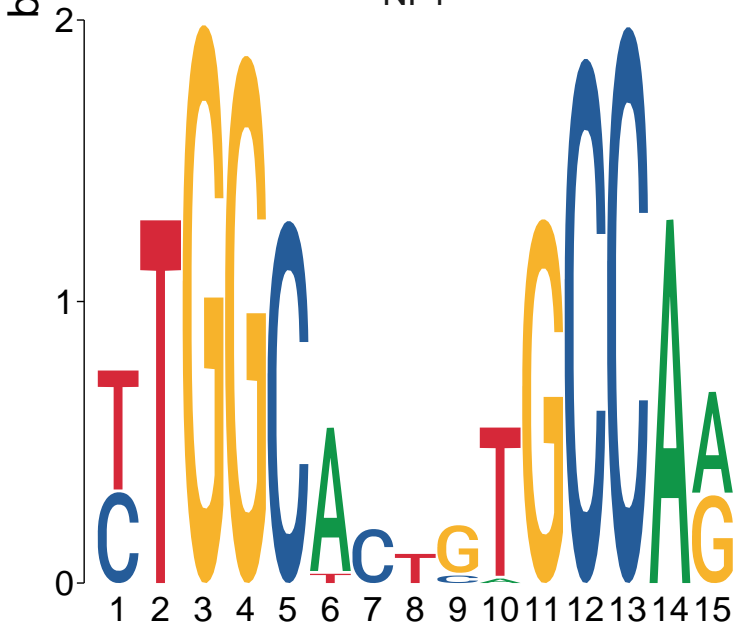
GATA:SCL



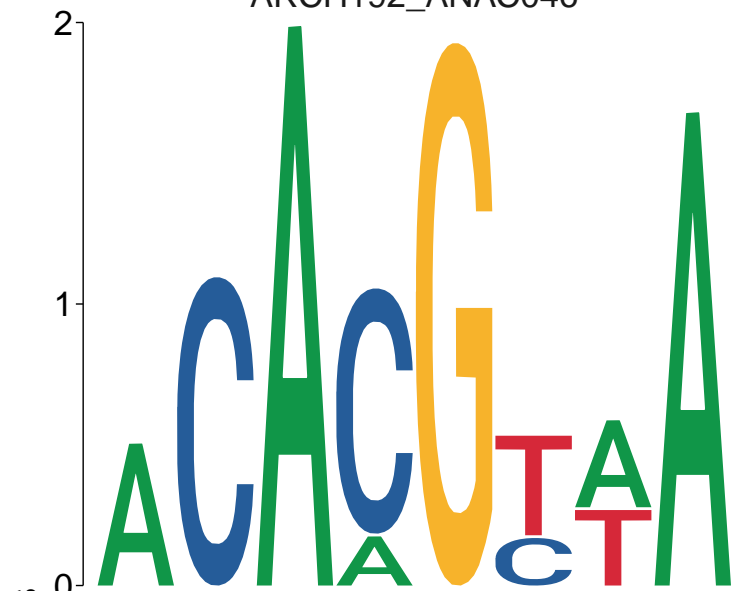
ARCH186_NF1



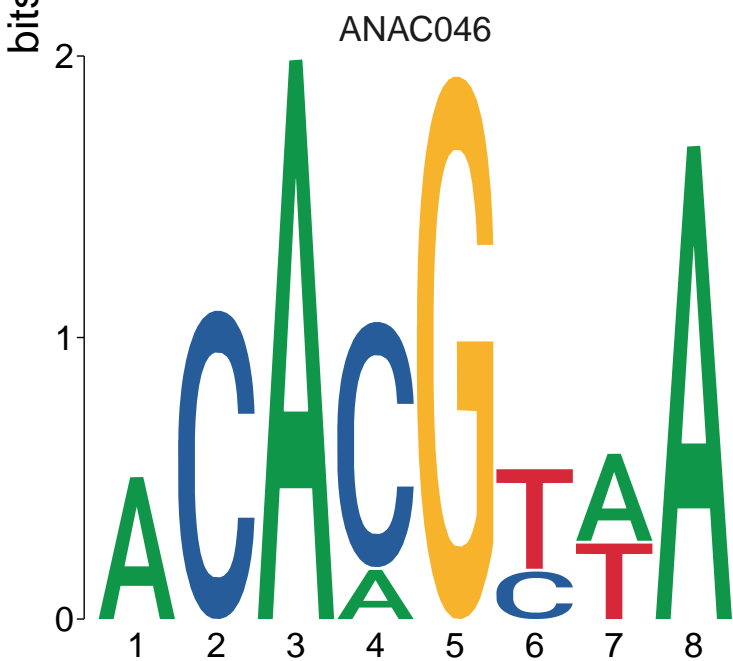
NF1



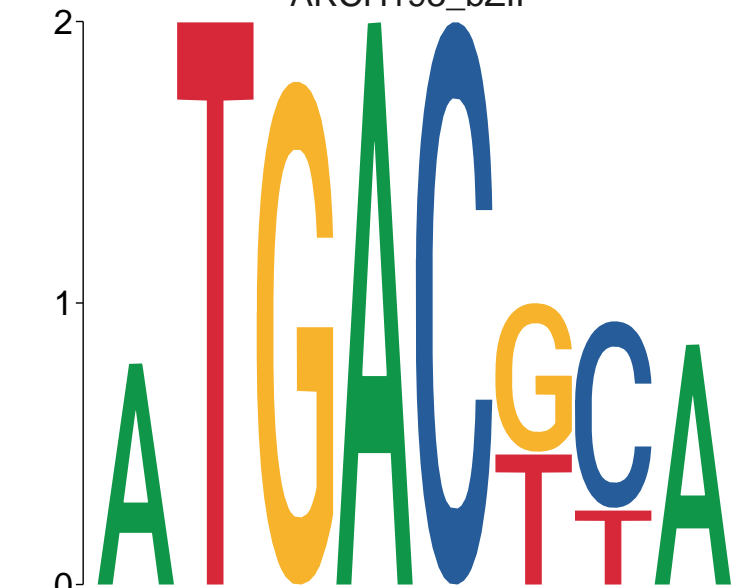
ARCH192_ANAC046



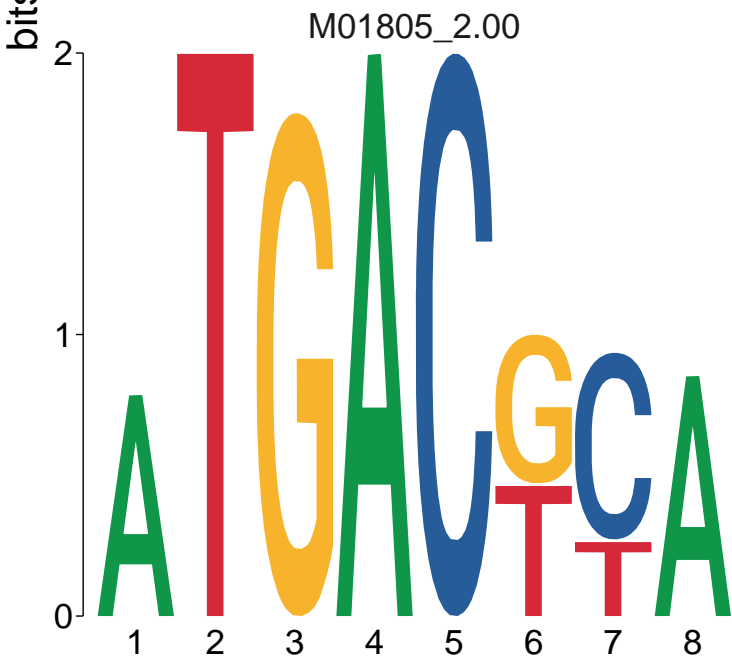
ANAC046



ARCH193_bZIP



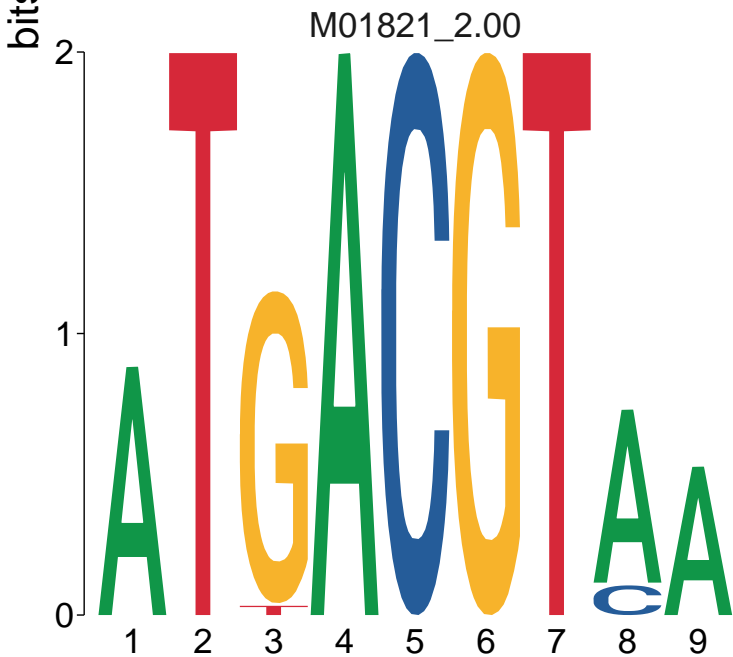
M01805_2.00



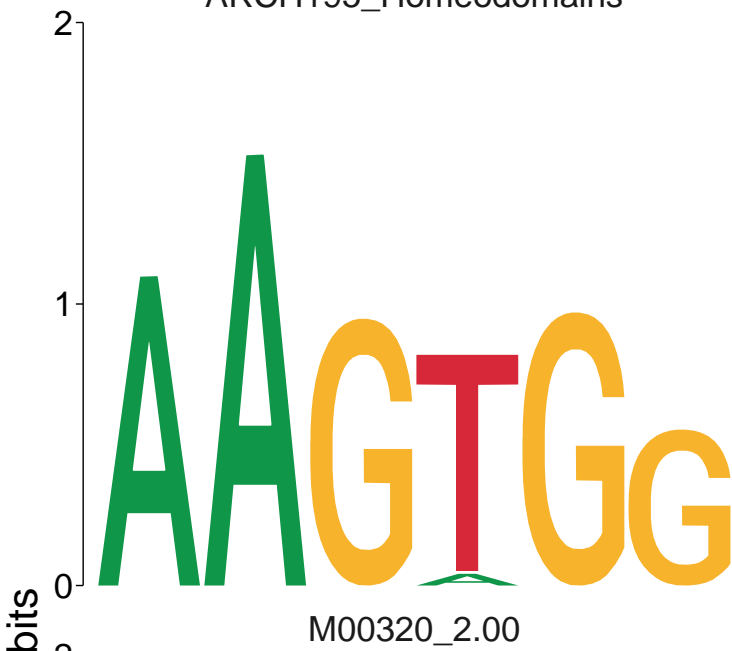
ARCH194_bZIP



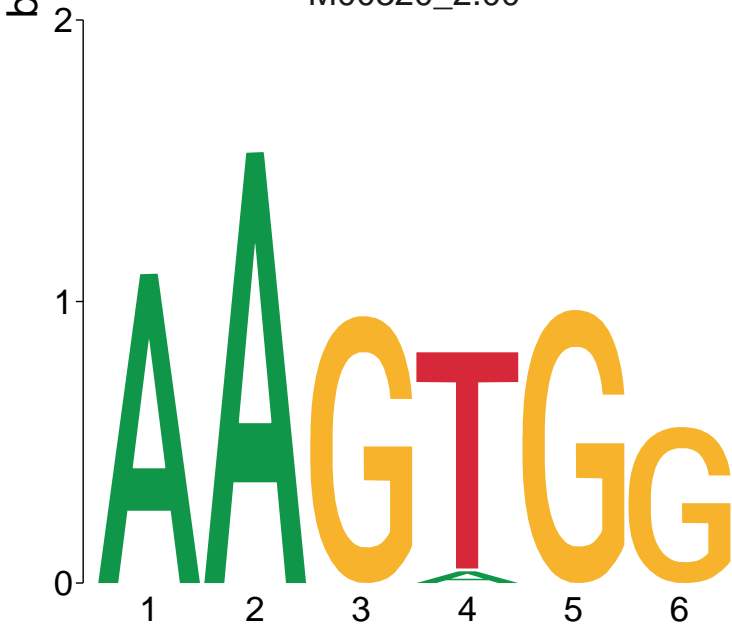
M01821_2.00



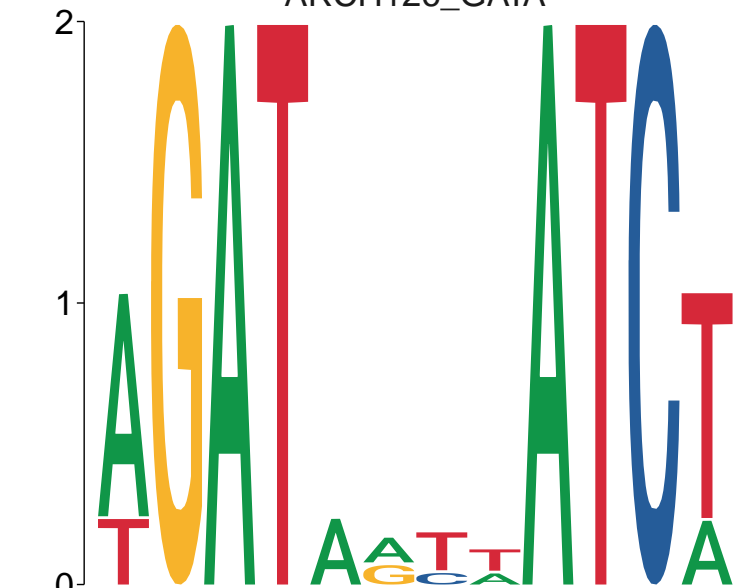
ARCH195_Homeodomains



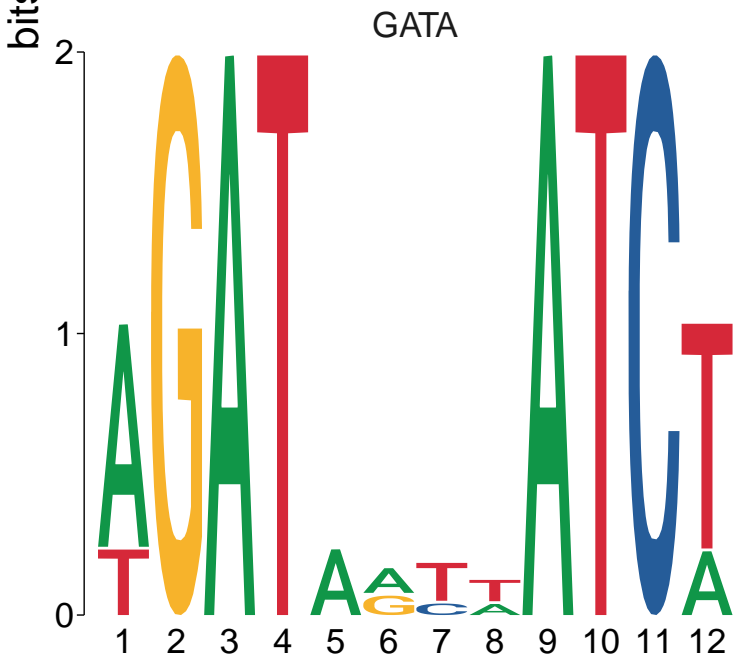
M00320_2.00



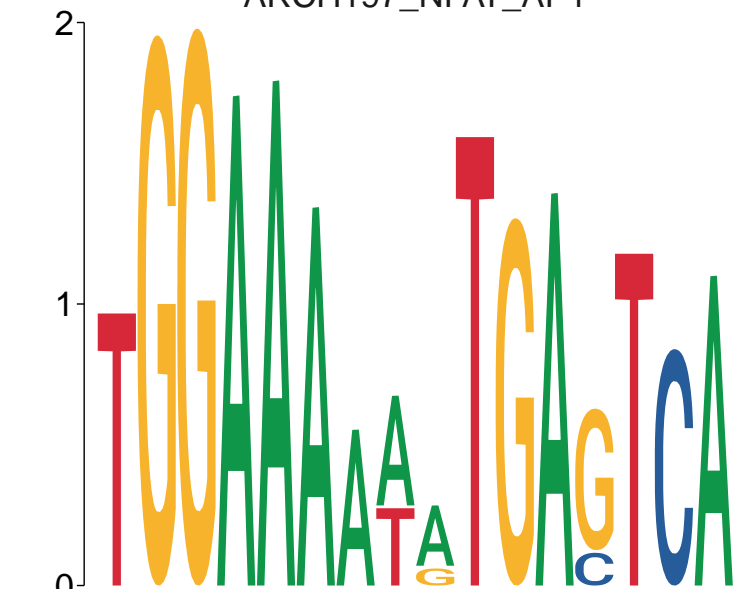
ARCH126_GATA



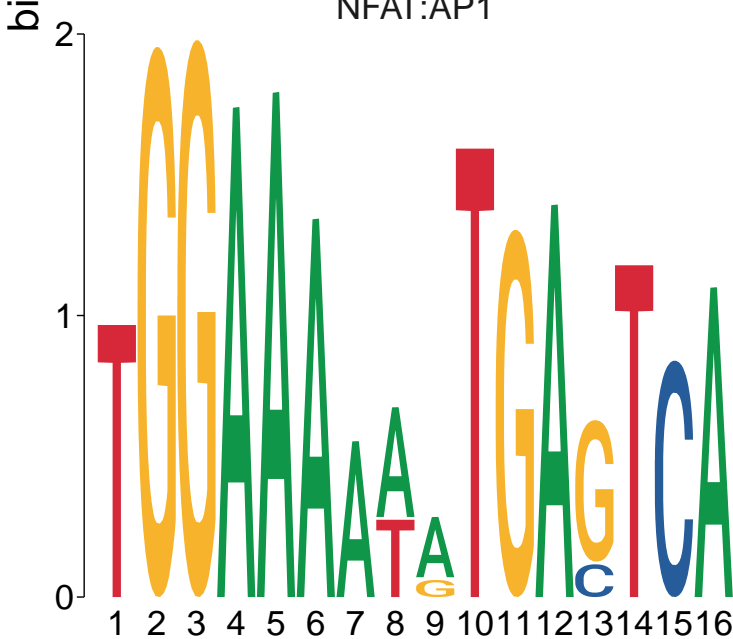
GATA



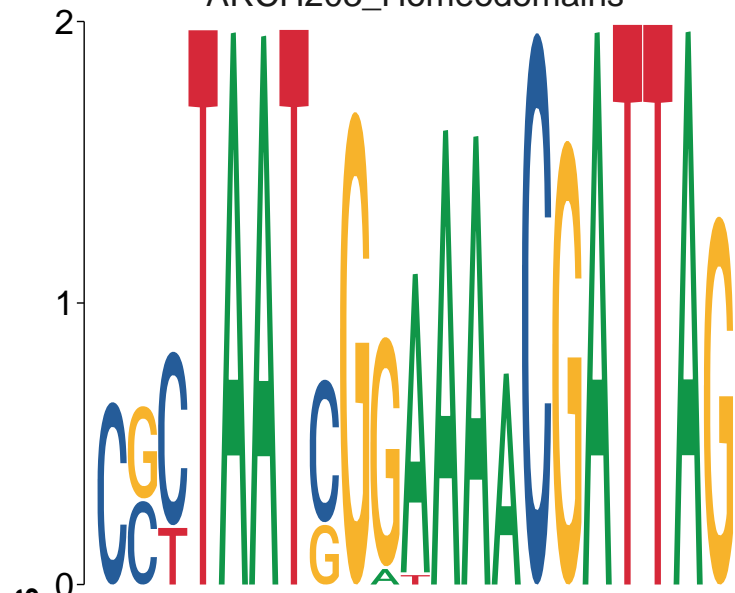
ARCH197_NFAT_AP1



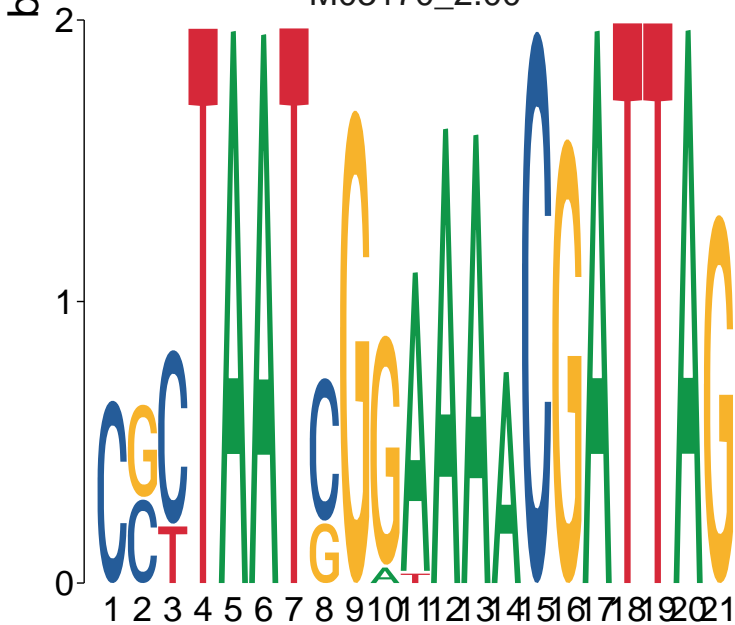
NFAT:AP1

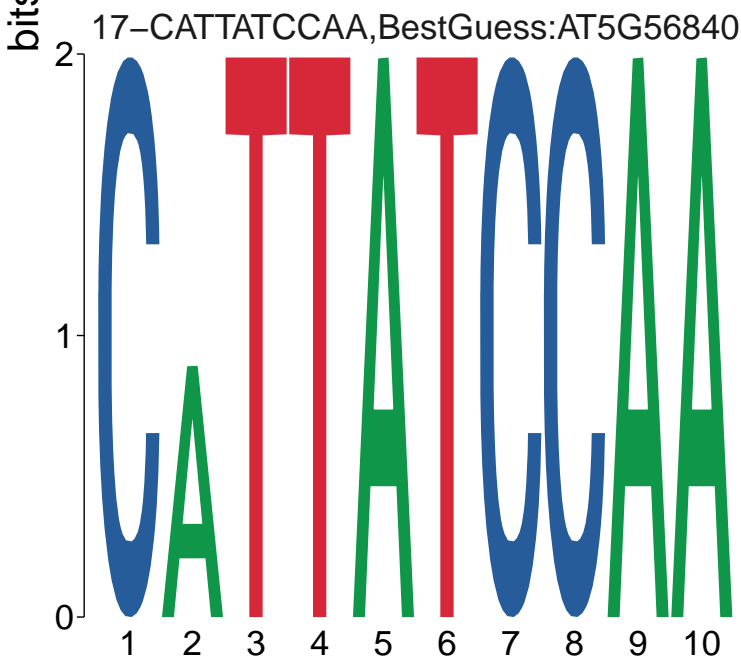
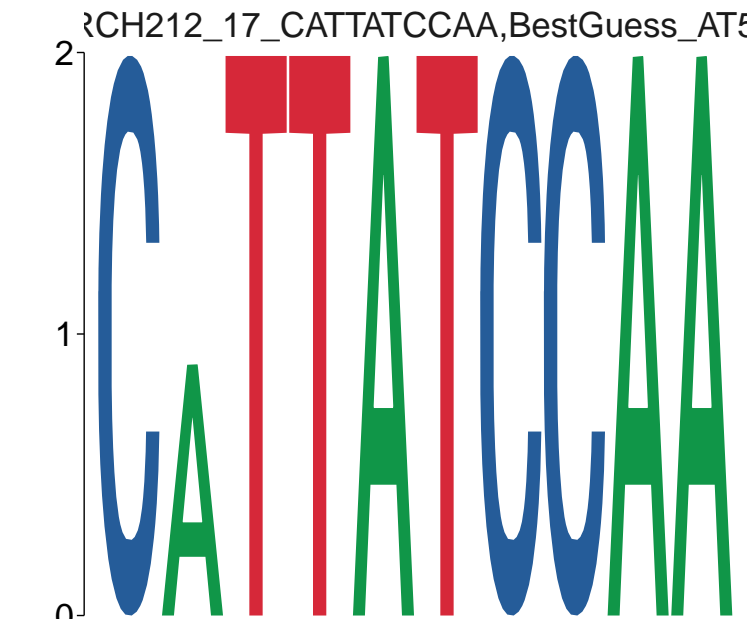


ARCH203_Homeodomains



M03170_2.00





RCH213_EWS_ERG_fusion_EWS_FLI1_fu



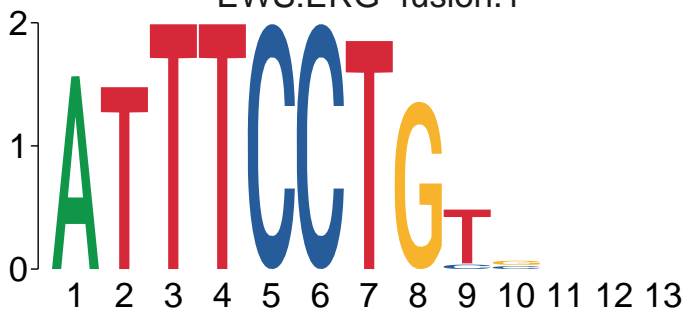
EWS:ERG-fusion



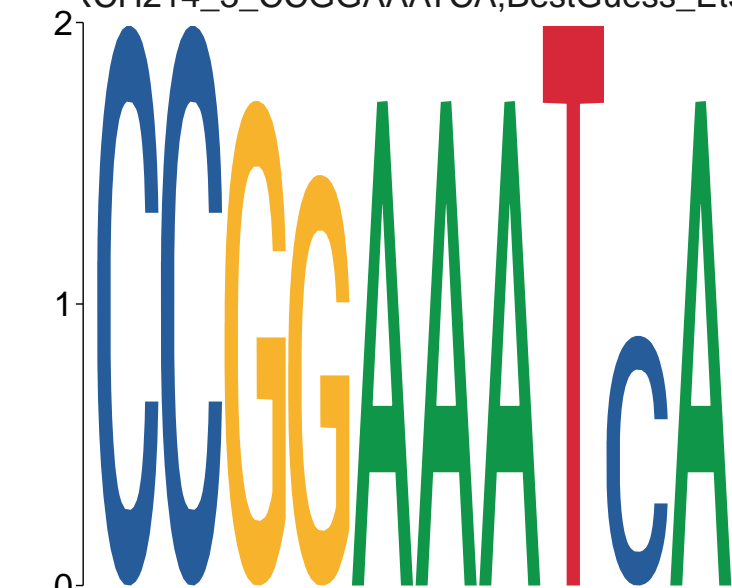
EWS:FLI1-fusion



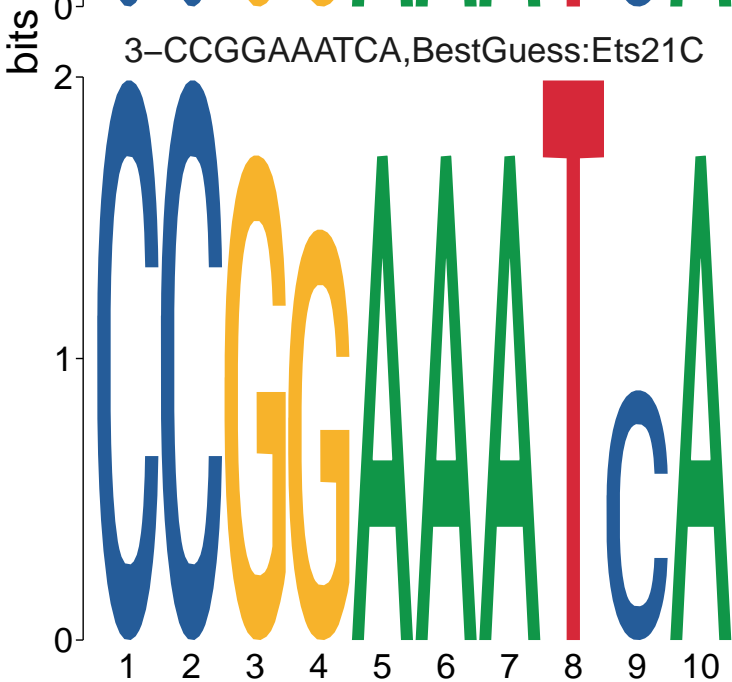
EWS:ERG-fusion.1



CH214_3_CCGGAAATCA,BestGuess_Ets



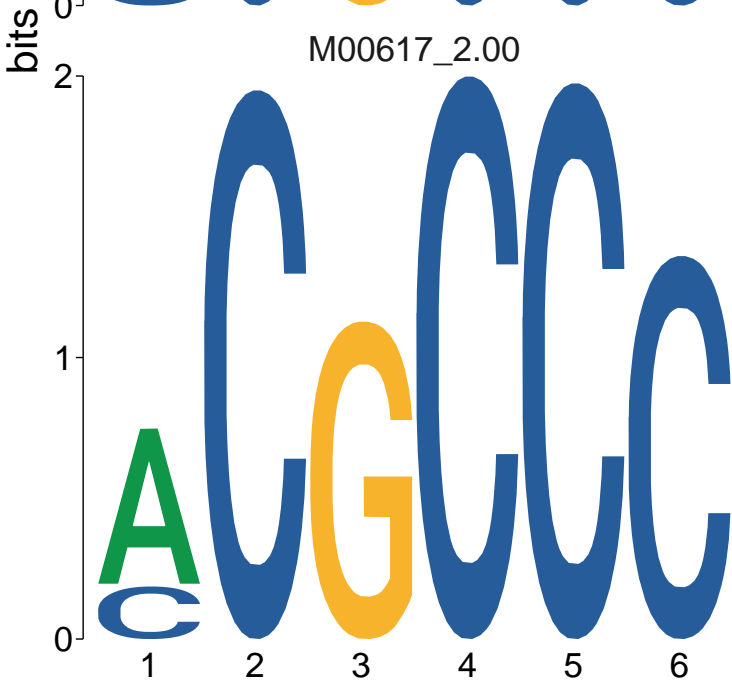
3-CCGGAAATCA,BestGuess:Ets21C



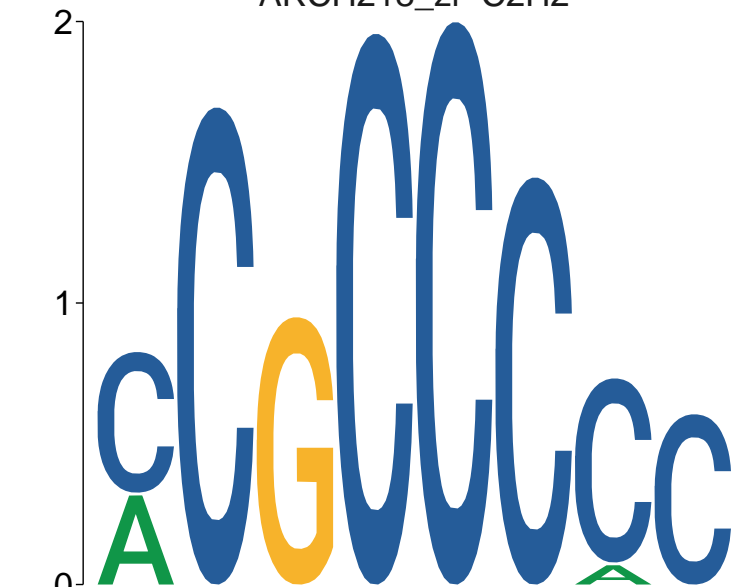
ARCH217_zf-C2H2



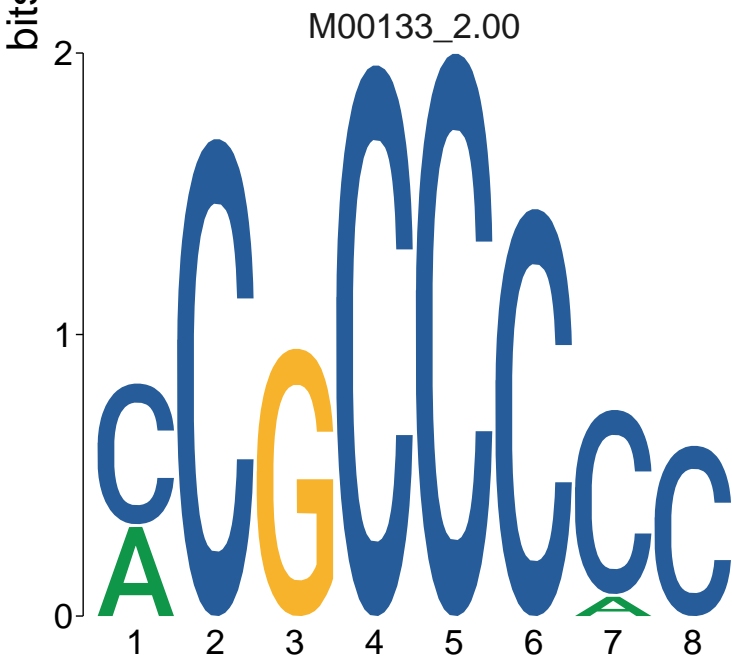
M00617_2.00



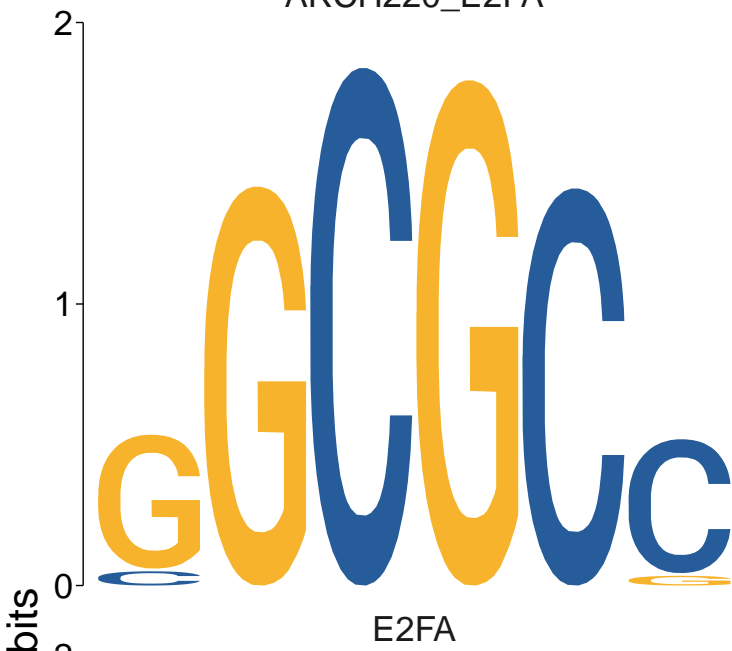
ARCH218_zf-C2H2



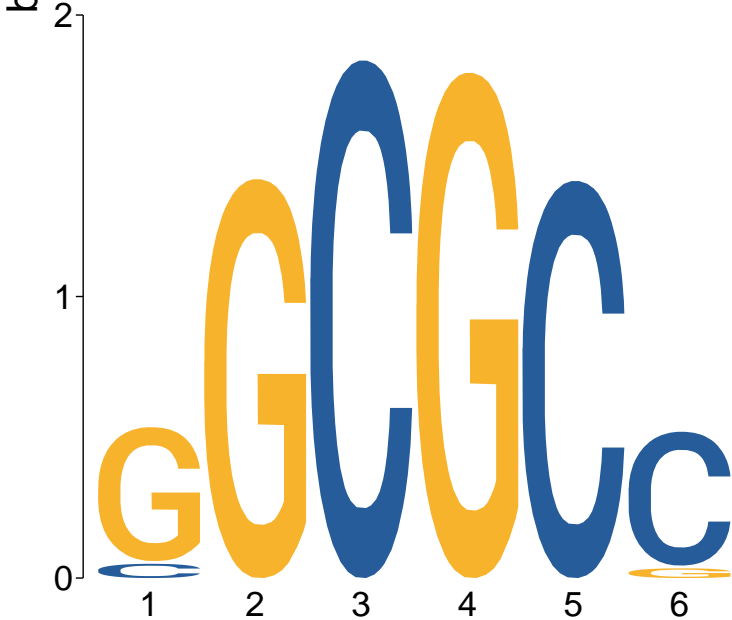
M00133_2.00



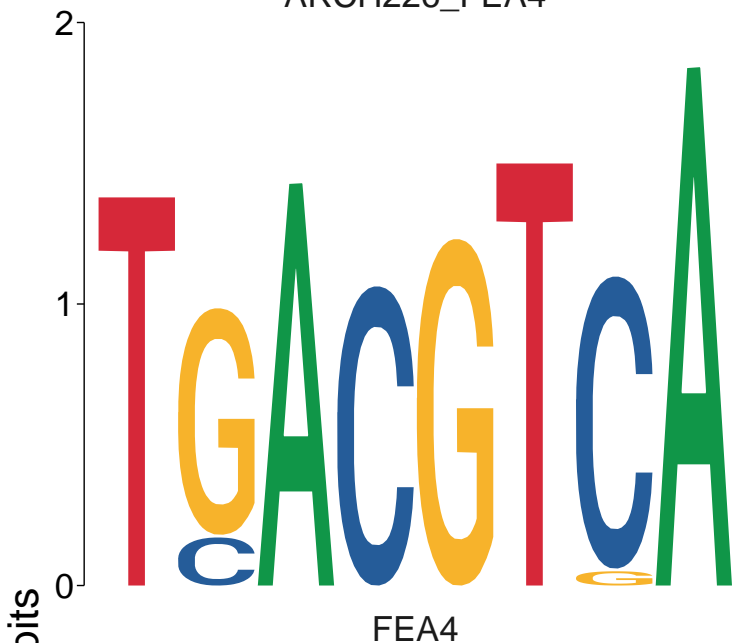
ARCH220_E2FA



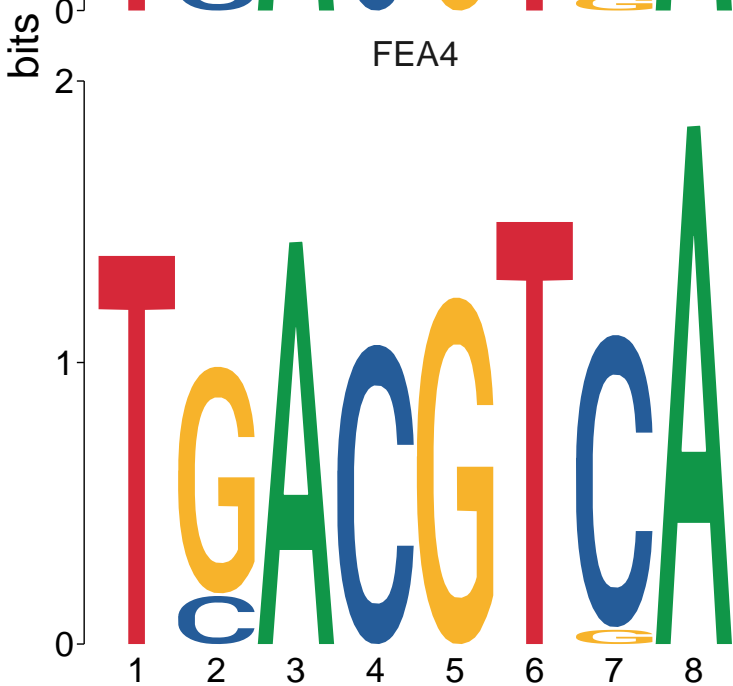
E2FA



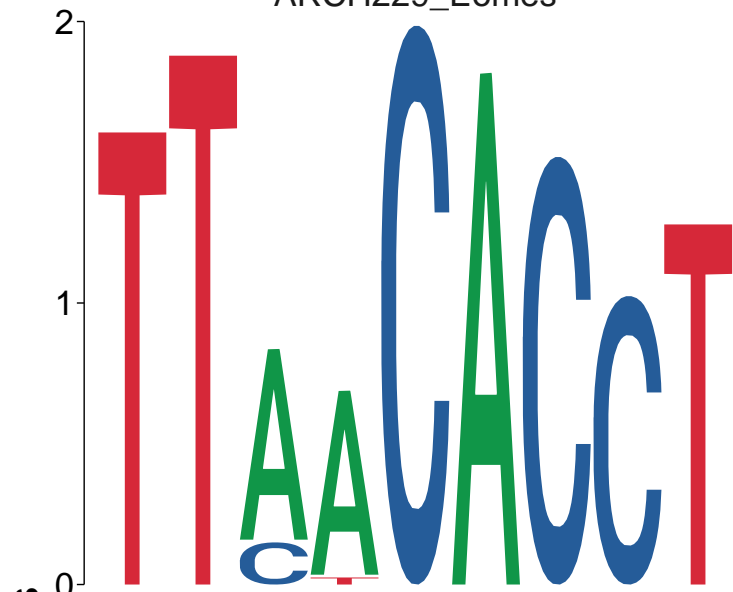
ARCH226_FEA4



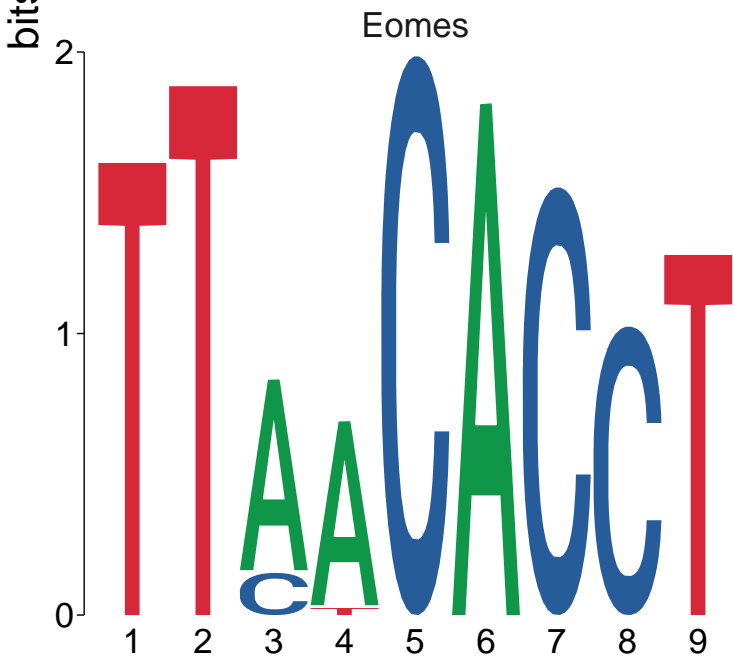
FEA4



ARCH229_Eomes



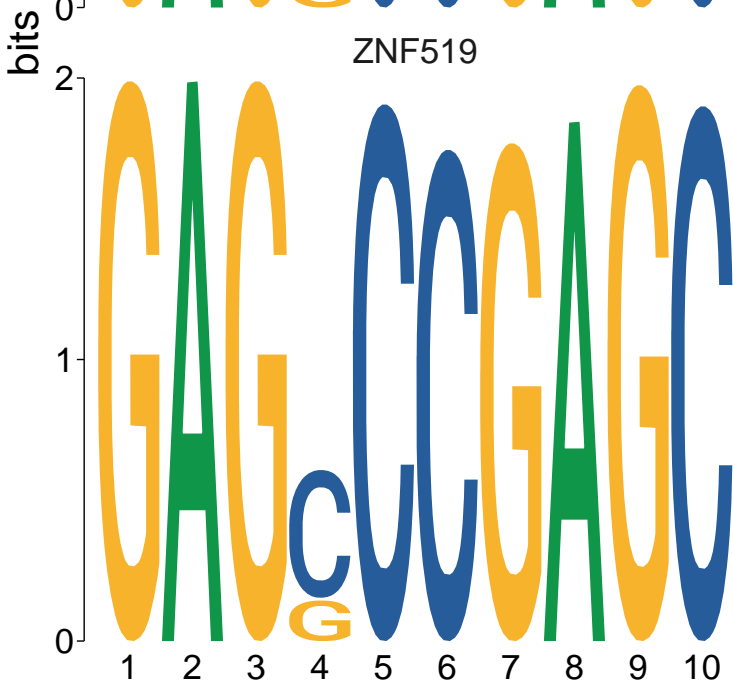
Eomes



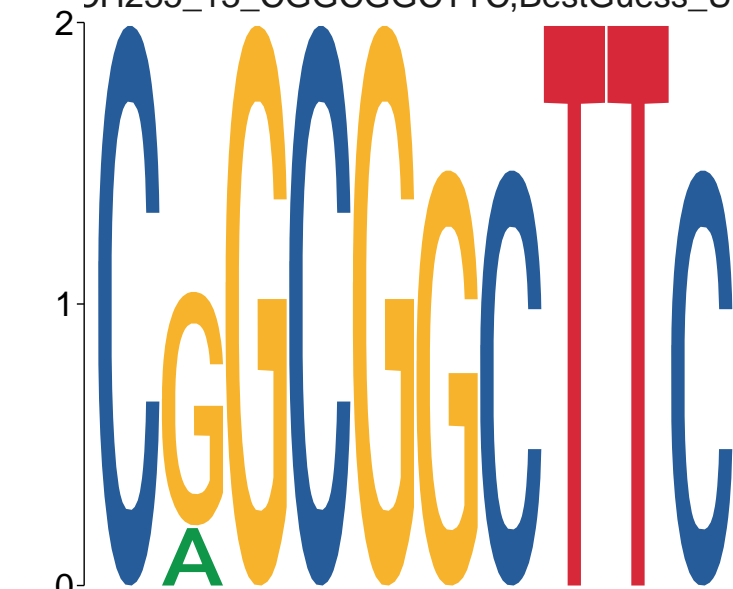
ARCH234_ZNF519



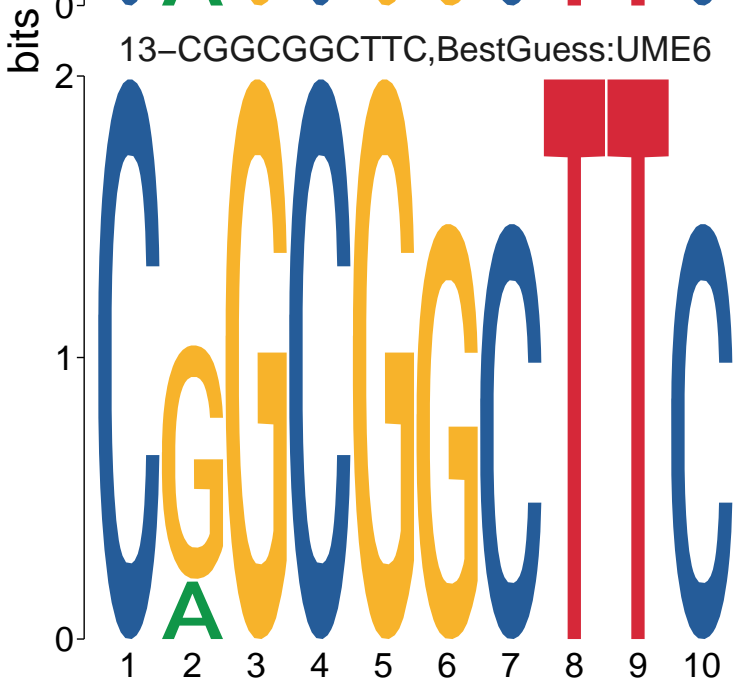
ZNF519



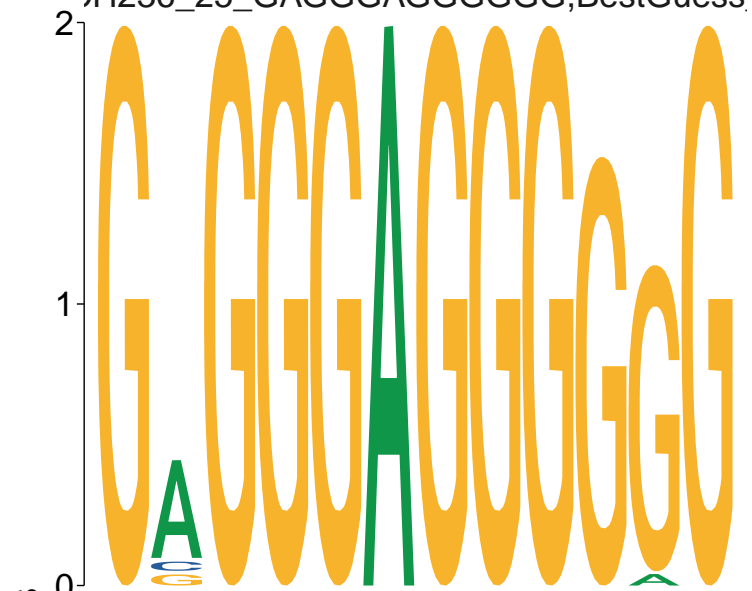
CH235_13_CGGCGGCTTC,BestGuess_UN



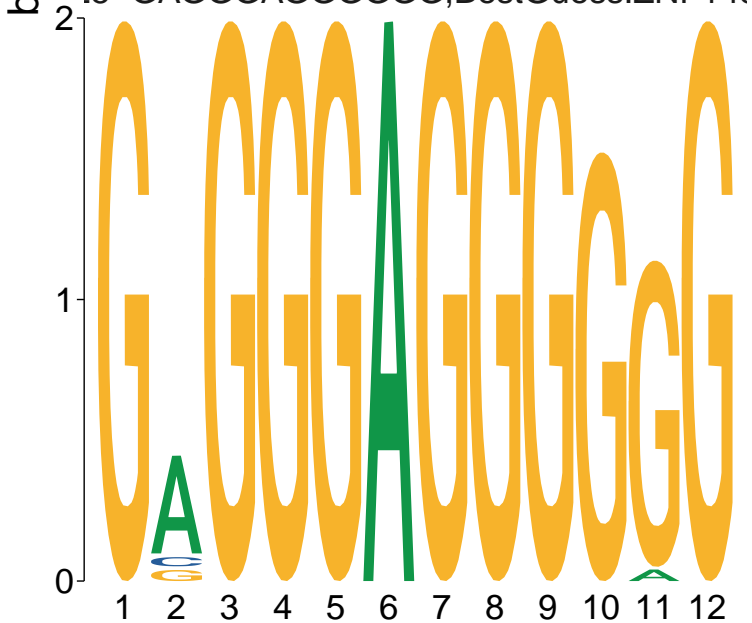
13-CGGCGGCTTC,BestGuess:UME6



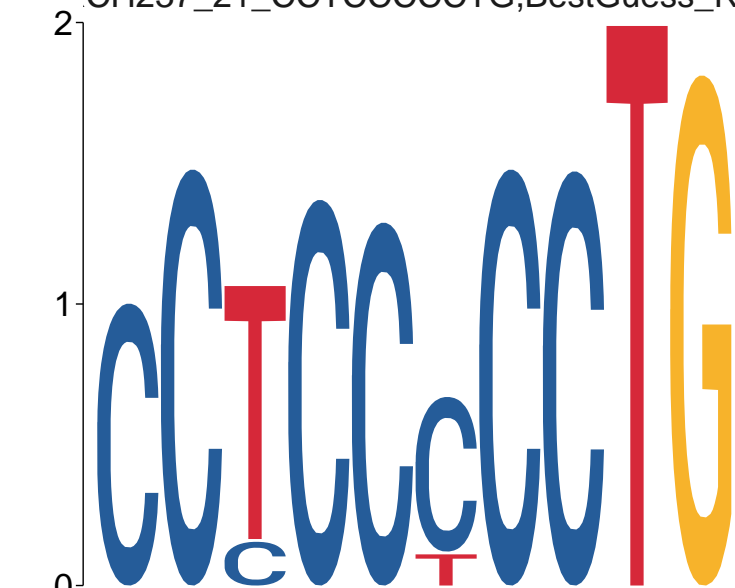
2:H236_25_GAGGGAGGGGGG,BestGuess:



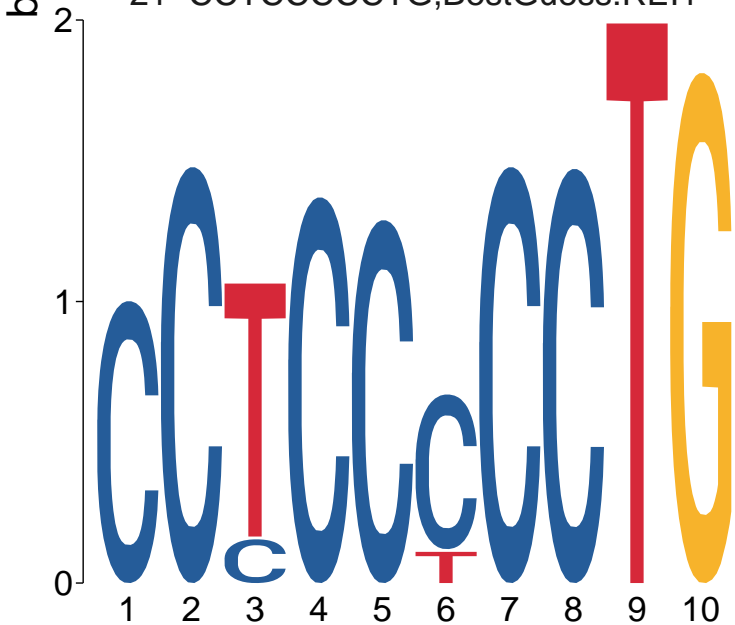
25-GAGGGAGGGGGG,BestGuess:ZNF148



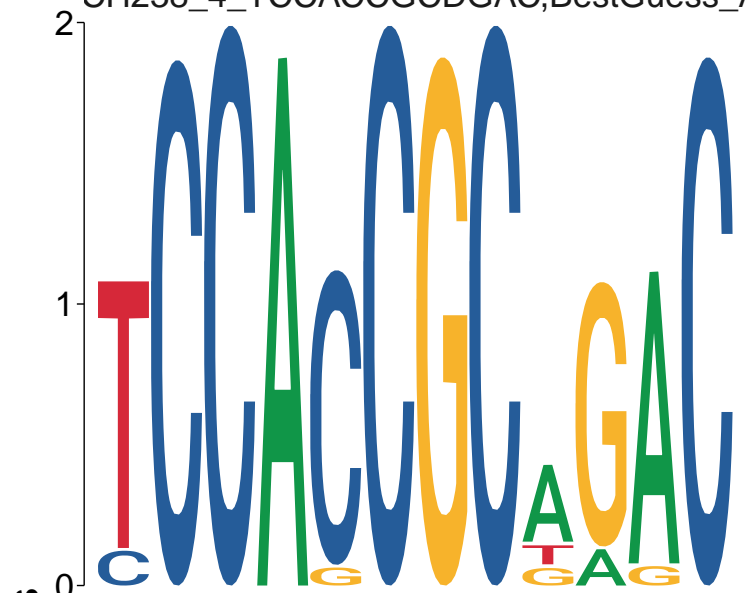
CH237_21_CCTCCCCCTG,BestGuess_RI



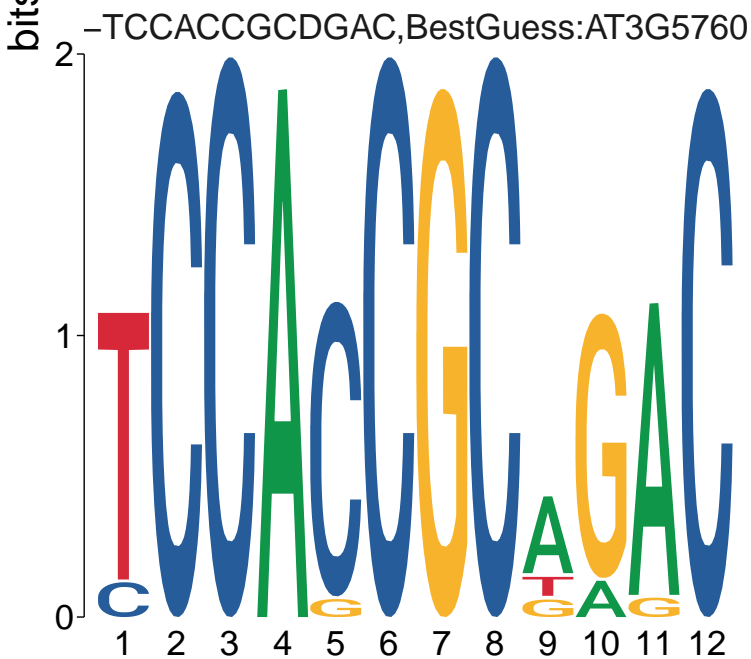
21-CCTCCCCCTG,BestGuess:REI1



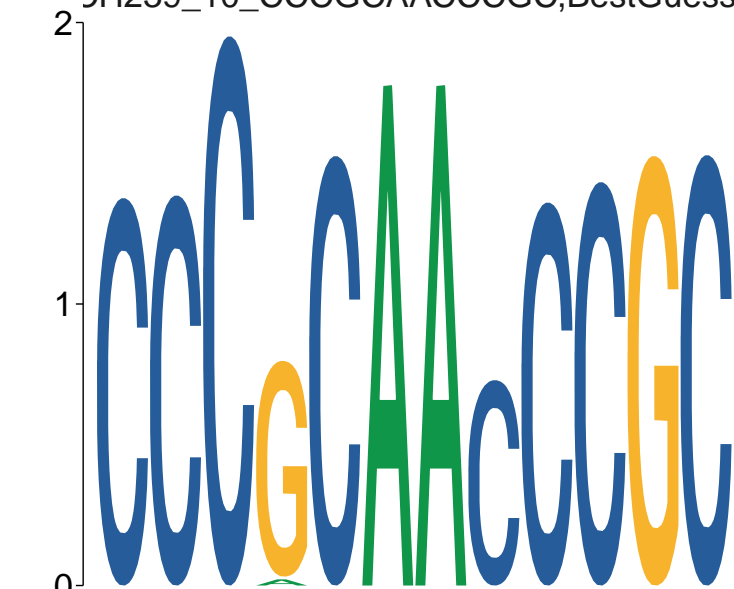
CH238_4_TCCACCGCDGAC,BestGuess_1



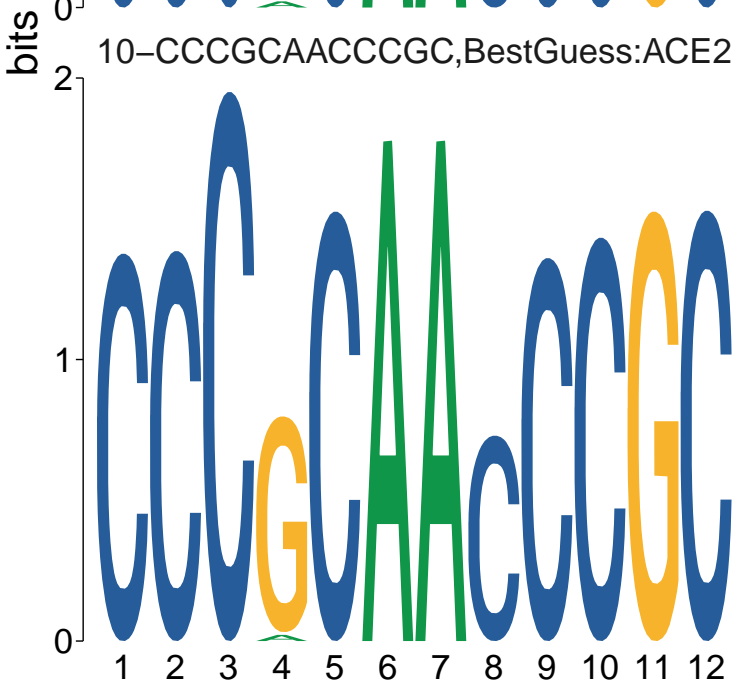
-TCCACCGCDGAC,BestGuess:AT3G5760



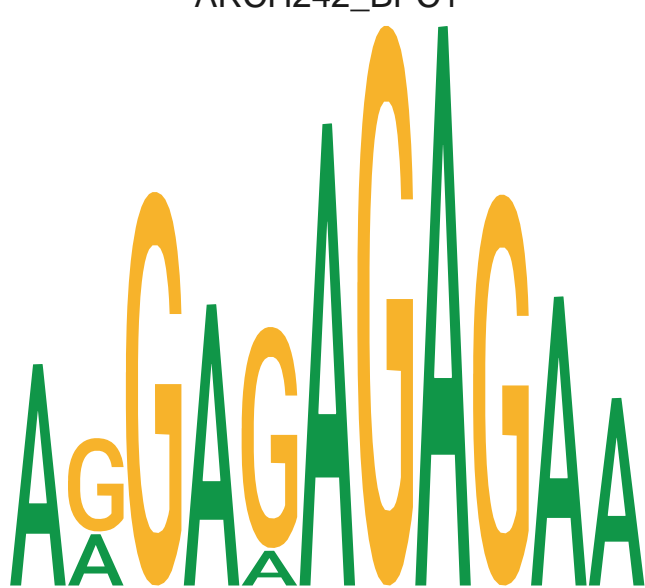
CH239_10_CCCGCAACCCGC,BestGuess_



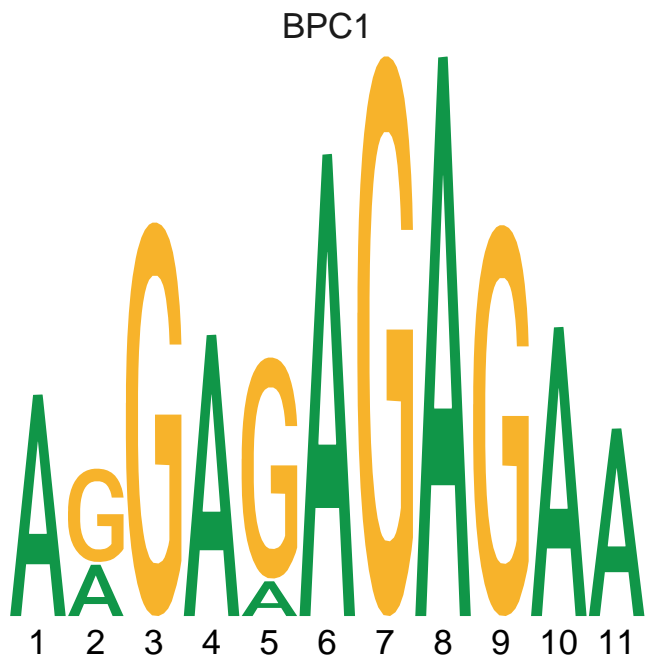
10-CCCGCAACCCGC,BestGuess:ACE2



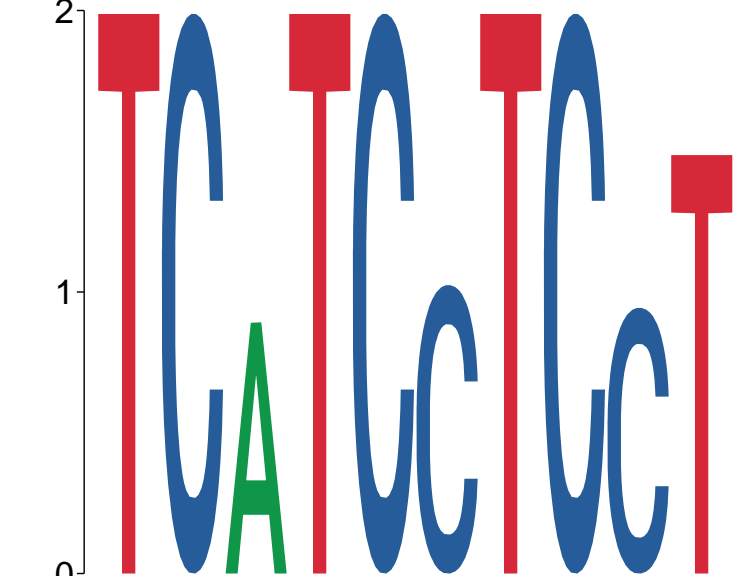
ARCH242_BPC1



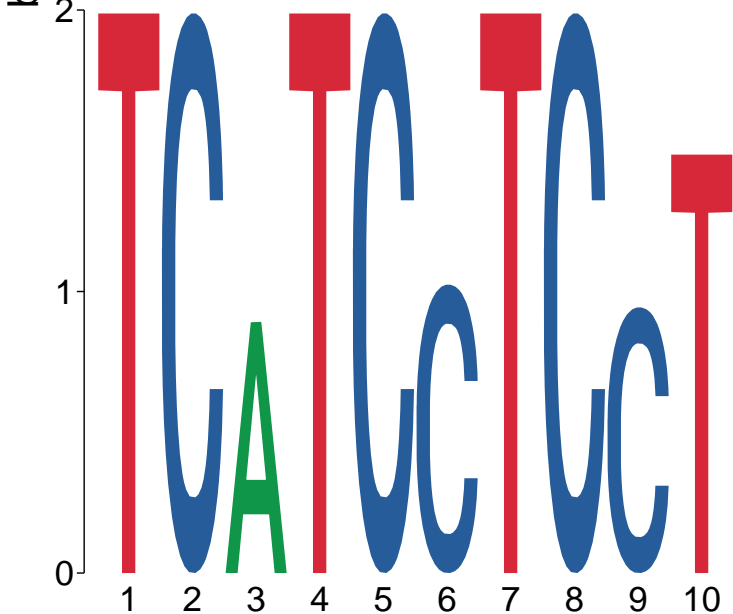
BPC1



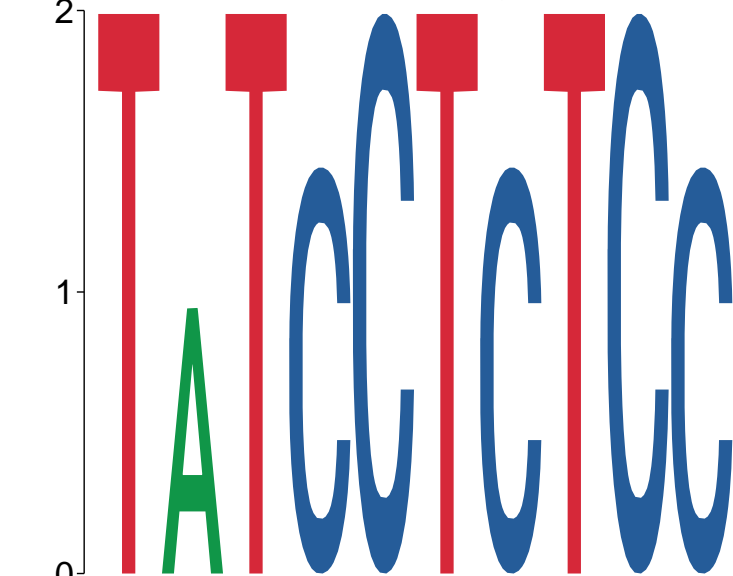
CH243_19_TCATCCTCCT,BestGuess_TF:



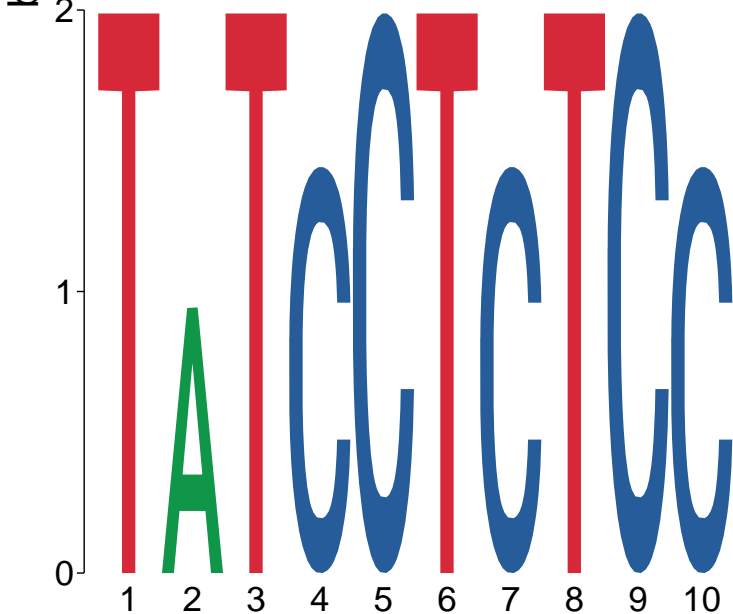
19-TCATCCTCCT,BestGuess:TF3A



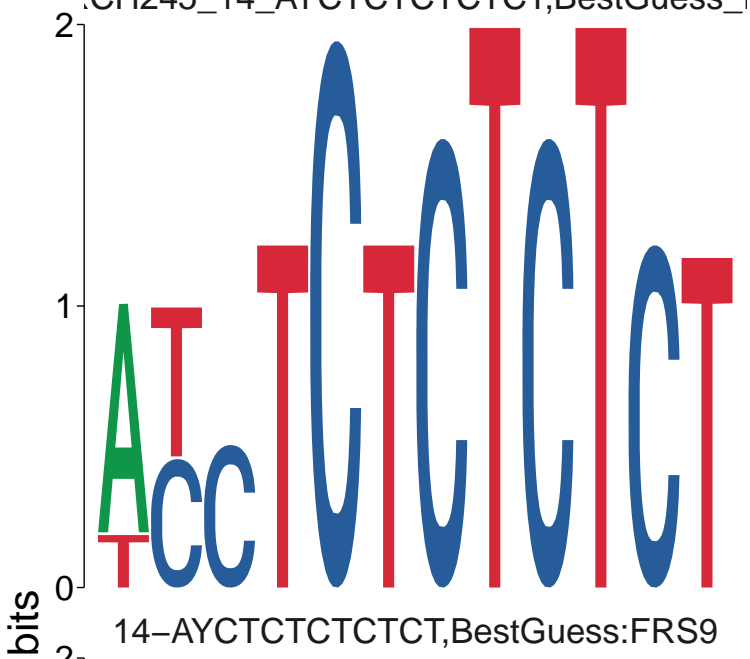
CH244_11_TATCCTCTCC,BestGuess_SR



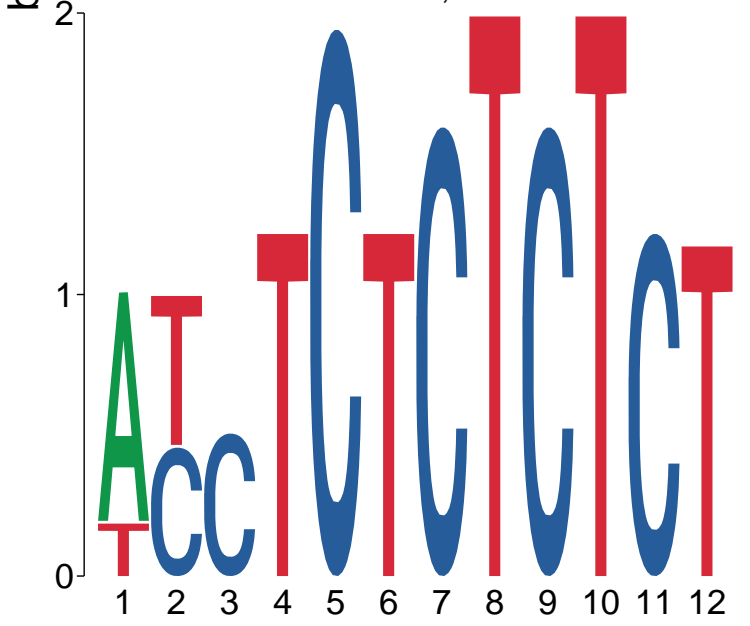
11-TATCCTCTCC,BestGuess:SRSF2



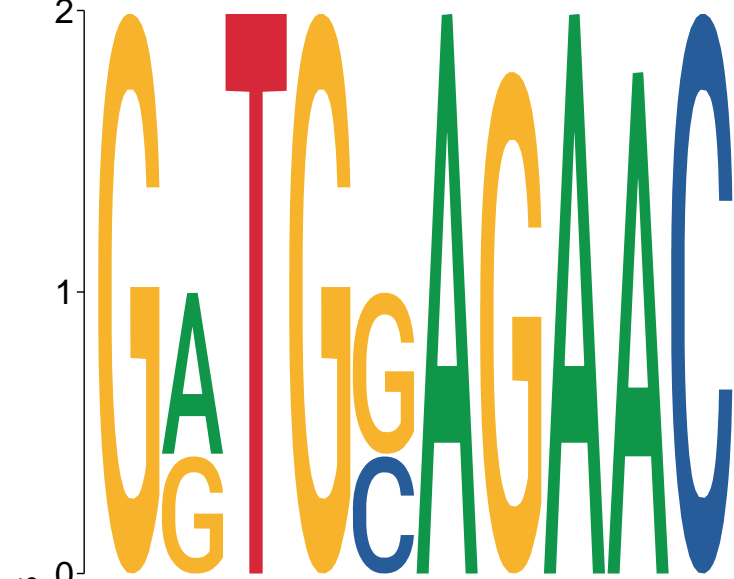
CH245_14_AYCTCTCTCTCT, BestGuess_



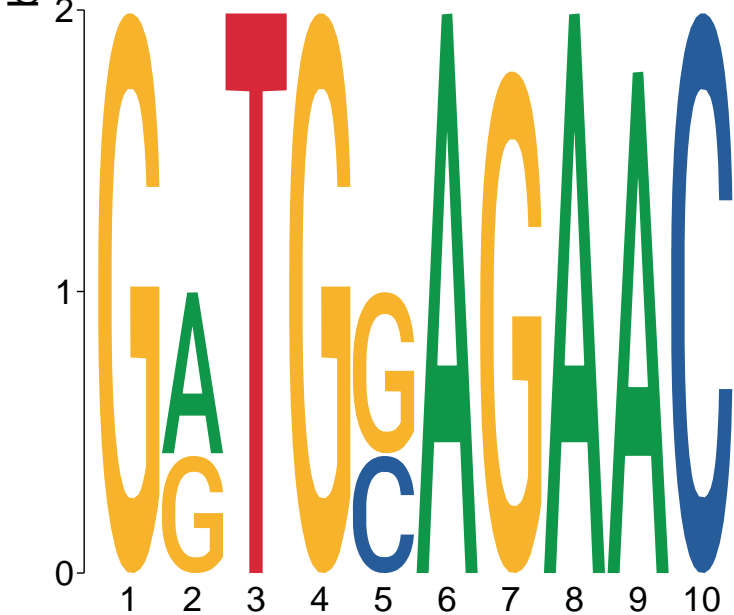
14-AYCTCTCTCTCT, BestGuess:FRS9



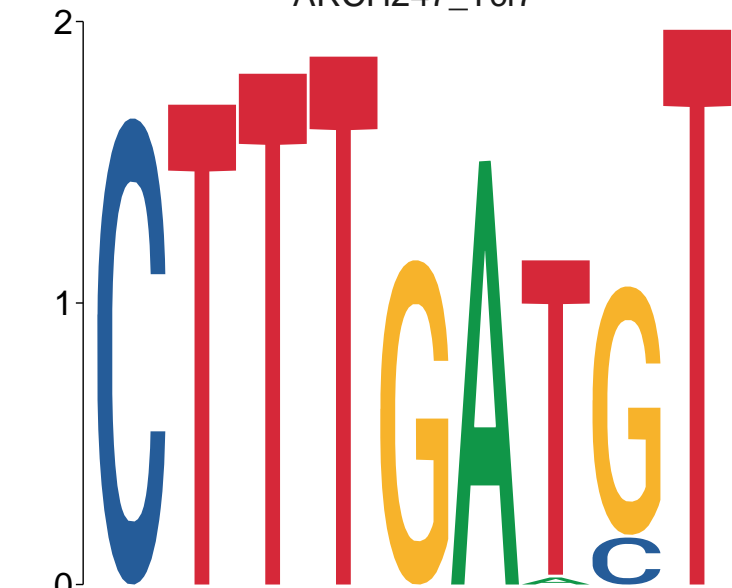
CH246_1_GRTGSAGAAC,BestGuess_LIN



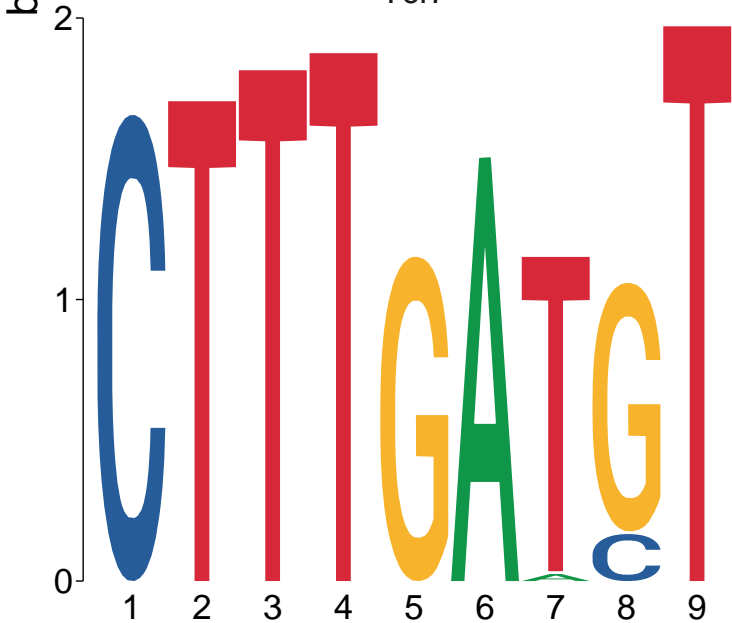
1-GRTGSAGAAC,BestGuess:LIN28A



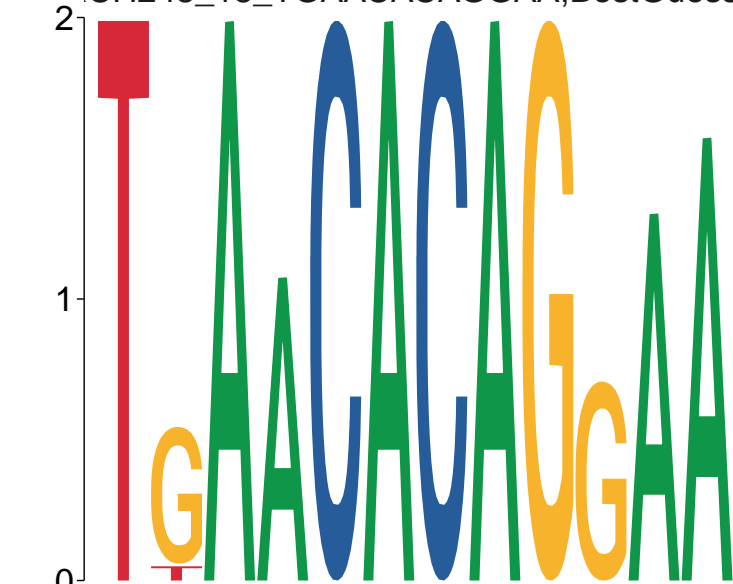
ARCH247_Tcf7



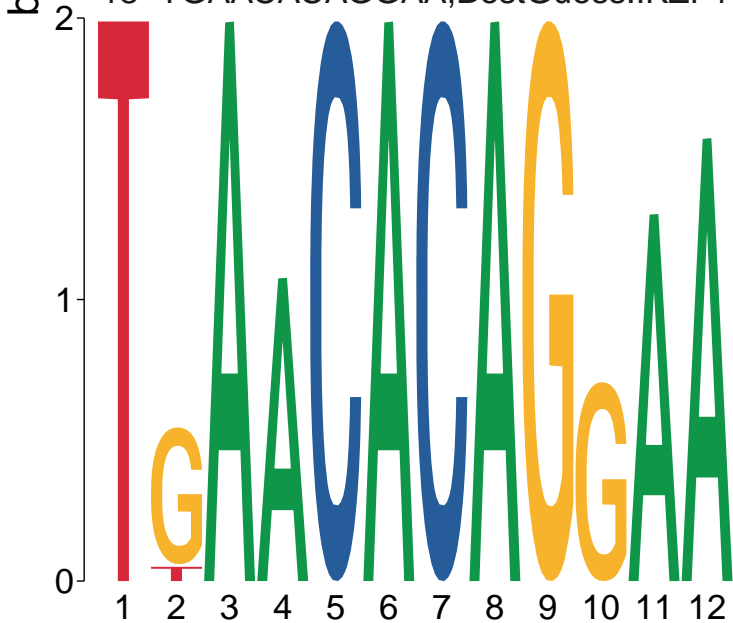
Tcf7



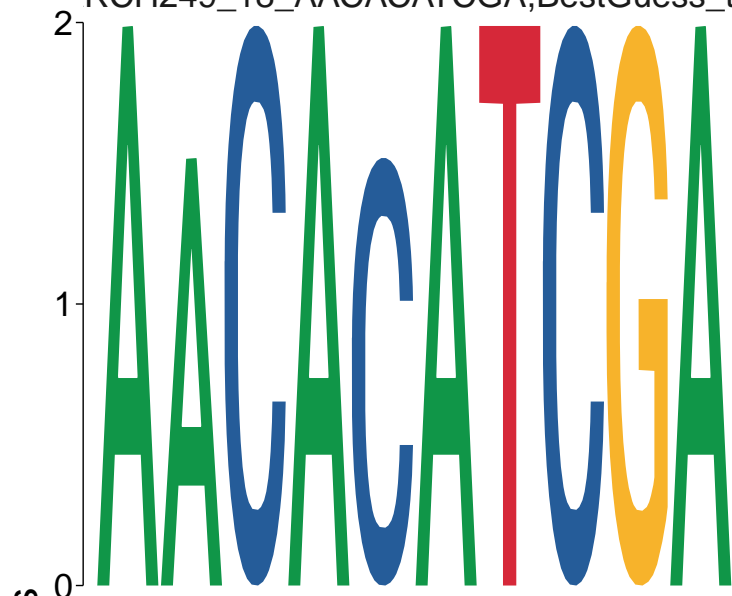
CH248_18_TGAACACAGGAA,BestGuess_



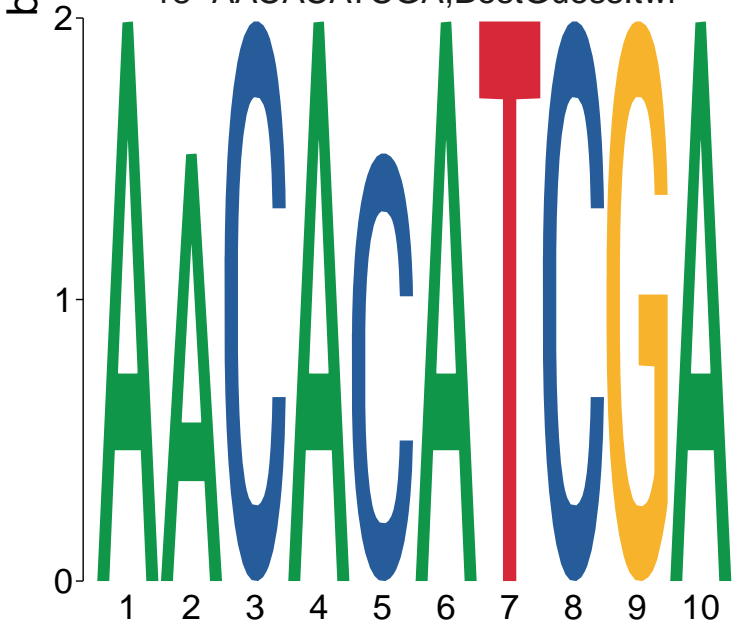
18-TGAACACAGGAA,BestGuess:IKZF1



RCH249_18_AACACATCGA,BestGuess_tv



18-AACACATCGA,BestGuess:twi



CH250_11_ACTCACAGAAAA,BestGuess_

2

1

0

bits

11-ACTCACAGAAAA,BestGuess:Tv_0257

2

1

0

1

2

3

4

5

6

7

8

9

10

11

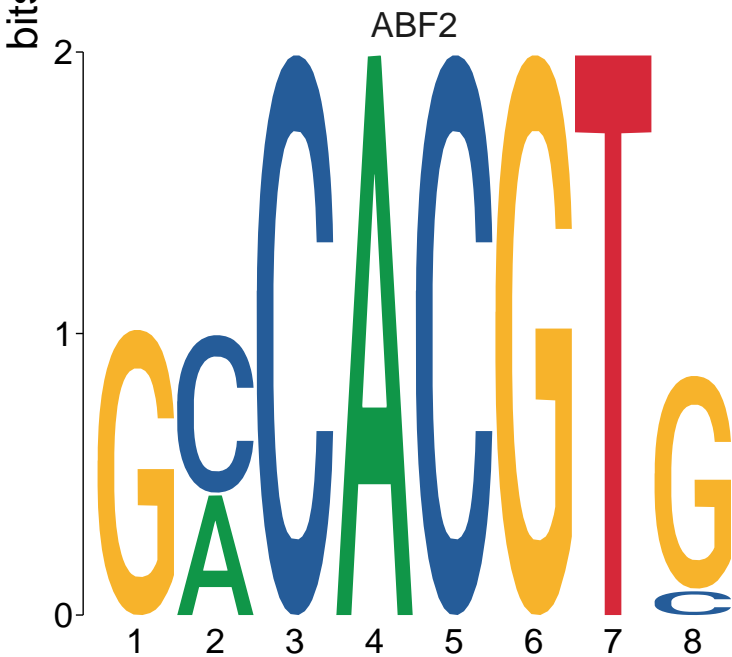
12



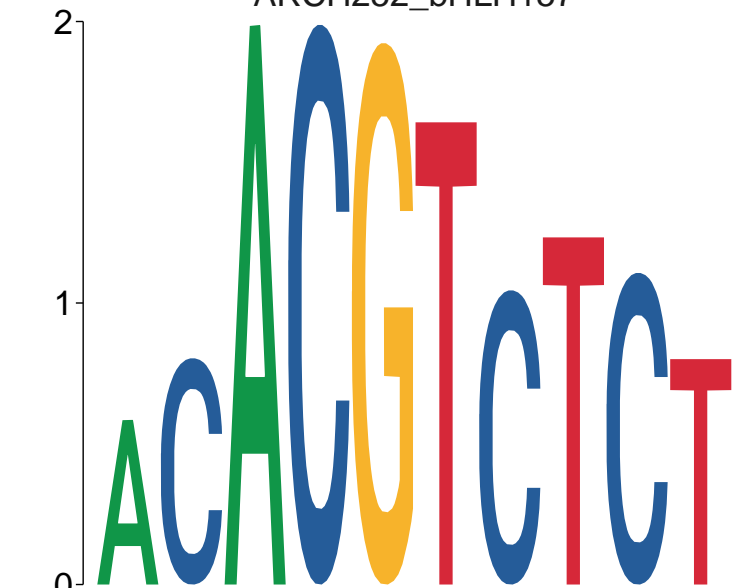
ARCH251_ABIF2



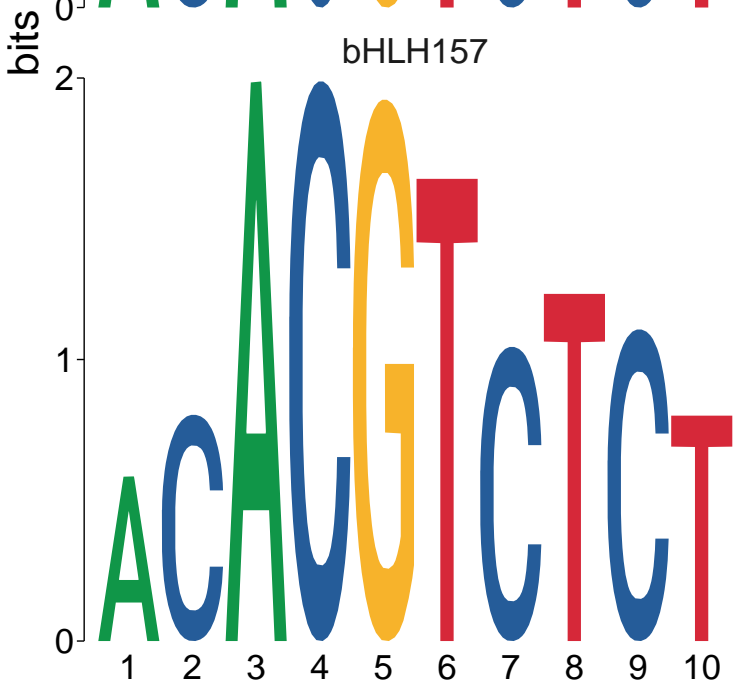
ABIF2



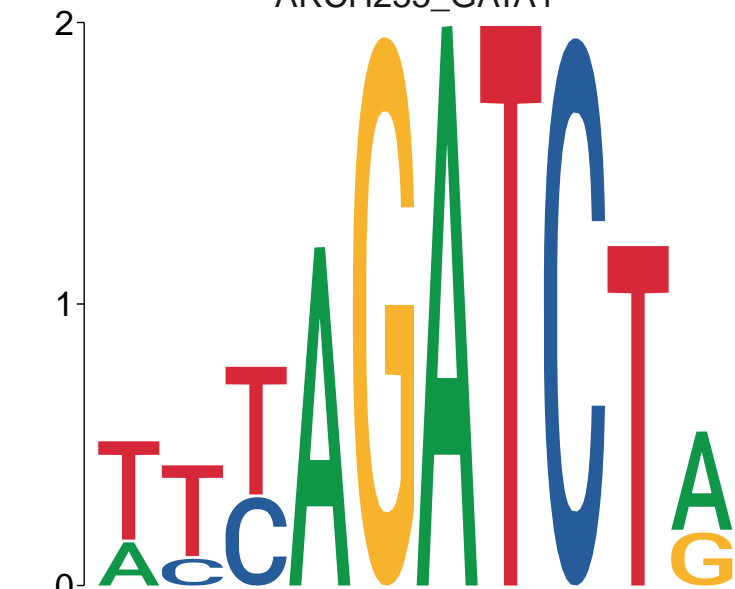
ARCH252_bHLH157



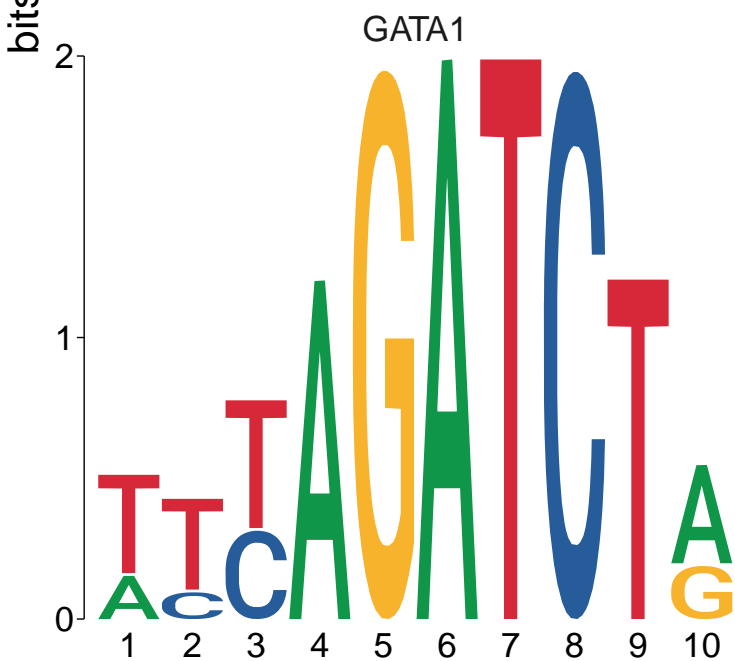
bHLH157



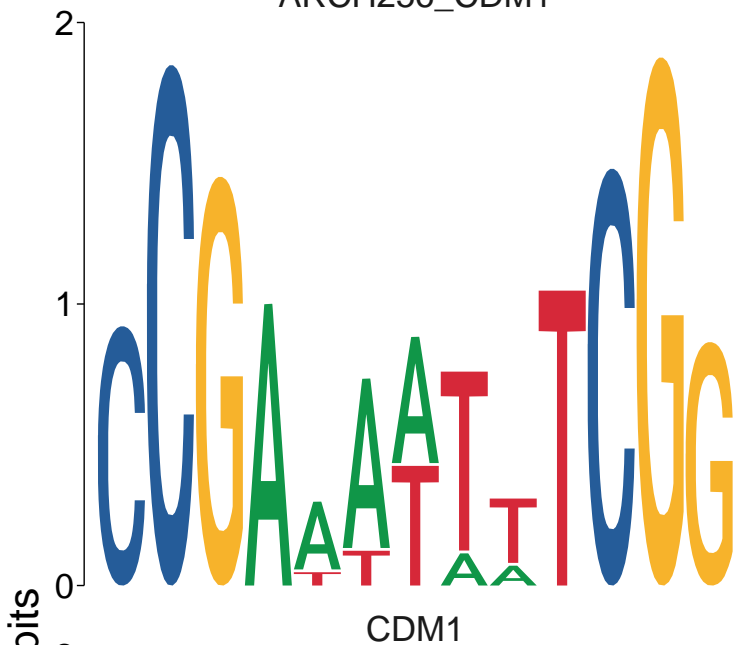
ARCH255_GATA1



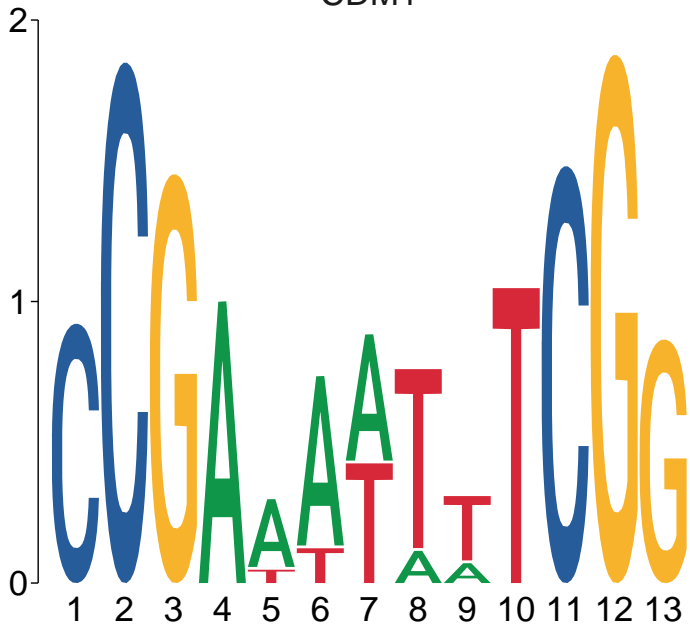
GATA1



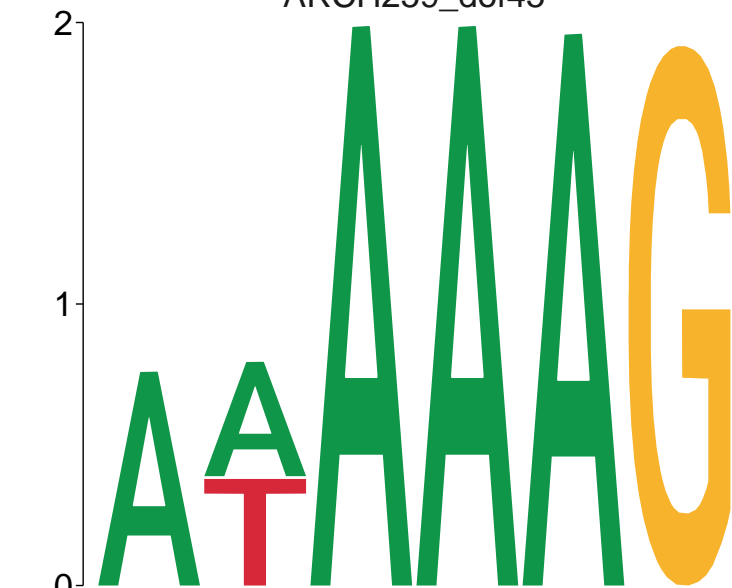
ARCH256_CDM1



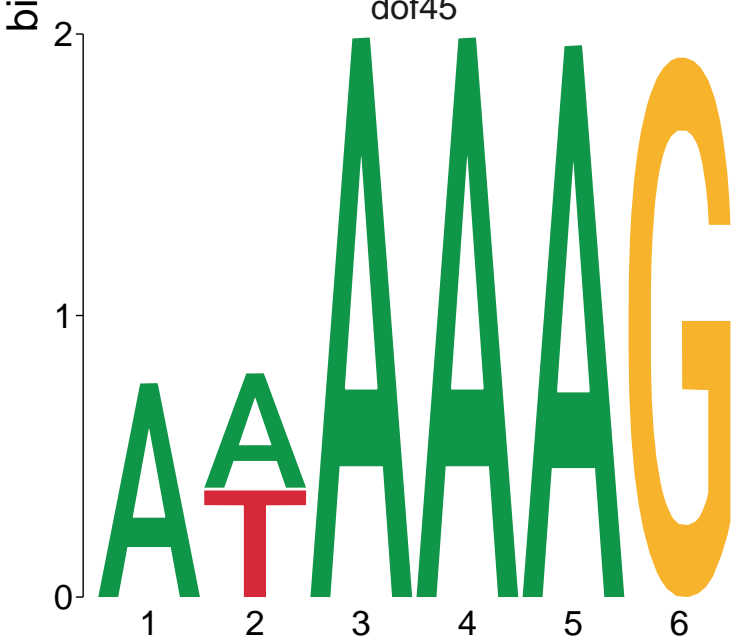
CDM1



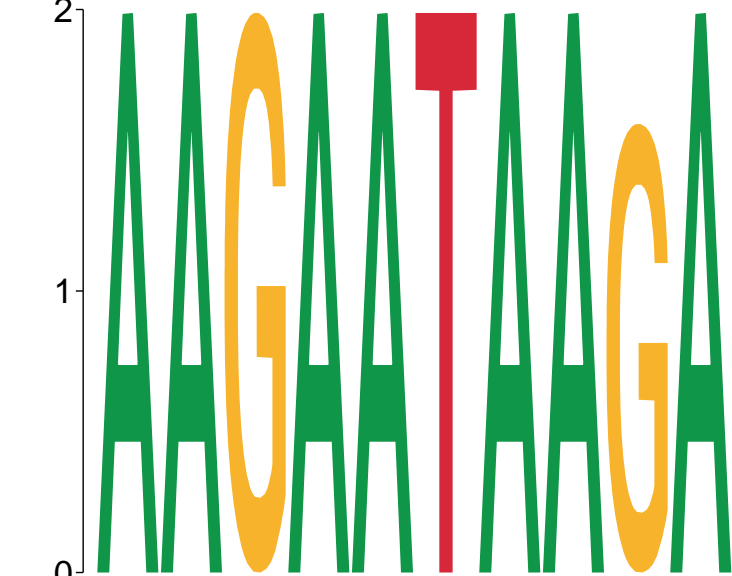
ARCH259_dof45



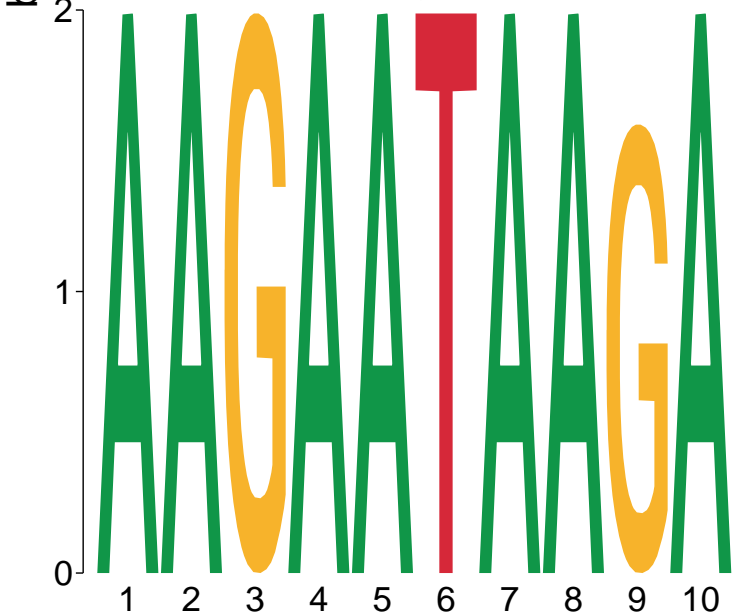
dof45



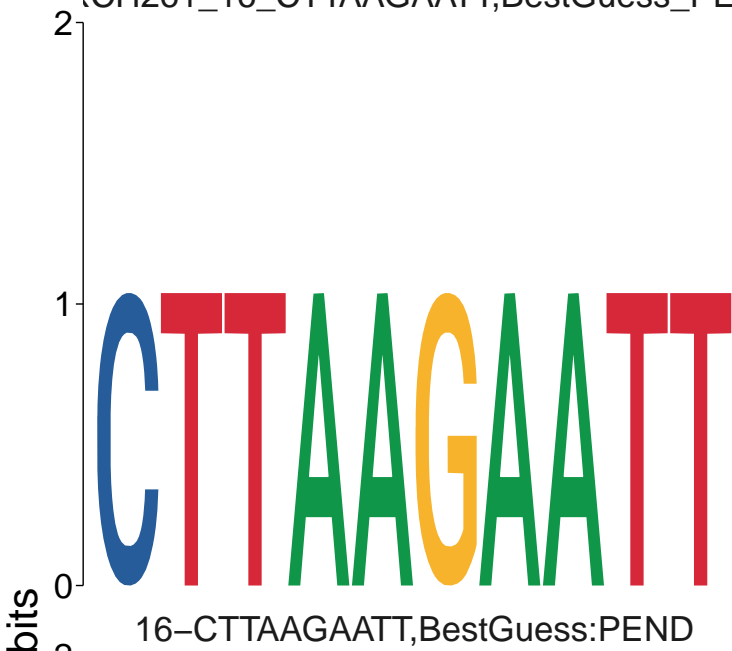
CH260_18_AAGAATAAGA,BestGuess_KA



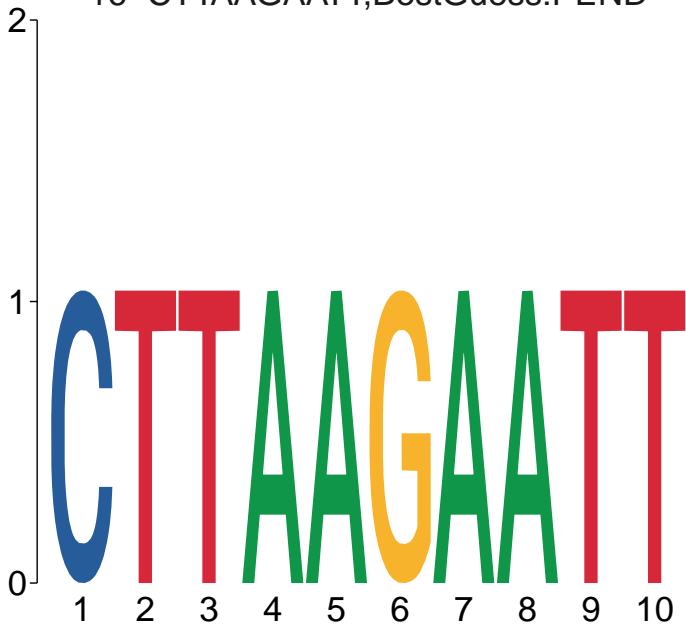
18-AAGAATAAGA,BestGuess:KAN2



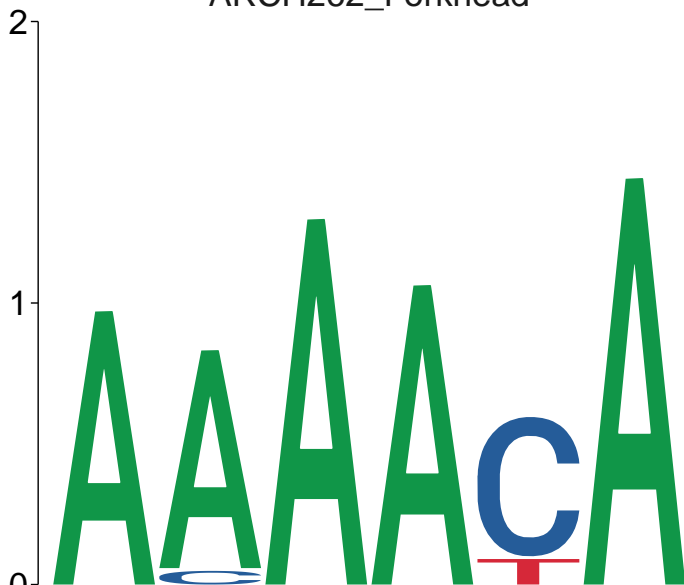
CH261_16_CTTAAGAATT,BestGuess_PEN



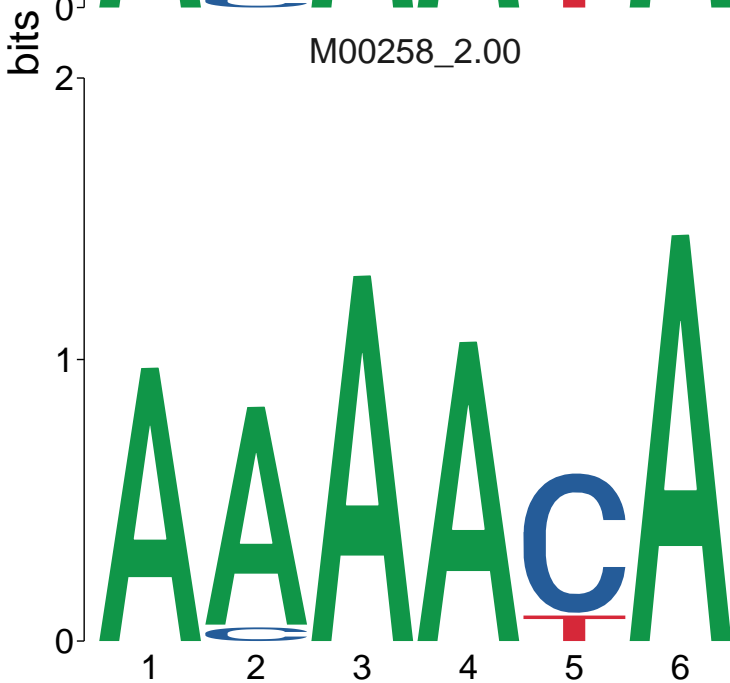
16-CTTAAGAATT,BestGuess:PEND



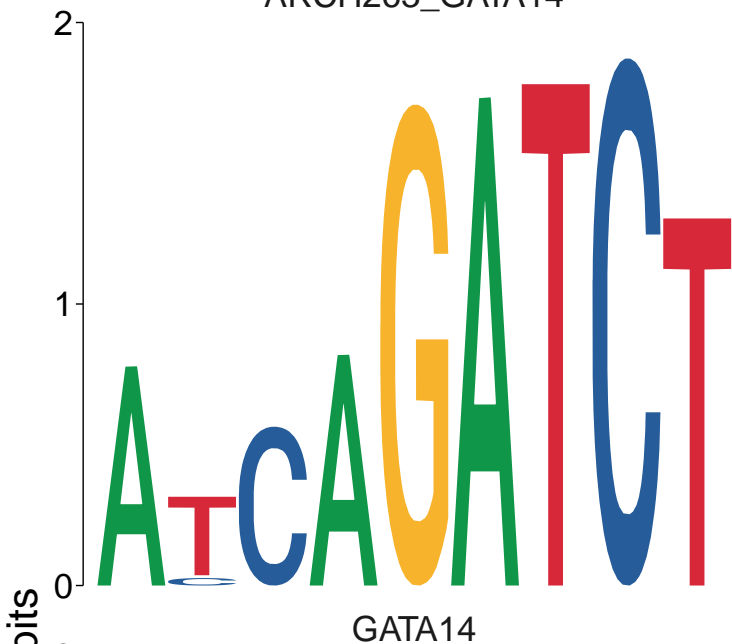
ARCH262_Forkhead



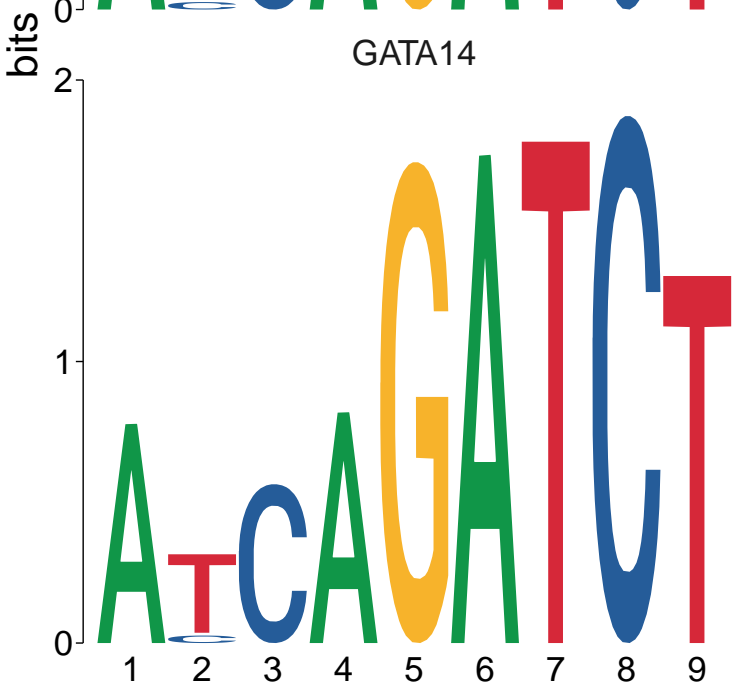
M00258_2.00



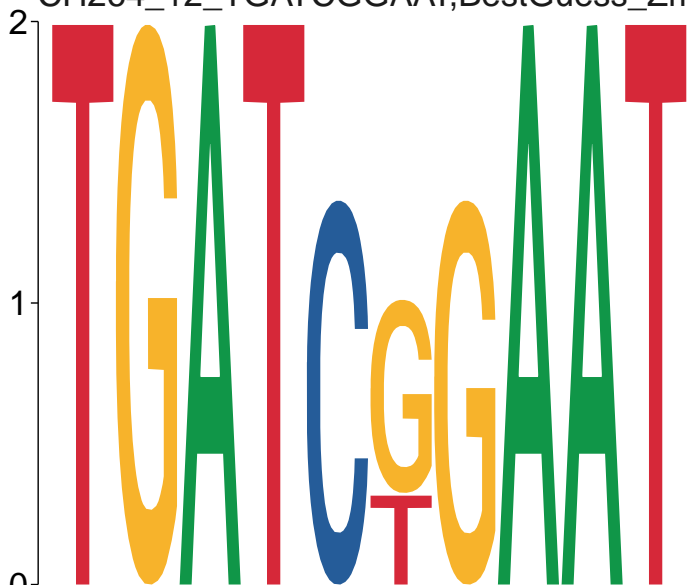
ARCH263_GATA14



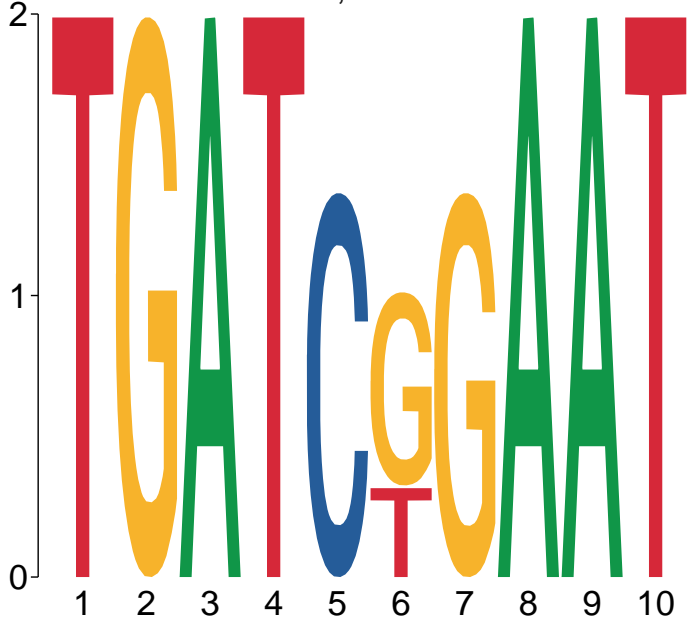
GATA14



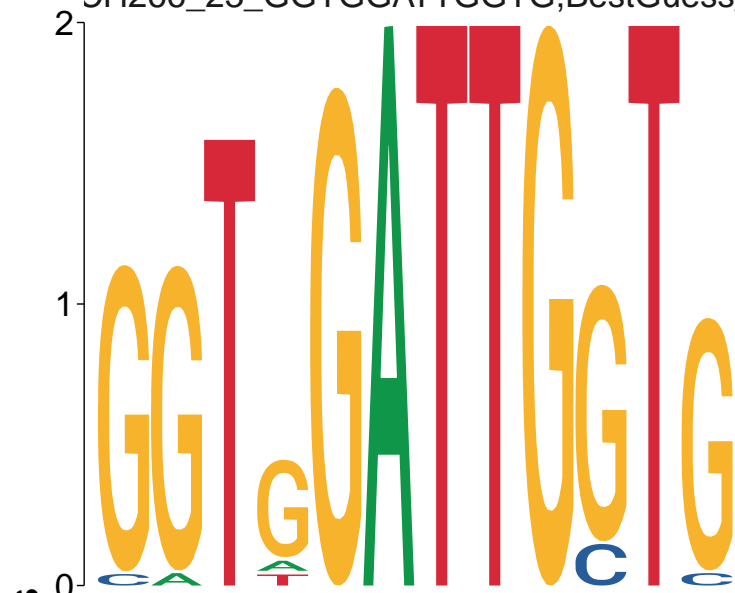
CH264_12_TGATCGGAAT,BestGuess_ZmI



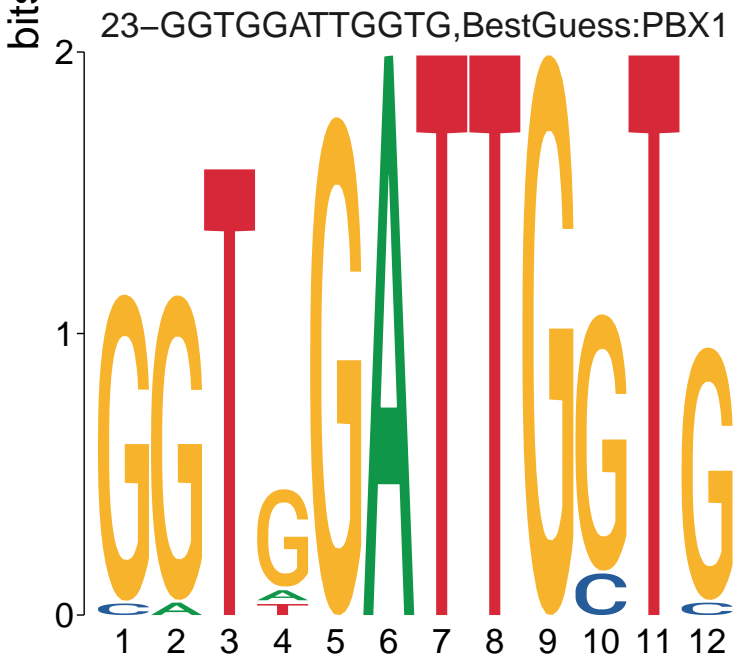
12-TGATCGGAAT,BestGuess:ZmHOX2a



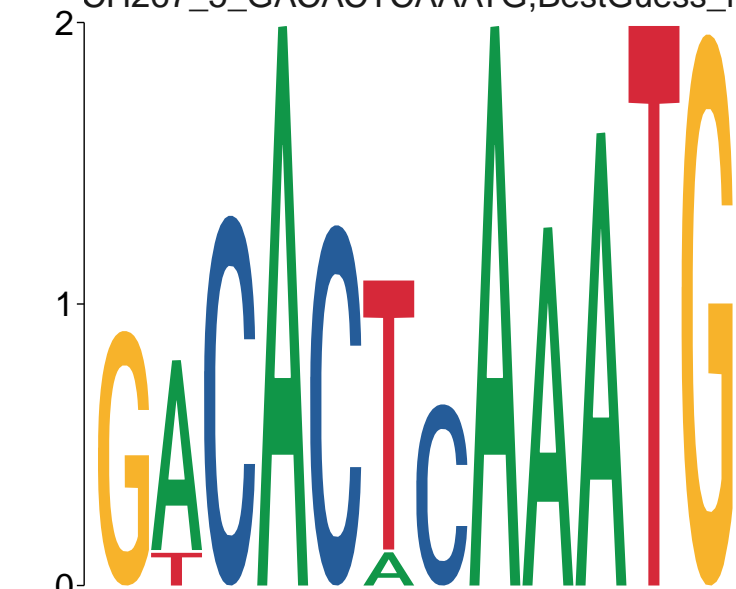
CH266_23_GGTGGATTGGTG,BestGuess_



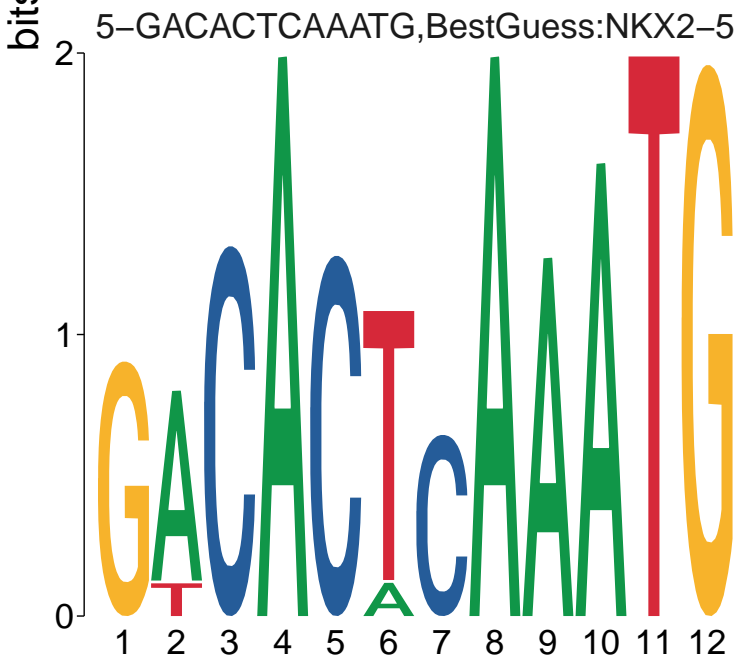
23-GGTGGATTGGTG,BestGuess:PBX1



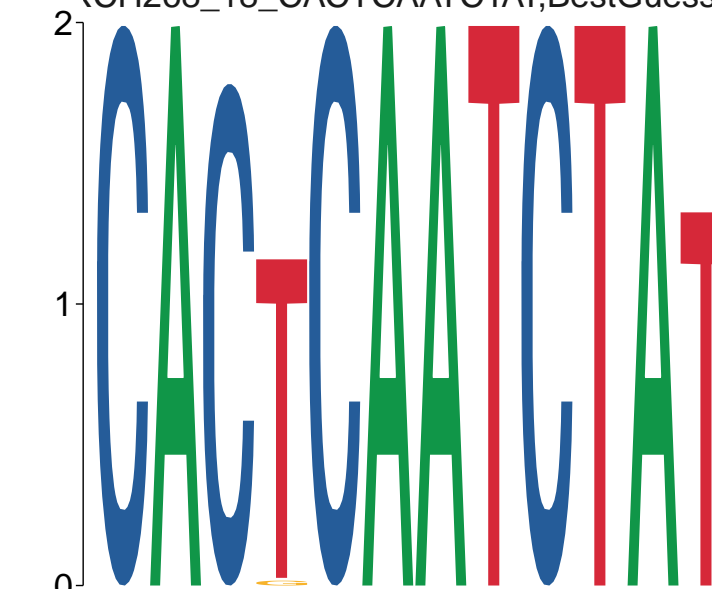
CH267_5_GACACTCAAATG,BestGuess_N



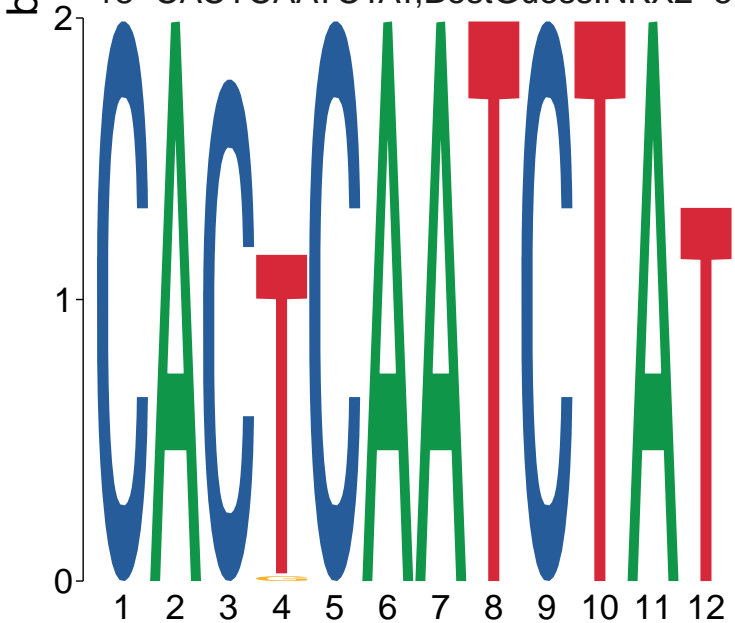
5-GACACTCAAATG,BestGuess:NKX2-5



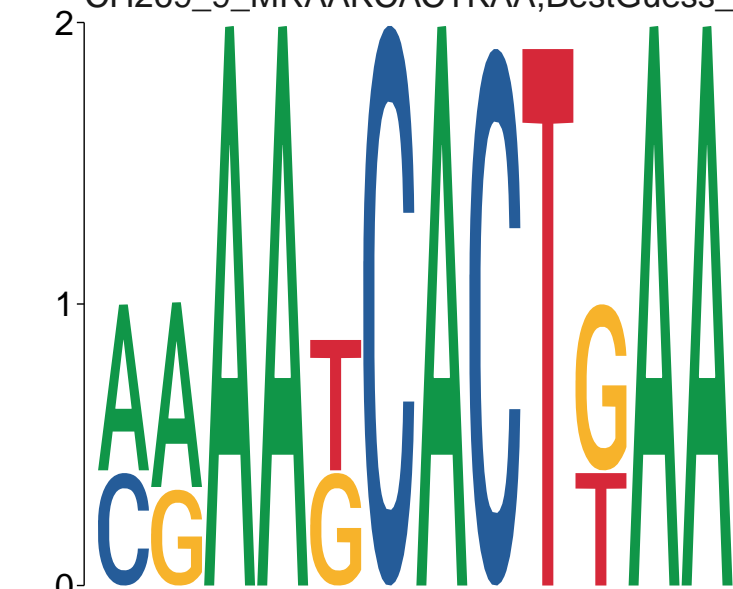
CH268_18_CACTCAATCTAT,BestGuess_1



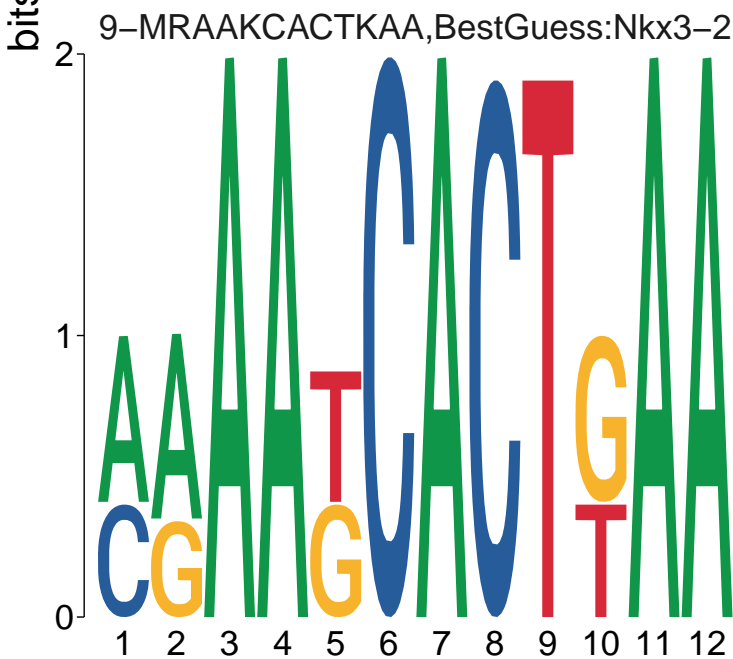
18-CACTCAATCTAT,BestGuess:NKX2-5



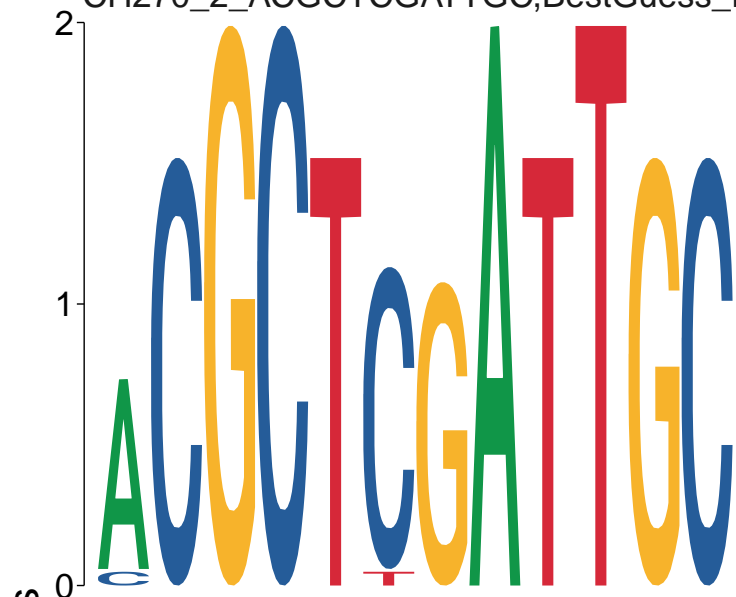
CH269_9_MRAAKCACTKAA,BestGuess_1



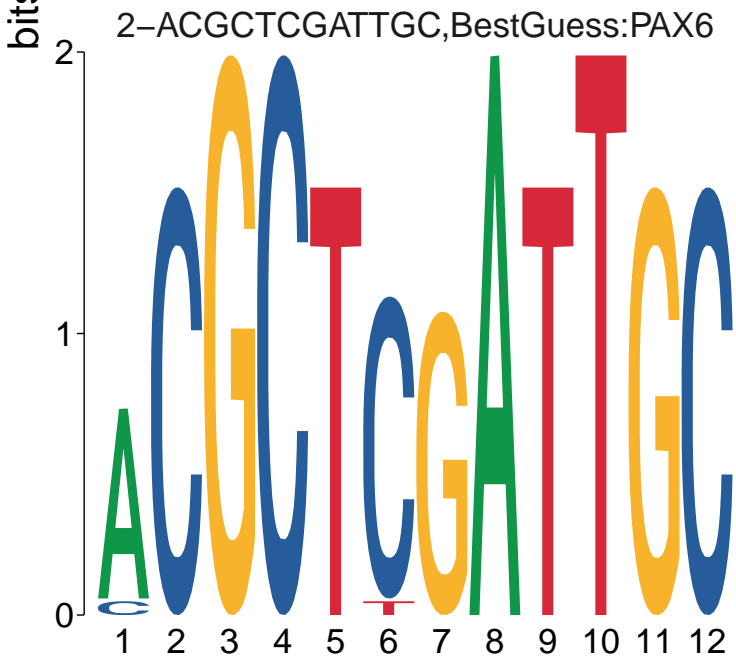
9-MRAAKCACTKAA,BestGuess:Nkx3-2



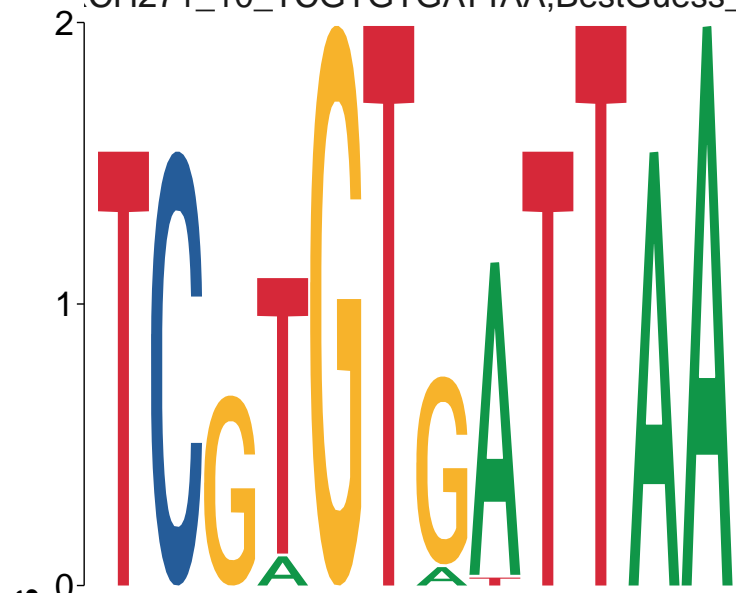
CH270_2_ACGCTCGATTGC,BestGuess_F



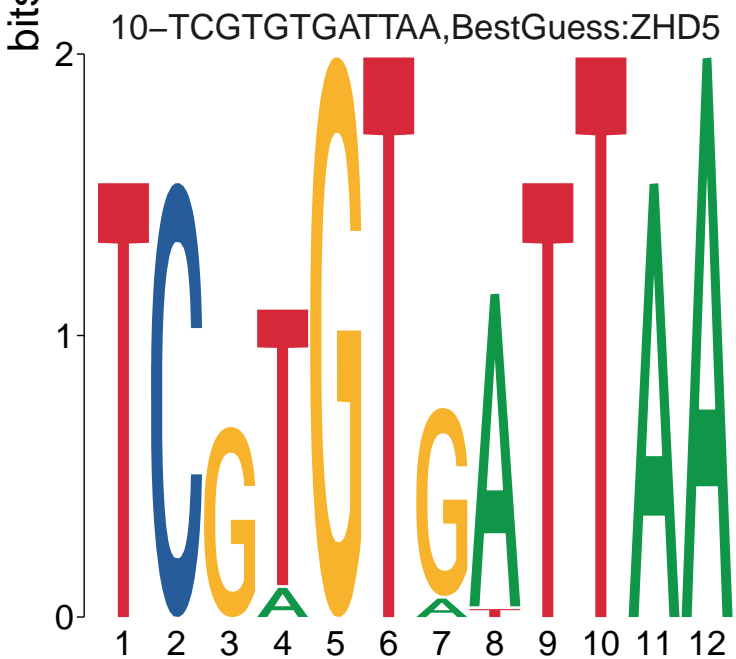
2-ACGCTCGATTGC,BestGuess:PAX6



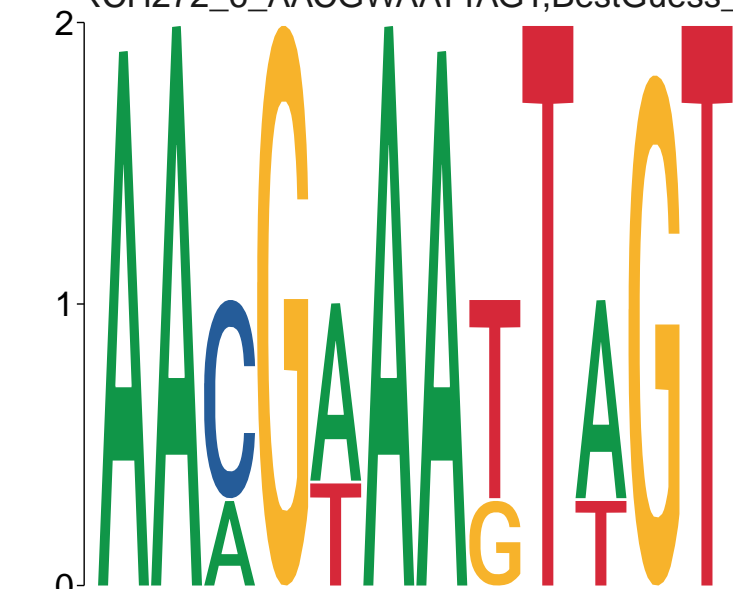
CH271_10_TCGTGTGATTAA,BestGuess_



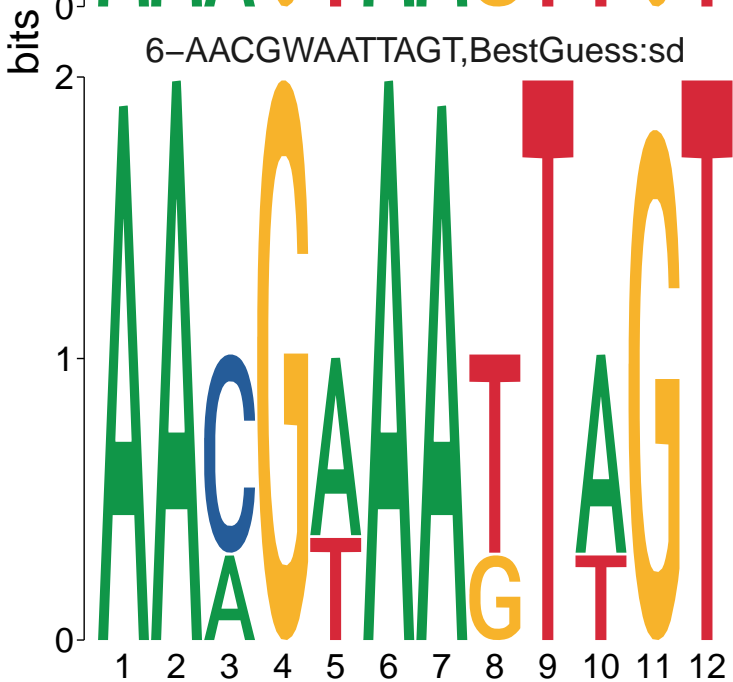
10-TCGTGTGATTAA,BestGuess:ZHD5



RCH272_6_AACGWAATTAGT,BestGuess_9



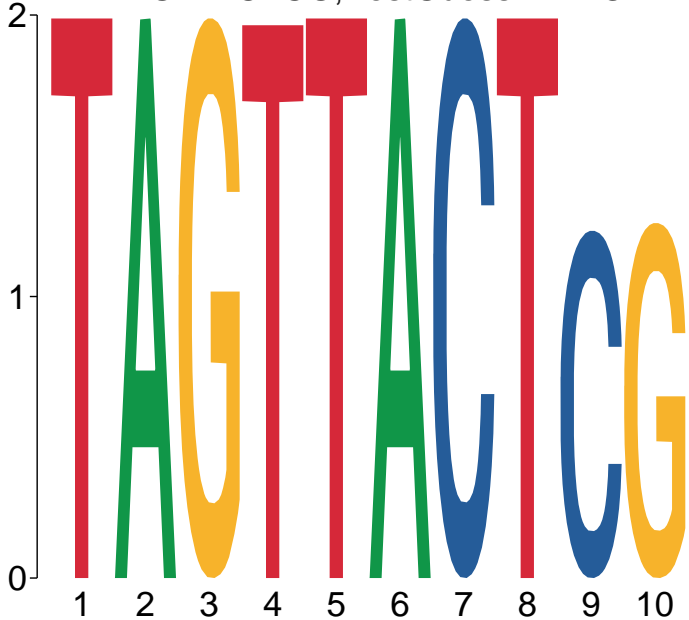
6-AACGWAATTAGT,BestGuess:sd



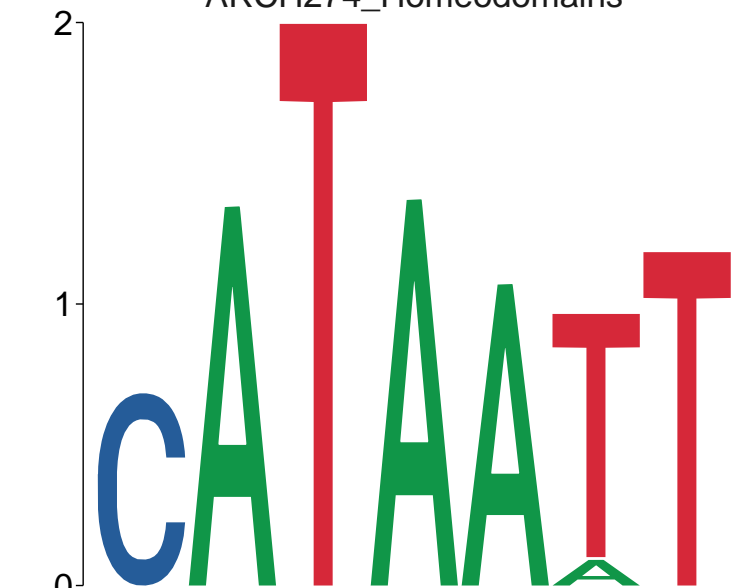
CH273_7_TAGTTACTCG,BestGuess_HMB



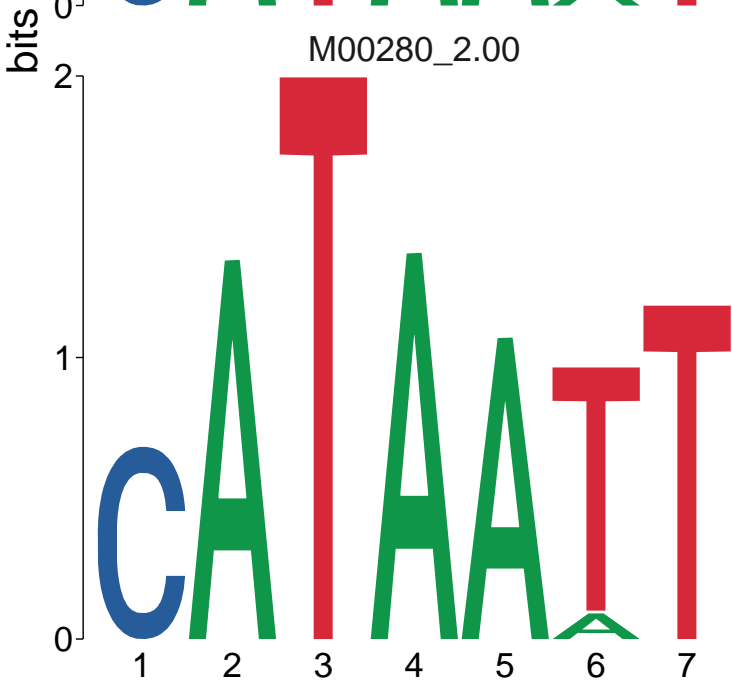
7-TAGTTACTCG,BestGuess:HMBOX1



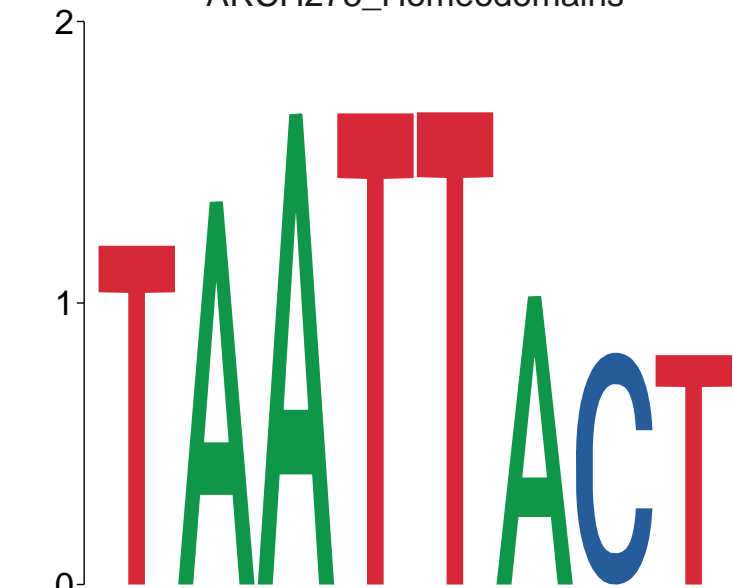
ARCH274_Homeodomains



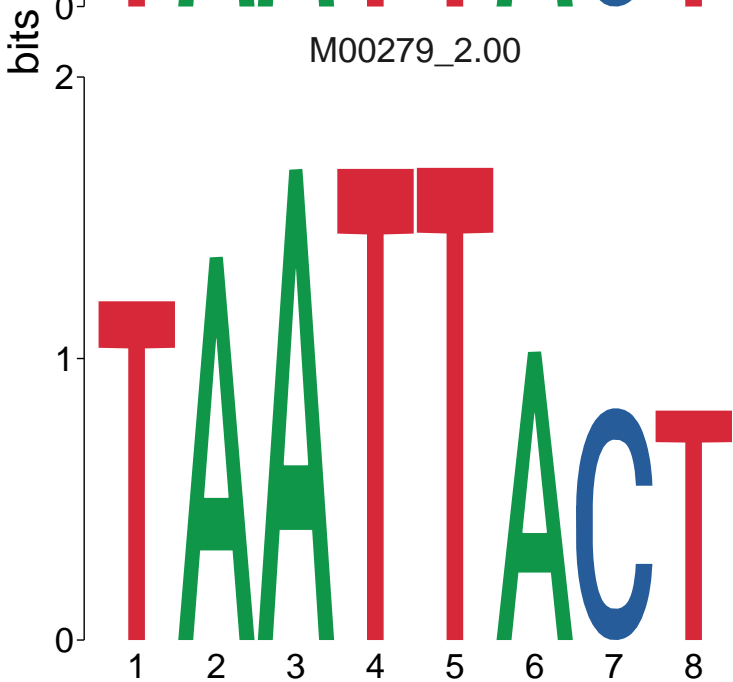
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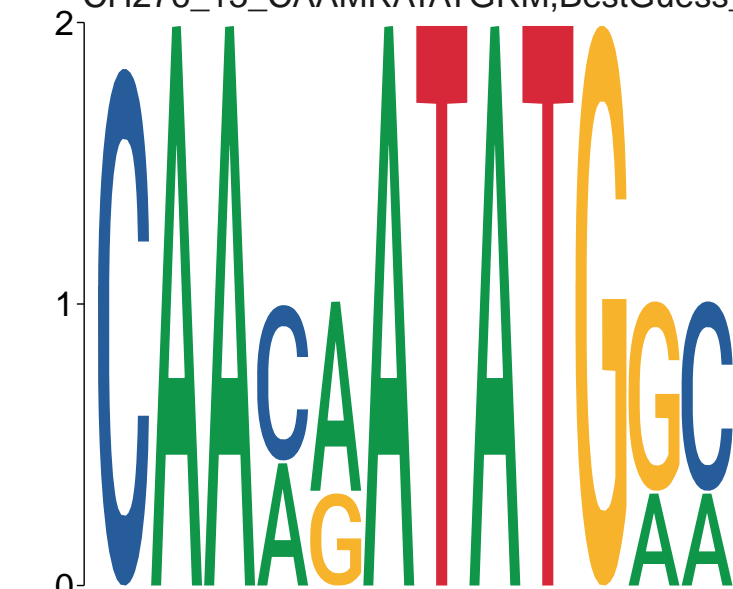
ARCH275_Homeodomains



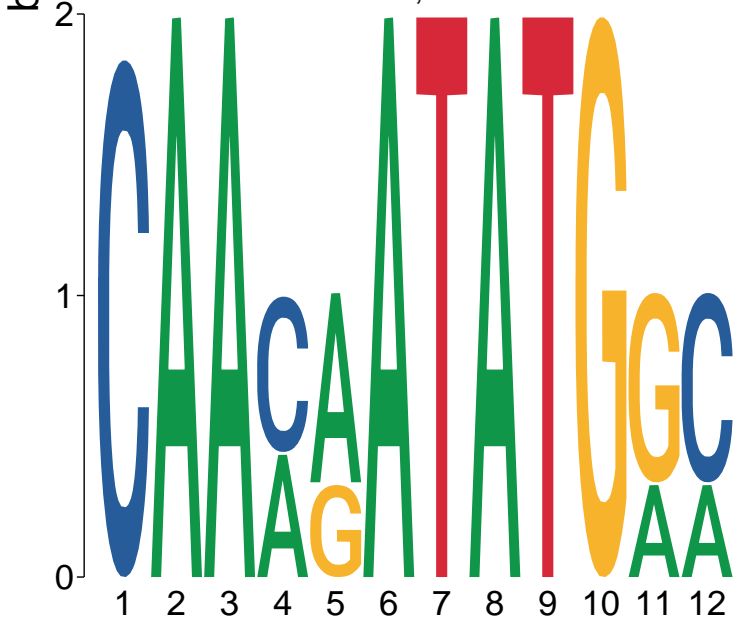
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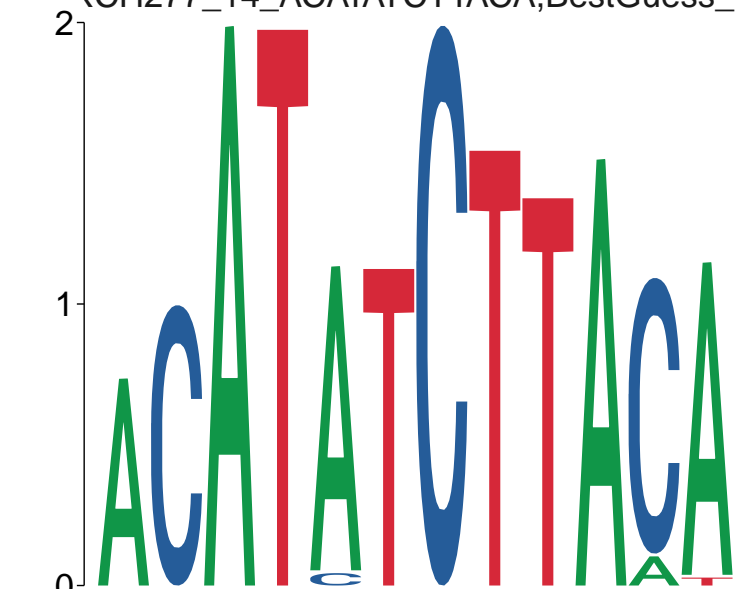
CH276_13_CAAMRATATGRM,BestGuess_



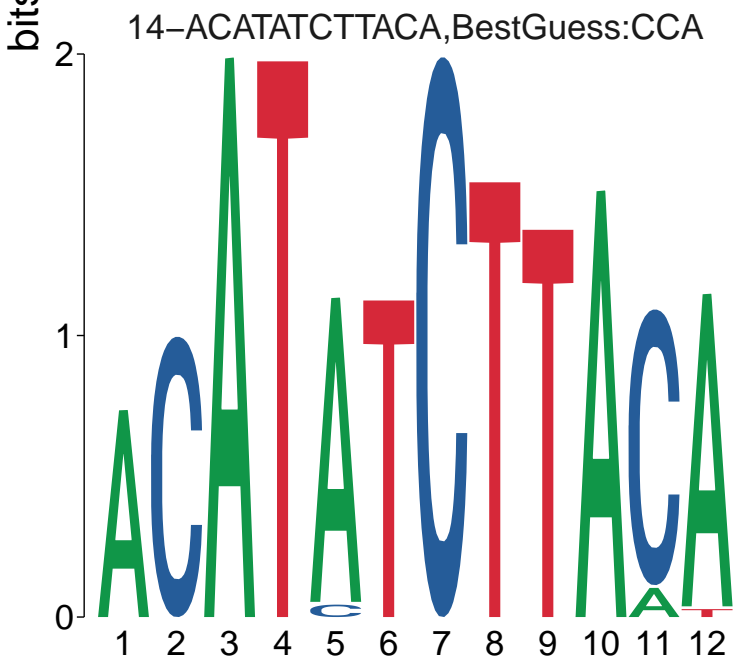
13-CAAMRATATGRM,BestGuess:BHLHE23



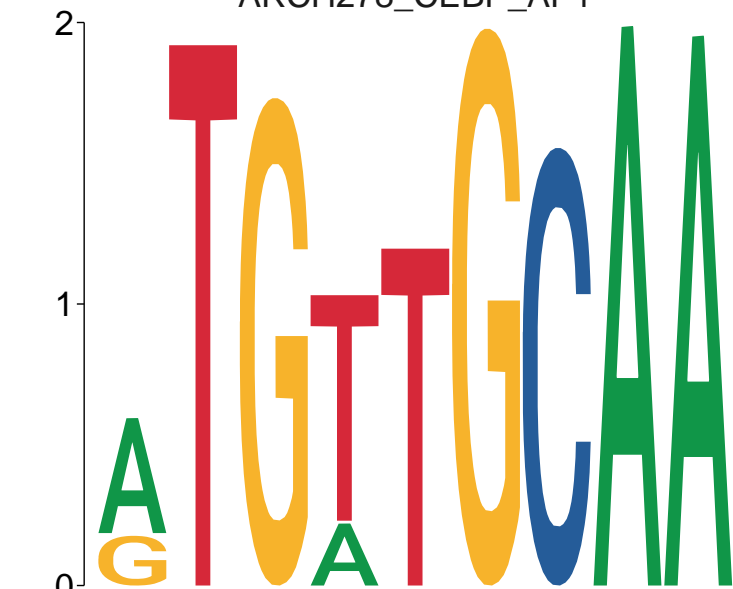
2CH277_14_ACATATCTTACA,BestGuess_C



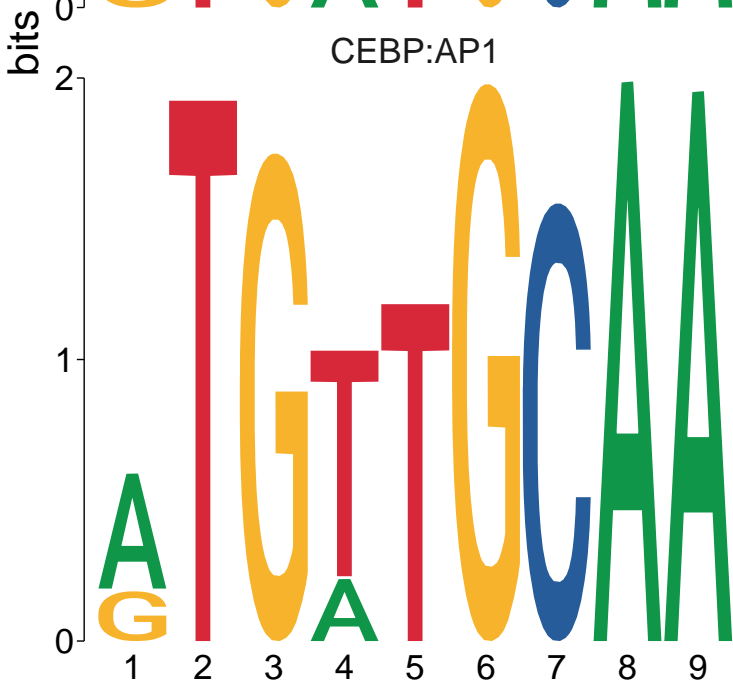
14-ACATATCTTACA,BestGuess:CCA



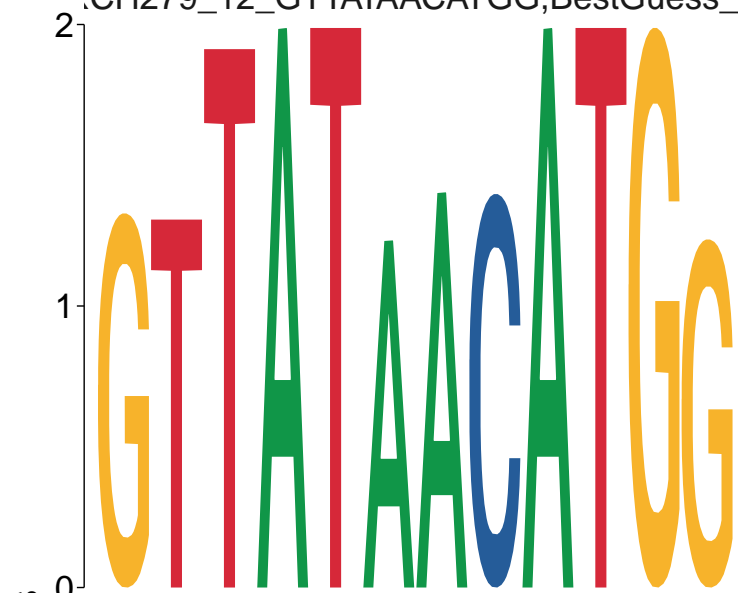
ARCH278_CEBP_AP1



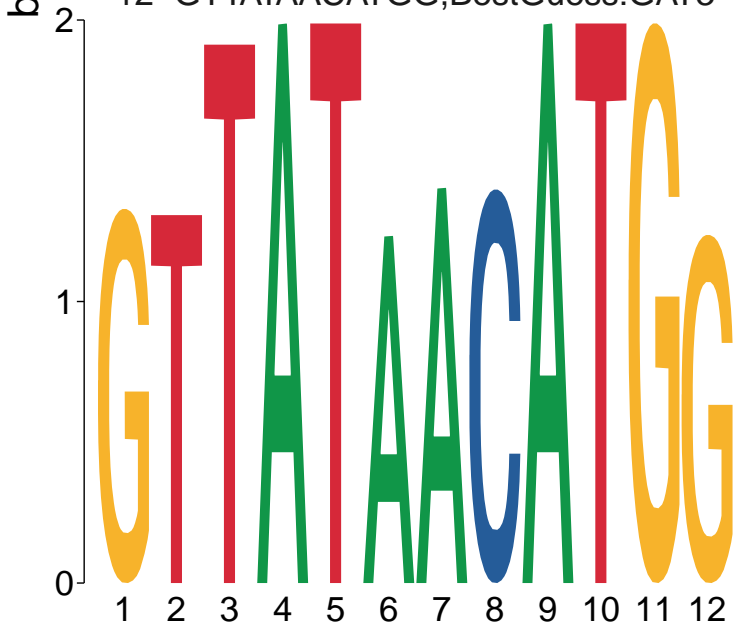
CEBP:AP1



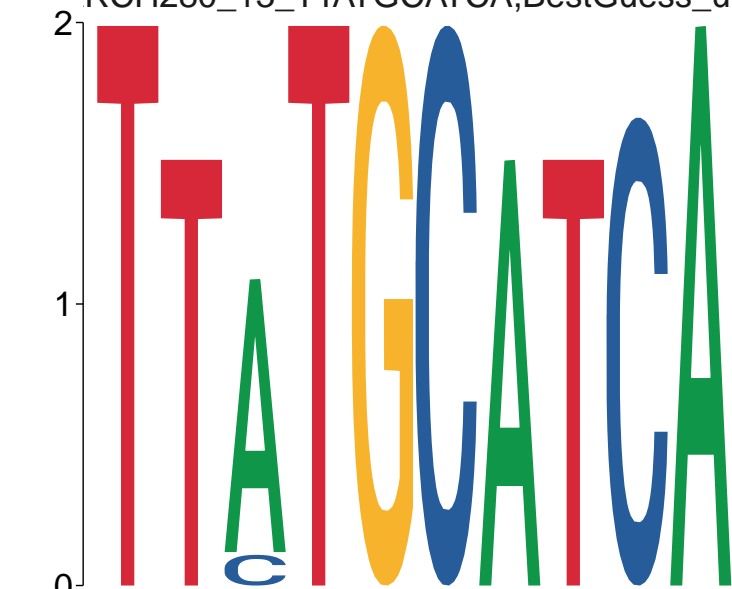
CH279_12_GTTATAACATGG,BestGuess_(



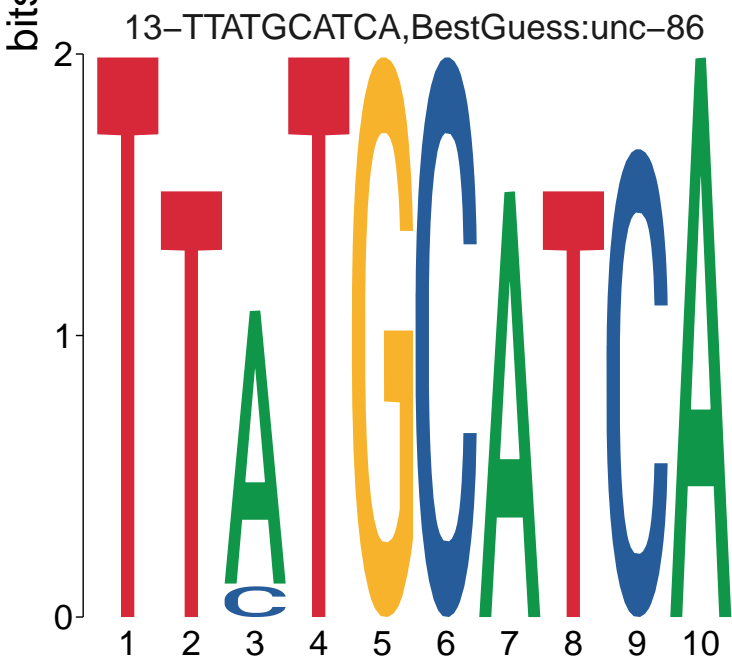
12-GTTATAACATGG,BestGuess:GAT3



RCH280_13_TTATGCATCA,BestGuess_un



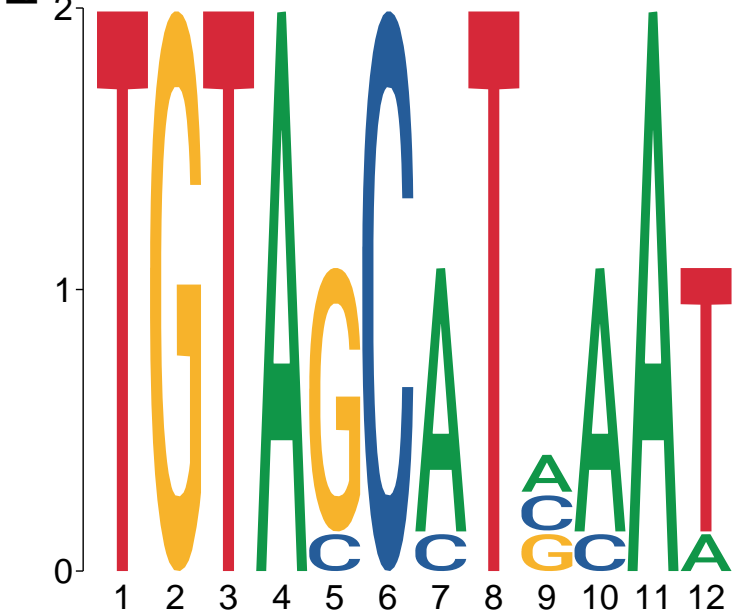
13-TTATGCATCA,BestGuess:unc-86



CH281_1_TGTCAGCATVAAT,BestGuess_DM



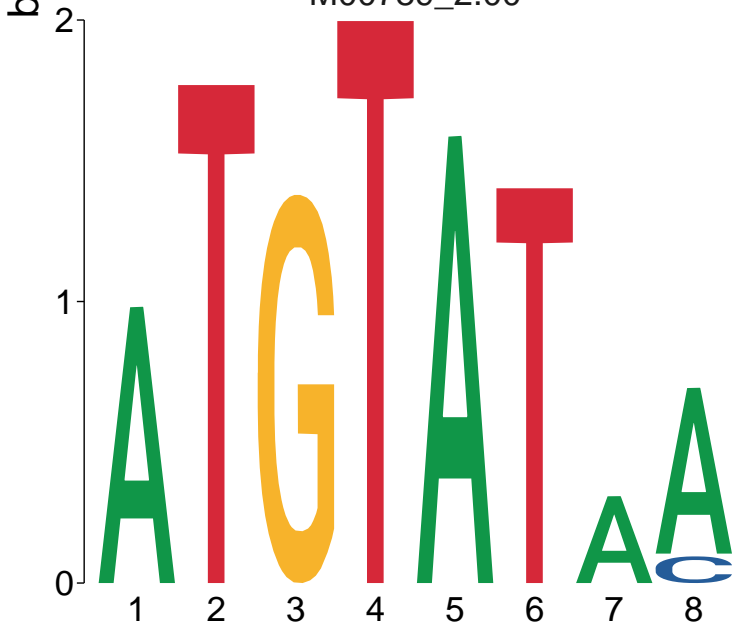
1-TGTCAGCATVAAT,BestGuess:DMRT3



ARCH282_Doublesex_DM



M00789_2.00



RCH283_15_TGATAAATTGTT,BestGuess_F

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'GATAAATTGTT,BestGuess:PB0066.1_Sox

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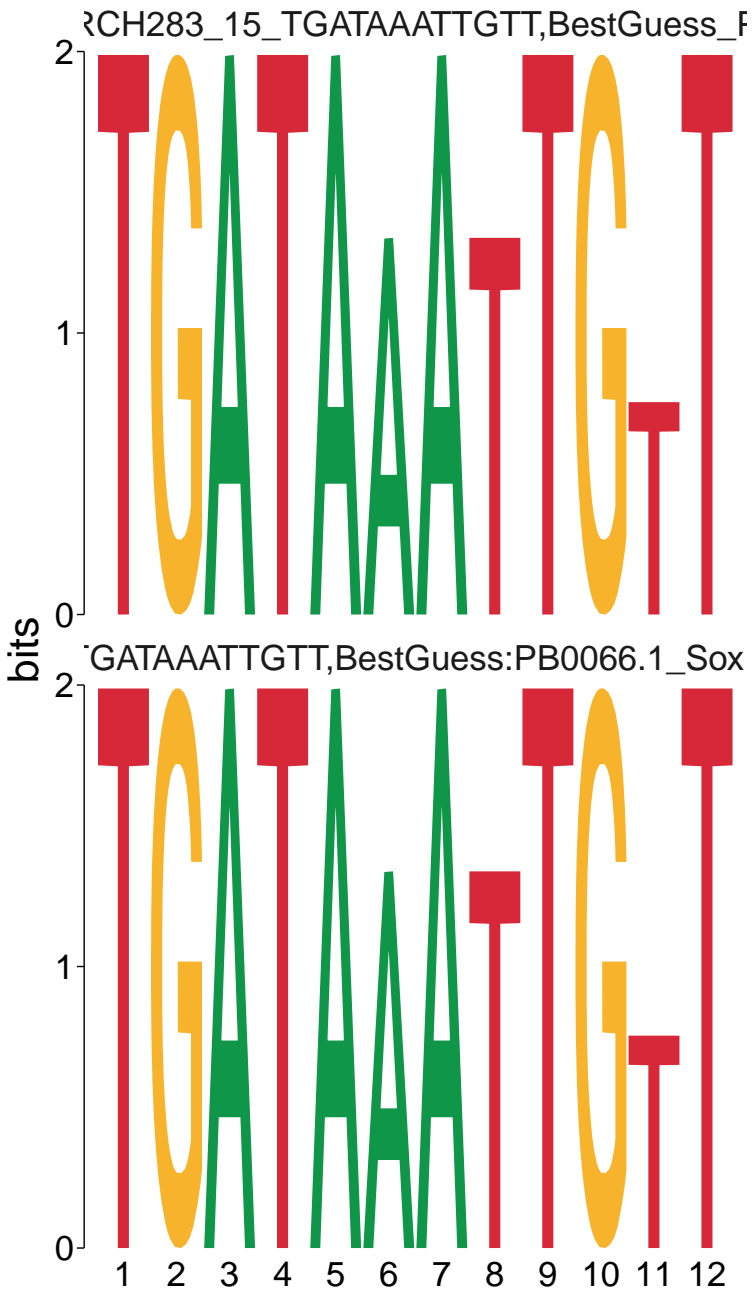
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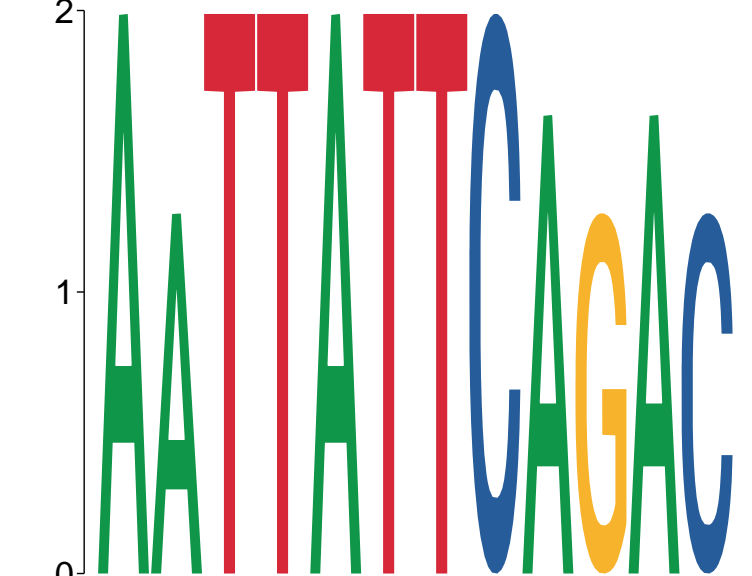
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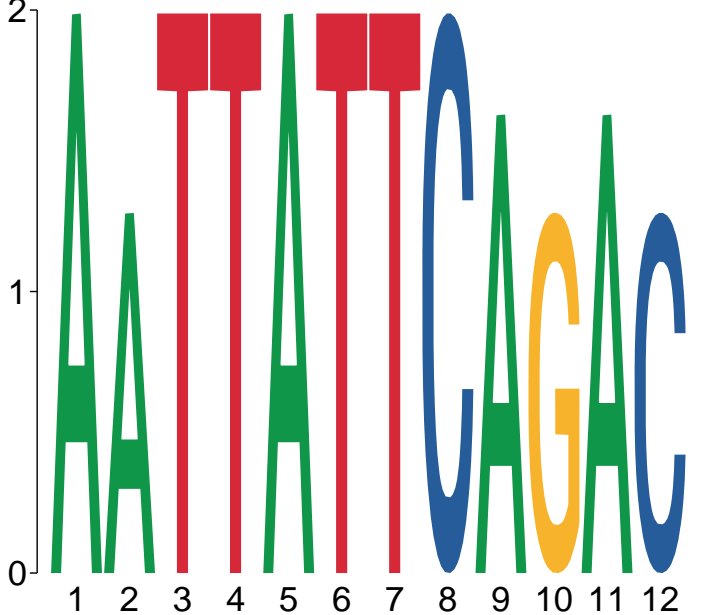
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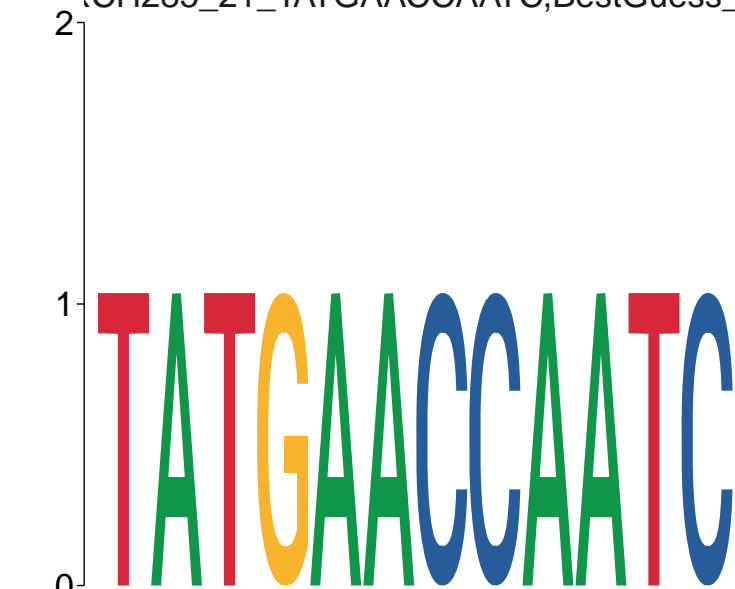
CH284_14_AATTATTCAGAC,BestGuess_1



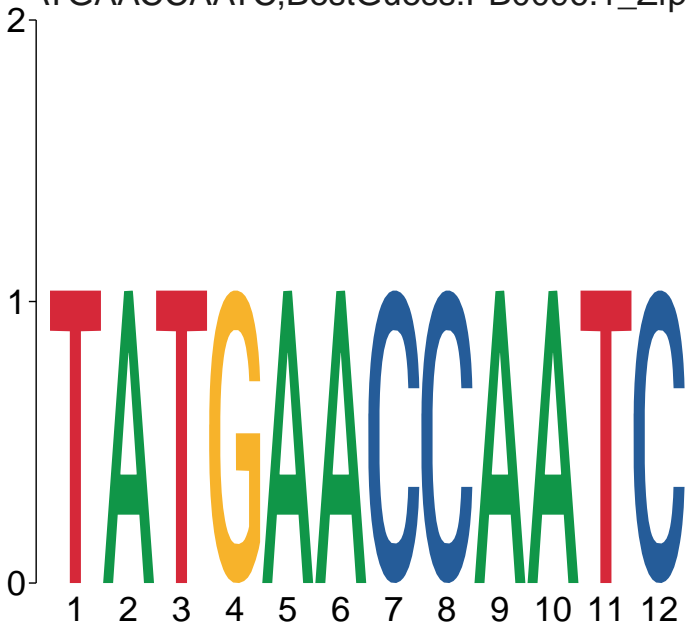
ATTCAGAC,BestGuess:MF0010.1_Homeok



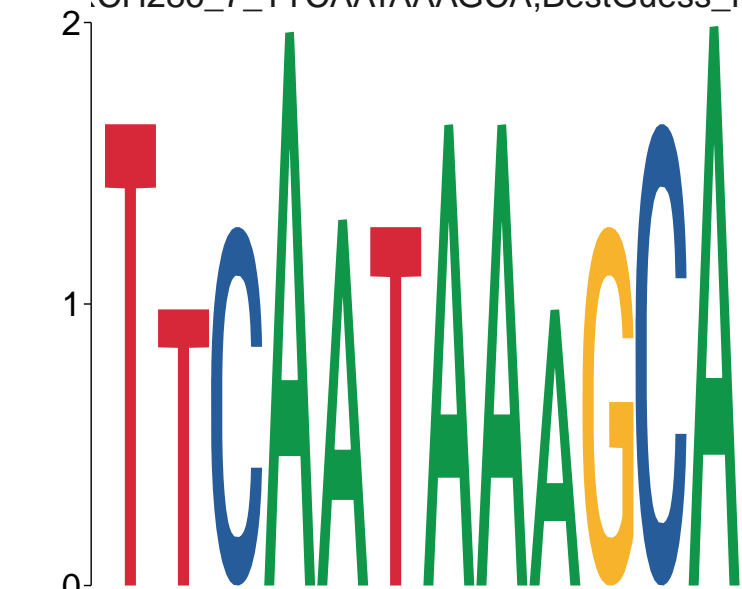
CH285_21_TATGAACCAATC,BestGuess_I



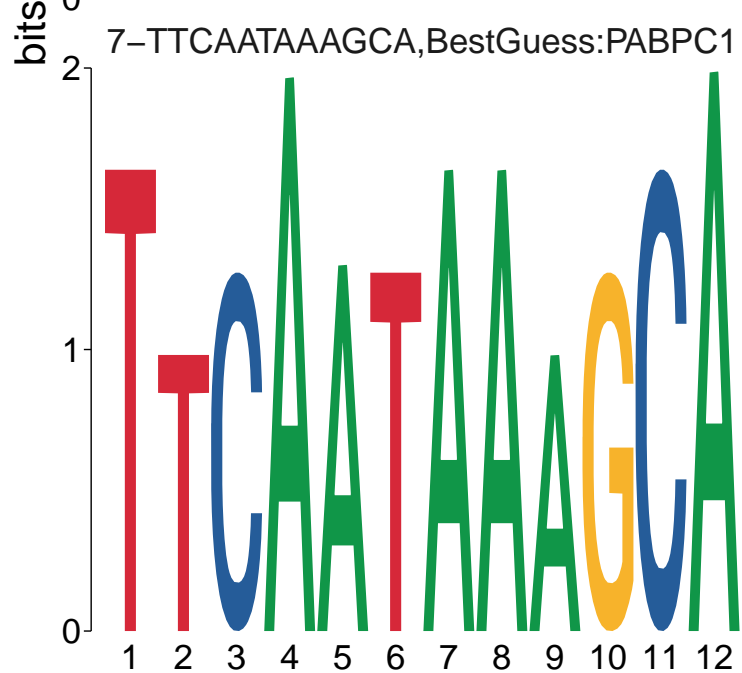
ATGAACCAATC,BestGuess:PB0096.1_Zfp1



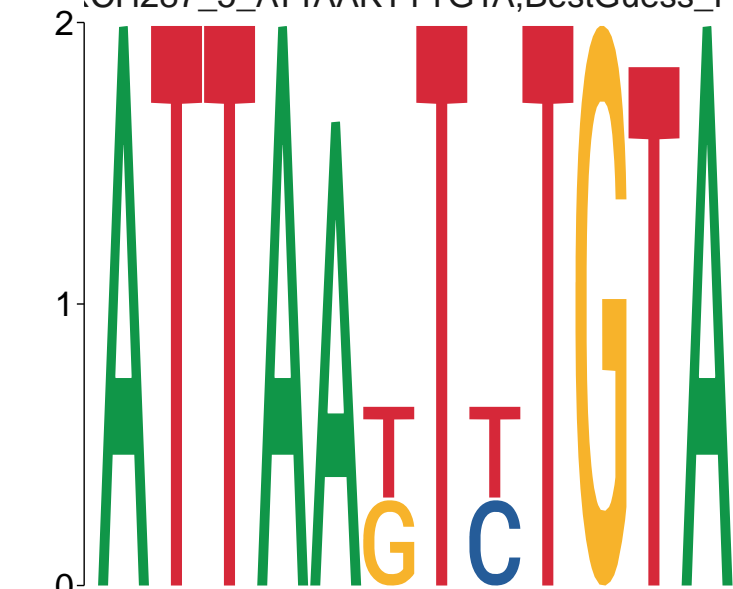
CH286_7_TTCAATAAAGCA,BestGuess_P



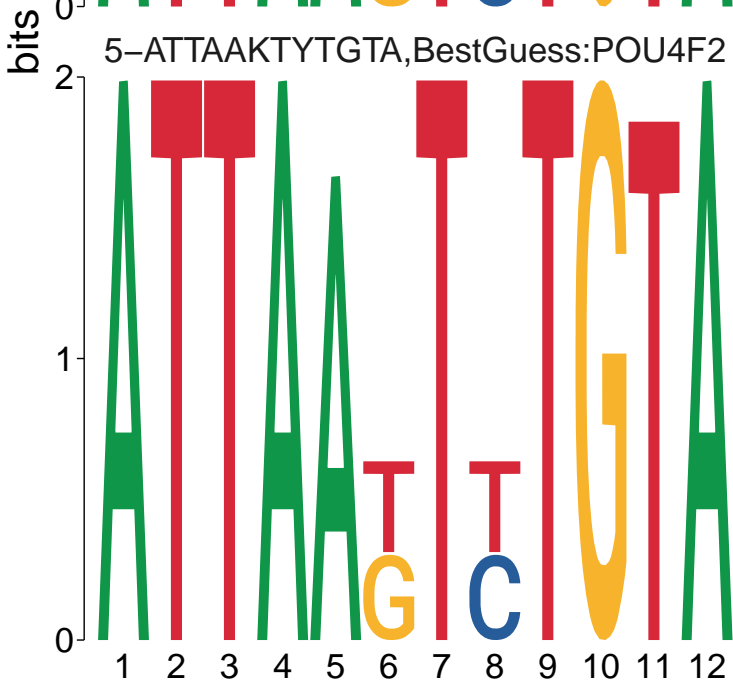
7-TTCAATAAAGCA,BestGuess:PABPC1



CH287_5_ATTAAKTYTGTA,BestGuess_PC



5-ATTAAKTYTGTA,BestGuess:POU4F2



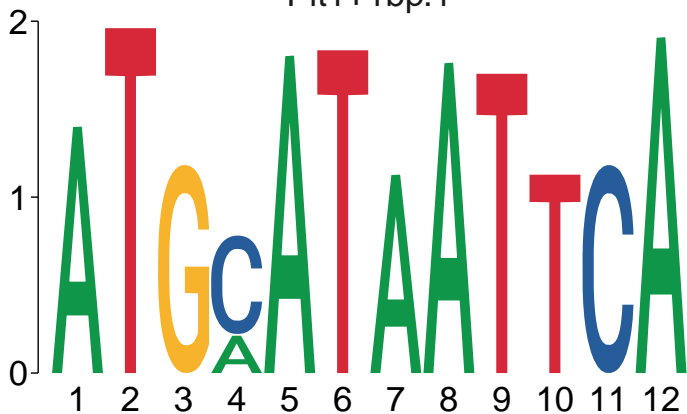
ARCH288_Pit1+1bp_Pit1+1bp



Pit1+1bp



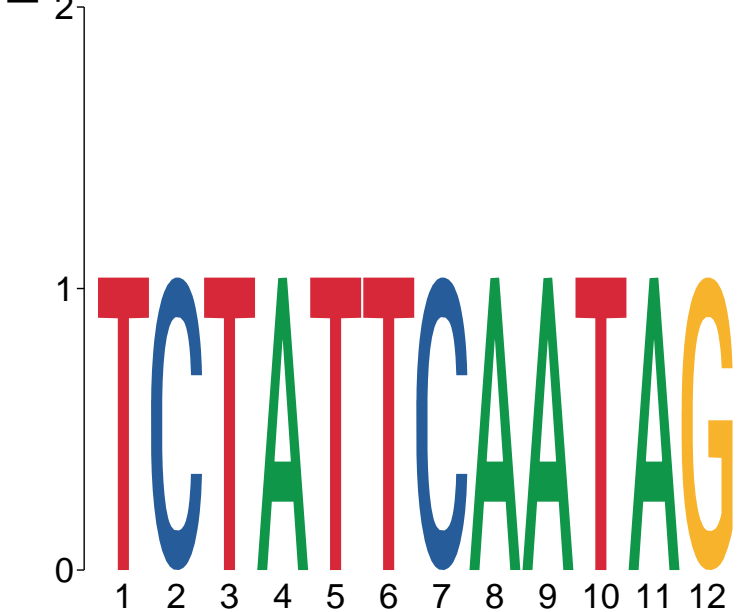
Pit1+1bp.1



RCH289_23_TCTATTCAATAG,BestGuess_F



TCTATTCAATAG,BestGuess:PB0068.1_Sox



RCH290_8_ATGGTTCATTTG,BestGuess_g

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8-ATGGTTCATTTG,BestGuess:grh

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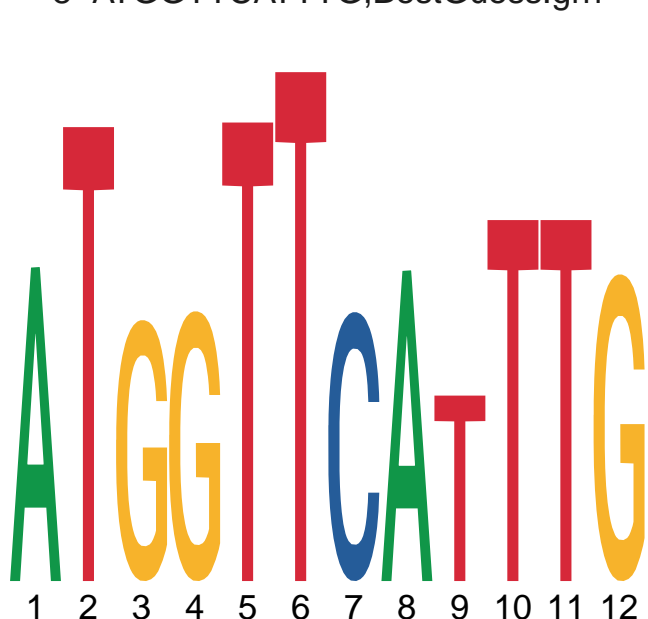
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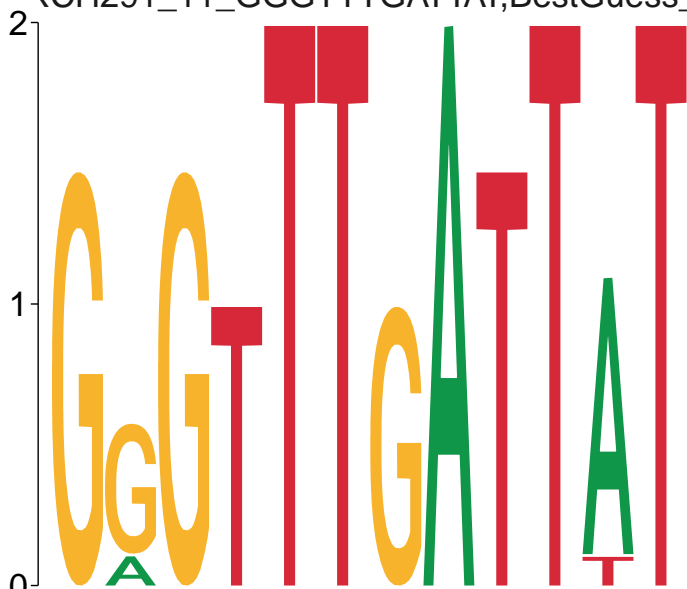
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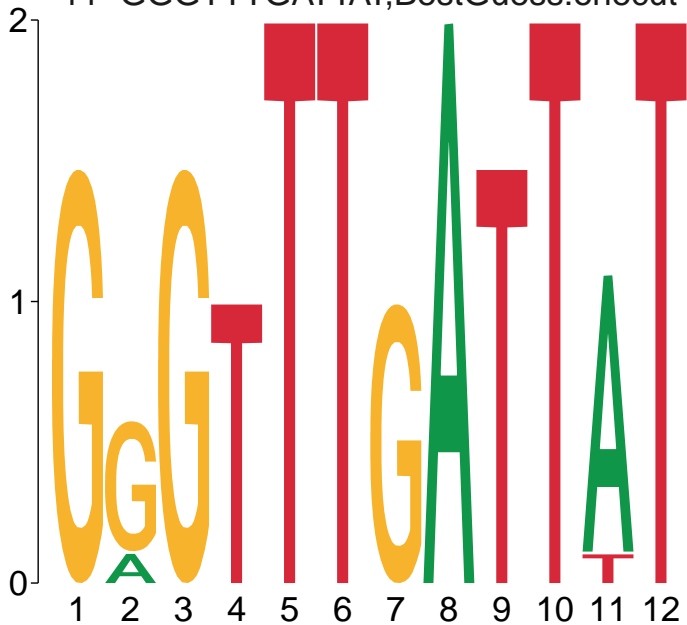
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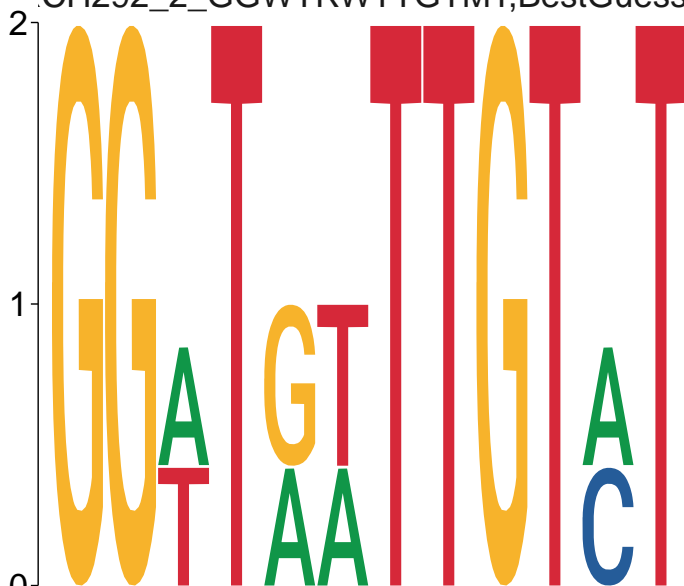
RCH291_11_GGGTTTGATTAT,BestGuess_



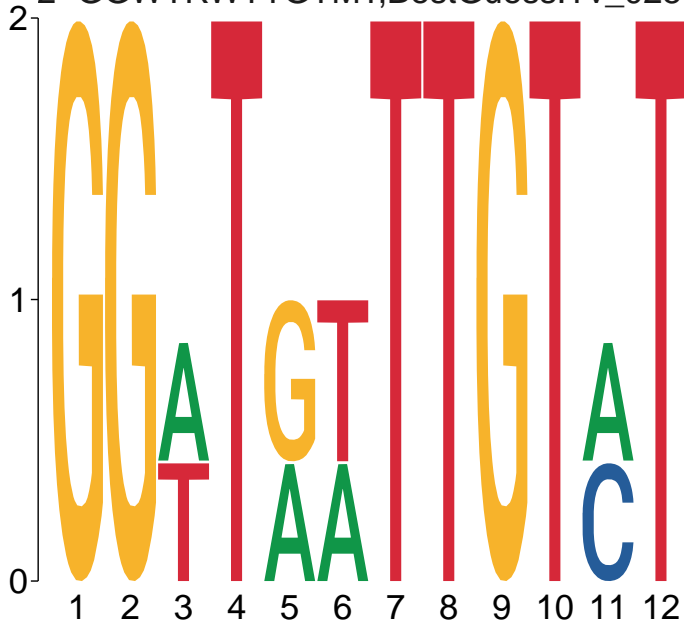
11-GGGTTTGATTAT,BestGuess:onecut



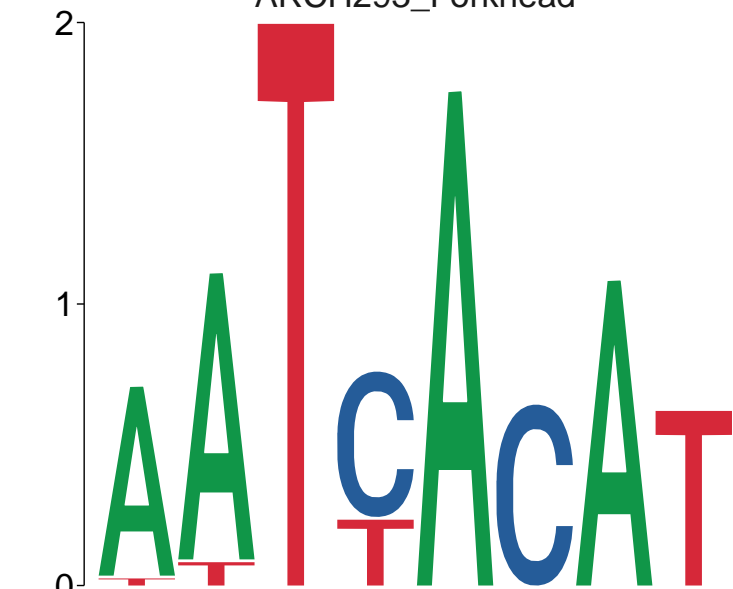
CH292_2_GGWTRWTTGTMT,BestGuess_



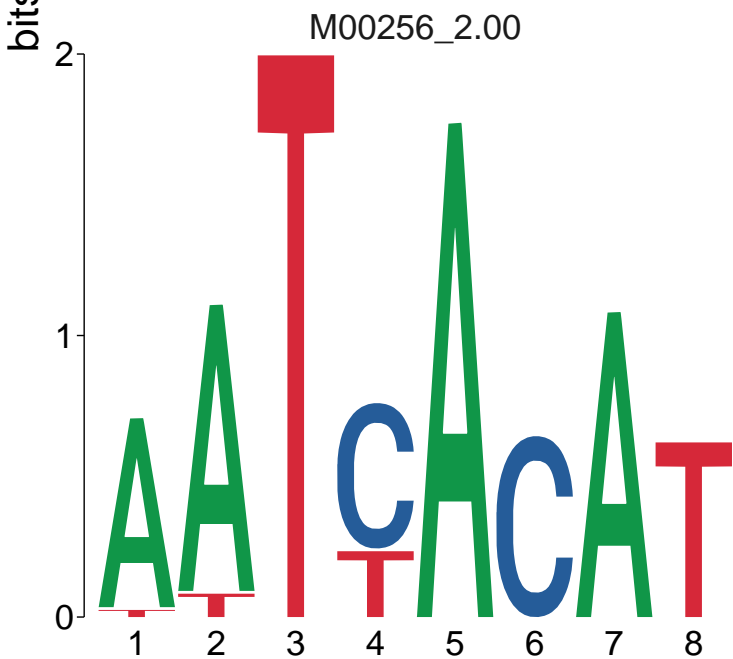
2-GGWTRWTTGTMT,BestGuess:Tv_0258



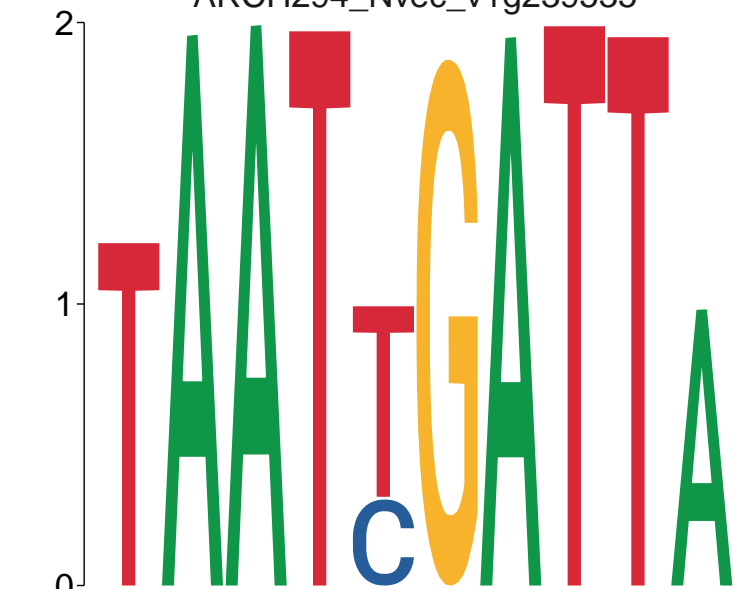
ARCH293_Forkhead



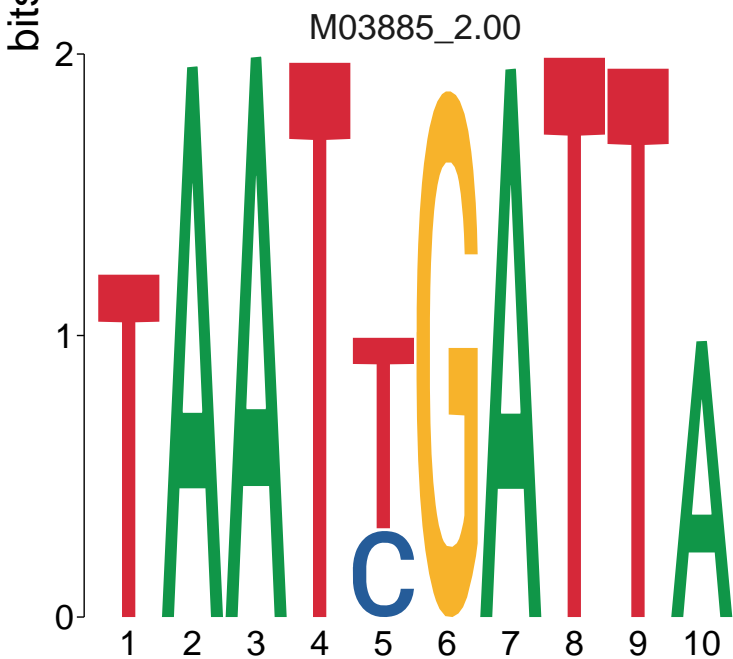
M00256_2.00



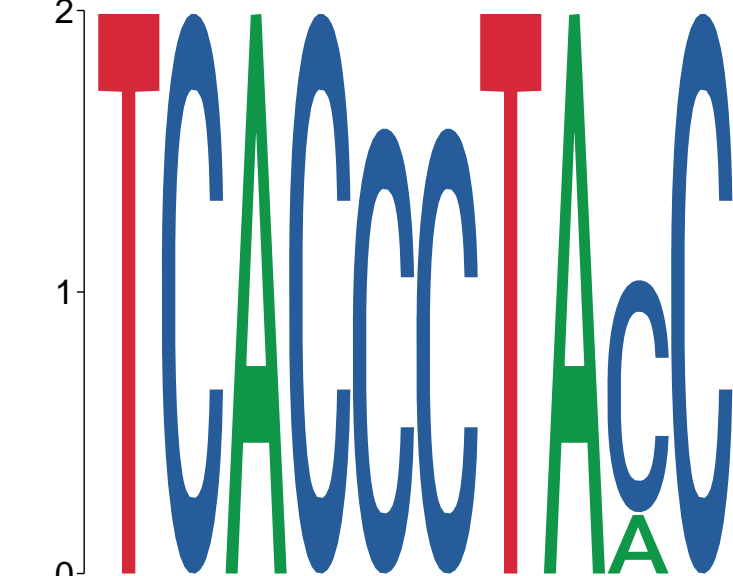
ARCH294_Nvec_v1g239535



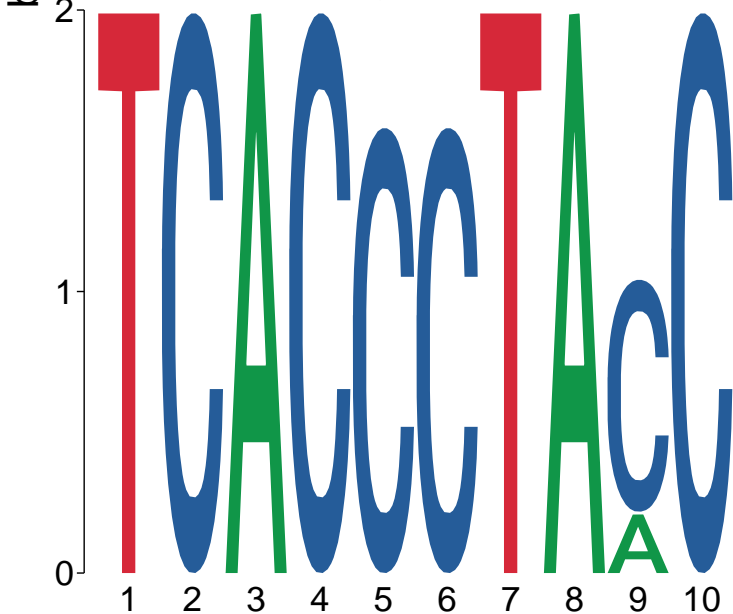
M03885_2.00



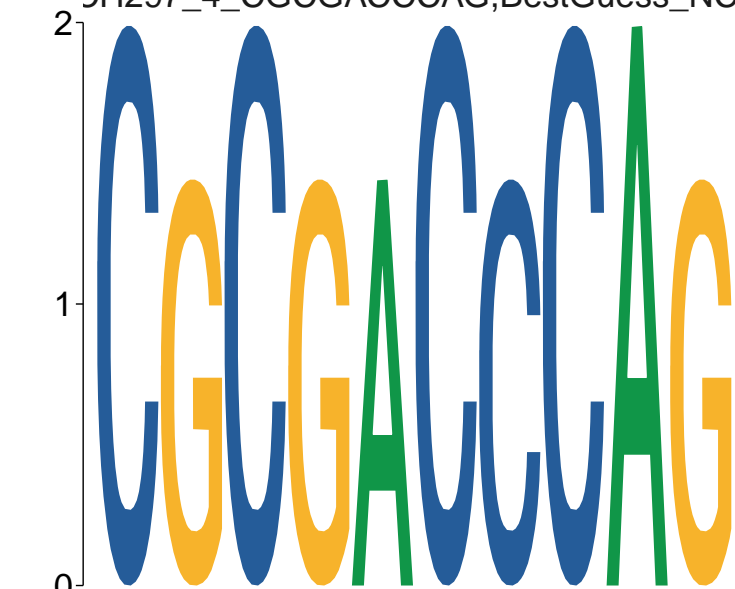
CH296_9_TCACCCTACC,BestGuess_HRE



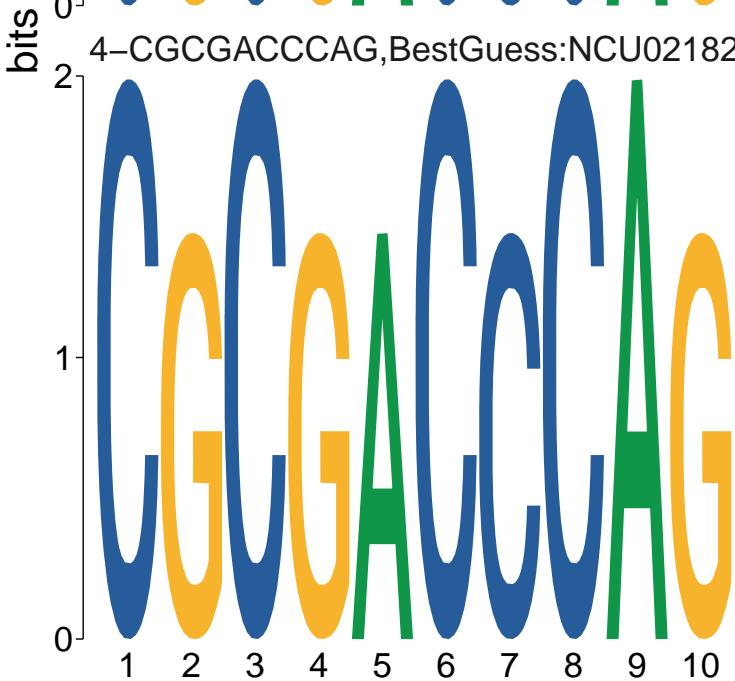
9-TCACCCTACC,BestGuess:HRB98DE



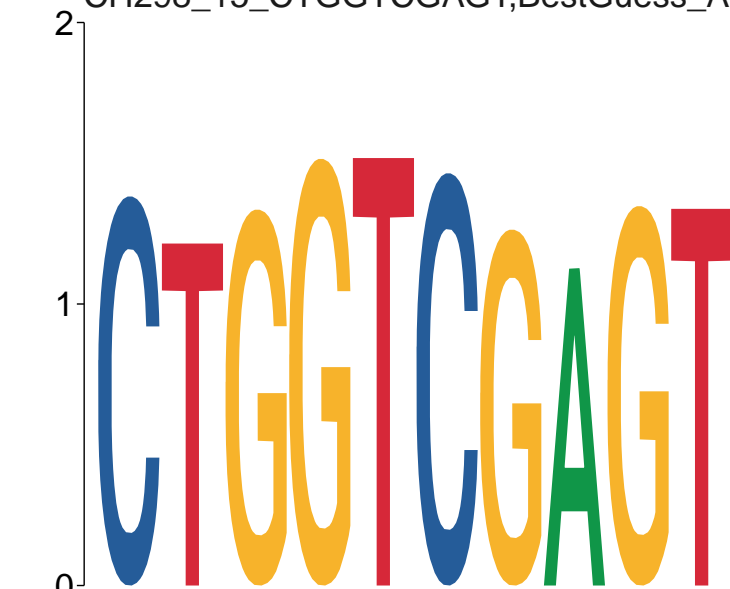
CH297_4_CGCGACCCAG,BestGuess_NCI



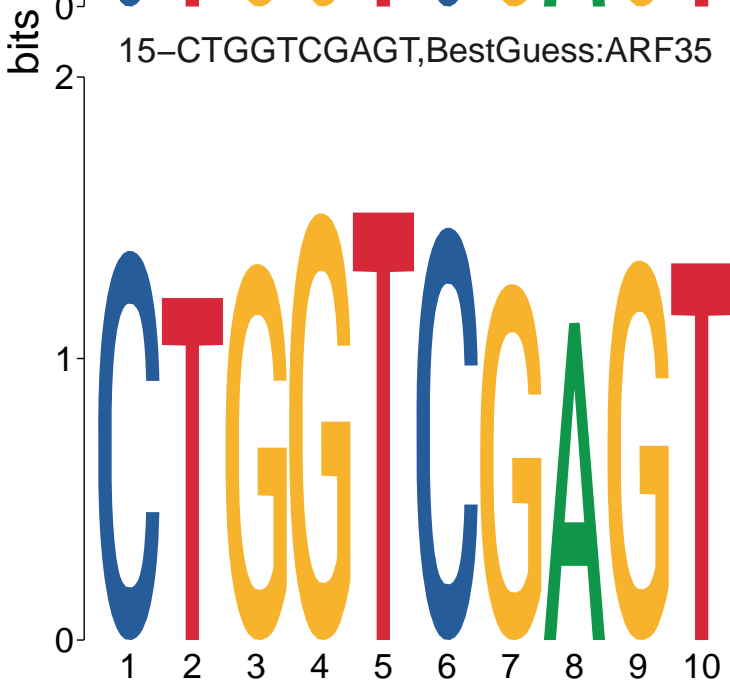
4-CGCGACCCAG,BestGuess:NCU02182



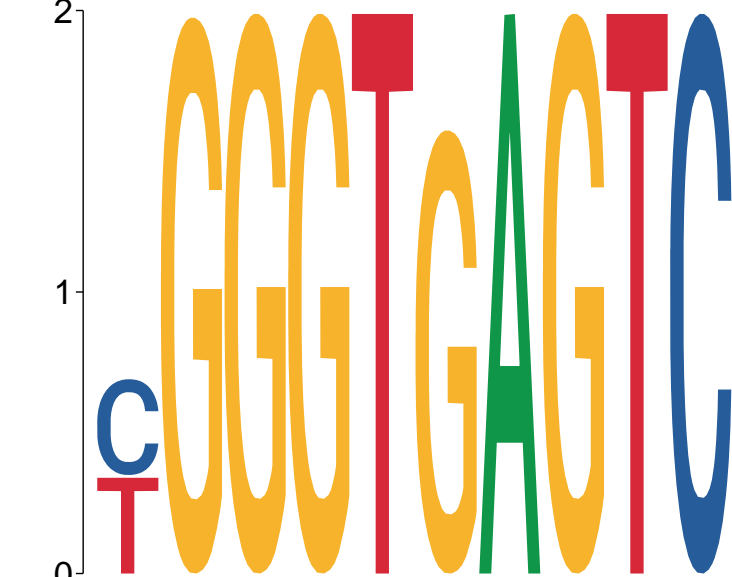
CH298_15_CTGGTCGAGT,BestGuess_ARF



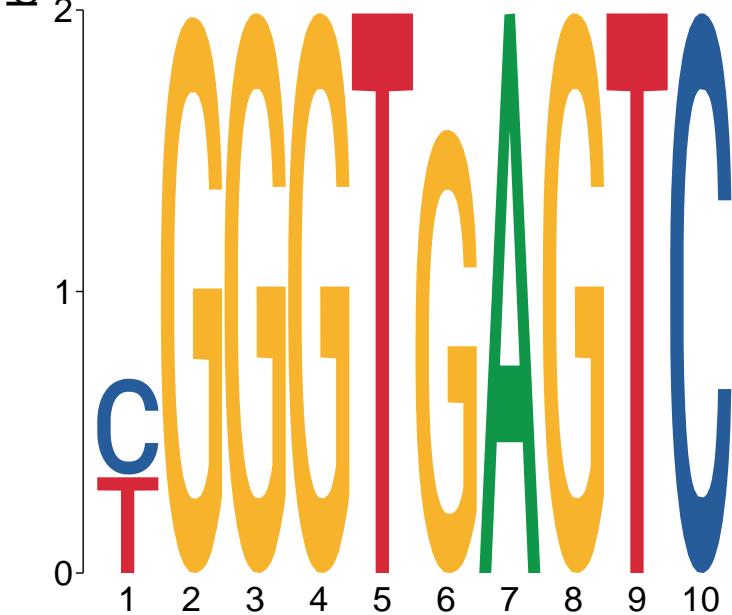
15-CTGGTCGAGT,BestGuess:ARF35



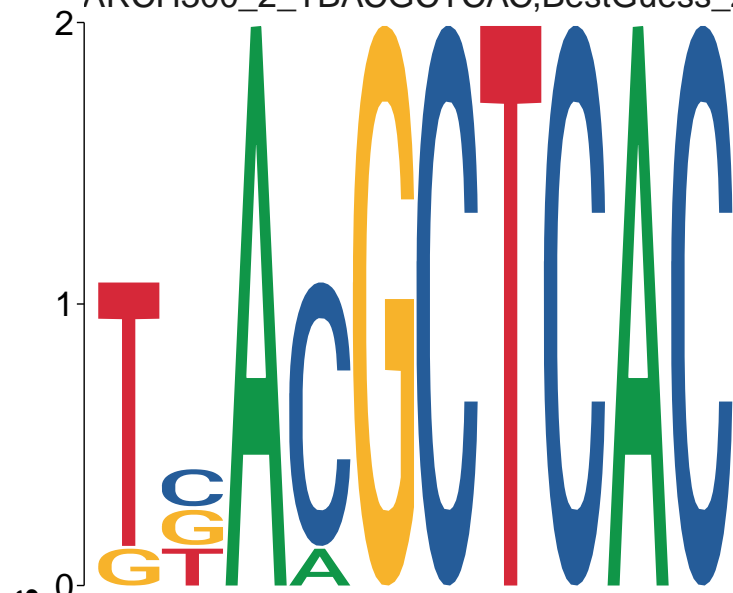
CH299_1_YGGGTGAGTC,BestGuess_fos



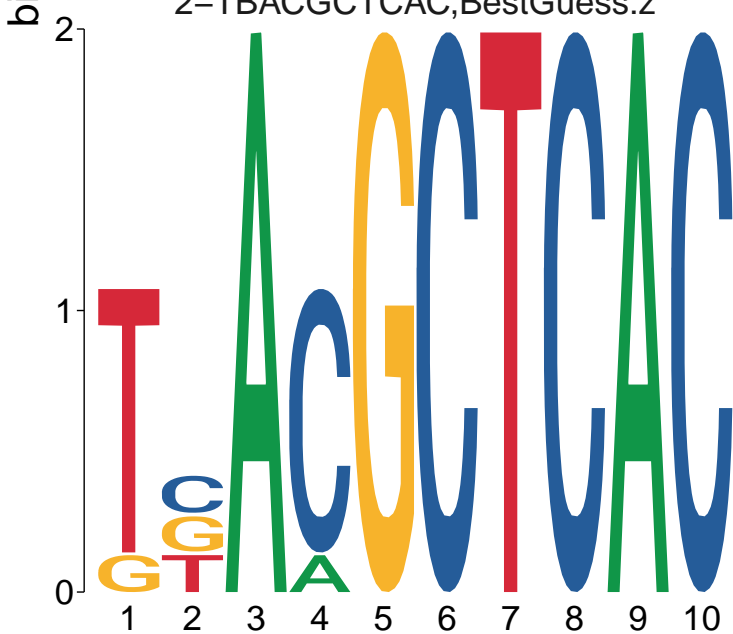
1-YGGGTGAGTC,BestGuess:fos-1



ARCH300_2_TBACGCTCAC,BestGuess_z



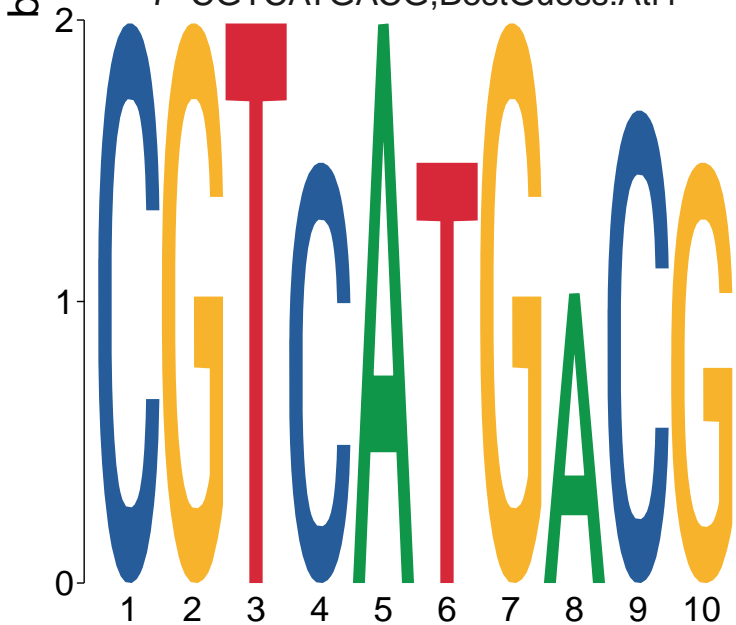
2-TBACGCTCAC,BestGuess:z



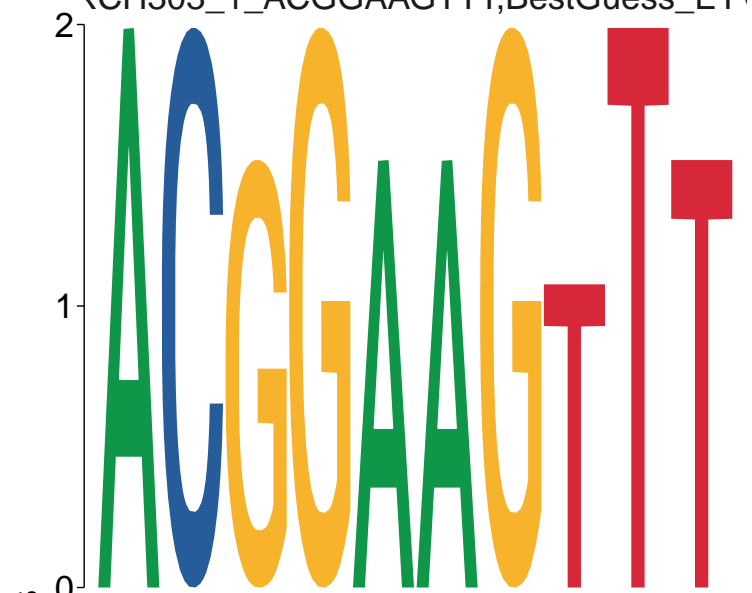
RCH302_7_CGTCATGACG,BestGuess_At1



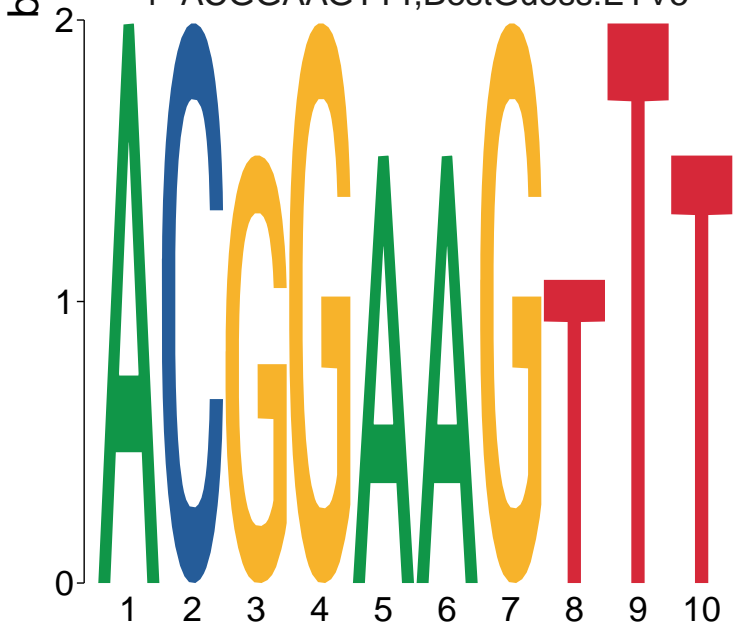
7-CGTCATGACG,BestGuess:Atf1



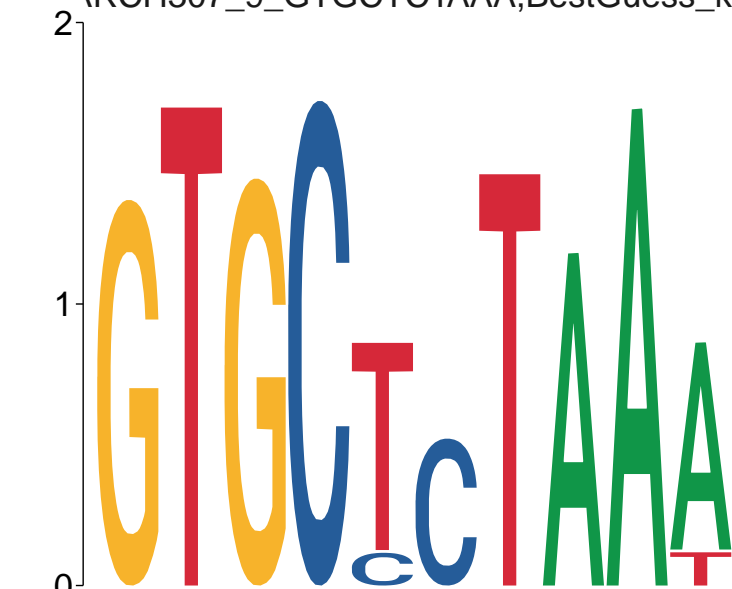
RCH303_1_ACGGAAGTTT,BestGuess_ETV



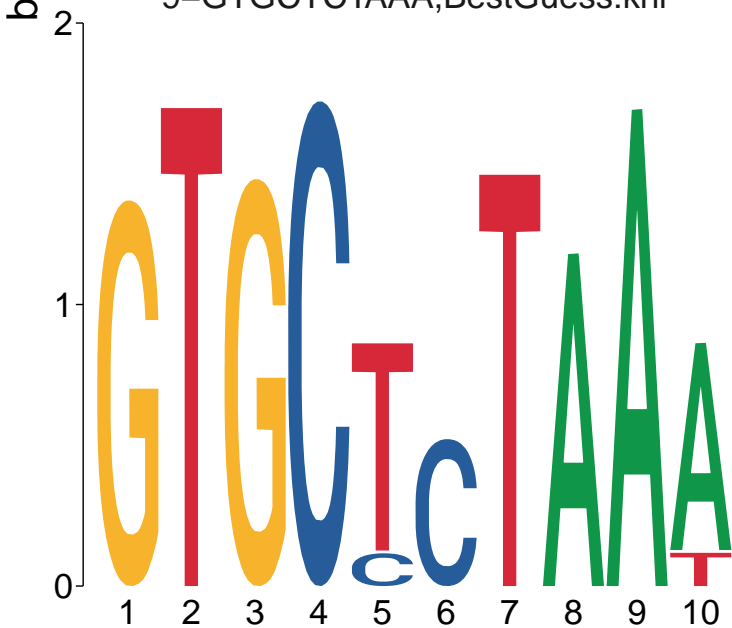
1-ACGGAAGTTT,BestGuess:ETV5



ARCH307_9_GTGCTCTAAA,BestGuess_kn



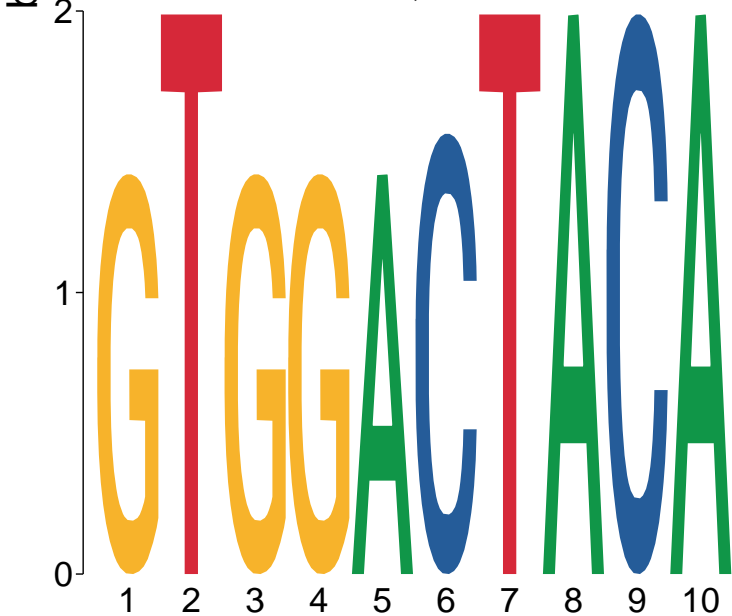
9-GTGCTCTAAA,BestGuess:kni



CH308_19_GTGGACTACA,BestGuess_Rb

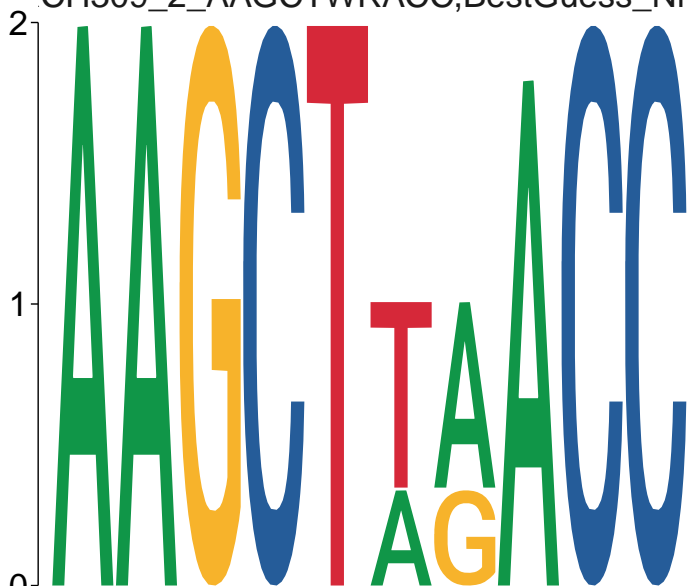


19-GTGGACTACA,BestGuess:Rbm42

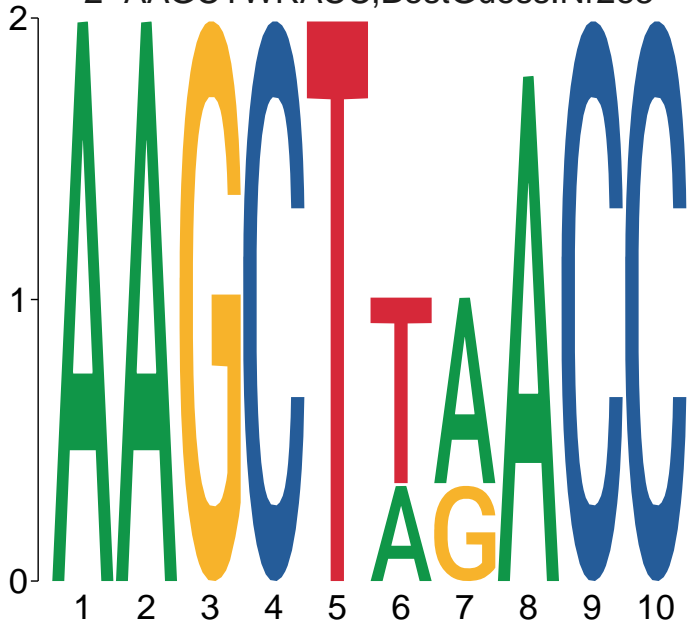


CH309_2_AAGCTWRACC,BestGuess_Nr2

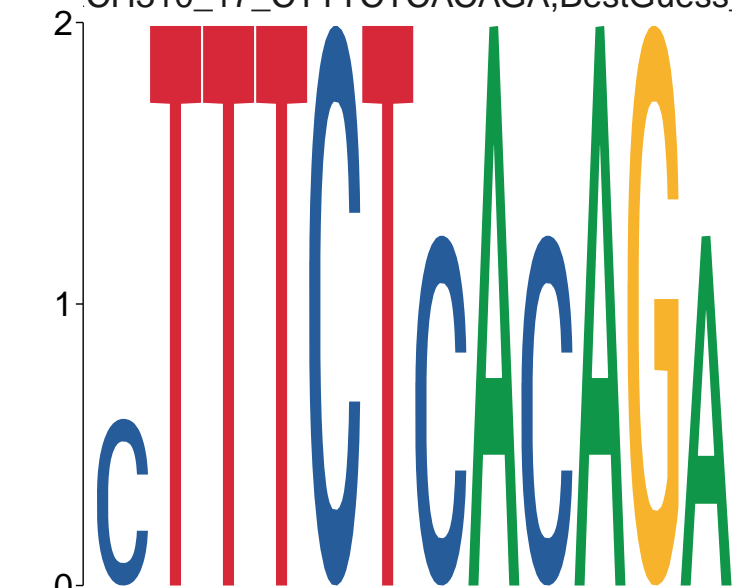
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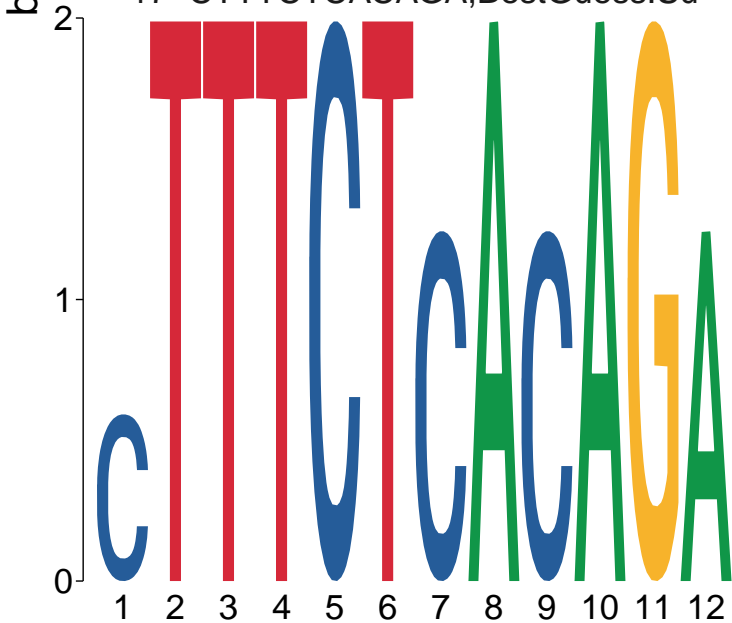
2-AAGCTWRACC,BestGuess:Nr2e3



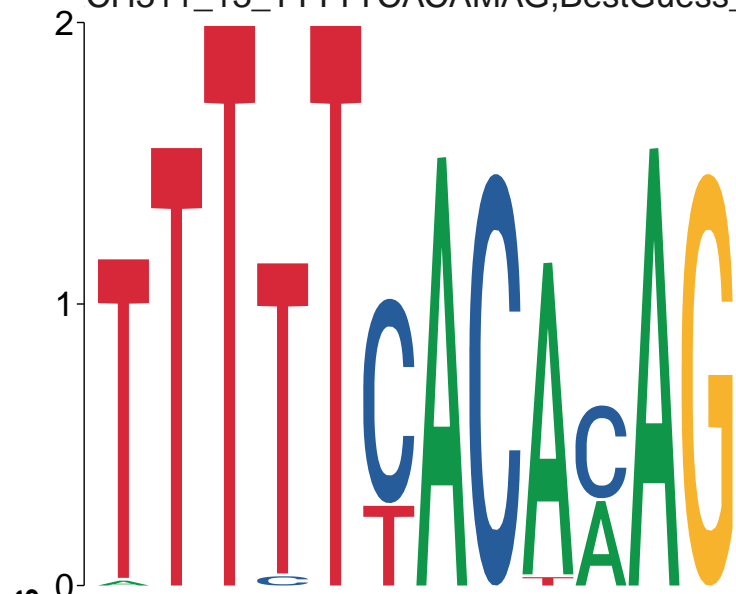
CH310_17_CTTTCTCACAGA,BestGuess_



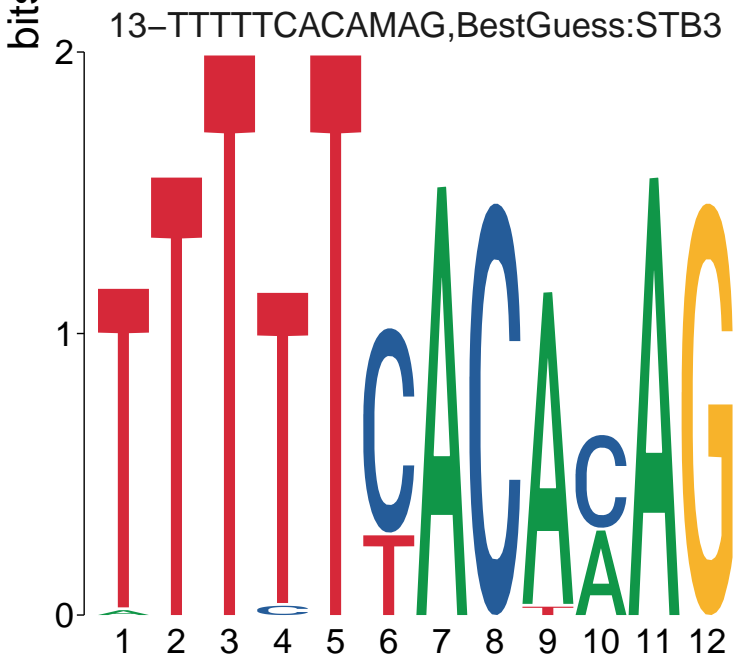
17-CTTTCTCACAGA,BestGuess:Su



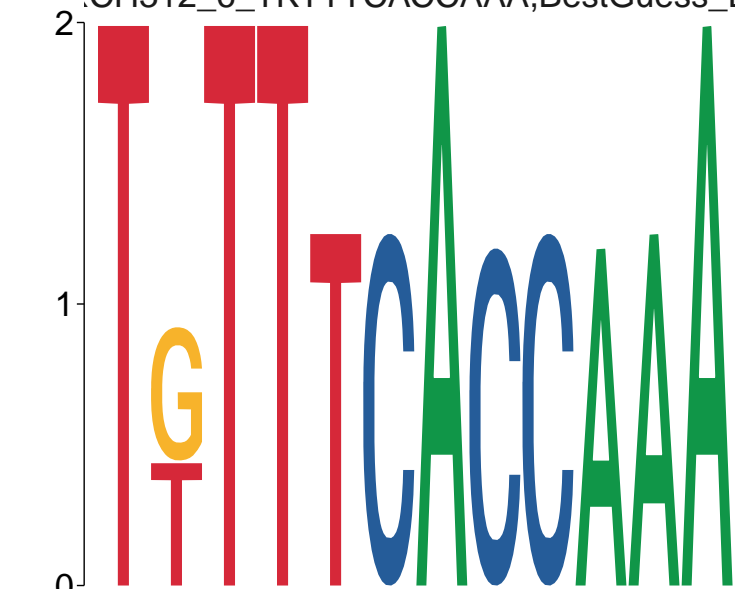
CH311_13_TTTTTCACAMAG,BestGuess_



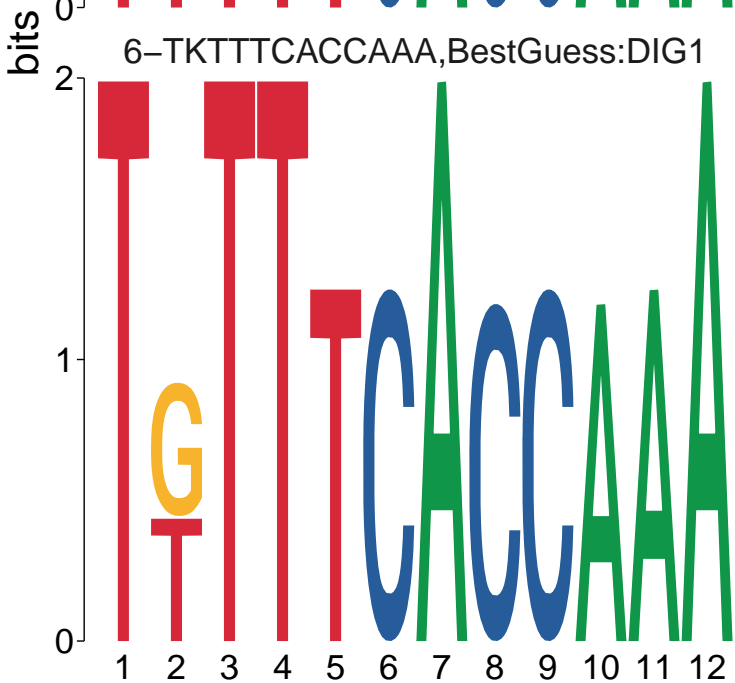
13-TTTTTCACAMAG,BestGuess:STB3



CH312_6_TKTTTCACCAAA,BestGuess_D

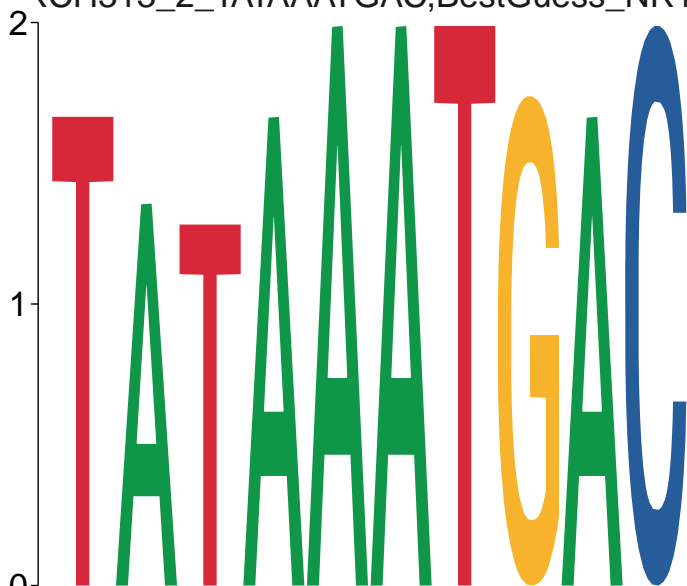


6-TKTTTCACCAAA,BestGuess:DIG1

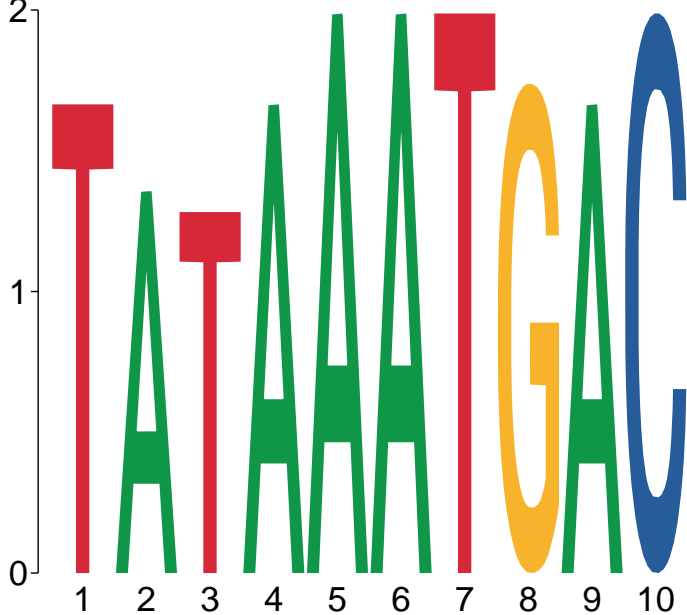


2-CH313_2_TATAAATGAC,BestGuess_NR1H4

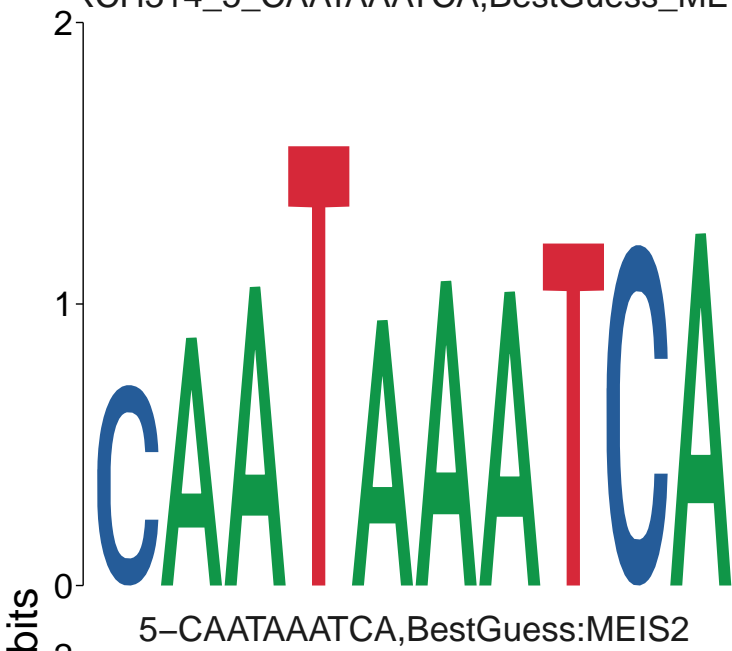
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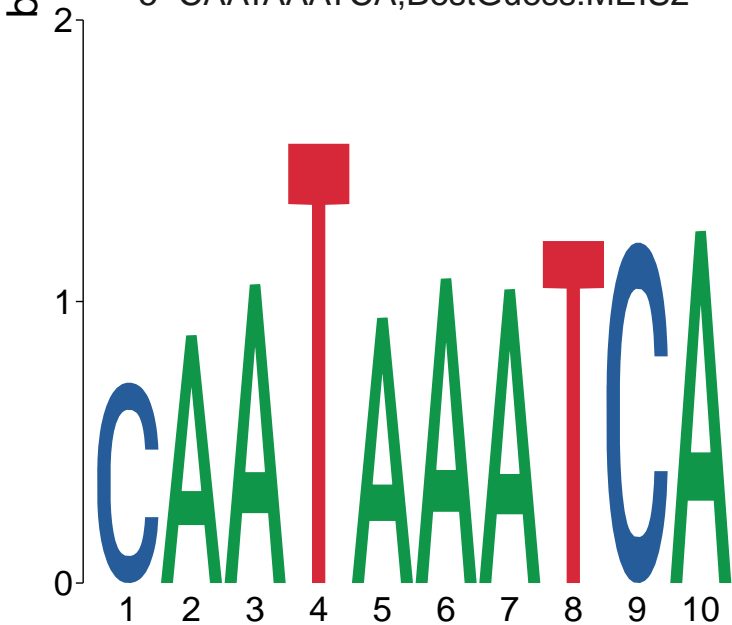
2-TATAAATGAC,BestGuess:NR1H4



5-CAATAAATCA, BestGuess_MEIS2



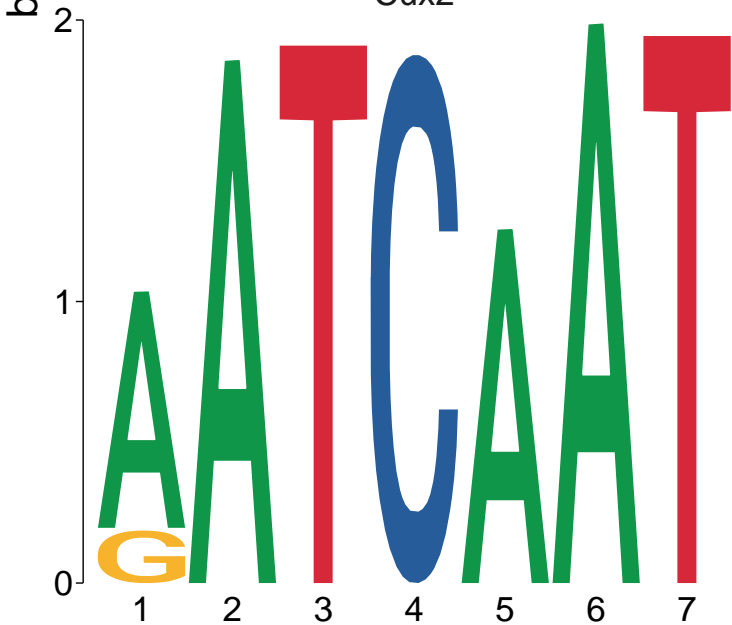
5-CAATAAATCA, BestGuess:MEIS2



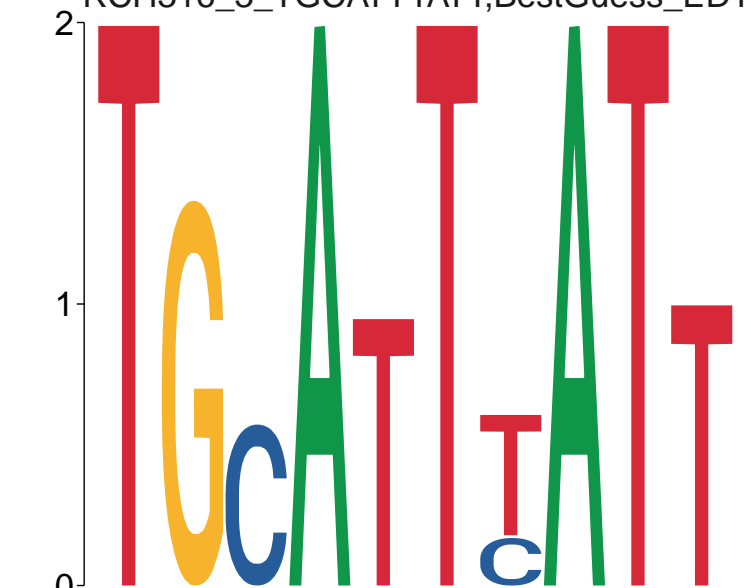
ARCH315_Cux2



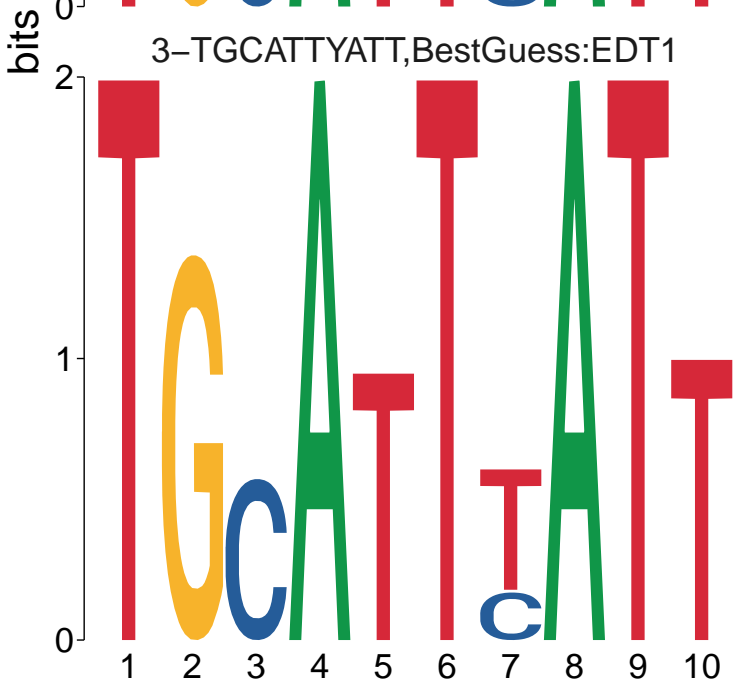
Cux2



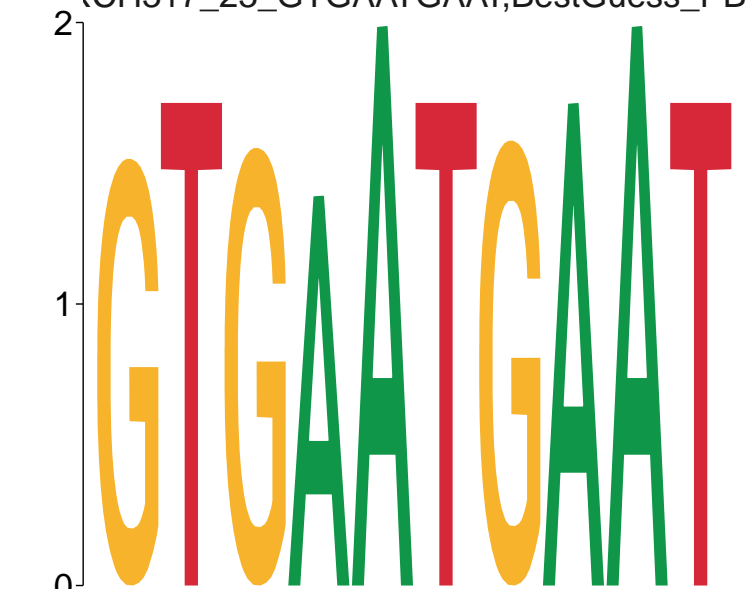
RCH316_3_TGCATTYATT,BestGuess_EDT



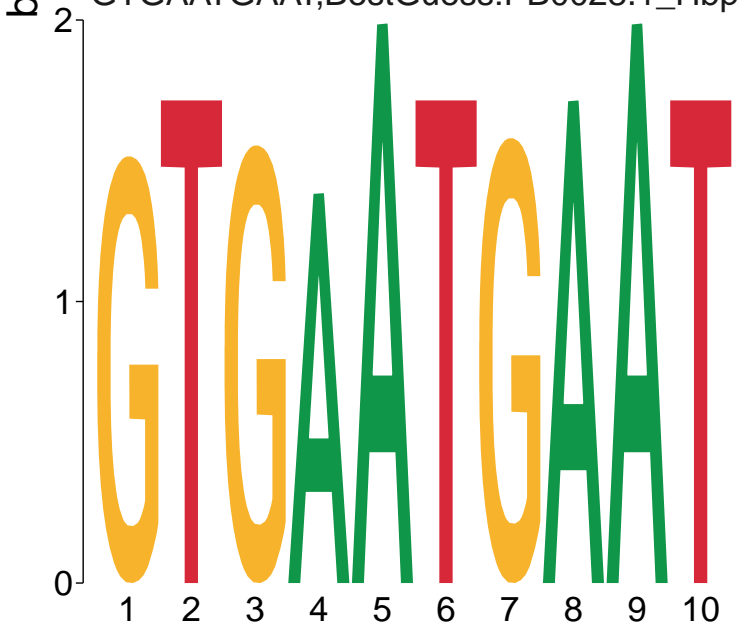
3-TGCATTYATT,BestGuess:EDT1



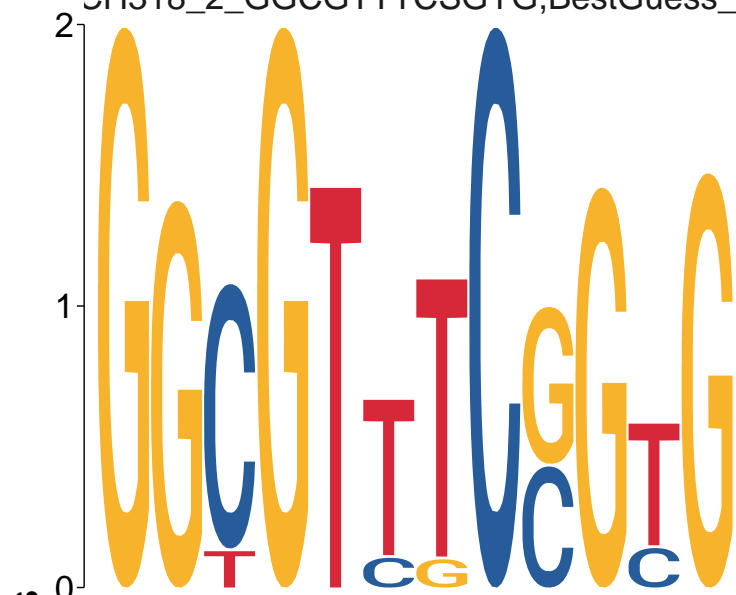
CH317_23_GTGAATGAAT,BestGuess_PB



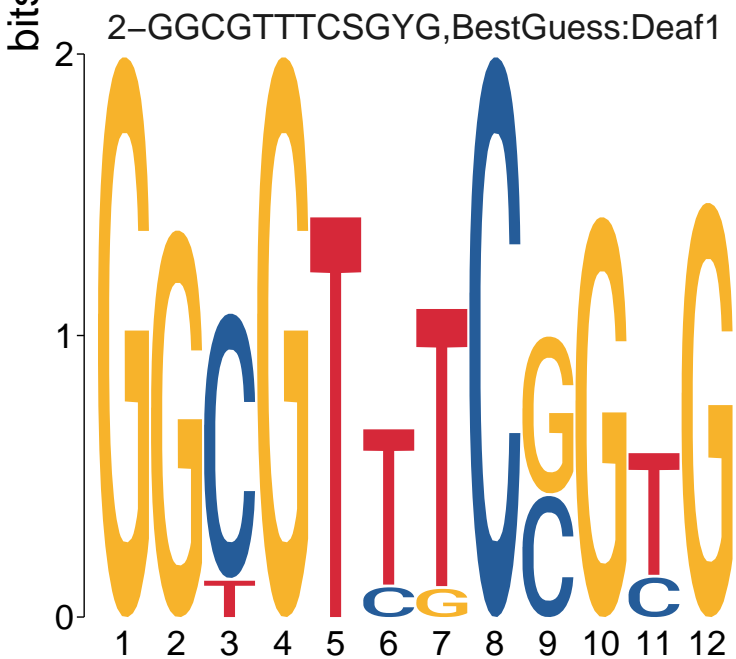
-GTGAATGAAT,BestGuess:PB0028.1_Hbp'



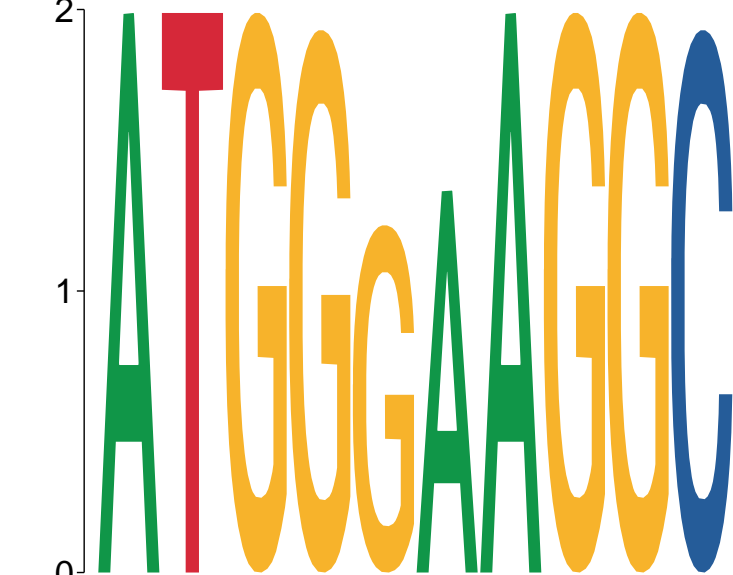
CH318_2_GGCGTTTCSGYG,BestGuess_I



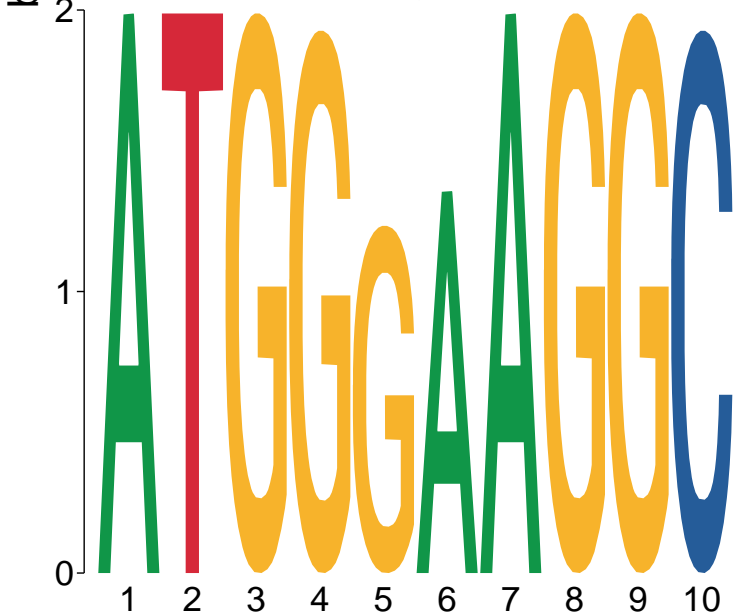
2-GGCGTTTCSGYG,BestGuess:Deaf1



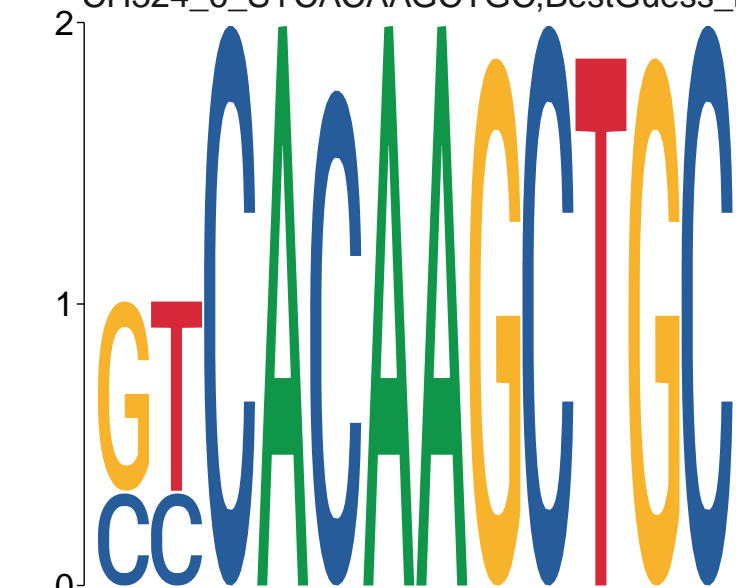
CH319_14_ATGGGAAGGC,BestGuess_PC



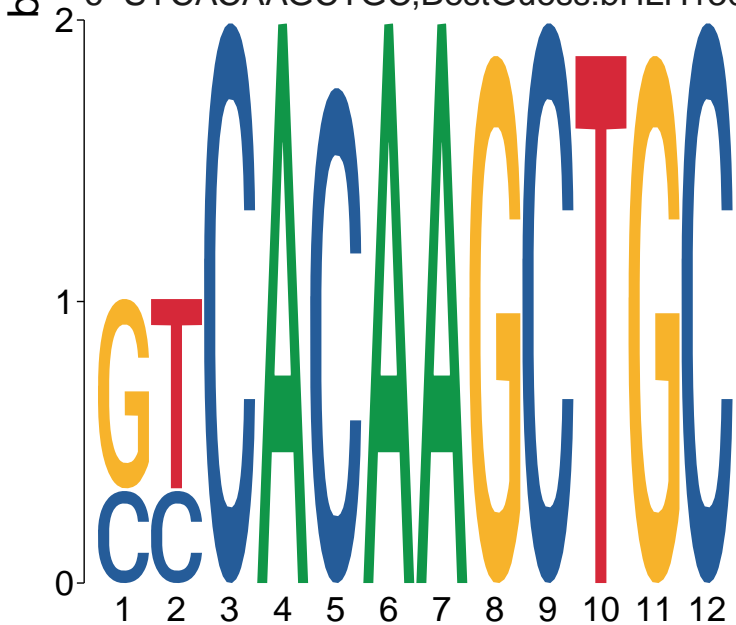
14-ATGGGAAGGC,BestGuess:PCBP2



CH324_6_SYCACAAAGCTGC,BestGuess_b



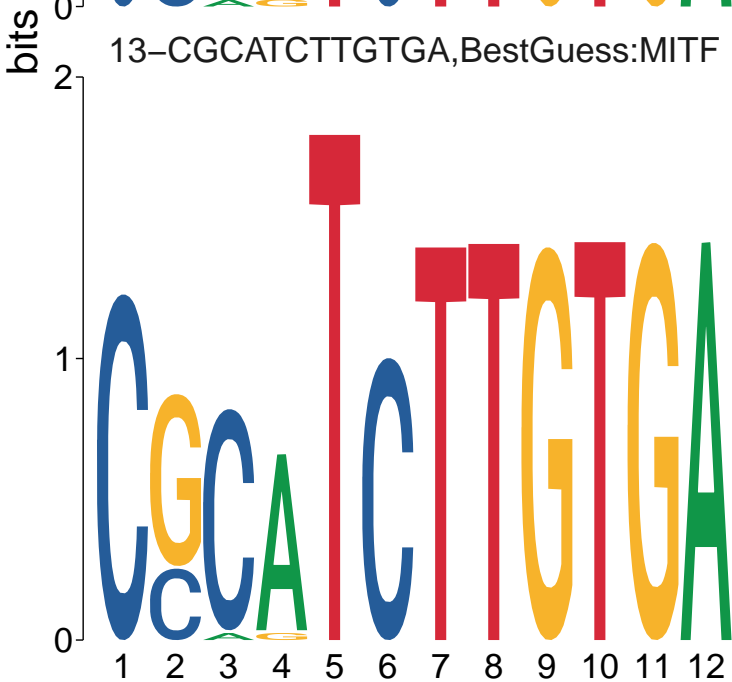
6-SYCACAAAGCTGC,BestGuess:bHLH130



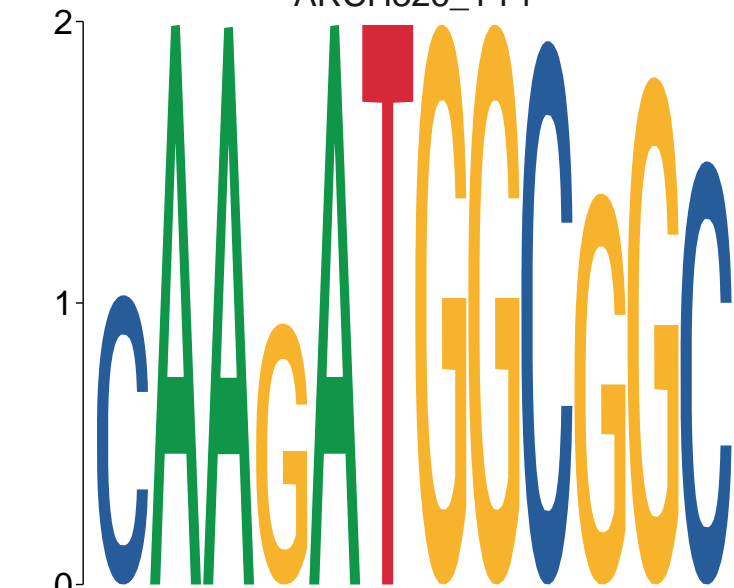
CH325_13_CGCATCTTGTGA,BestGuess_



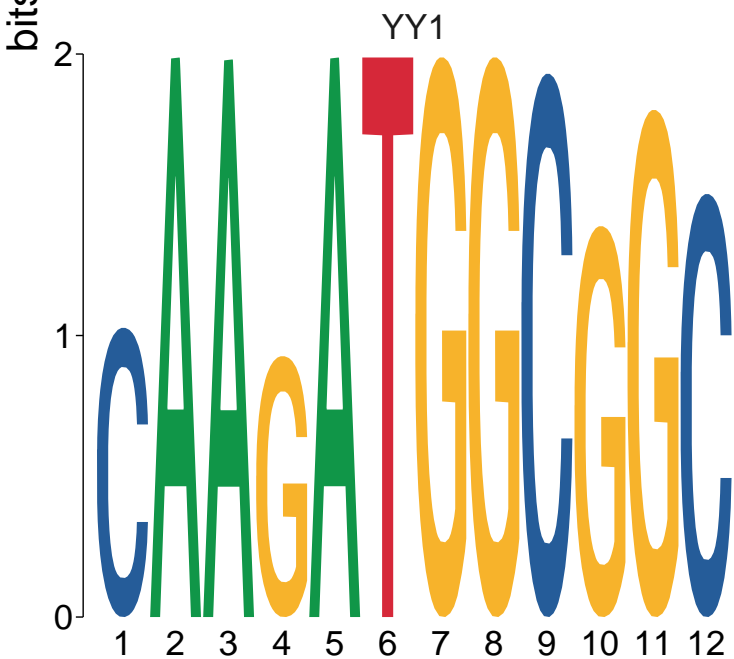
13-CGCATCTTGTGA,BestGuess:MITF



ARCH326_YY1



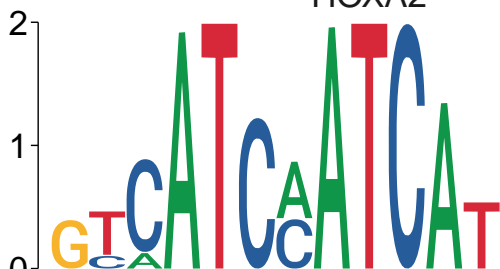
YY1



ARCH328_Hoxb4_Hoxb4_HOXA2



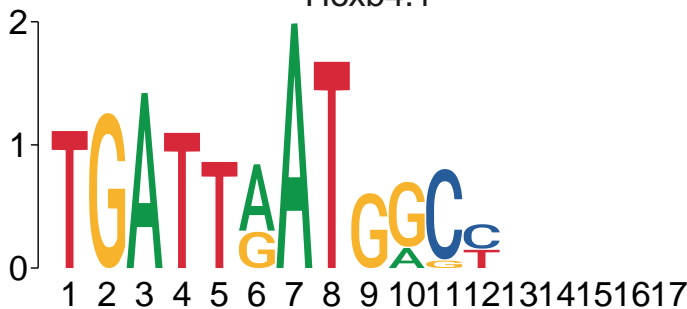
HOXA2



Hoxb4



Hoxb4.1



ARCH329_LIN_39_HOXA1_LIN_39_Pdx1



Pdx1 [RC]



LIN-39



Pdx1.1 [RC]



LIN-39.1



HOXA1

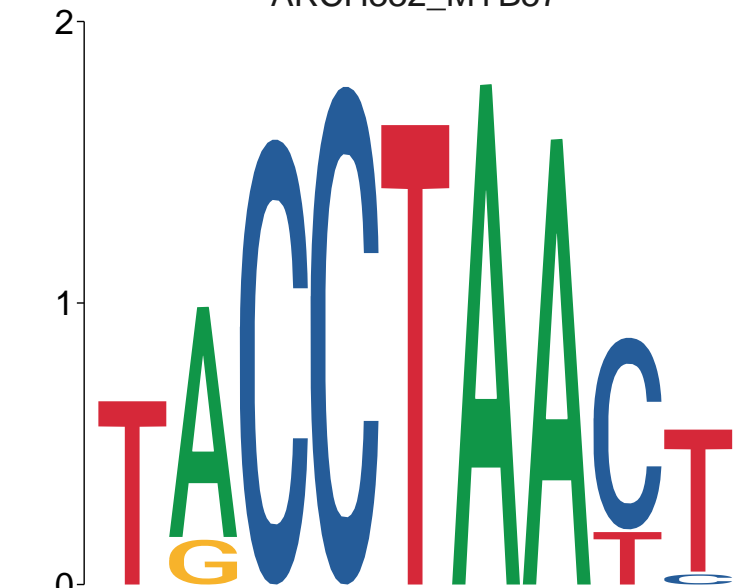


LIN-39.2

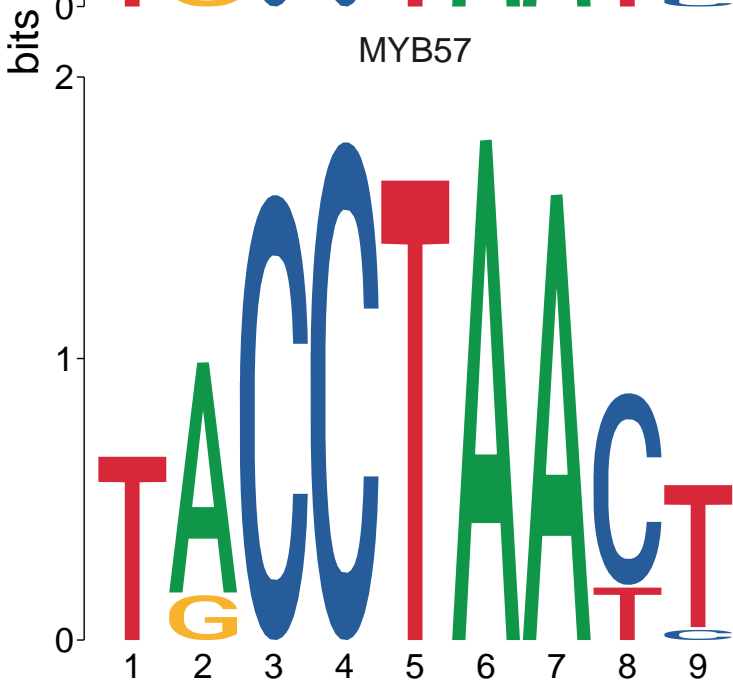


1 2 3 4 5 6 7 8 9 10

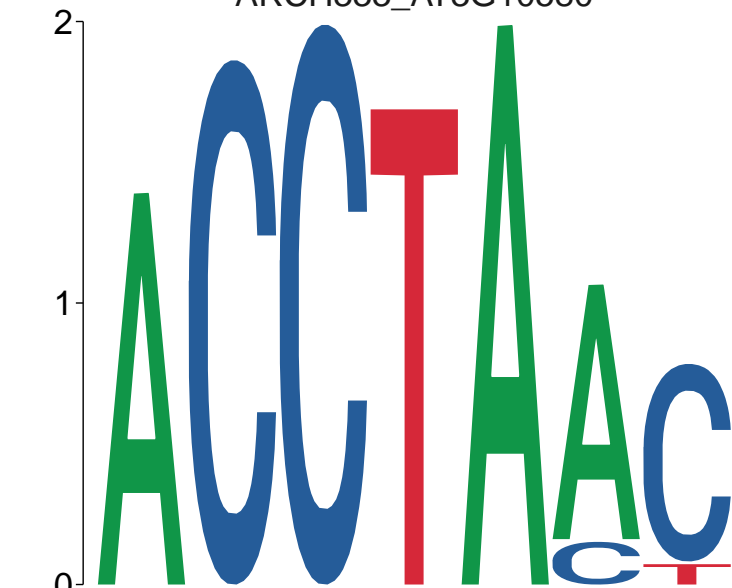
ARCH332_MYB57



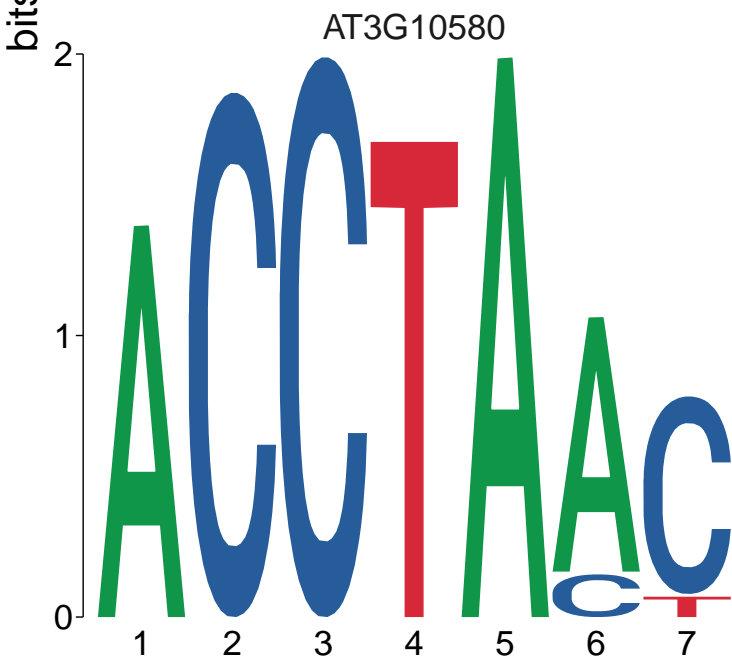
MYB57



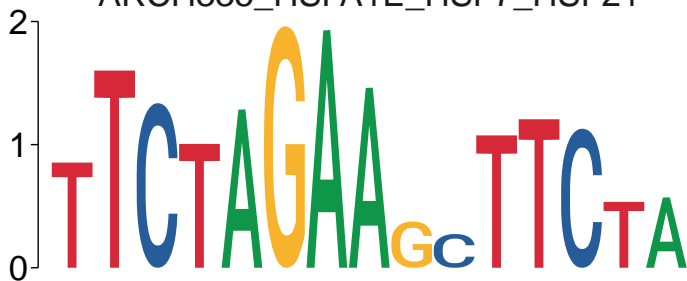
ARCH333_AT3G10580



AT3G10580



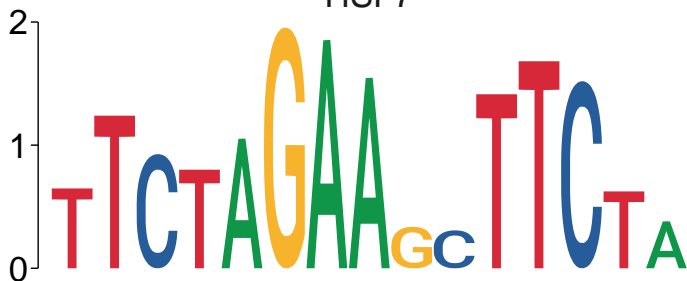
ARCH335_HSFA1E_HSF7_HSF21



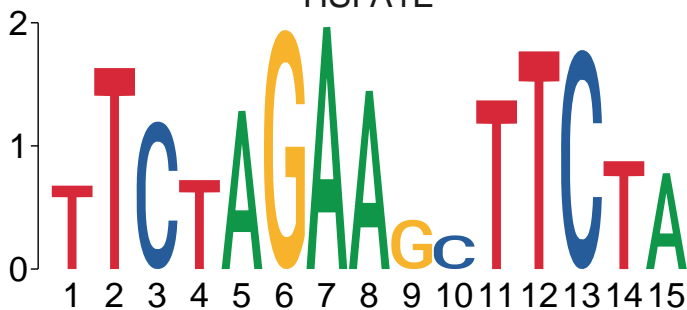
HSF21



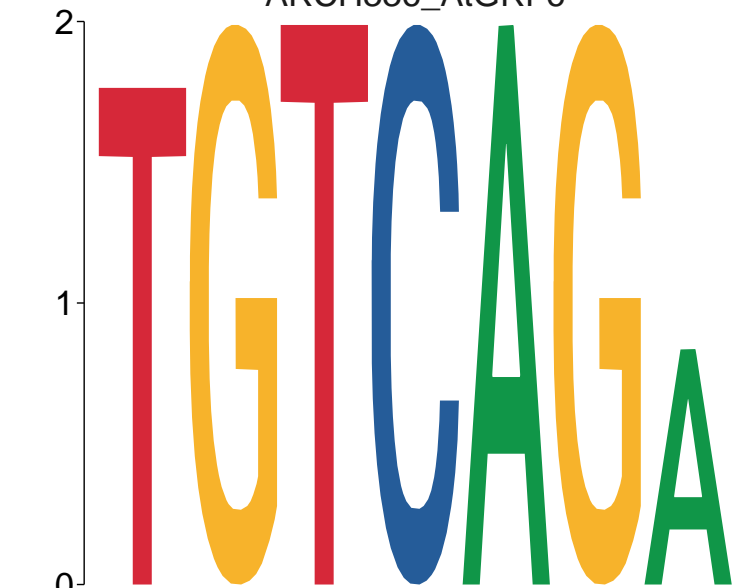
HSF7



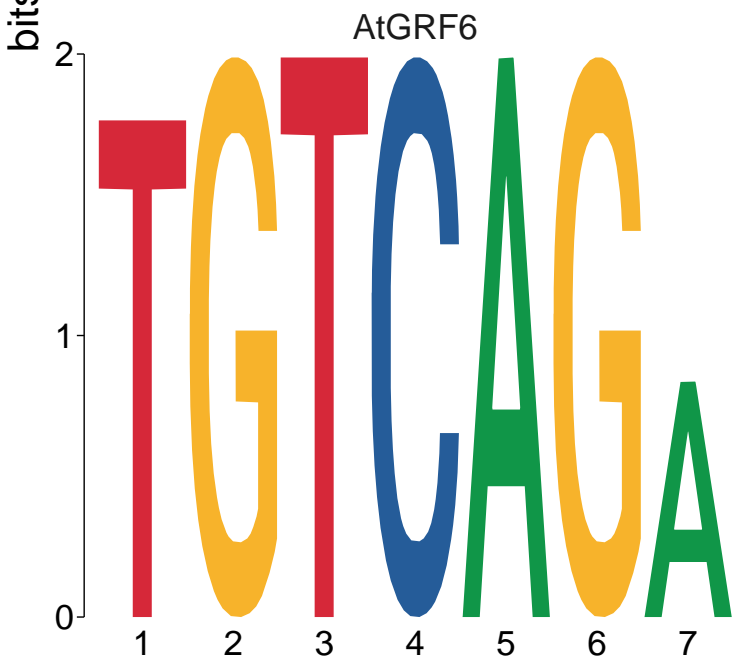
HSFA1E



ARCH336_AtGRF6



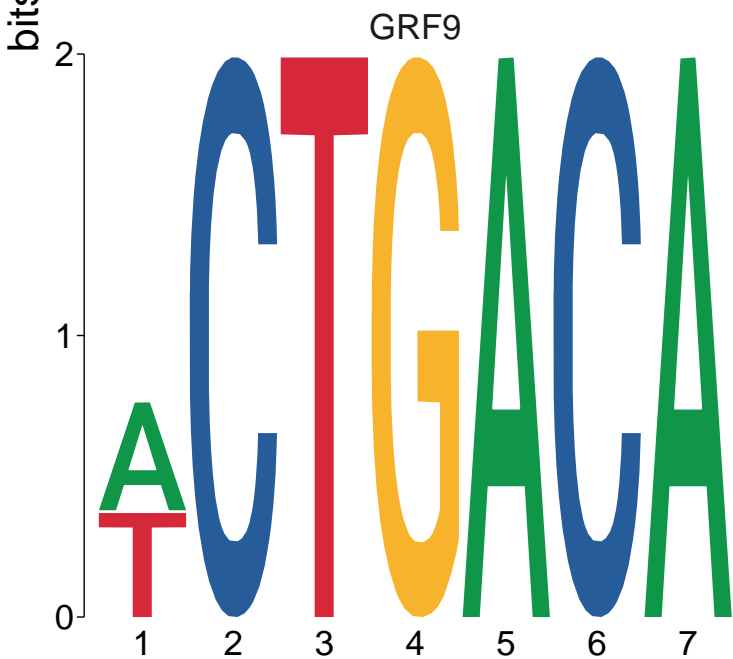
AtGRF6



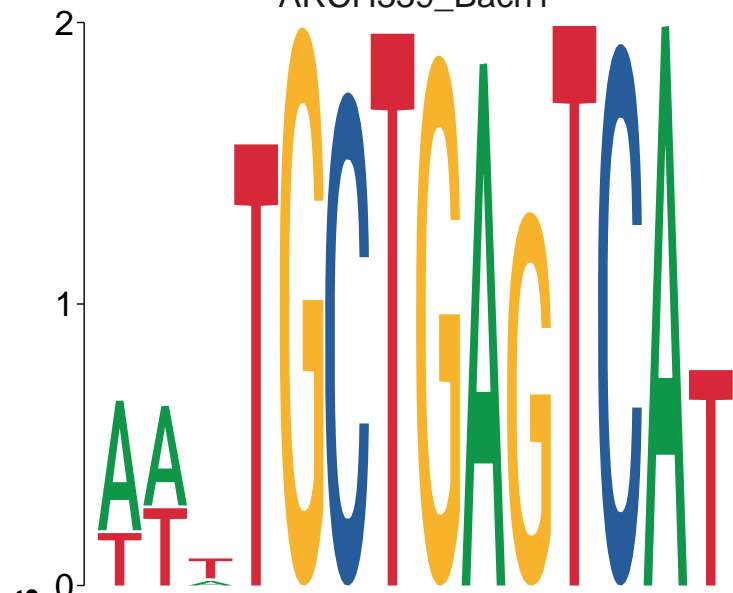
ARCH337_GRF9



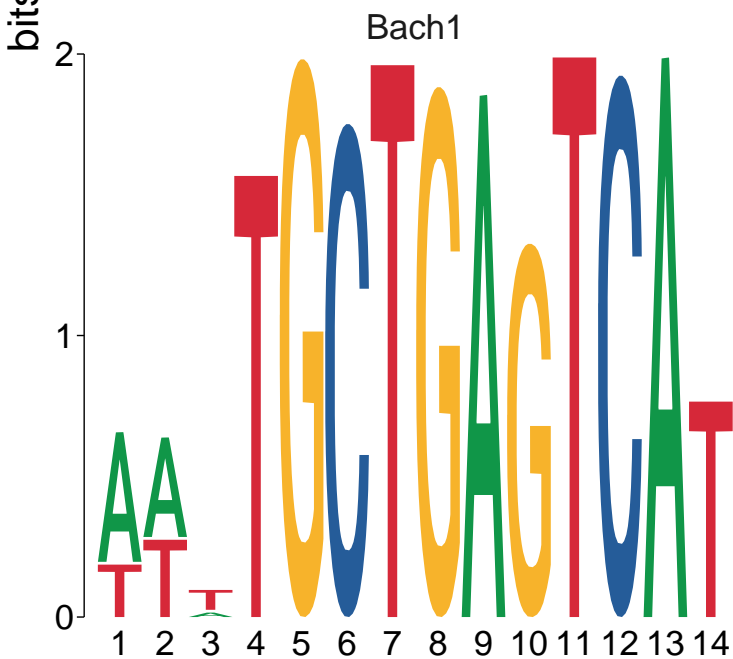
GRF9



ARCH339_Bach1



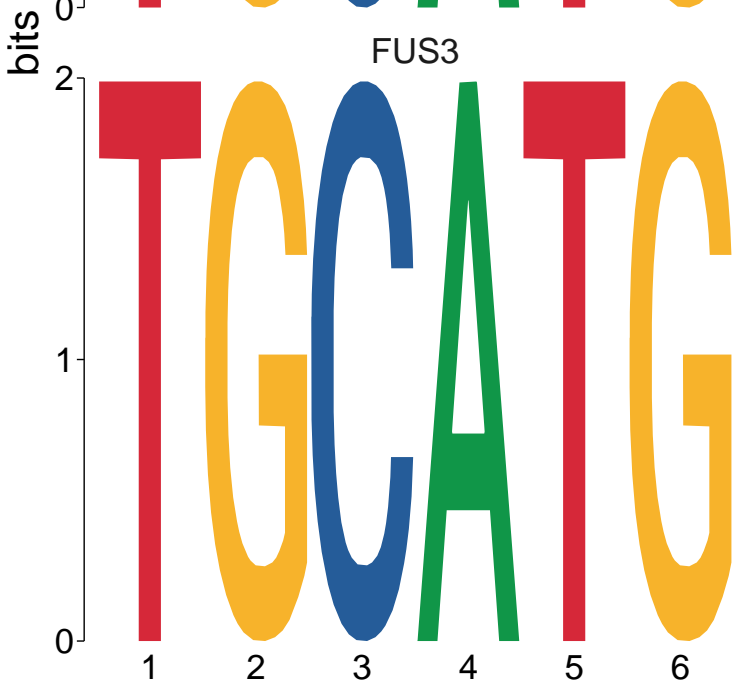
Bach1



ARCH340_FUS3



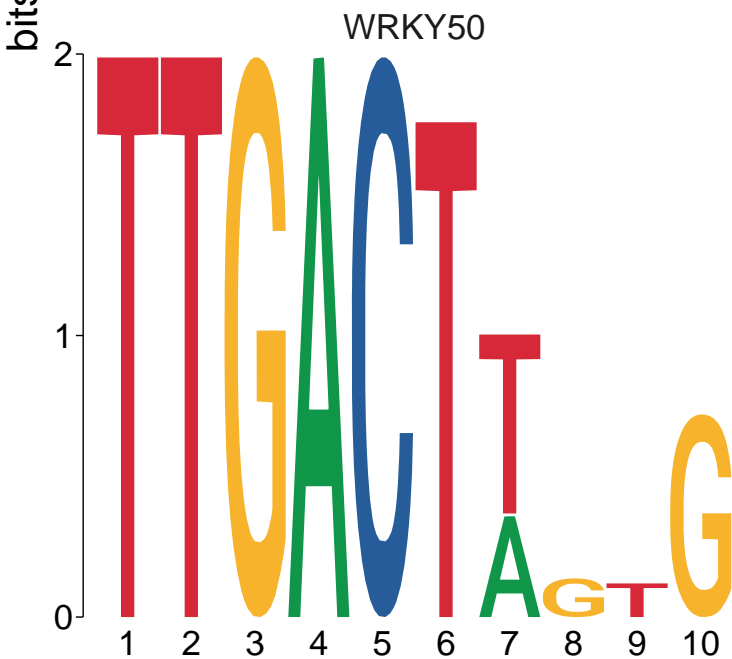
FUS3



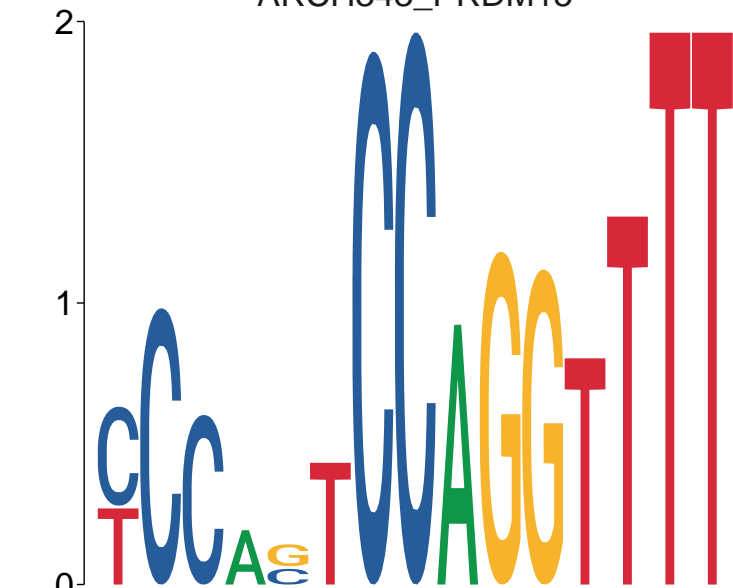
ARCH341_WRKY50



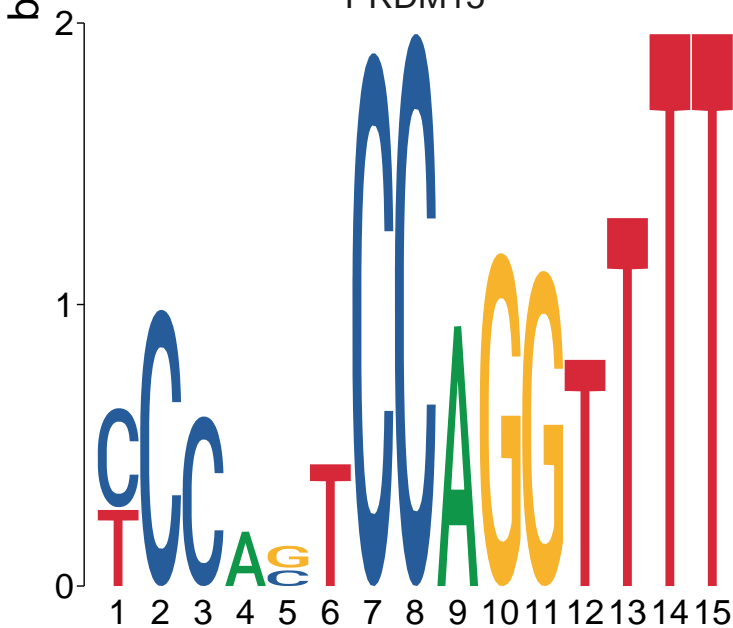
WRKY50



ARCH343_PRDM15



PRDM15



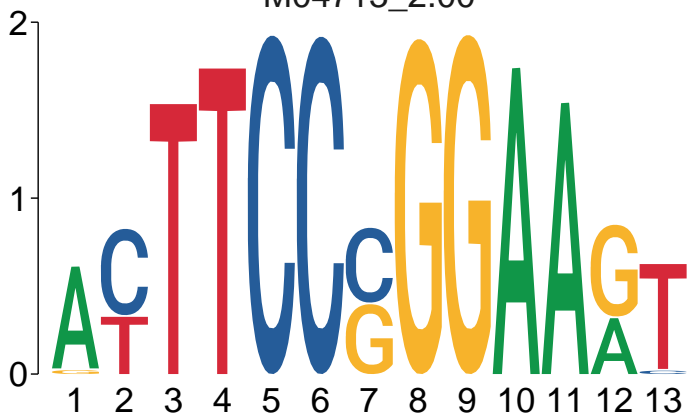
ARCH351_Ets



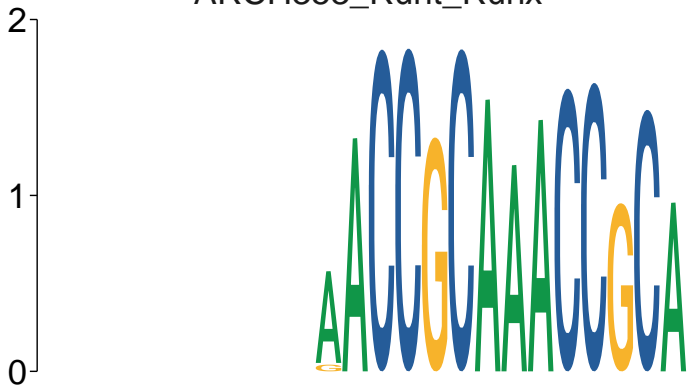
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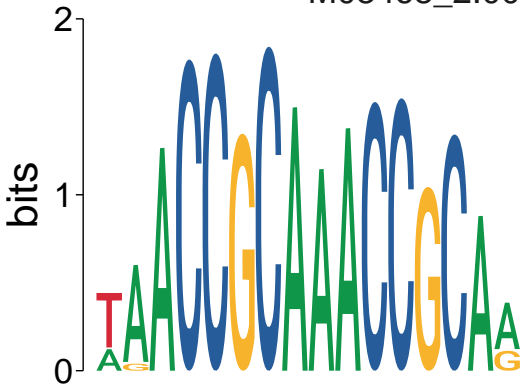
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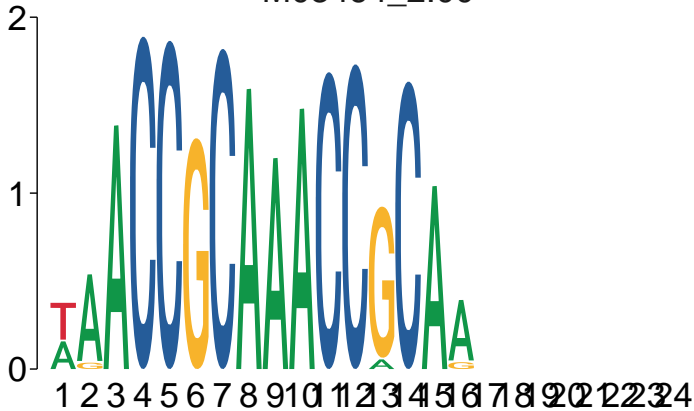
ARCH353_Runt_Runx



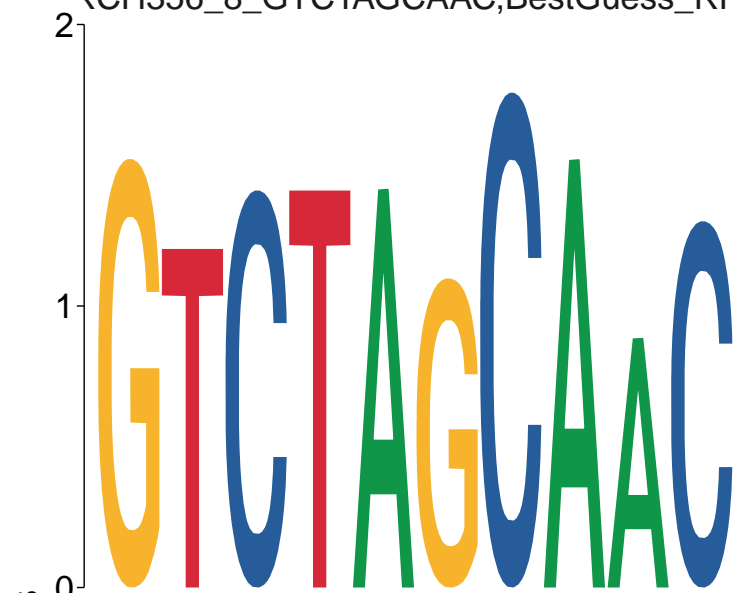
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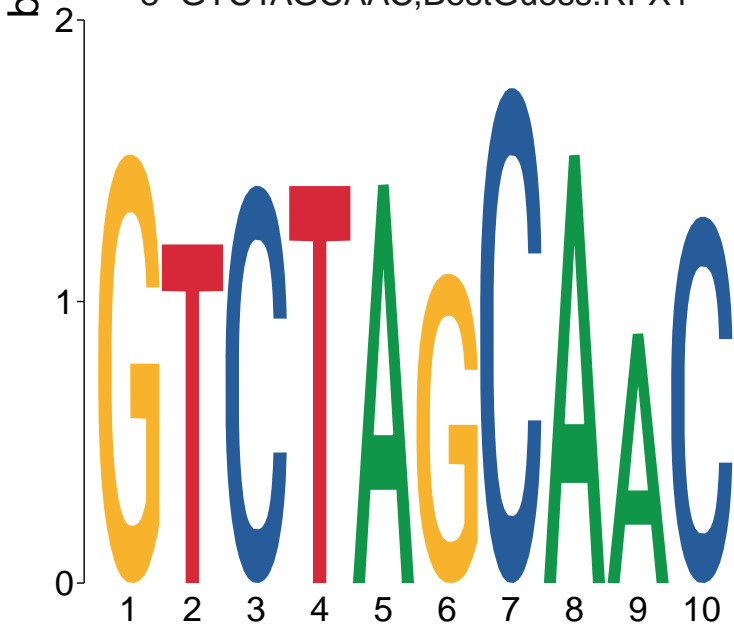
M03464_2.00



RCH356_8_GTCTAGCAAC,BestGuess_RF)



8-GTCTAGCAAC,BestGuess:RFX1



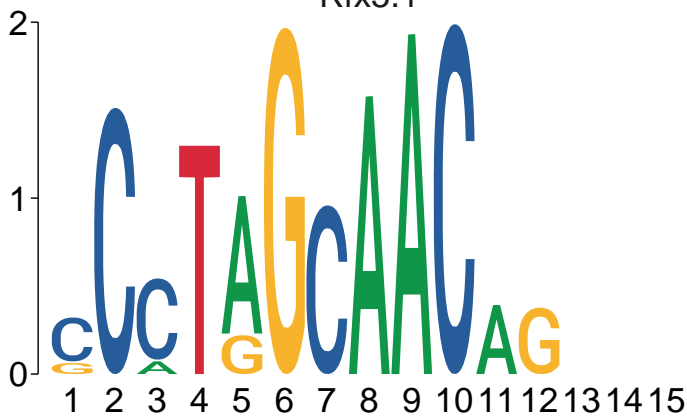
ARCH357_Rfx5_Rfx5



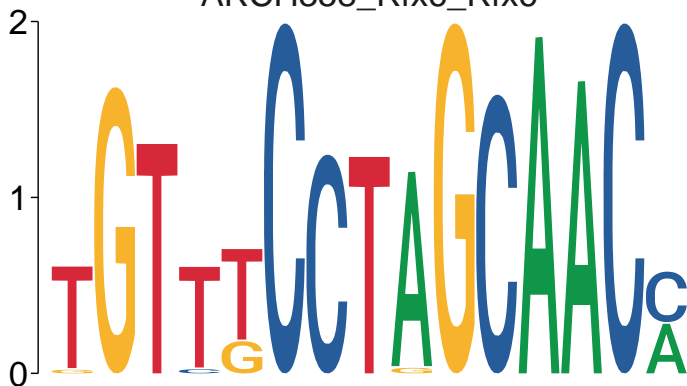
Rfx5



Rfx5.1



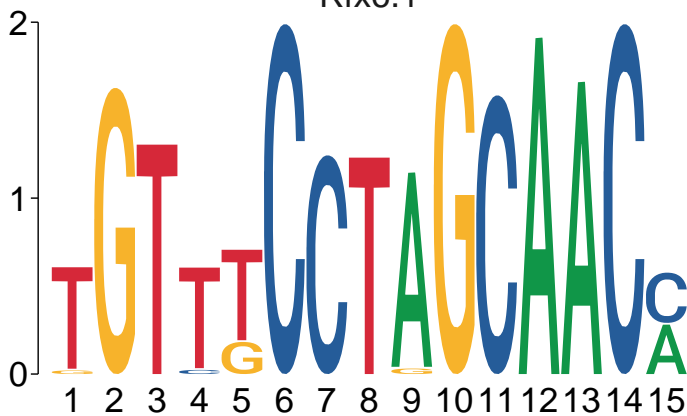
ARCH358_Rfx6_Rfx6



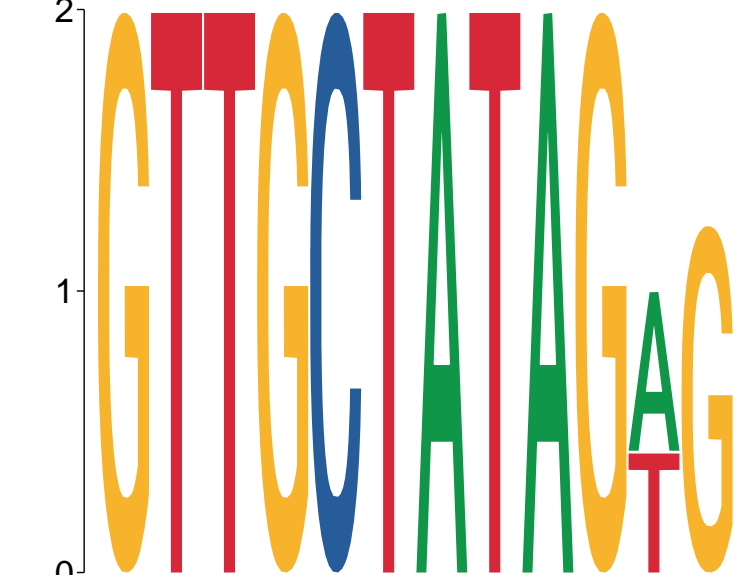
Rfx6



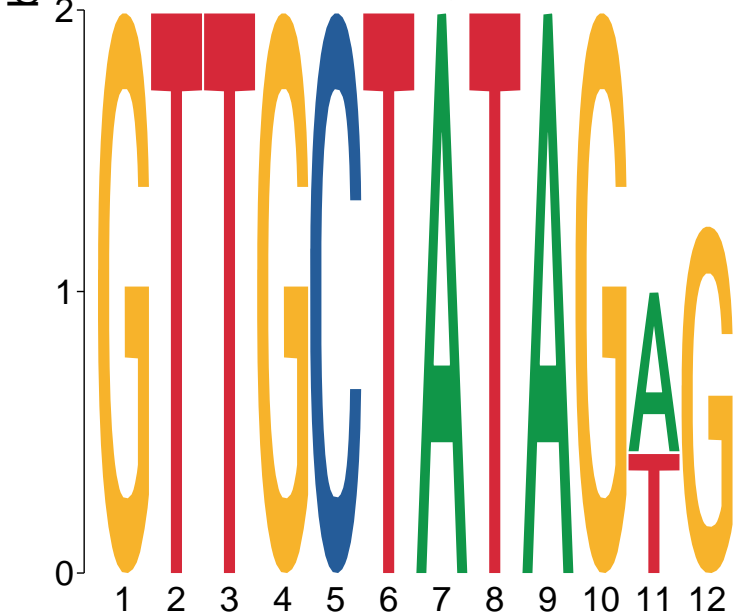
Rfx6.1



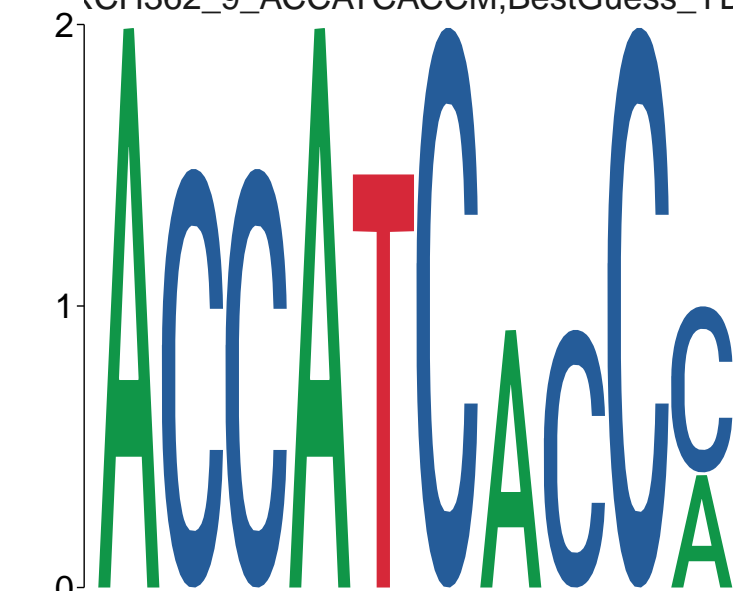
CH359_23_GTTGCTATAGWG,BestGuess_



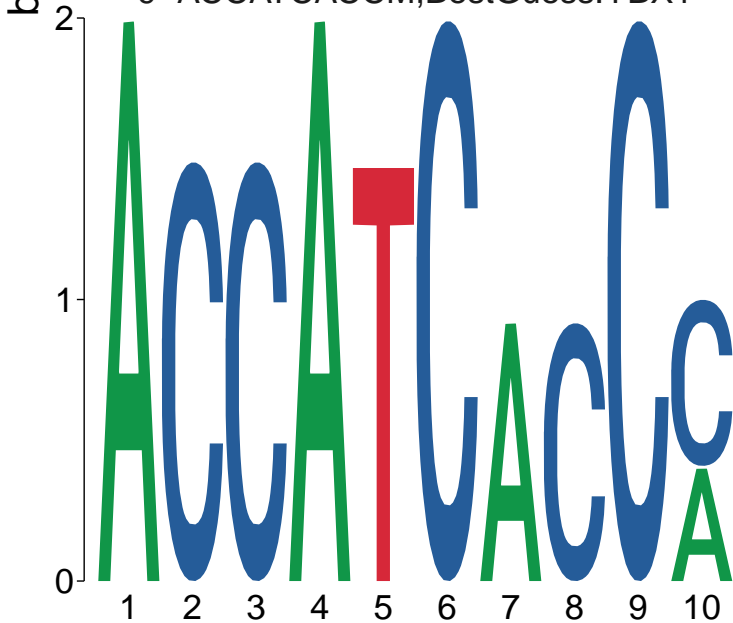
23-GTTGCTATAGWG,BestGuess:RFX1



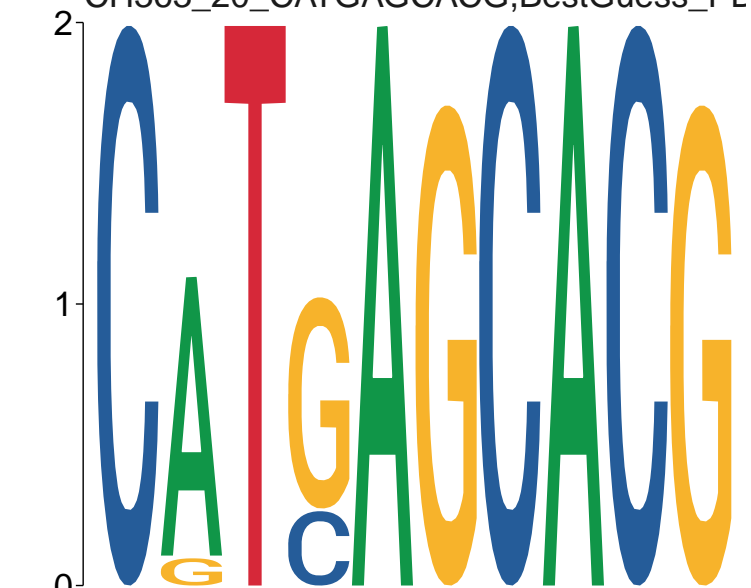
CH362_9_ACCATCACCM,BestGuess_YB



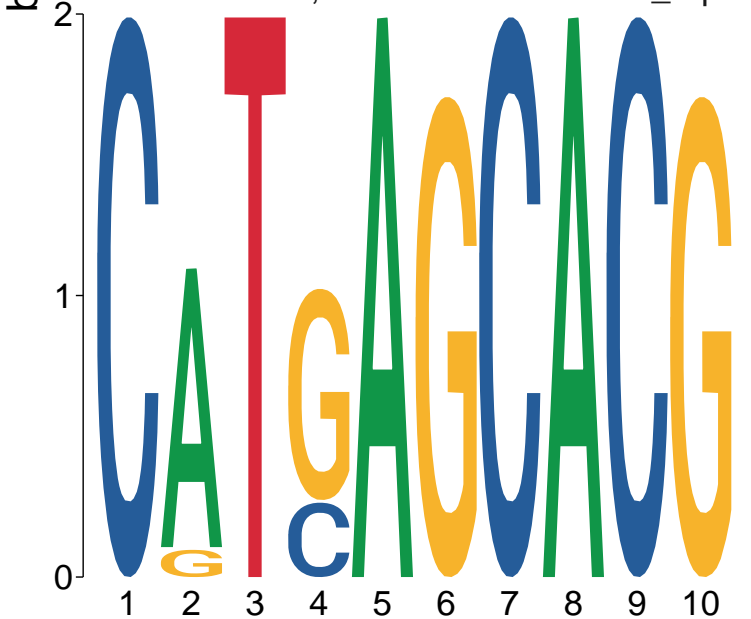
9-ACCATCACCM,BestGuess:YBX1



CH363_20_CATGAGCACG,BestGuess_PE



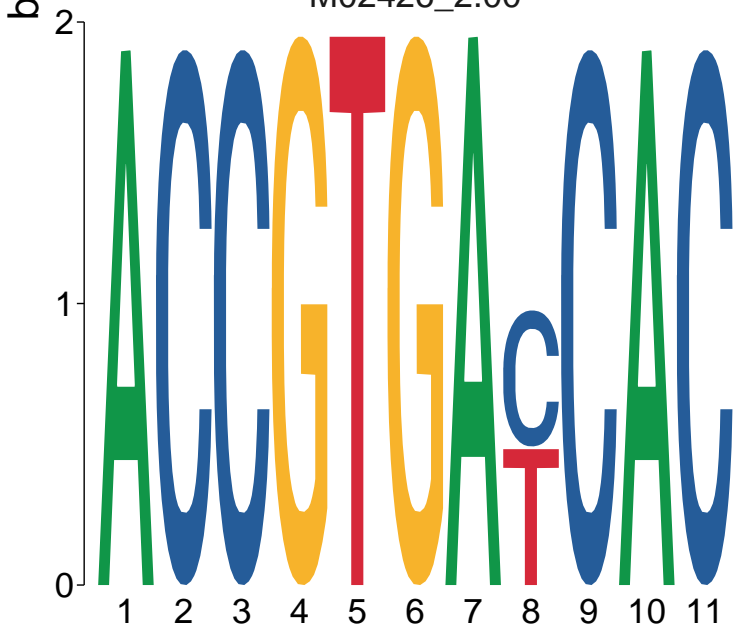
CATGAGCACG,BestGuess:PB0099.1_Zfp69



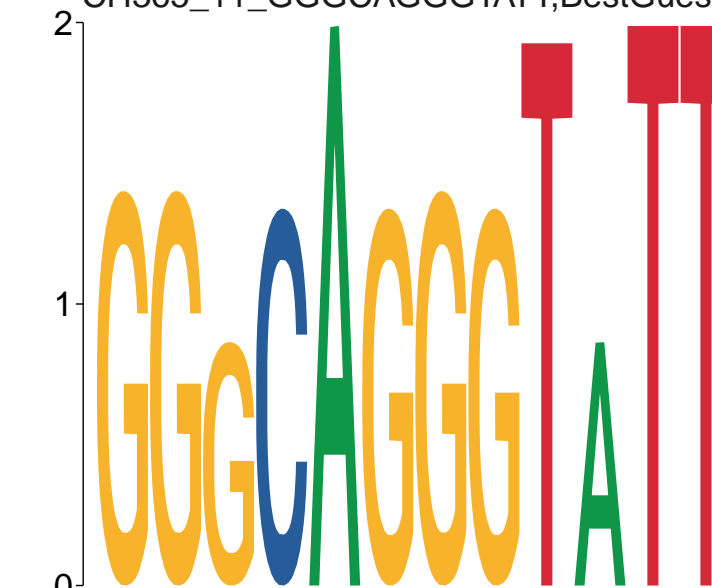
ARCH364_Homeodomains



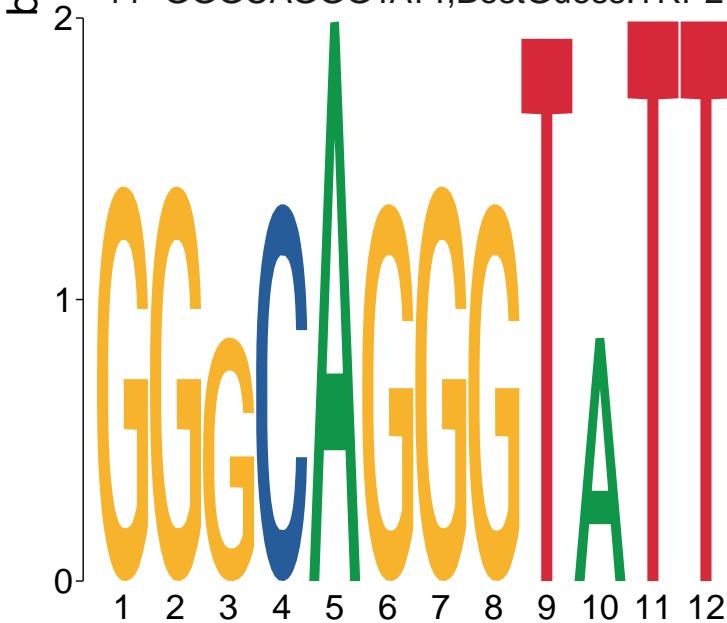
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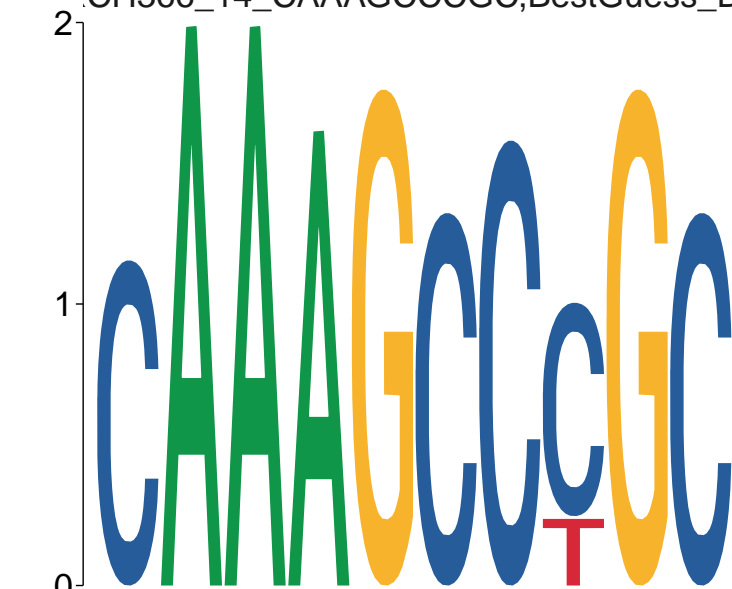
CH365_11_GGGCAGGGTATT,BestGuess_



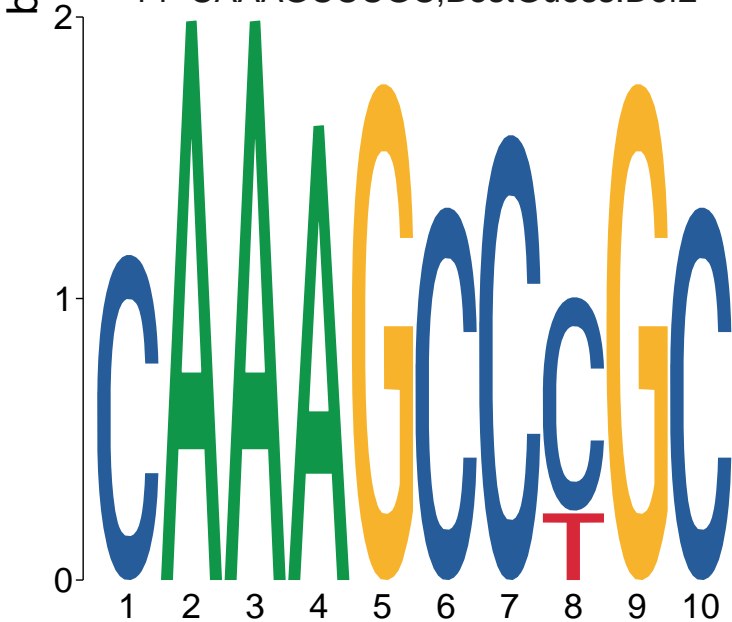
11-GGGCAGGGTATT,BestGuess:TRP2



CH366_14_CAAAGCCCGC,BestGuess_Do



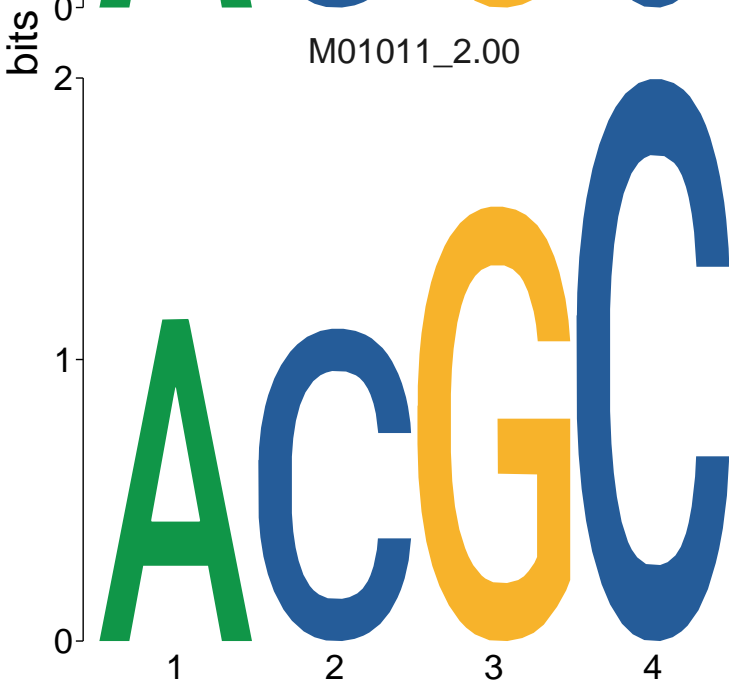
14-CAAAGCCCGC,BestGuess:Dof2



ARCH367_Forkhead



M01011_2.00



RCH369_11_GGTCATTAAT,BestGuess_PHI

2

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bits

-GGTCATTAAT,BestGuess:PH0073.1_Hox

2

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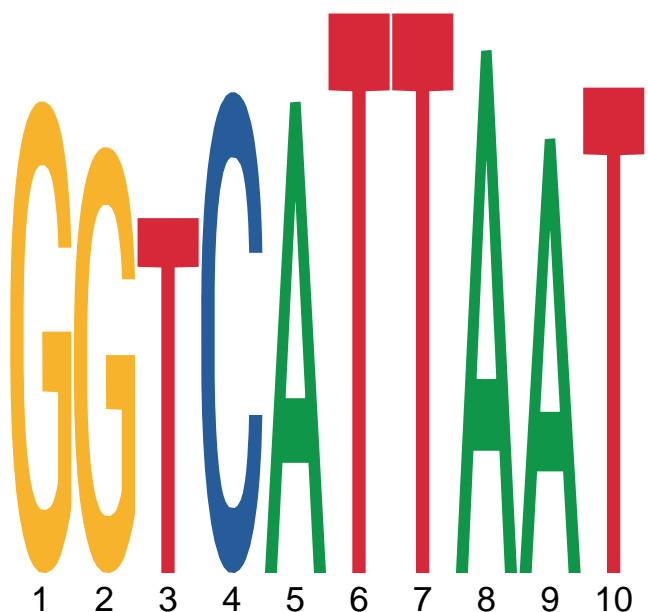
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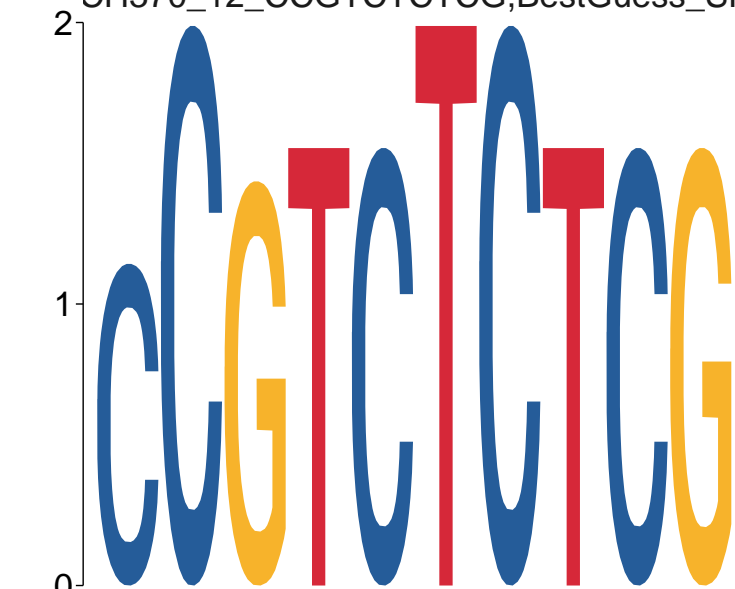
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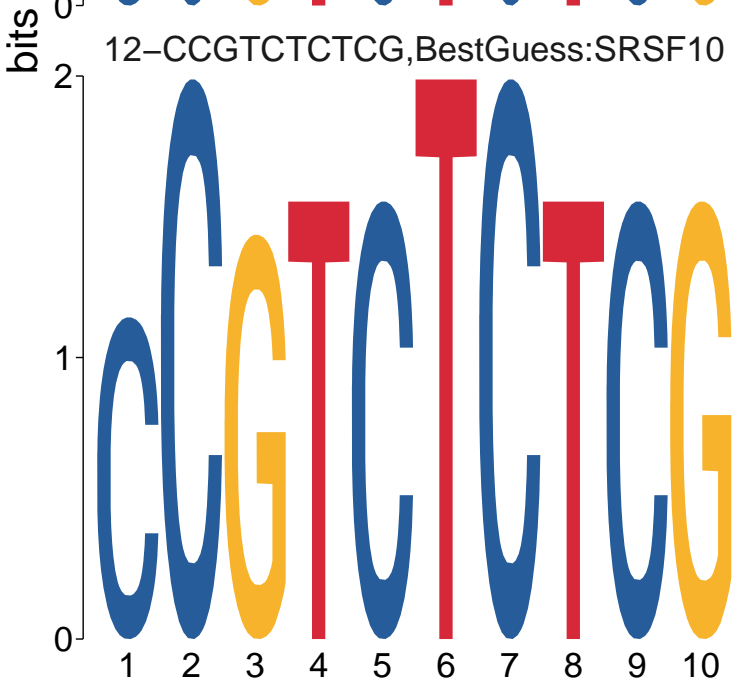
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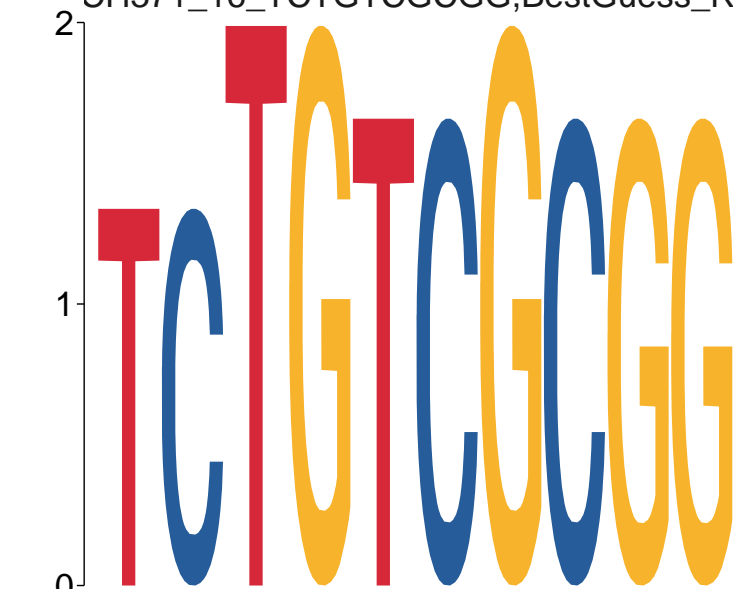
CH370_12_CCGTCTCTCTCG,BestGuess_SR



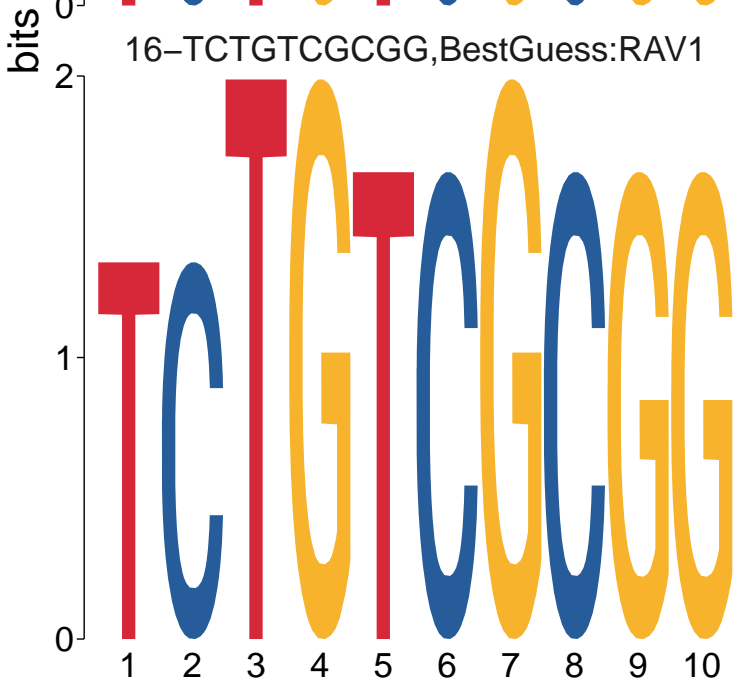
12-CCGTCTCTCTCG,BestGuess:SRSF10



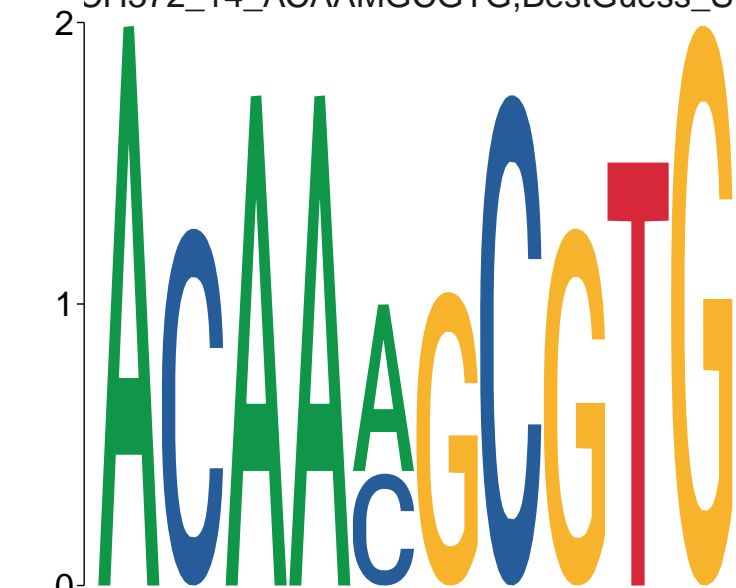
CH371_16_TCTGTCGCGG,BestGuess_R/



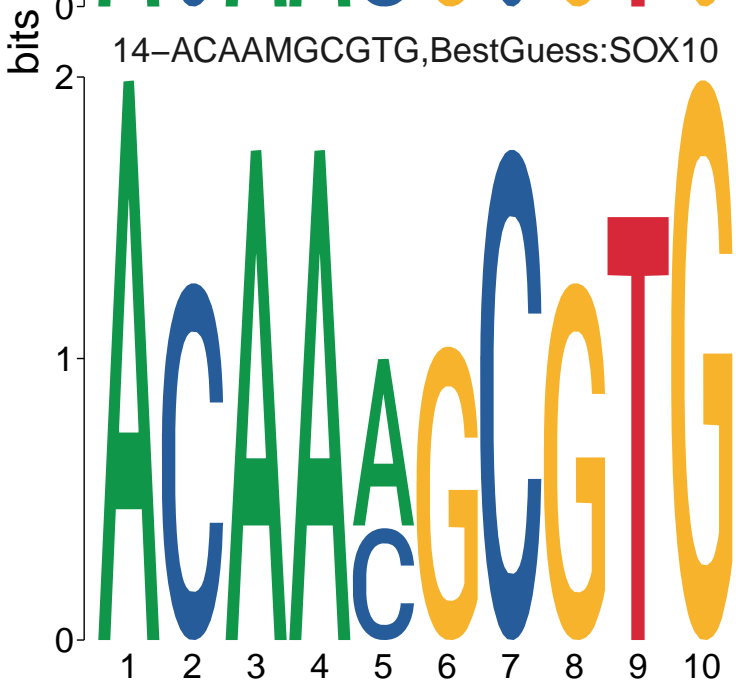
16-TCTGTCGCGG,BestGuess:RAV1



CH372_14_ACAAMGCGTG,BestGuess_SC



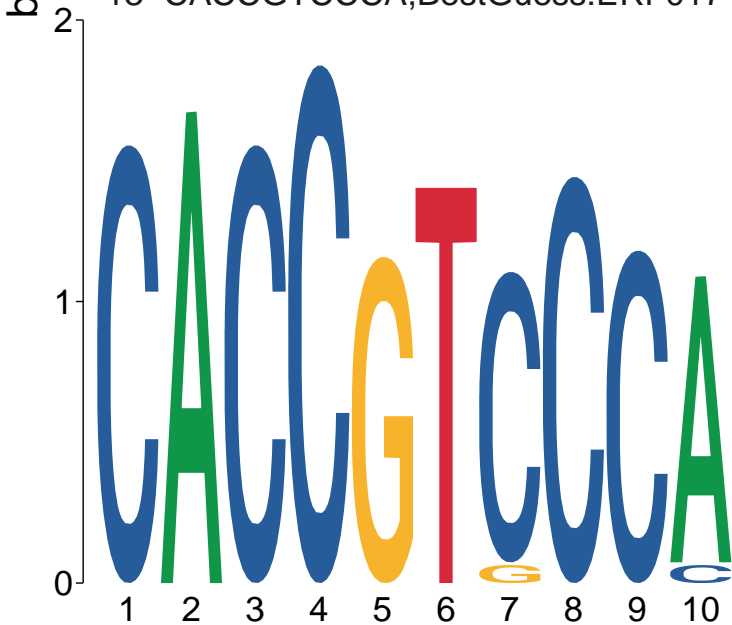
14-ACAAMGCGTG,BestGuess:SOX10



CH373_13_CACCGTCCCA,BestGuess_EF



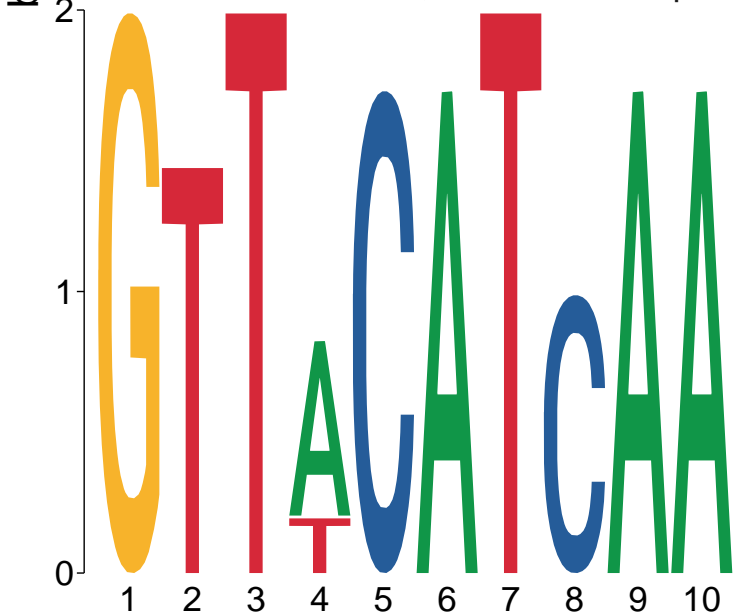
13-CACCGTCCCA,BestGuess:ERF017



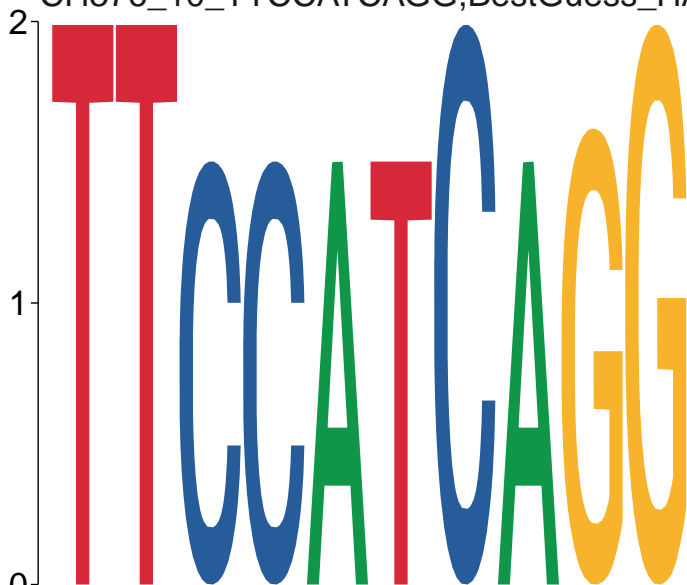
CH375_14_GTTACATCAA,BestGuess_Ch



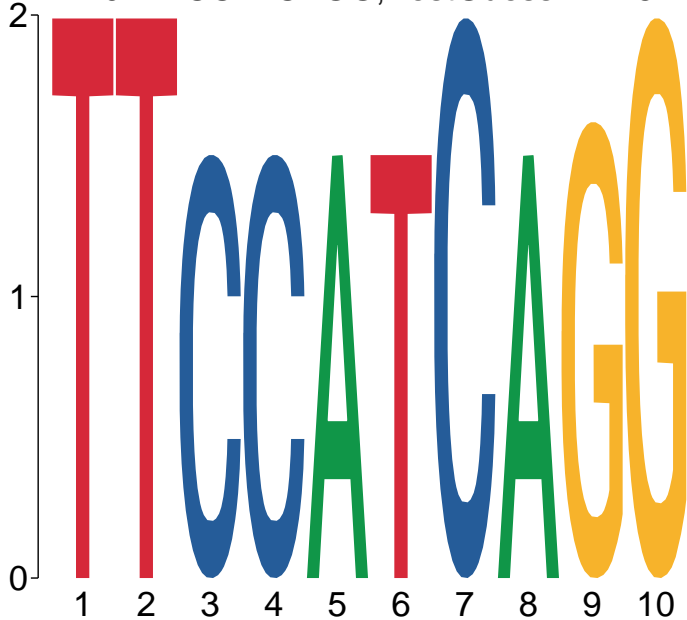
14-GTTACATCAA,BestGuess:Chop



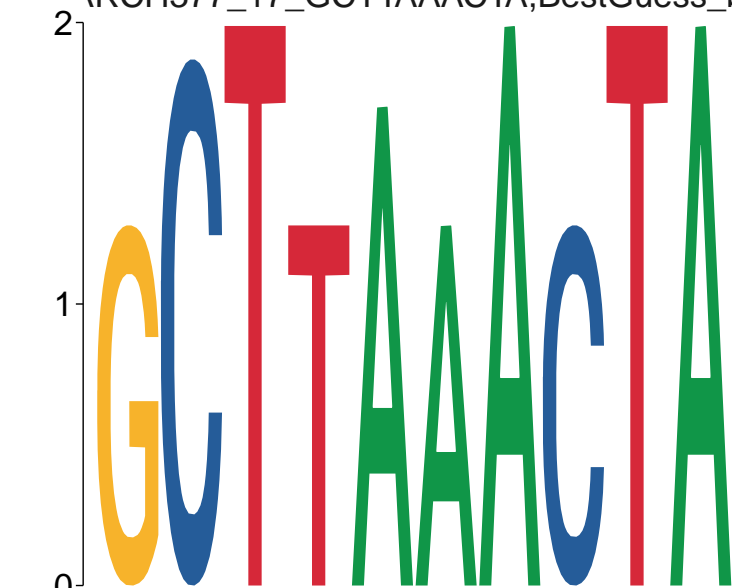
CH376_10_TTCCATCAGG,BestGuess_HA



10-TTCCATCAGG,BestGuess:HAP3

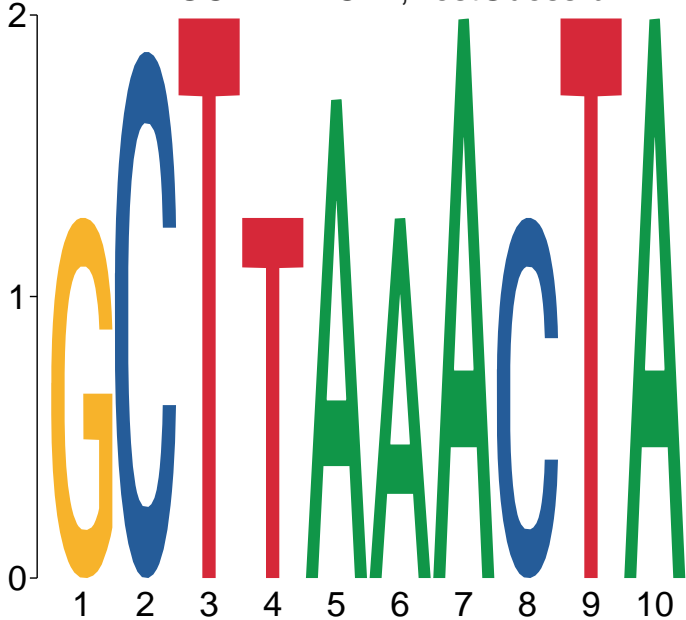


ARCH377_17_GCTTAAACTA,BestGuess_b



bits

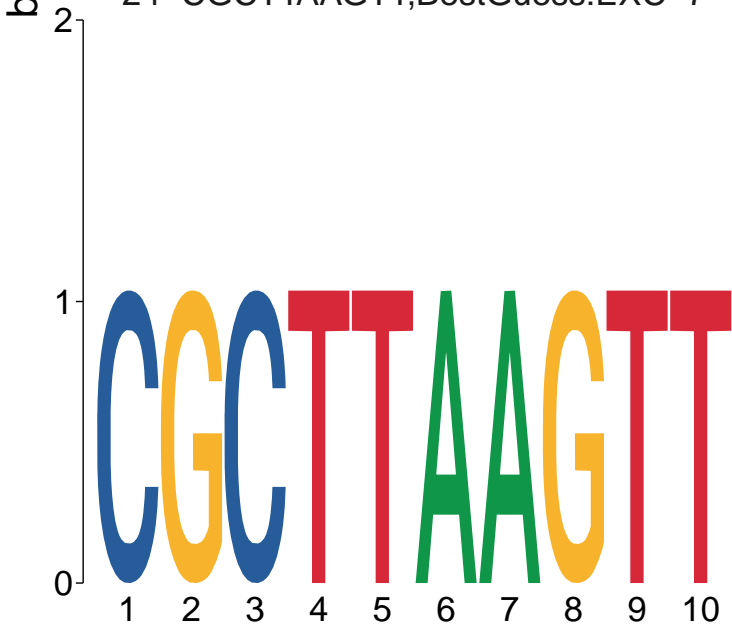
17-GCTTAAACTA,BestGuess:br



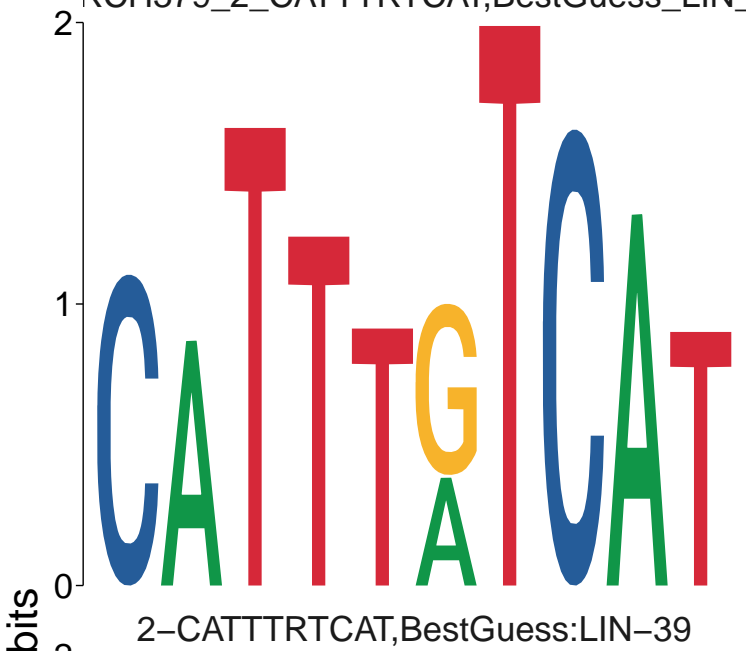
RCH378_24_CGCTTAAGTT,BestGuess_EX



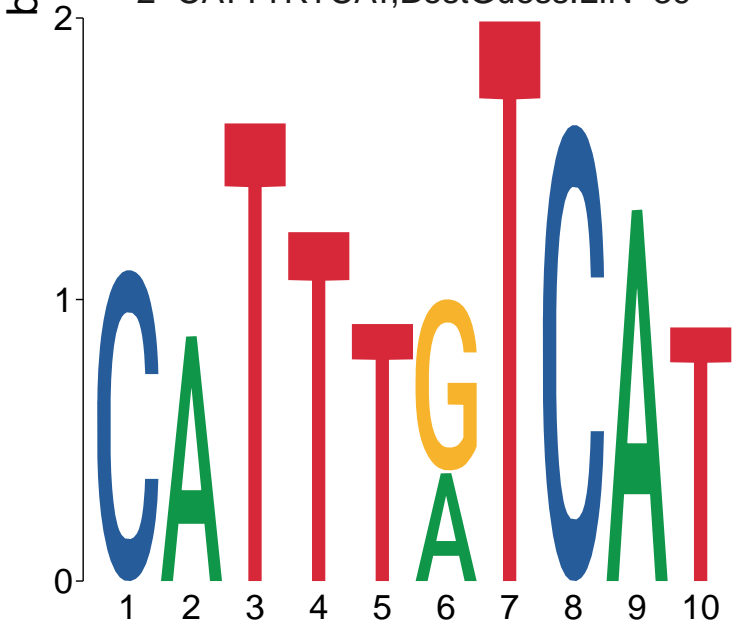
24-CGCTTAAGTT,BestGuess:EXC-7



RCH379_2_CATTTRTCAT,BestGuess_LIN_



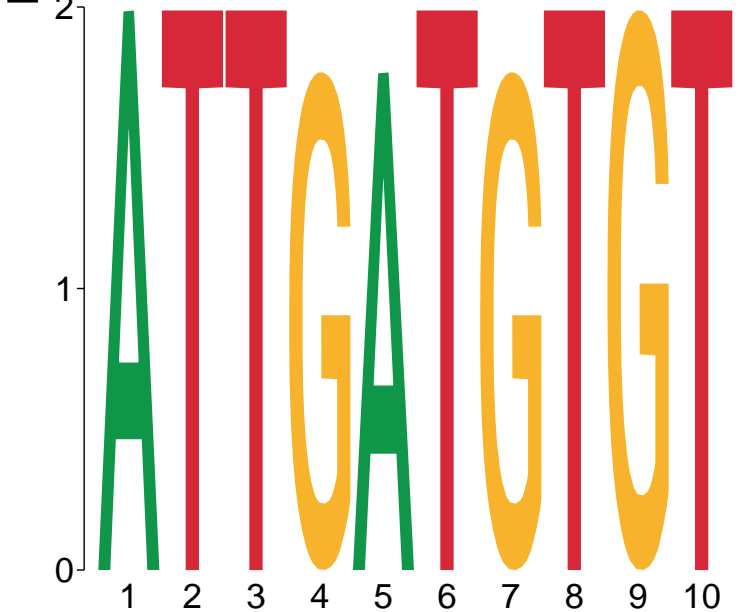
2-CATTTRTCAT,BestGuess:LIN-39



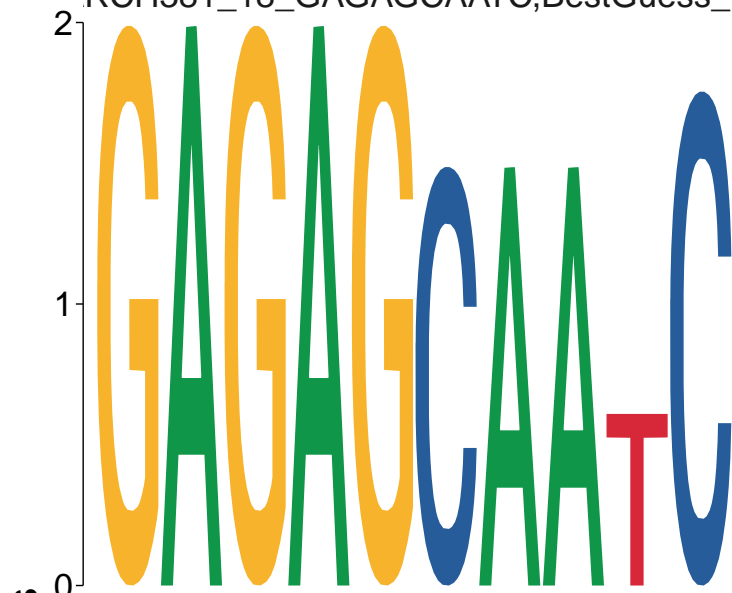
CH380_17_ATTGATGTGT,BestGuess_PH



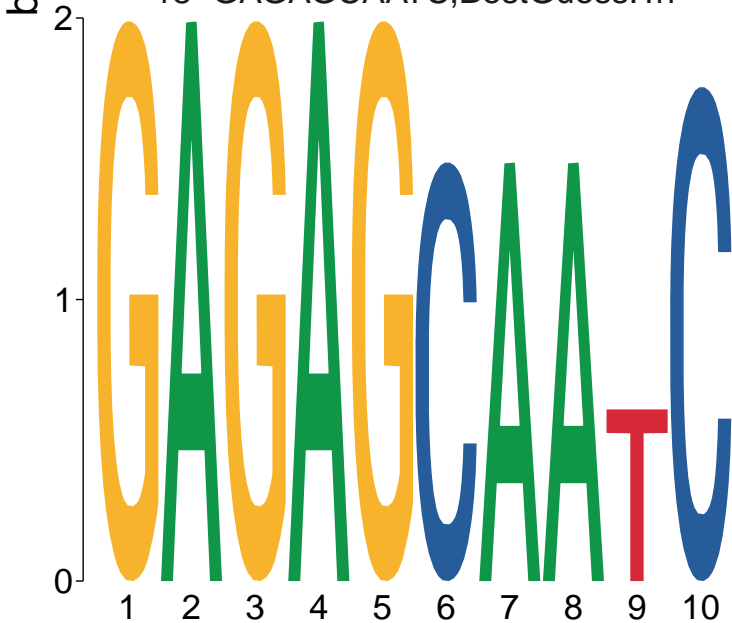
7-ATTGATGTGT,BestGuess:PH0134.1_Pb



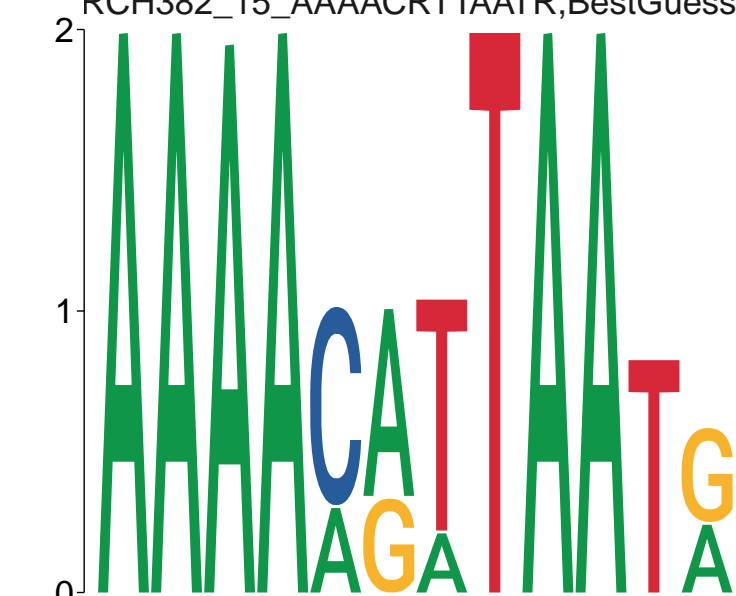
RCH381_18_GAGAGCAATC,BestGuess_T



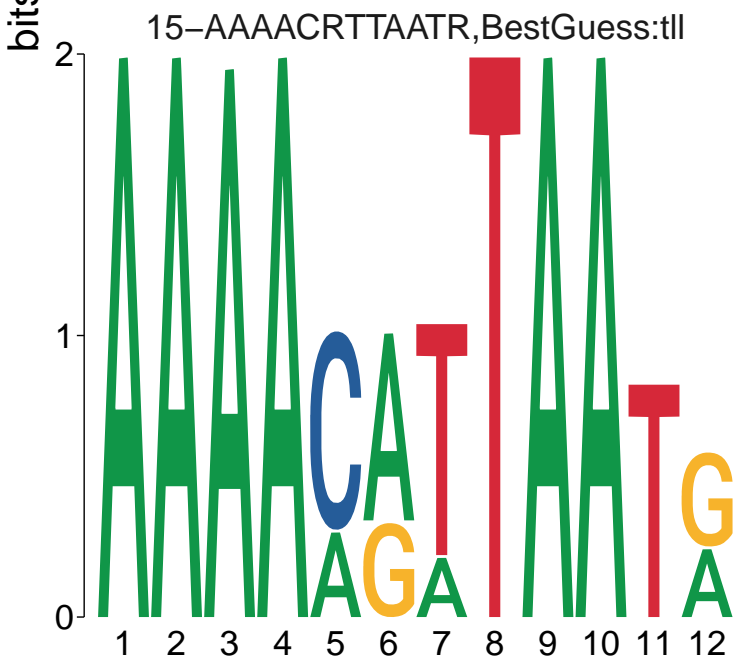
18-GAGAGCAATC,BestGuess:Trl



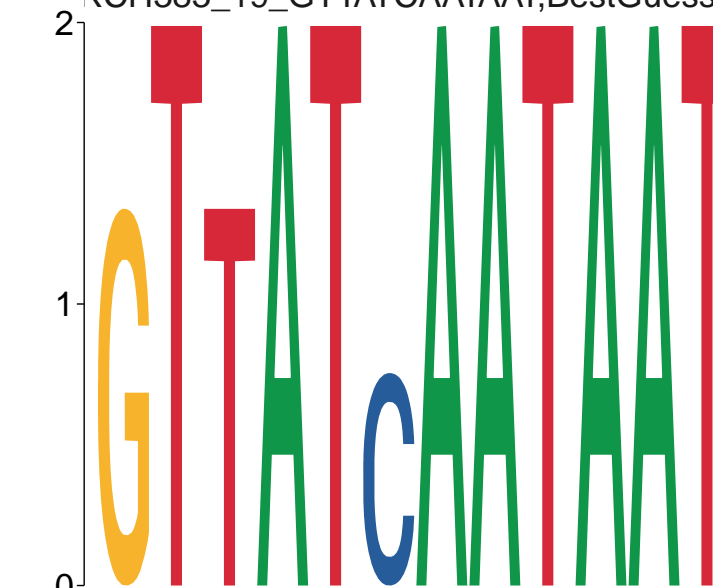
RCH382_15_AAAACRTTAATR,BestGuess_



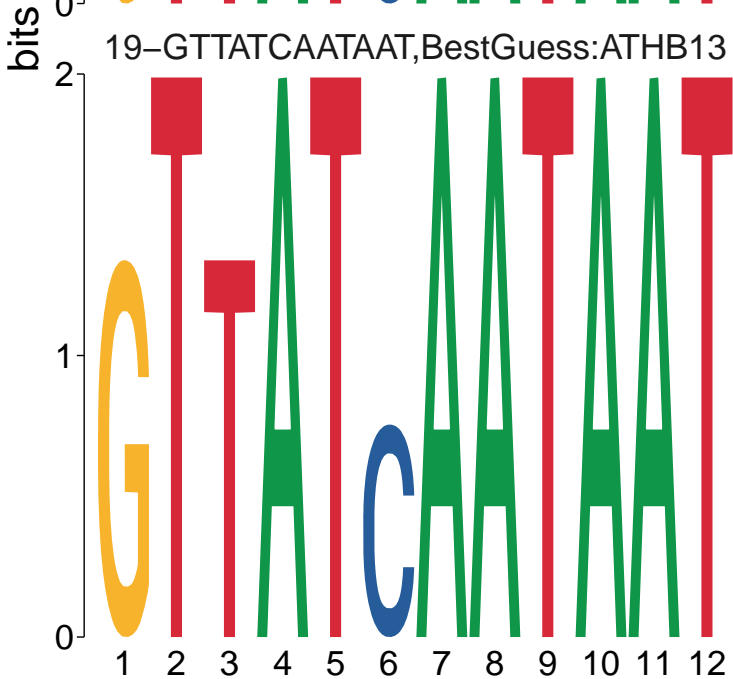
15-AAAACRTTAATR,BestGuess:tl



RCH383_19_GTTATCAATAAT,BestGuess_1



19-GTTATCAATAAT,BestGuess:ATHB13



1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19



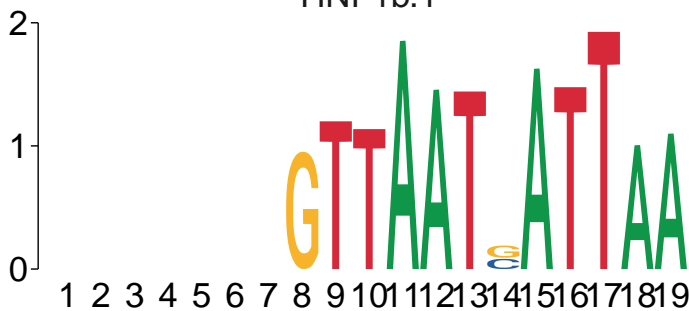
Hnf1



HNF1b



HNF1b.1



RCH385_22_TAGTCATTTTTT,BestGuess_1

2

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bits

2-TAGTCATTTTTT,BestGuess:HNRNPCL'

2

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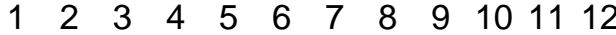
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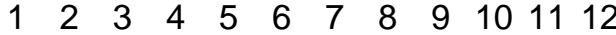
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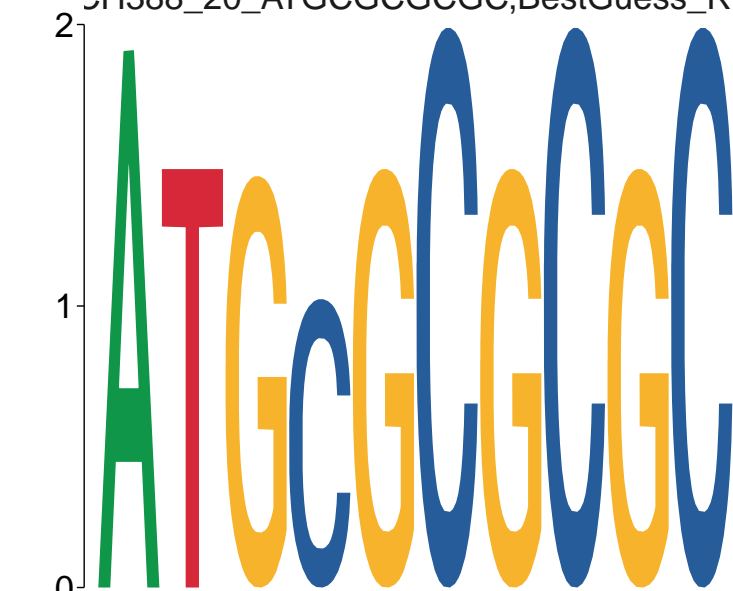
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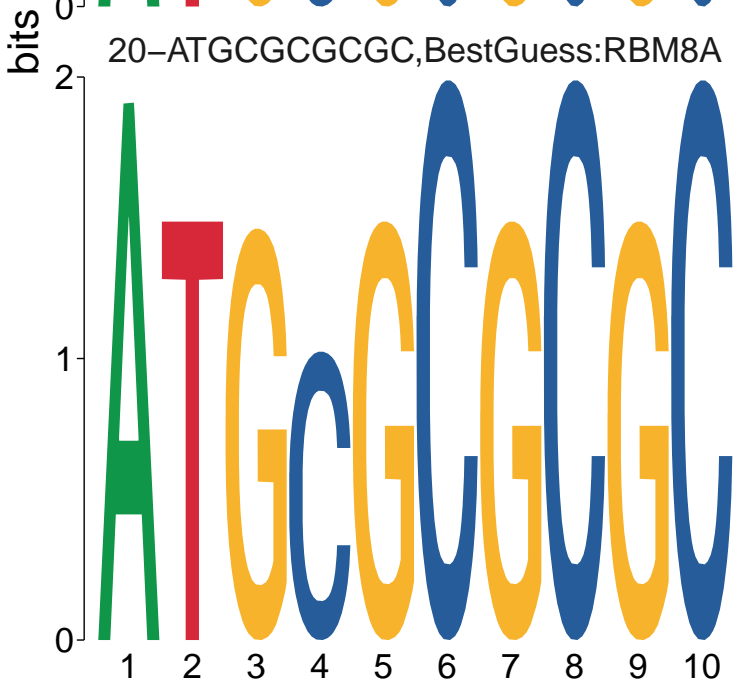
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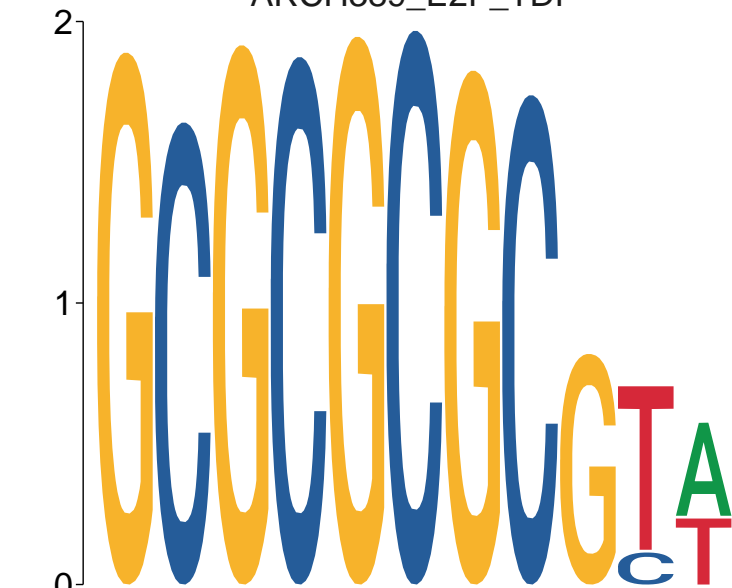
CH388_20_ATGCGCGCGC,BestGuess_RE



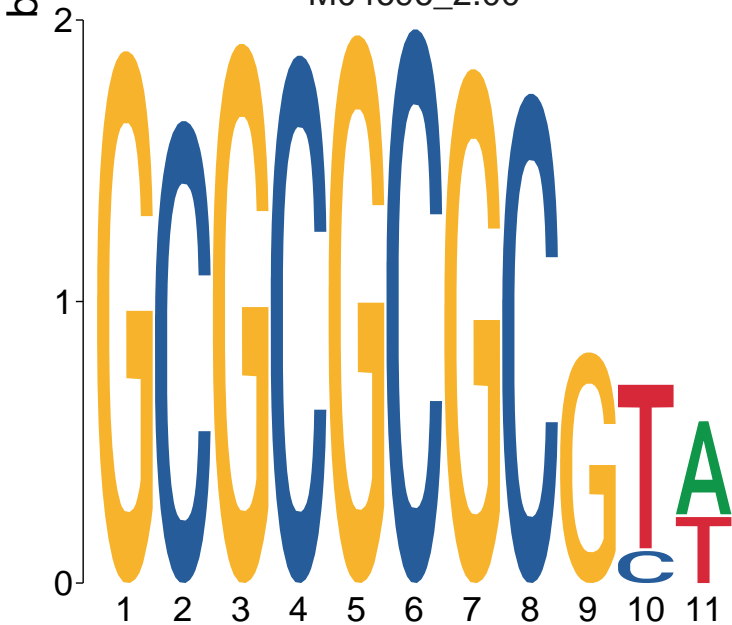
20-ATGCGCGCGC,BestGuess:RBM8A



ARCH389_E2F_TDP



M04696_2.00



Nvec_v1g200125_Nvec_v1g235633_Nvec_

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bits

M01960_2.00

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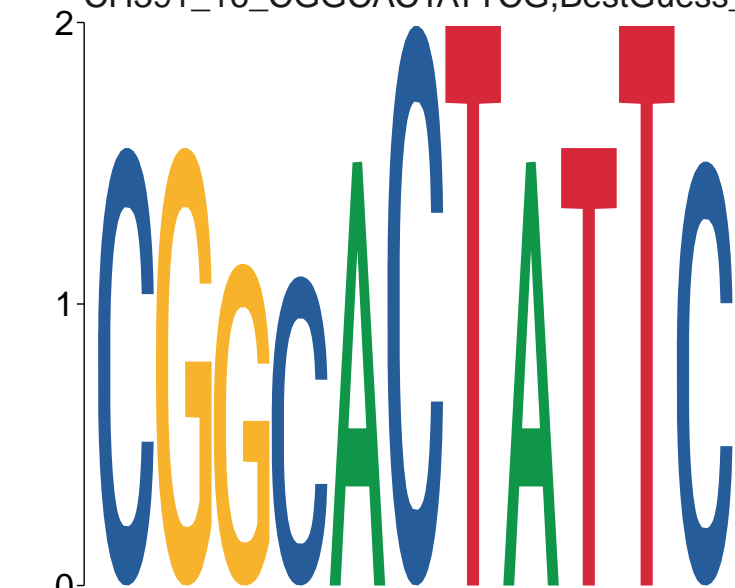
2

3

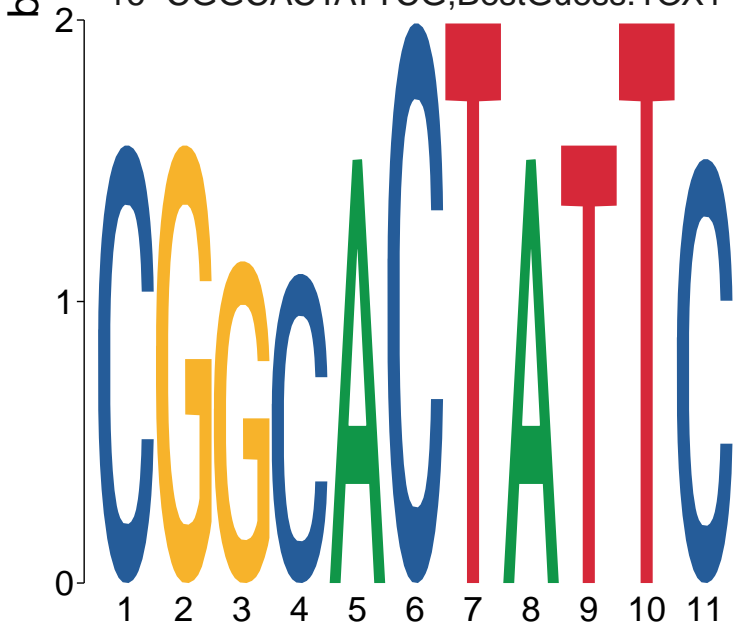
4



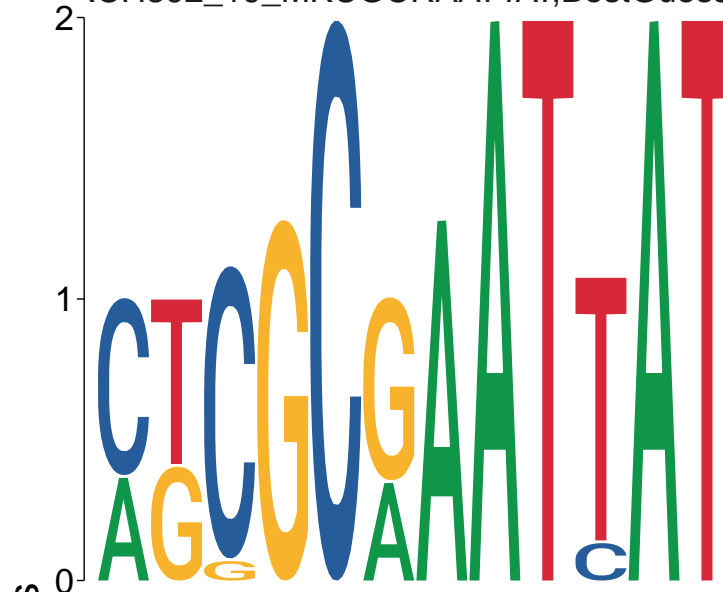
CH391_16_CGGCACTATTTCG,BestGuess_



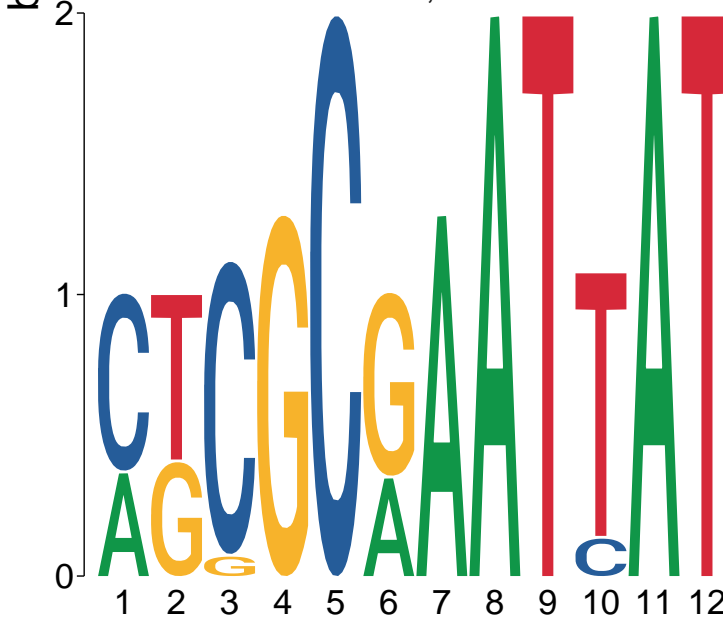
16-CGGCACTATTTCG,BestGuess:YOX1



RCH392_19_MKCGCRAATTAT,BestGuess_



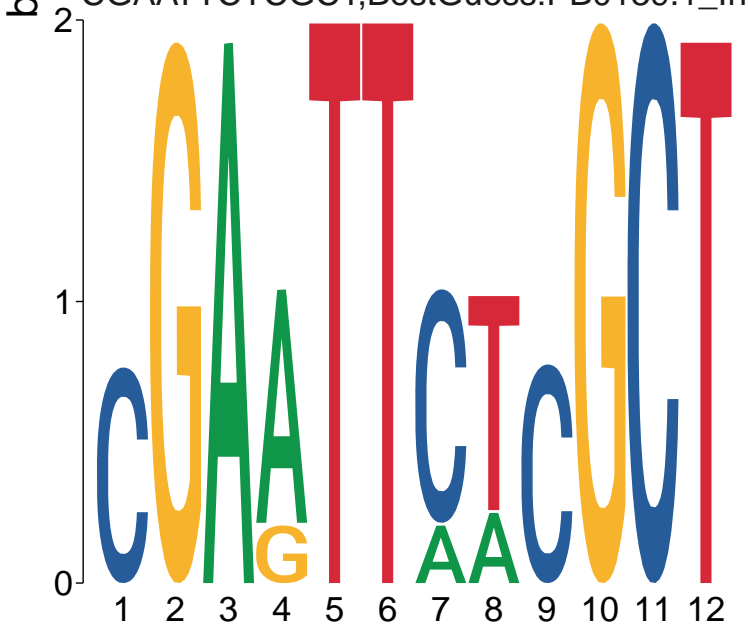
19-MKCGCRAATTAT,BestGuess:AtHB32



CH393_12_CGAATTCTCGCT,BestGuess_



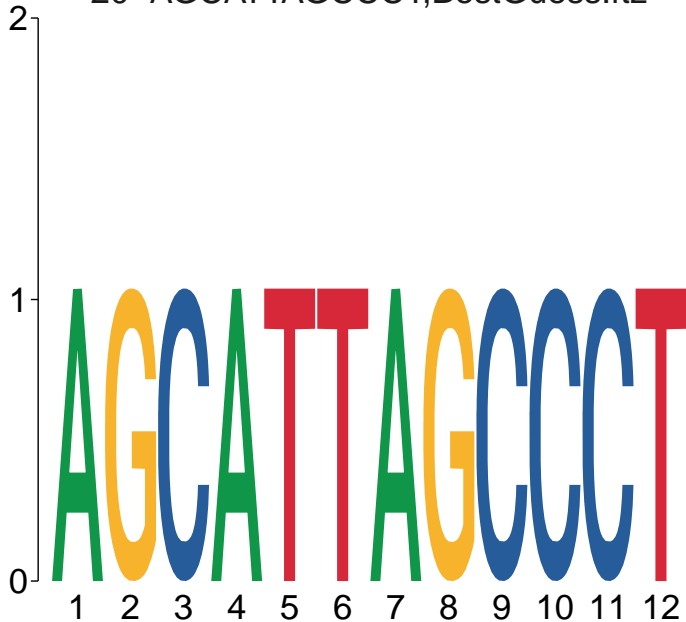
CGAATTCTCGCT,BestGuess:PB0139.1_Irf



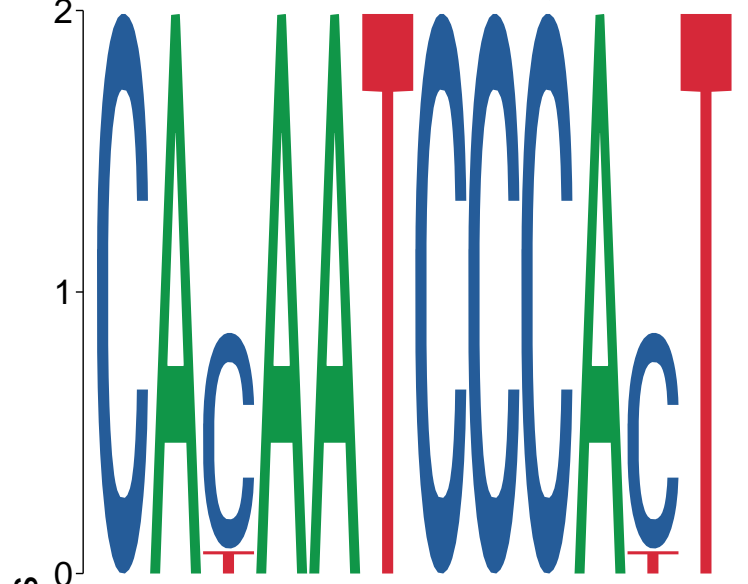
RCH394_20_AGCATTAGCCCT,BestGuess_



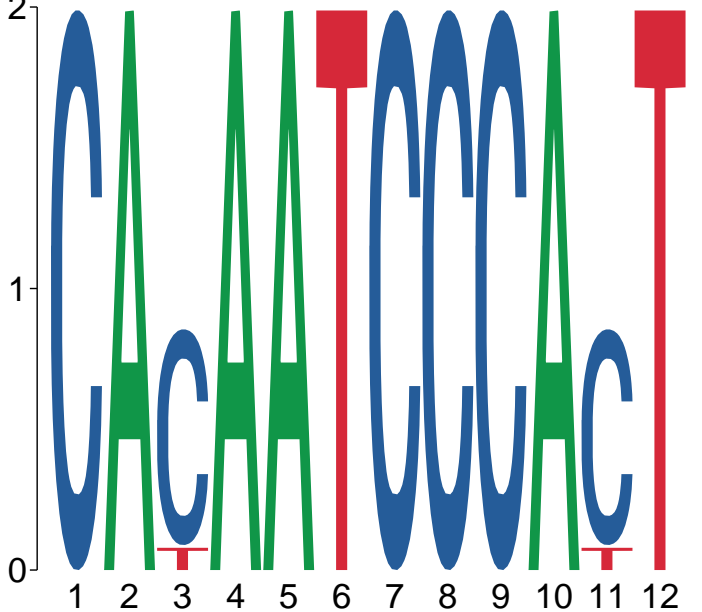
20-AGCATTAGCCCT,BestGuess:ftz



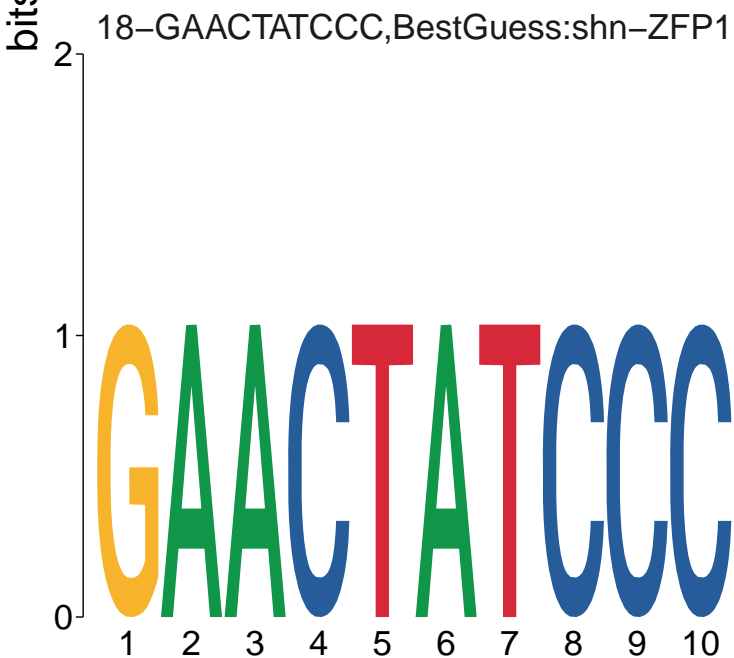
CH395_15_CACAATCCCCT, BestGuess_



CACAATCCCCT, BestGuess:PB0114.1_Eg



RCH396_18_GAACTATCCC,BestGuess_sr



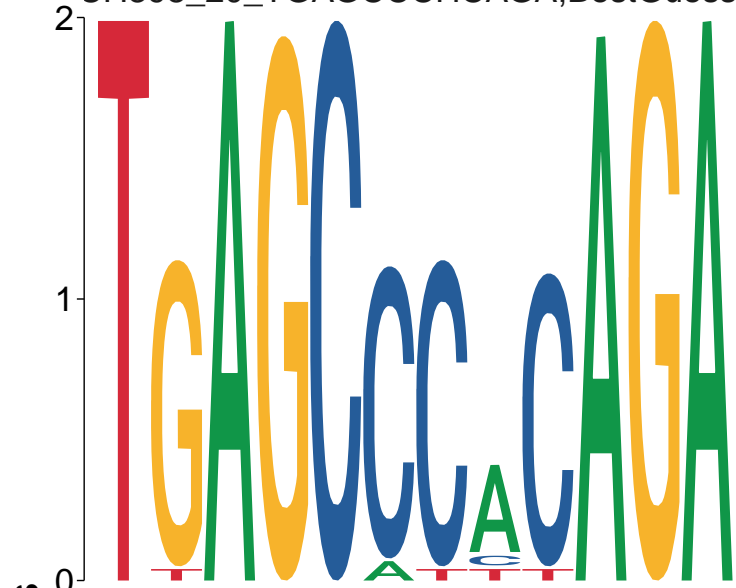
CH397_25_AATCTCGCTG,BestGuess_PB



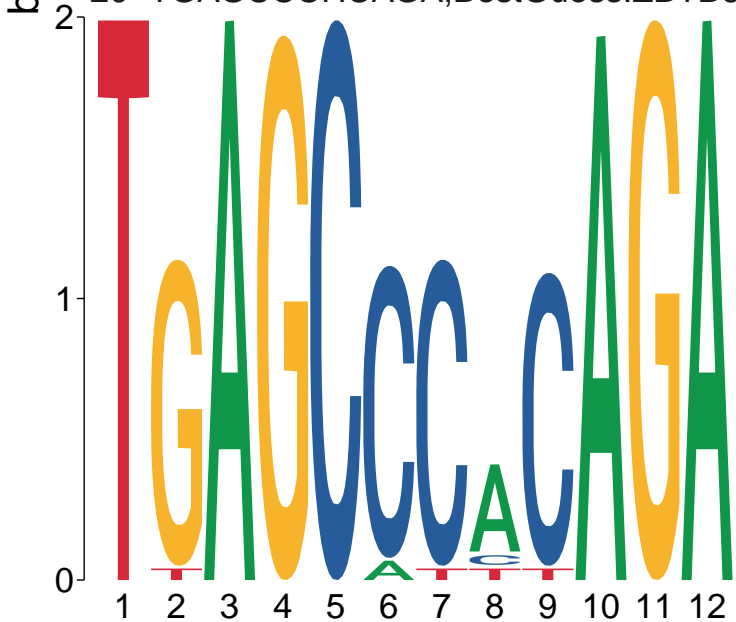
bits -AATCTCGCTG,BestGuess:PB0139.1_Irf5



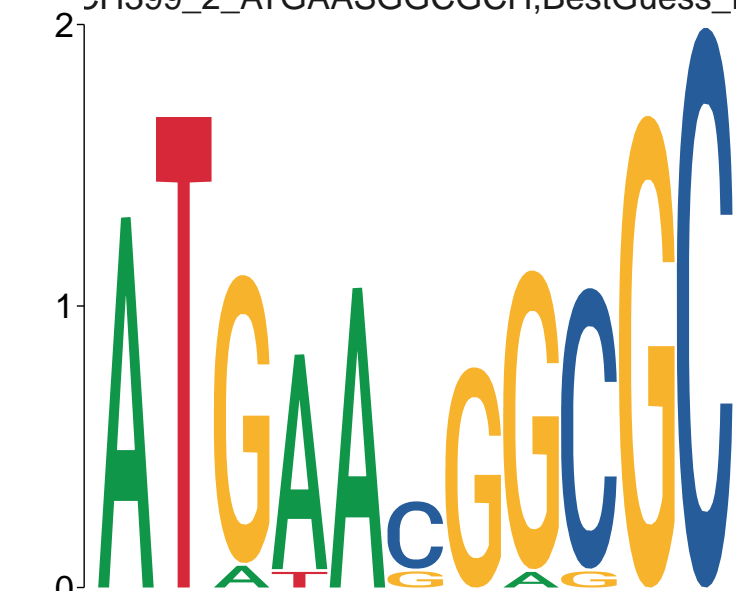
CH398_20_TGAGCCCHCAGA,BestGuess_



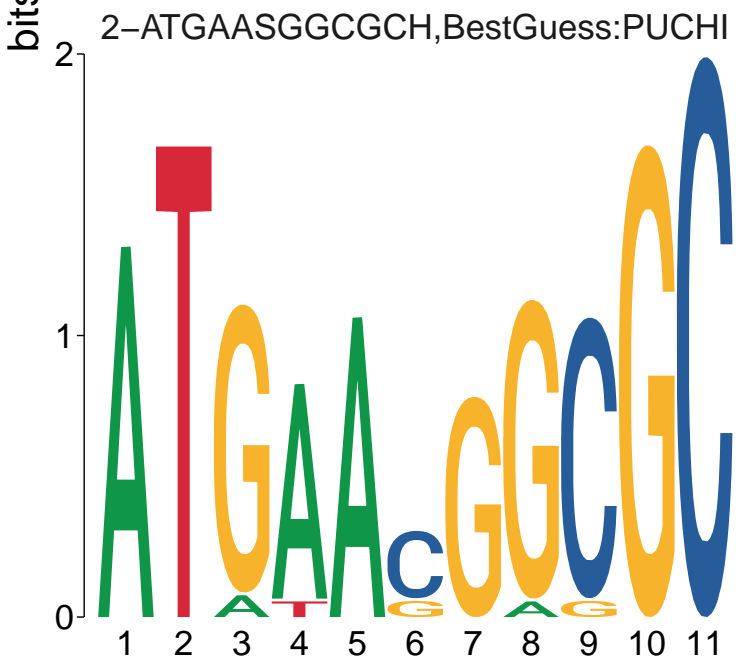
20-TGAGCCCHCAGA,BestGuess:ZBTB6



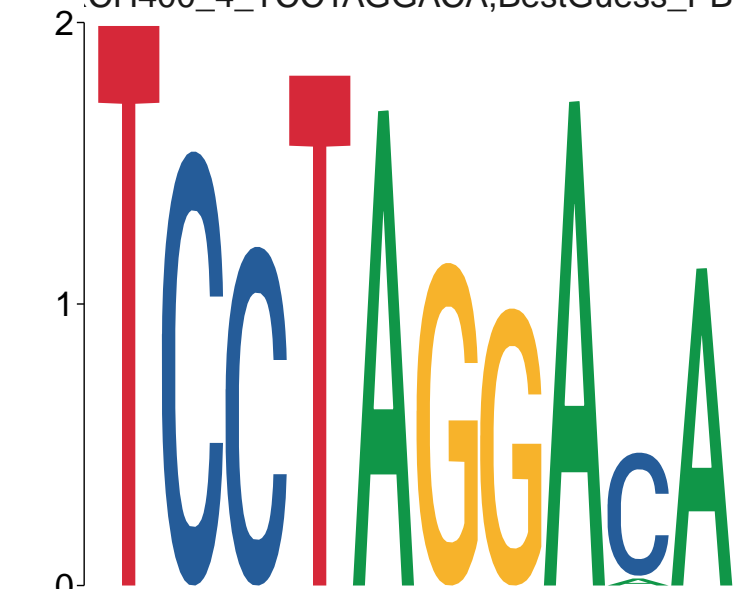
CH399_2_ATGAASGGCGCH,BestGuess_F



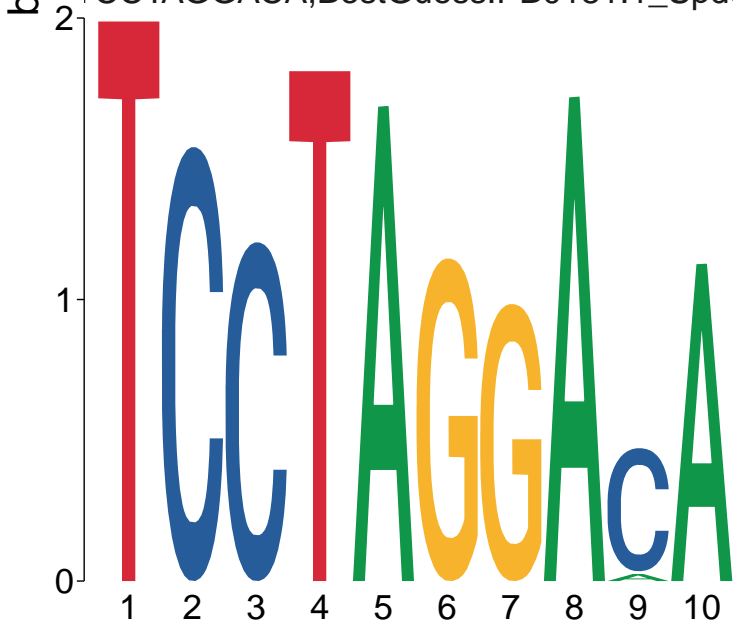
2-ATGAASGGCGCH,BestGuess:PUCHI



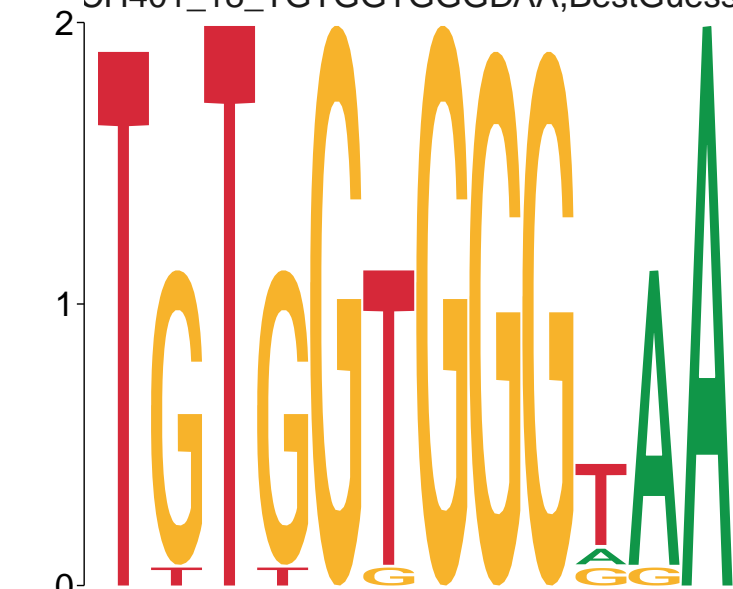
CH400_4_TCCTAGGACA,BestGuess_PBC



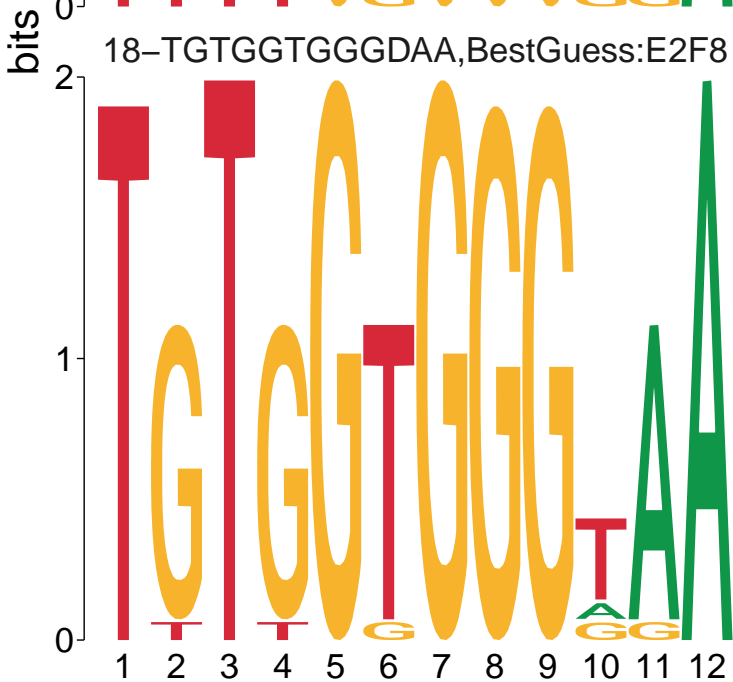
CCTAGGACA,BestGuess:PB0181.1_Spde



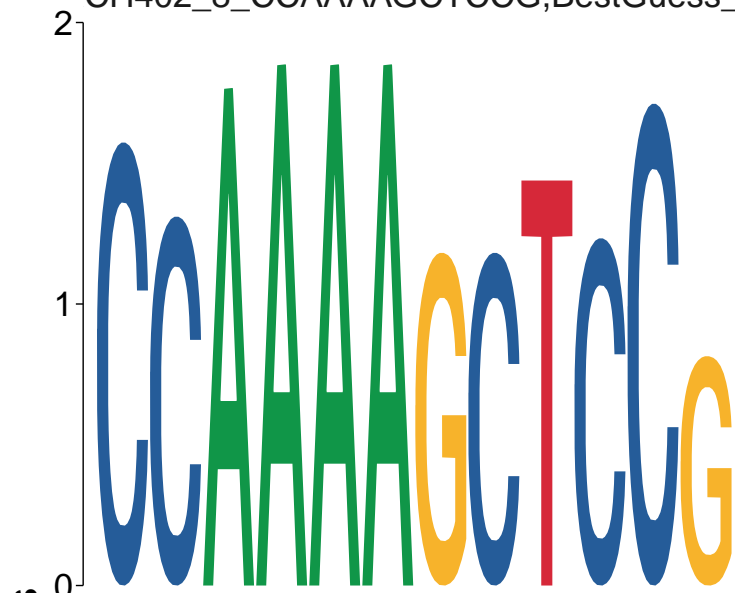
CH401_18_TGTGGTGGGDAA,BestGuess_



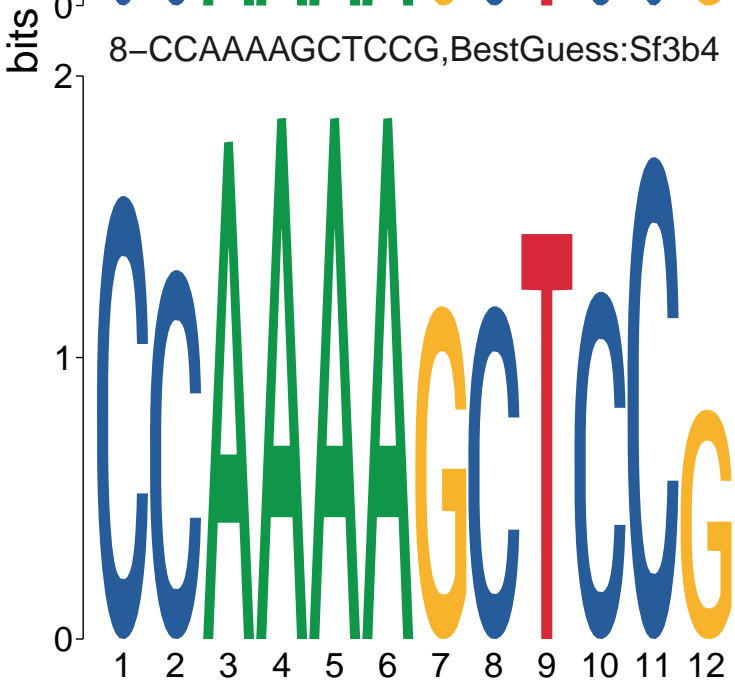
18-TGTGGTGGGDAA,BestGuess:E2F8



CH402_8_CCAAAAGCTCCG,BestGuess_!



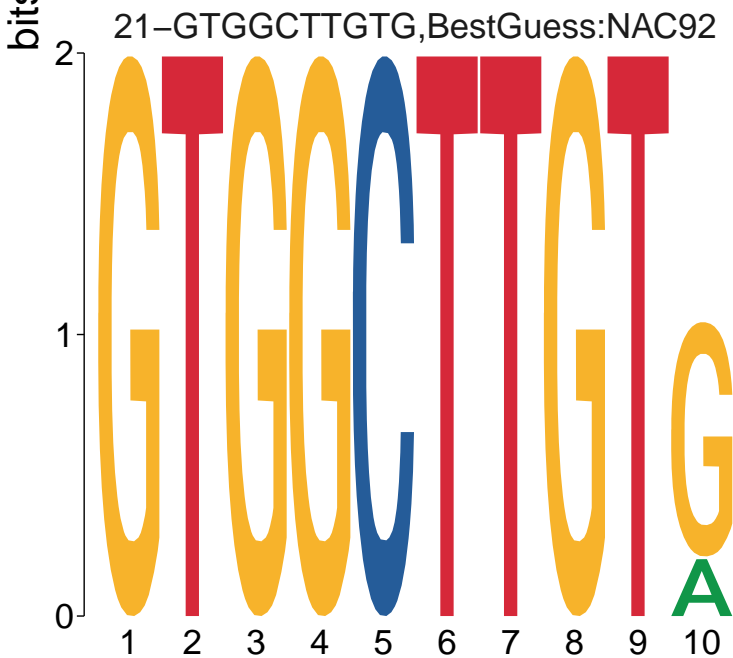
8-CCAAAAGCTCCG,BestGuess:Sf3b4



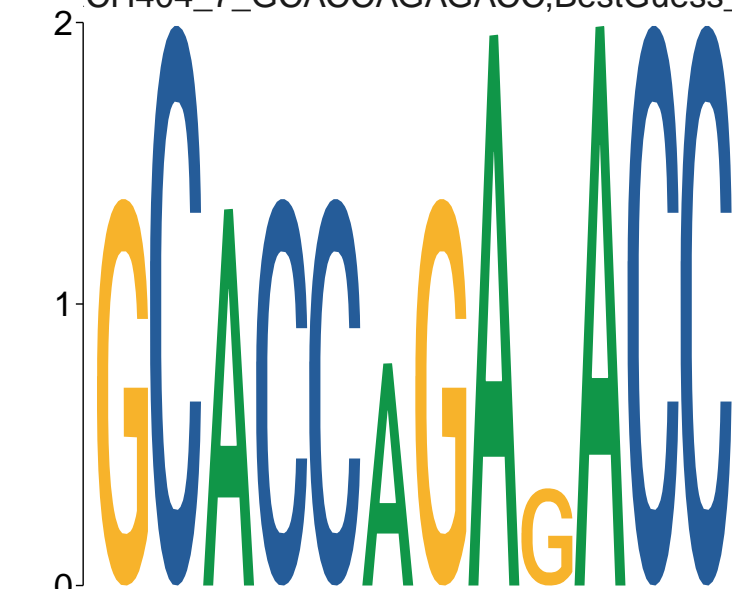
CH403_21_GTGGCTTGTG,BestGuess_NA



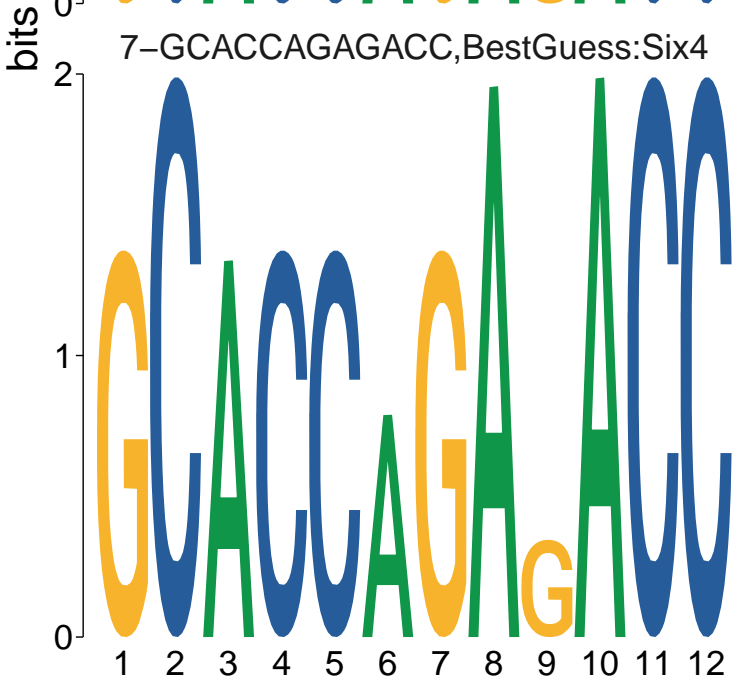
21-GTGGCTTGTG,BestGuess:NAC92



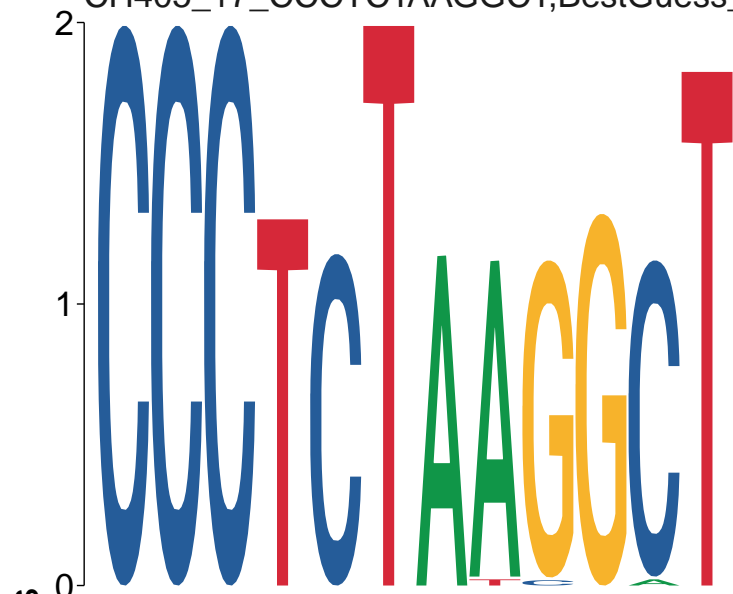
CH404_7_GCACCAGAGACC,BestGuess_



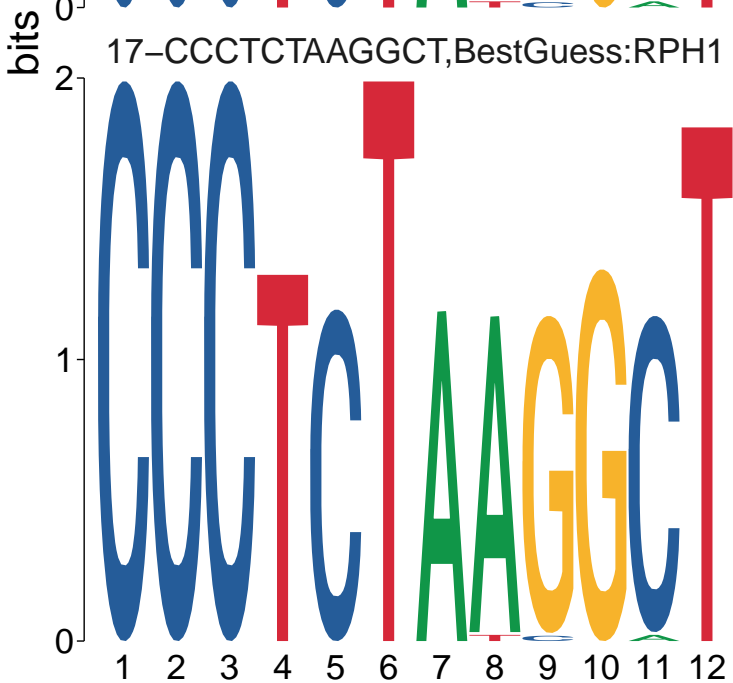
7-GCACCAGAGACC,BestGuess:Six4



CH405_17_CCCTCTAAGGCT,BestGuess_



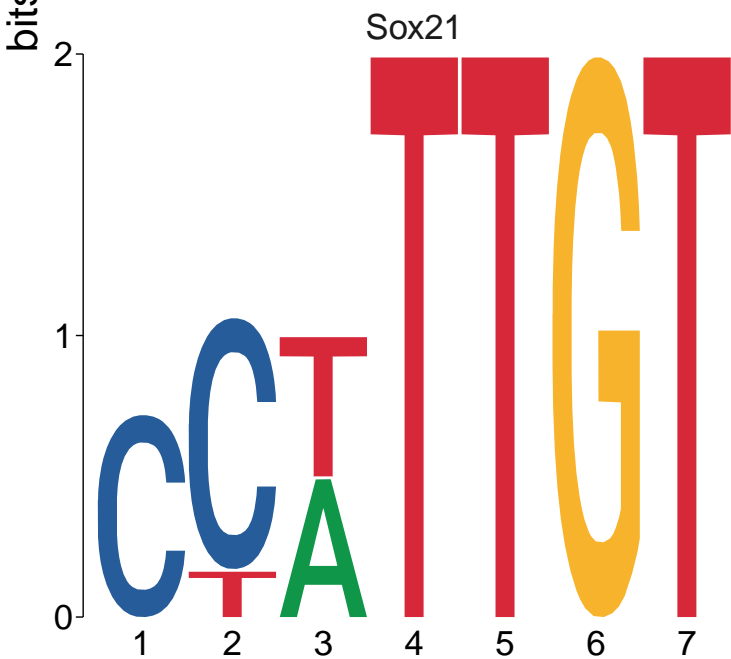
17-CCCTCTAAGGCT,BestGuess:RPH1



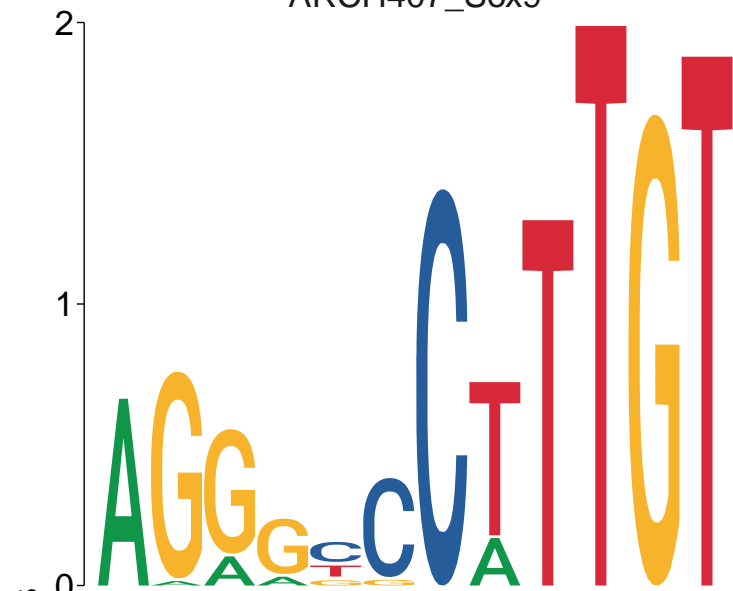
ARCH406_Sox21



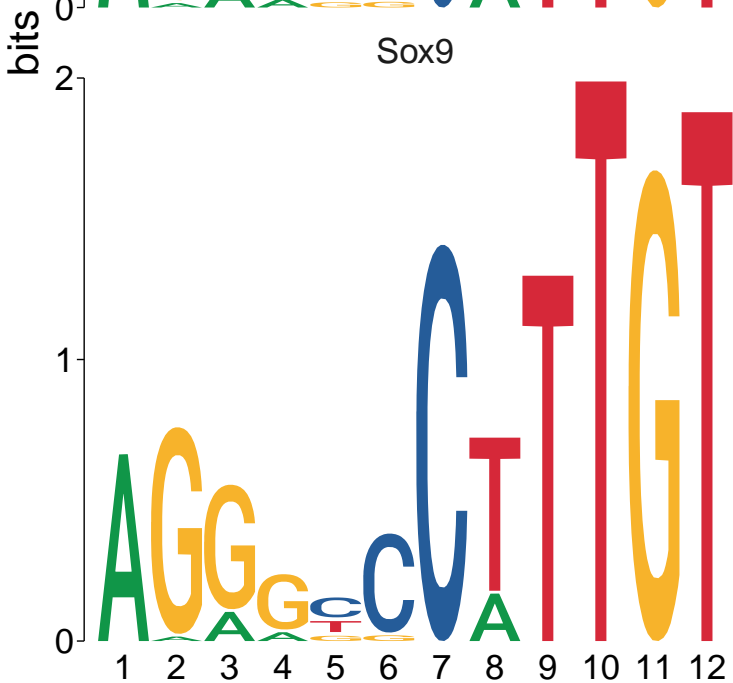
Sox21



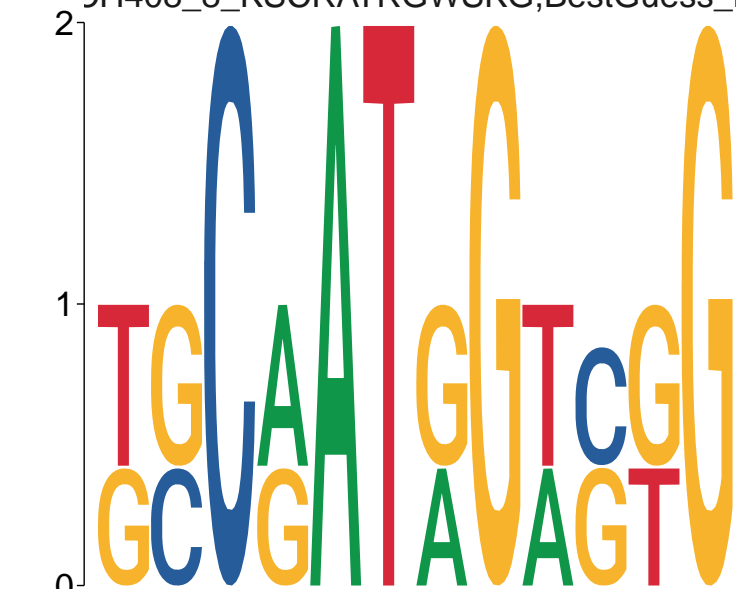
ARCH407_Sox9



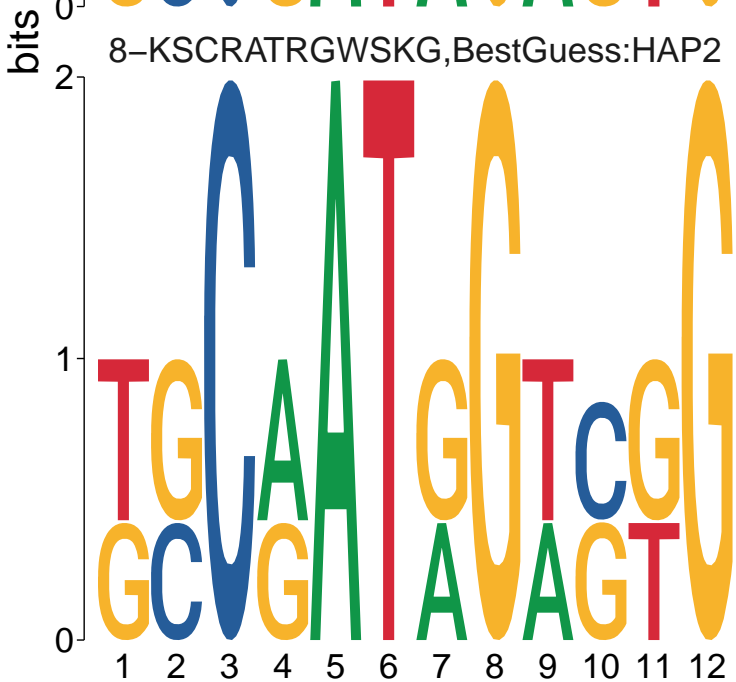
Sox9



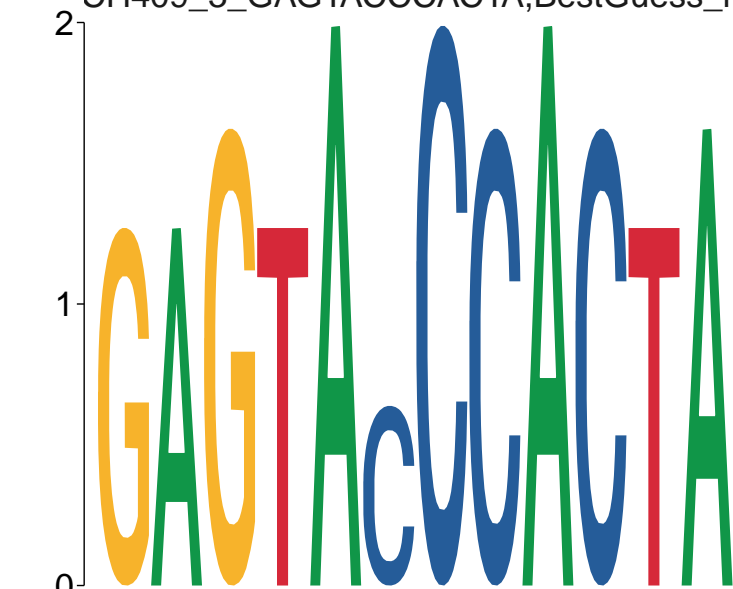
CH408_8_KSCRATRGWSKG,BestGuess_F



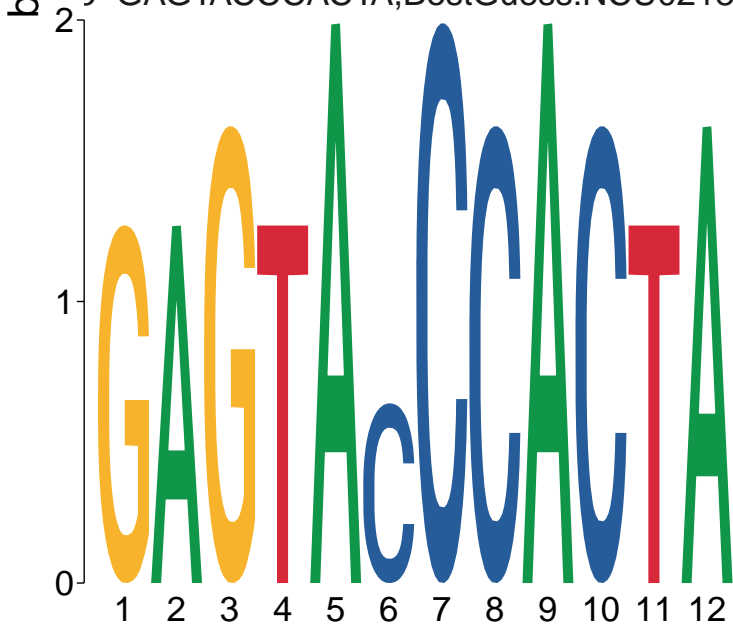
8-KSCRATRGWSKG,BestGuess:HAP2



CH409_3_GAGTACCCACTA,BestGuess_N



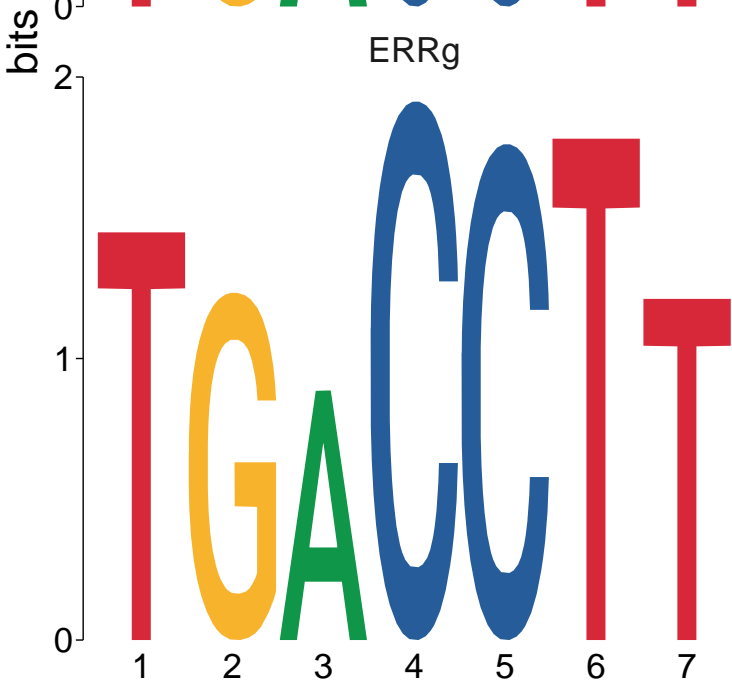
3-GAGTACCCACTA,BestGuess:NCU02182



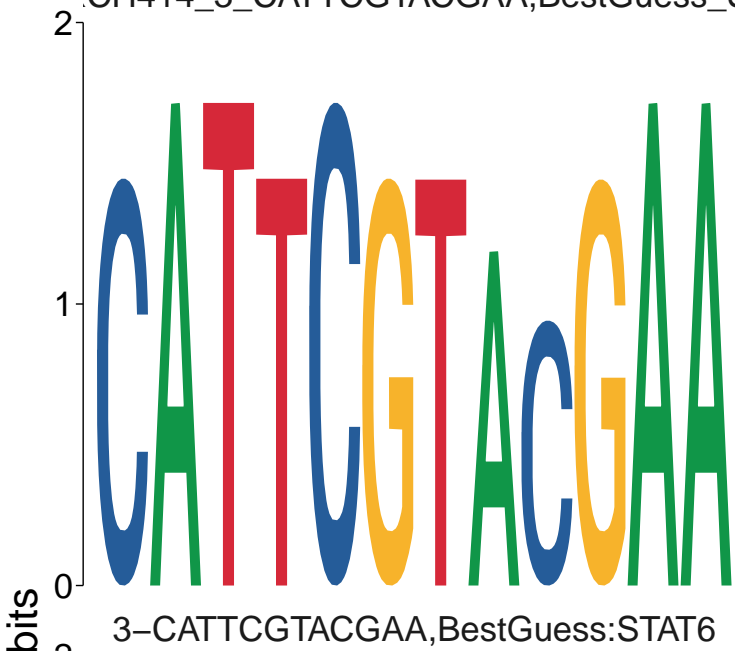
ARCH411_ERRg



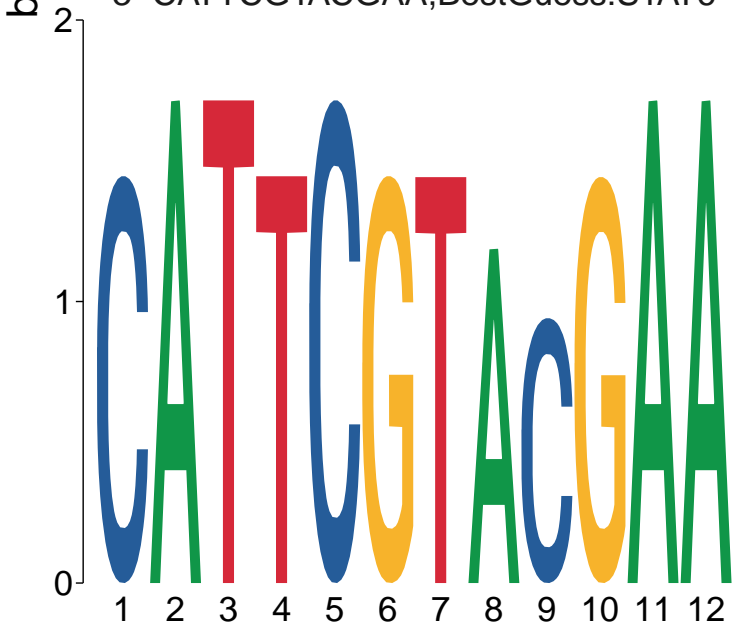
ERRg



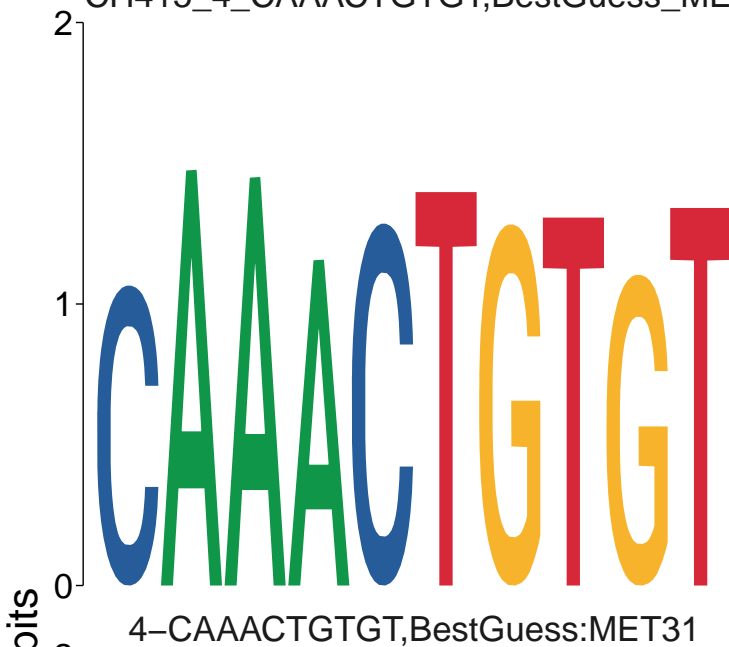
CH414_3_CATTCTGACGAA,BestGuess_S



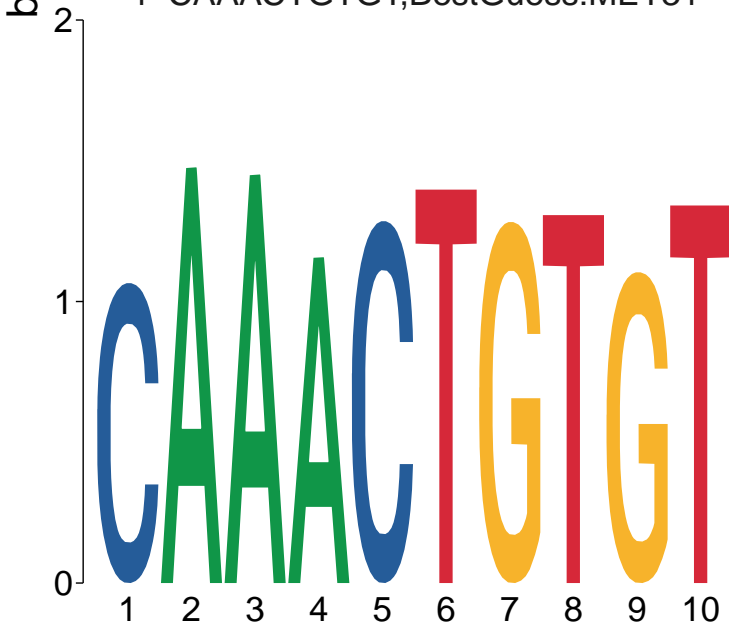
3-CATTCTGACGAA,BestGuess:STAT6



CH415_4_CAAACTGTGT,BestGuess_MET



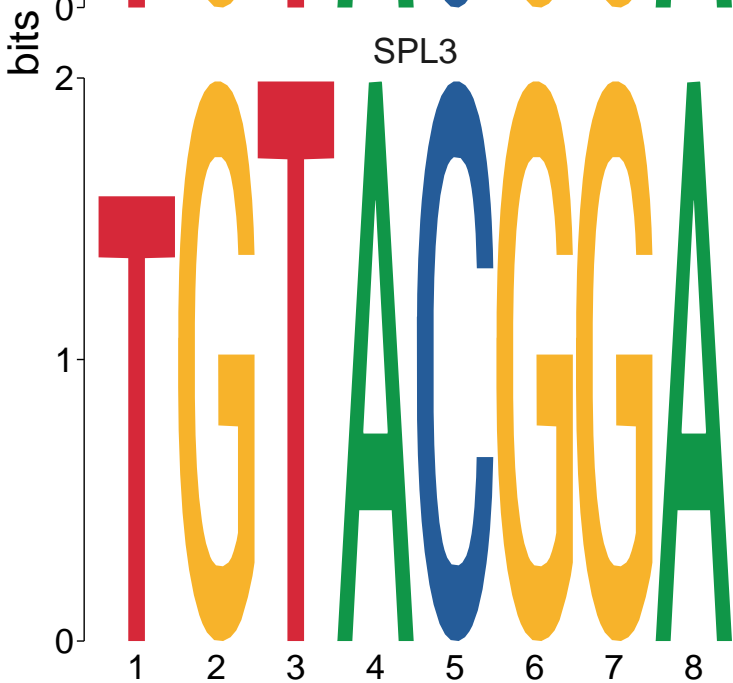
4-CAAACTGTGT,BestGuess:MET31



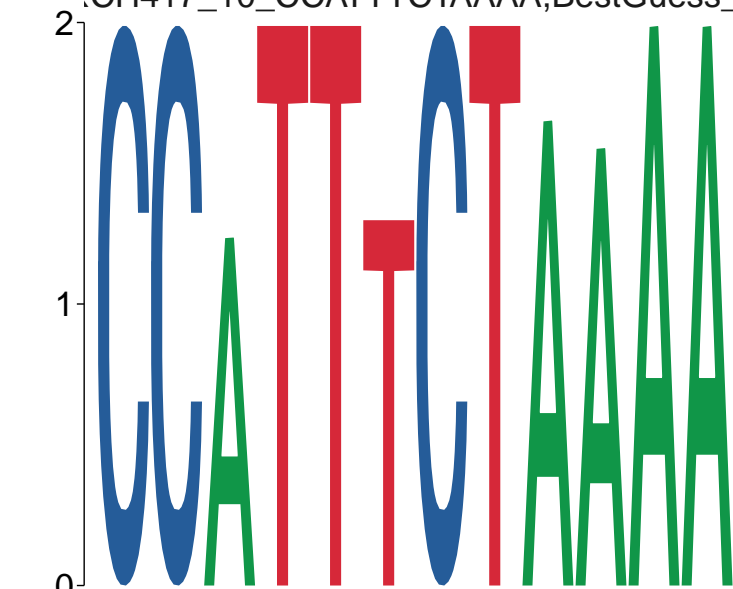
ARCH416_SPL3



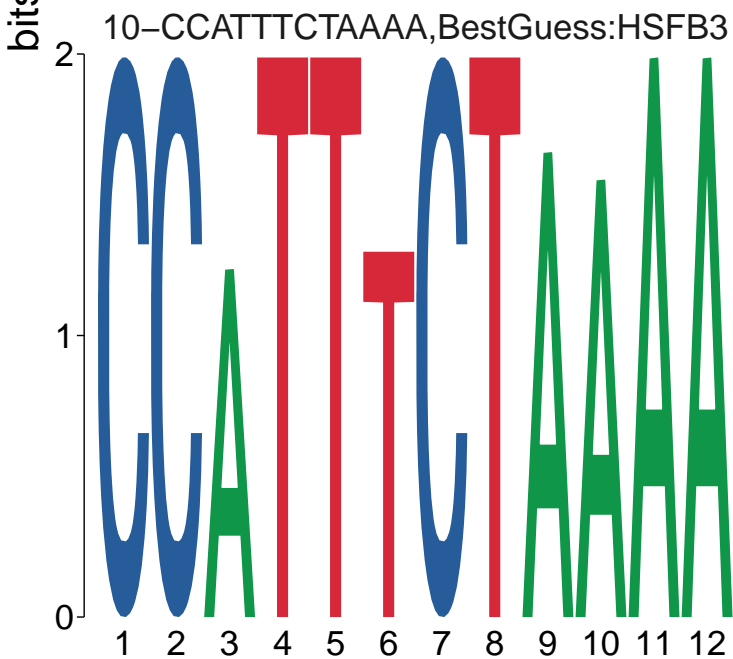
SPL3



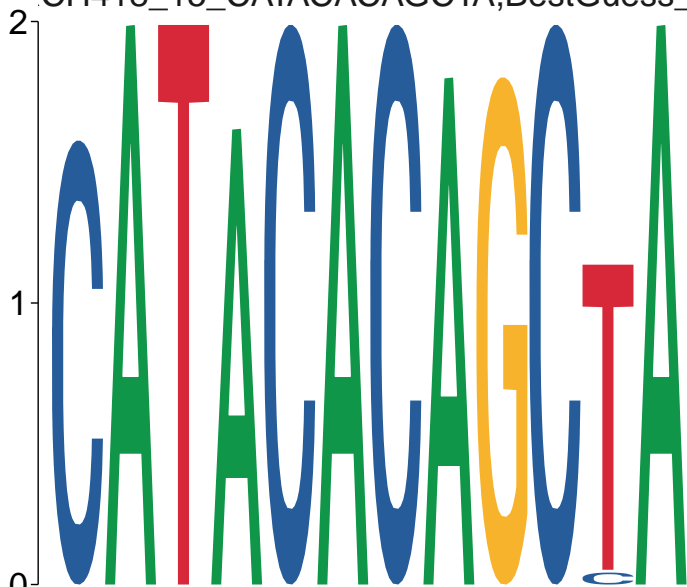
CH417_10_CCATTCTCTAAAA, BestGuess_I



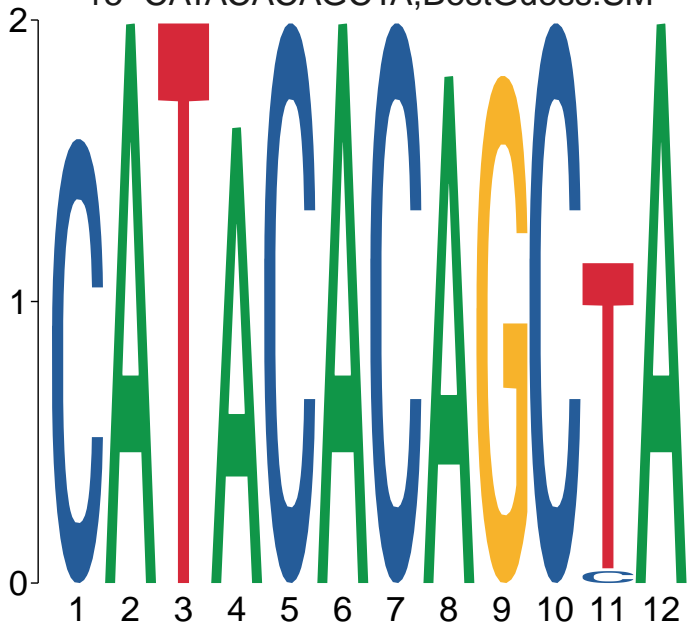
10-CCATTCTCTAAAA, BestGuess:HSFB3



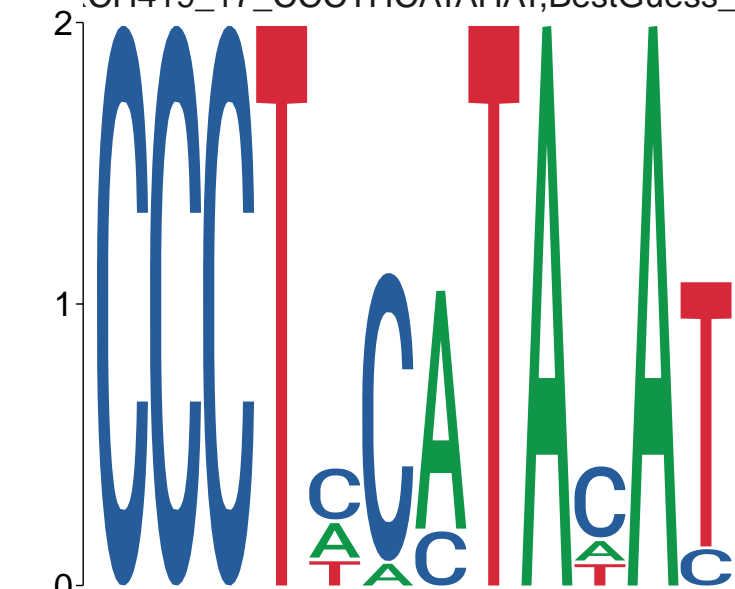
CH418_15_CATACACAGCTA,BestGuess_5



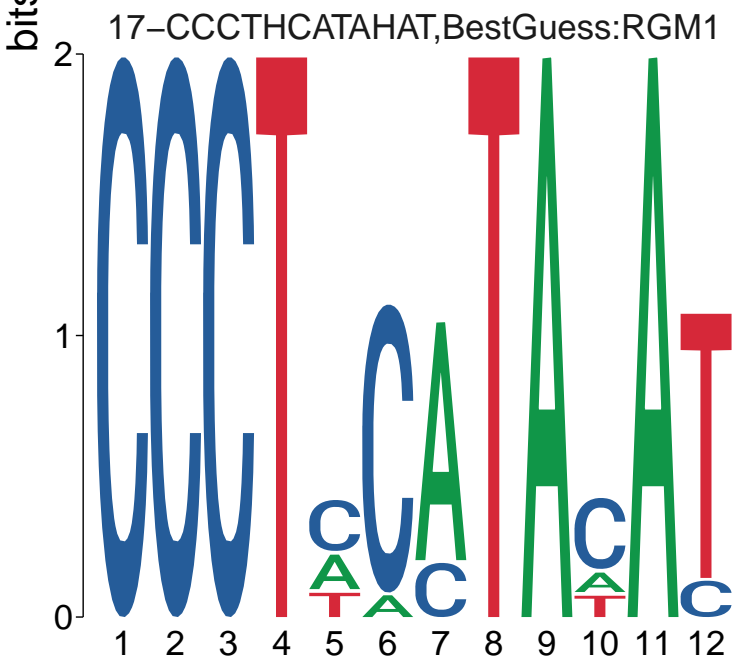
15-CATACACAGCTA,BestGuess:SM



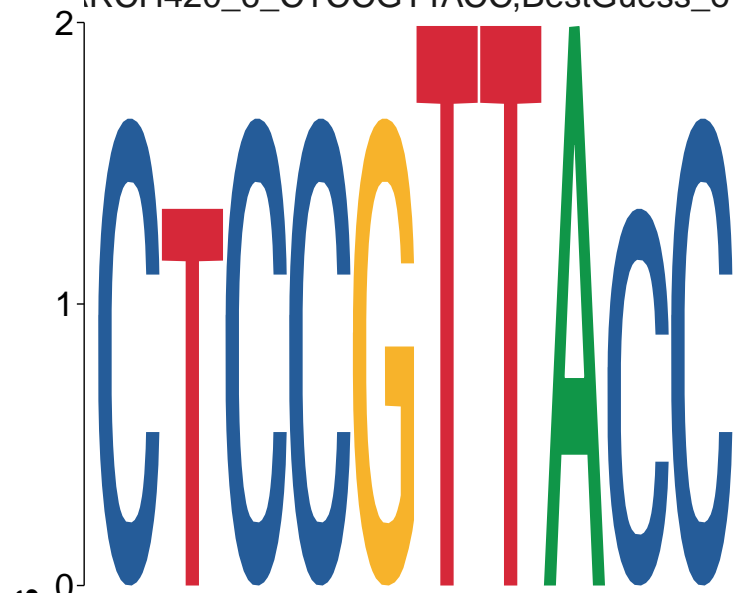
CH419_17_CCCTHCATAHAT,BestGuess_f



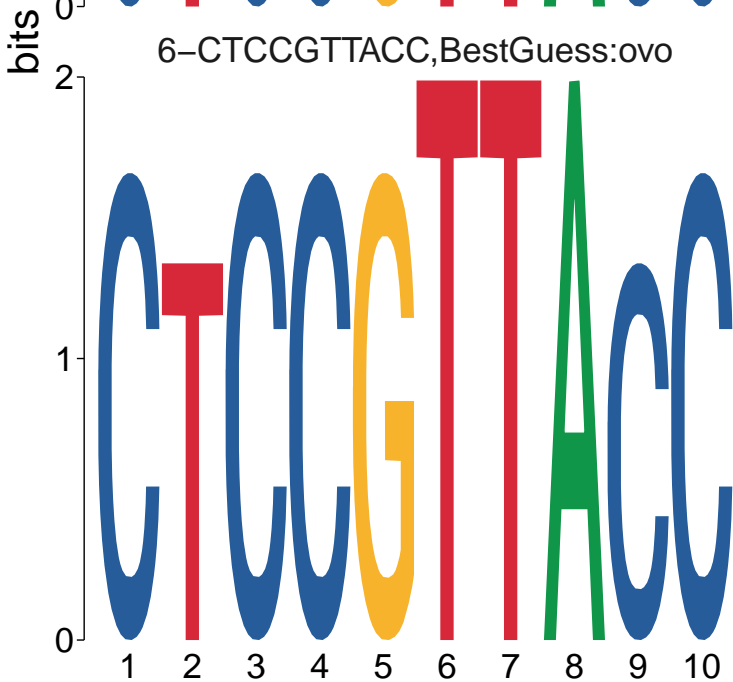
17-CCCTHCATAHAT,BestGuess:RGM1



RCH420_6_CTCCGTTACC,BestGuess_ov



6-CTCCGTTACC,BestGuess:ovo



ARCH421_Rfx1_Rfx2_X_box_RFX_Rfx1



Rfx1 [RC]



RFX



X-box



Rfx2

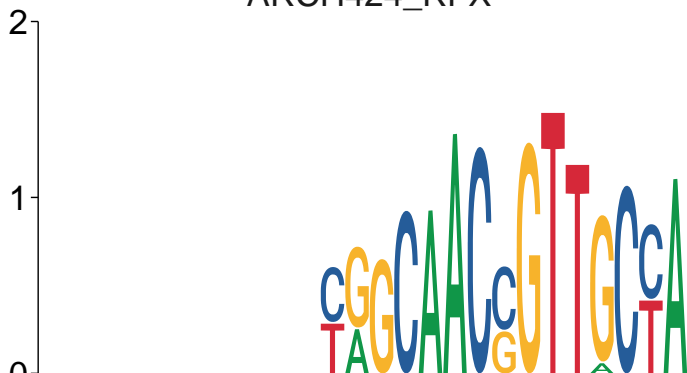


Rfx1.1 [RC]

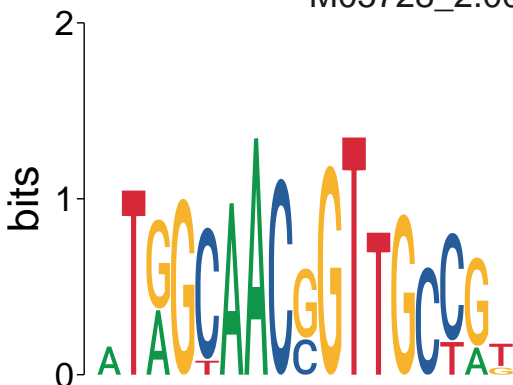


1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24

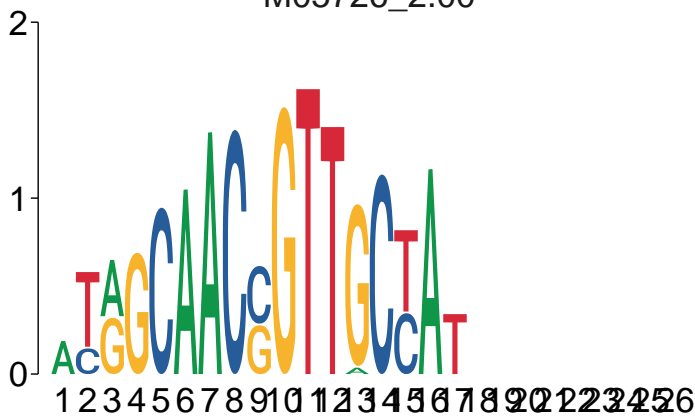
ARCH424_RFX



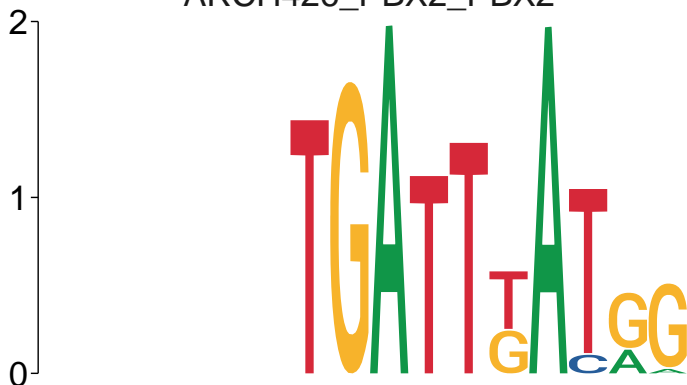
M05728_2.00



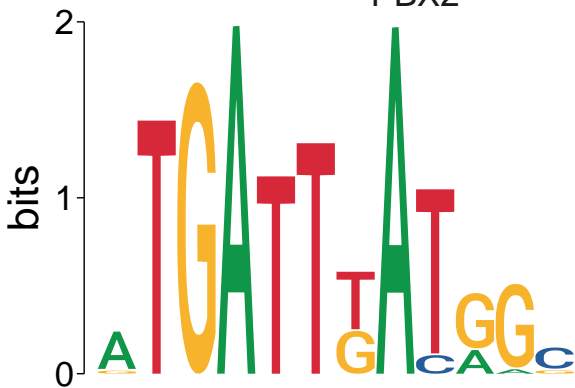
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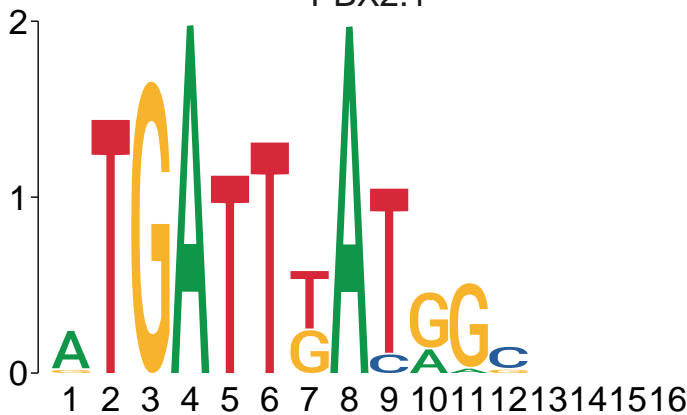
ARCH426_PBX2_PBX2



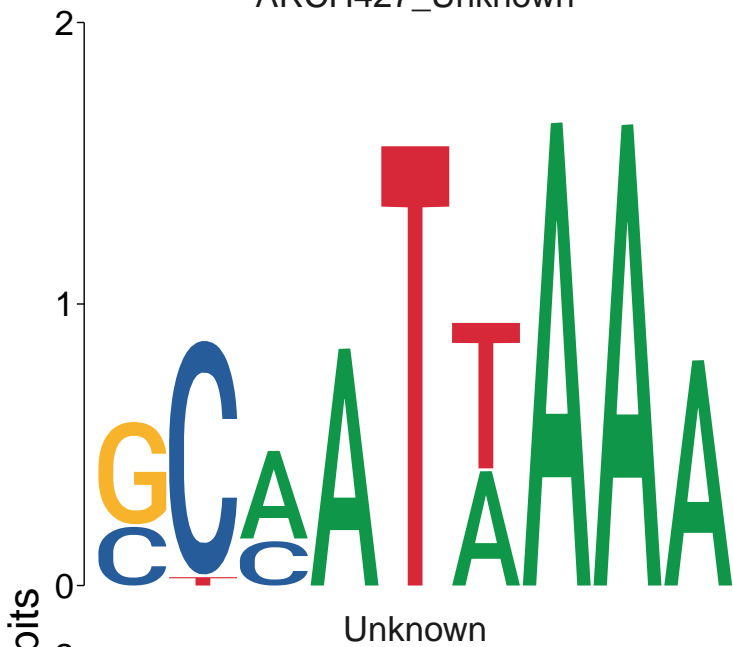
PBX2



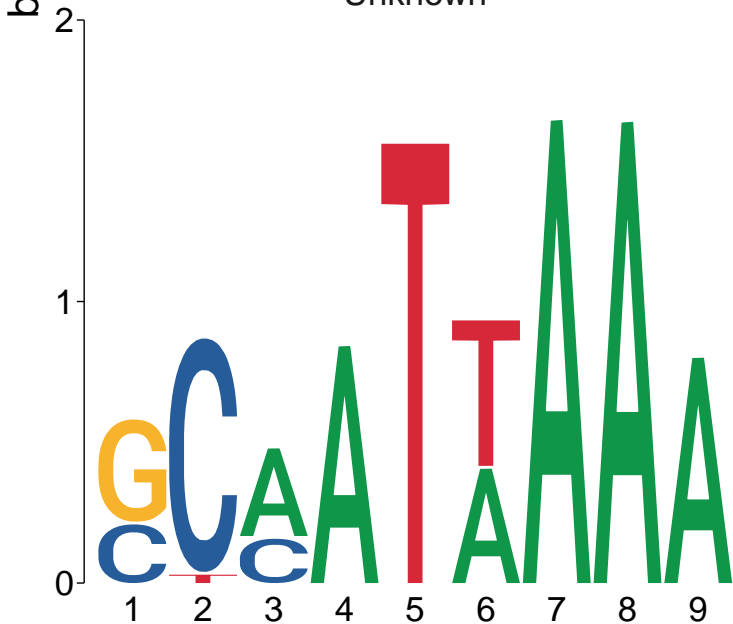
PBX2.1



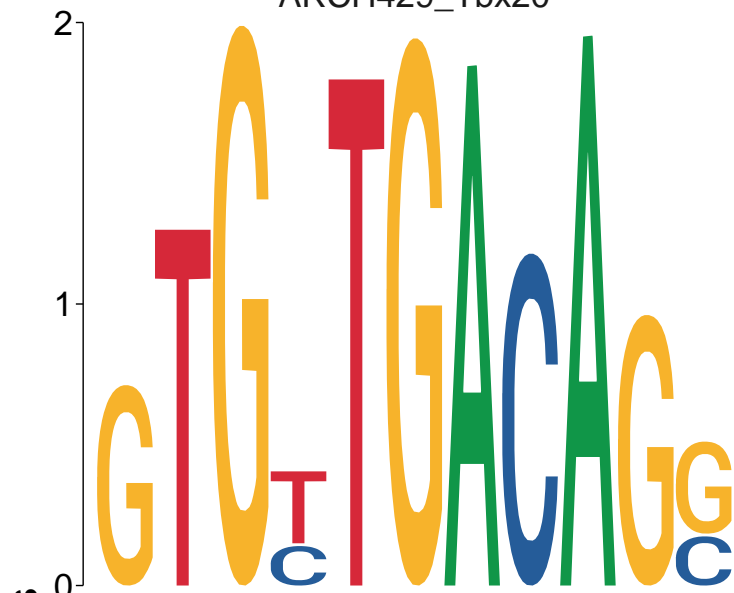
ARCH427_Unknown



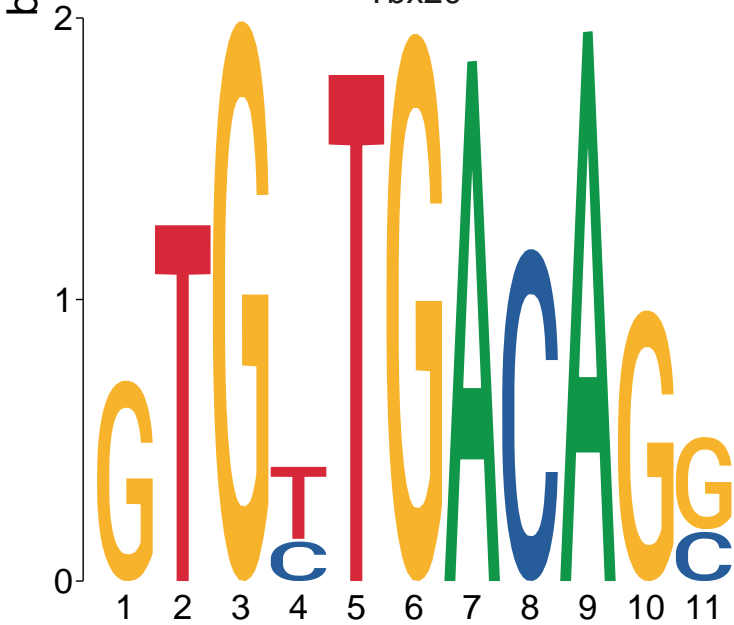
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ARCH429_Tbx20



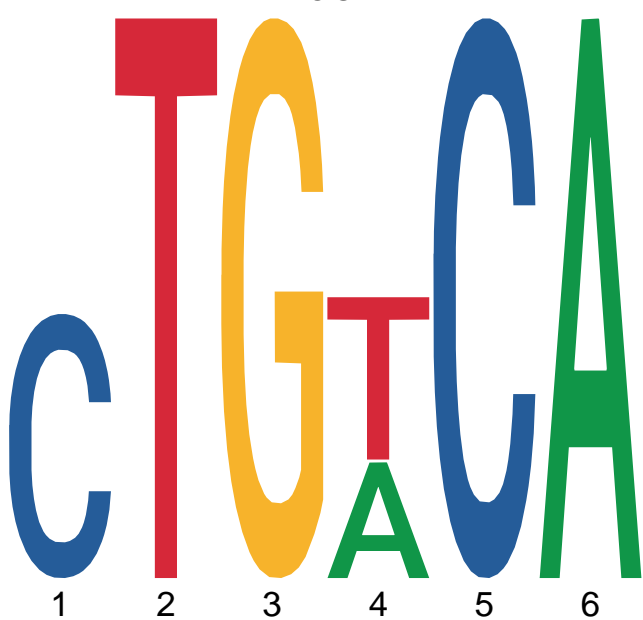
Tbx20



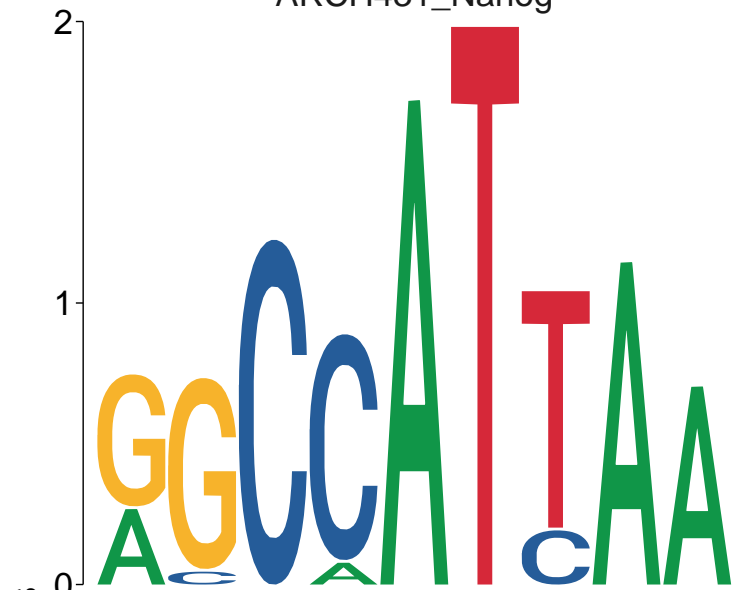
ARCH430_Meis1



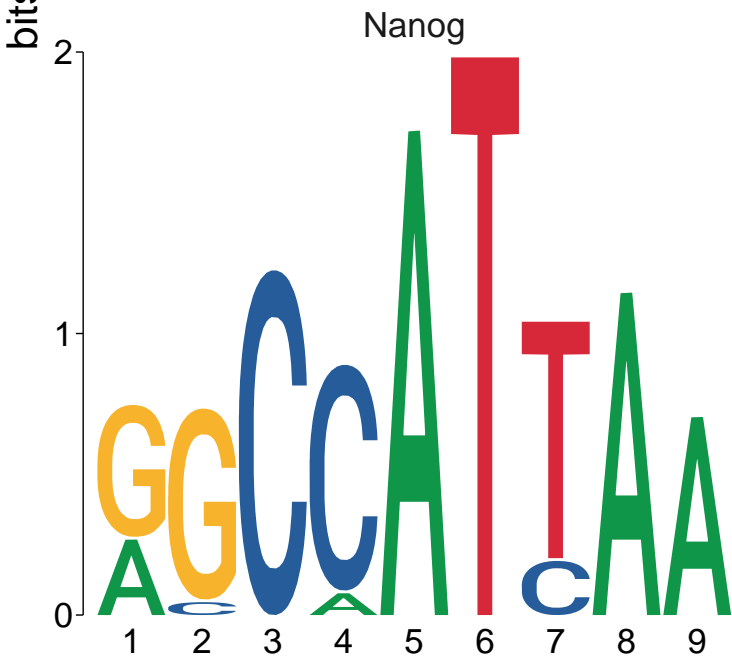
Meis1



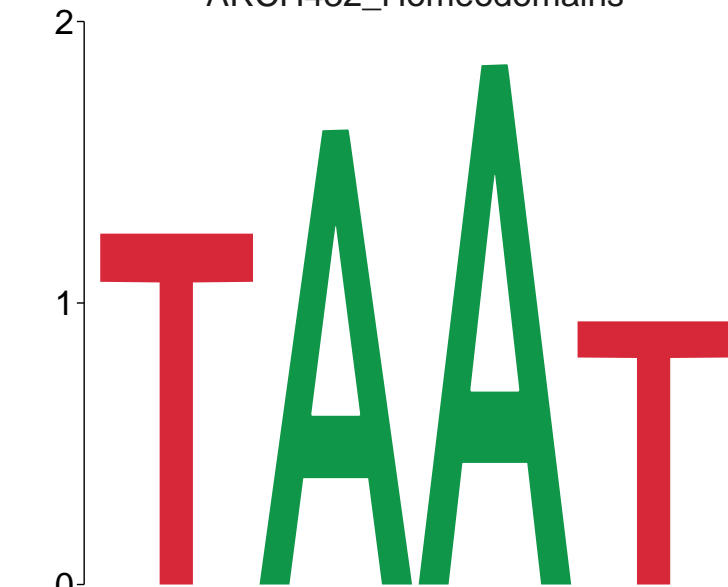
ARCH431_Nanog



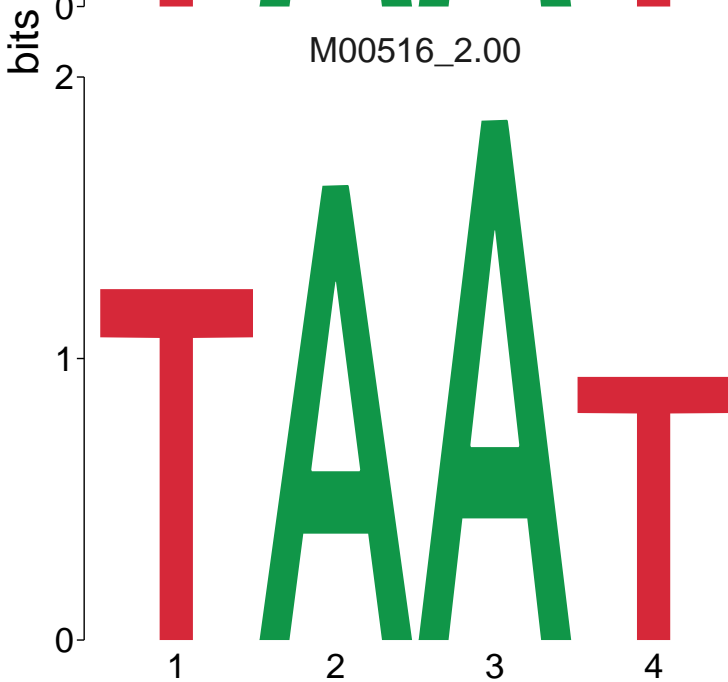
Nanog



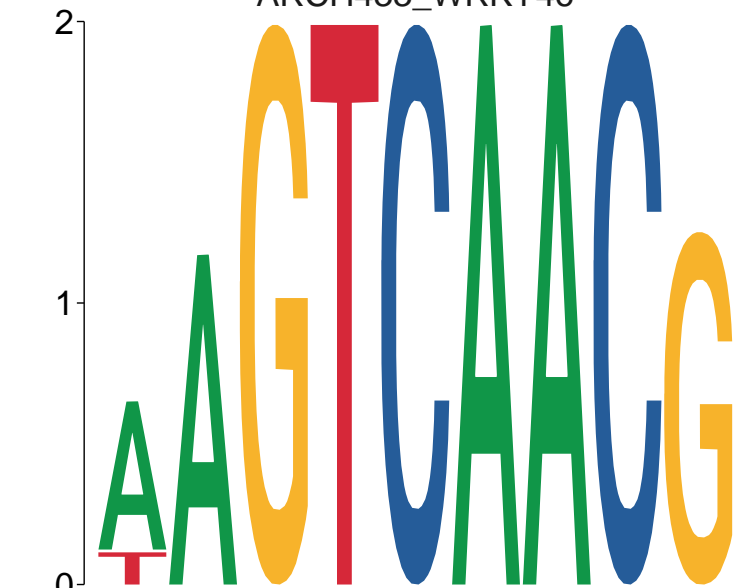
ARCH432_Homeodomains



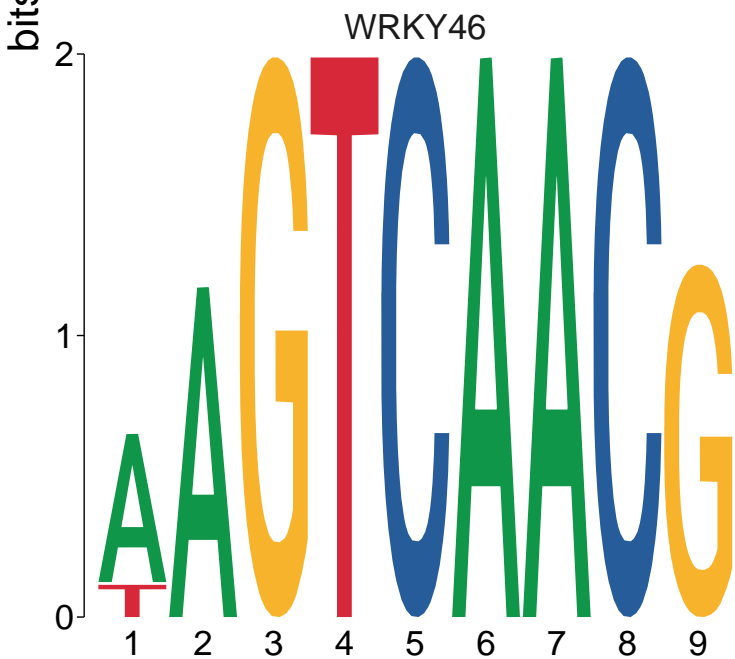
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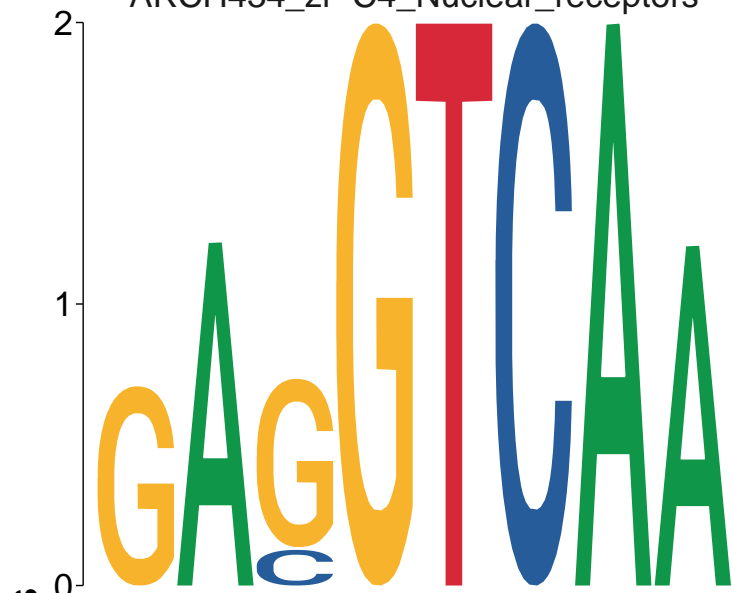
ARCH433_WRKY46



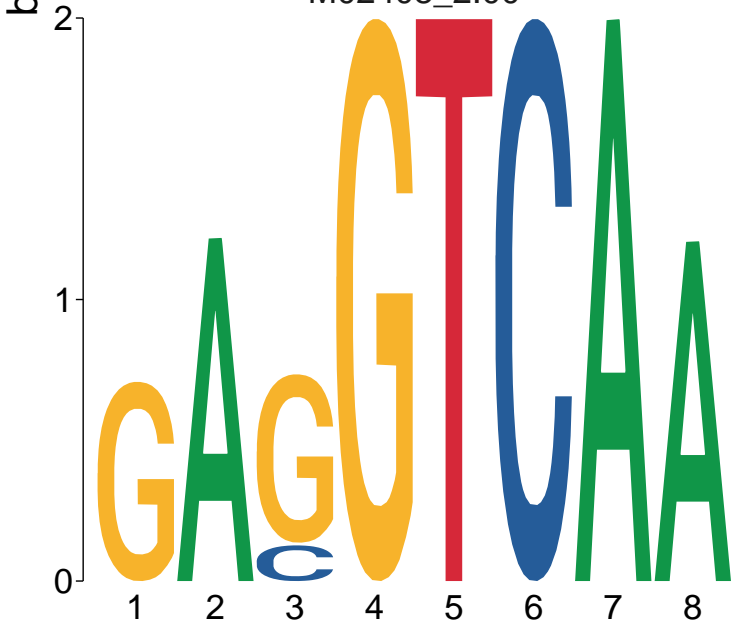
WRKY46



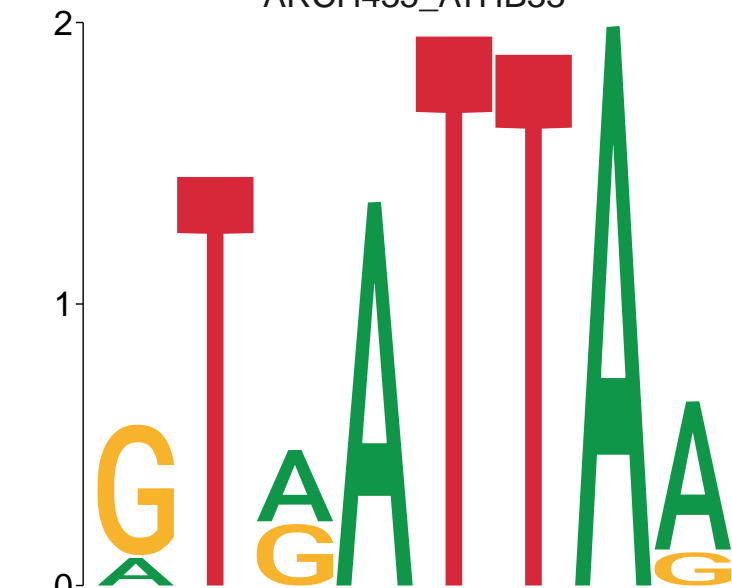
ARCH434_zf-C4_Nuclear_receptors



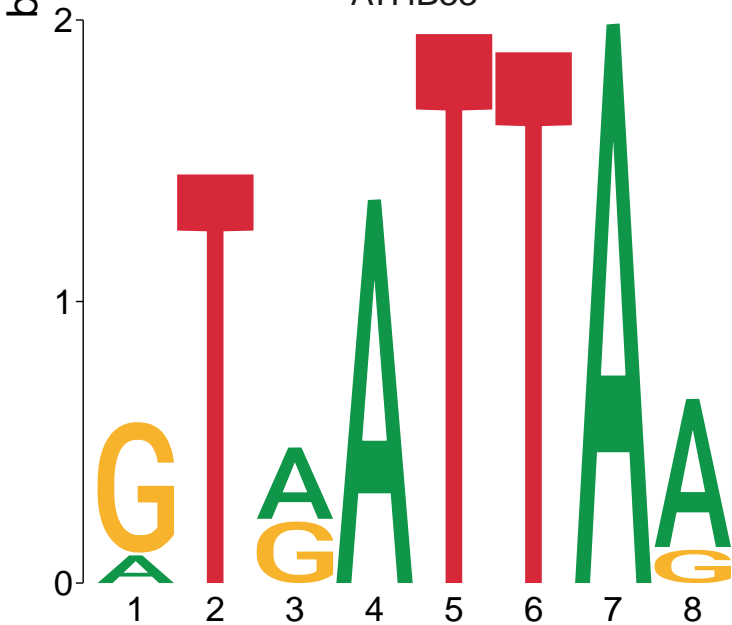
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ARCH435_ATHB33



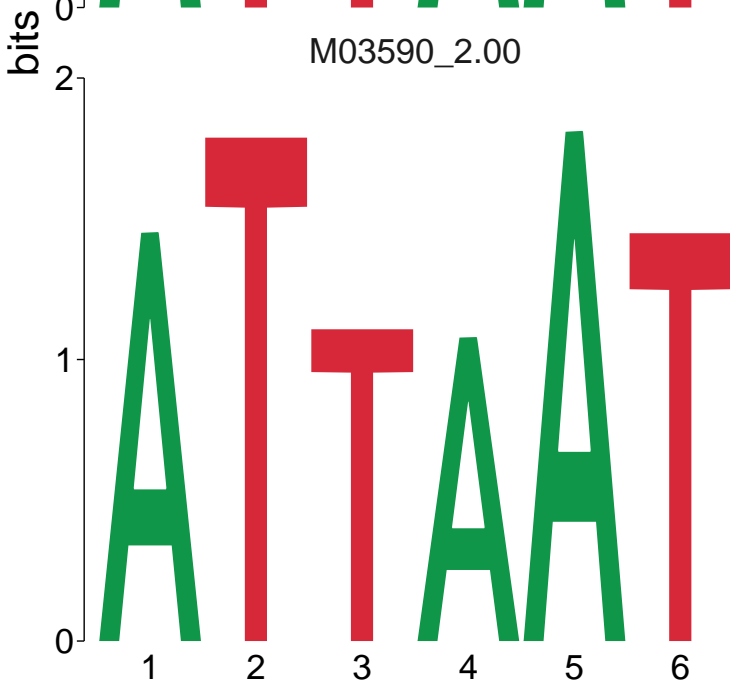
ATHB33



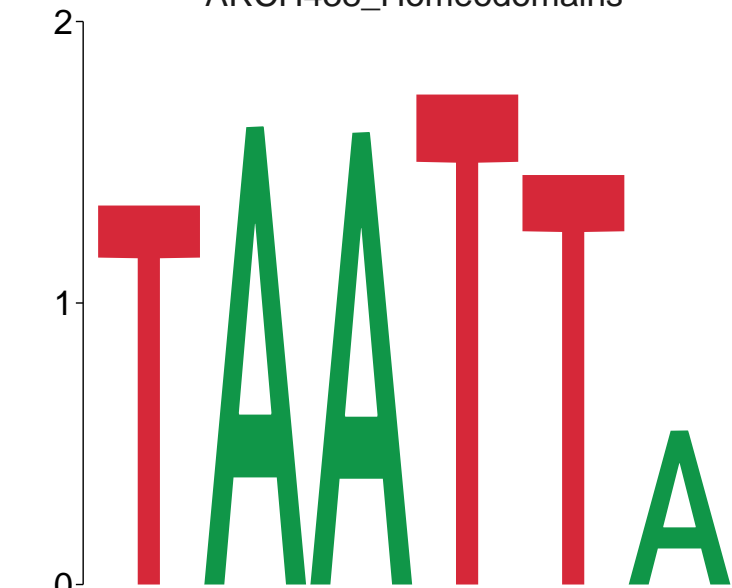
ARCH436_ARID_BRIGHT



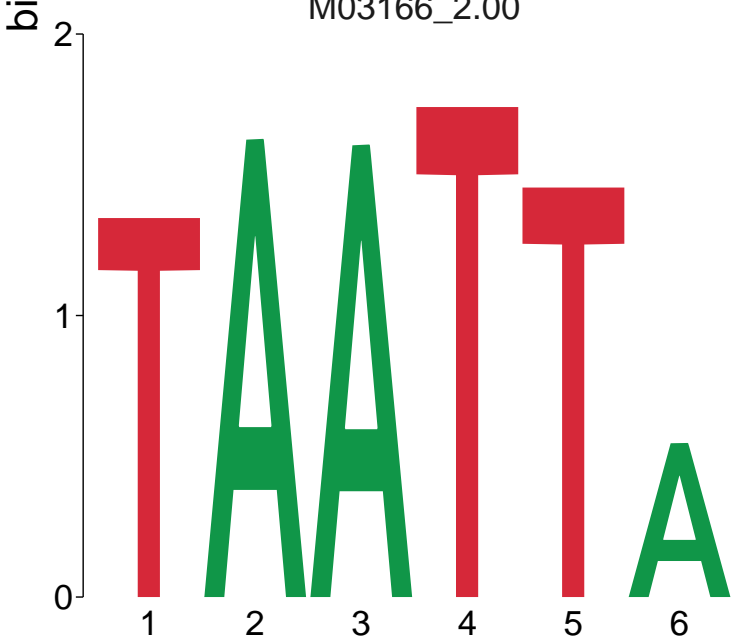
M03590_2.00



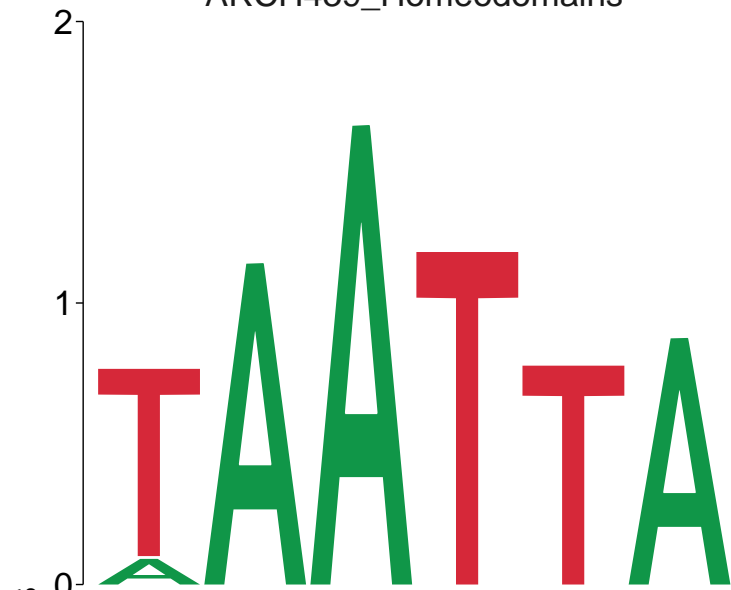
ARCH438_Homeodomains



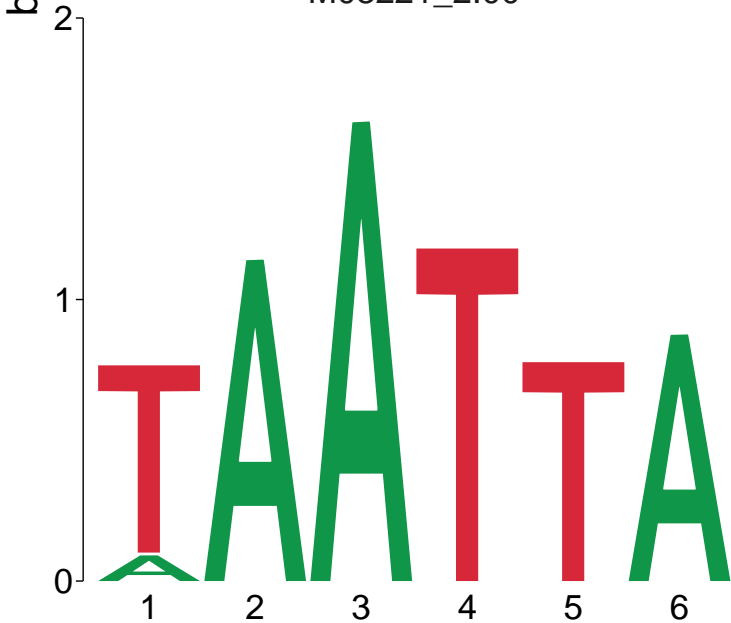
M03166_2.00



ARCH439_Homeodomains



M03221_2.00



ARCH446_ERF4_RRTF1_RAP212_ABR1_F



RAP26



ABR1



RAP212



RRTF1

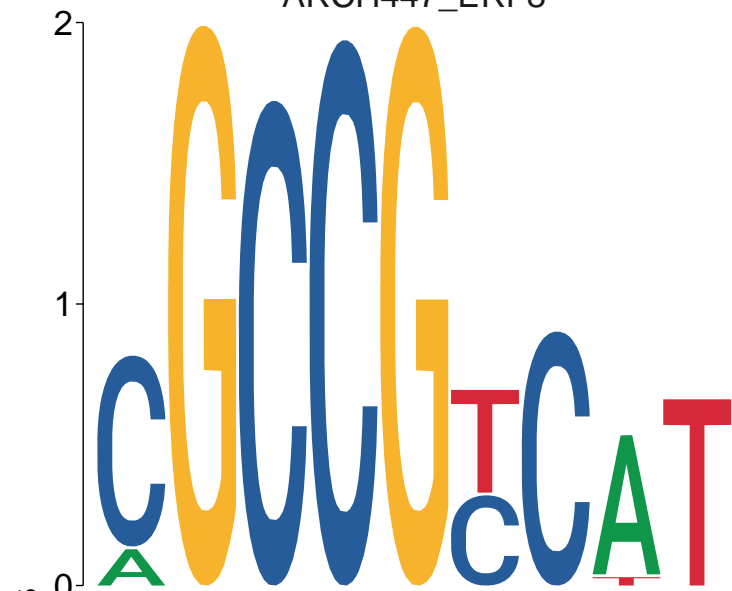


ERF4

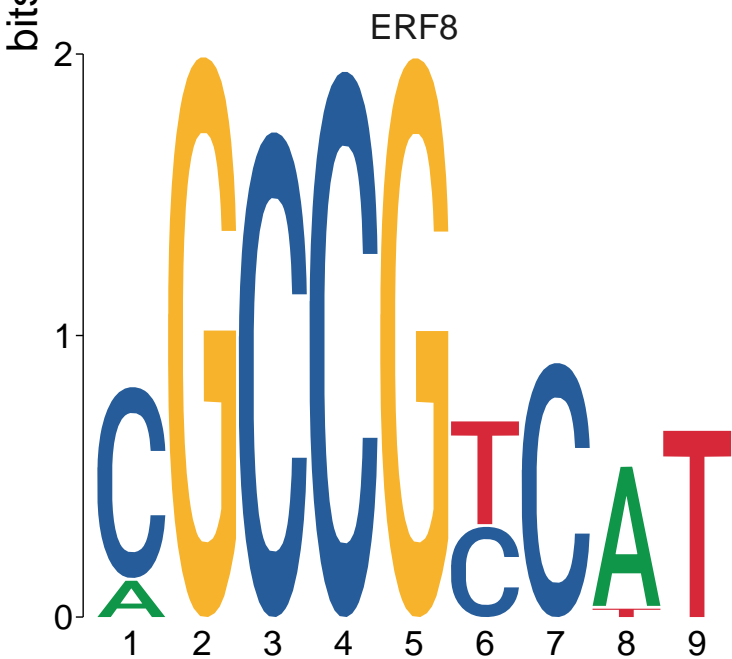


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ARCH447_ERF8



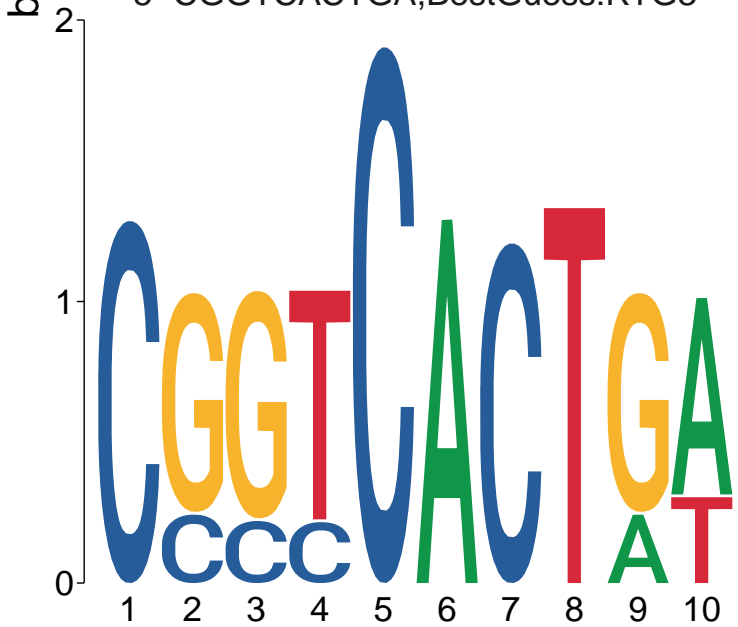
ERF8



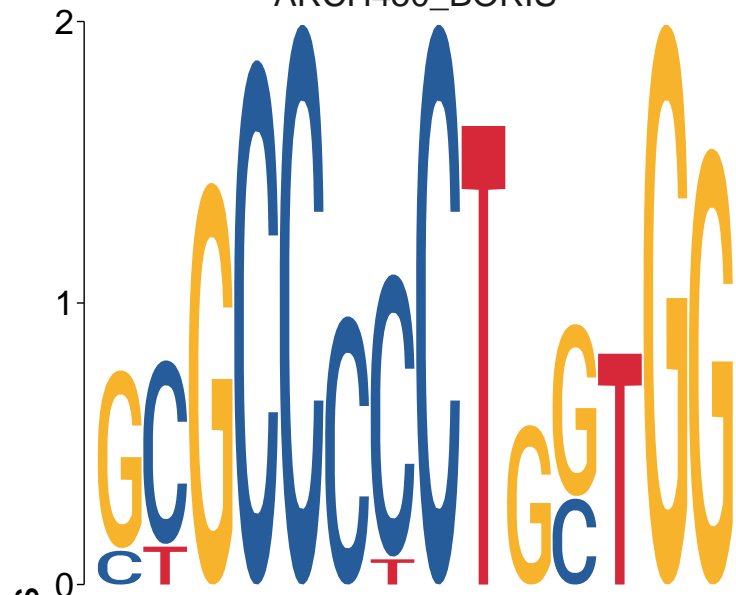
CH448_5_CGGTCACTGA,BestGuess_RT0



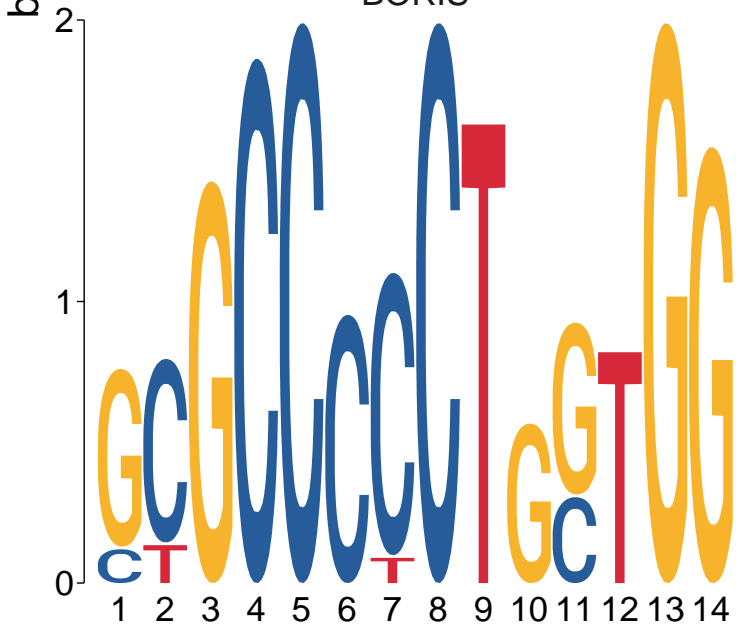
5-CGGTCACTGA,BestGuess:RTG3



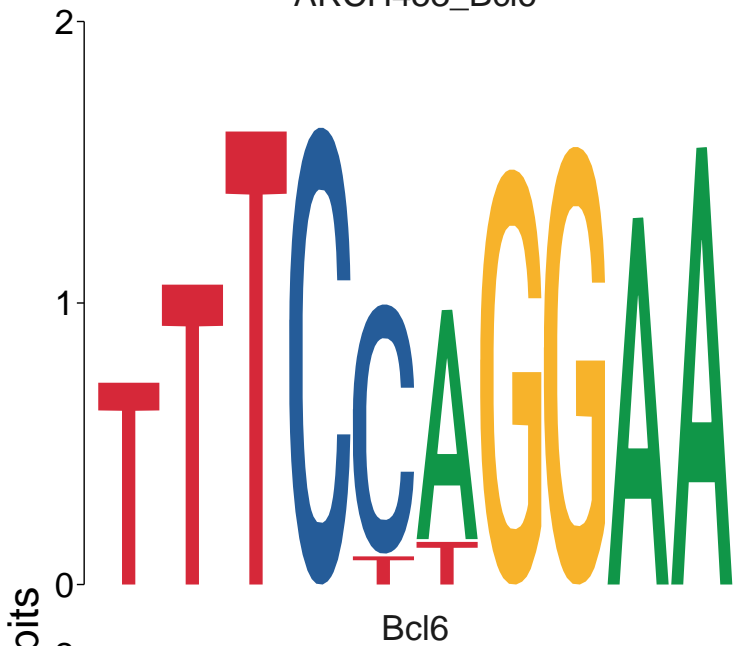
ARCH450_BORIS



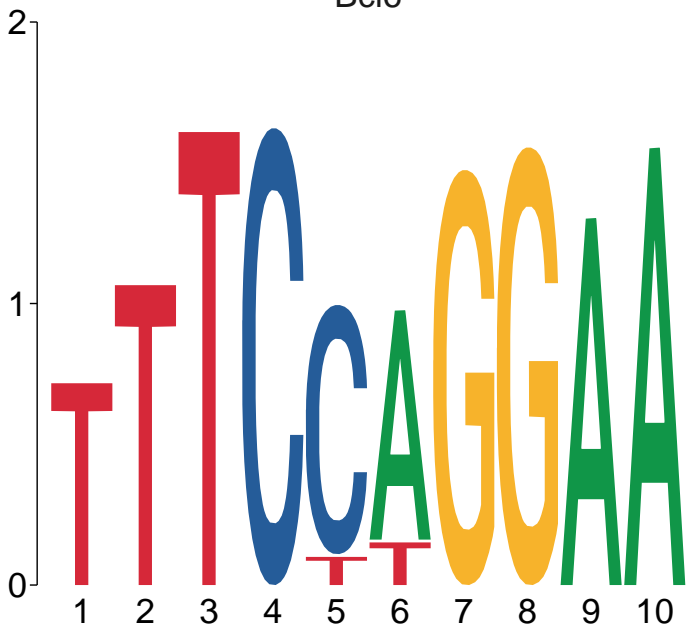
BORIS



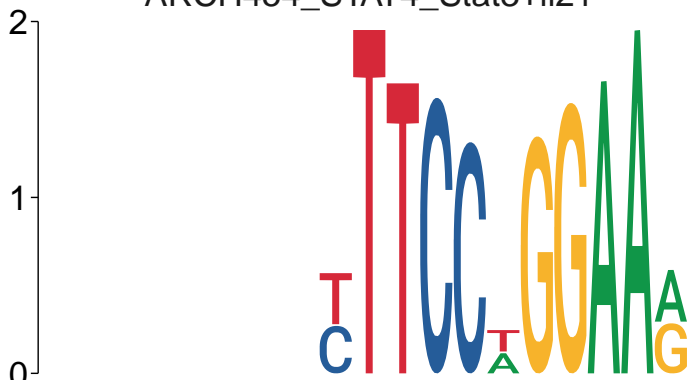
ARCH453_Bcl6



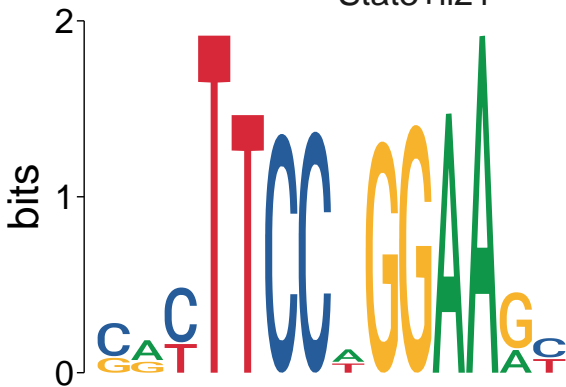
Bcl6



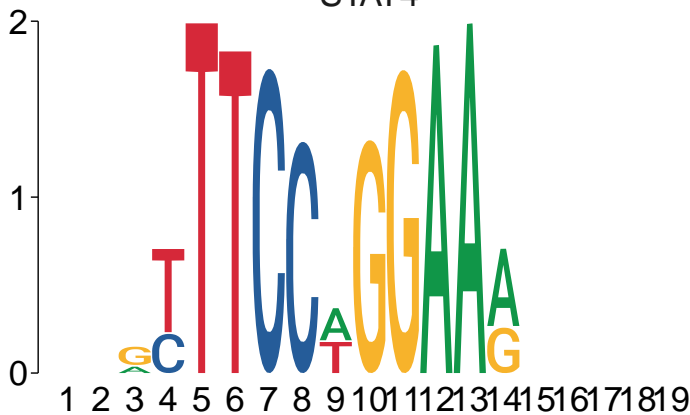
ARCH454_STAT4_Stat3+il21



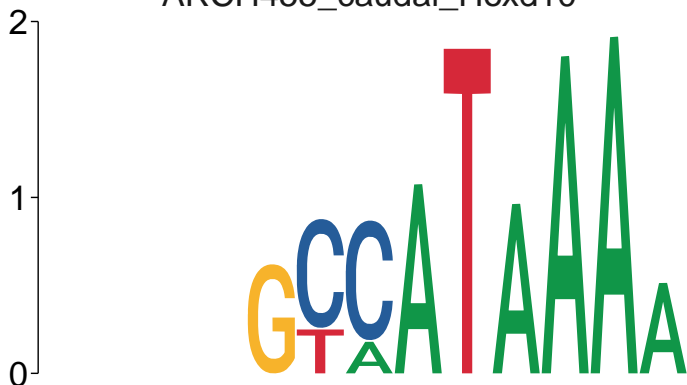
Stat3+il21



STAT4



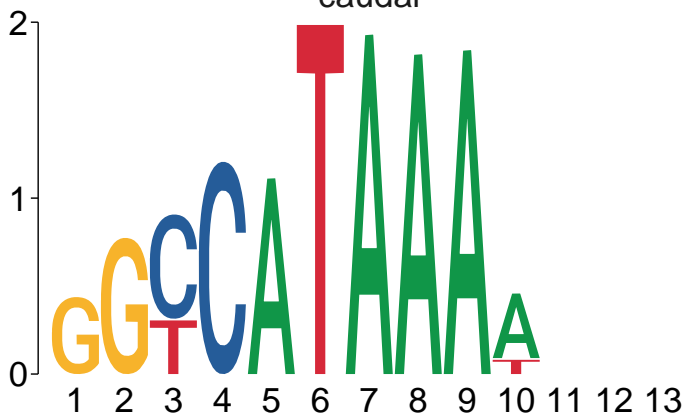
ARCH455_caudal_Hoxd10



Hoxd10



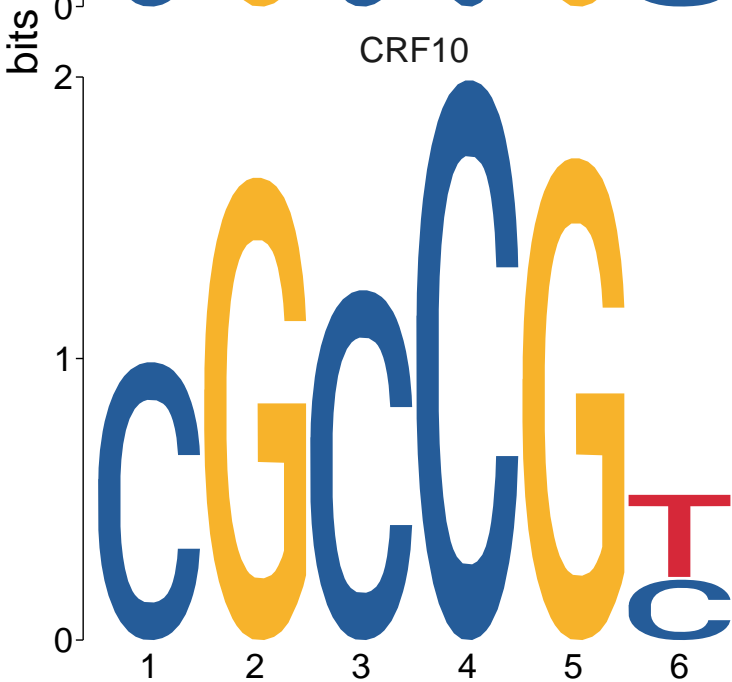
caudal



ARCH458_CRF10



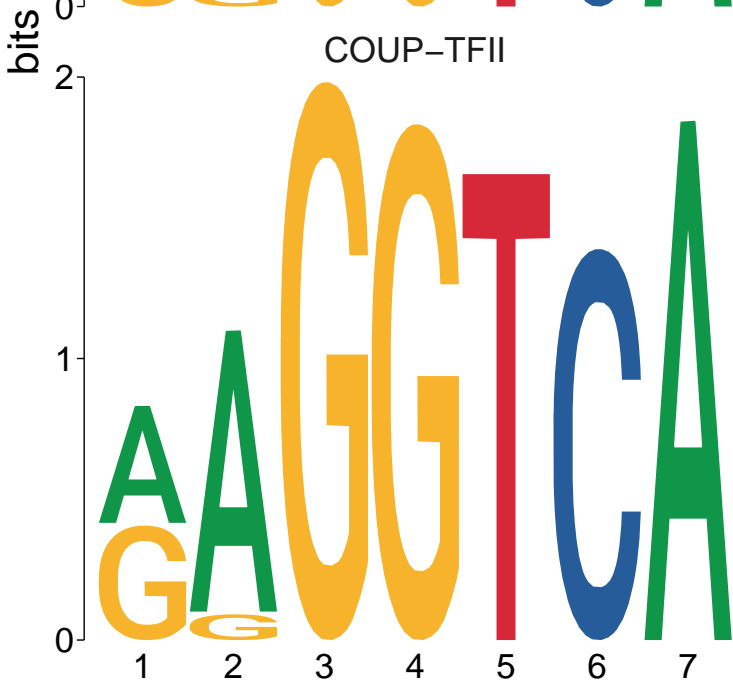
CRF10



ARCH459_COUP_TFII



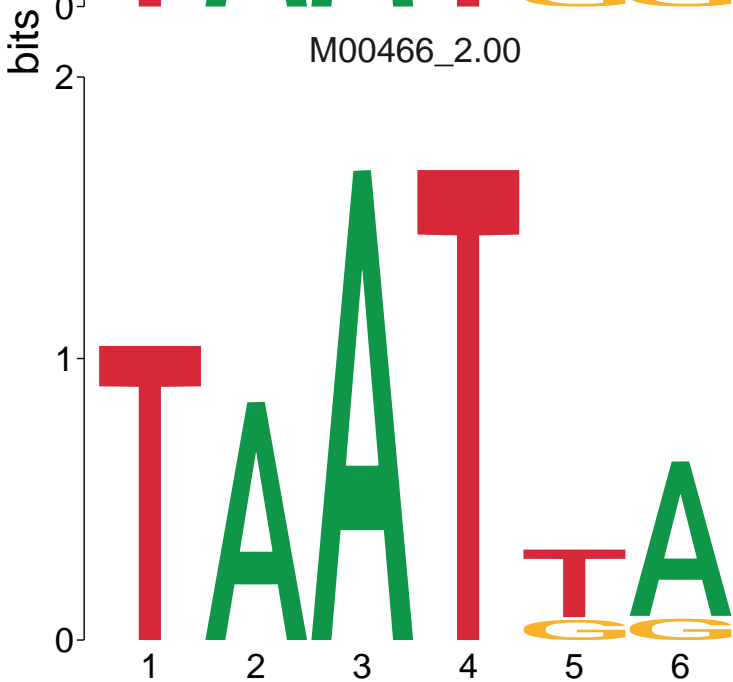
COUP-TFII



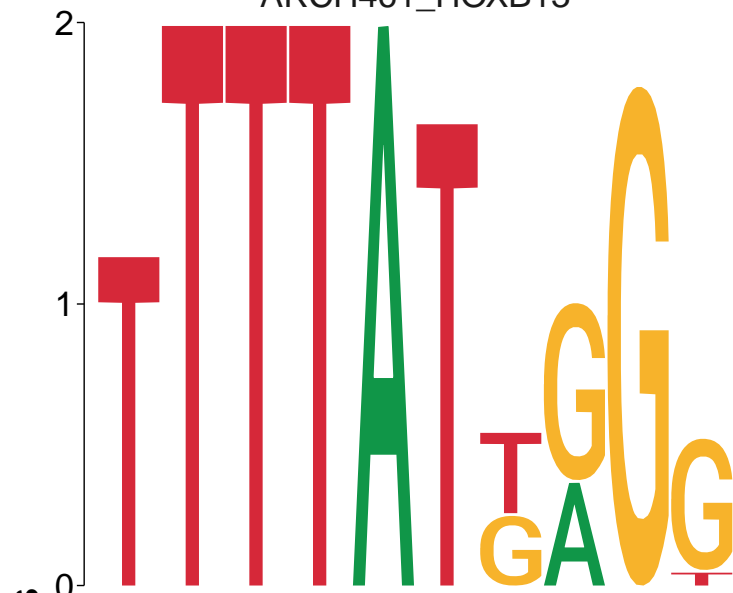
ARCH460_Homeodomains



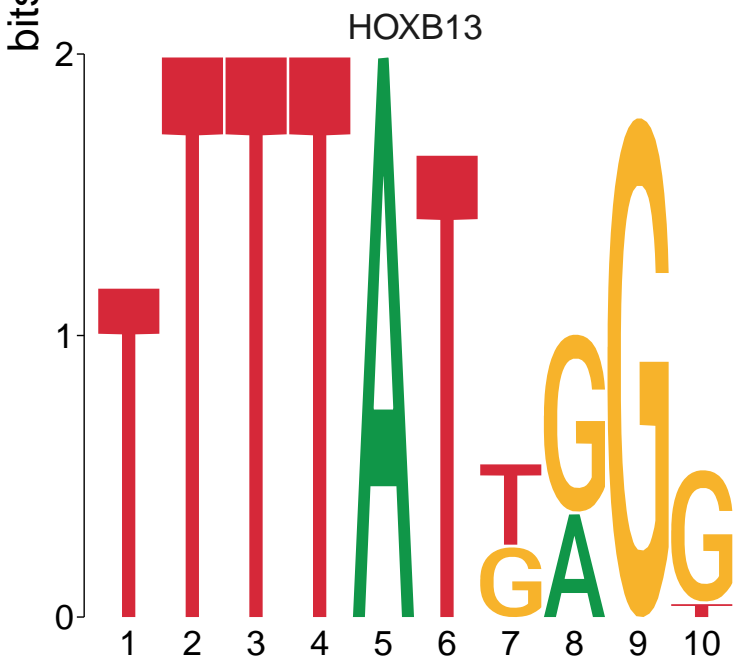
M00466_2.00



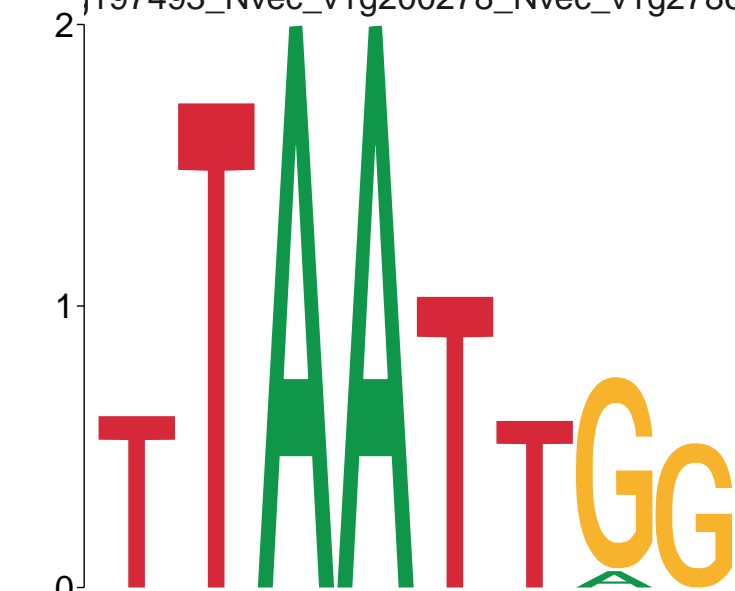
ARCH461_HOXB13



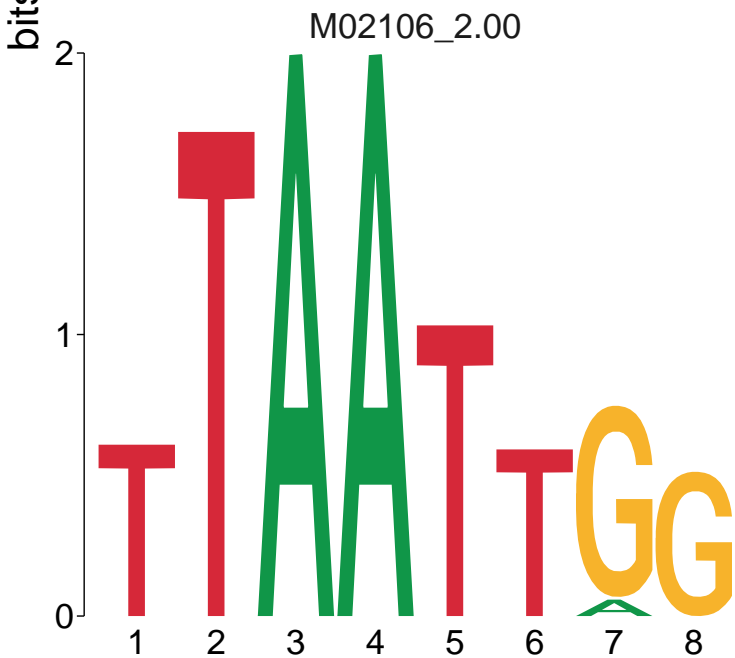
HOXB13



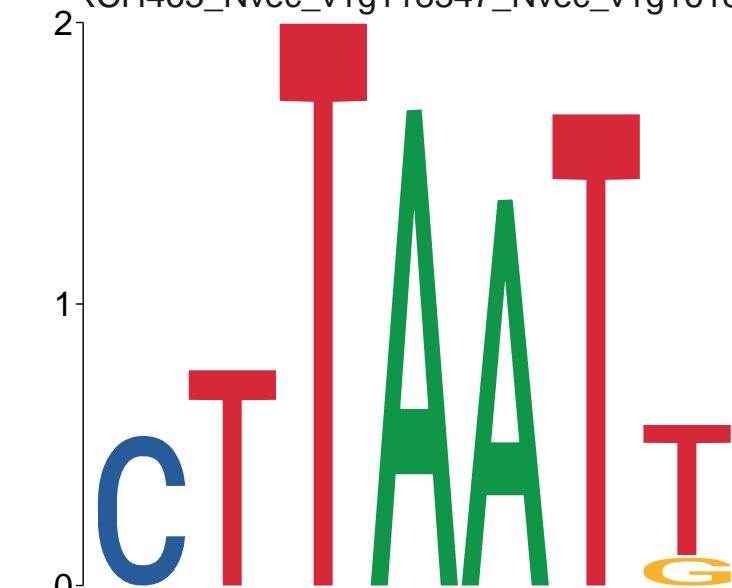
197493_Nvec_v1g200278_Nvec_v1g2786:



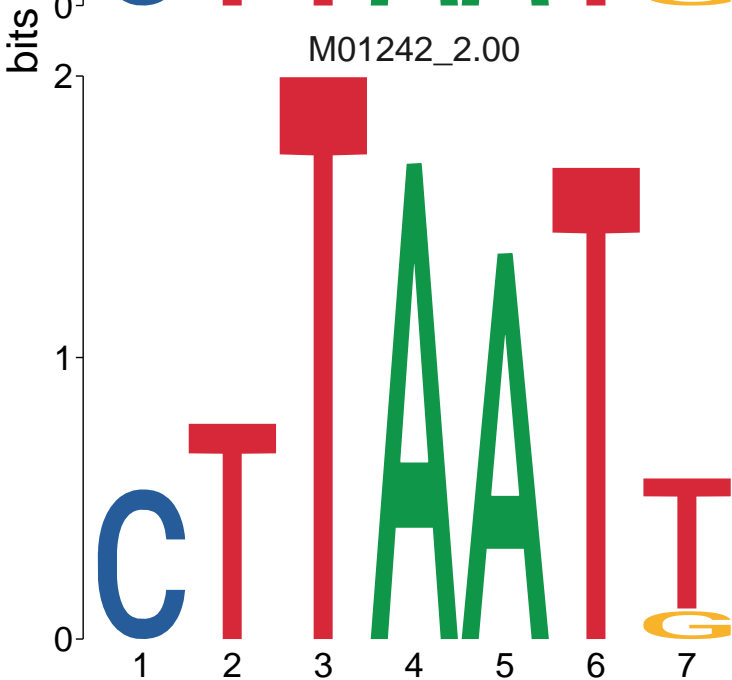
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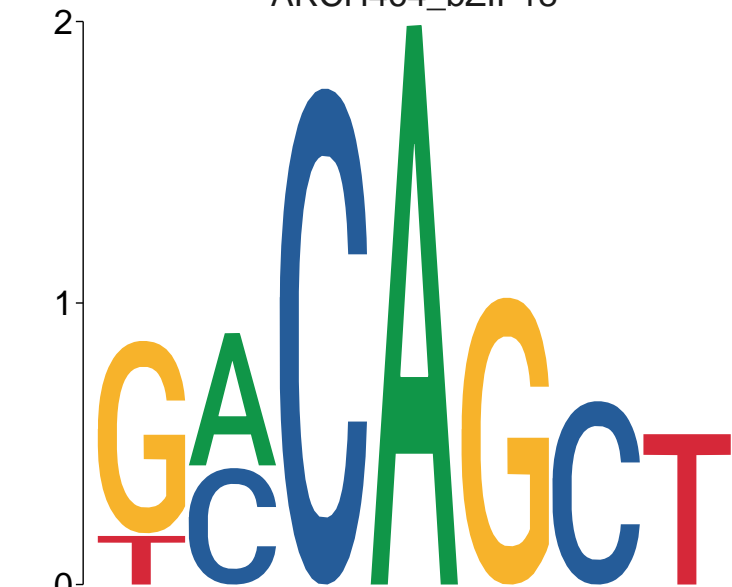
RCH463_Nvec_v1g118347_Nvec_v1g16180



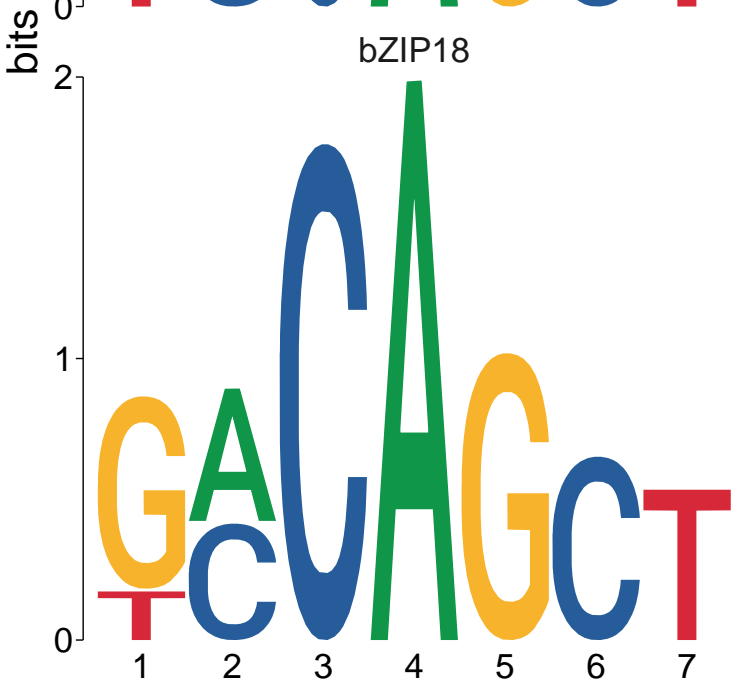
M01242_2.00



ARCH464_bZIP18



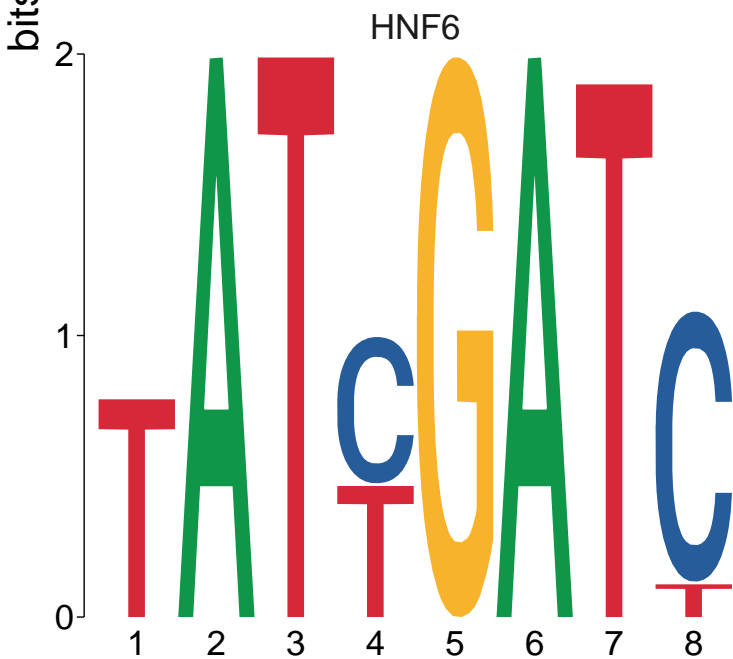
bZIP18



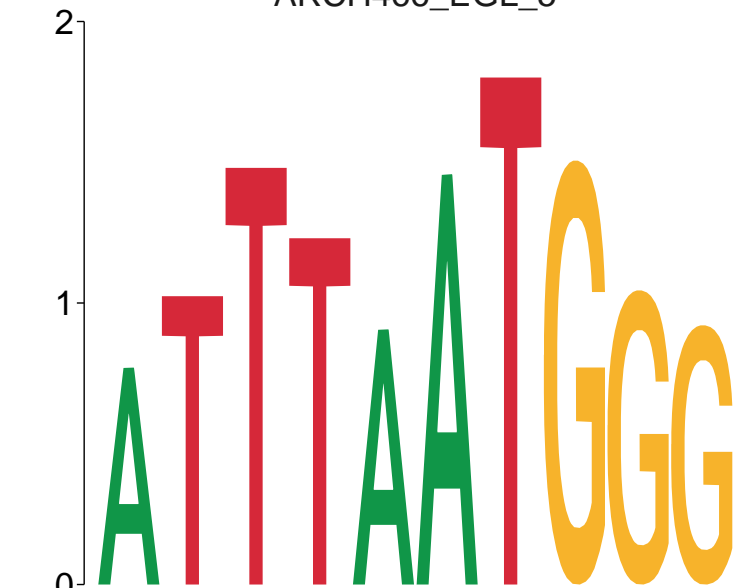
ARCH465_HNF6



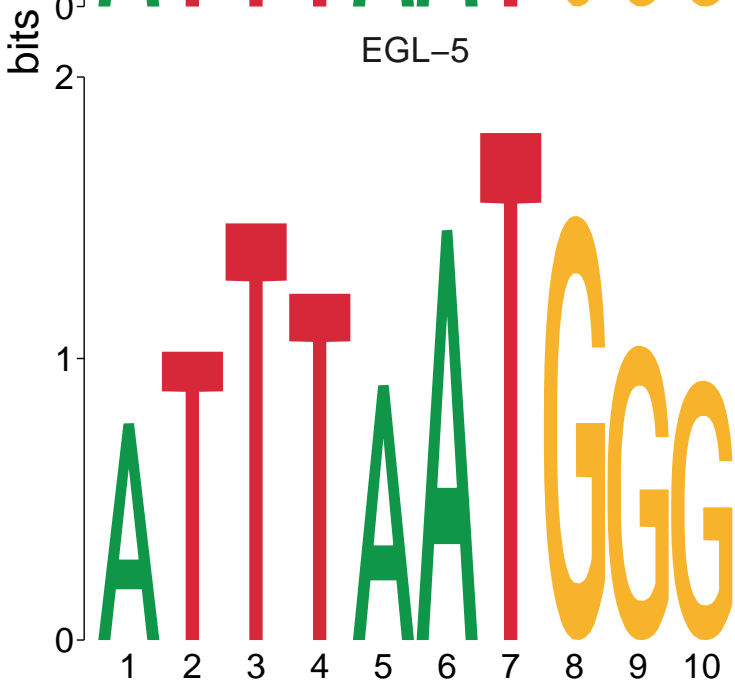
HNF6



ARCH466_EGL_5



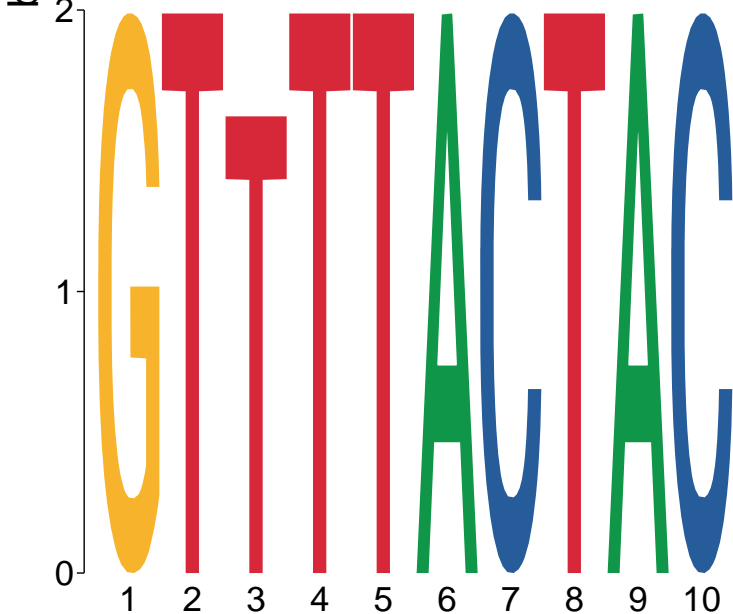
EGL-5



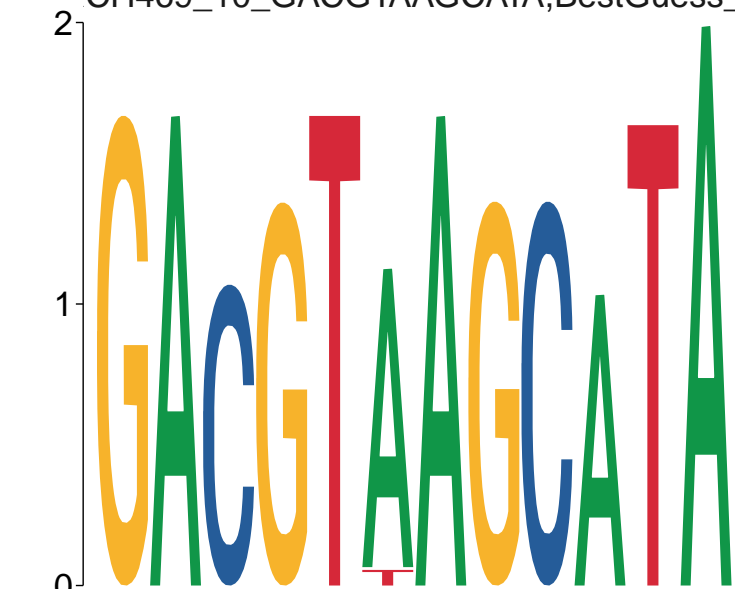
CH468_8_GTTTTACTAC,BestGuess_HOX



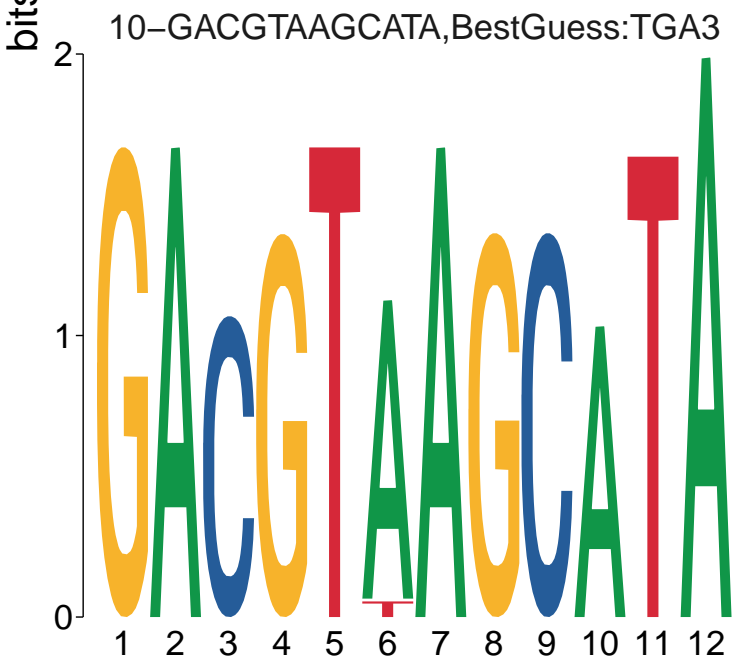
8-GTTTTACTAC,BestGuess:HOXC12



CH469_10_GACGTAAGCATA,BestGuess_



10-GACGTAAGCATA,BestGuess:TGA3



CH470_19_GTTGTGTCAGCA,BestGuess_

2

1

0

bits

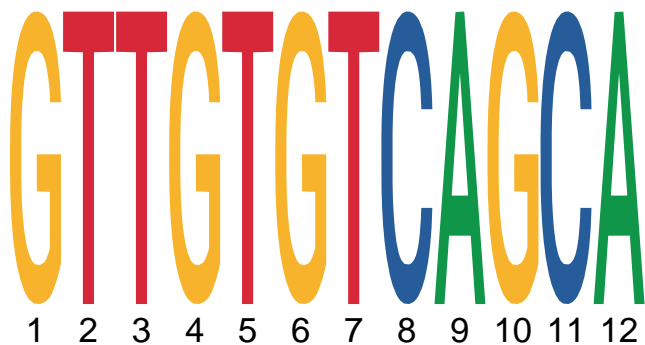
19-GTTGTGTCAGCA,BestGuess:MafA

2

1

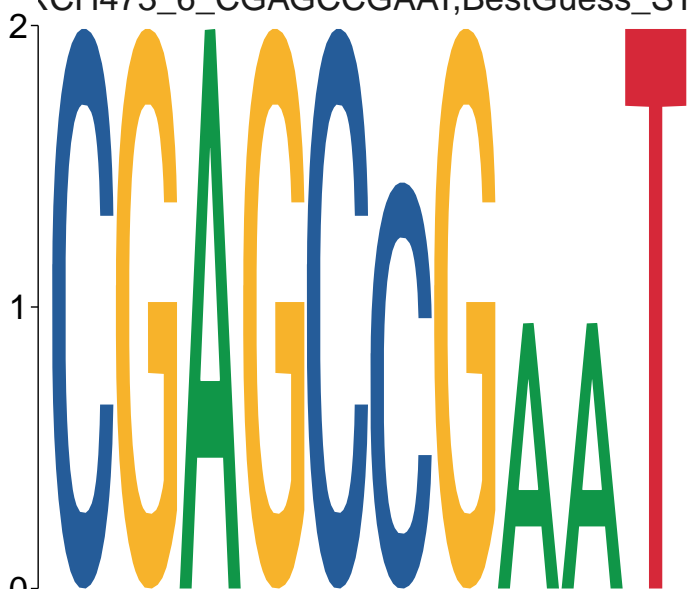
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1 2 3 4 5 6 7 8 9 10 11 12

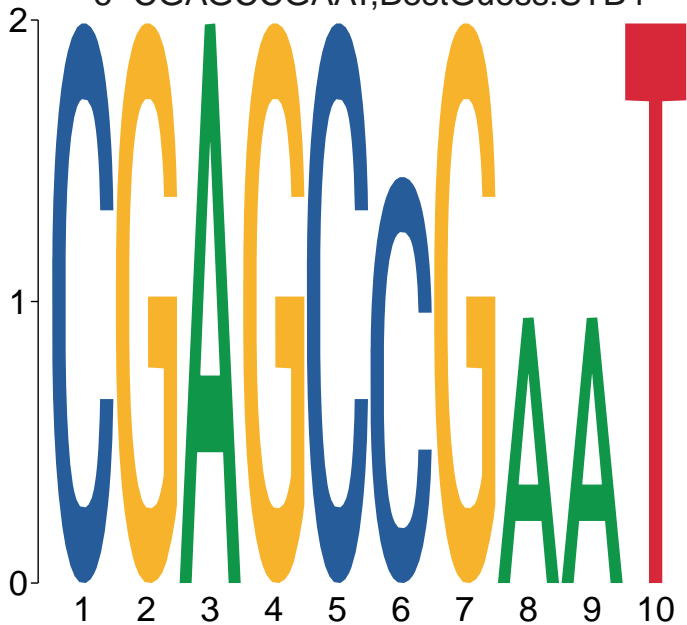


2CH473_6_CGAGCCGAAT,BestGuess_STI

bits



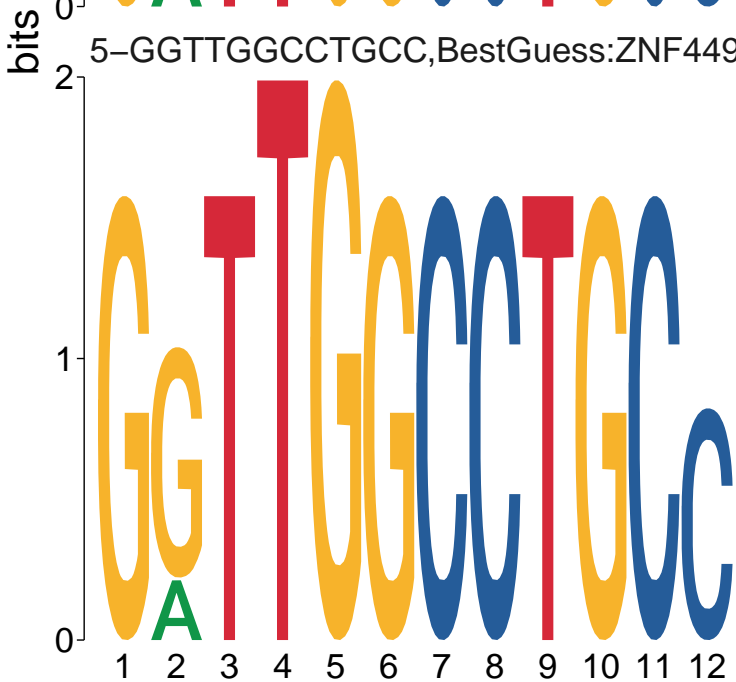
6-CGAGCCGAAT,BestGuess:STB4



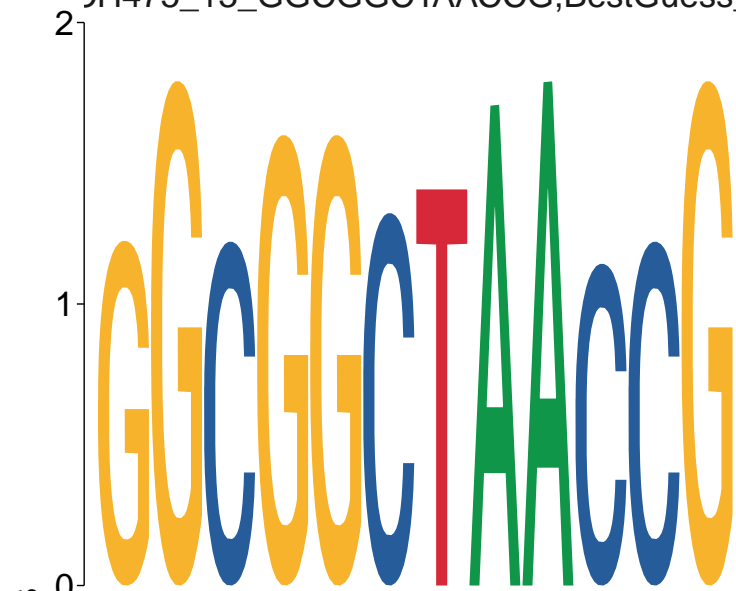
CH474_5_GGTTGGCCTGCC,BestGuess_2



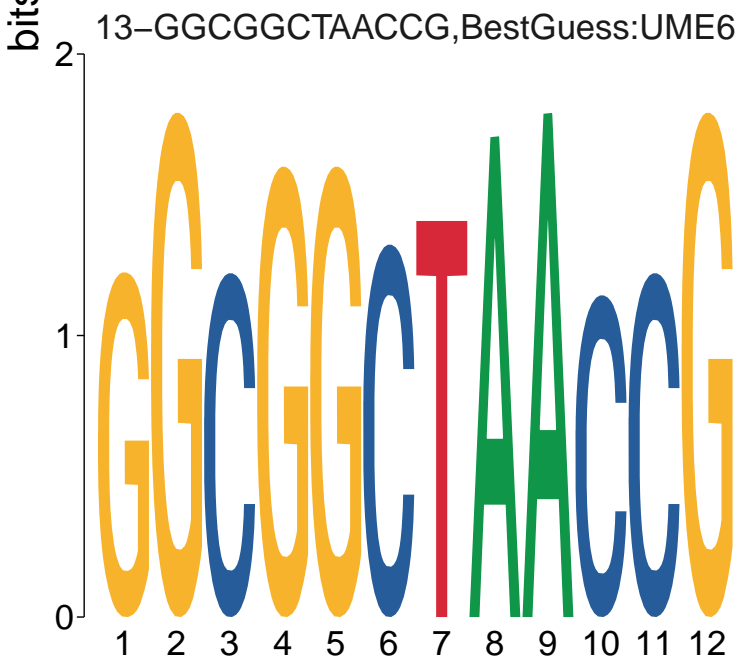
5-GGTTGGCCTGCC,BestGuess:ZNF449



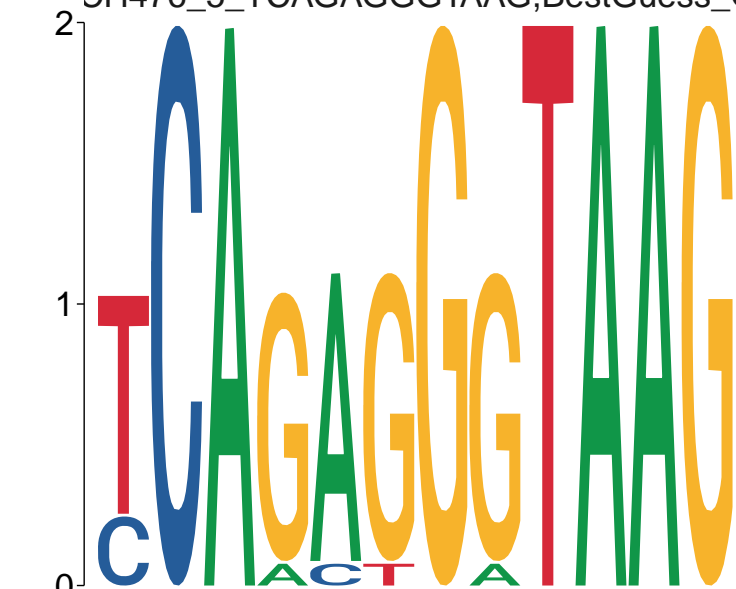
CH475_13_GGCGGCTAACCG,BestGuess_



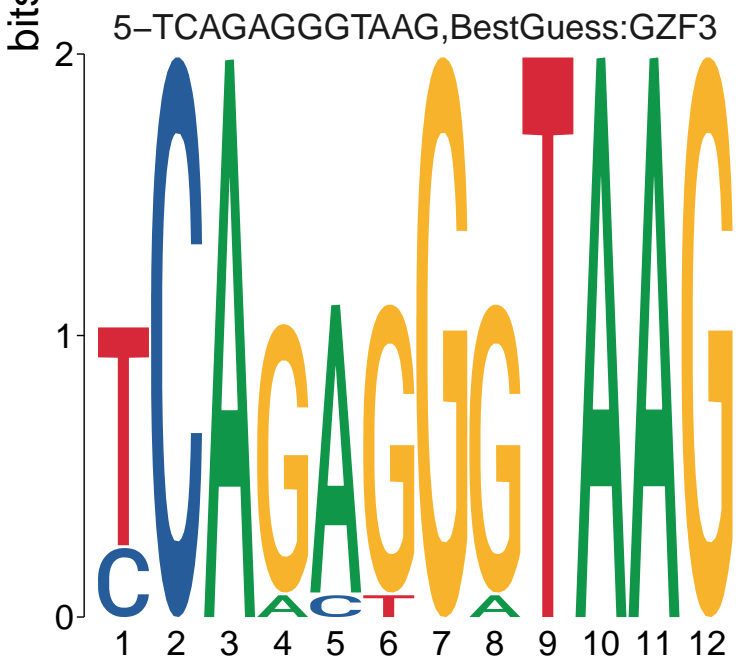
13-GGCGGCTAACCG,BestGuess:UME6



CH476_5_TCAGAGGGGTAAG,BestGuess_C



5-TCAGAGGGGTAAG,BestGuess:GZF3



CH477_21_AGAGGGTAGT,BestGuess_RB

2

1

0

bits

21-AGAGGGTAGT,BestGuess:RBM28

2

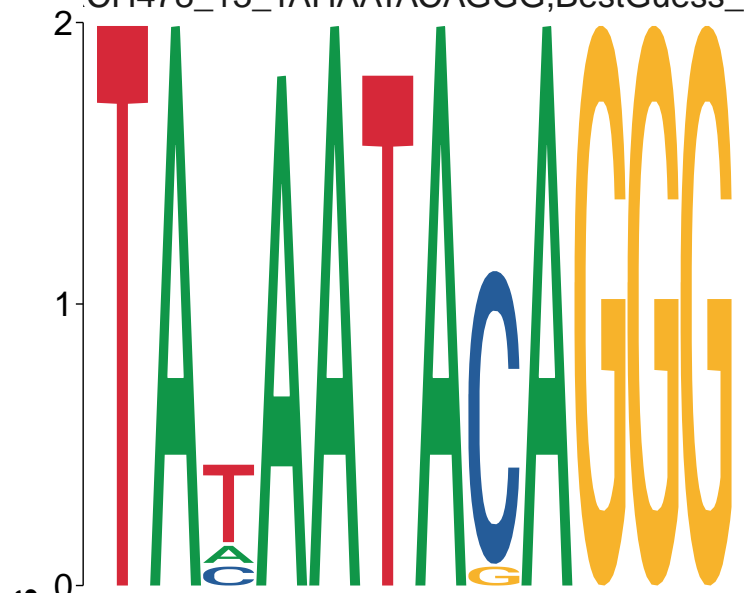
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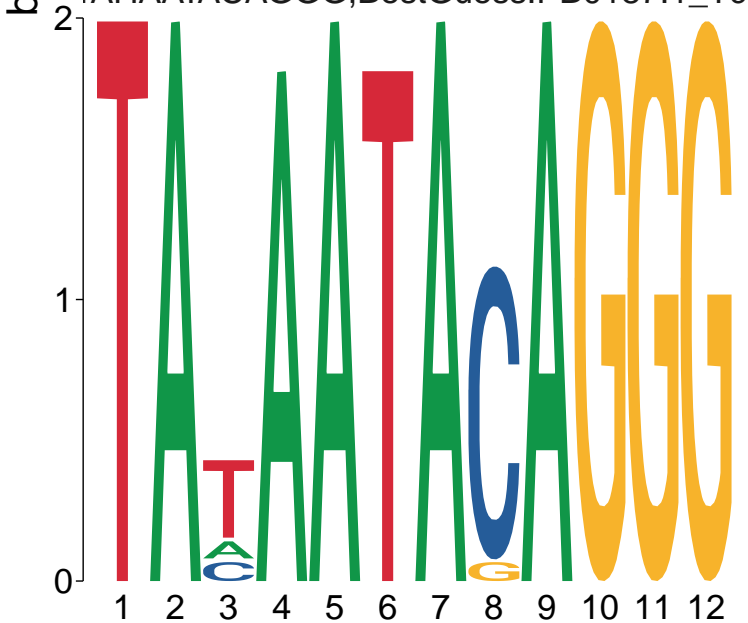
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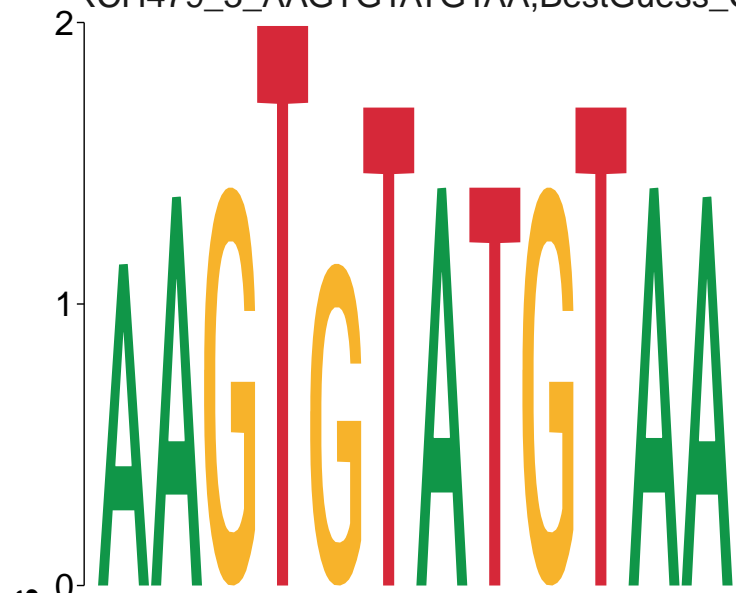
CH478_13_TAHAATACAGGG, BestGuess_



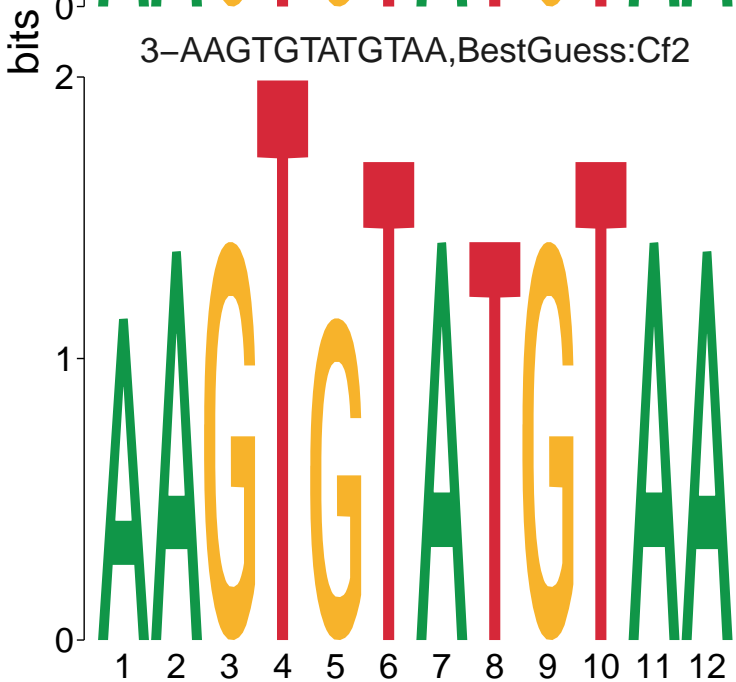
TAHAATACAGGG, BestGuess:PB0187.1_Tc



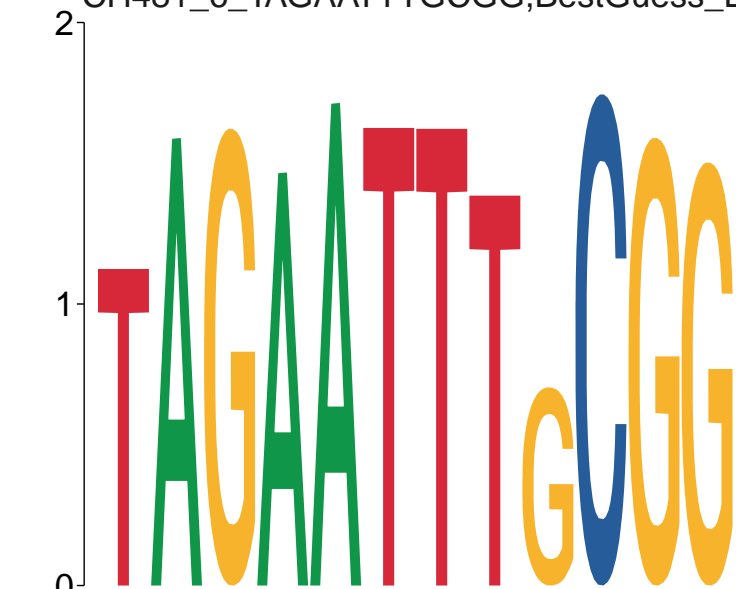
RCH479_3_AAGTGTATGTAA,BestGuess_C



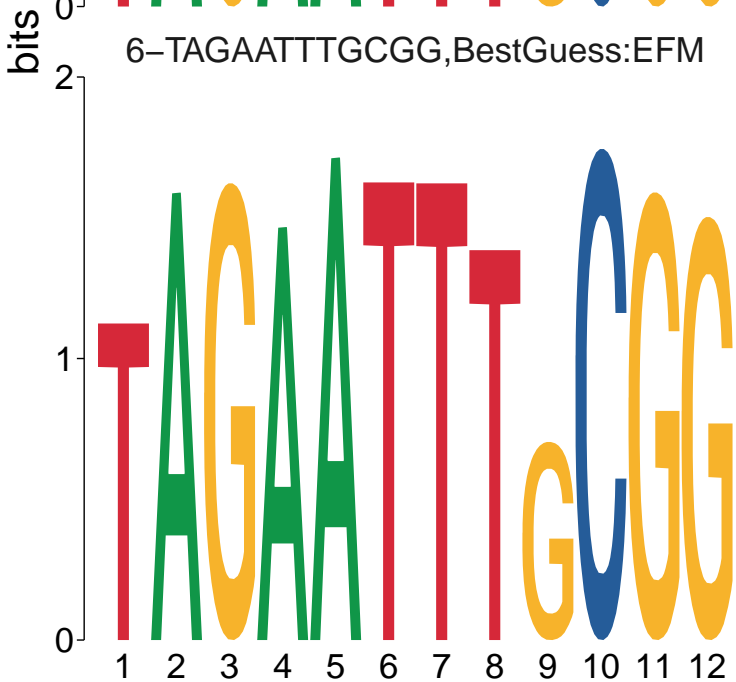
3-AAGTGTATGTAA,BestGuess:Cf2



CH481_6_TAGAATTTGCGG,BestGuess_E



6-TAGAATTTGCGG,BestGuess:EFM



CH482_19_TAGTGGAAATAG,BestGuess_I

2

1

0

bits



19-TAGTGGAAATAG,BestGuess:MOD

2

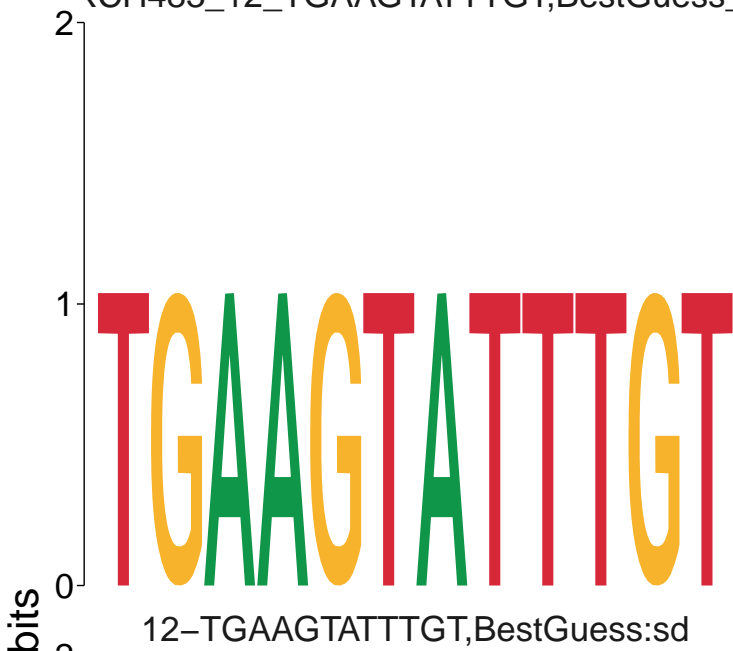
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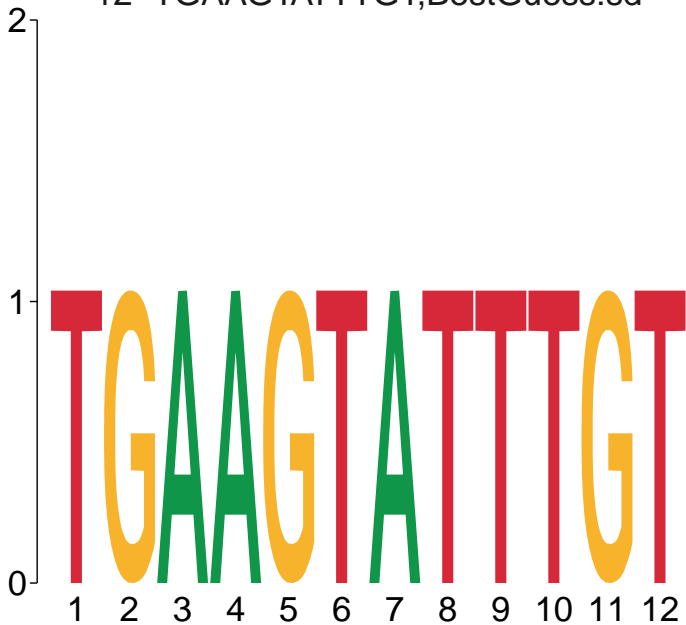
1 2 3 4 5 6 7 8 9 10 11 12



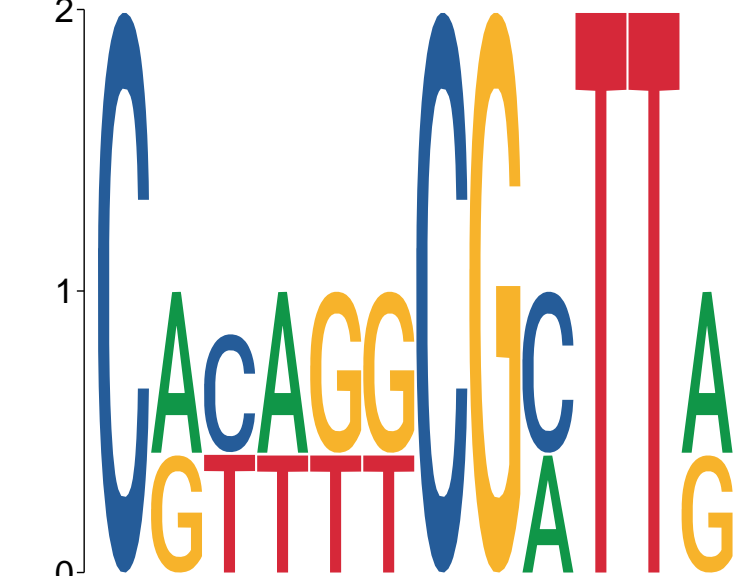
RCH483_12_TGAAGTATTTGT,BestGuess_



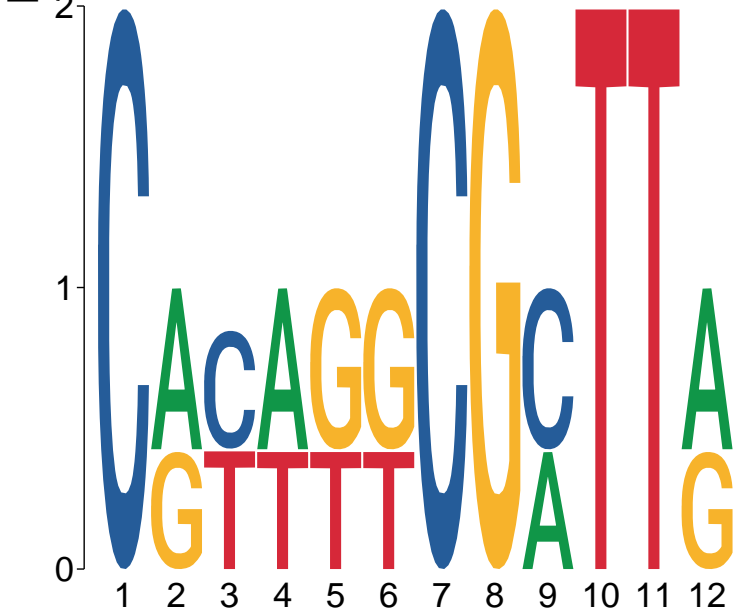
12-TGAAGTATTTGT,BestGuess:sd



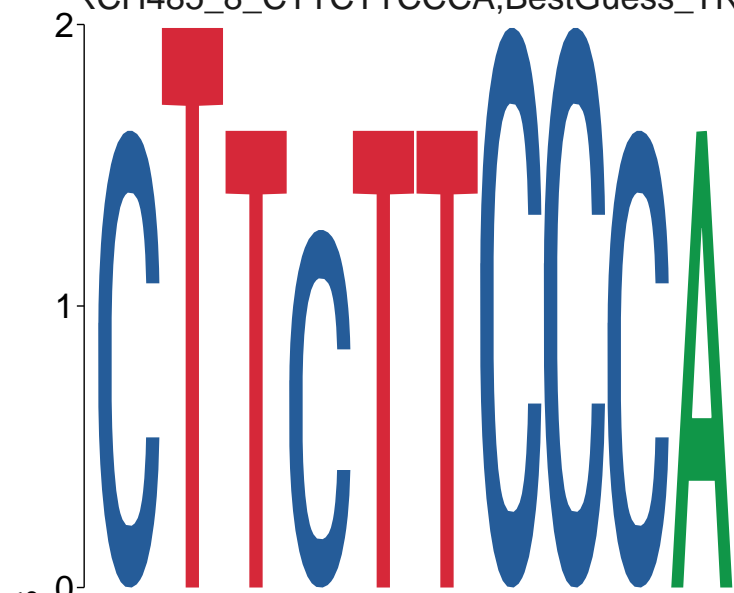
CH484_5_CRYWKKCGMTTR,BestGuess_M



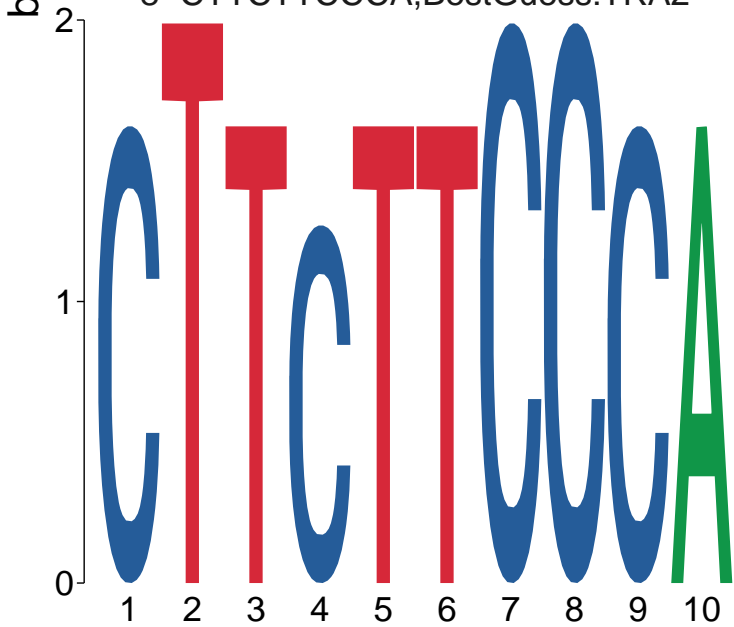
CRYWKKCGMTTR,BestGuess:MF0009.1_T



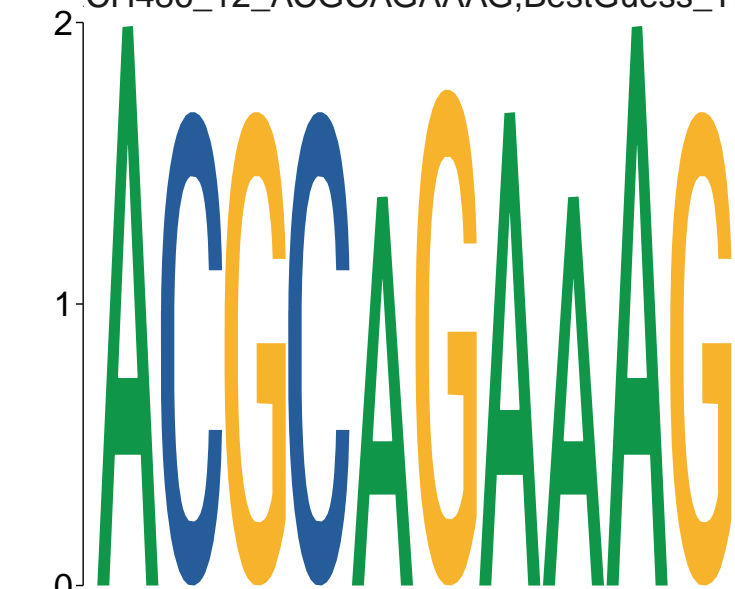
RCH485_8_CTTCTTCCCA,BestGuess_TR/



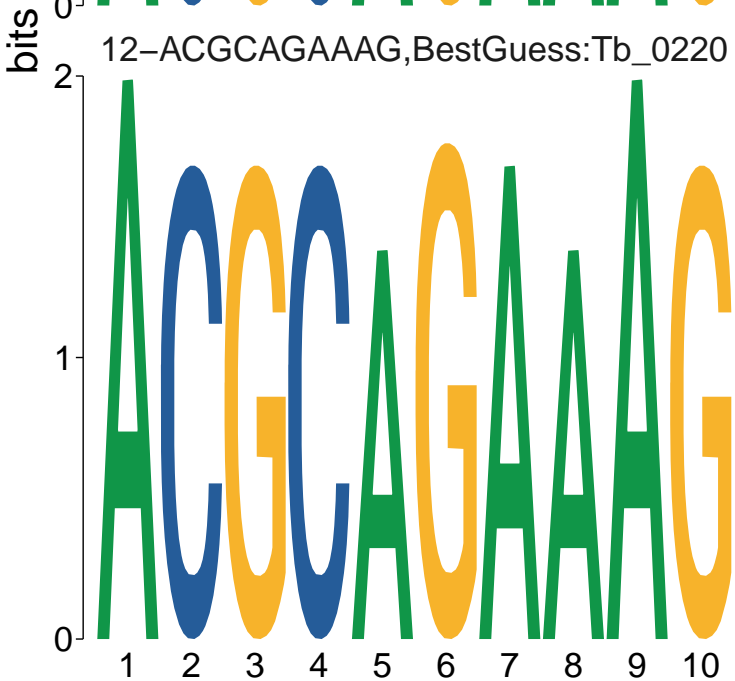
8-CTTCTTCCCA,BestGuess:TRA2



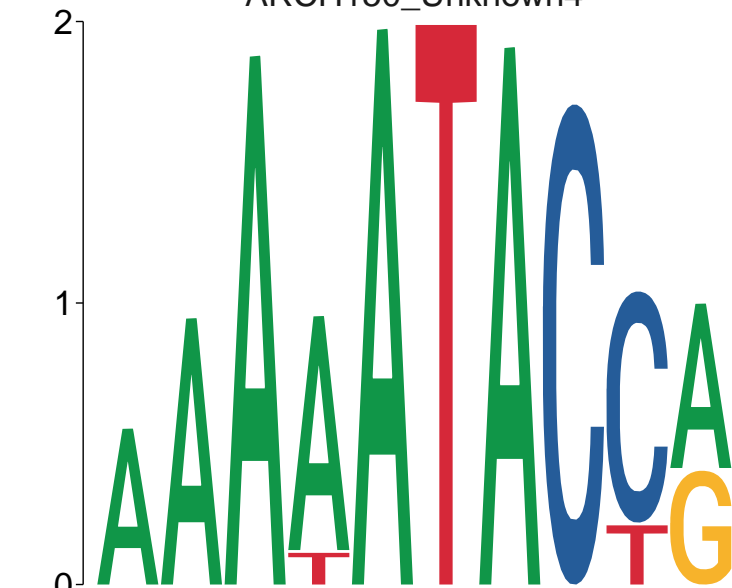
CH486_12_ACGCAGAAAG,BestGuess_Tb



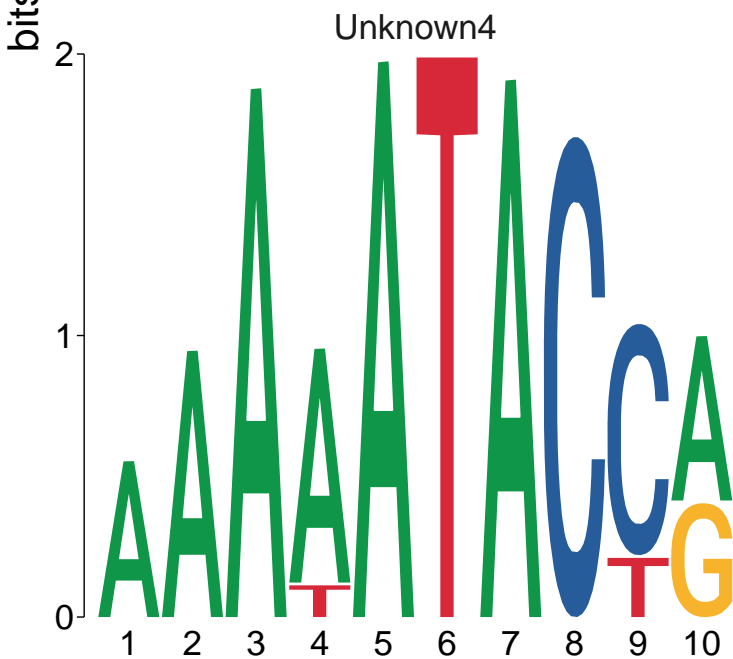
12-ACGCAGAAAG,BestGuess:Tb_0220



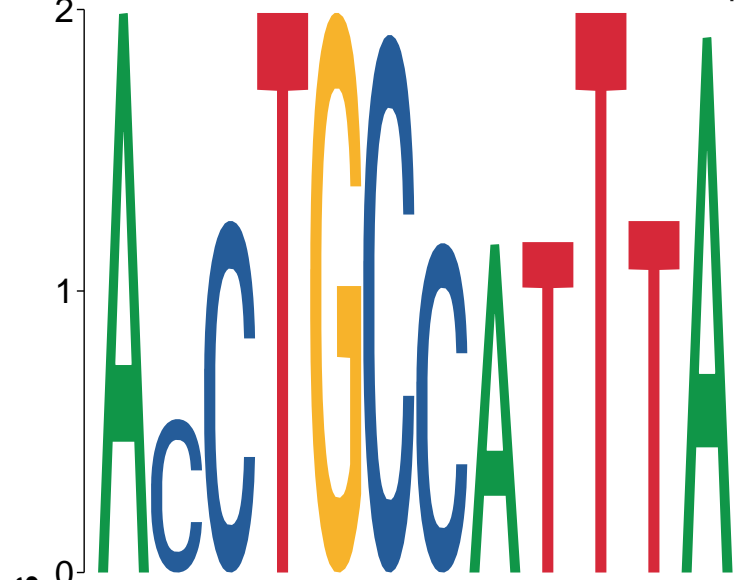
ARCH150_Unknown4



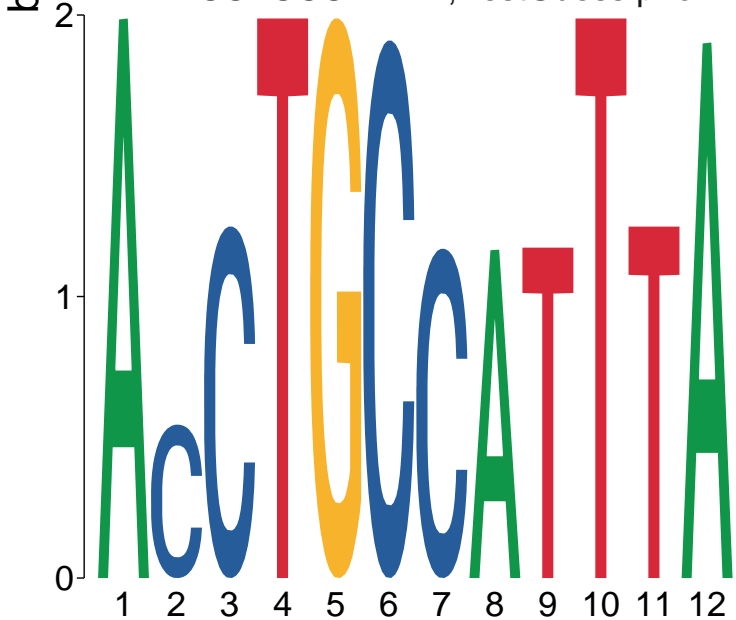
Unknown4



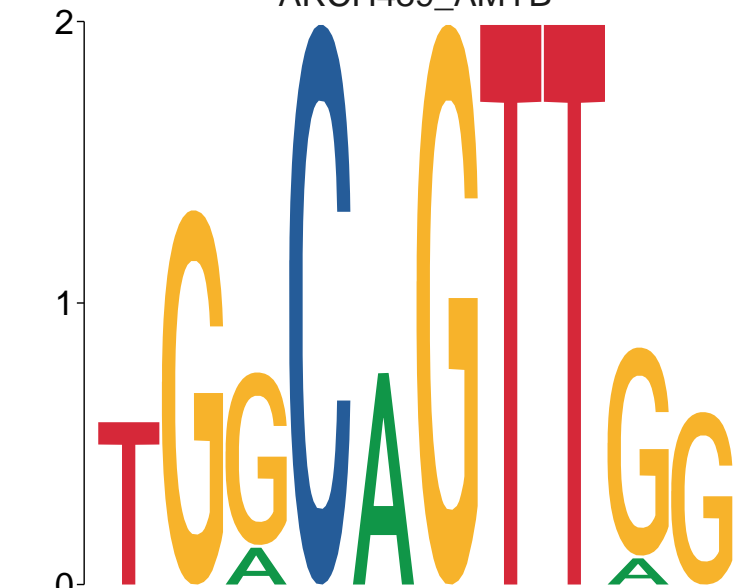
CH488_2_ACCTGCCATTTA,BestGuess_p



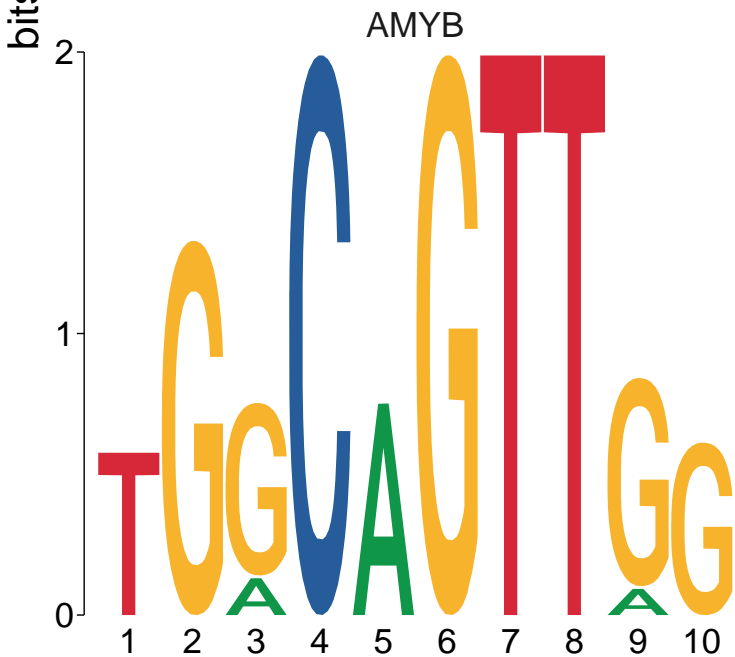
2-ACCTGCCATTTA,BestGuess:pho



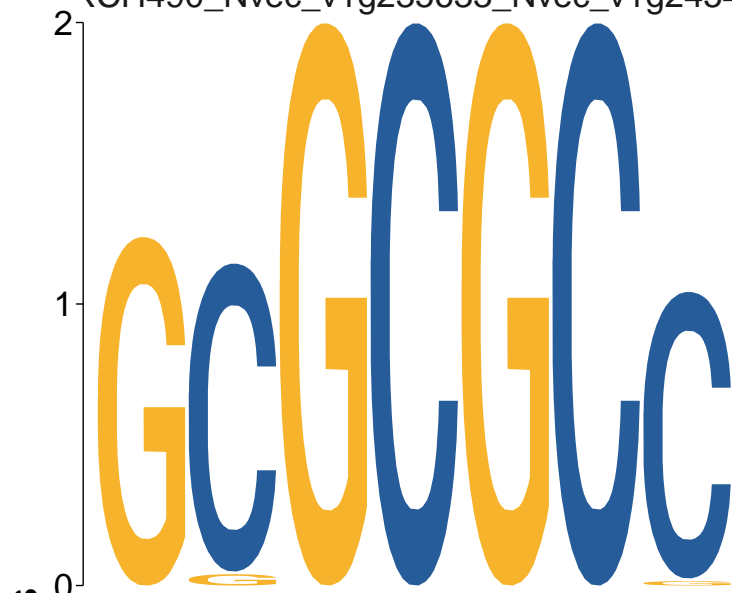
ARCH489_AMYB



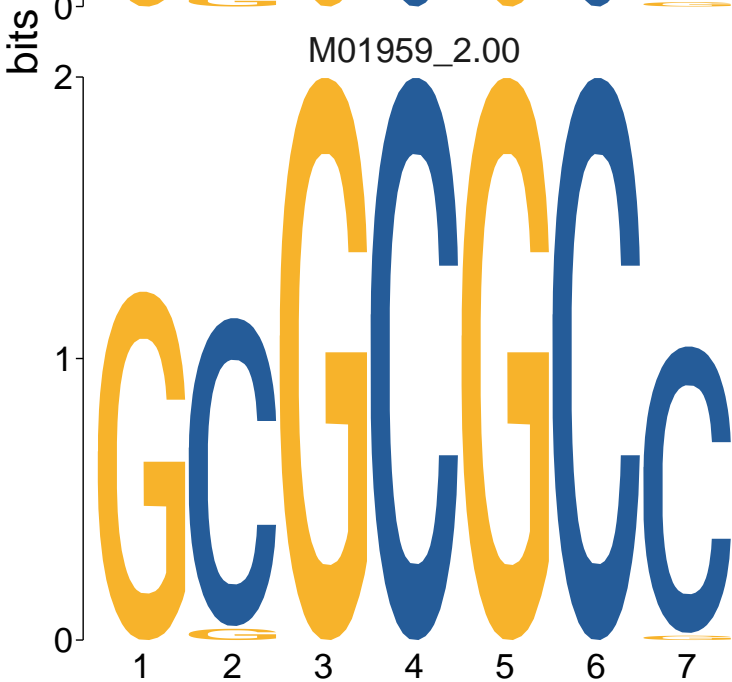
AMYB



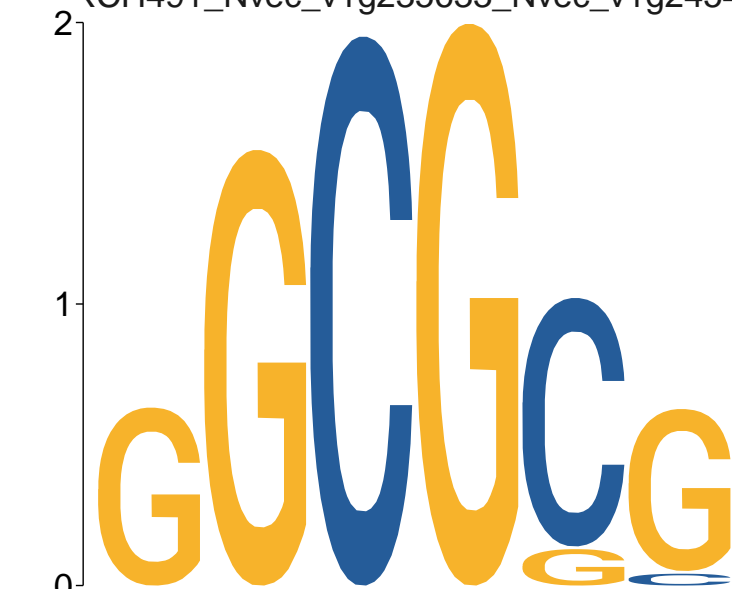
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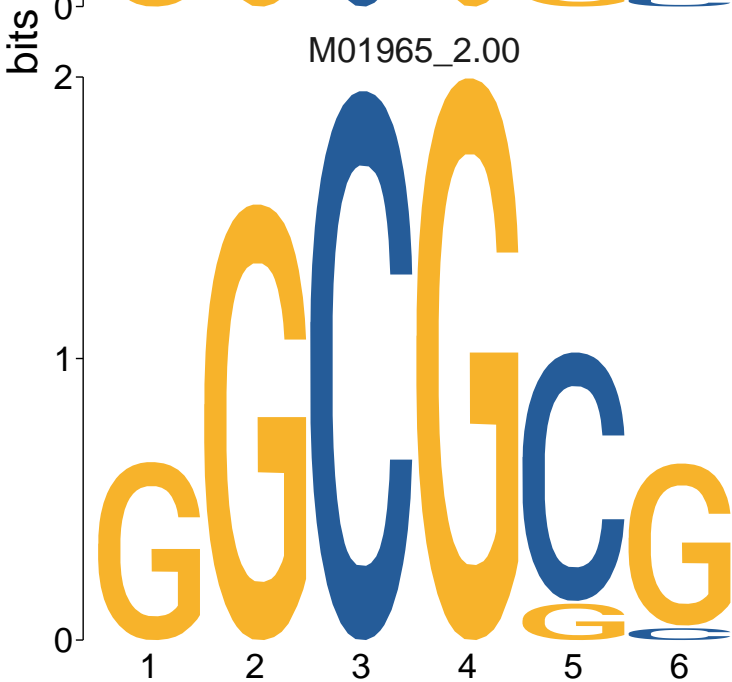
M01959_2.00



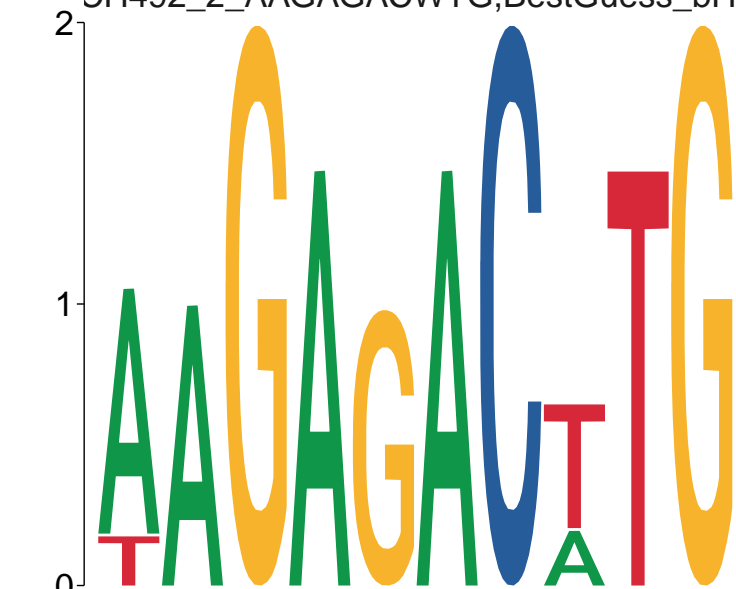
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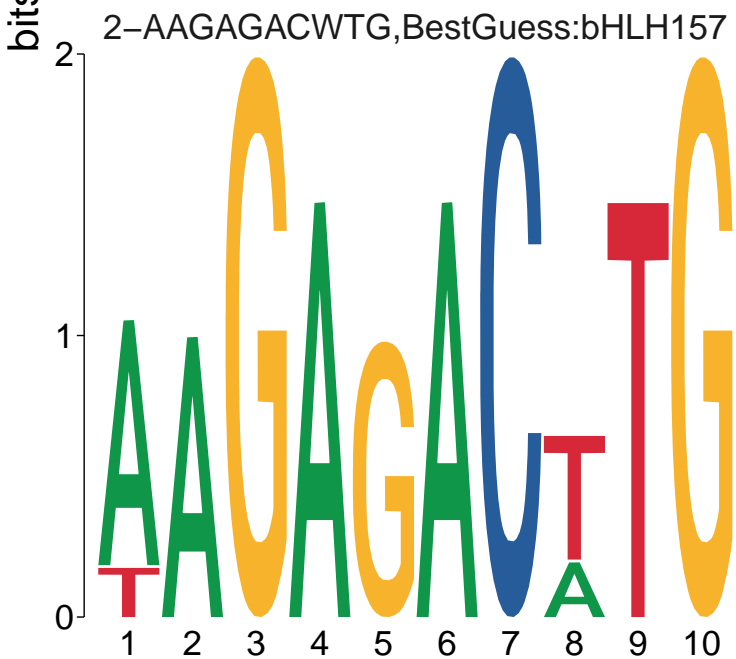
M01965_2.00



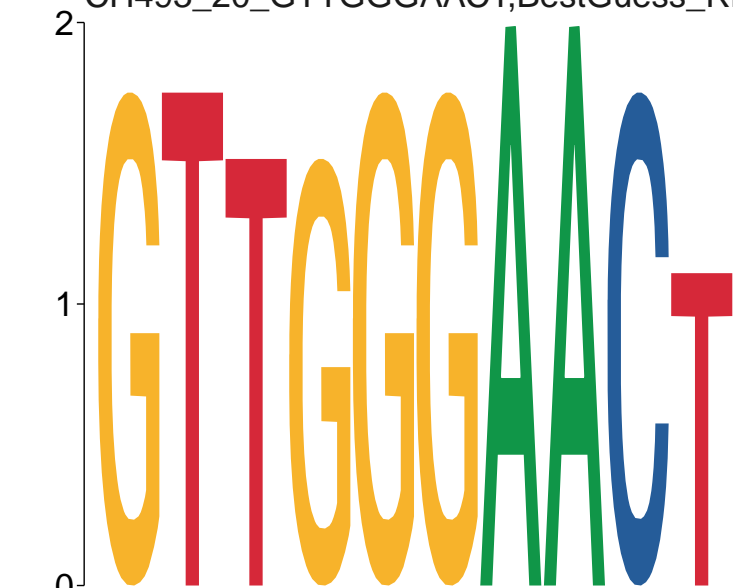
CH492_2_AAGAGACWTG,BestGuess_bHL



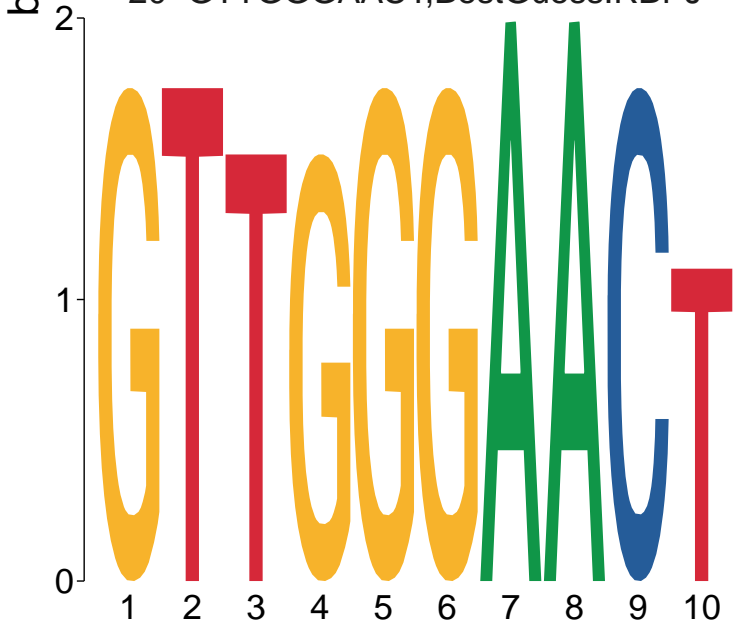
2-AAGAGACWTG,BestGuess:bHLH157



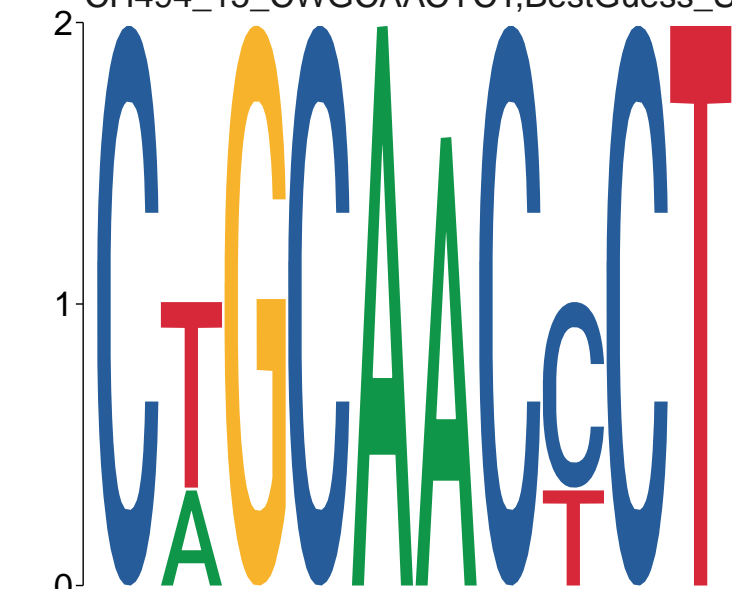
CH493_20_GTTGGGAACT,BestGuess_RE



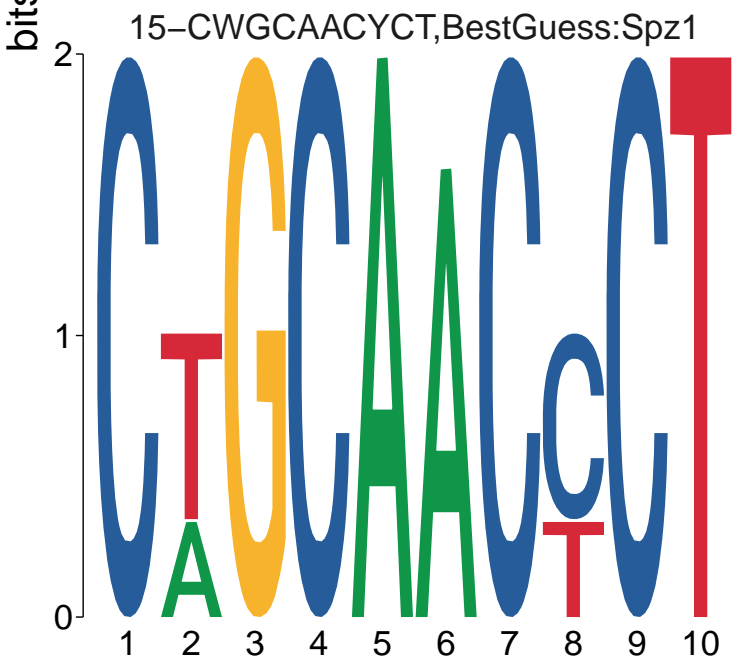
20-GTTGGGAACT,BestGuess:RBPJ



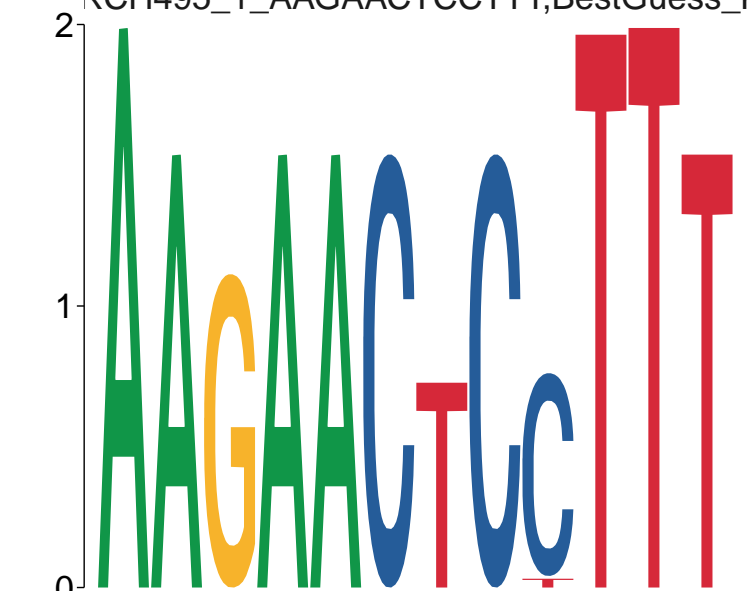
CH494_15_CWGCAACYCT,BestGuess_Sp



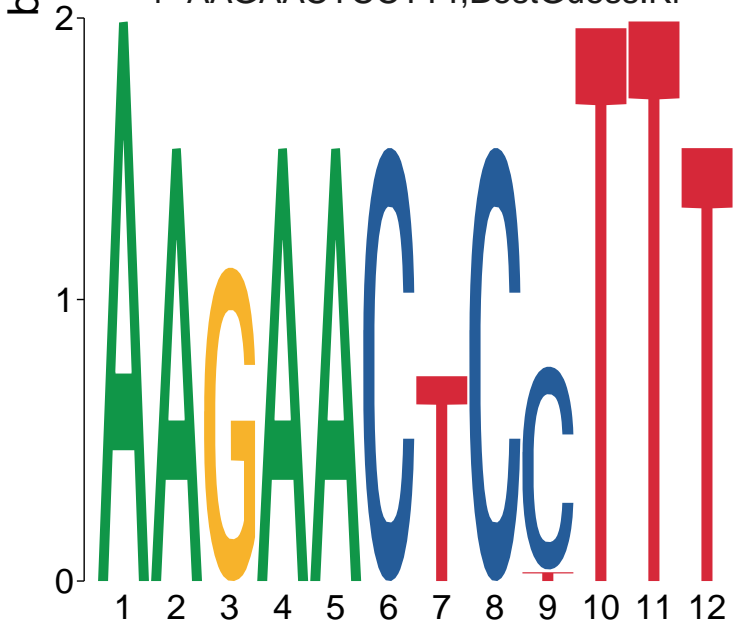
15-CWGCAACYCT,BestGuess:Spz1



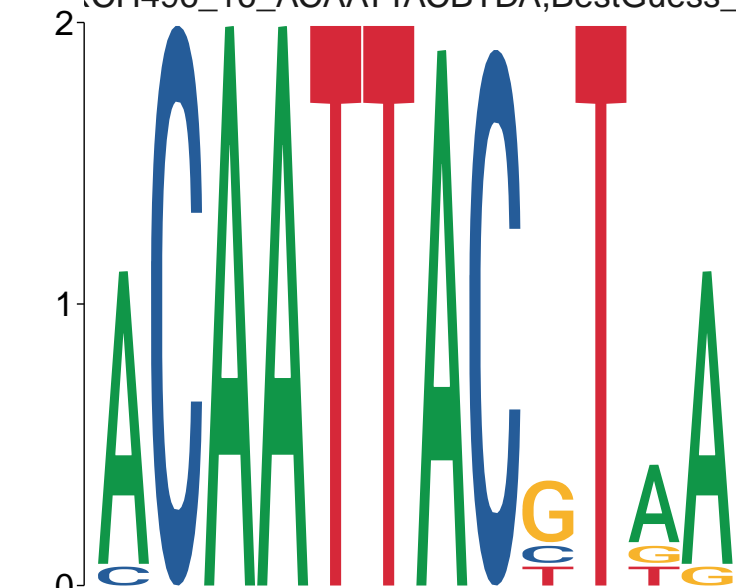
RCH495_1_AAGAACTCCTTT,BestGuess_I



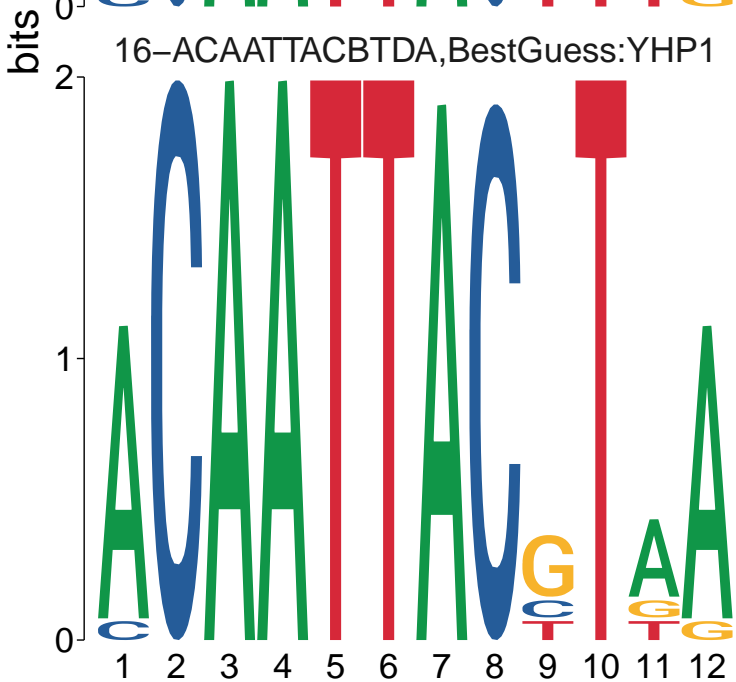
1-AAGAACTCCTTT,BestGuess:Kr



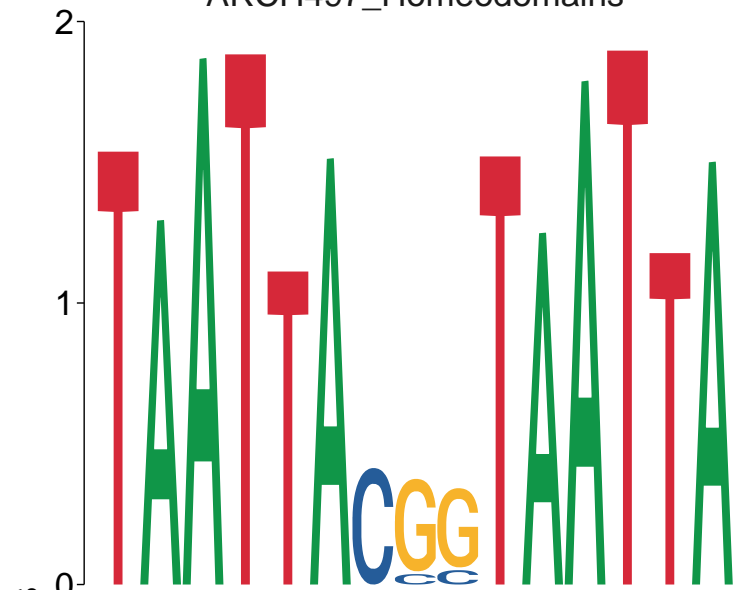
CH496_16_ACAATTACBTDA,BestGuess_`



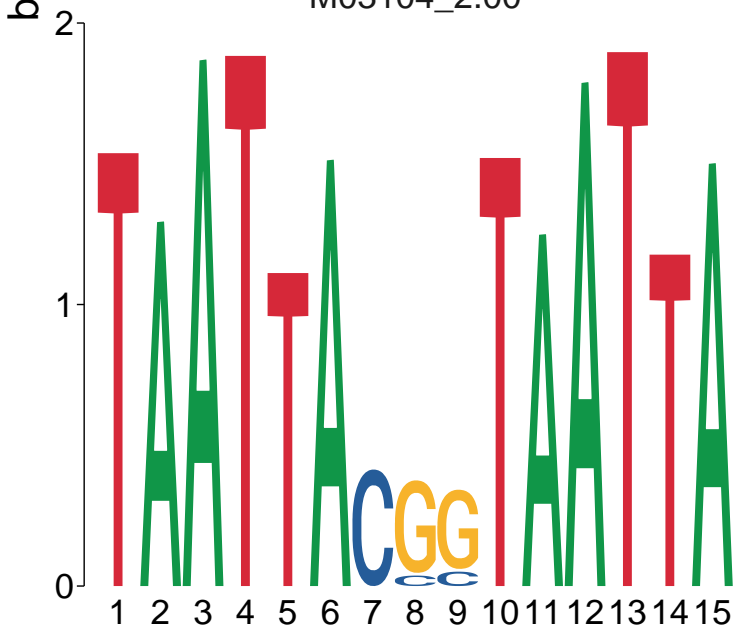
16-ACAATTACBTDA,BestGuess:YHP1



ARCH497_Homeodomains



M03104_2.00



ARCH499_Homeodomains



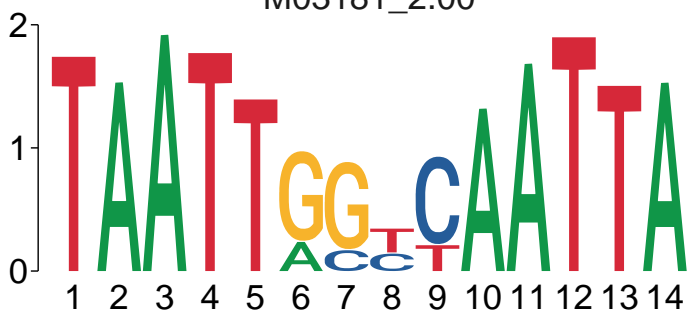
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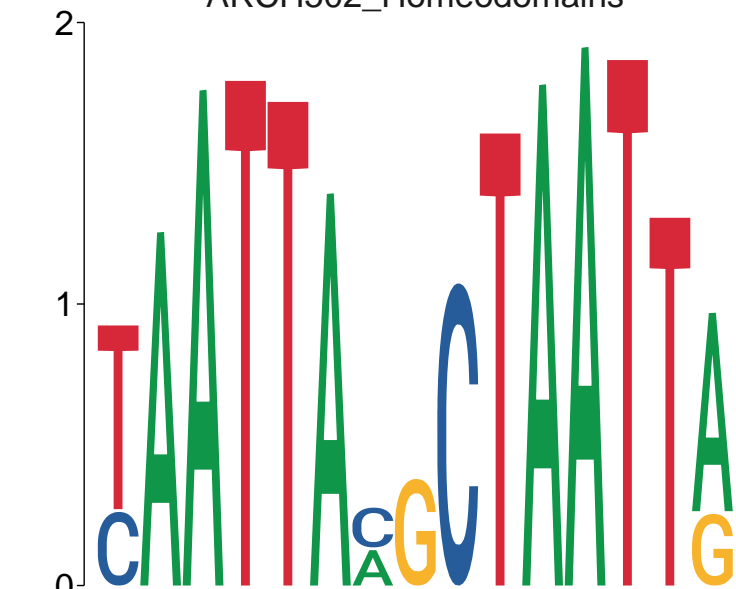
M03183_2.00



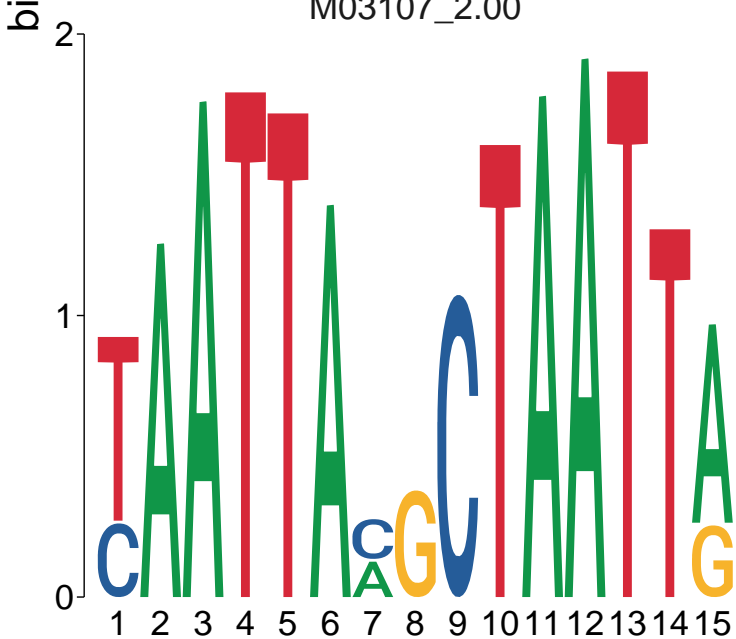
M03181_2.00



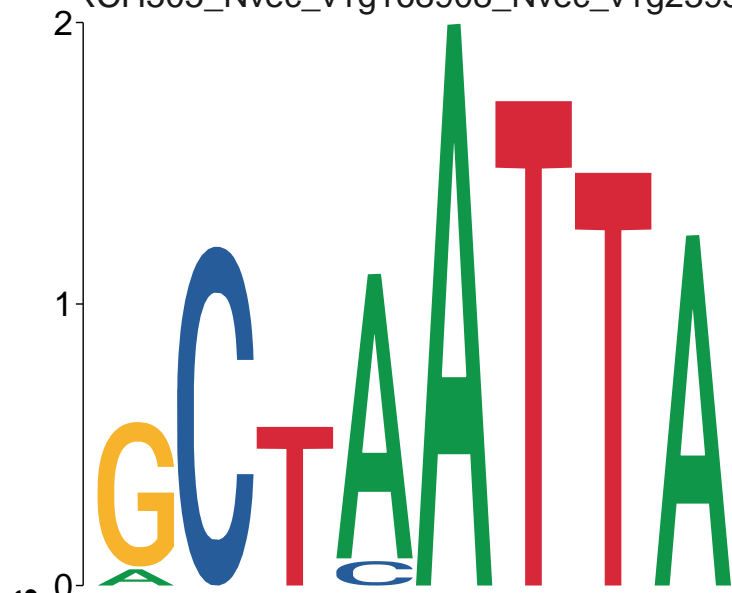
ARCH502_Homeodomains



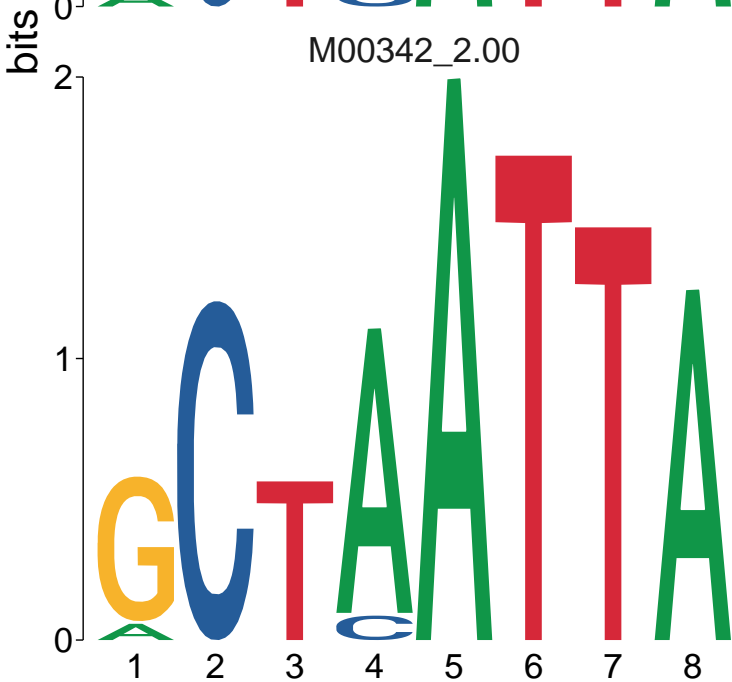
M03107_2.00



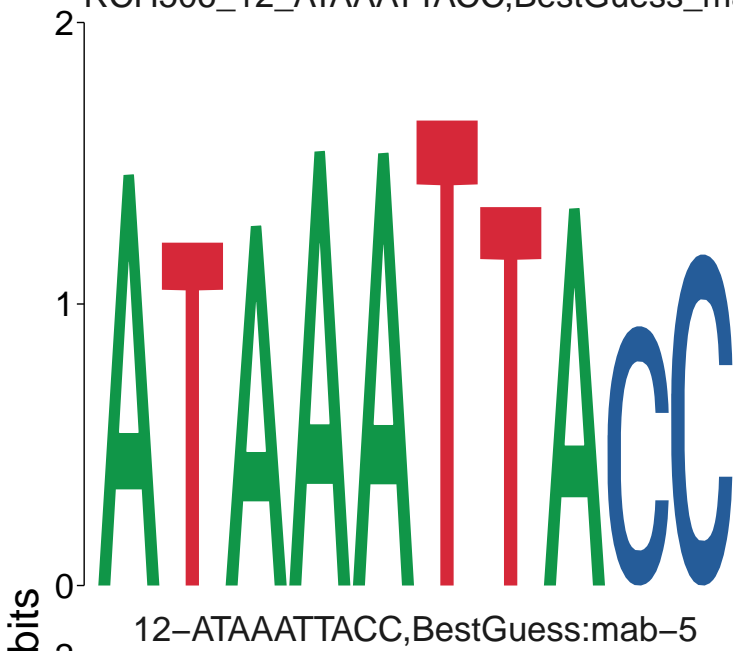
RCH505_Nvec_v1g168908_Nvec_v1g2395:



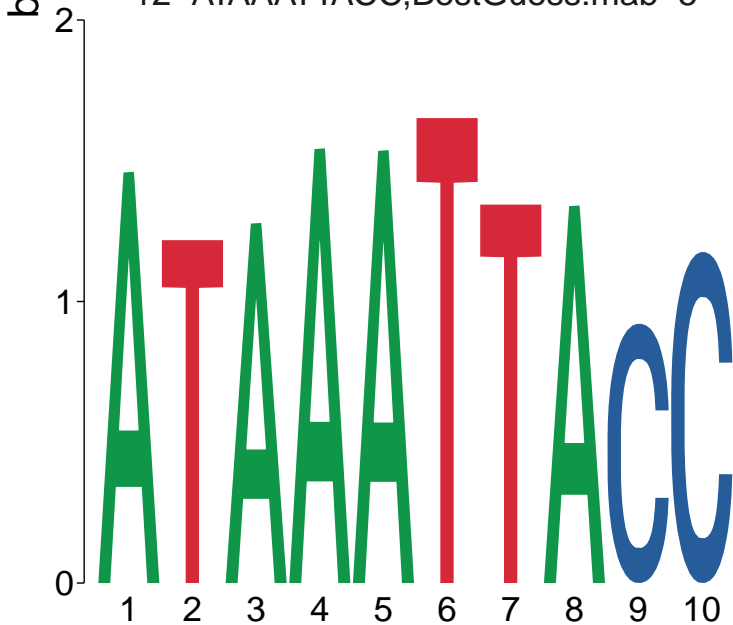
M00342_2.00



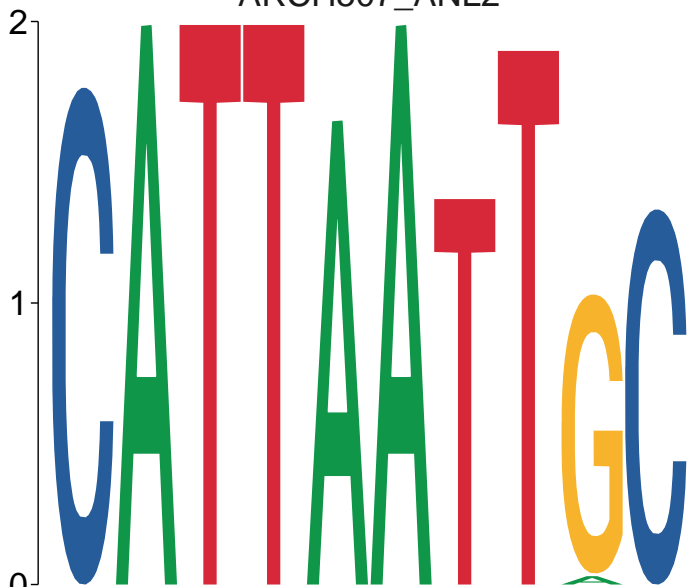
RCH506_12_ATAAATTACC,BestGuess_ma



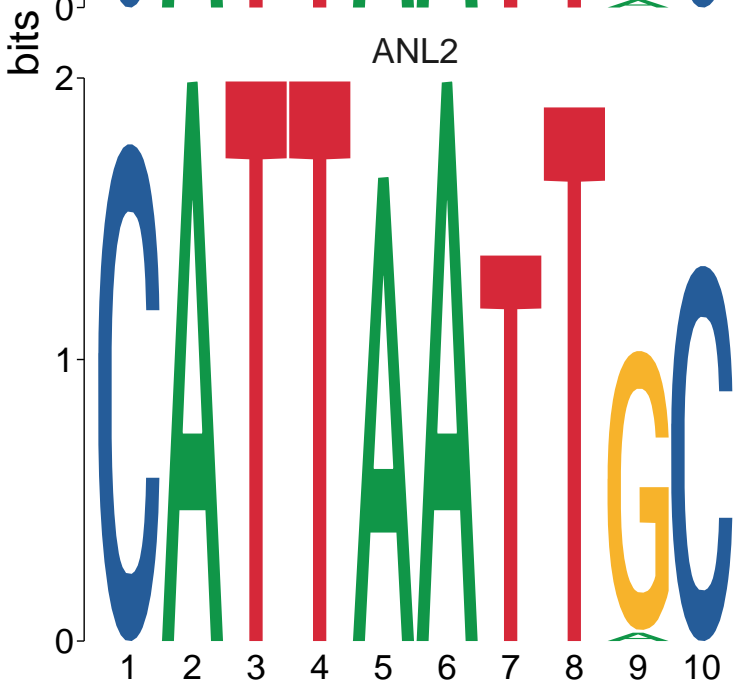
12-ATAAATTACC,BestGuess:mab-5



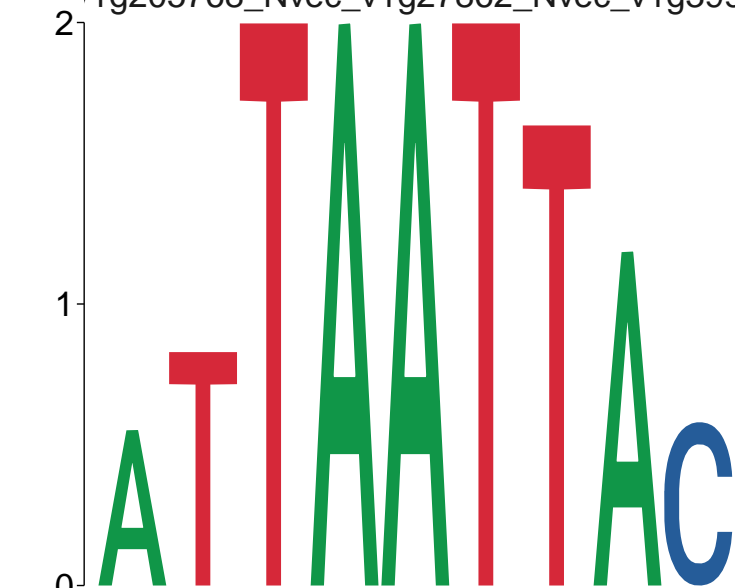
ARCH507_ANL2



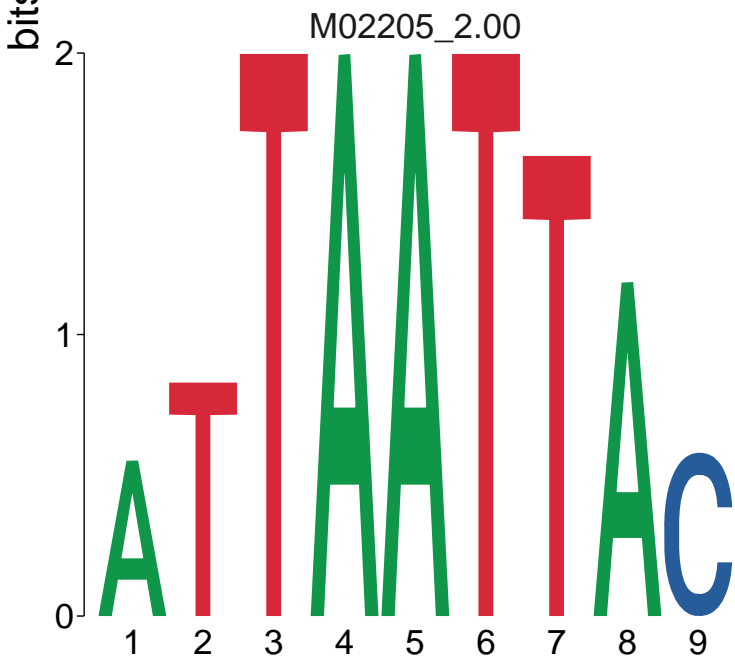
ANL2



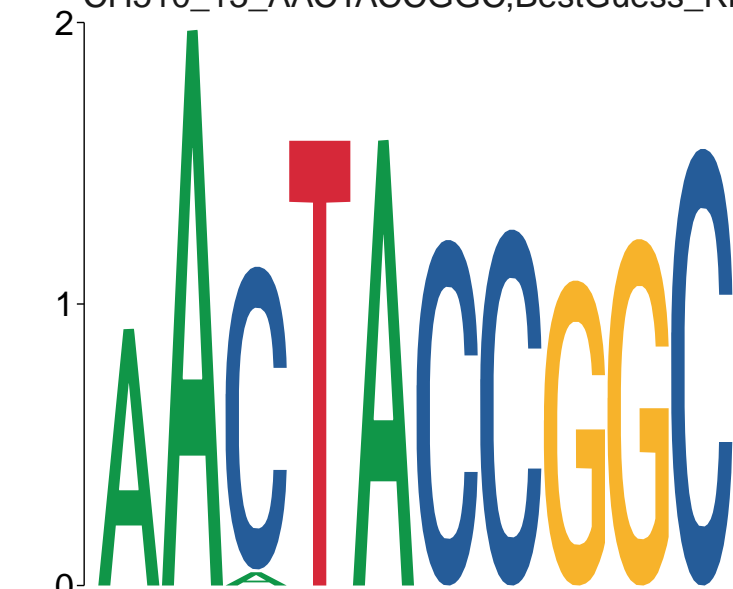
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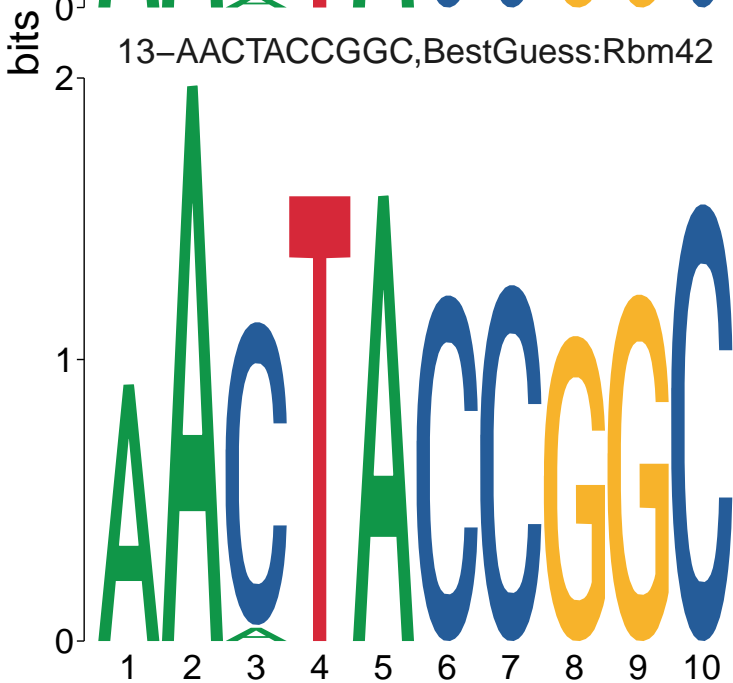
M02205_2.00



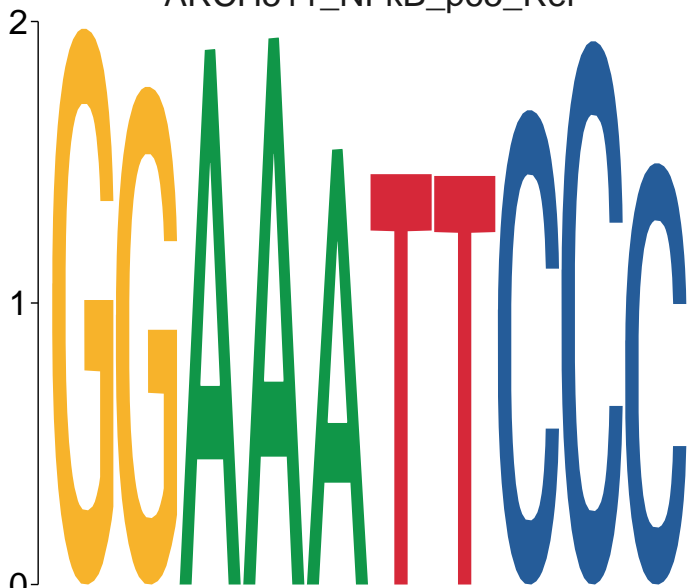
CH510_13_AACTACCGGC,BestGuess_Rb



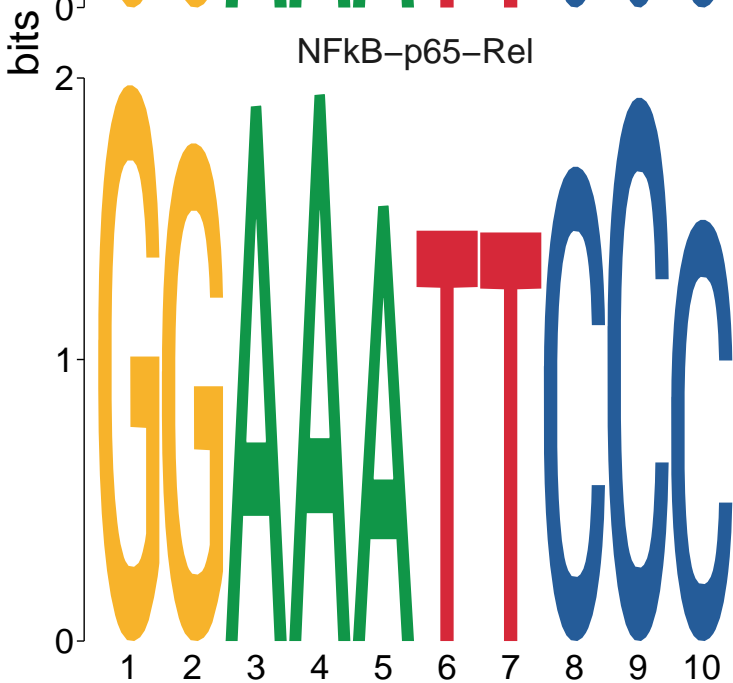
13-AACTACCGGC,BestGuess:Rbm42



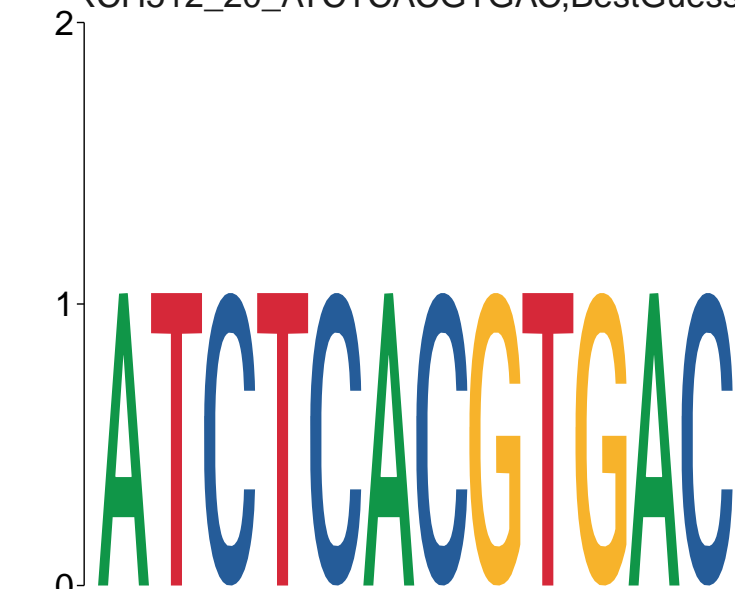
ARCH511_NFkB_p65_Rel



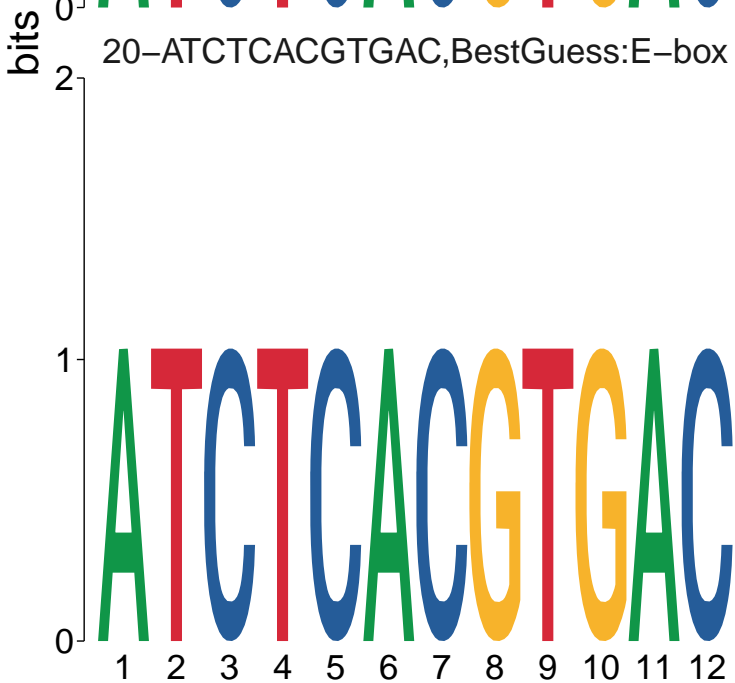
NFkB-p65-Rel



RCH512_20_ATCTCACGTGAC,BestGuess_

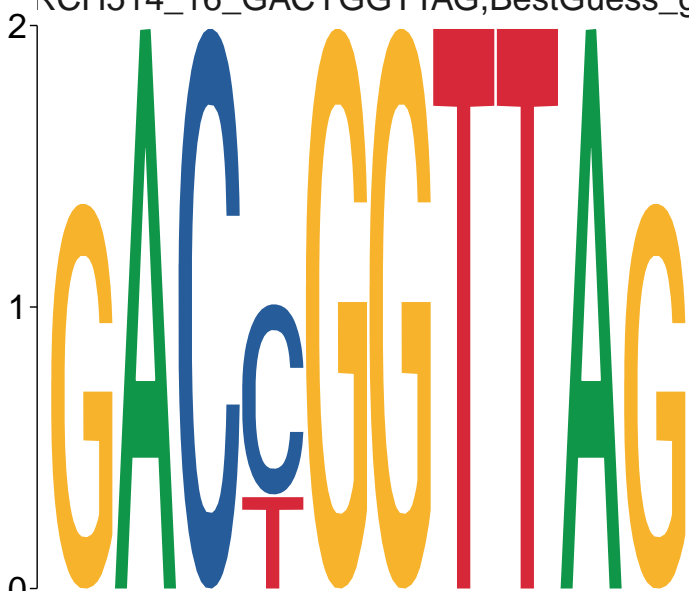


20-ATCTCACGTGAC,BestGuess:E-box

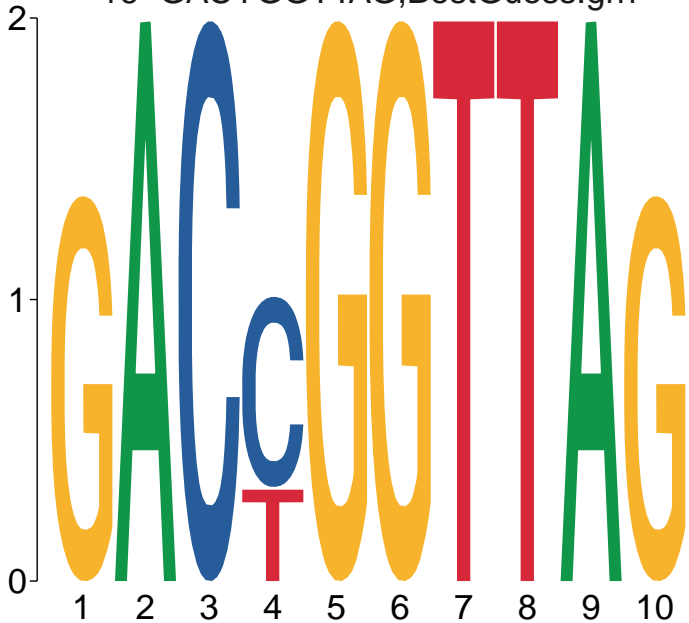


RCH514_16_GACYGGTTAG,BestGuess_g

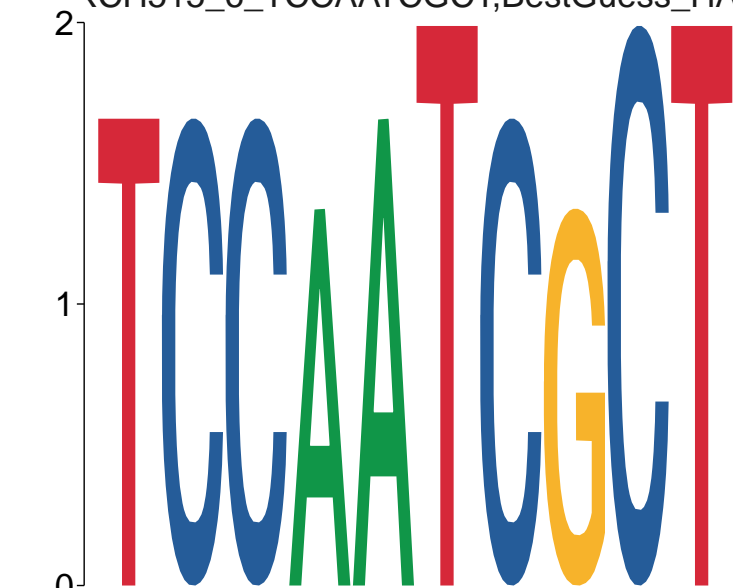
bits



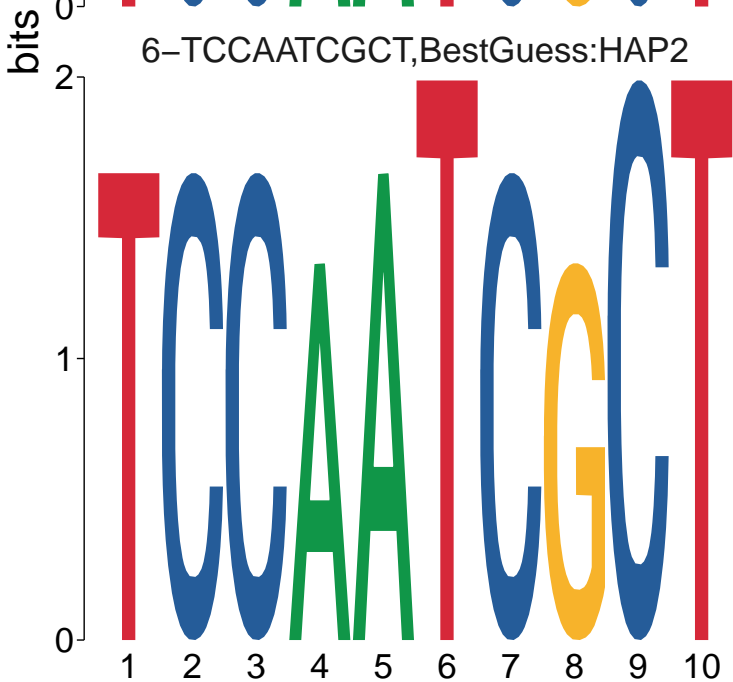
16-GACYGGTTAG,BestGuess:grh



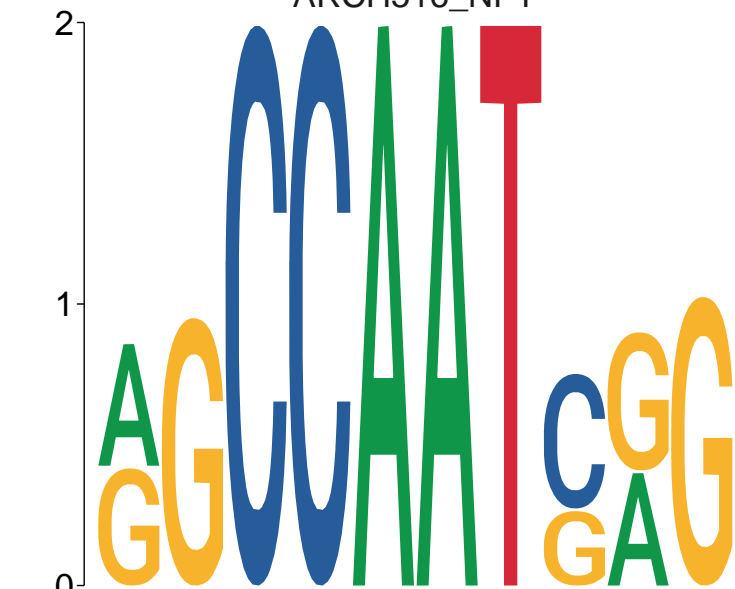
RCH515_6_TCCAATCGCT,BestGuess_HAF



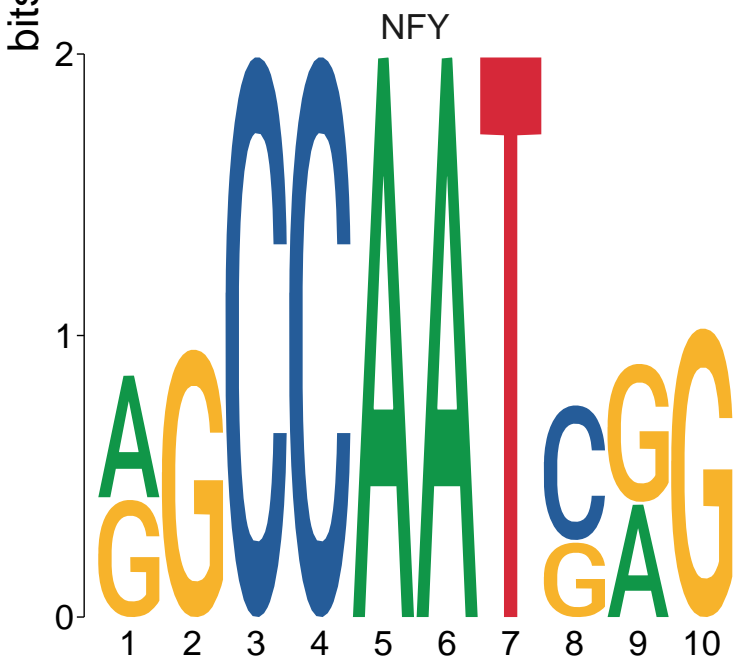
6-TCCAATCGCT,BestGuess:HAP2



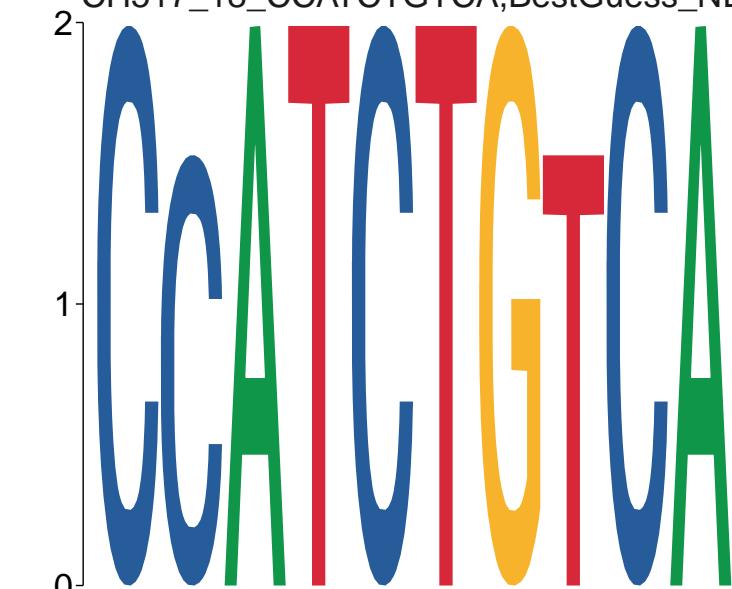
ARCH516_NFY



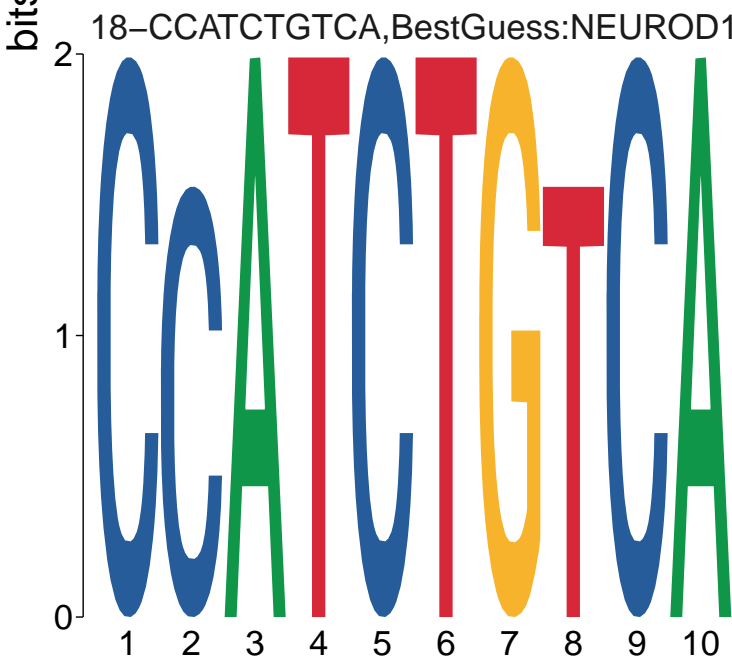
NFY



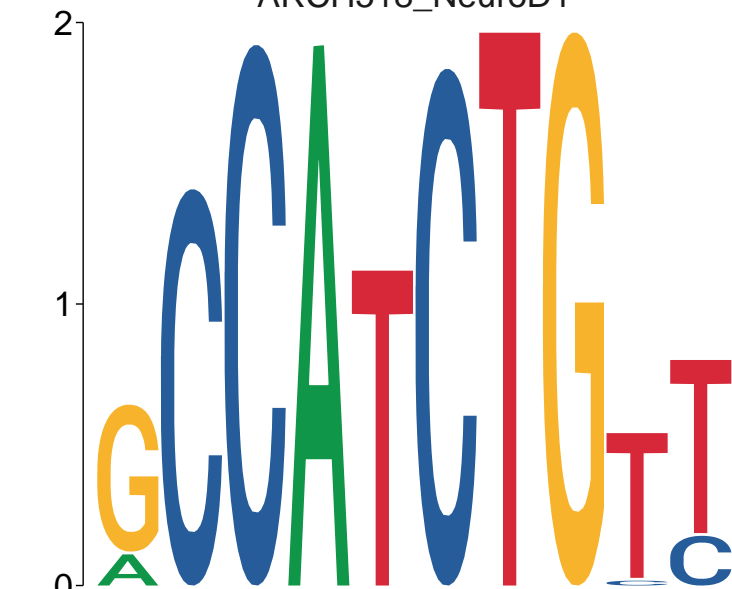
CH517_18_CCATCTGTCA,BestGuess_NE



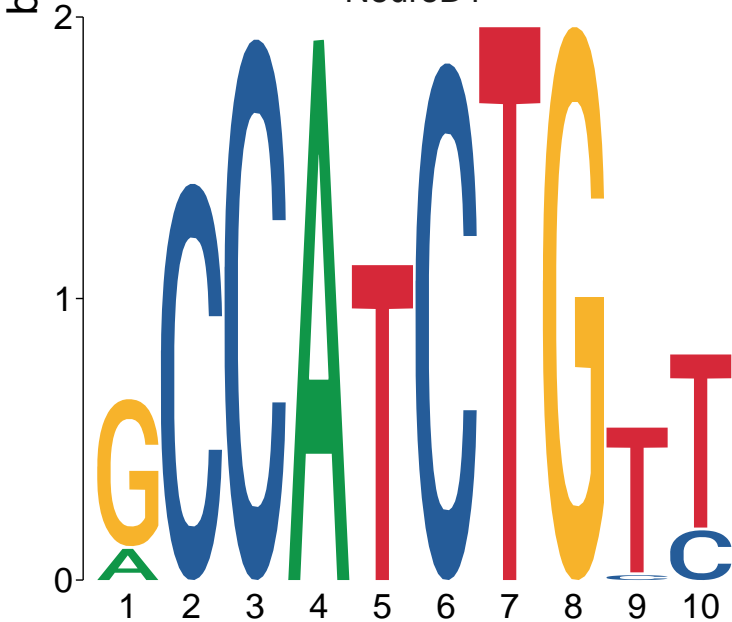
18-CCATCTGTCA,BestGuess:NEUROD1



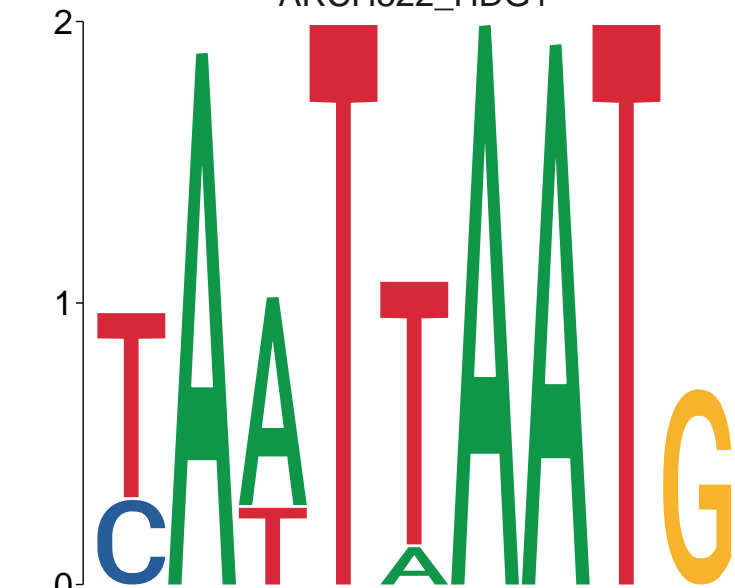
ARCH518_NeuroD1



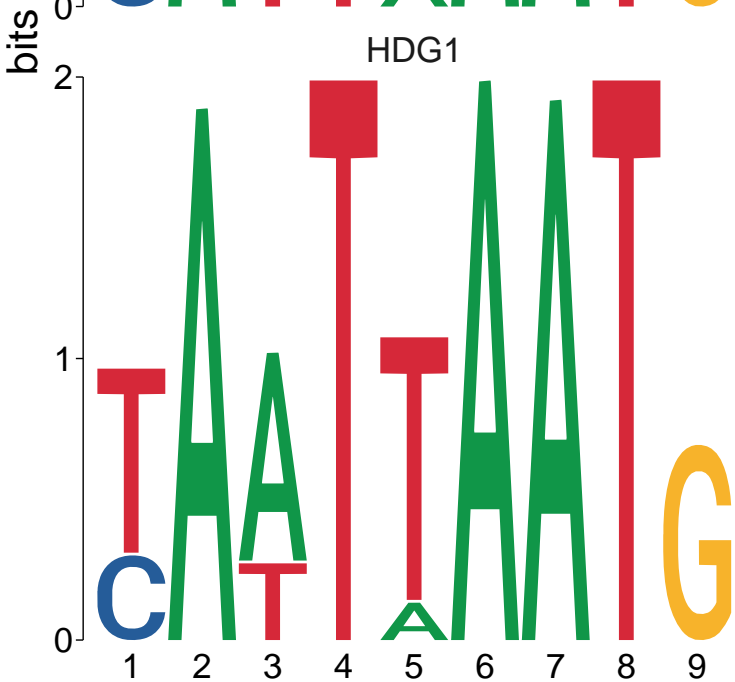
NeuroD1



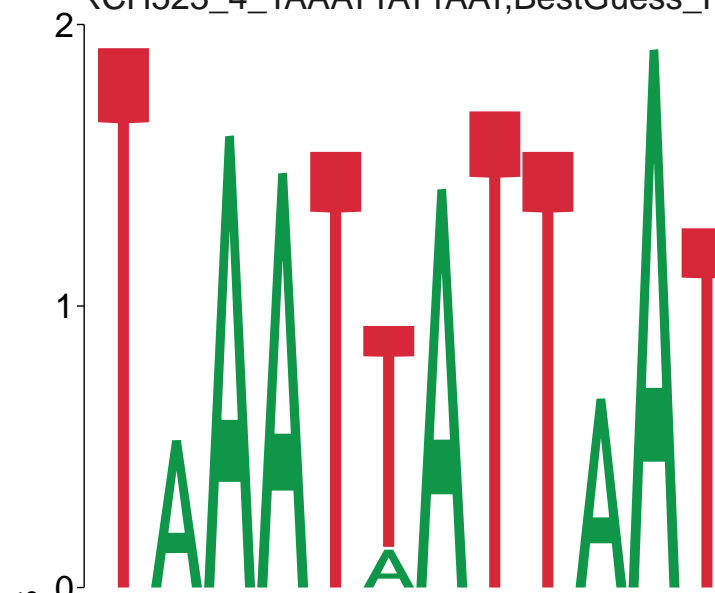
ARCH522_HDG1



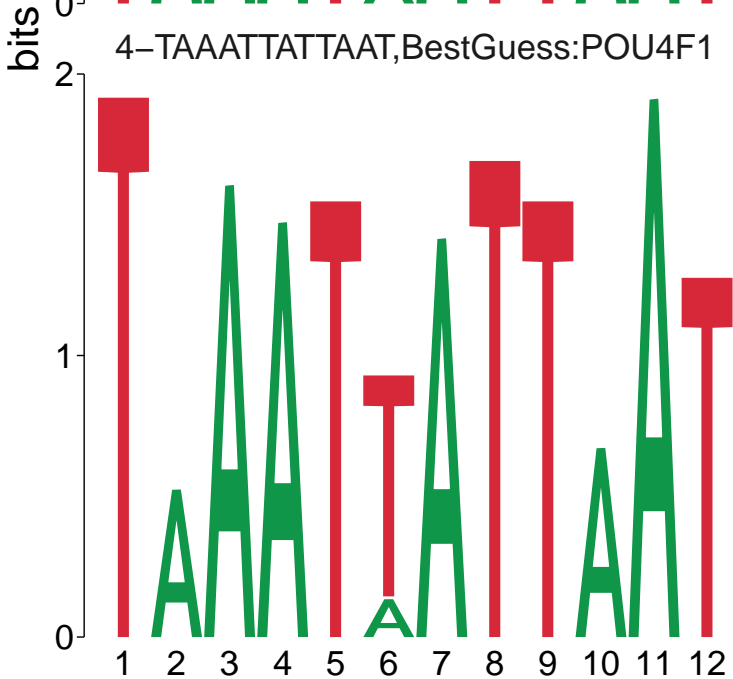
HDG1



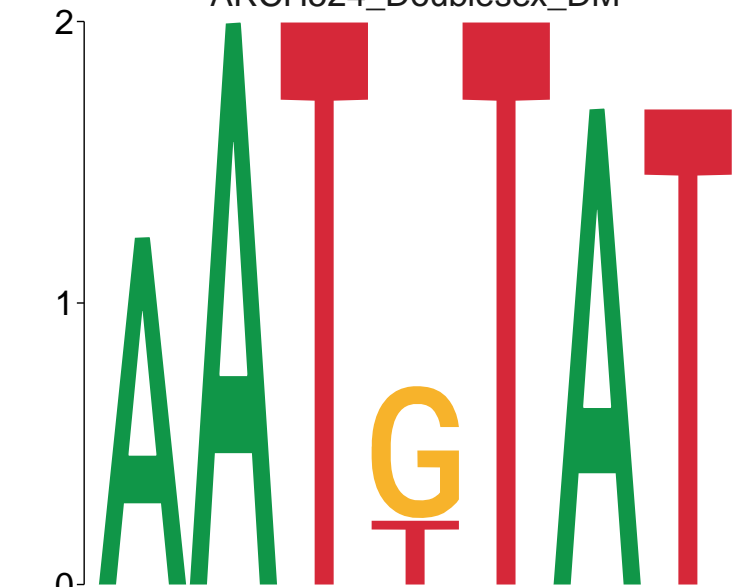
RCH523_4_TAAATTATTAAT,BestGuess_PC



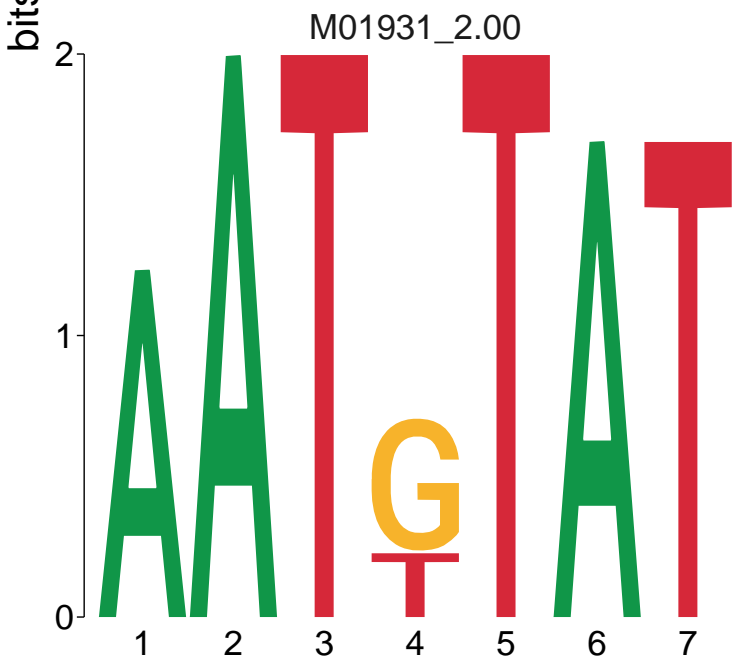
4-TAAATTATTAAT,BestGuess:POU4F1



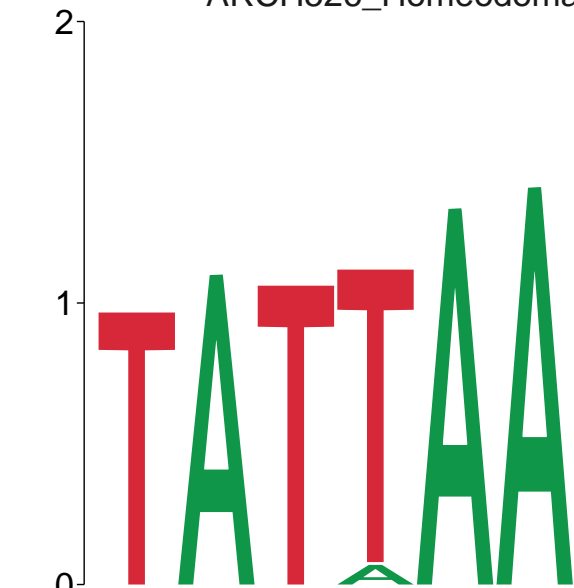
ARCH524_Doublesex_DM



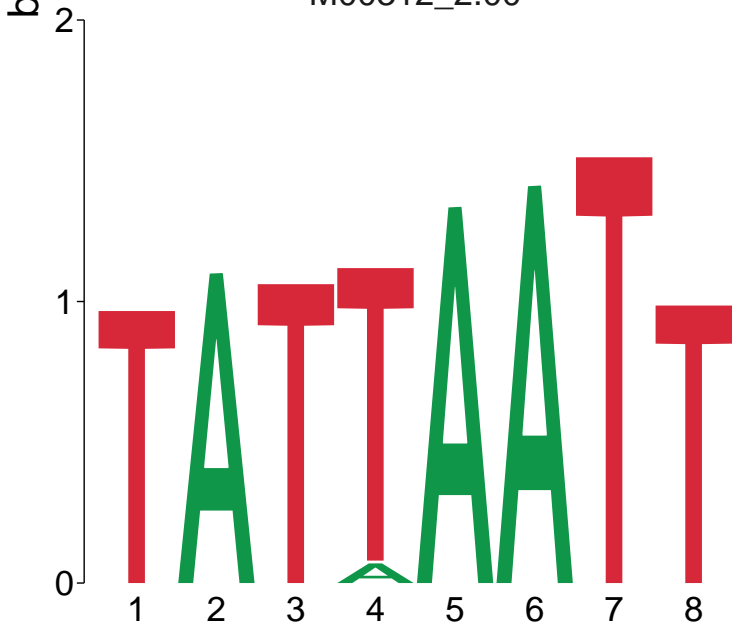
M01931_2.00



ARCH526_Homeodomains



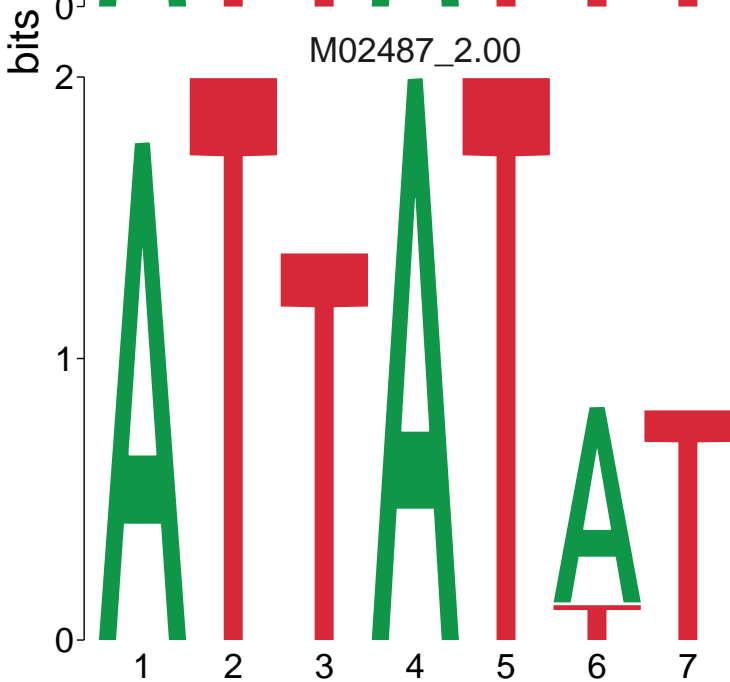
M00312_2.00



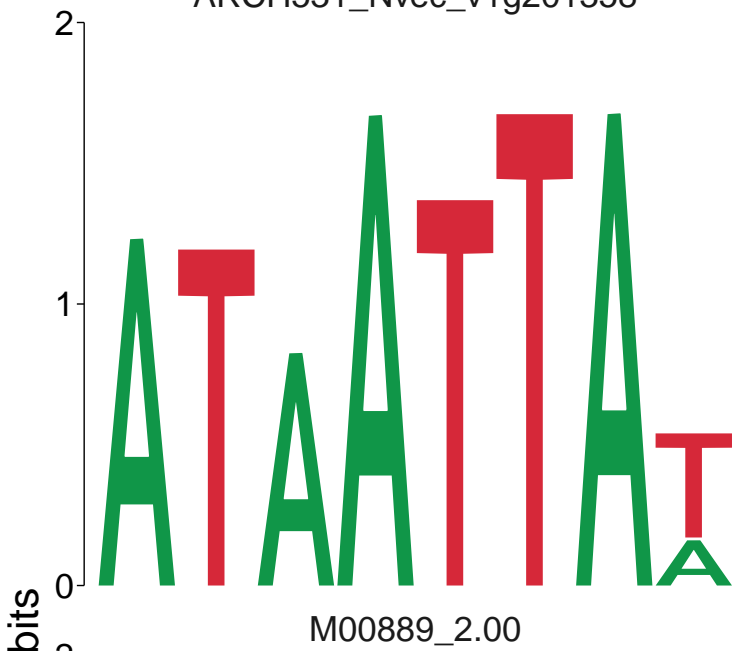
ARCH530_HMGbox_Sox



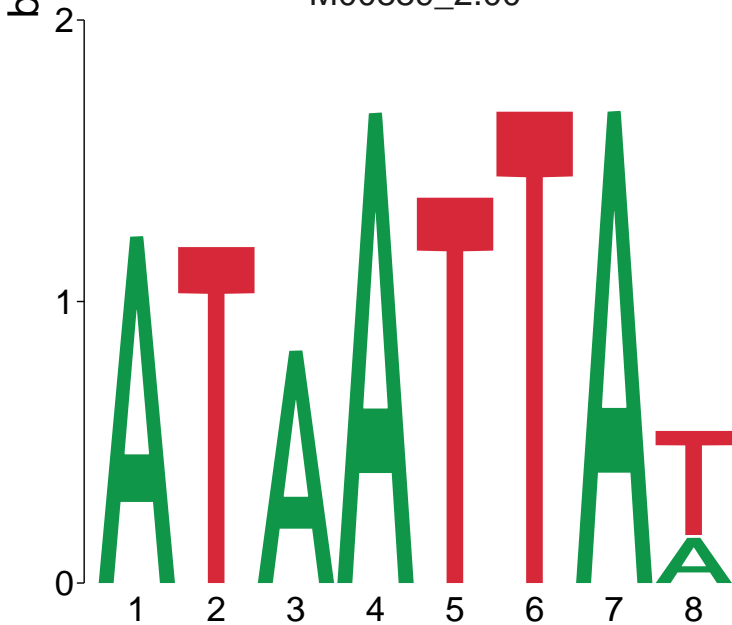
M02487_2.00



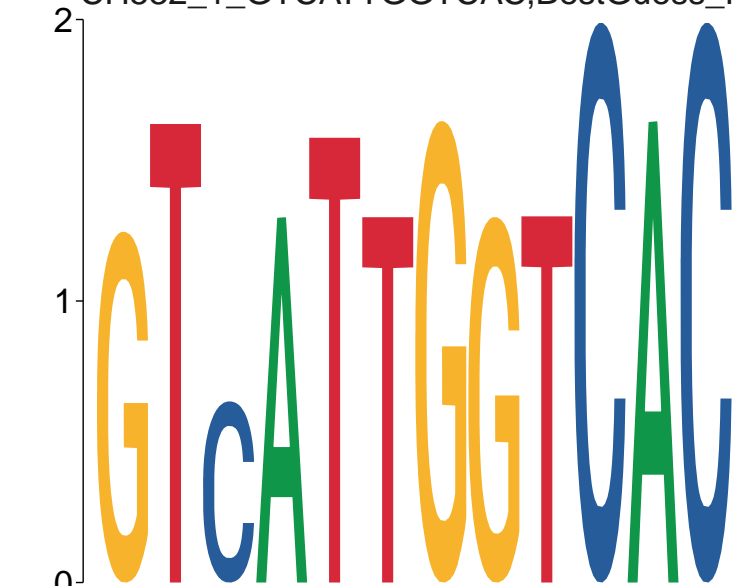
ARCH531_Nvec_v1g201358



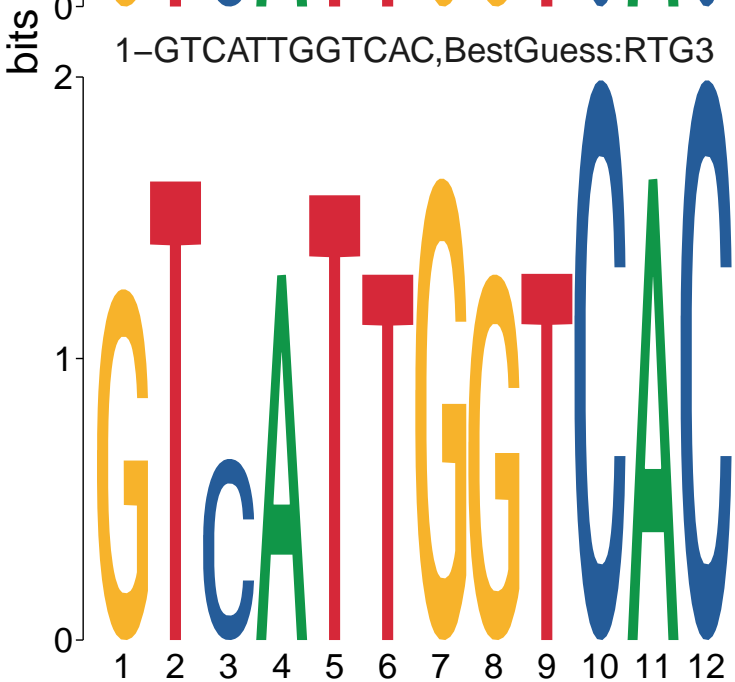
M00889_2.00



CH532_1_GTCATTGGTCAC,BestGuess_R



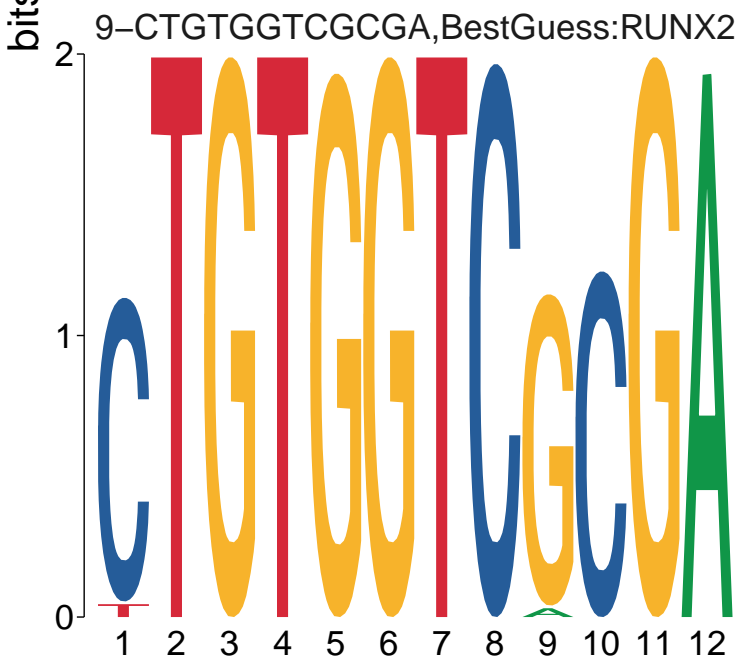
1-GTCATTGGTCAC,BestGuess:RTG3



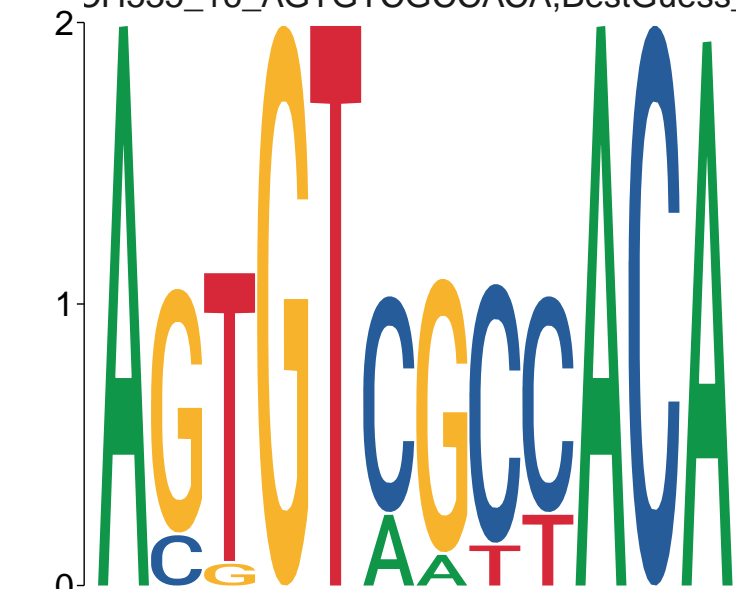
CH534_9_CTGTGGTCGCGA,BestGuess_F



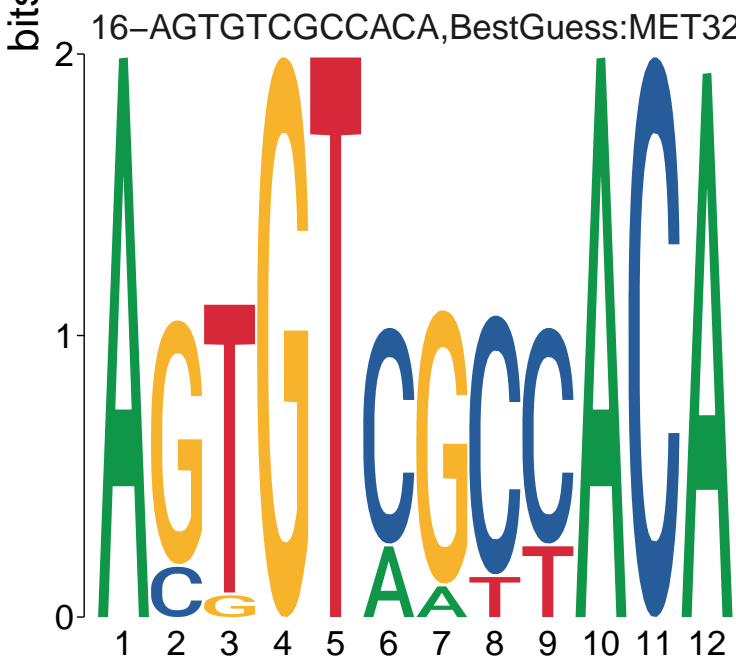
9-CTGTGGTCGCGA,BestGuess:RUNX2



CH535_16_AGTGTCGCCACA,BestGuess_



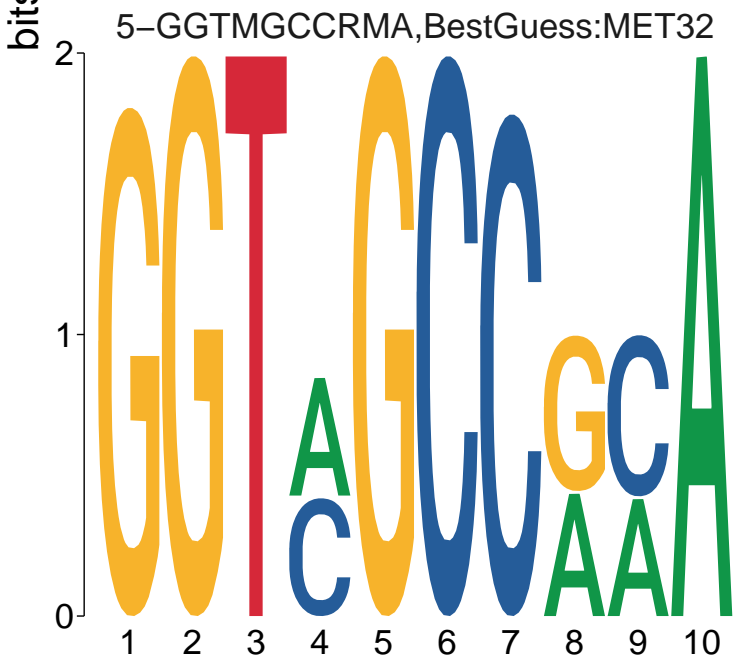
16-AGTGTCGCCACA,BestGuess:MET32



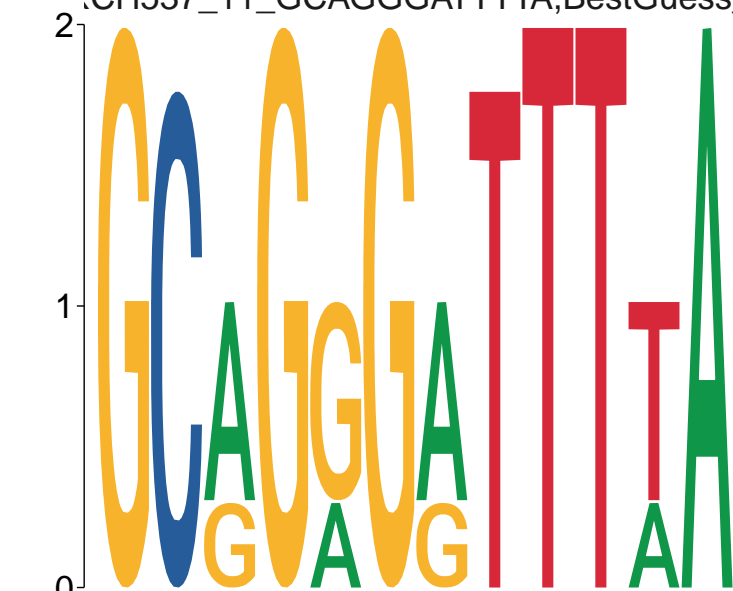
CH536_5_GGTMGCCRMA,BestGuess_ME



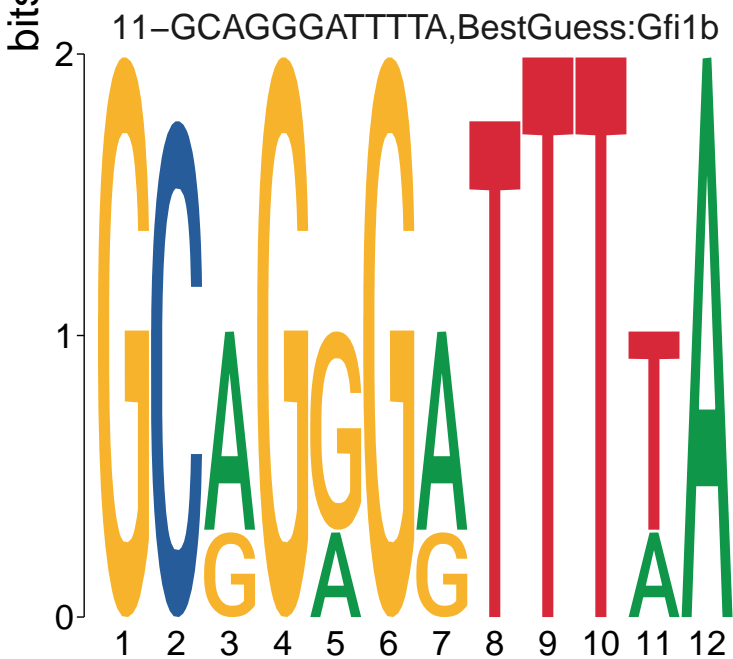
5-GGTMGCCRMA,BestGuess:MET32



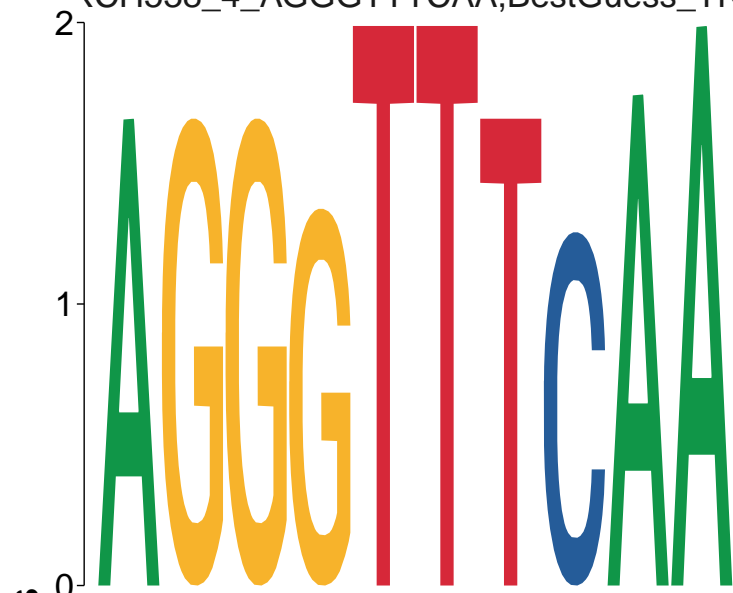
CH537_11_GCAGGGATTTTA,BestGuess_



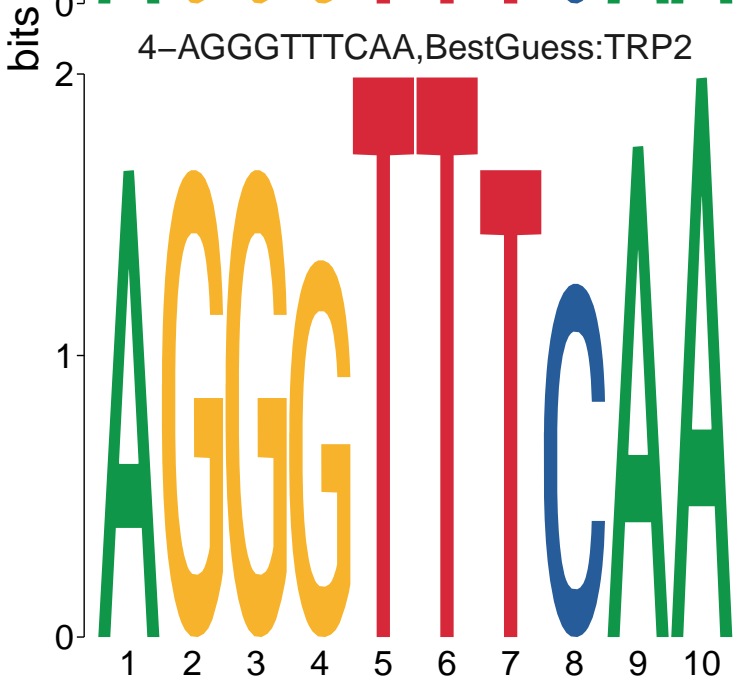
11-GCAGGGATTTTA,BestGuess:Gfi1b



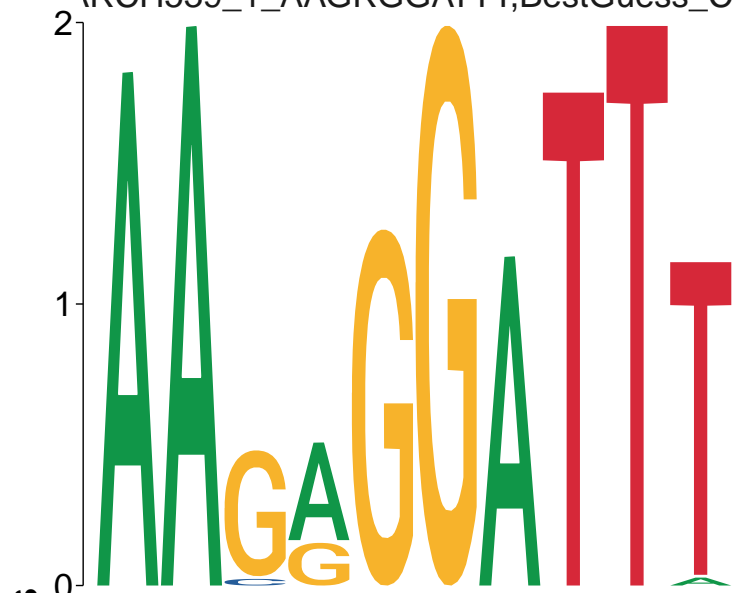
TRCH538_4_AGGGTTTCAA,BestGuess_TRP



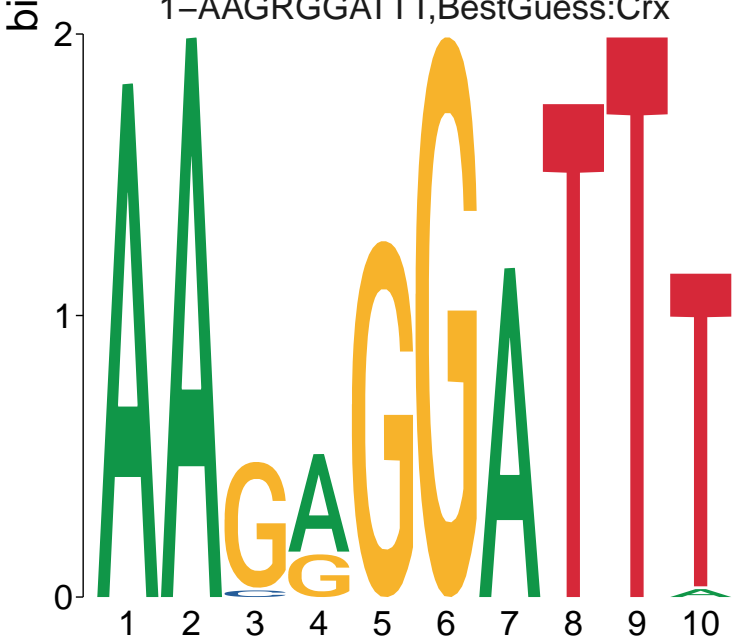
4-AGGGTTTCAA,BestGuess:TRP2



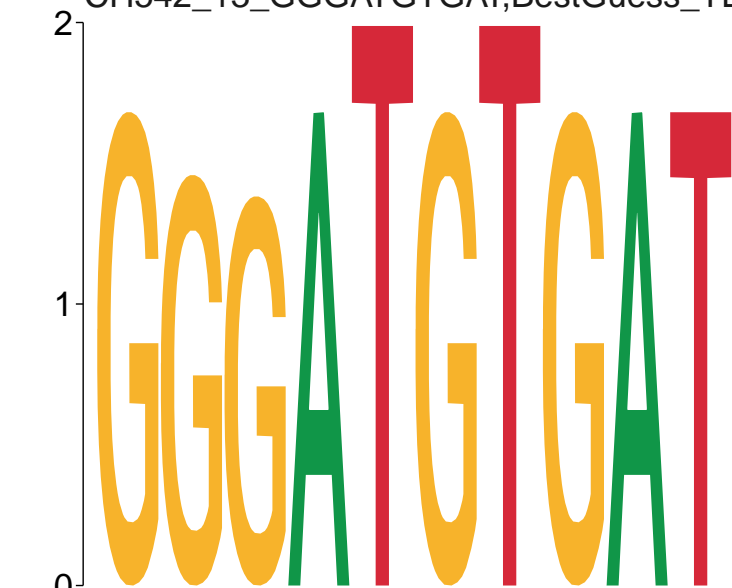
RCH539_1_AAGRGGATTT,BestGuess_Cr



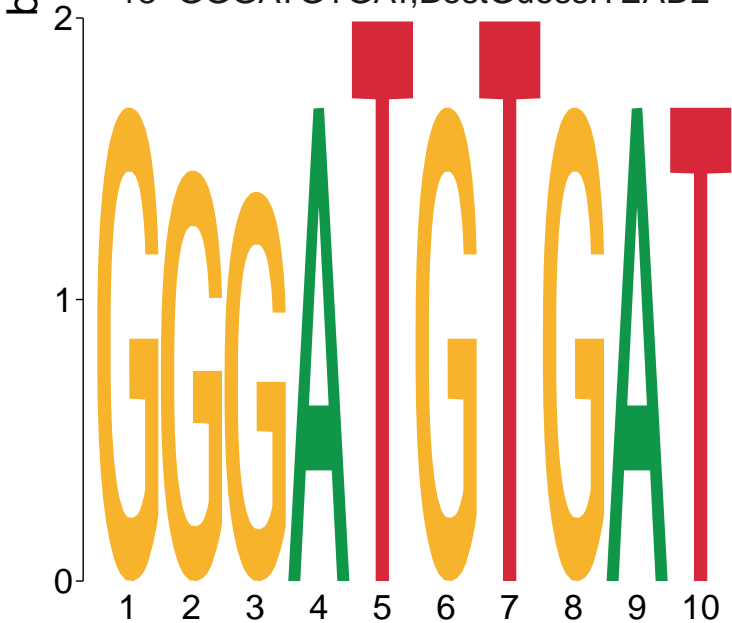
1-AAGRGGATTT,BestGuess:Crx



CH542_13_GGGATGTGAT,BestGuess_TE.



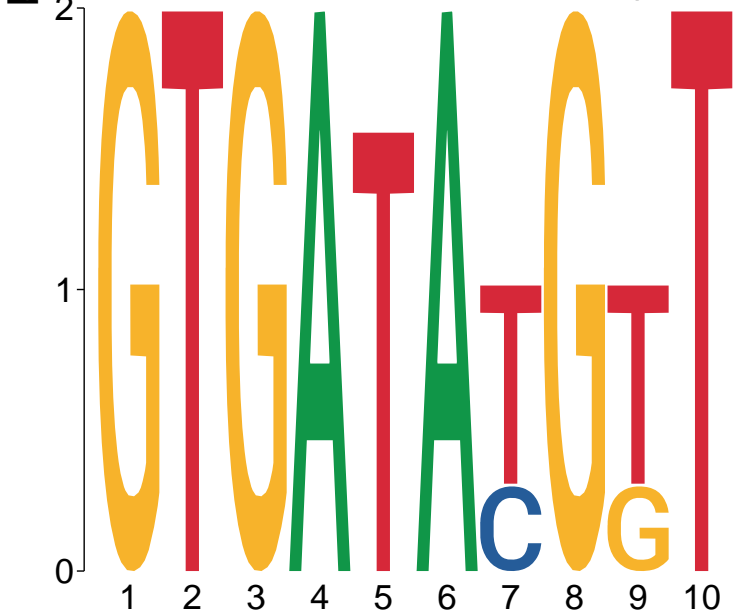
13-GGGATGTGAT,BestGuess:TEAD2



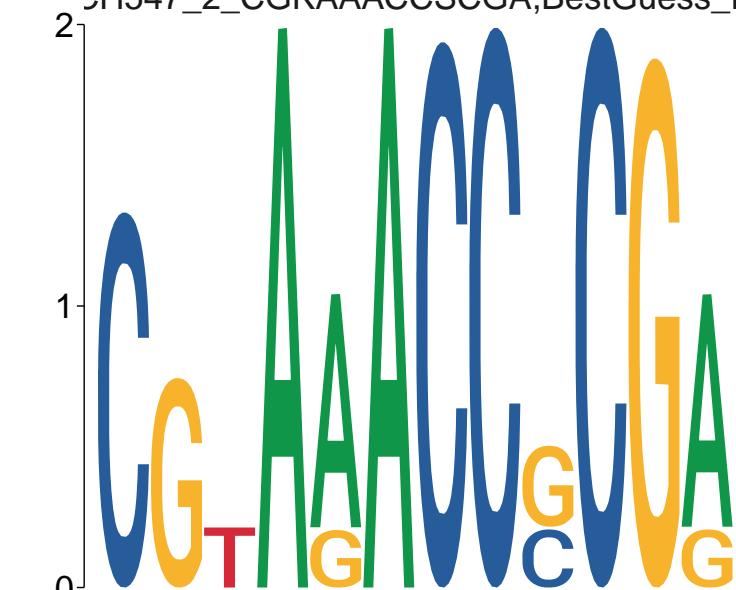
RCH545_18_GTGATATGTT,BestGuess_Op



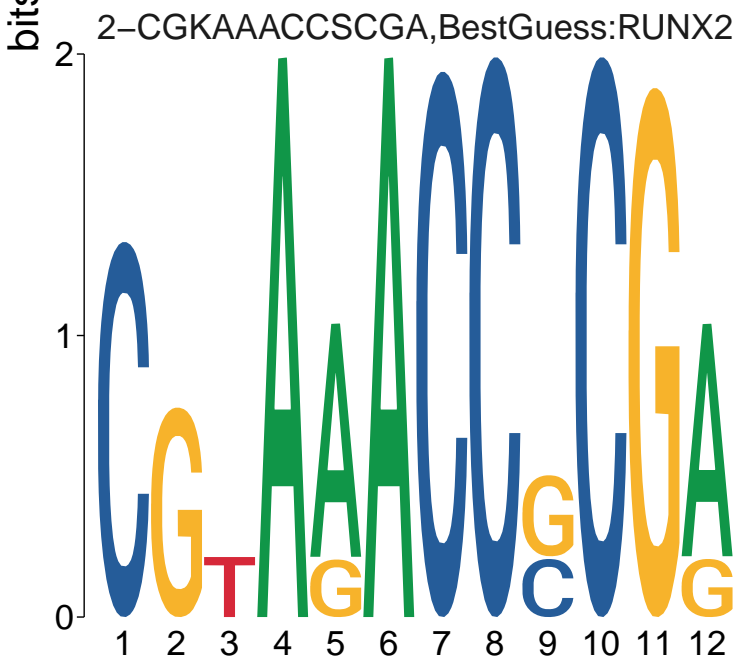
18-GTGATATGTT,BestGuess:Optix



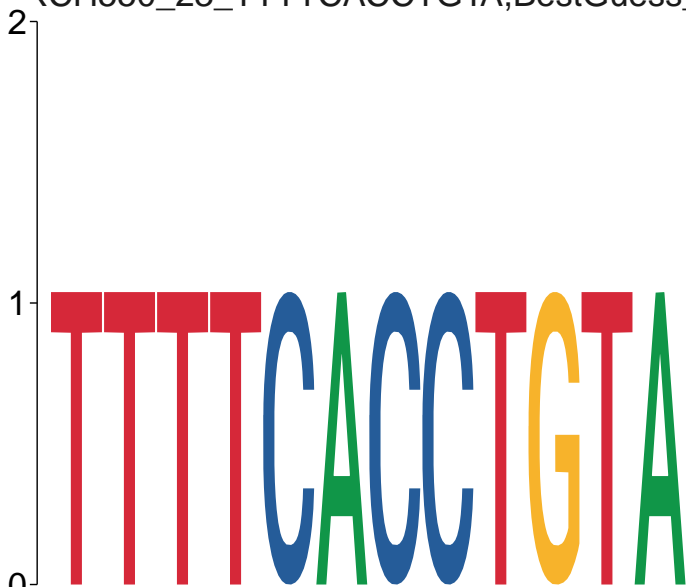
CH547_2_CGKAAACCSCGA,BestGuess_F



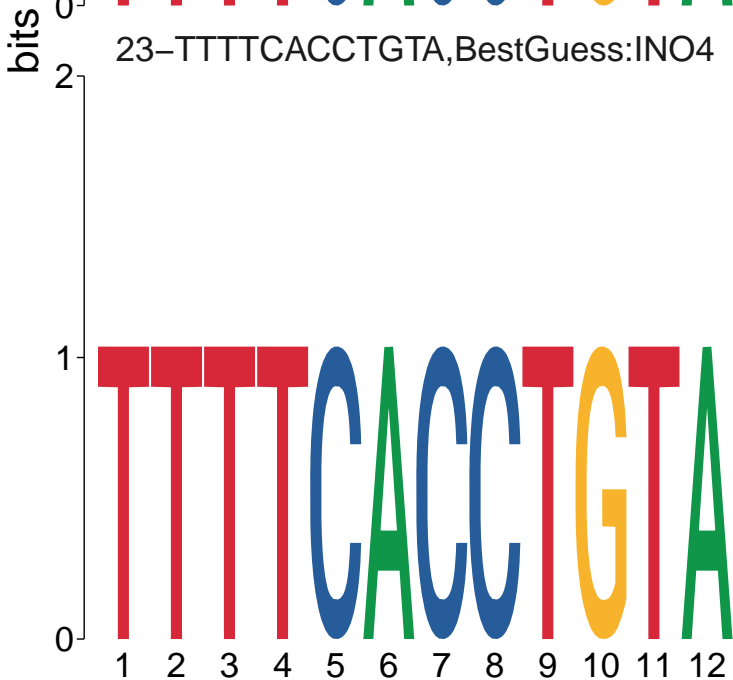
2-CGKAAACCSCGA,BestGuess:RUNX2



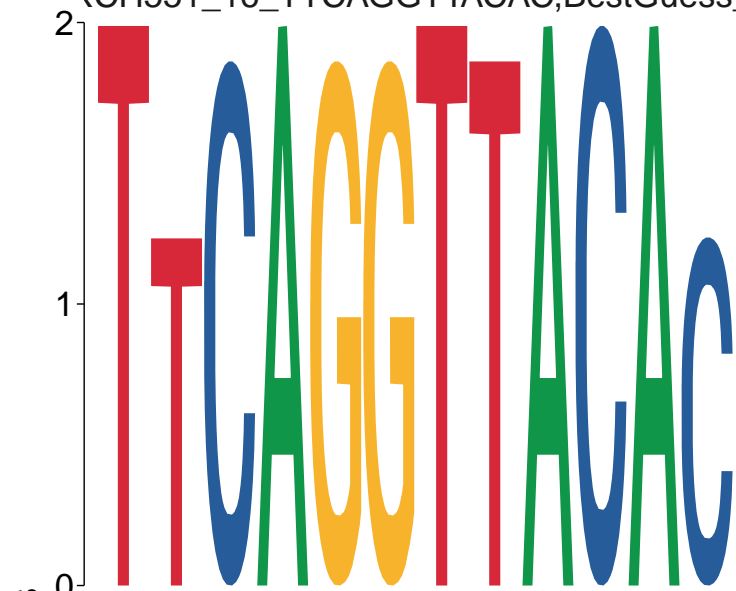
RCH550_23_TTTTCACCTGTA,BestGuess_



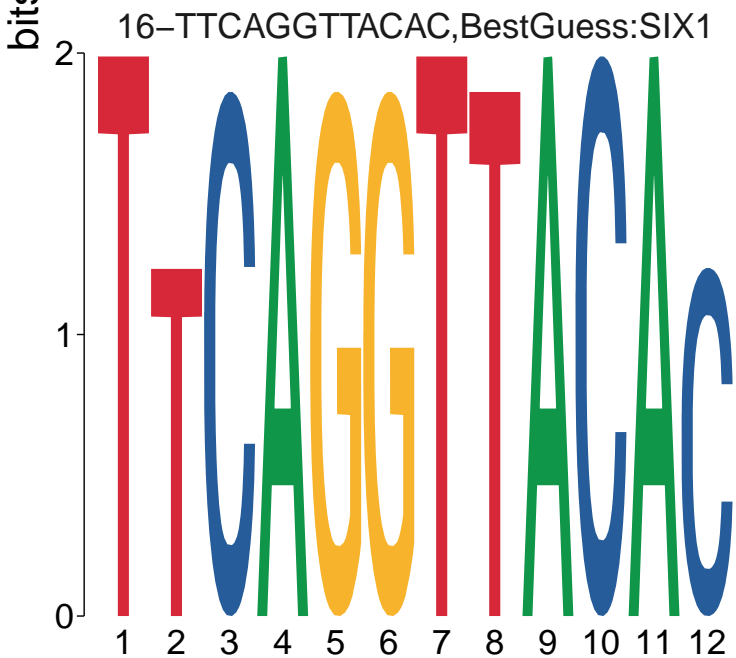
23-TTTTCACCTGTA,BestGuess:INO4



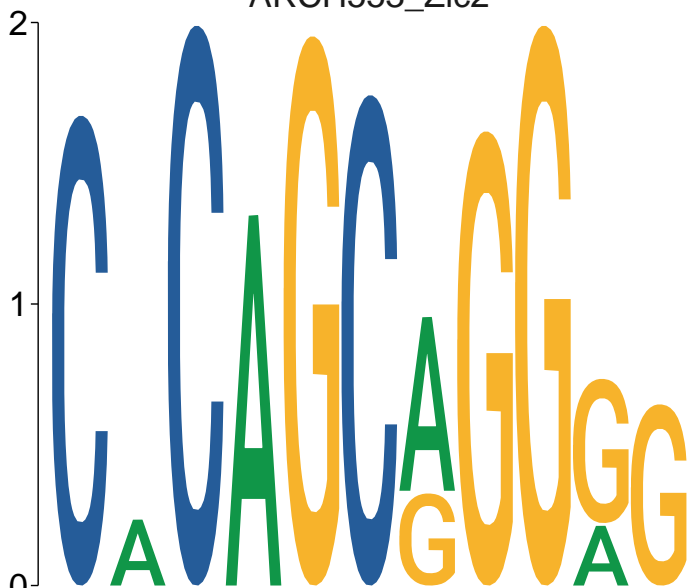
CH551_16_TTCAGGTTACAC,BestGuess_



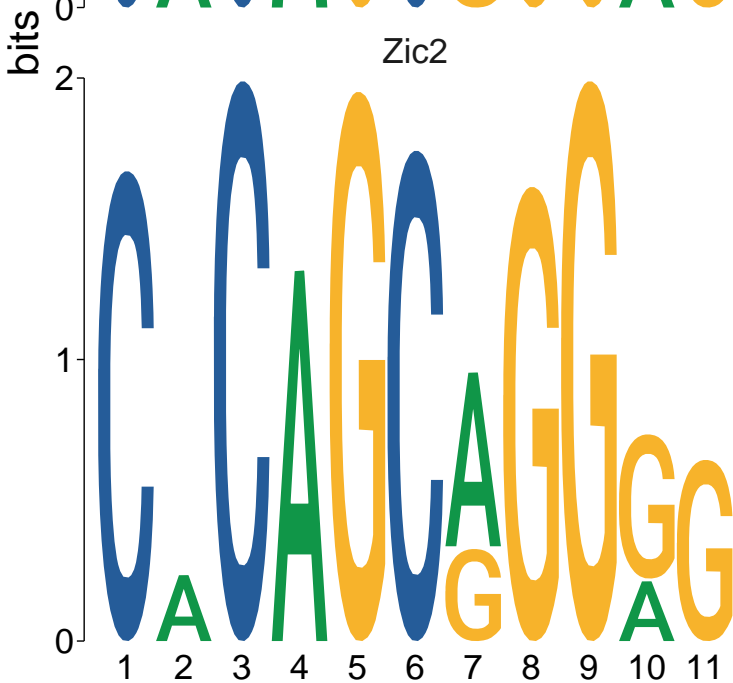
16-TTCAGGTTACAC,BestGuess:SIX1



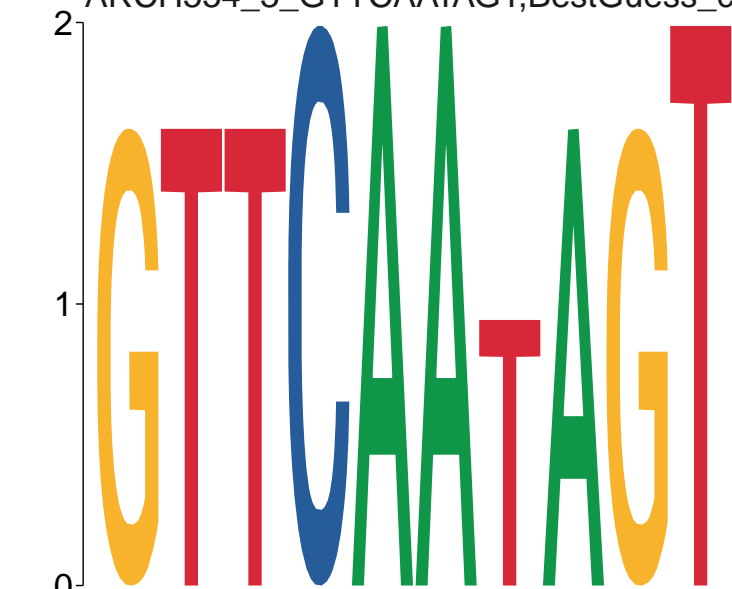
ARCH553_Zic2



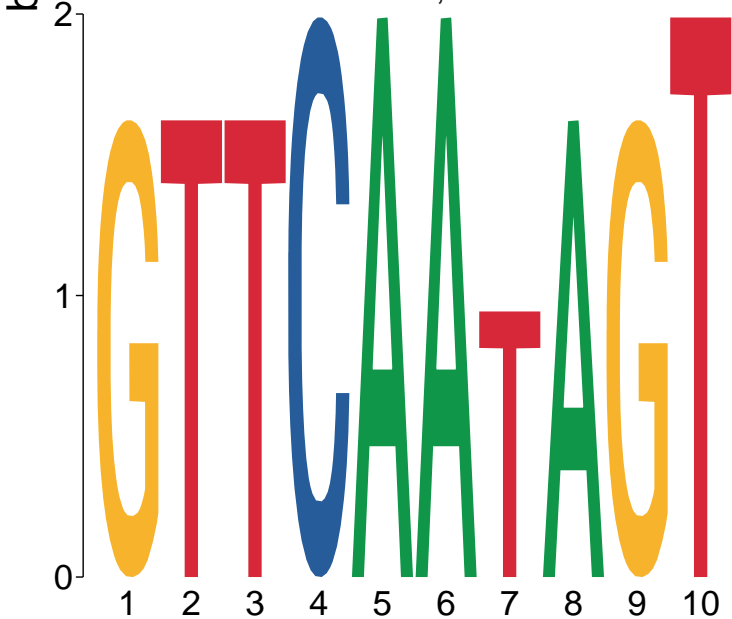
Zic2



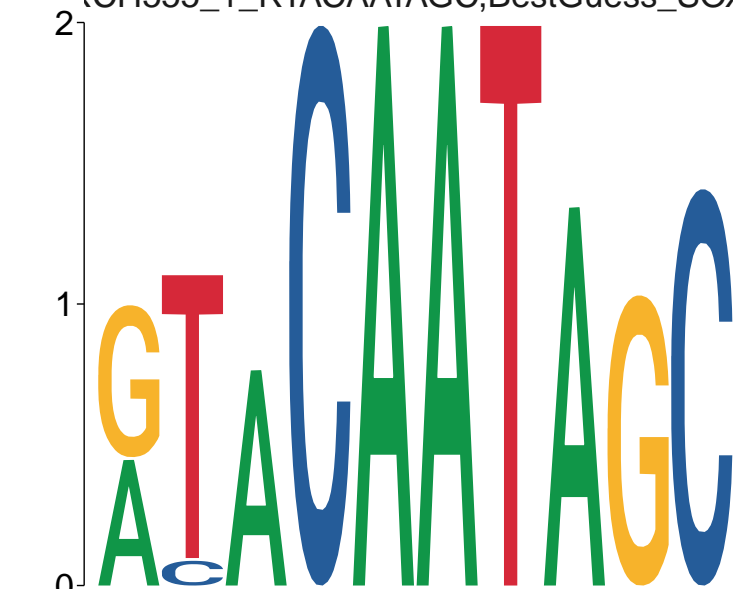
ARCH554_3_GTTCAATAGT,BestGuess_ct



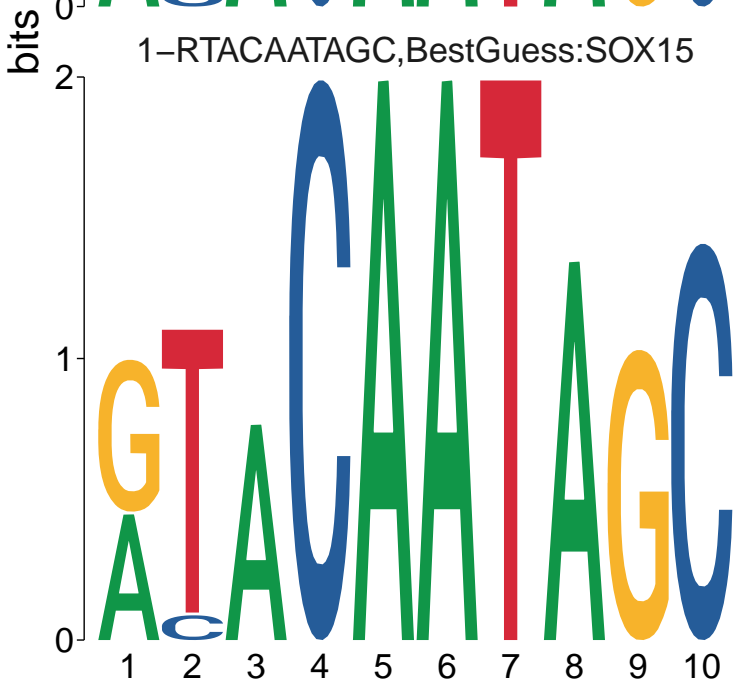
3-GTTCAATAGT,BestGuess:ct



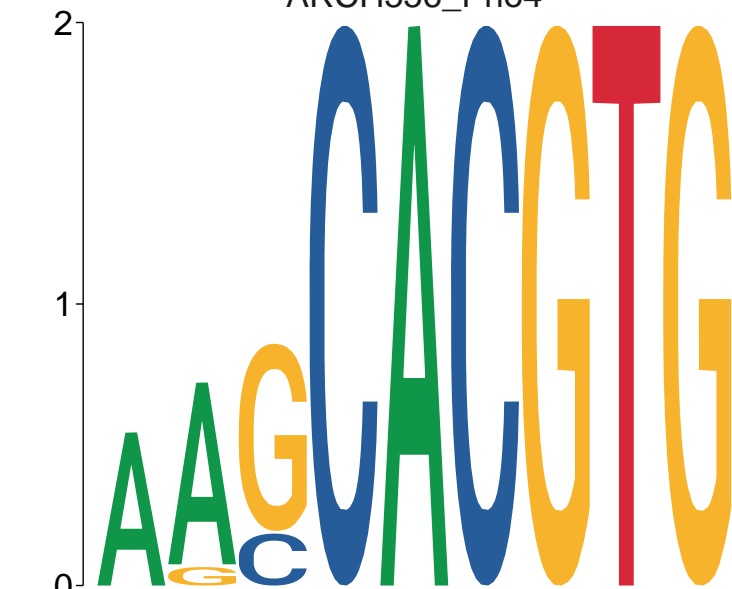
CH555_1_RTACAATAGC,BestGuess_SOX



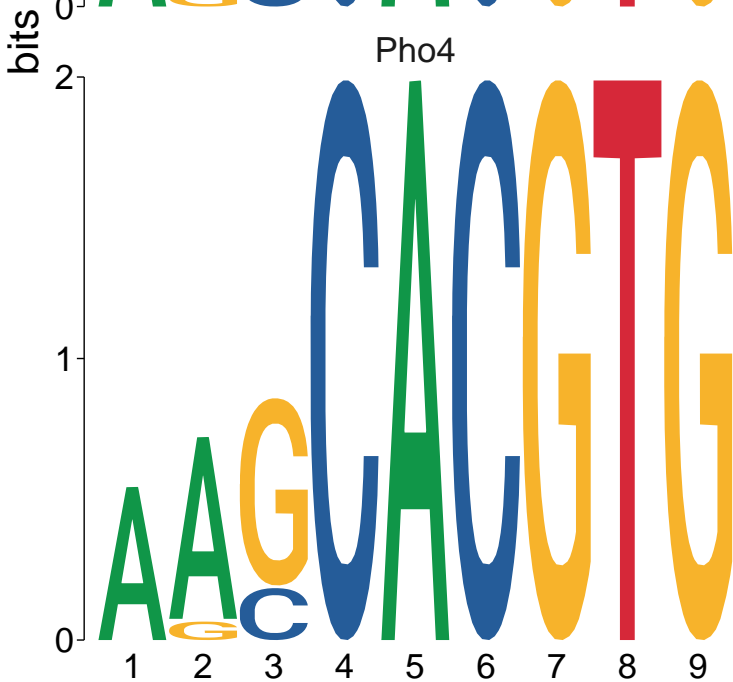
1-RTACAATAGC,BestGuess:SOX15



ARCH556_Ph04



Pho4



ARCH558_Fra2_At3_Fra1



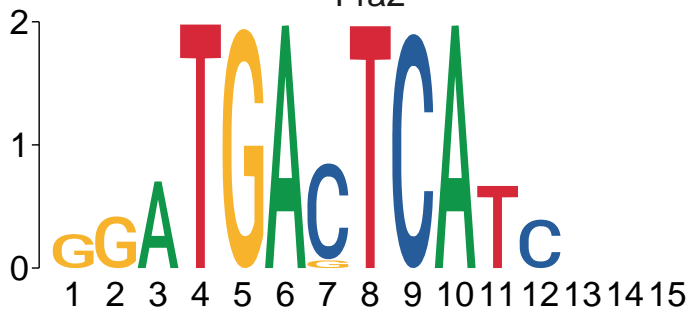
Fra1



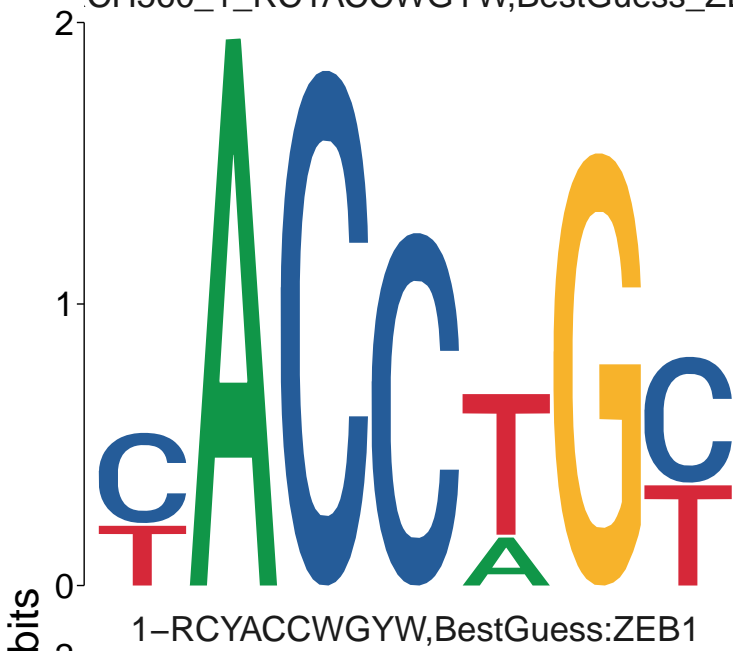
Atf3



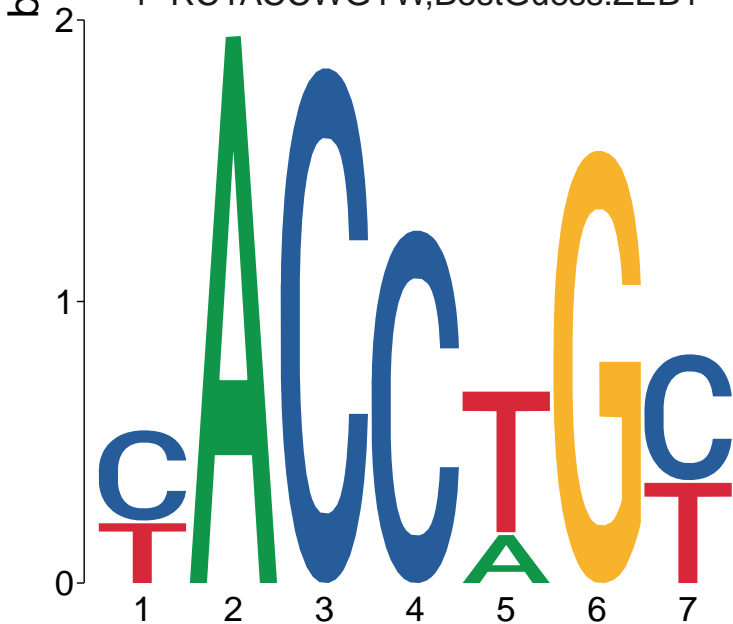
Fra2



CH560_1_RCYACCWGYW,BestGuess_ZE



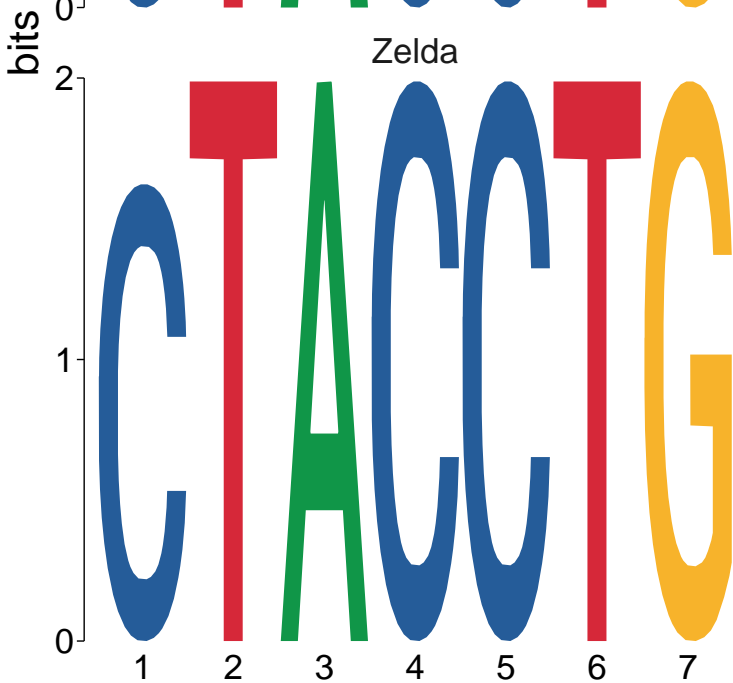
1-RCYACCWGYW,BestGuess:ZEB1



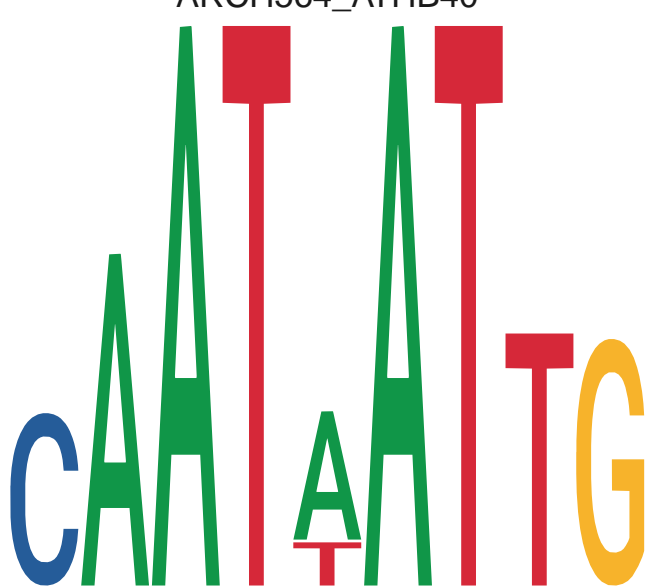
ARCH561_Zelda



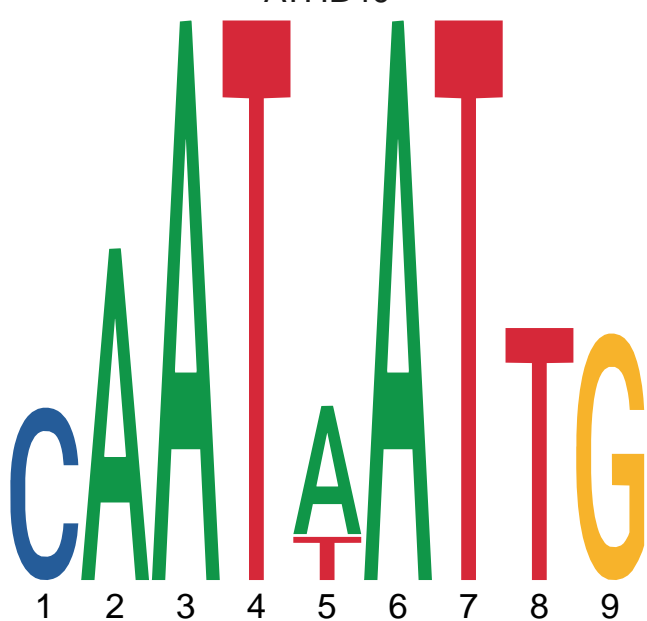
Zelda



ARCH564_ATHB40



ATHB40



CH565_RUNX1_RUNX1_RUNX_AML_RUI



RUNX



RUNX-AML



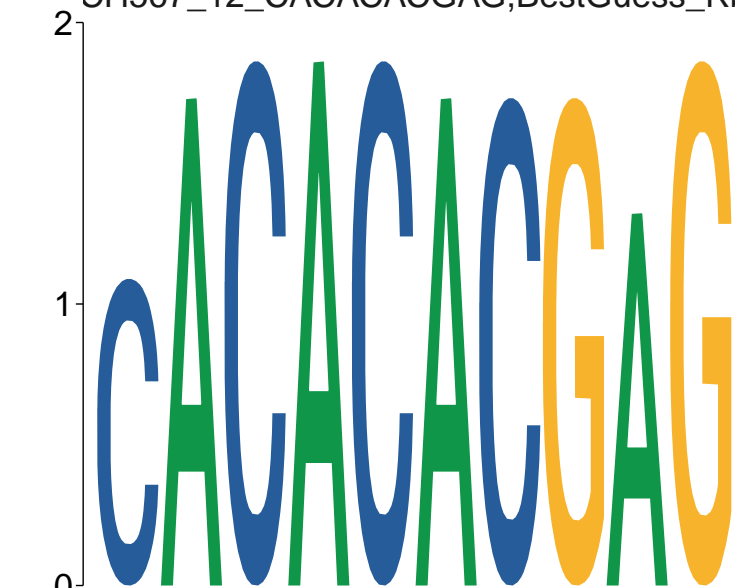
RUNX1



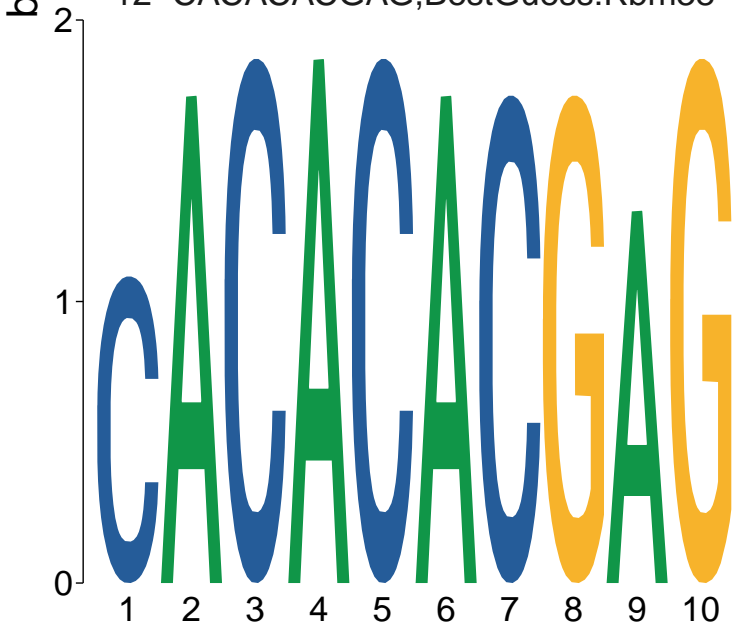
RUNX1.1



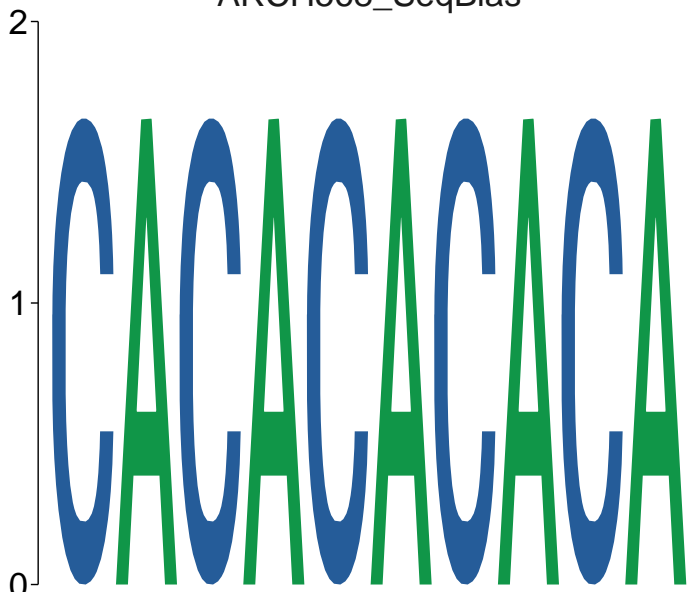
CH567_12_CACACACGAG,BestGuess_Rb



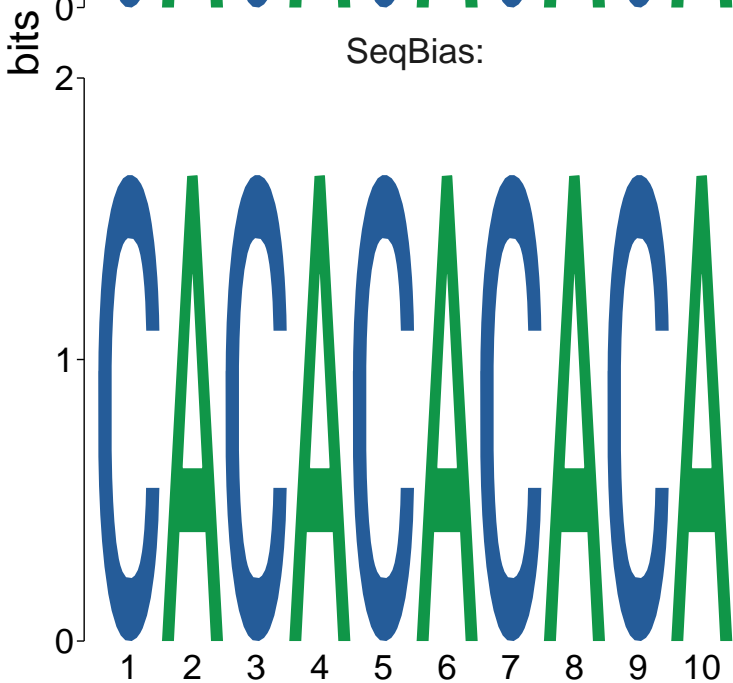
12-CACACACGAG,BestGuess:Rbm38



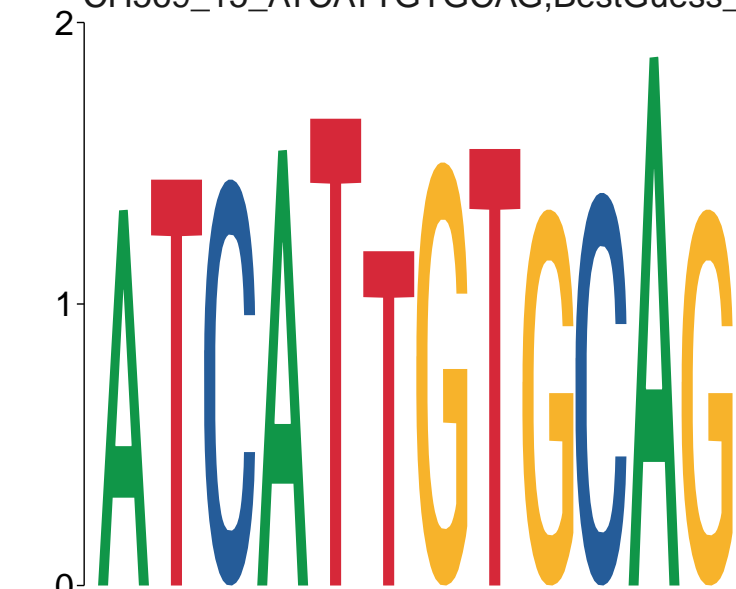
ARCH568_SeqBias



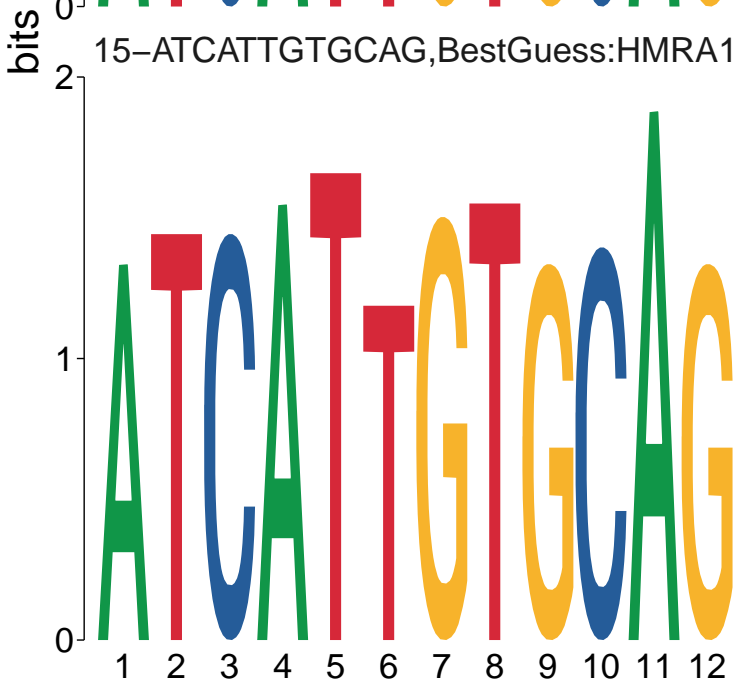
SeqBias:



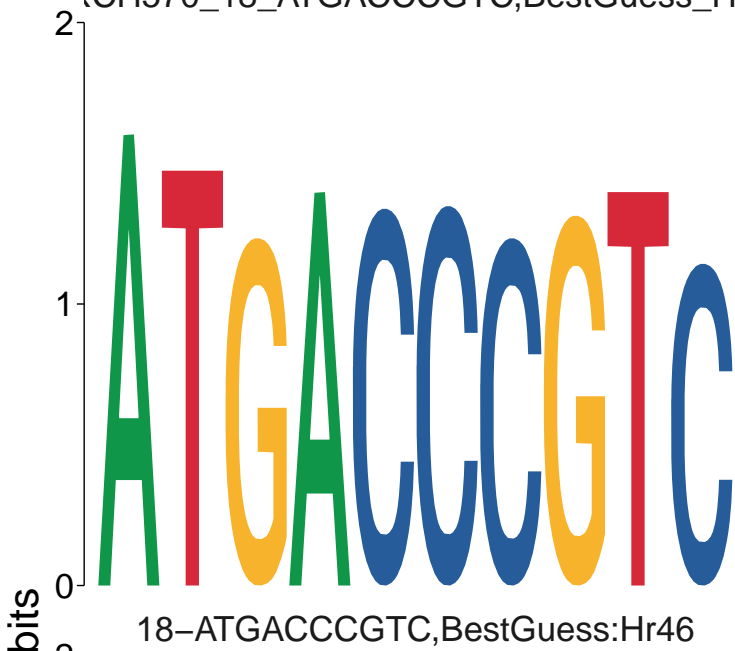
CH569_15_ATCATTGTGCAG,BestGuess_I



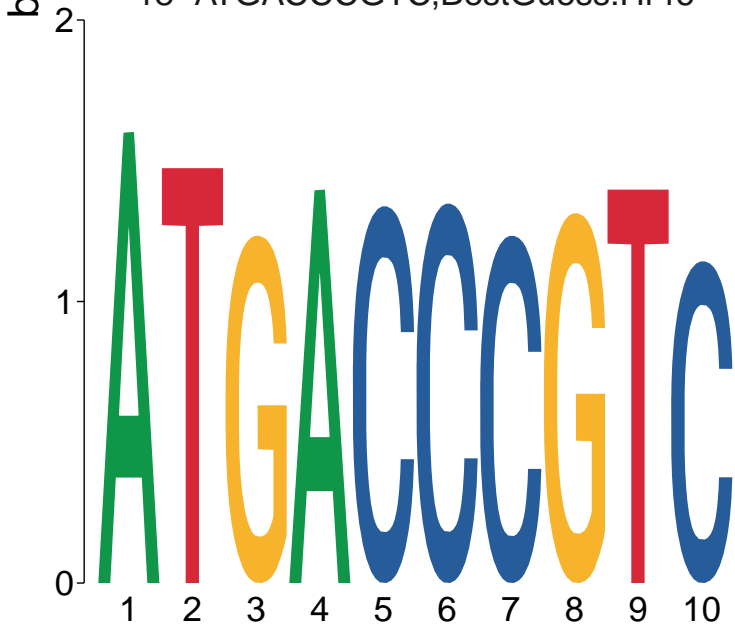
15-ATCATTGTGCAG,BestGuess:HMRA1



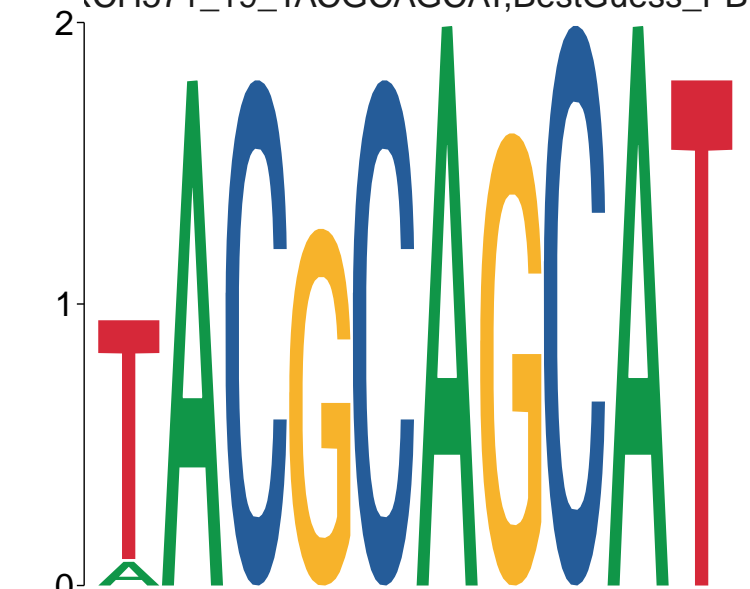
CH570_18_ATGACCCGTC,BestGuess_Hr



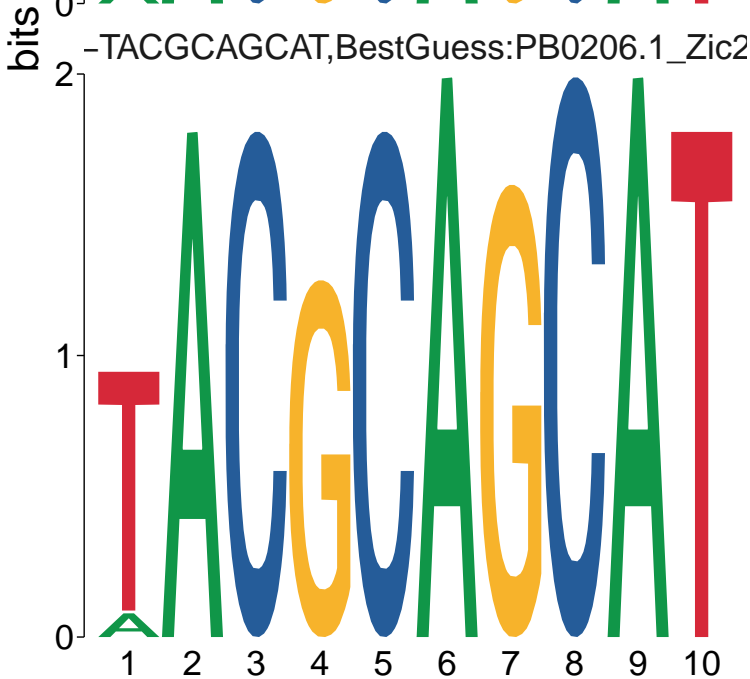
18-ATGACCCGTC,BestGuess:Hr46



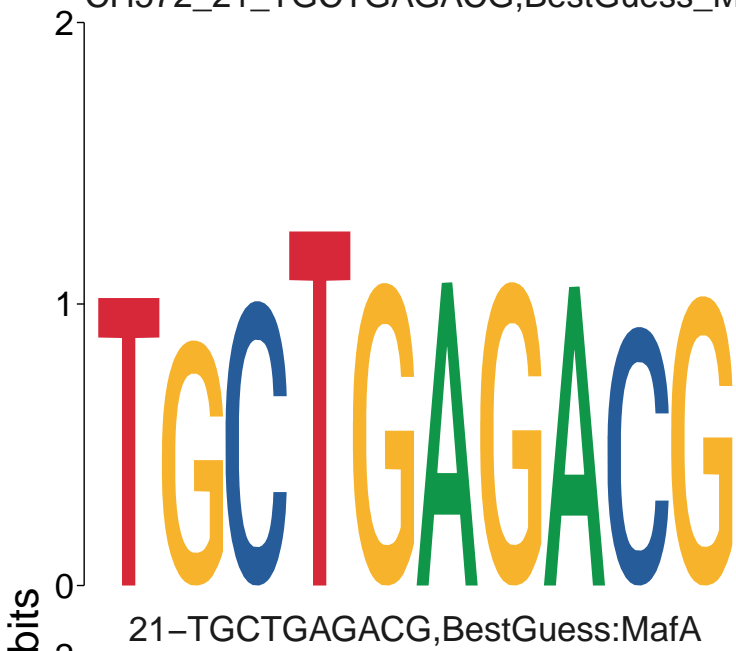
CH571_19_TACGCAGCAT,BestGuess_PB



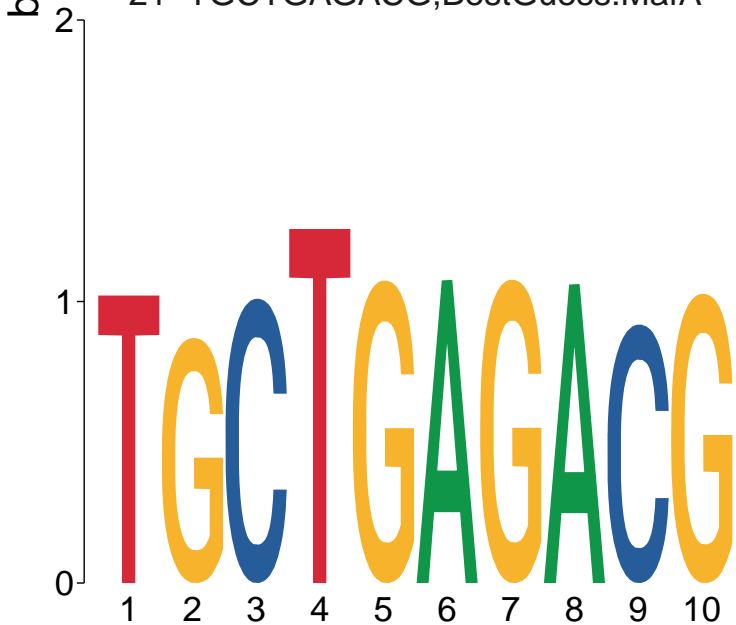
-TACGCAGCAT,BestGuess:PB0206.1_Zic2



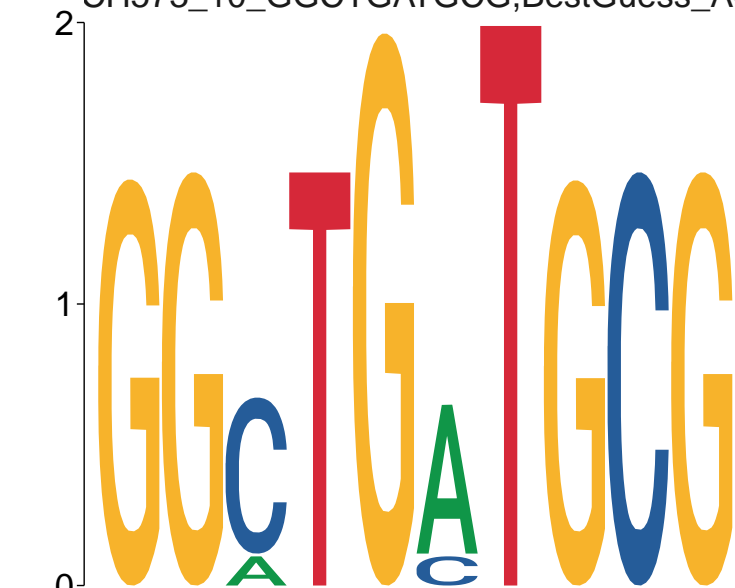
CH572_21_TGCTGAGACG,BestGuess_Ma



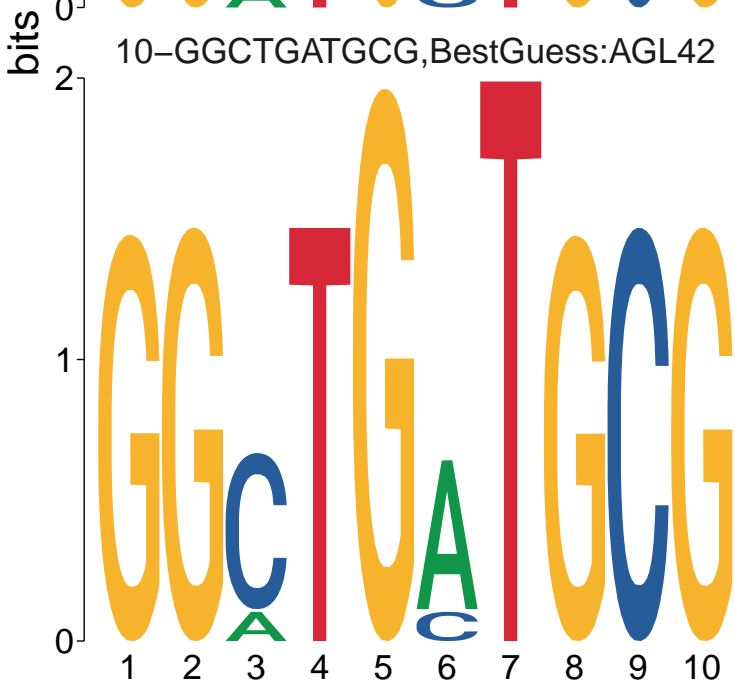
21-TGCTGAGACG,BestGuess:MafA



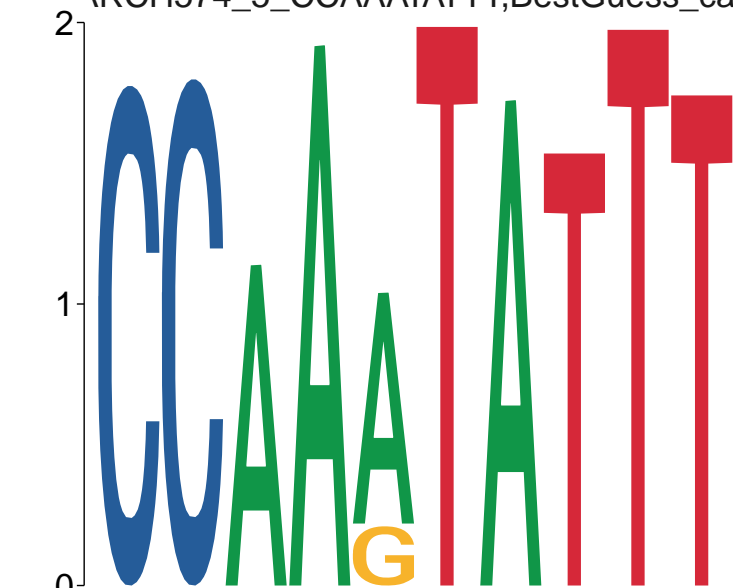
CH573_10_GGCTGATGCG,BestGuess_AC



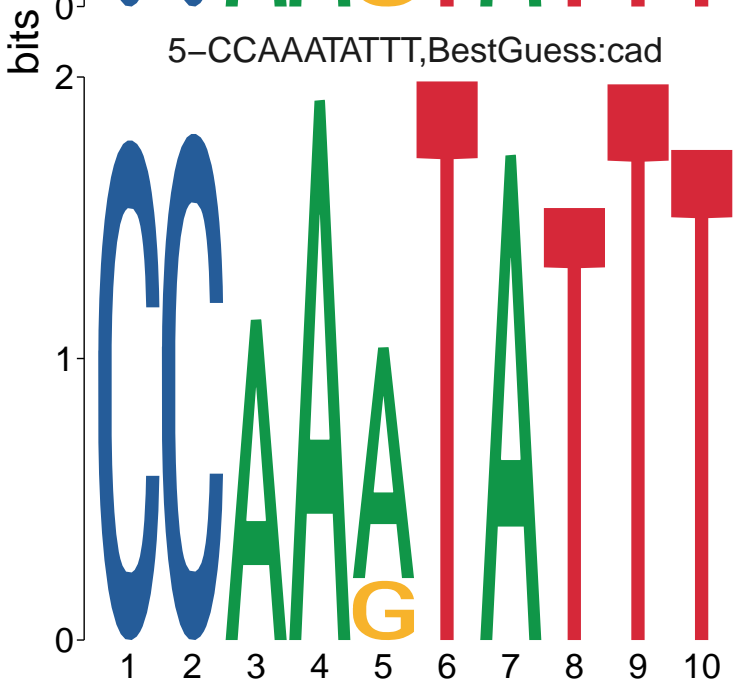
10-GGCTGATGCG,BestGuess:AGL42



ARCH574_5_CCAAATATTT,BestGuess_cac



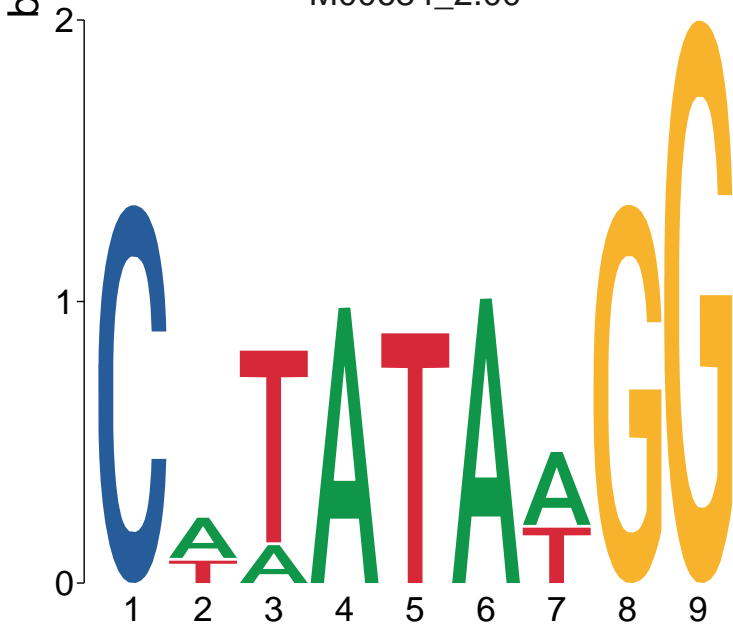
5-CCAAATATTT,BestGuess:cad



ARCH576_MADS-box_SRF



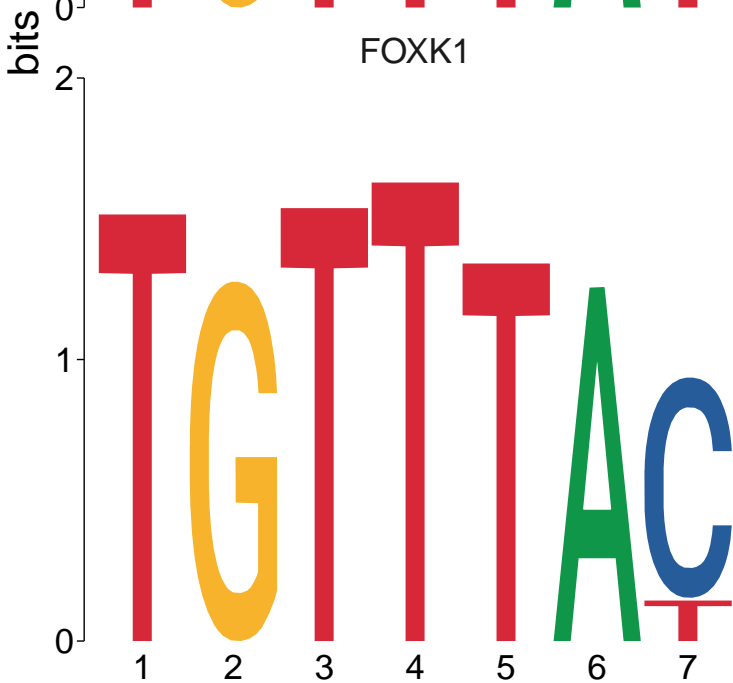
M00684_2.00



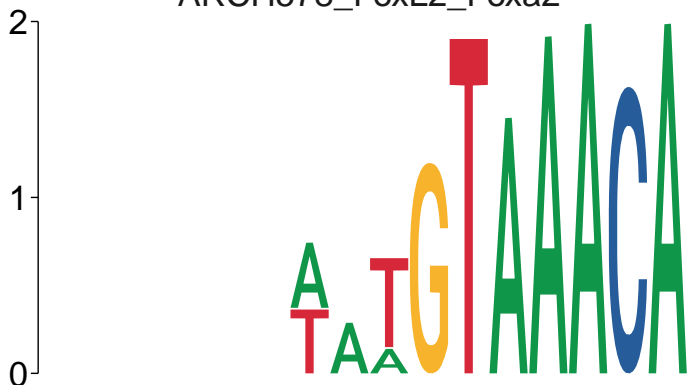
ARCH577_FOXK1



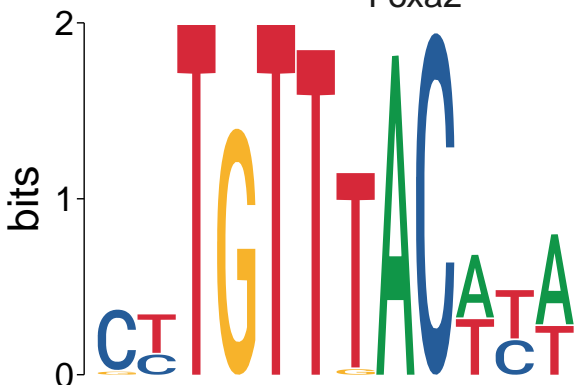
FOXK1



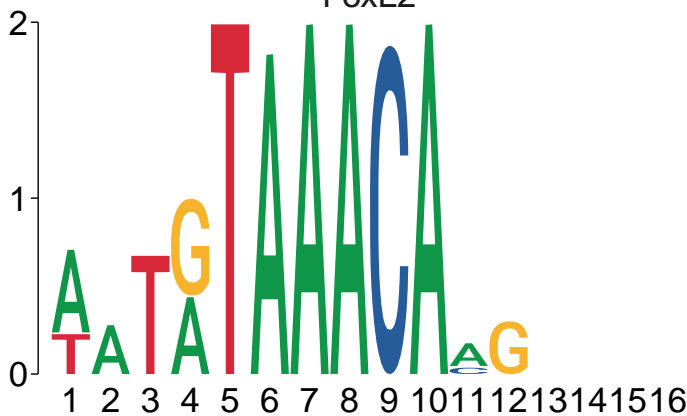
ARCH578_FoxL2_Foxa2



Foxa2



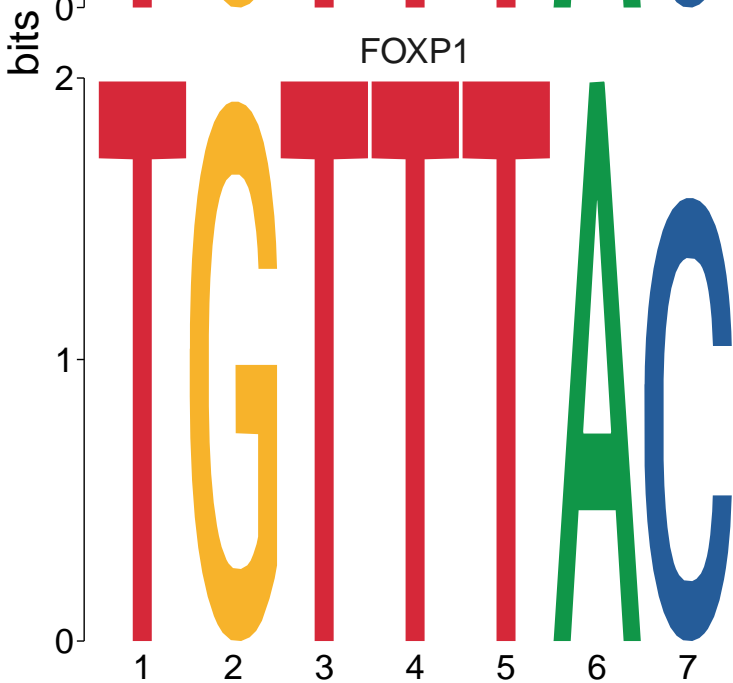
FoxL2



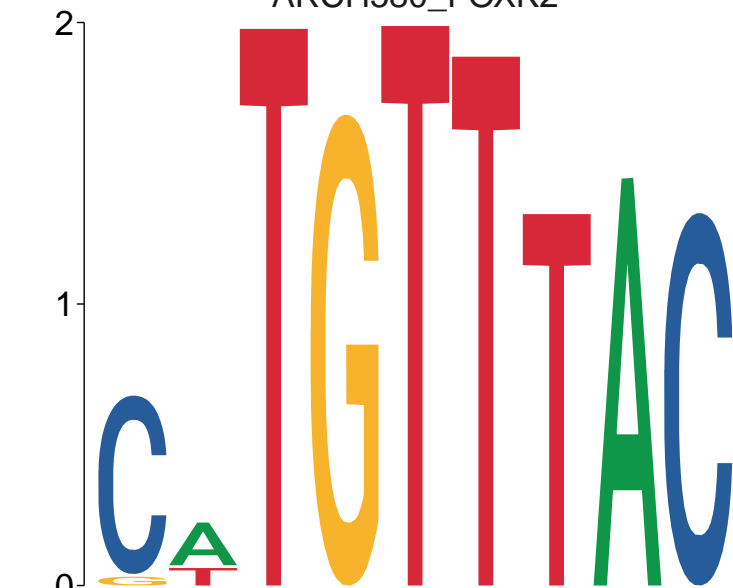
ARCH579_FOXP1



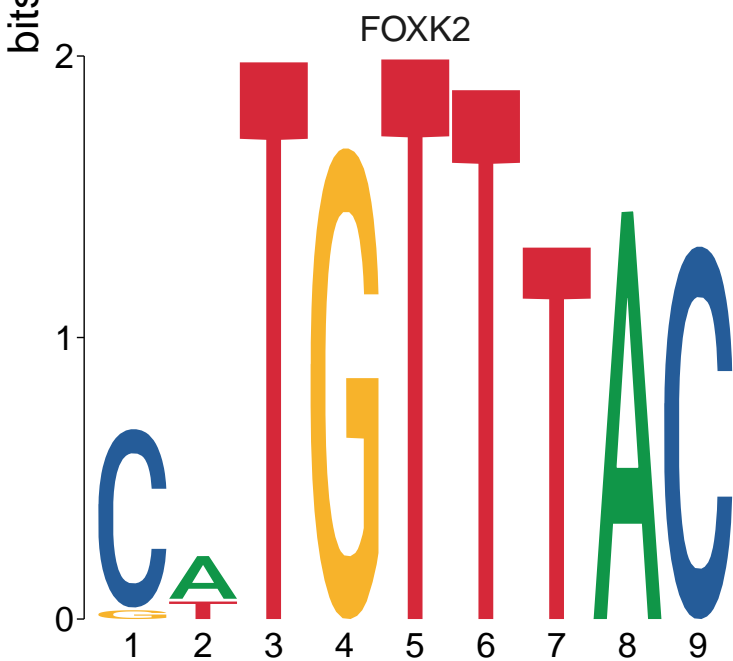
FOXP1



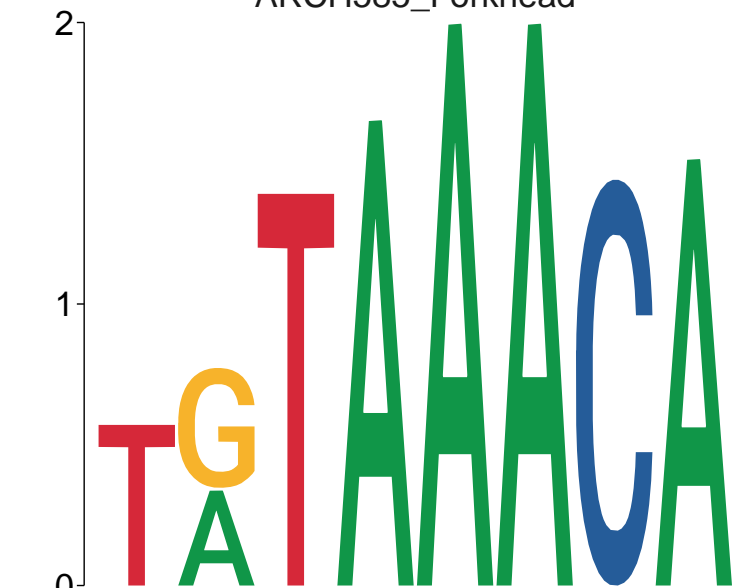
ARCH580_FOXK2



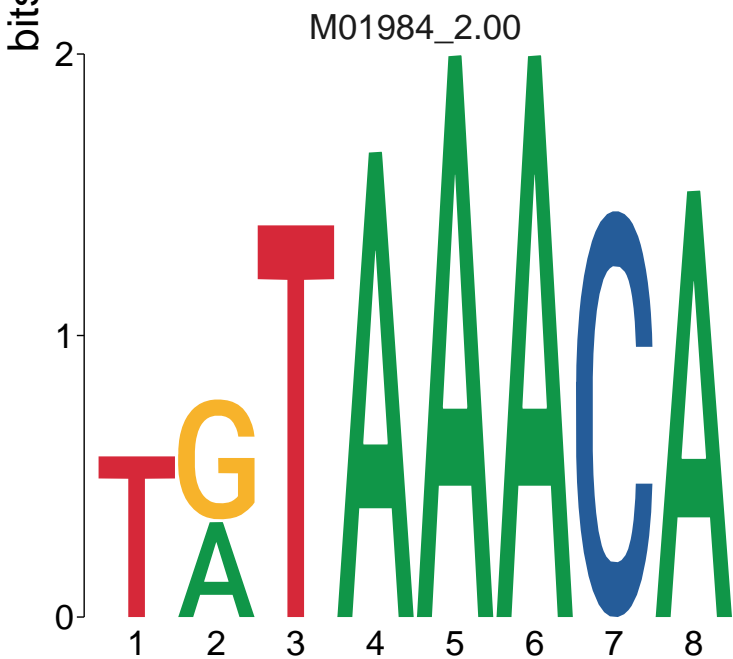
FOXK2



ARCH585_Forkhead



M01984_2.00



ARCH594_FOXA1_FOXA1



M01983_2.00 [RC]



M00796_2.00



M00164_2.00



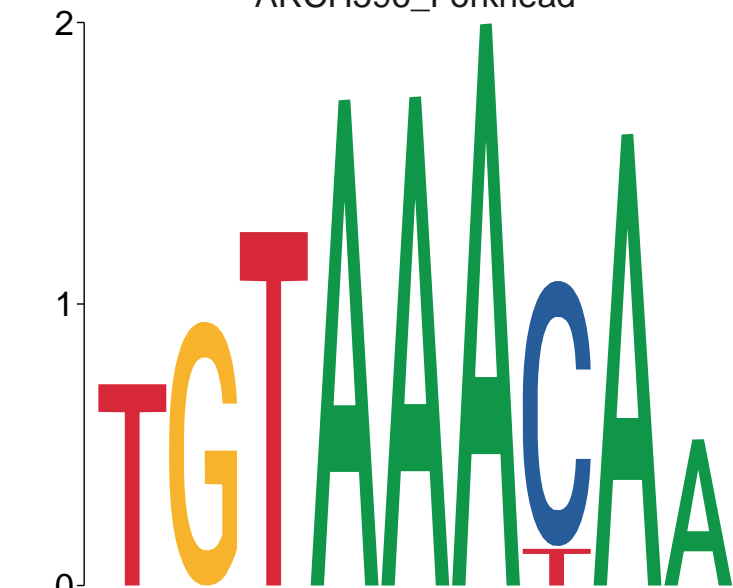
FOXA1



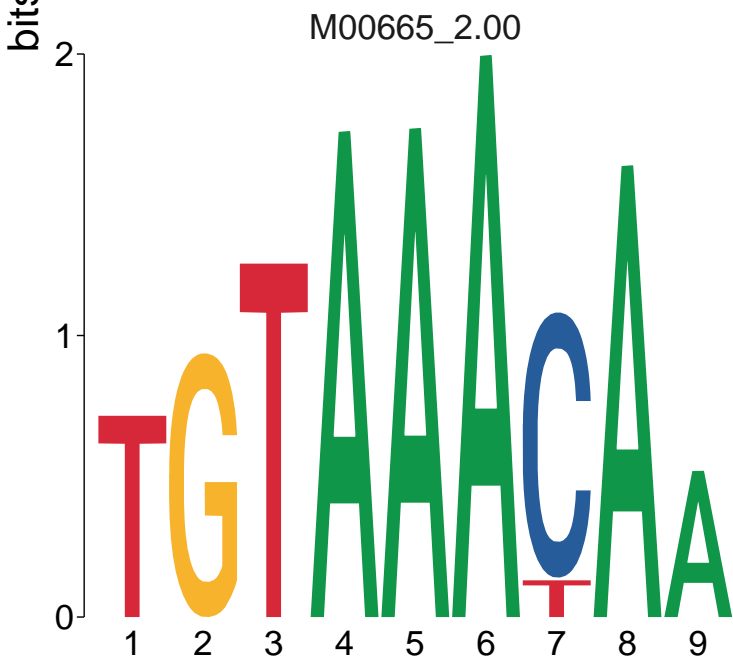
FOXA1.1



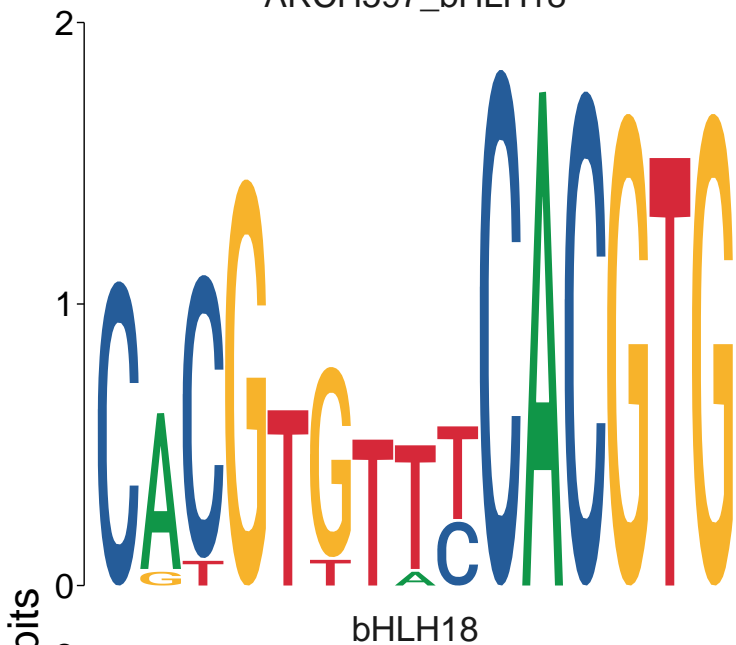
ARCH596_Forkhead



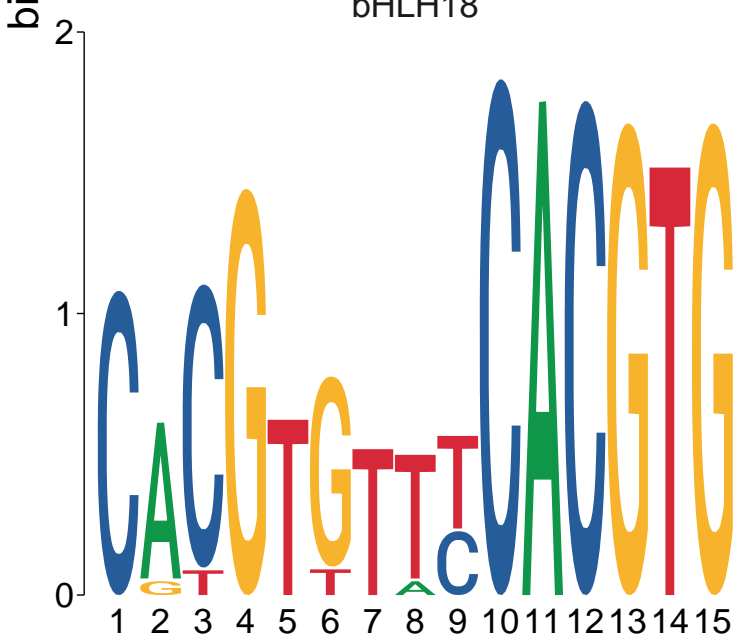
M00665_2.00



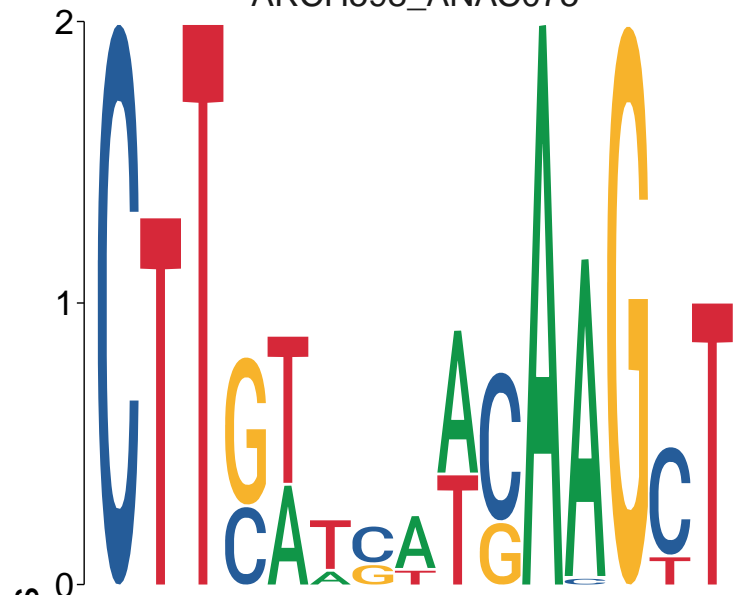
ARCH597_bHLH18



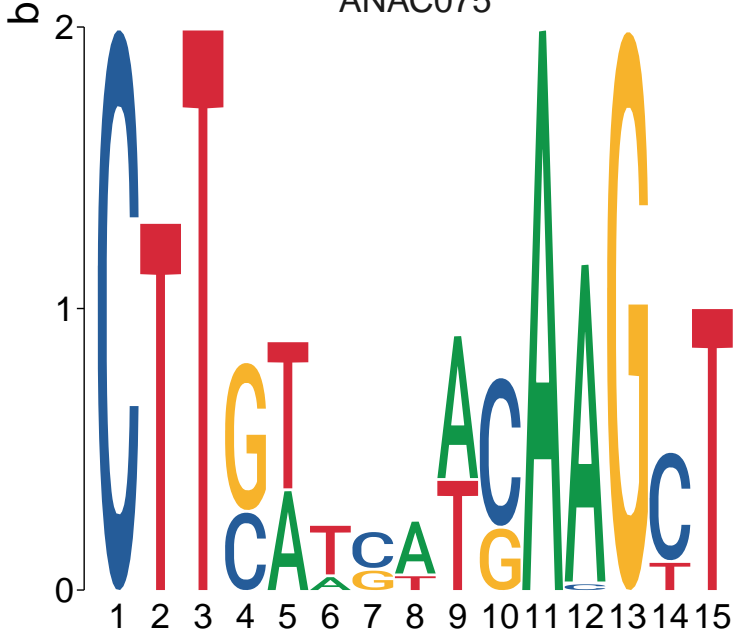
bHLH18



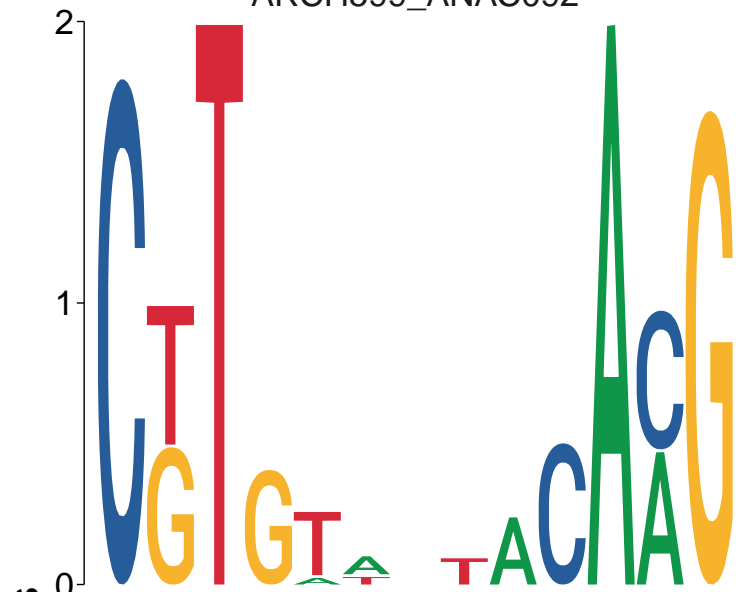
ARCH598_ANAC075



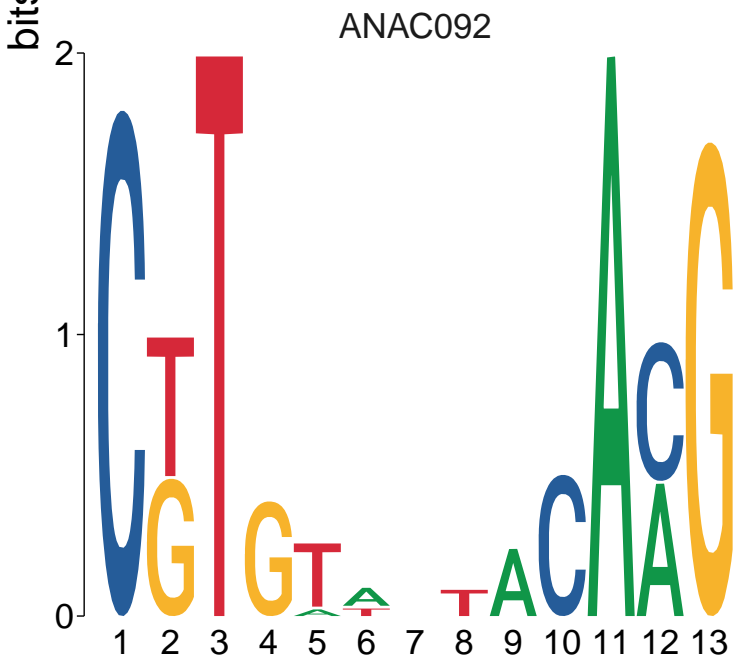
ANAC075



ARCH599_ANAC092



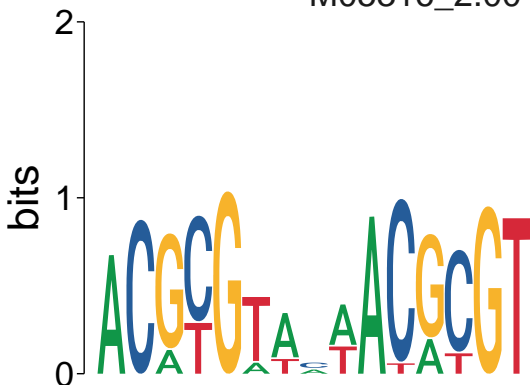
ANAC092



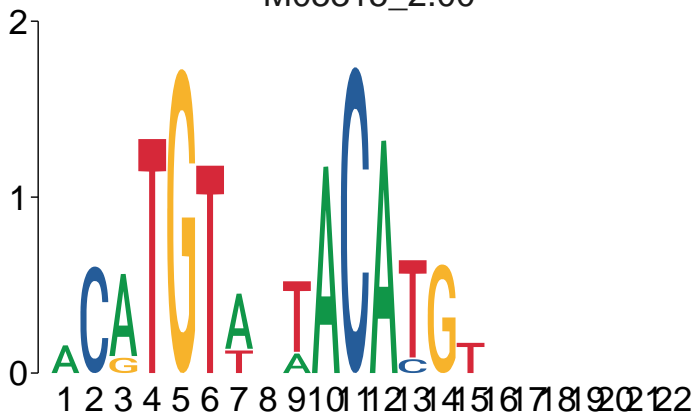
ARCH600_Homeodomains



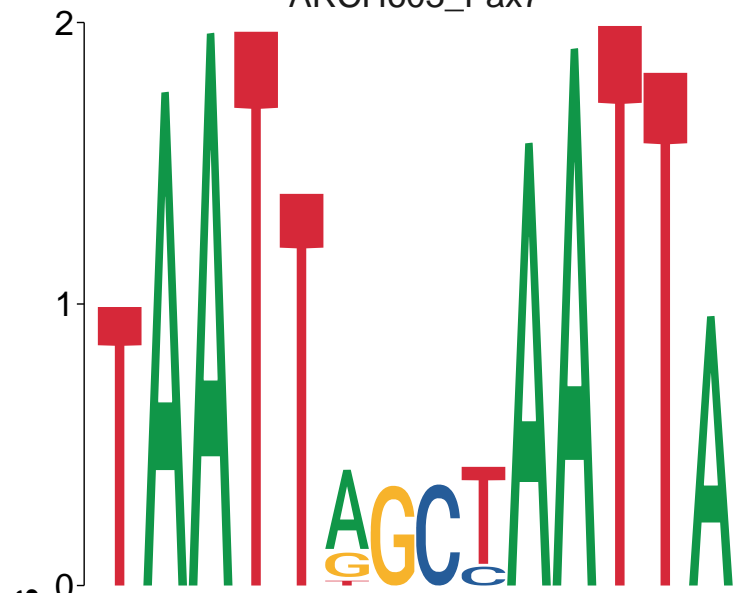
M05316_2.00



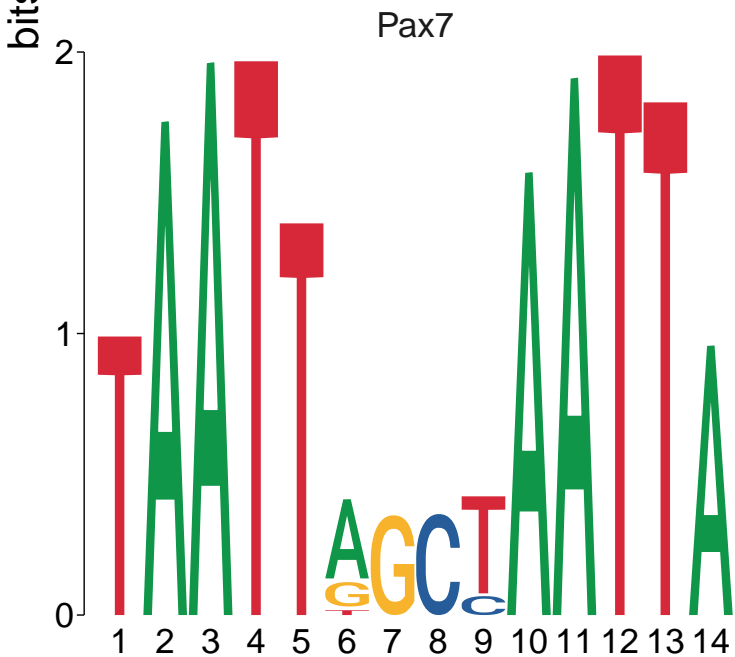
M05315_2.00



ARCH603_Pax7



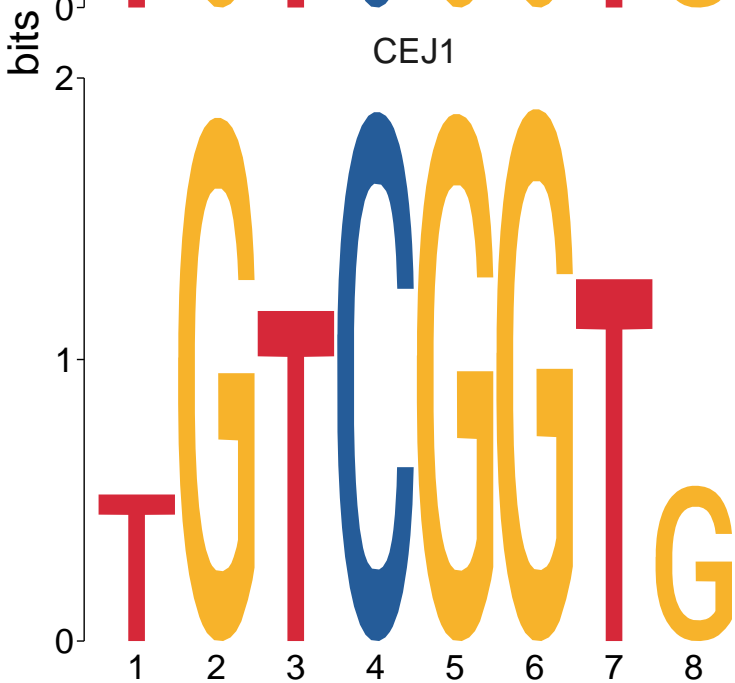
Pax7



ARCH606_CEJ1



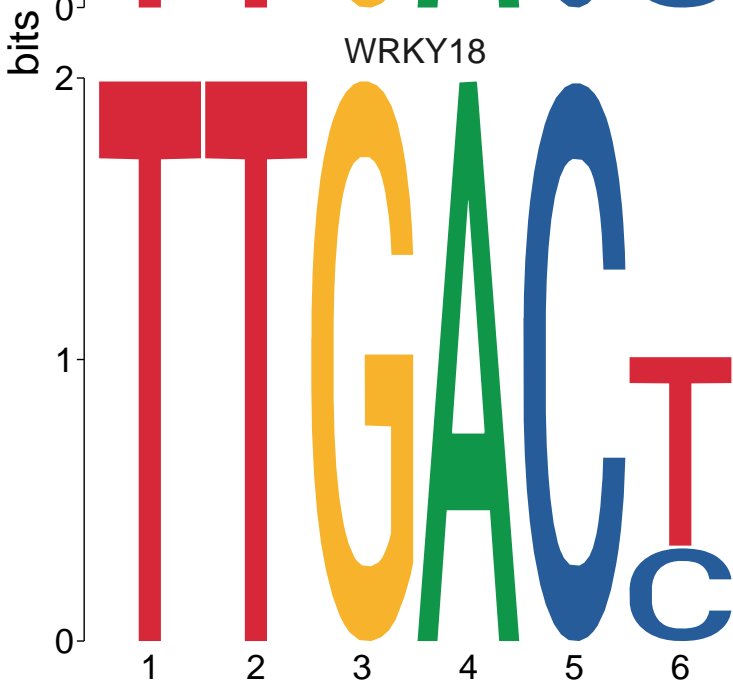
CEJ1



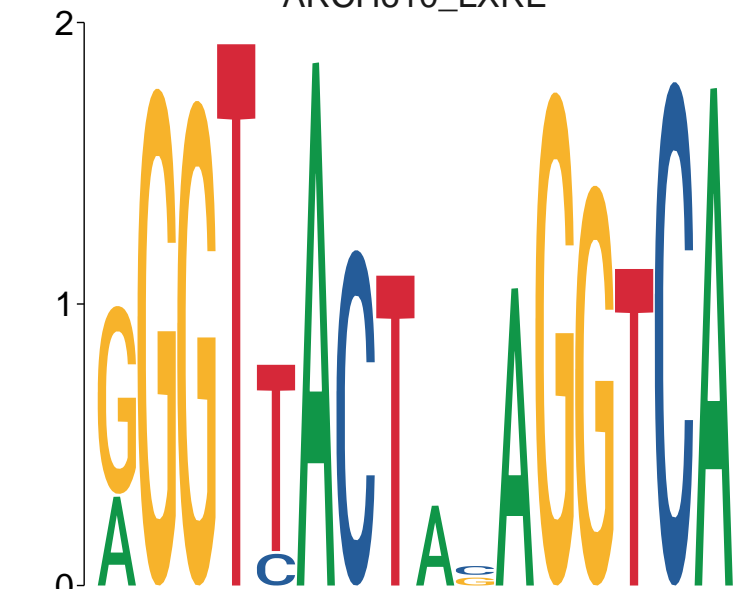
ARCH607_WRKY18



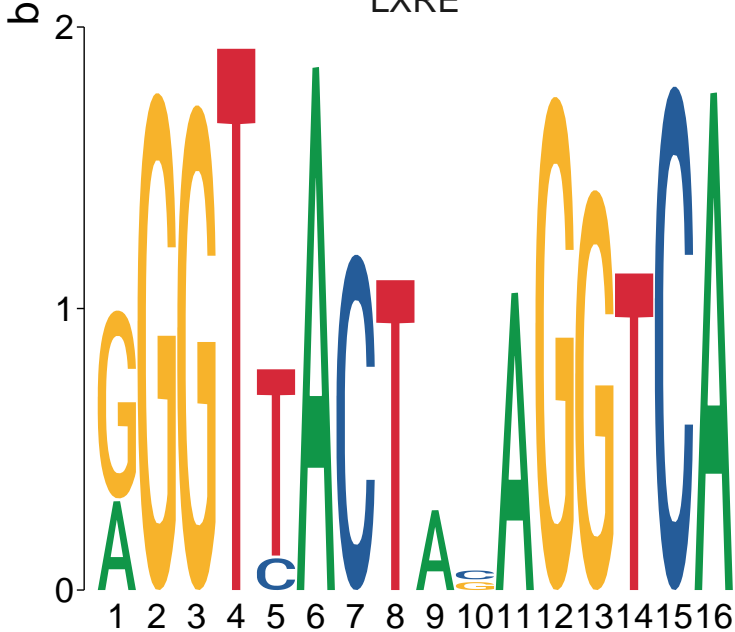
WRKY18



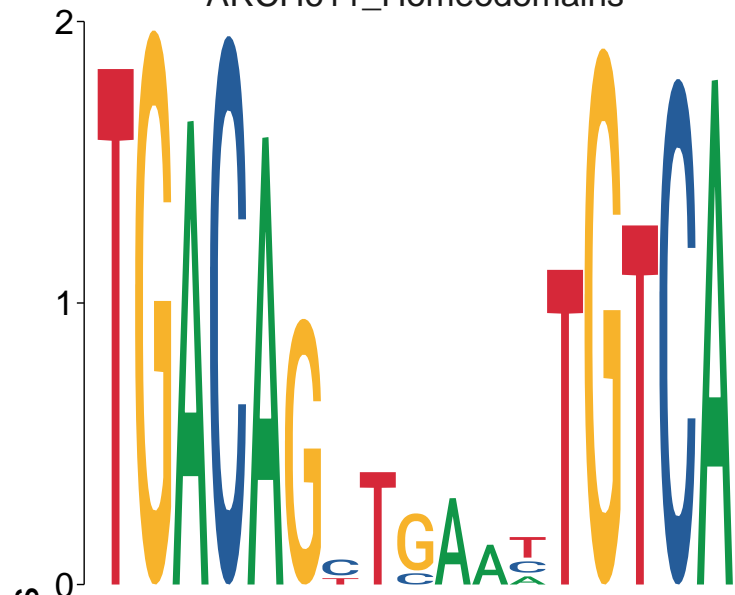
ARCH610_LXRE



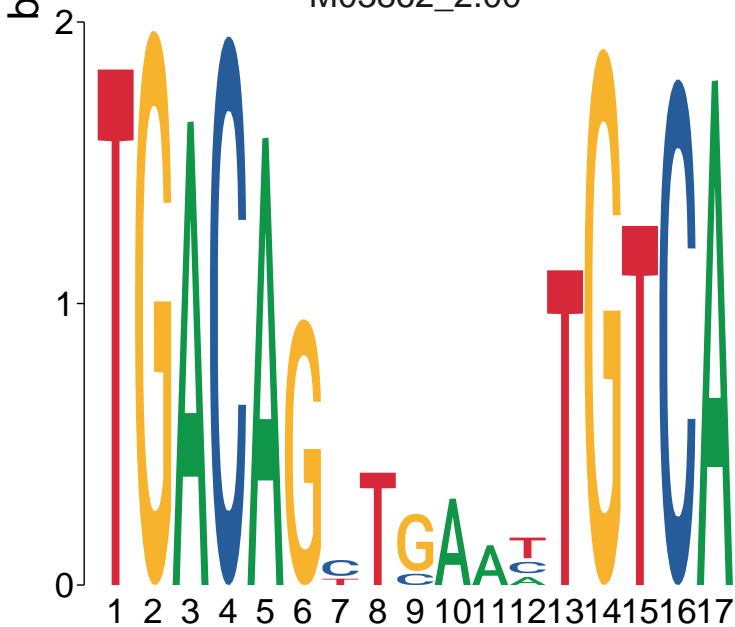
LXRE



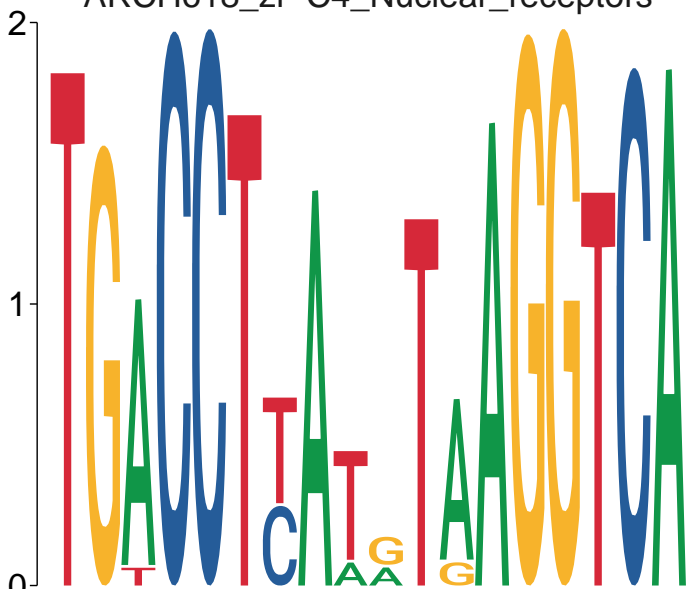
ARCH611_Homeodomains



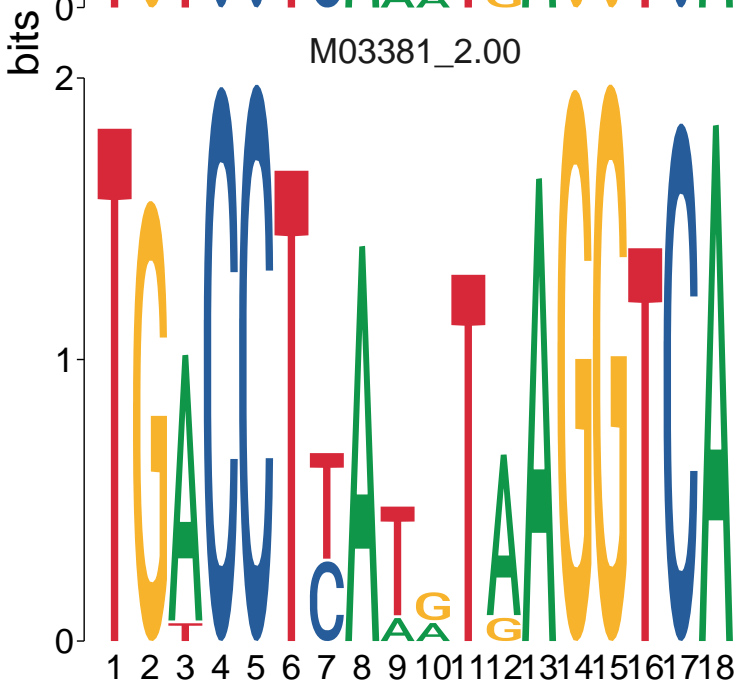
M03862_2.00



ARCH618_zf-C4_Nuclear_receptors



M03381_2.00



RCH629_TEAD3_TEAD2_TEAD_TEAD3_



TEAD2



TEAD4



TEAD3



TEAD



TEAD2.1



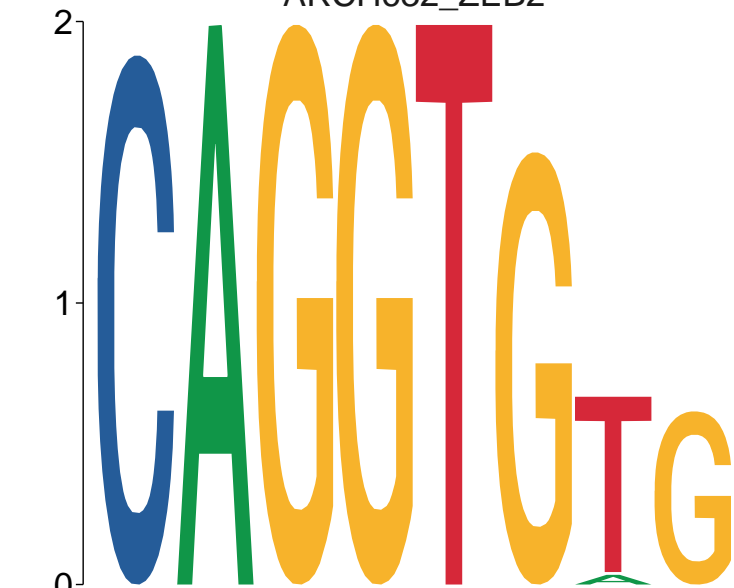
TEAD3.1



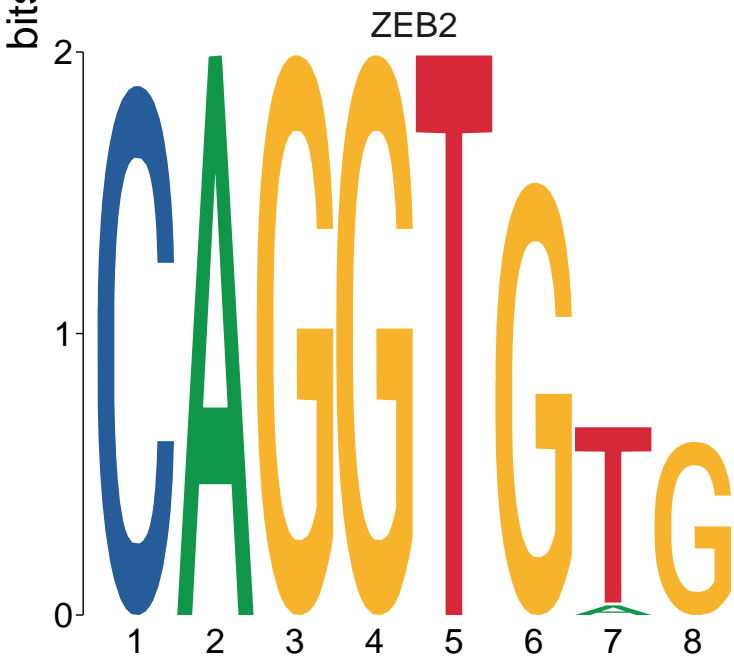
1 2 3 4 5 6 7 8 9 10 11 12 13

Sequence logo for the 10 bp motif. The y-axis represents information content in bits, ranging from 0 to 2. The x-axis shows positions 1 to 10. The sequence is CACACACACA. Positions 1, 3, 5, 7, and 9 are dominated by 'C' (blue), while positions 2, 4, 6, 8, and 10 are dominated by 'A' (green).

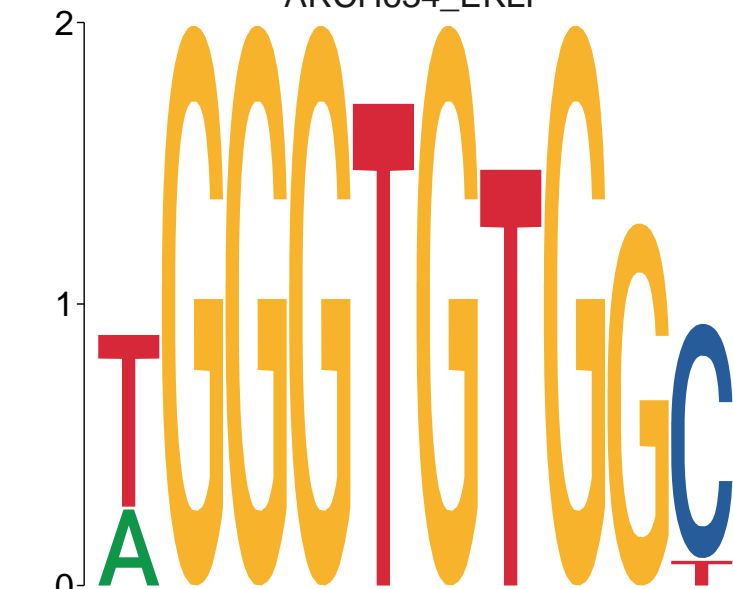
ARCH632_ZEB2



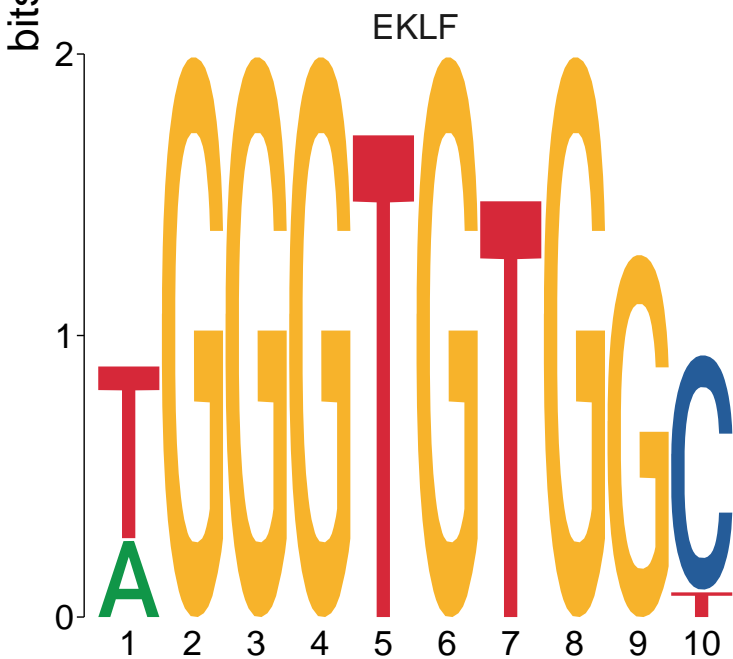
ZEB2



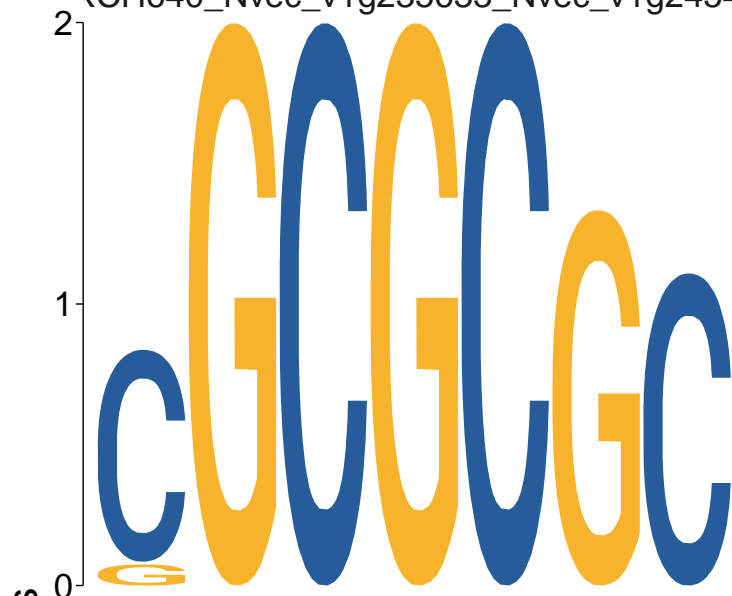
ARCH634_EKLF



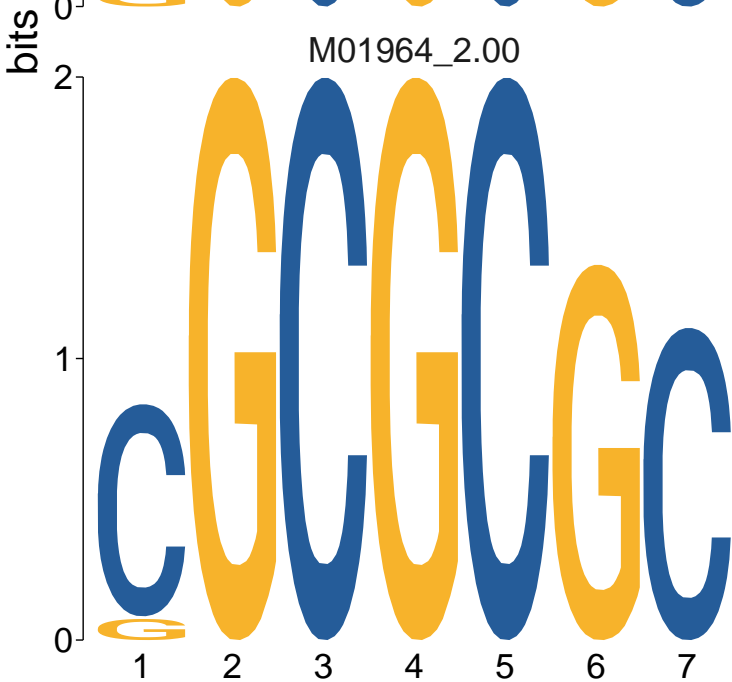
EKLF



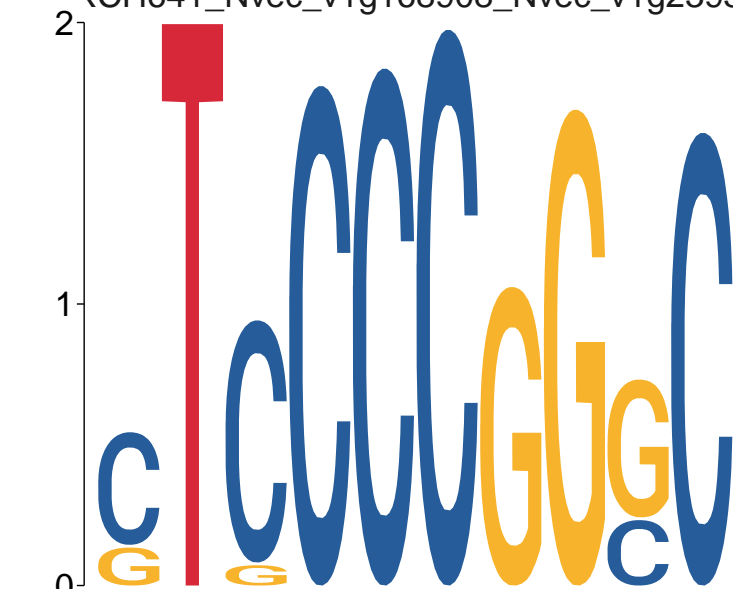
RCH640_Nvec_v1g235633_Nvec_v1g24540



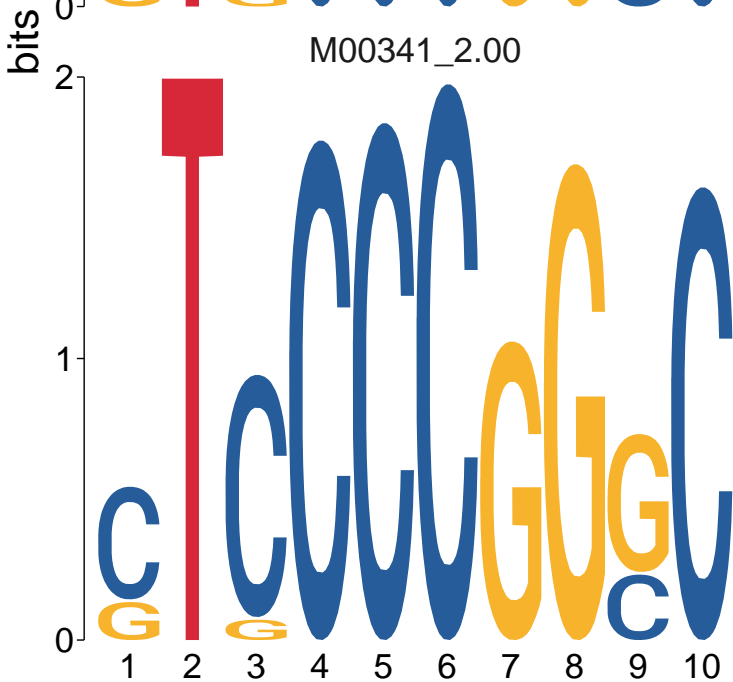
M01964_2.00



RCH641_Nvec_v1g168908_Nvec_v1g2395:



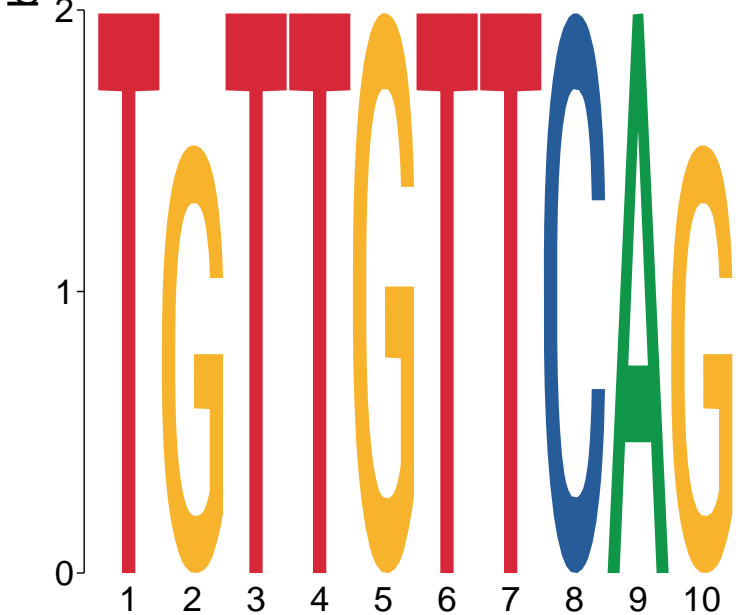
M00341_2.00



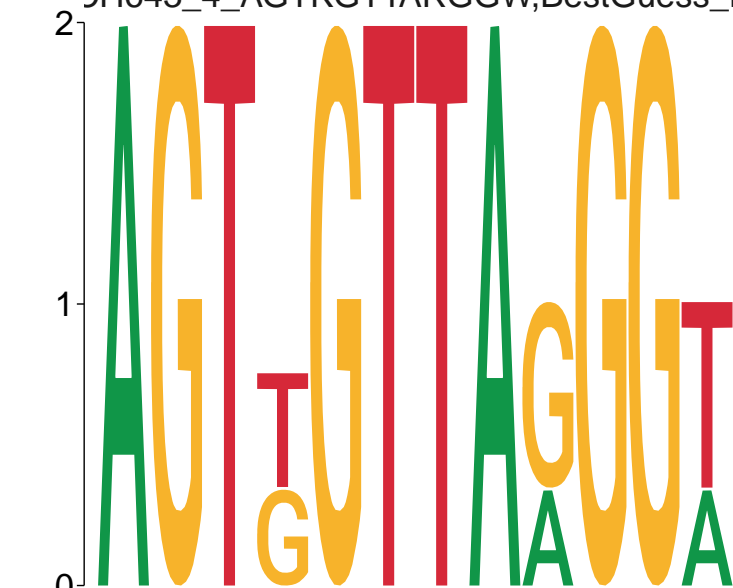
CH642_10_TGTTGTTTCAG,BestGuess_YB



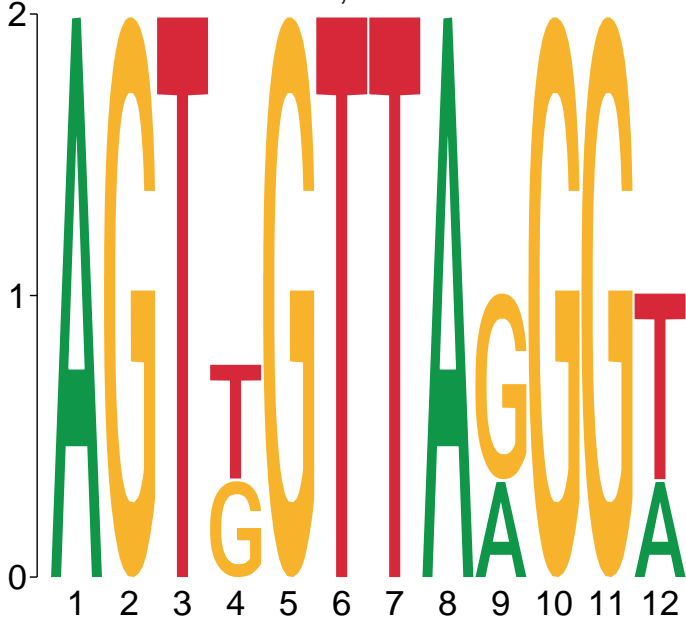
10-TGTTGTTTCAG,BestGuess:YBX2



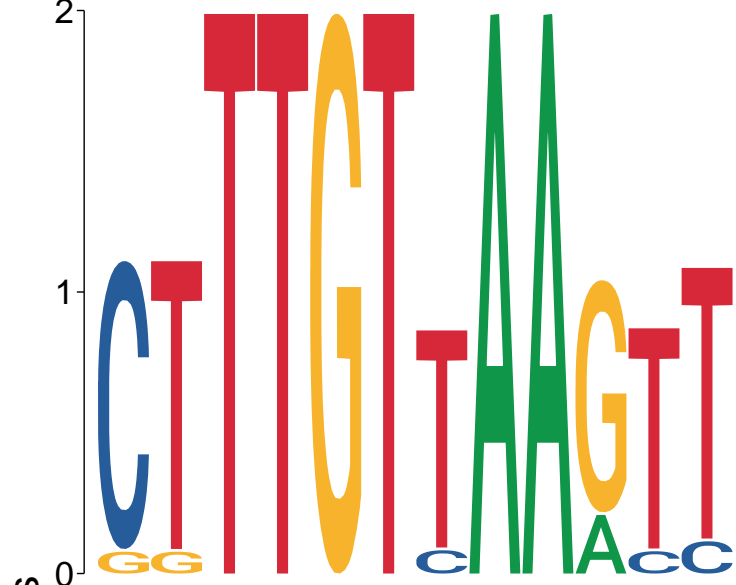
CH643_4_AGTKGTTARGGW,BestGuess_1



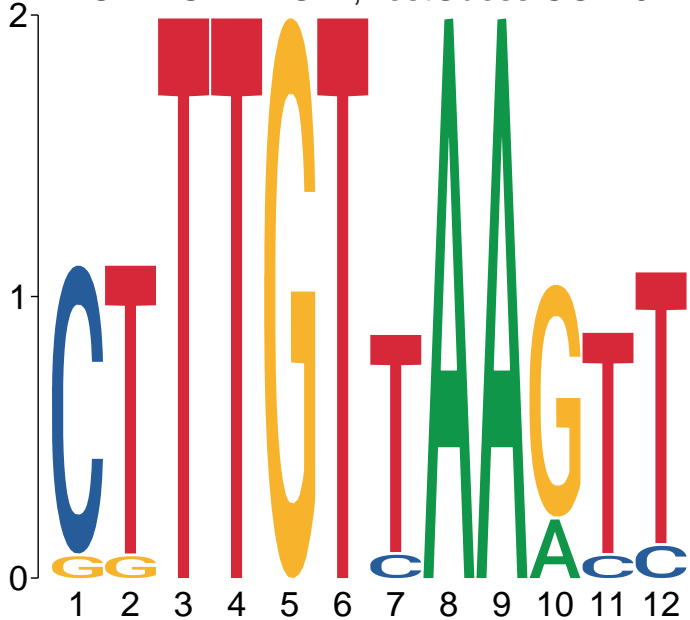
-AGTKGTTARGGW,BestGuess:HNRNPA1L



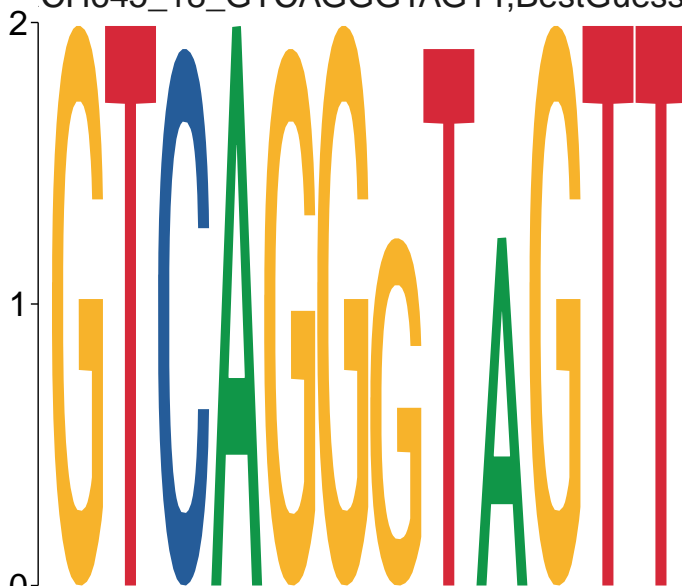
CH644_7_CTTTGTTAAGTT,BestGuess_C



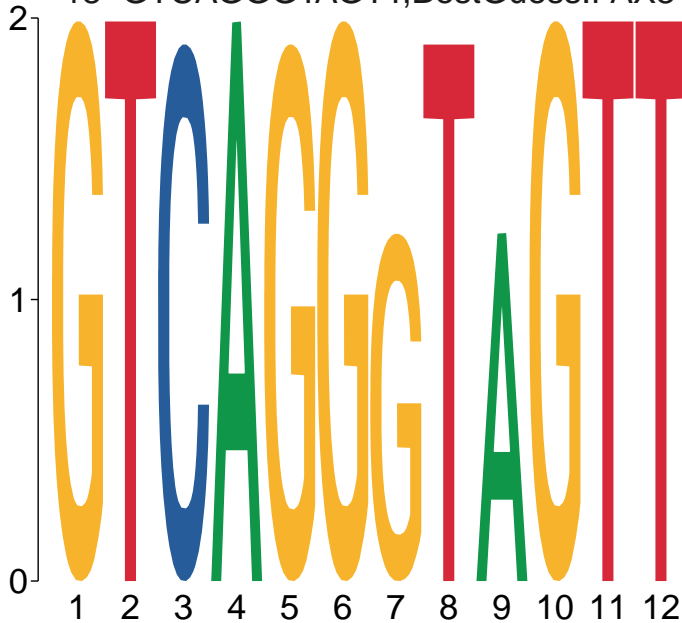
7-CTTTGTTAAGTT,BestGuess:CG11617



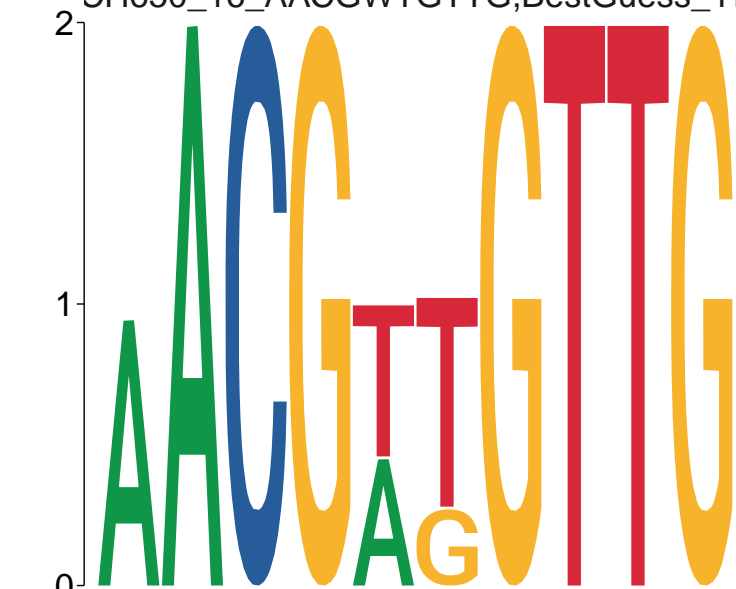
CH645_18_GTCAGGGTAGTT,BestGuess_



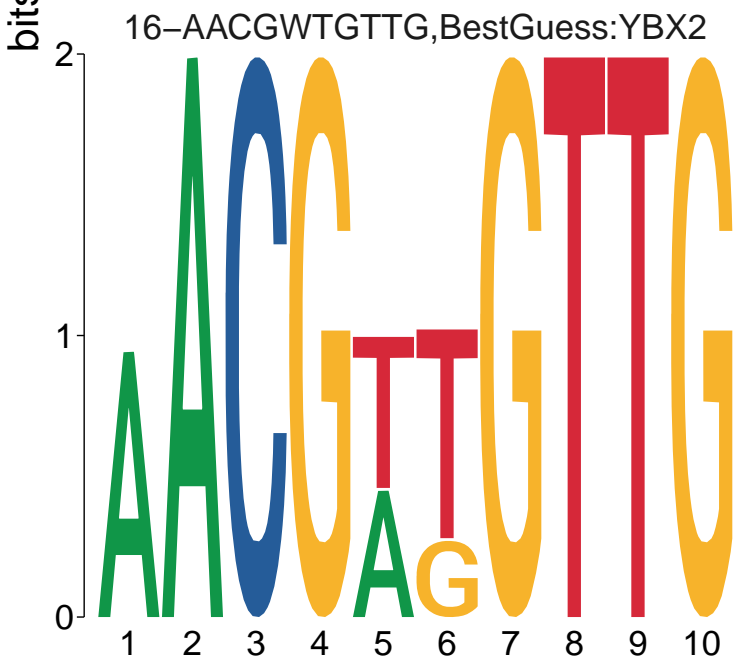
18-GTCAGGGTAGTT,BestGuess:PAX3



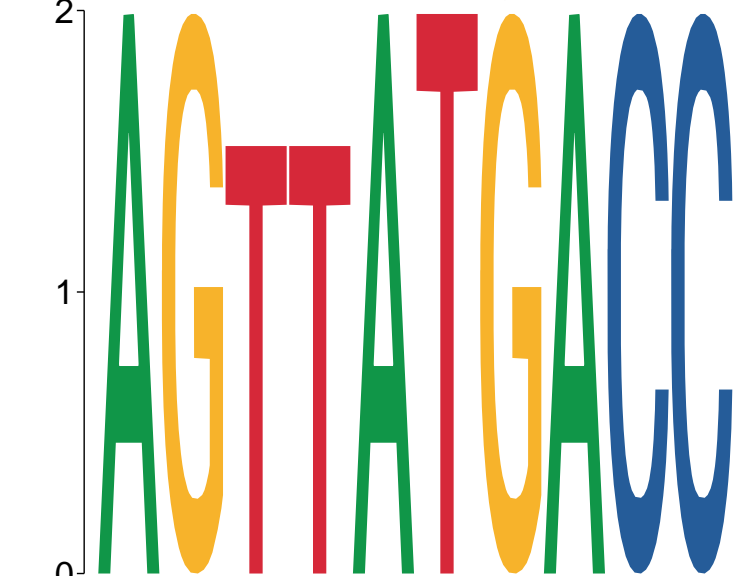
CH650_16_AACGWTGTTG,BestGuess_YE



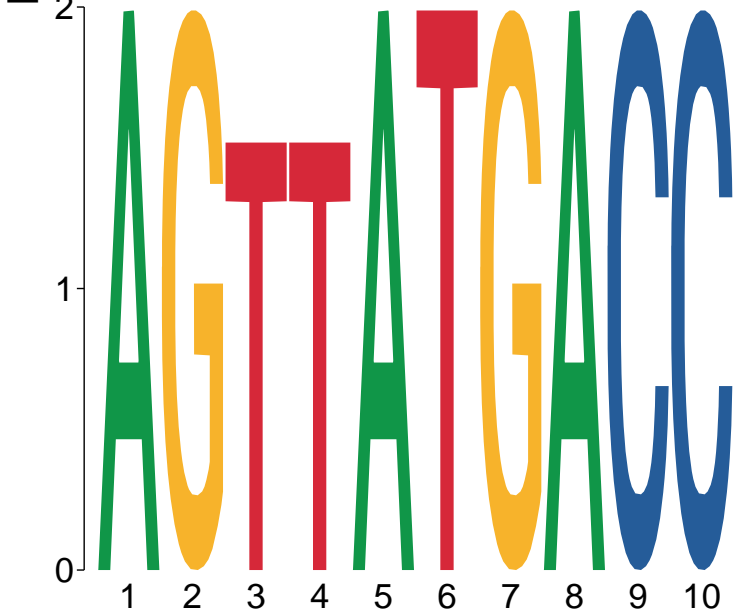
16-AACGWTGTTG,BestGuess:YBX2



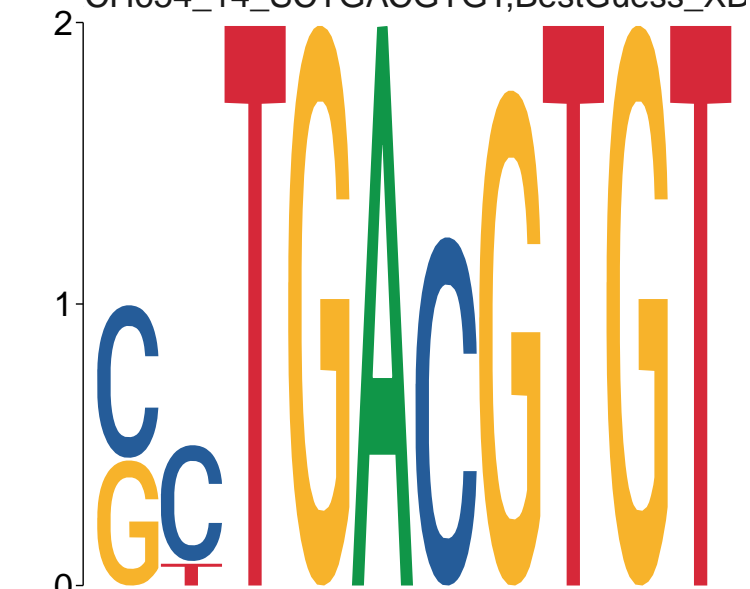
CH651_17_AGTTATGACC,BestGuess_MF



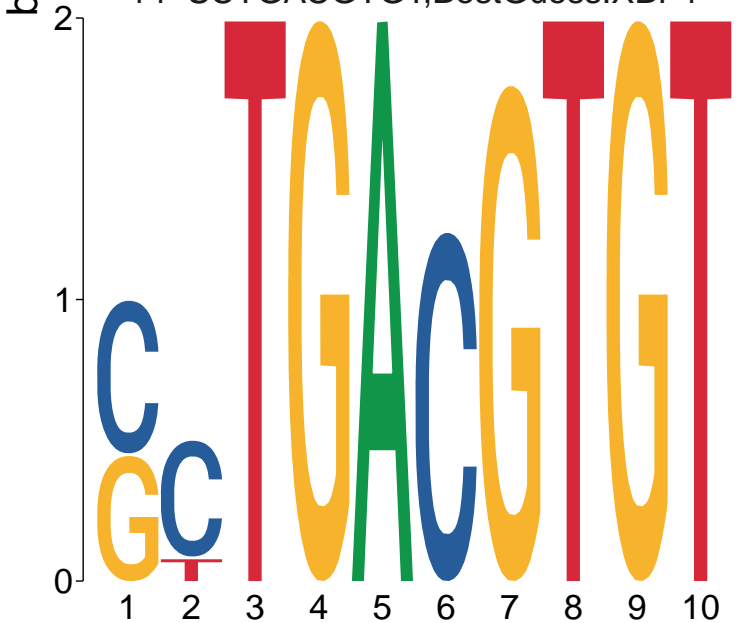
GACC,BestGuess:MF0004.1_Nuclear_Rec



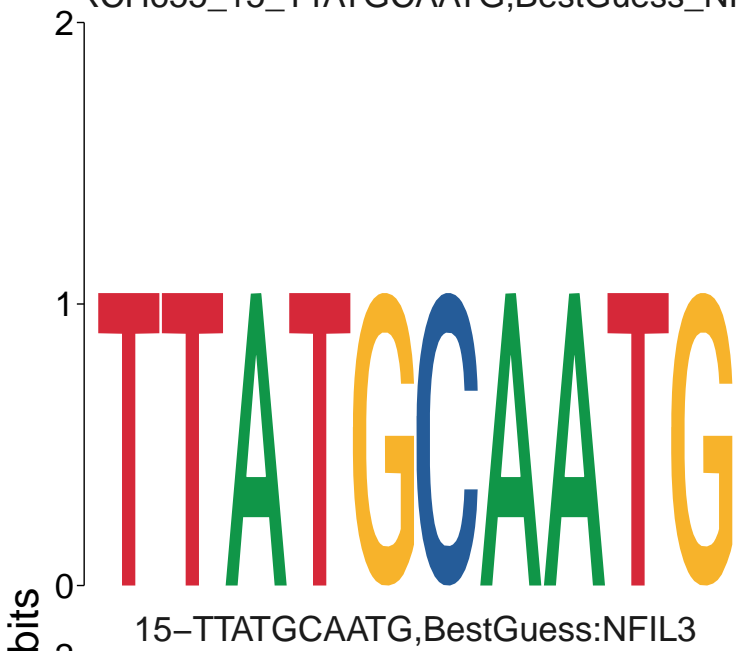
CH654_14_SCTGACGTGT,BestGuess_XB



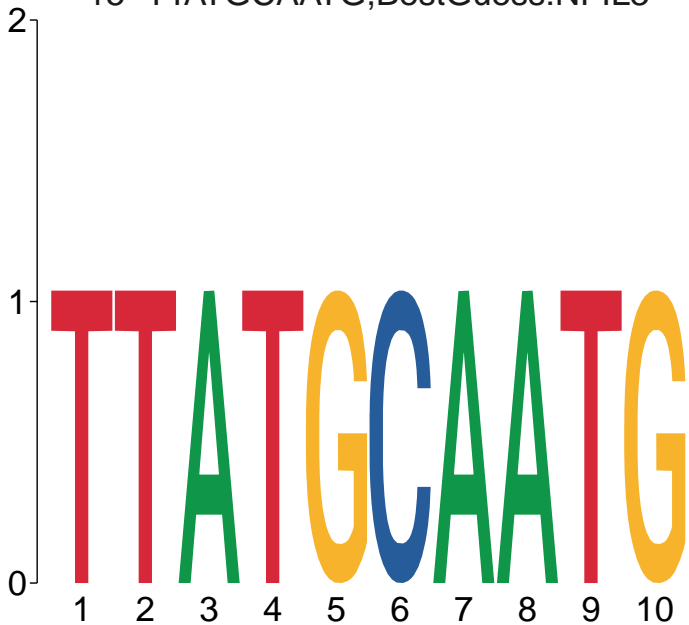
14-SCTGACGTGT,BestGuess:XBP1



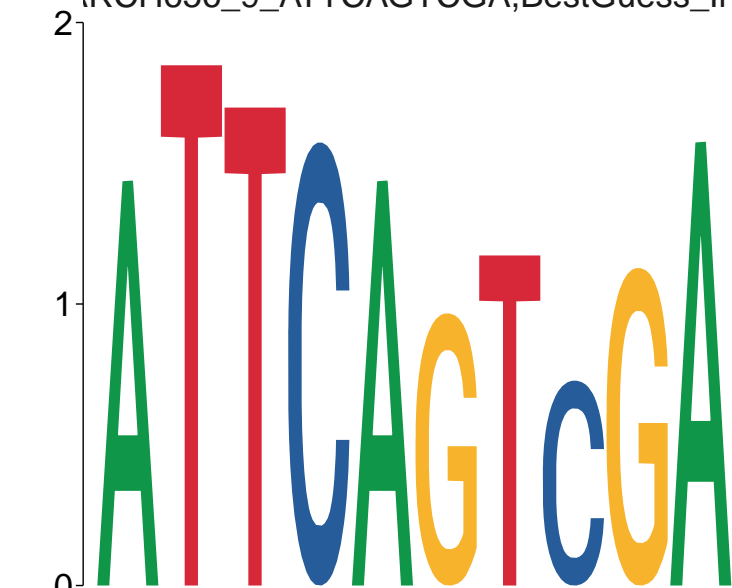
RCH655_15_TTATGCAATG,BestGuess_NF



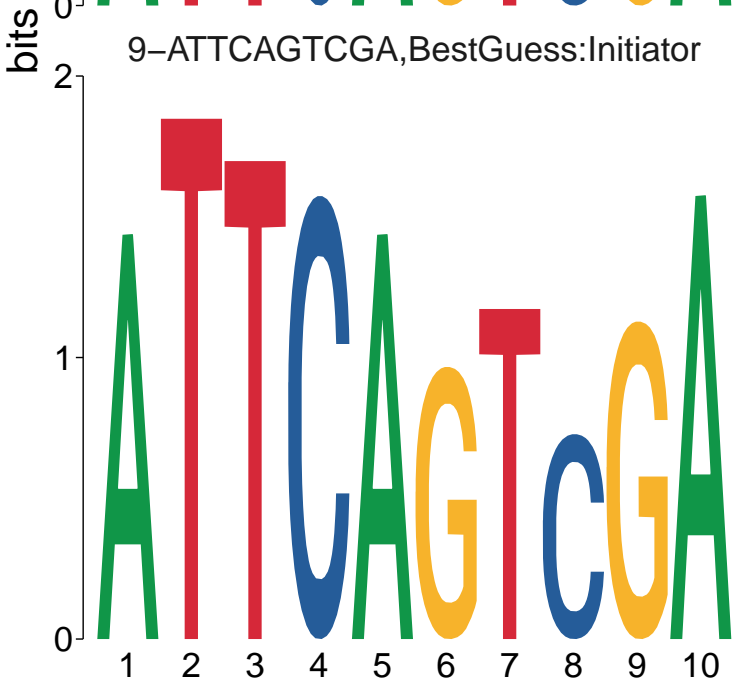
15-TTATGCAATG,BestGuess:NFIL3



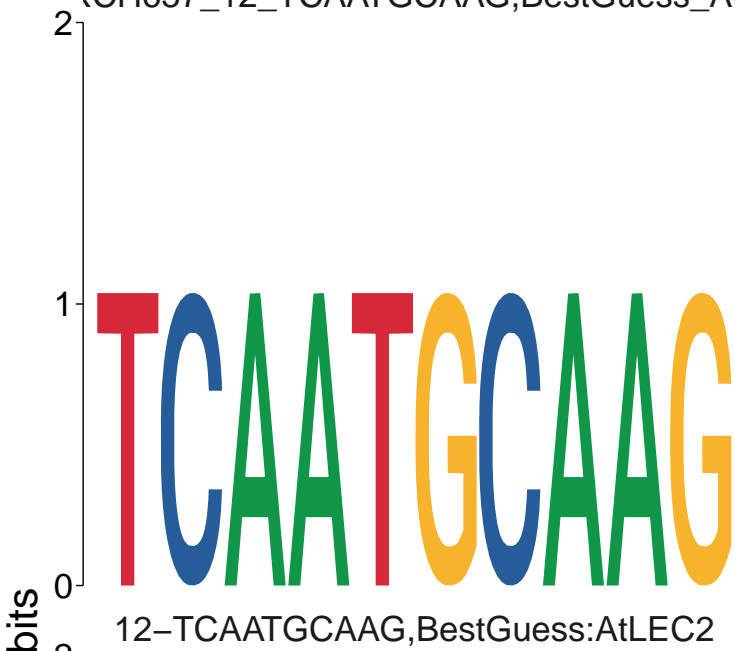
RCH656_9_ATTCAGTCGA,BestGuess_Ini



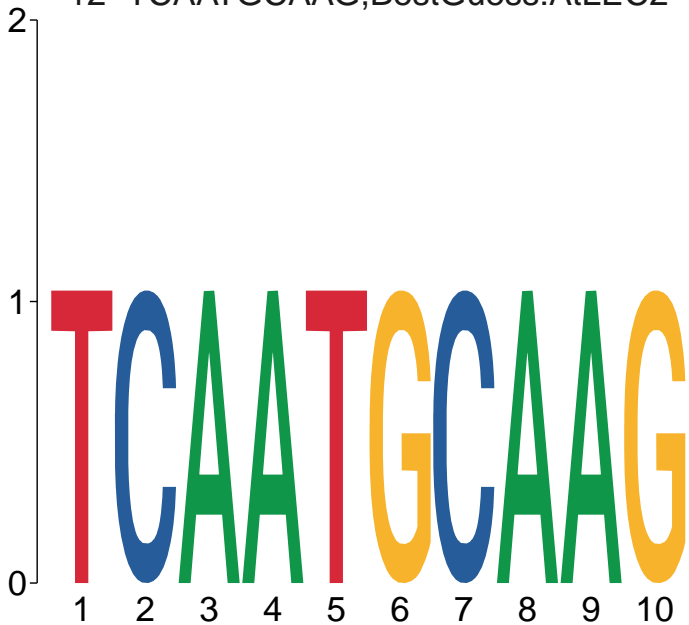
9-ATTCAGTCGA,BestGuess:Initiator



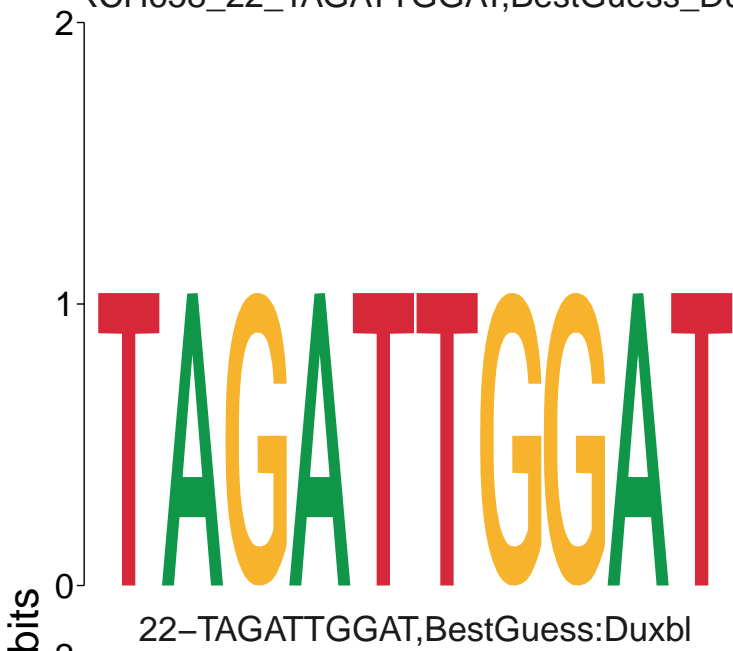
CH657_12_TCAATGCAAG,BestGuess_At



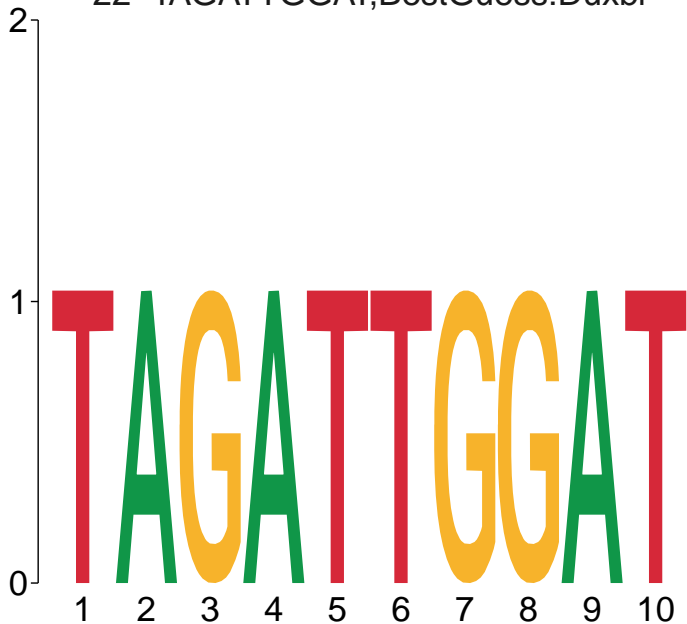
12-TCAATGCAAG,BestGuess:AtLEC2



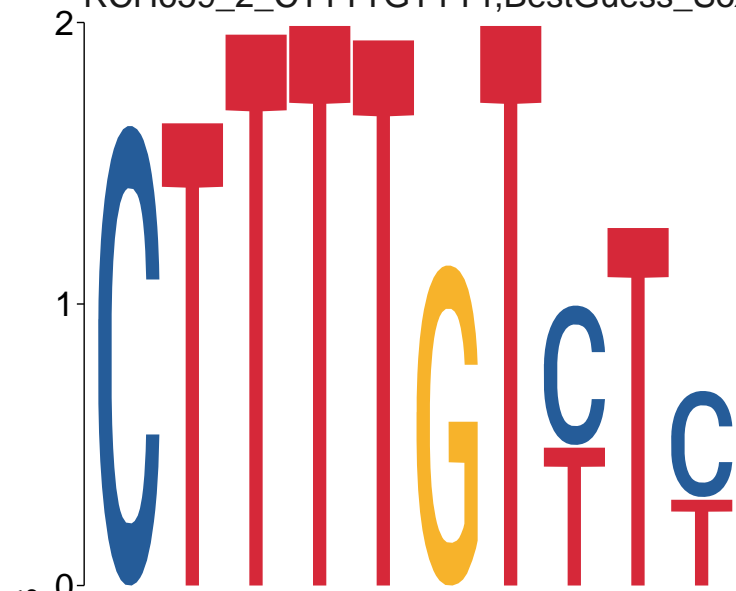
RCH658_22_TAGATTGGAT,BestGuess_Du:



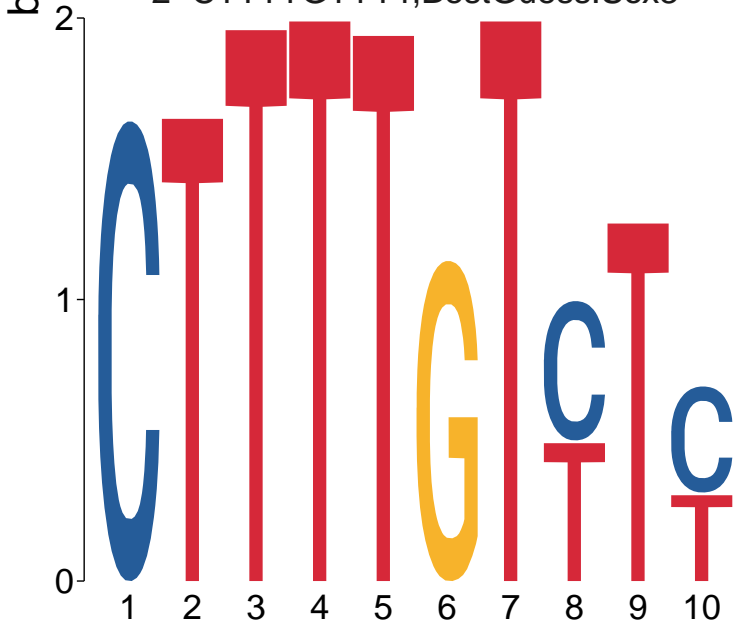
22-TAGATTGGAT,BestGuess:Duxbl



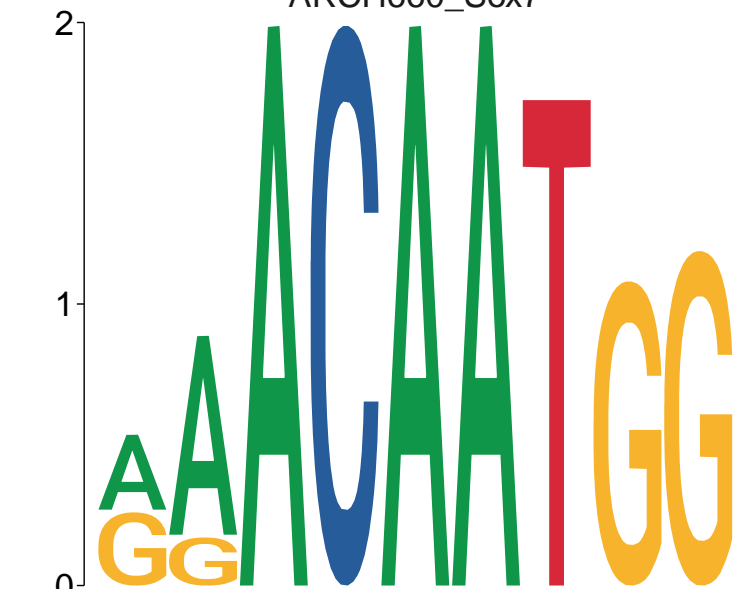
RCH659_2_CTTTTGTYTY,BestGuess_Sox



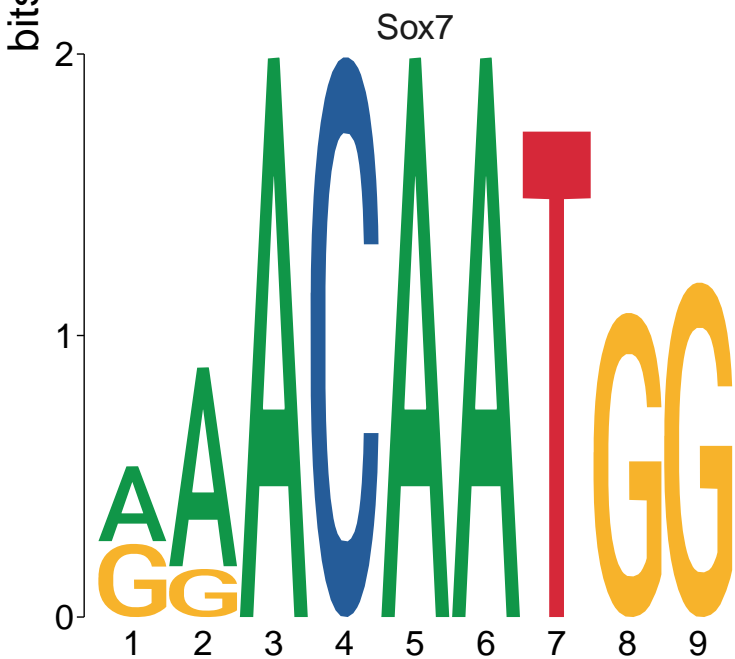
2-CTTTTGTYTY,BestGuess:Sox3



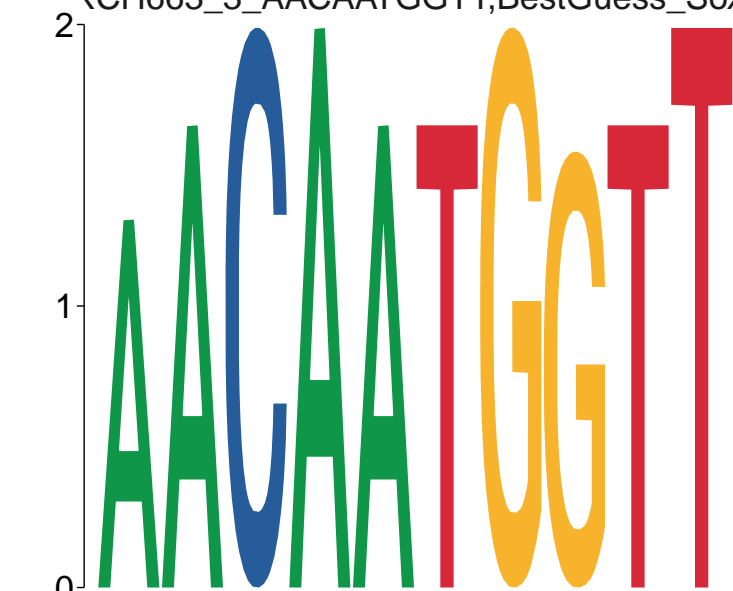
ARCH660_Sox7



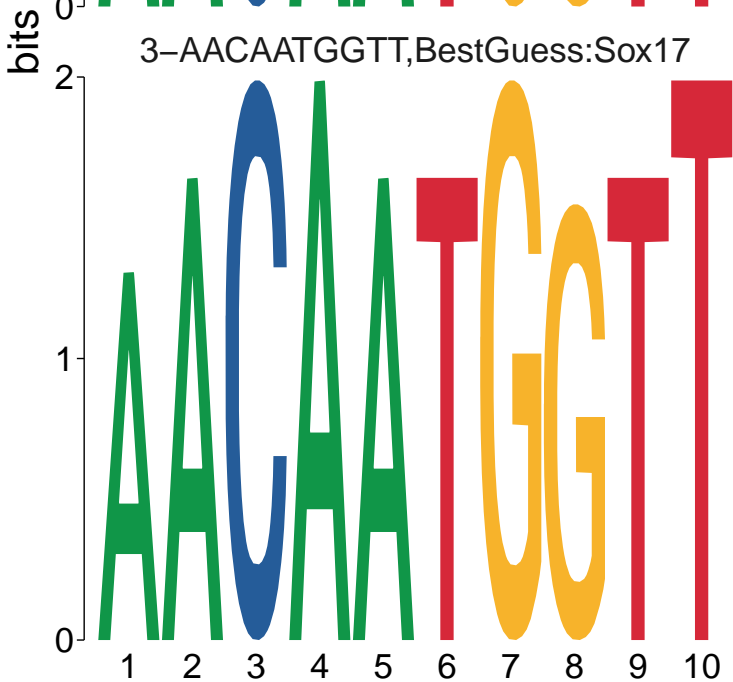
Sox7



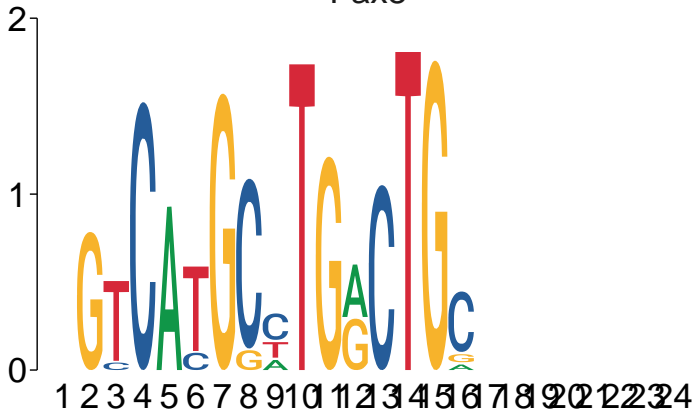
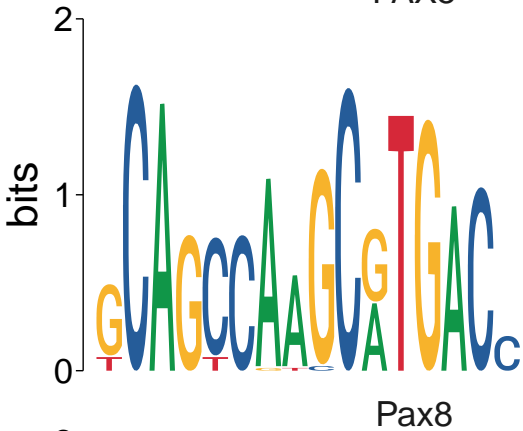
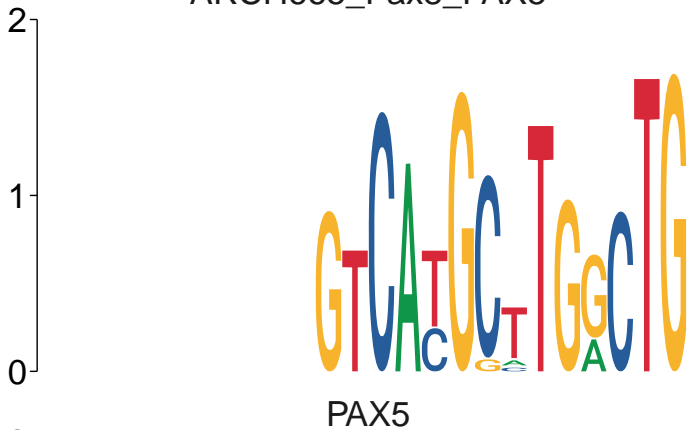
RCH663_3_AACAATGGTT,BestGuess_Sox



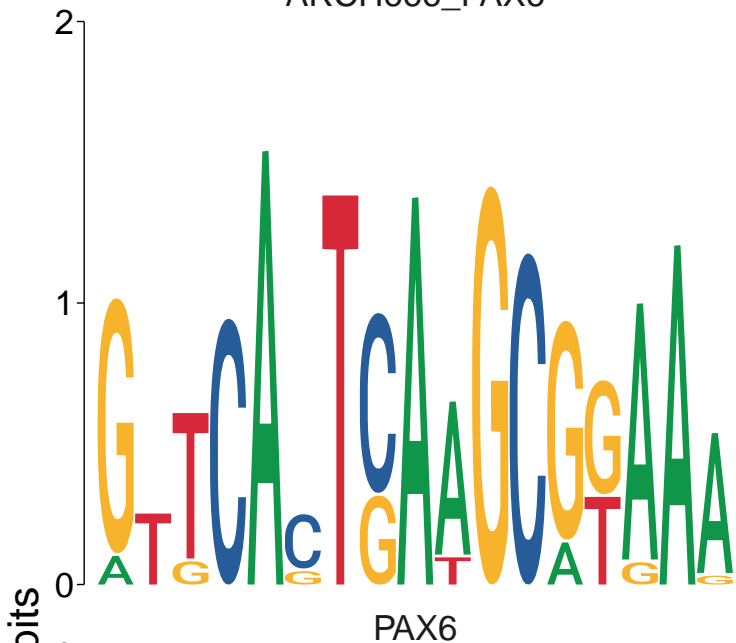
3-AACAATGGTT,BestGuess:Sox17



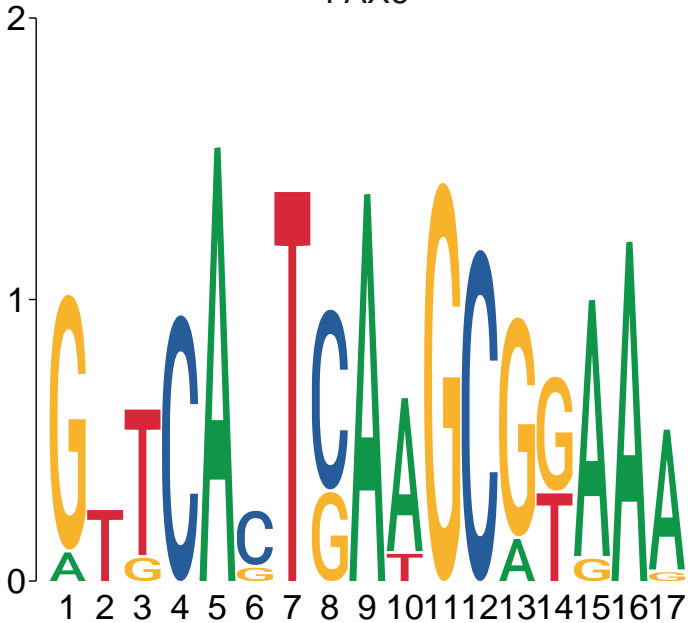
ARCH665_Pax8_PAX5



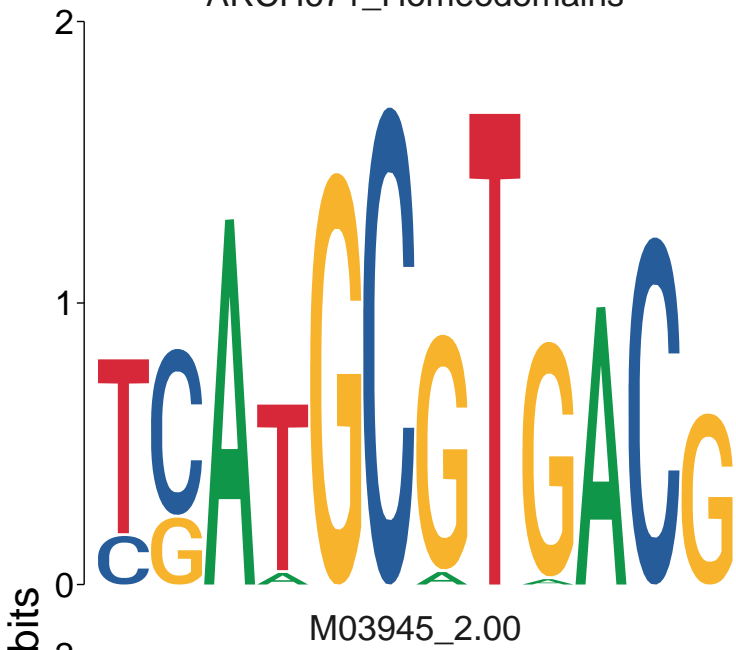
ARCH666_PAX6



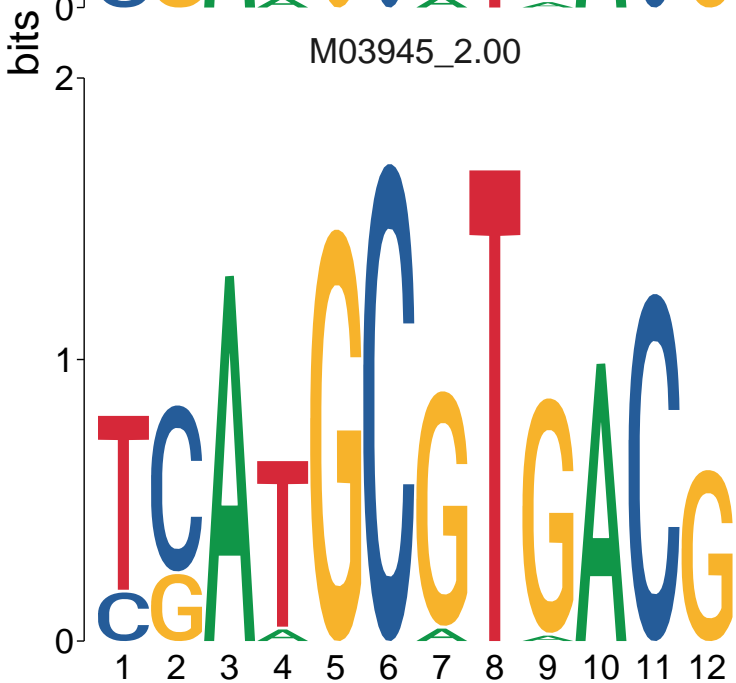
PAX6



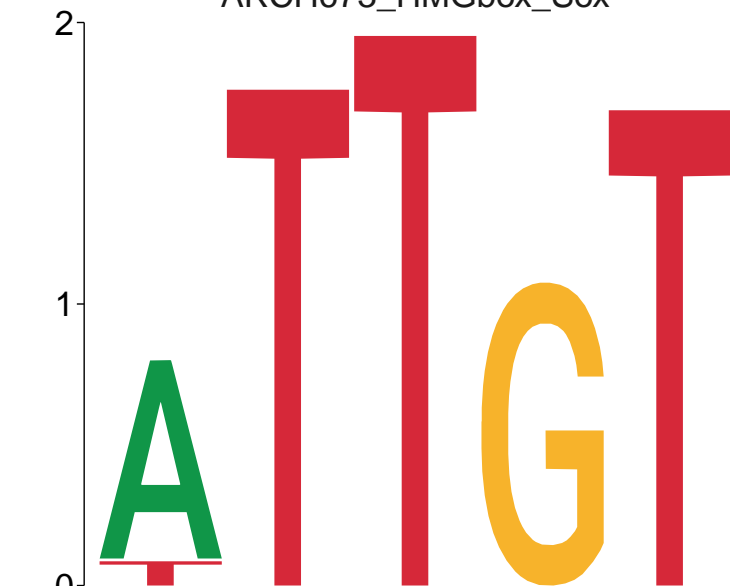
ARCH671_Homeodomains



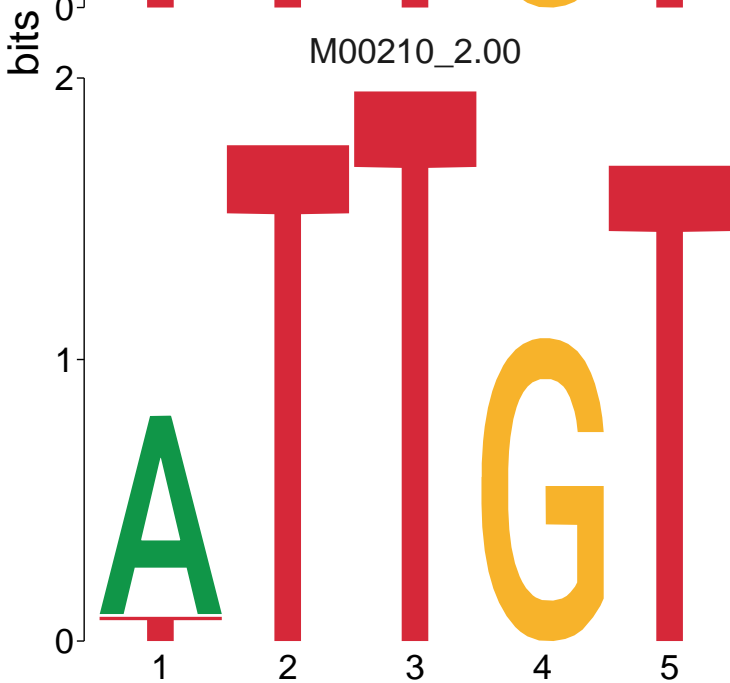
M03945_2.00



ARCH673_HMGbox_Sox



M00210_2.00



CH676_15_TTGTCTGCGT,BestGuess_AR

2

1

0

bits

15-TTGTCTGCGT,BestGuess:ARF27

2

1

0

1

2

3

4

5

6

7

8

9

10



CH679_20_ATTAGAACCA,BestGuess_PB

2

1

0

bits

ATTAGAACCA,BestGuess:PB0194.1_Zbtb1

2

1

0

1

2

3

4

5

6

7

8

9

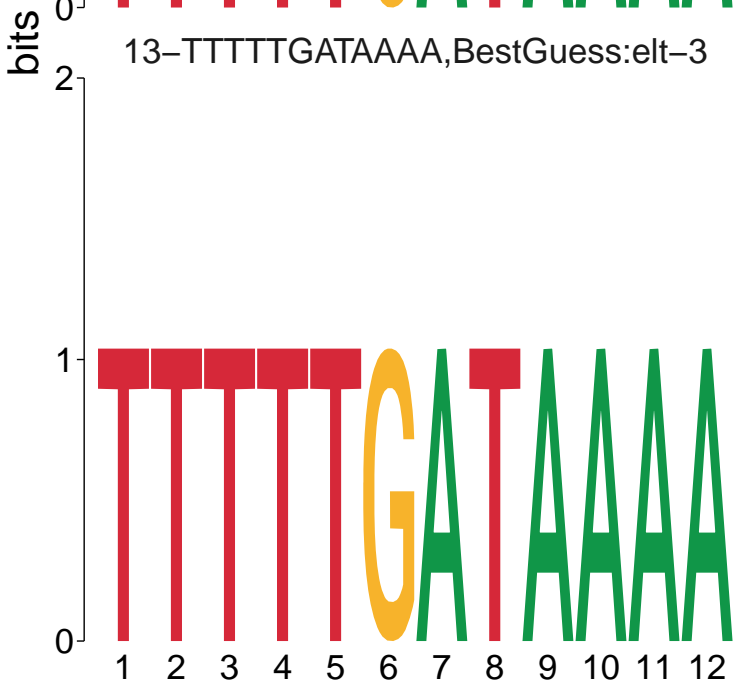
10



RCH680_13_TTTTTTGATAAAA,BestGuess_

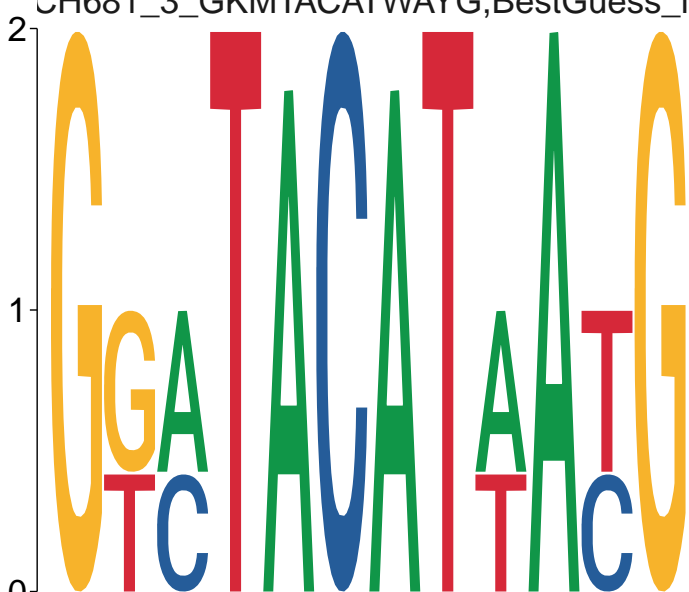


13-TTTTTGATAAAA,BestGuess:elt-3

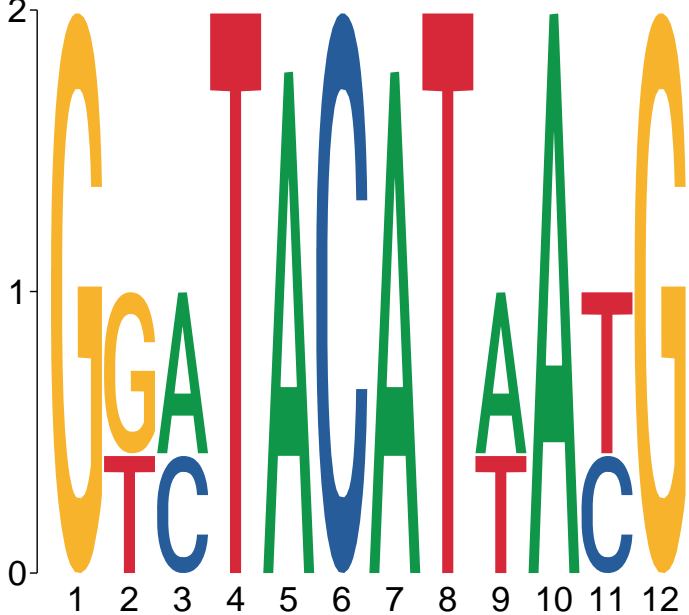


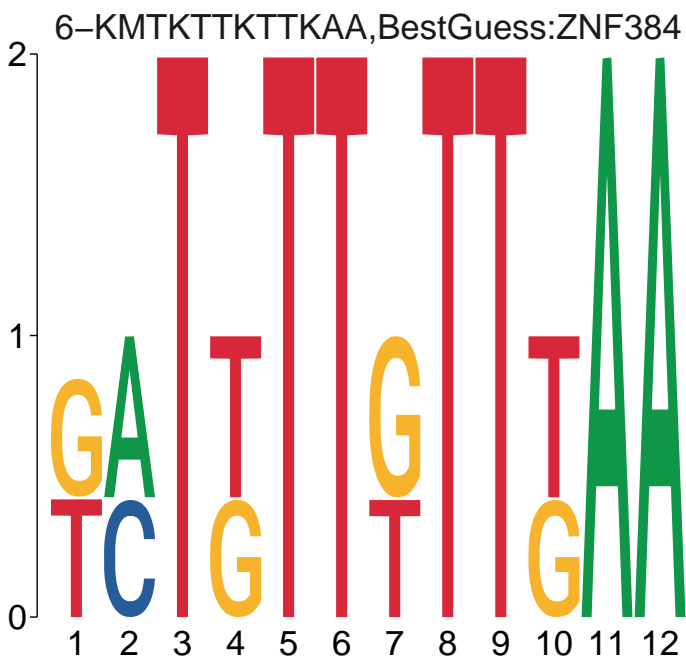
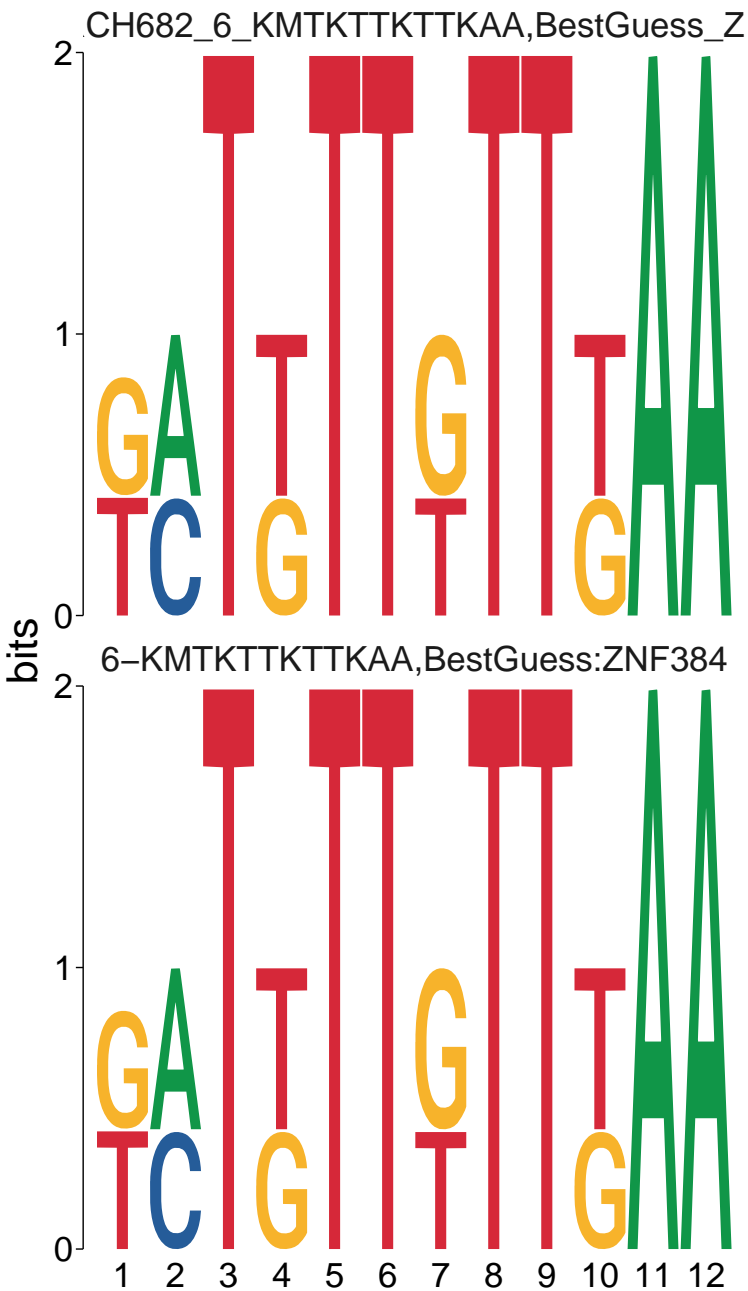
CH681_3_GKMTACATWAYG,BestGuess_N

bits



-GKMTACATWAYG,BestGuess:MAL8P1.4





CH686_18_CCATAAATGGAC,BestGuess_I

2

1

0

bits

ATAAATGGAC,BestGuess:MF0008.1_MAD:

2

1

0

1

2

3

4

5

6

7

8

9

10

11

12



_v1g229833_Nvec_v1g233675_Nvec_v1g2

2

1

0

bits

M01551_2.00

2

1

0

1

2

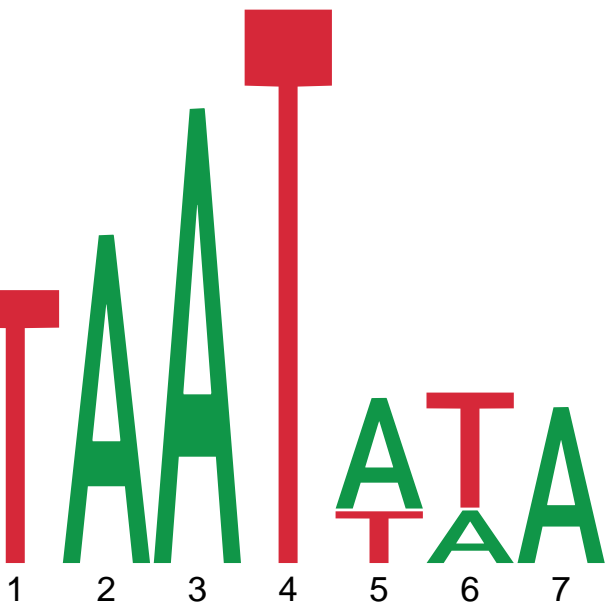
3

4

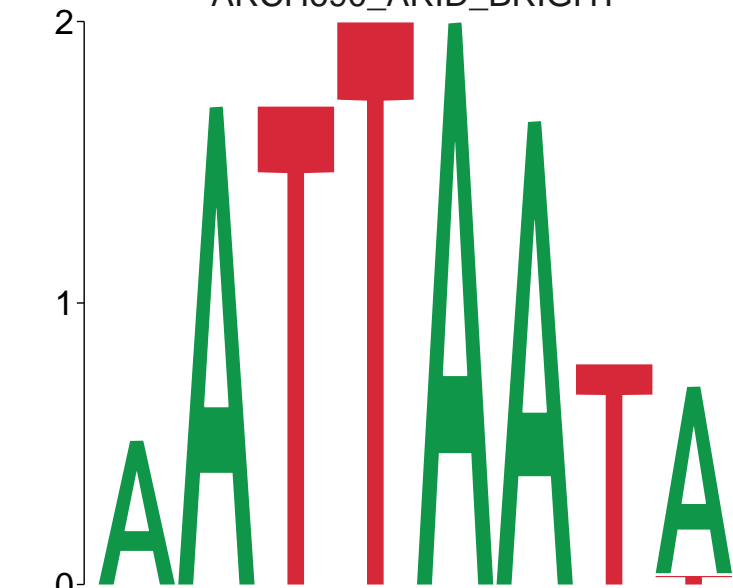
5

6

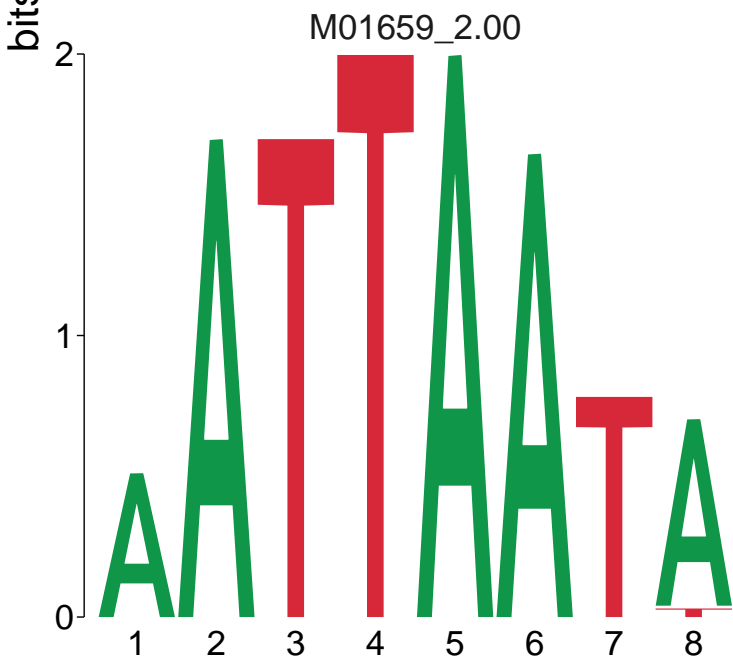
7



ARCH690_ARID_BRIGHT



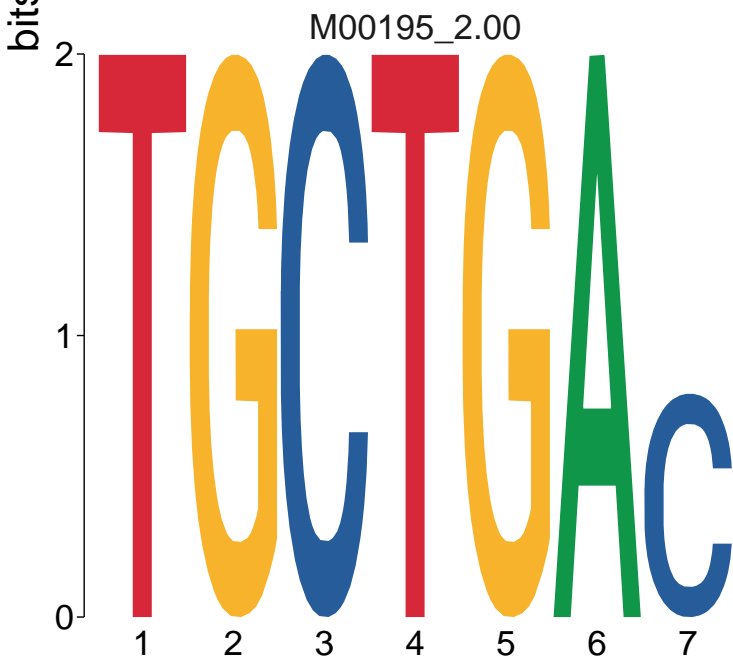
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ARCH694_HMGbox_Sox



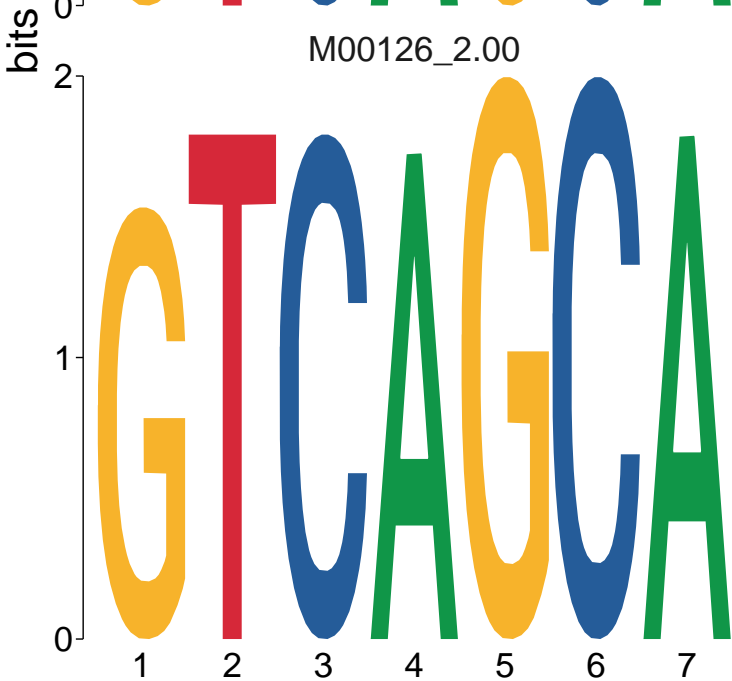
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ARCH695_bZIP



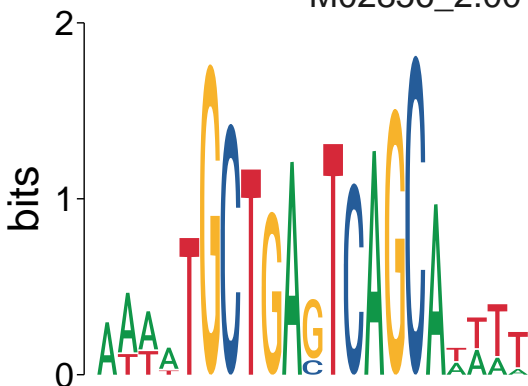
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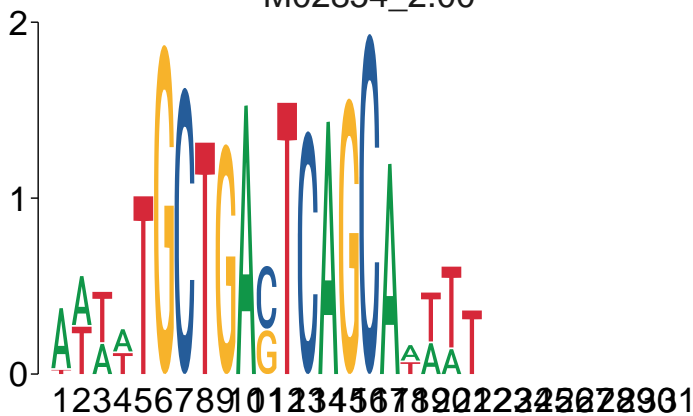
ARCH697_bZIP



M02856_2.00



M02854_2.00



ARCH698_bZIP



M04369 2.00



M04366_2.00



M04354 2.00



M04352 2.00



M04349 2.00



M04346 2.00



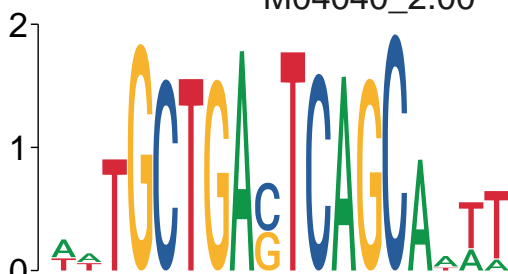
M02858 2.00



ARCH699_bZIP



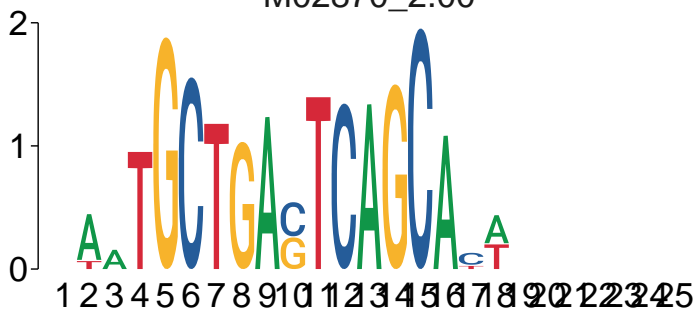
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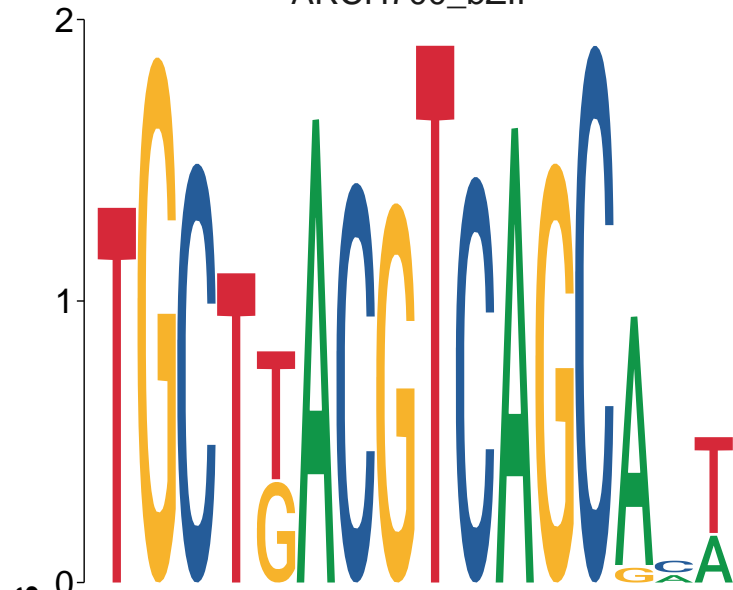
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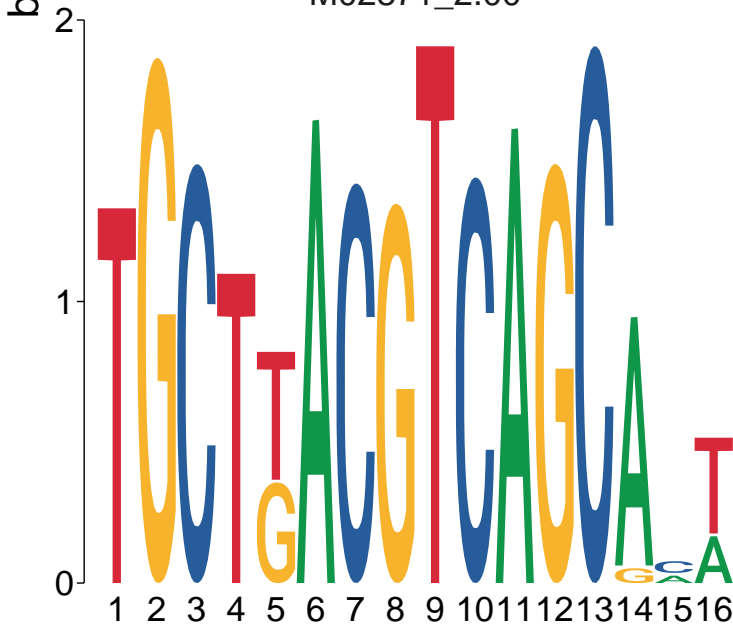
M02870_2.00



ARCH700_bZIP



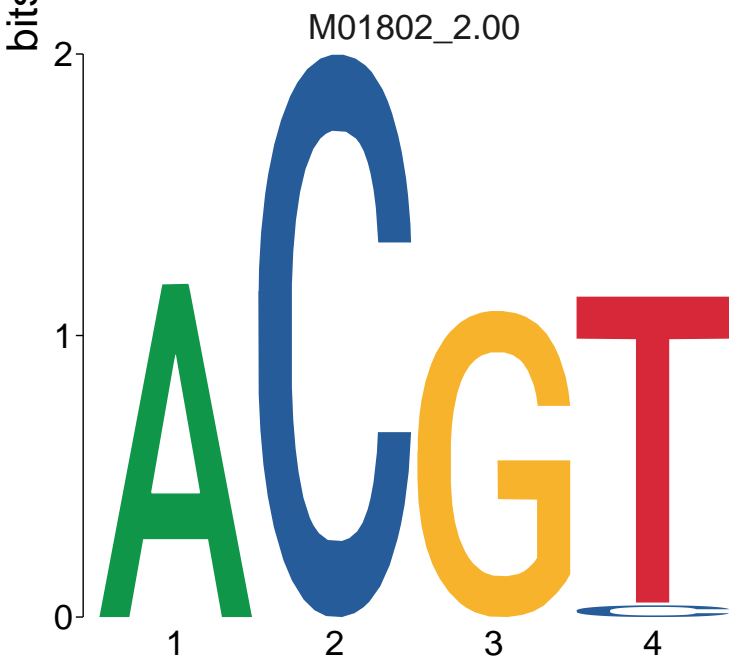
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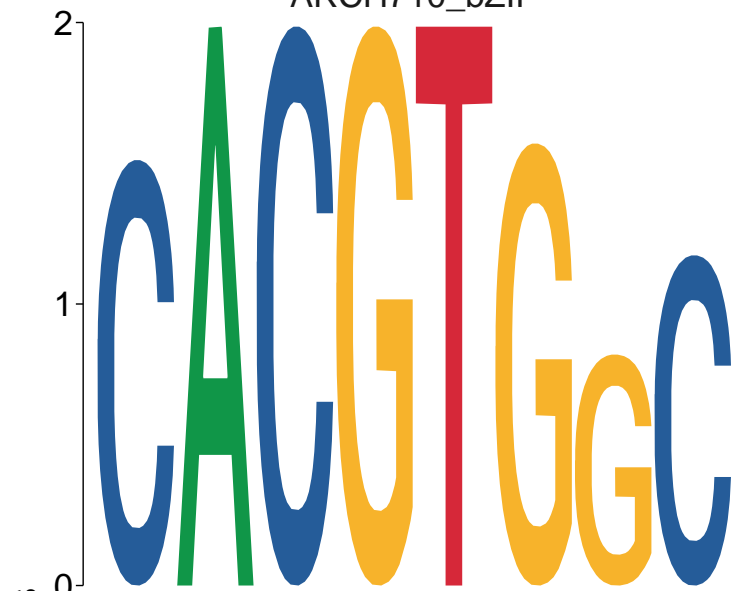
ARCH702_bZIP



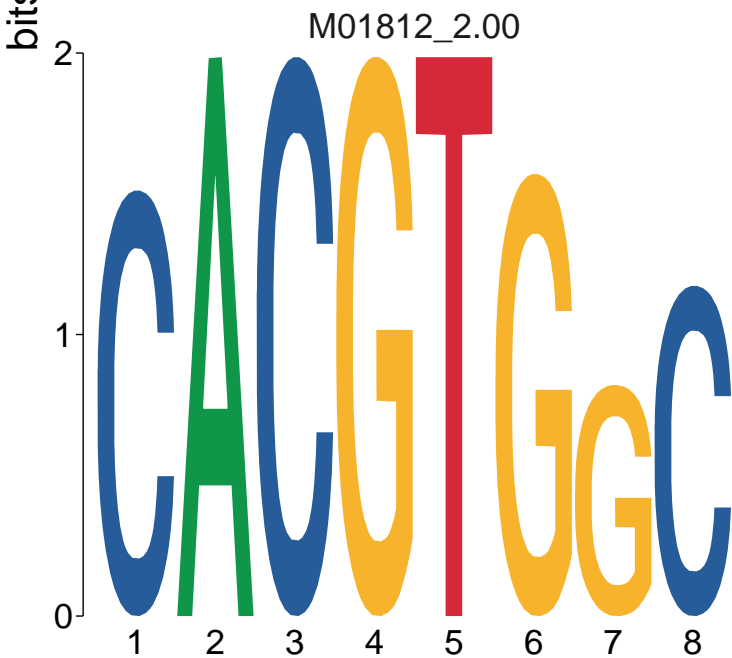
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ARCH710_bZIP



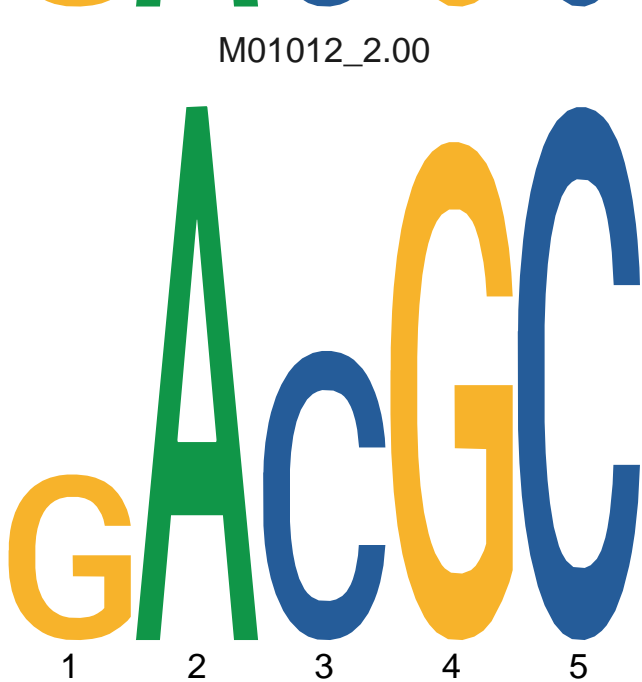
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ARCH712_Forkhead



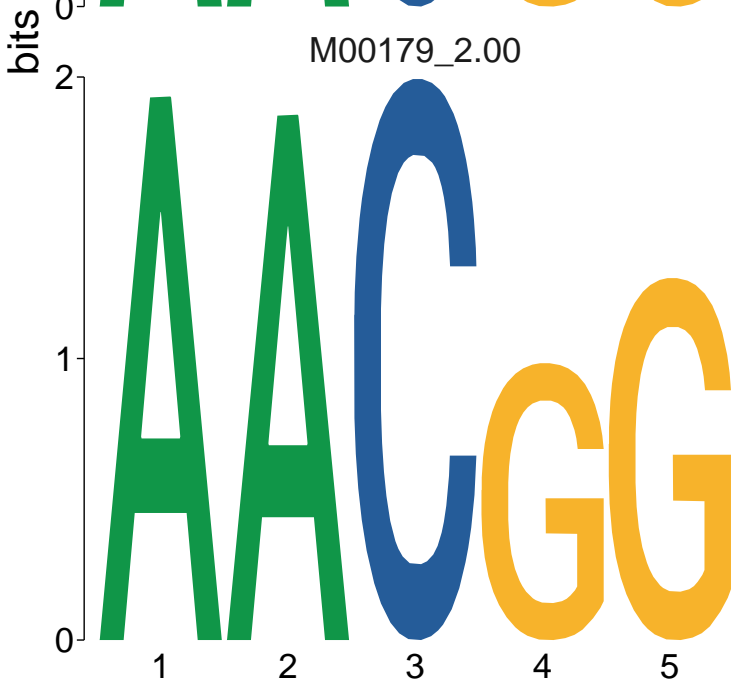
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ARCH713_Myb



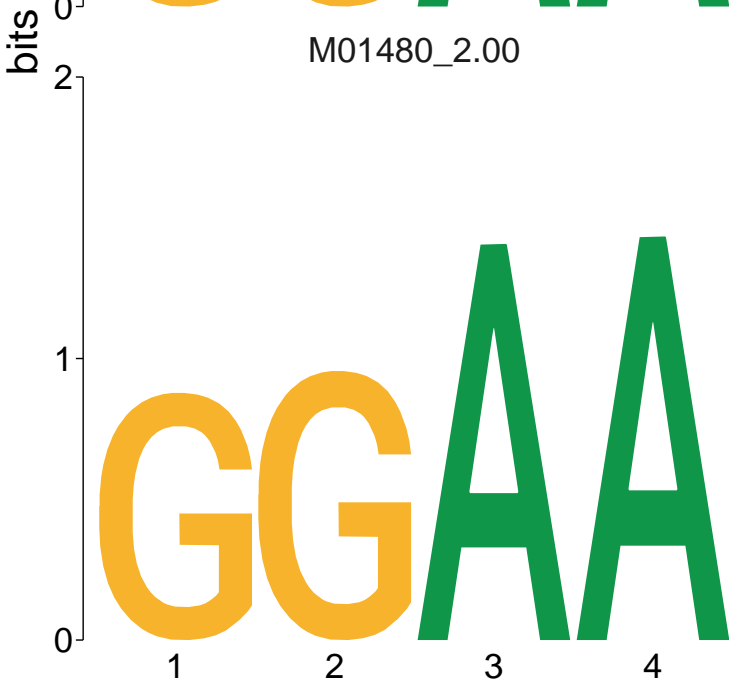
M00179_2.00



ARCH728_Ets



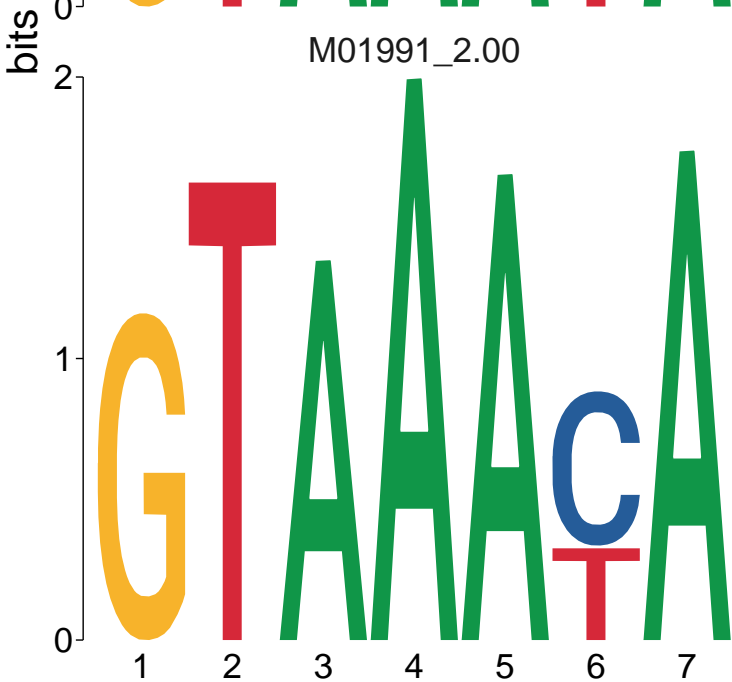
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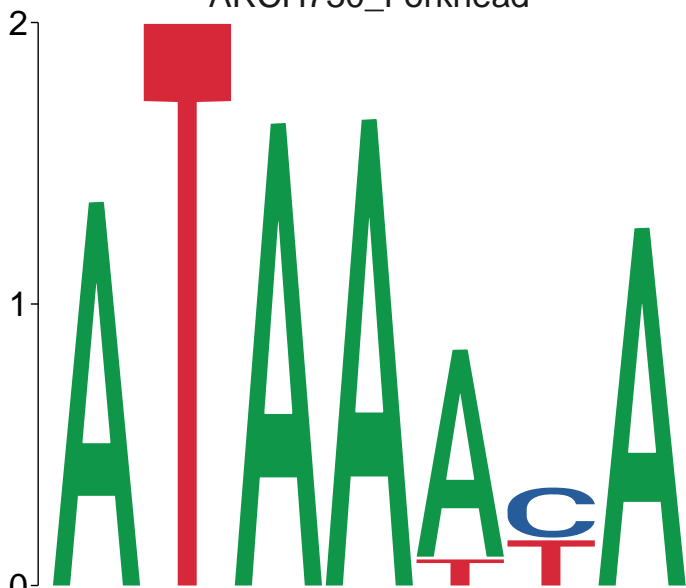
ARCH729_Nvec_v1g118122



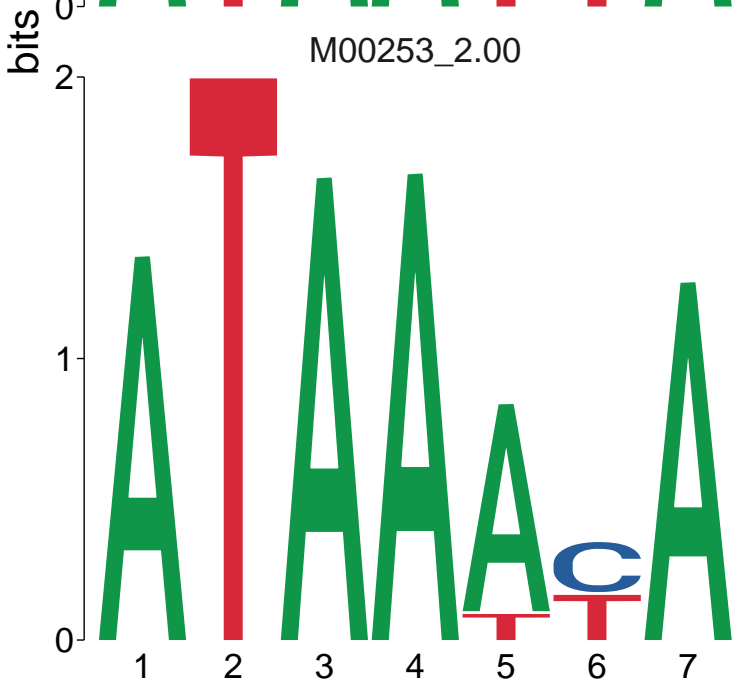
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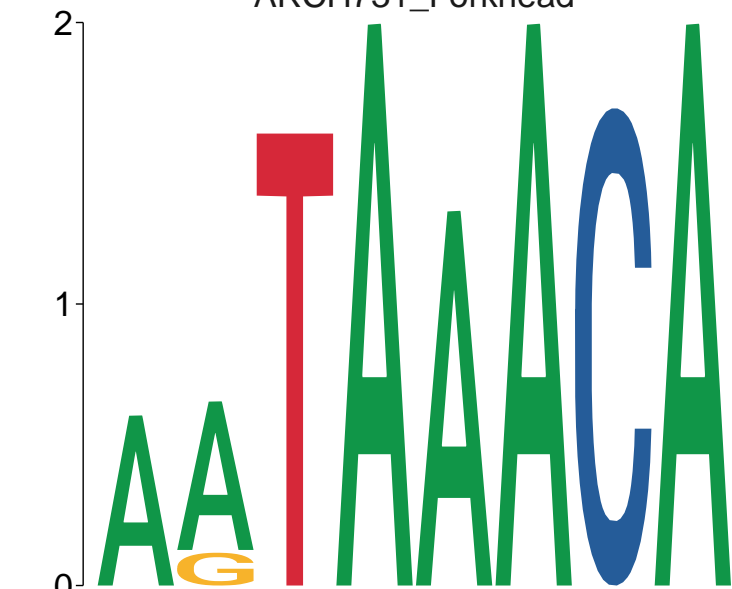
ARCH730_Forkhead



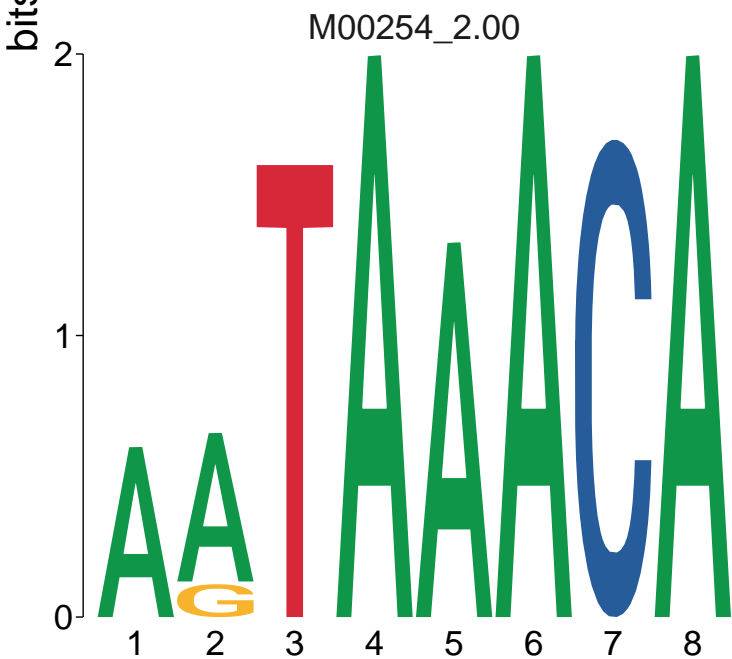
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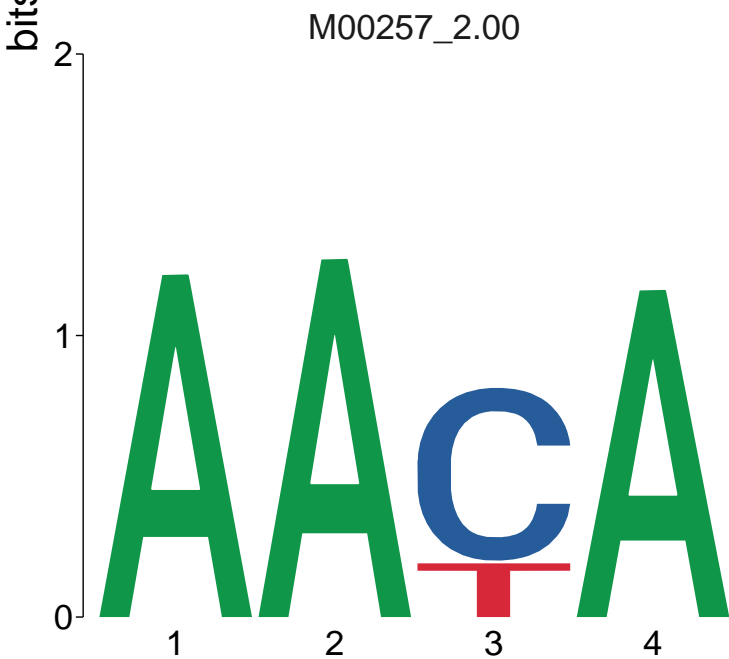
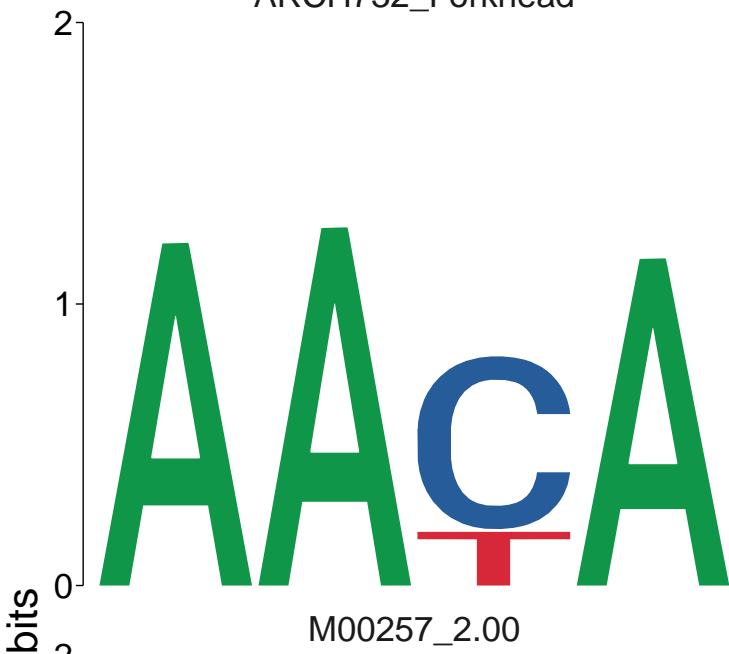
ARCH731_Forkhead



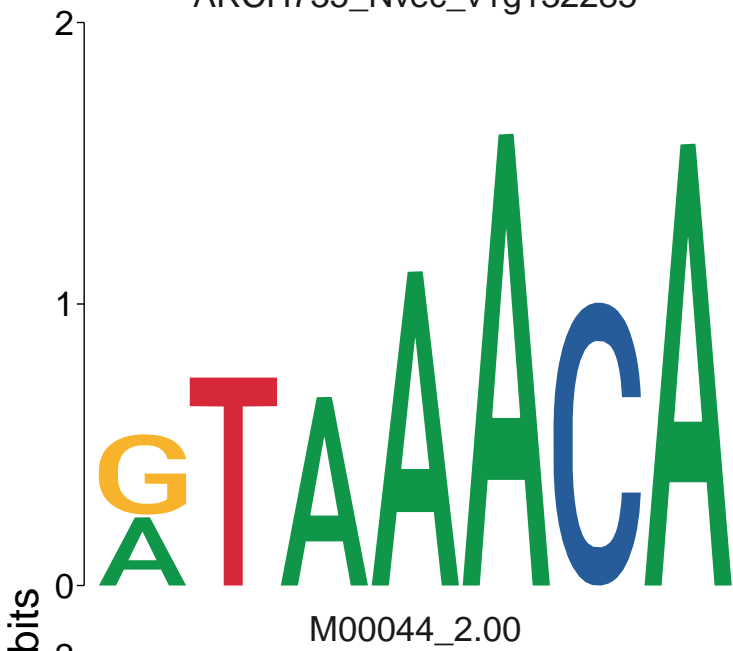
M00254_2.00



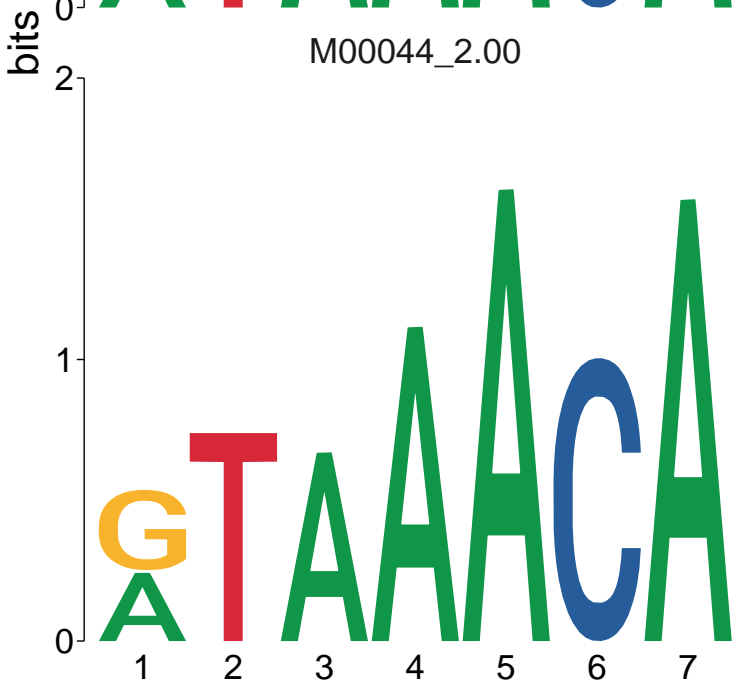
ARCH732_Forkhead



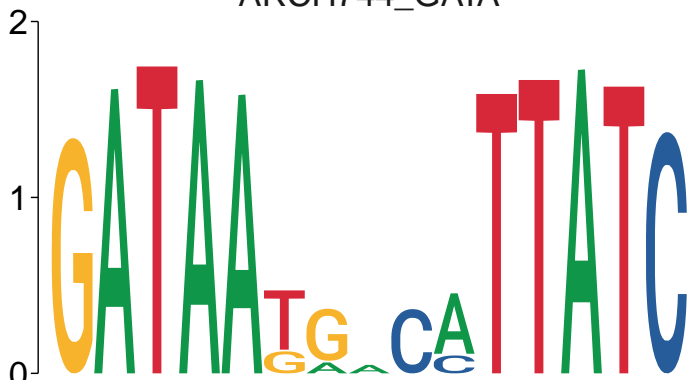
ARCH735_Nvec_v1g132285



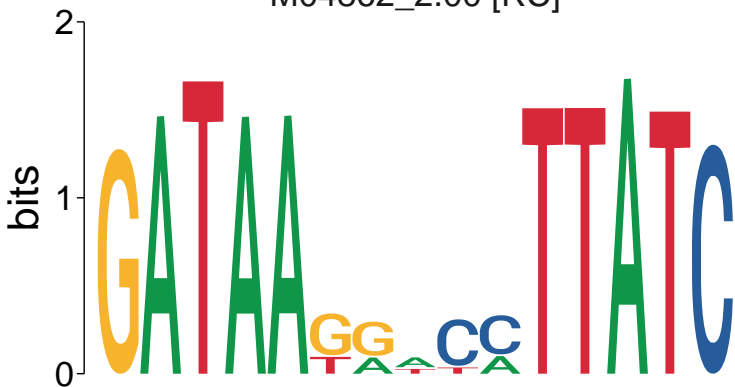
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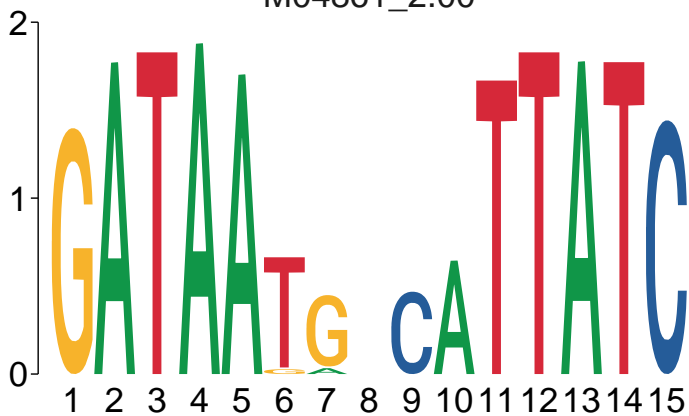
ARCH744_GATA



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M04861_2.00



33_Nvec_v1g233675_Nvec_v1g246590_N

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M00539_2.00

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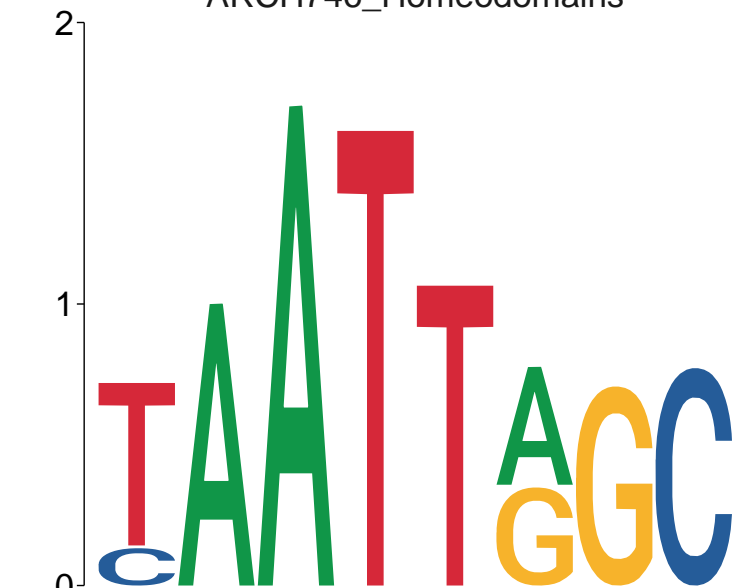
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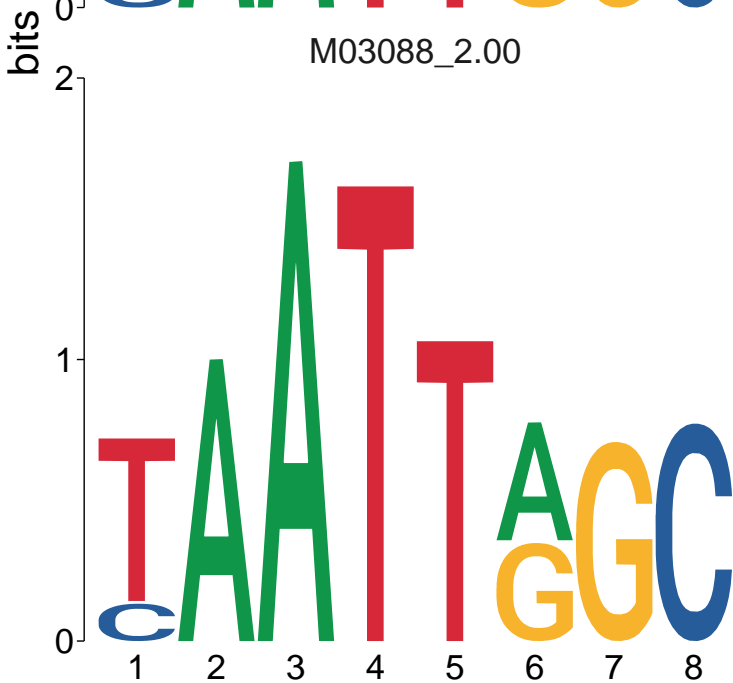
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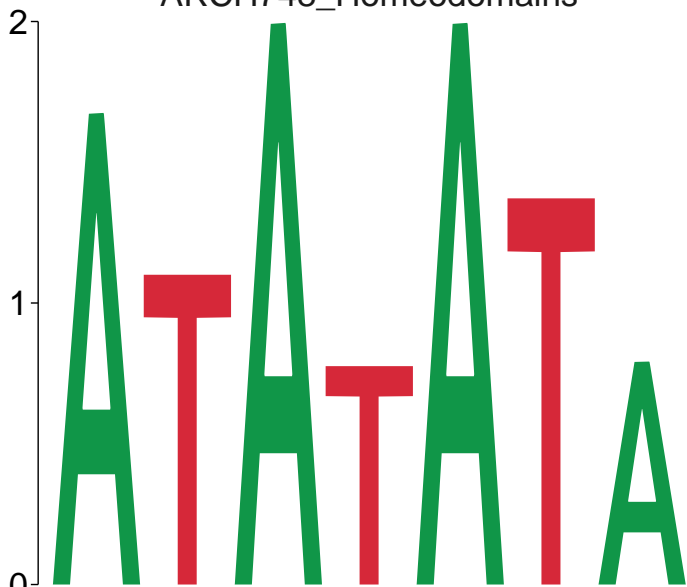
ARCH746_Homeodomains



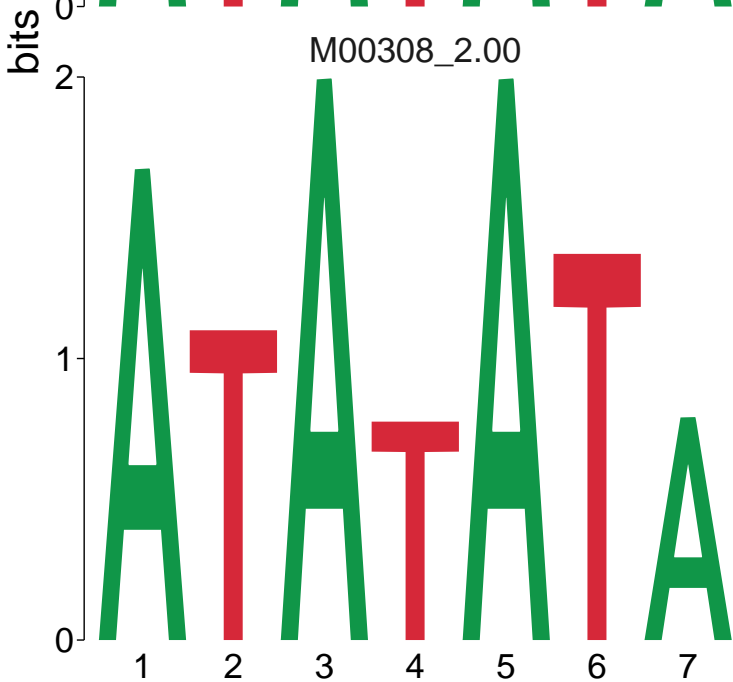
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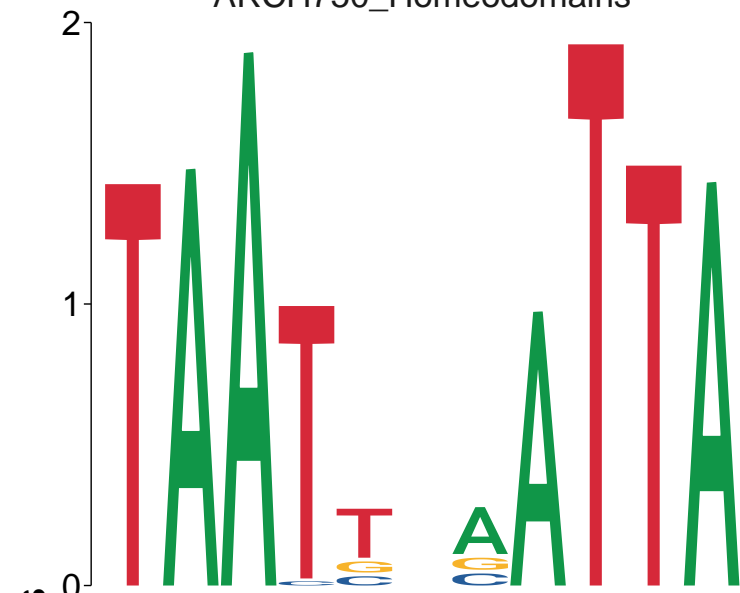
ARCH748_Homeodomains



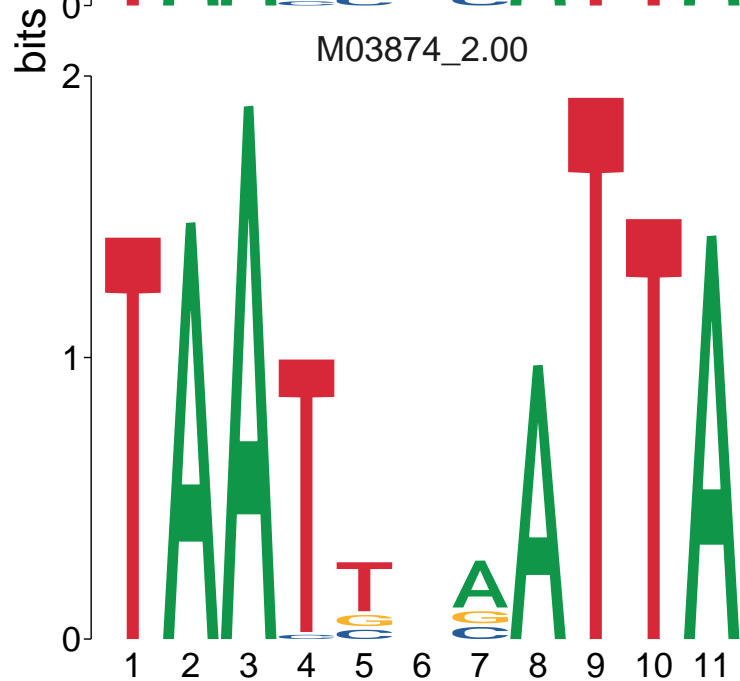
M00308_2.00



ARCH750_Homeodomains



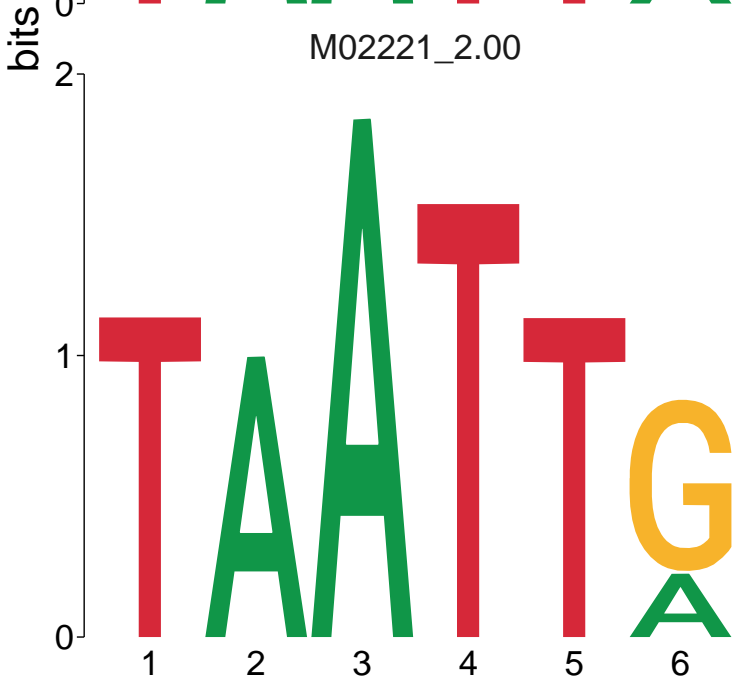
M03874_2.00



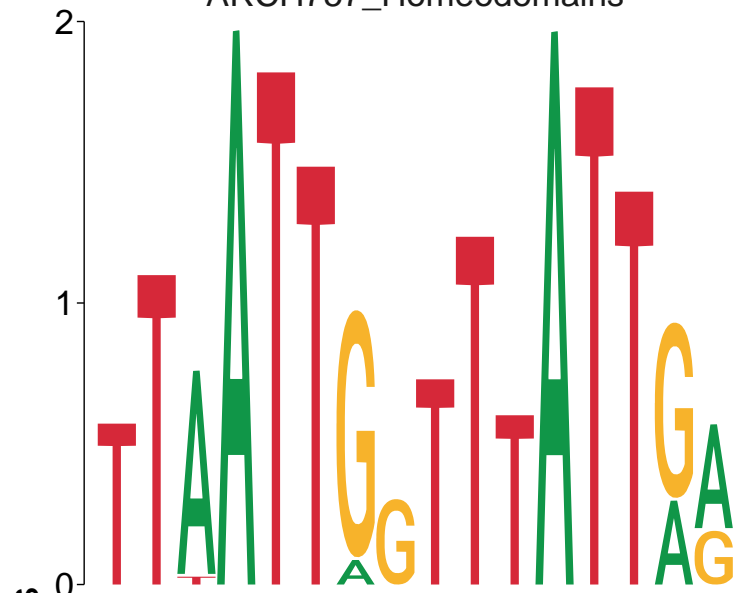
ARCH753_Homeodomains



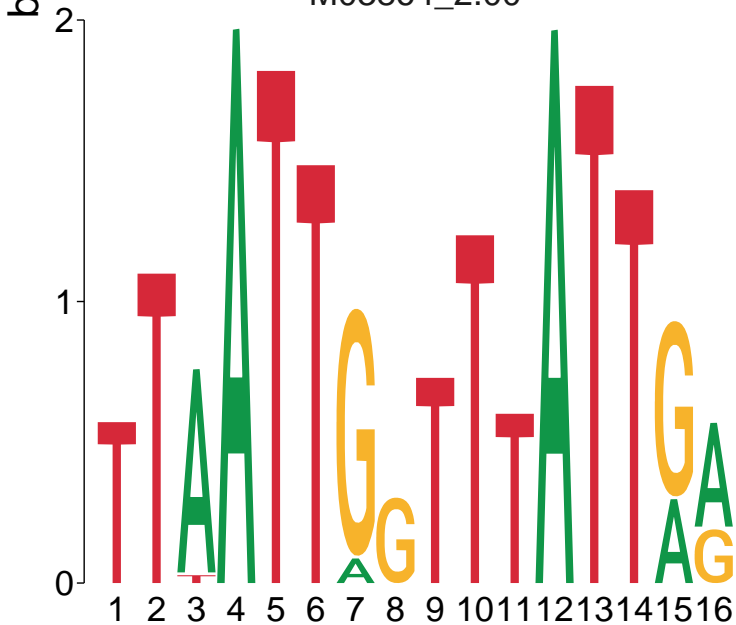
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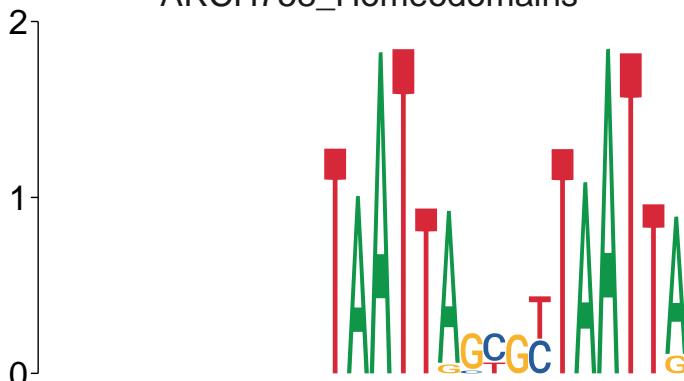
ARCH757_Homeodomains



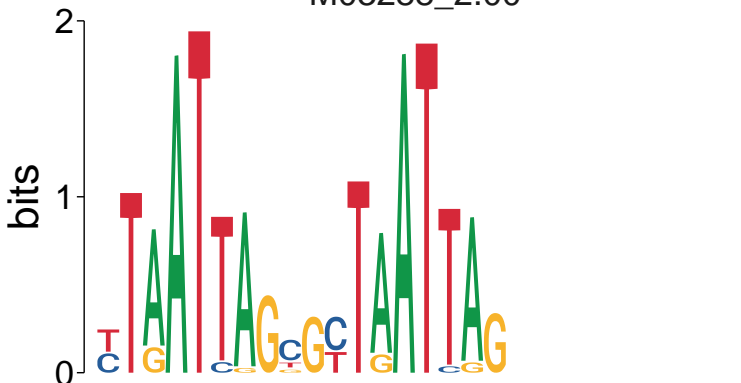
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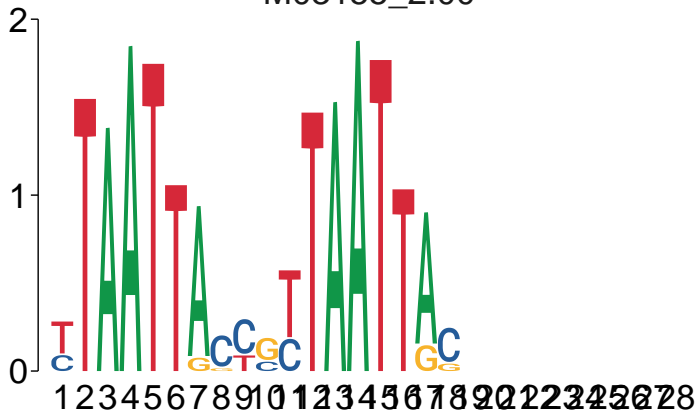
ARCH758_Homeodomains



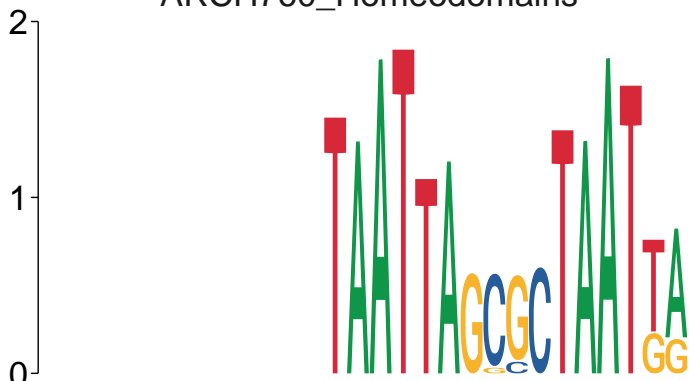
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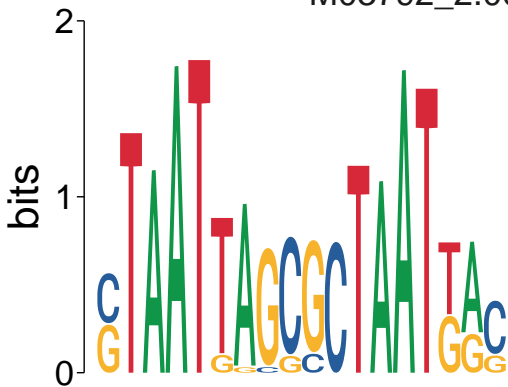
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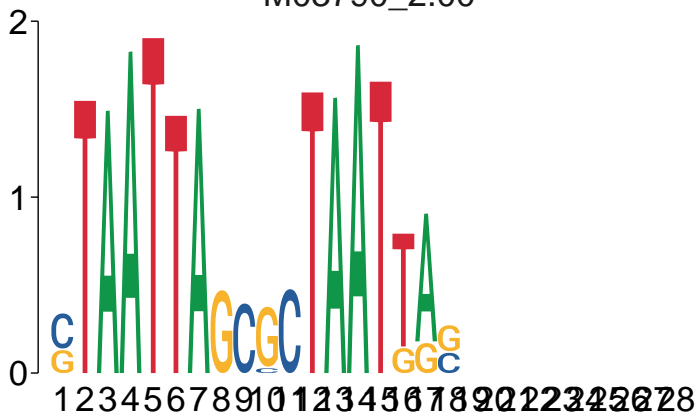
ARCH760_Homeodomains



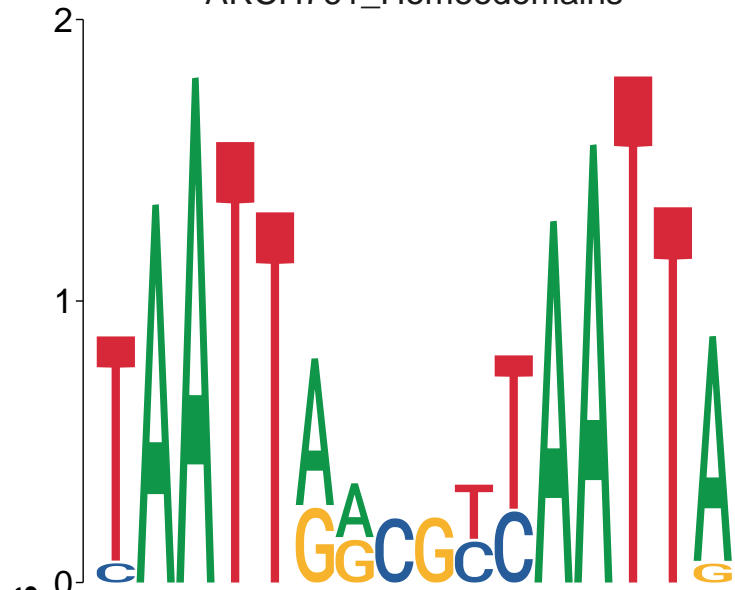
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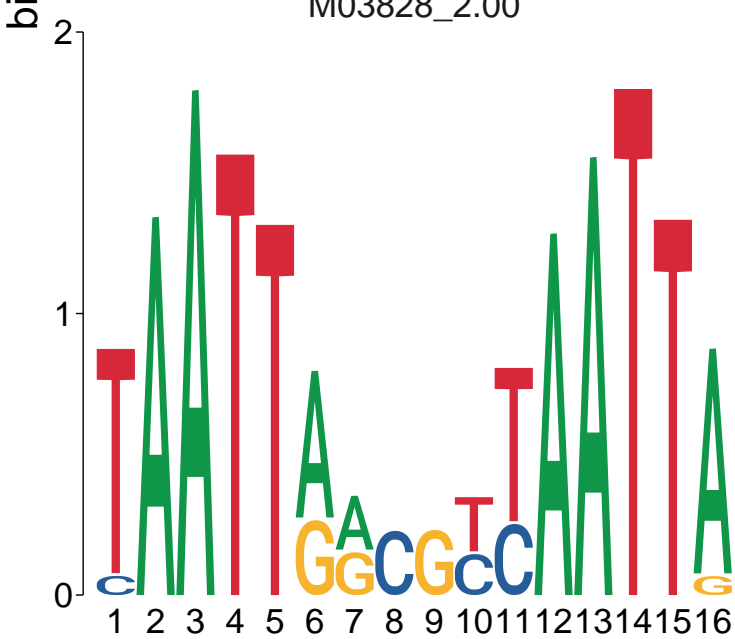
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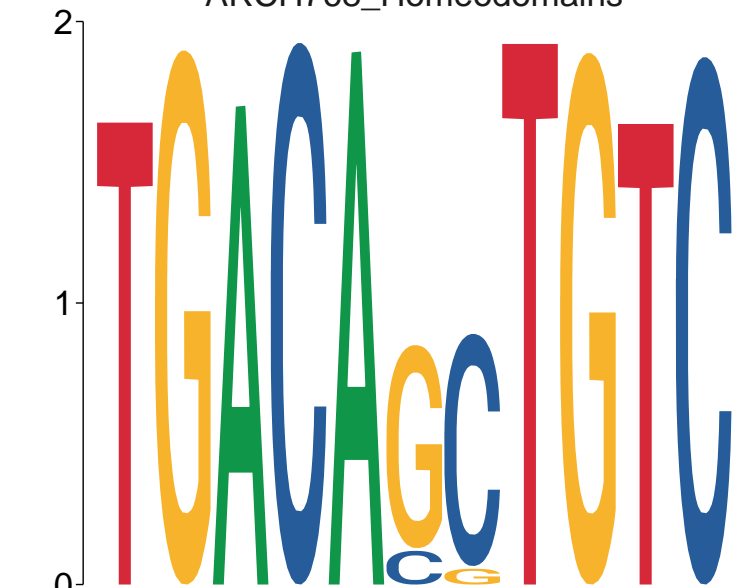
ARCH761_Homeodomains



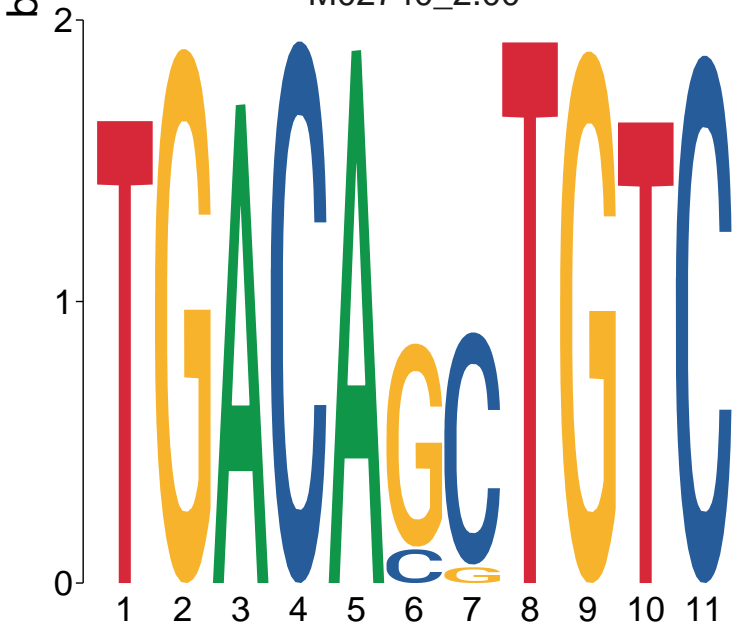
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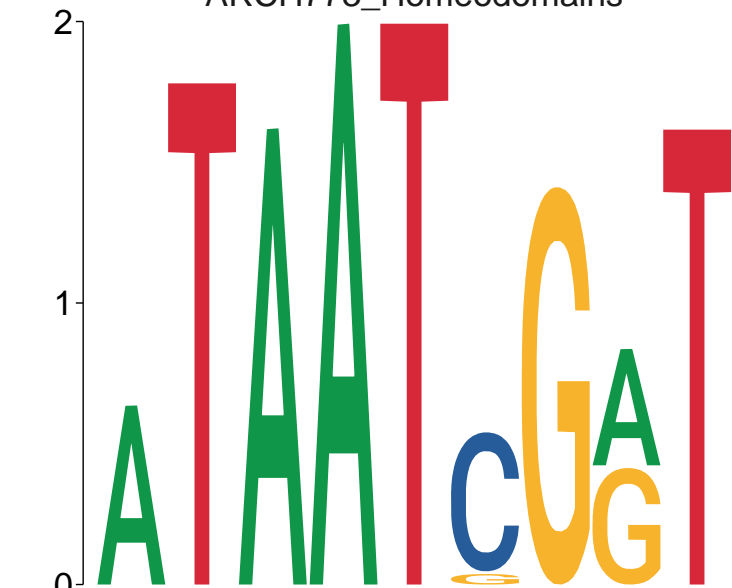
ARCH768_Homeodomains



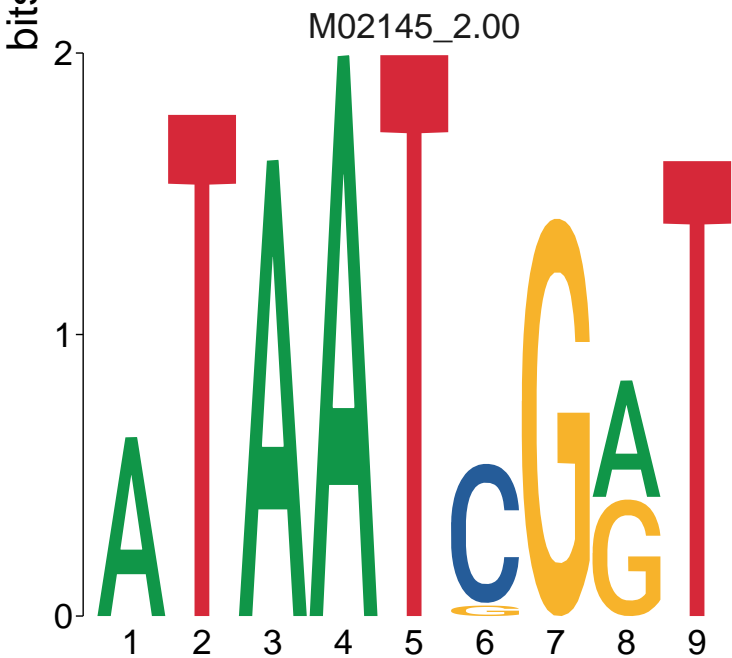
M02740_2.00



ARCH773_Homeodomains



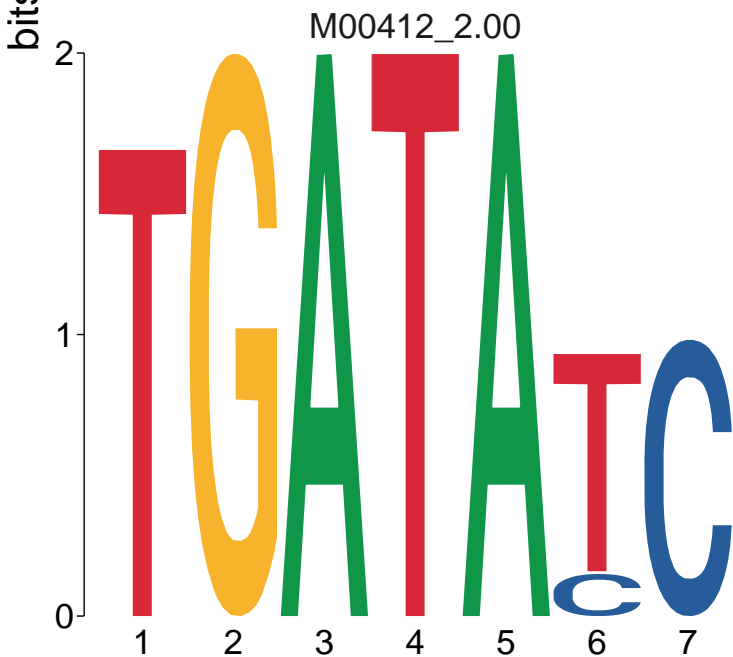
M02145_2.00



ARCH776_Homeodomains



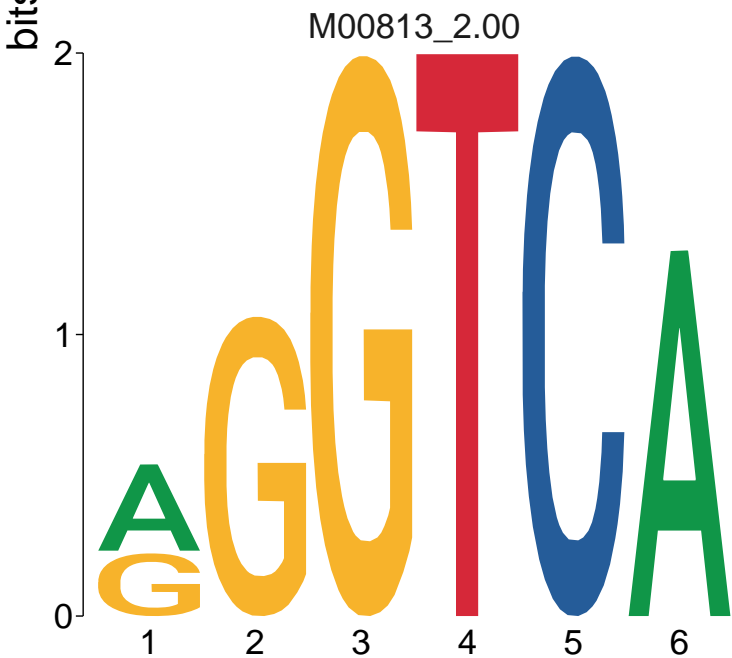
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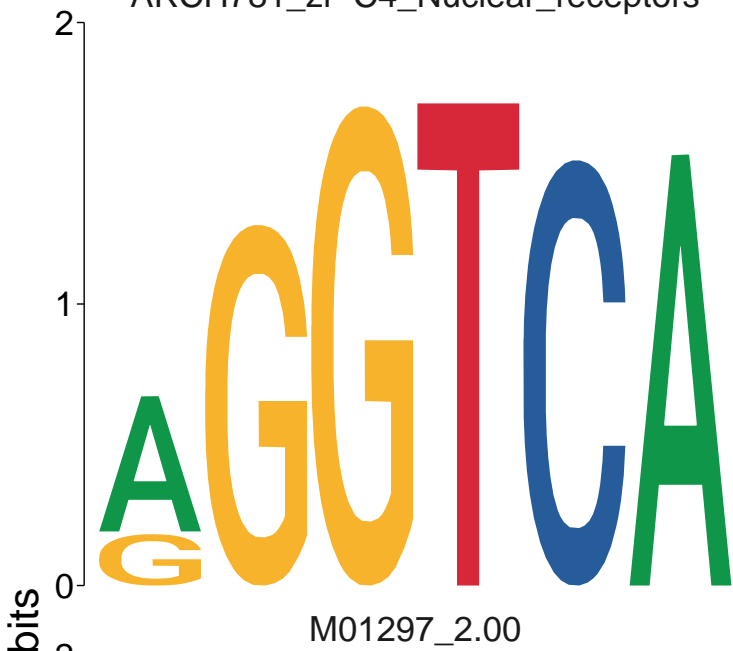
ARCH778_zf-C4_Nuclear_receptors



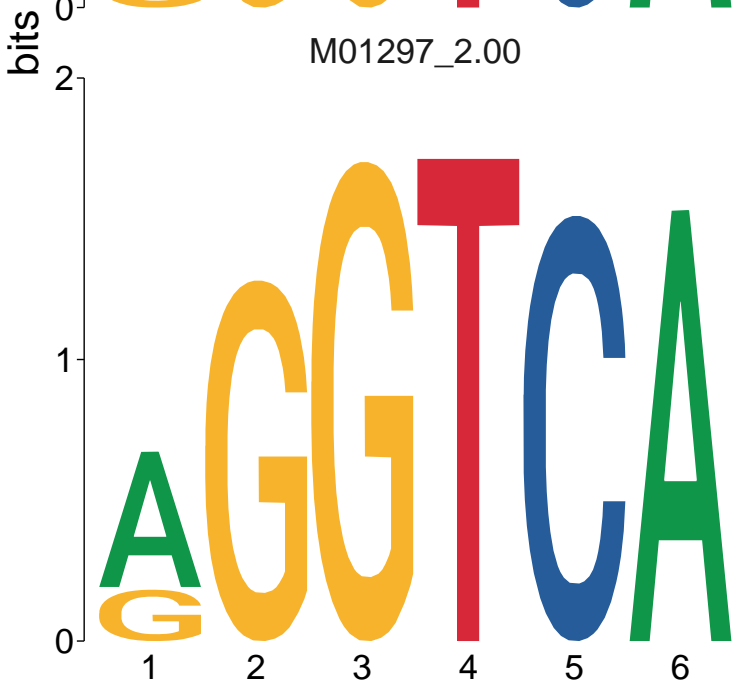
M00813_2.00



ARCH781_zf-C4_Nuclear_receptors



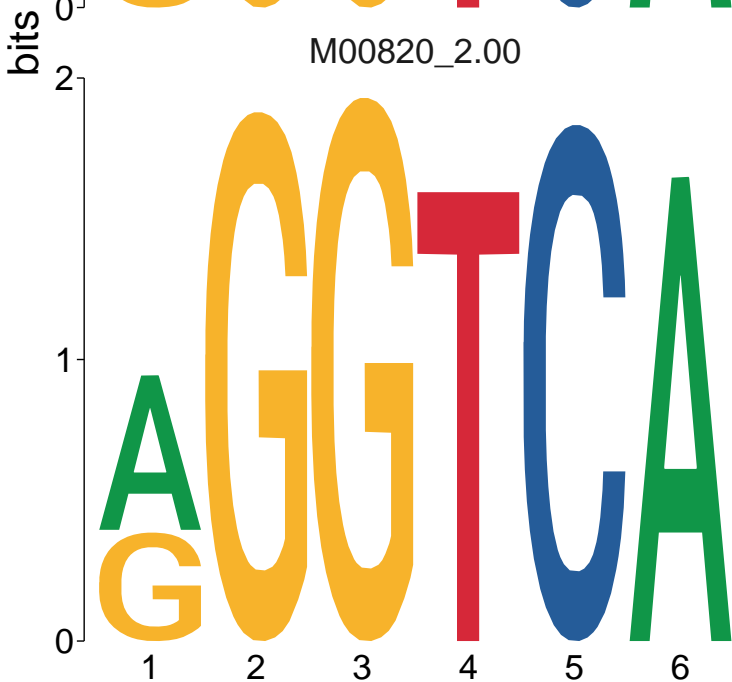
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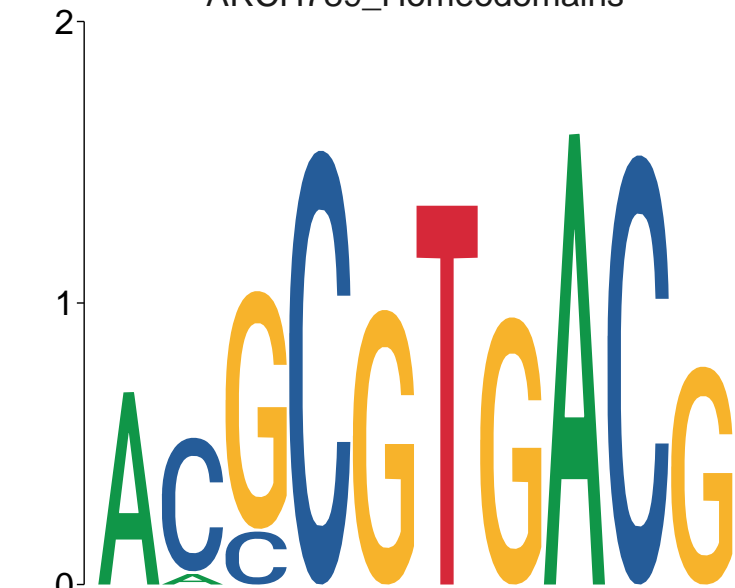
ARCH782_zf-C4_Nuclear_receptors



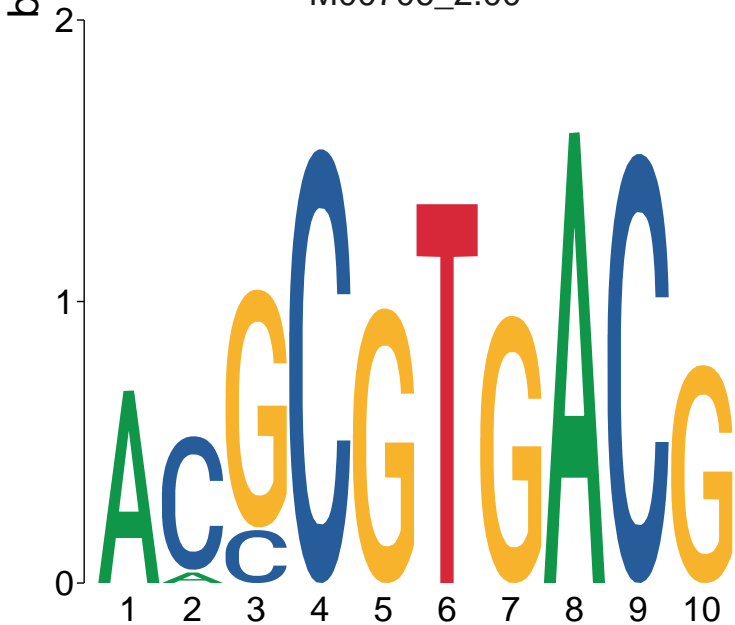
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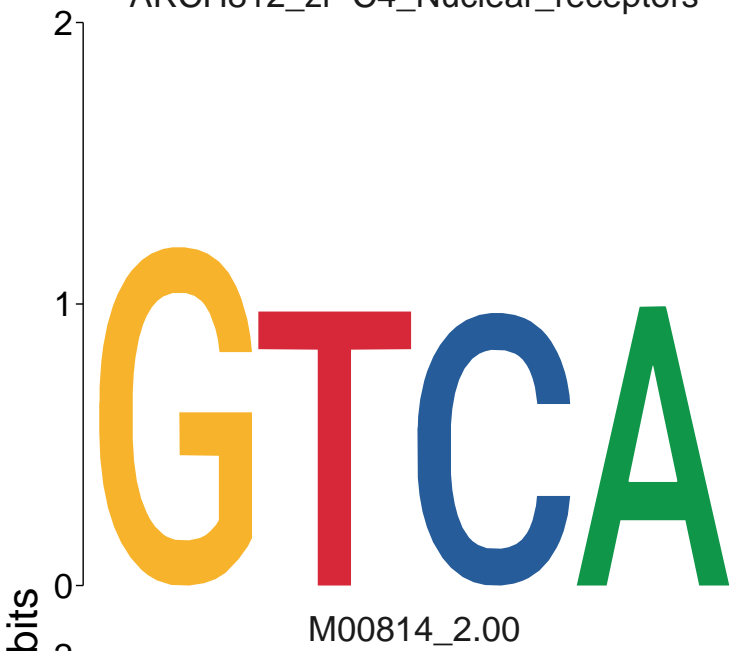
ARCH789_Homeodomains



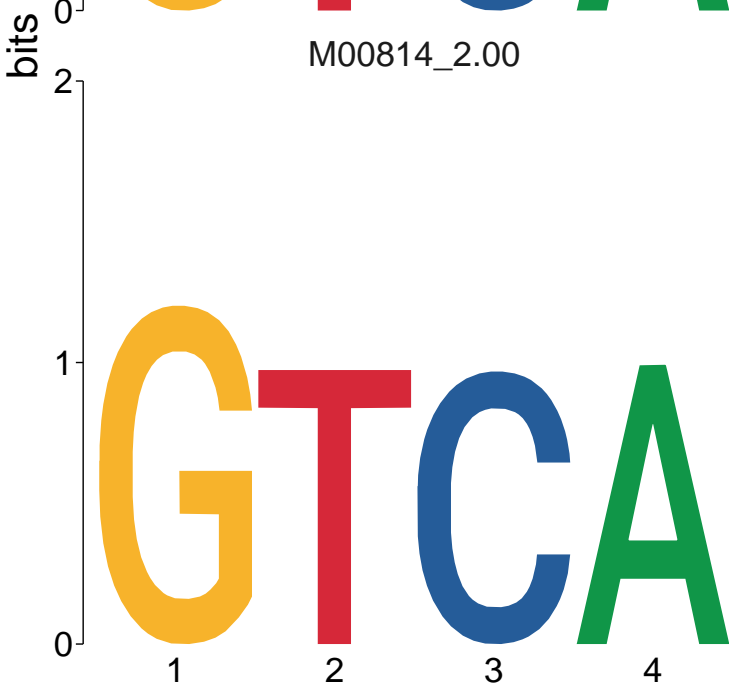
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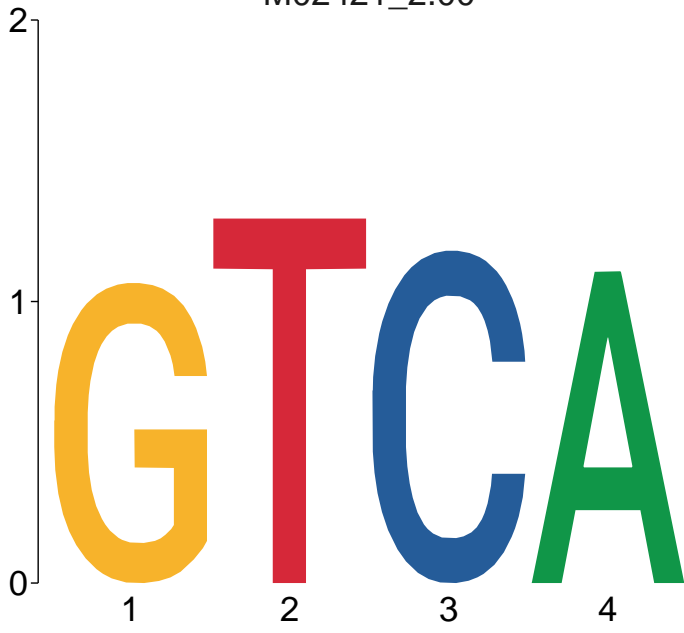
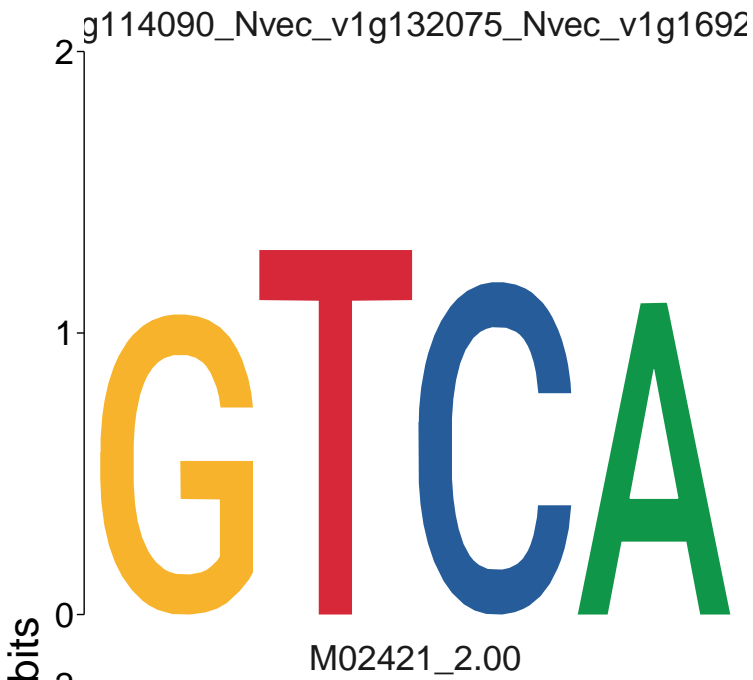


ARCH812_zf-C4_Nuclear_receptors

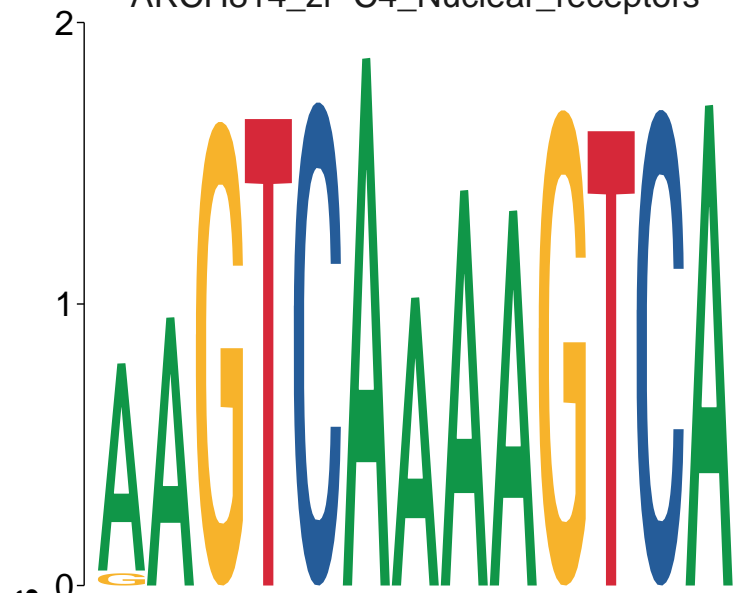


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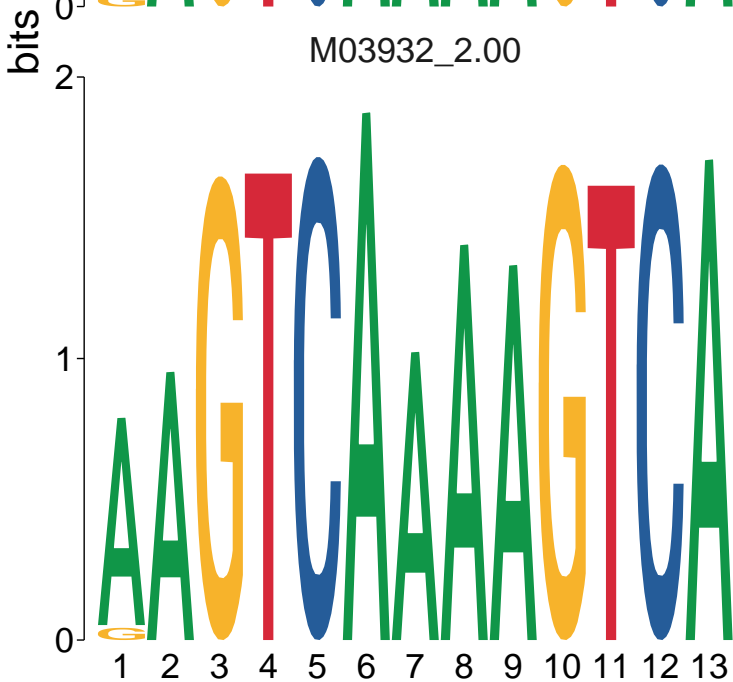




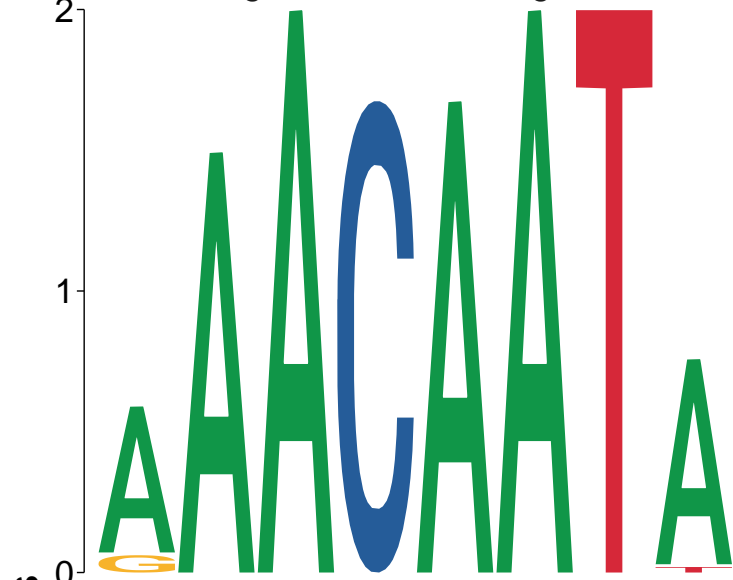
ARCH814_zf-C4_Nuclear_receptors



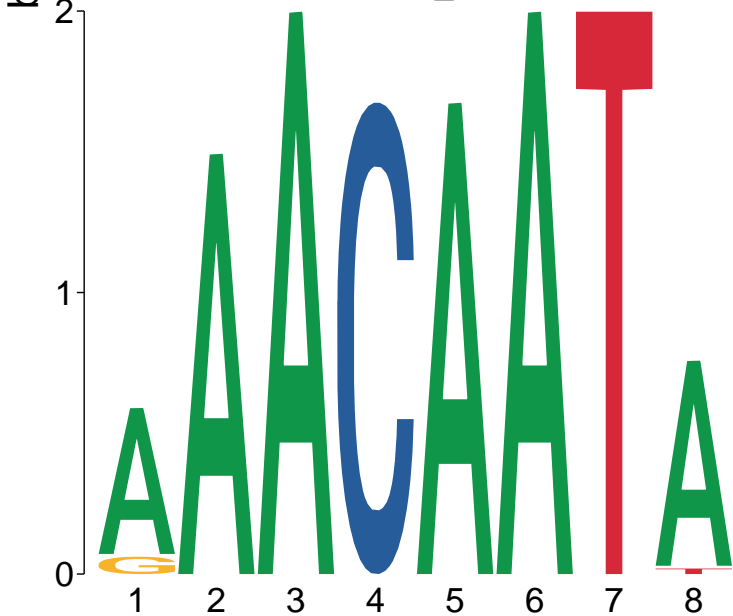
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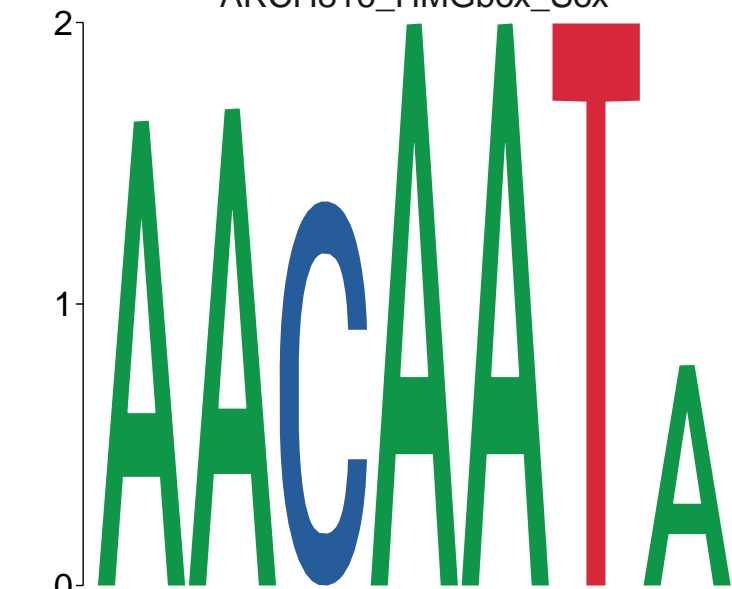
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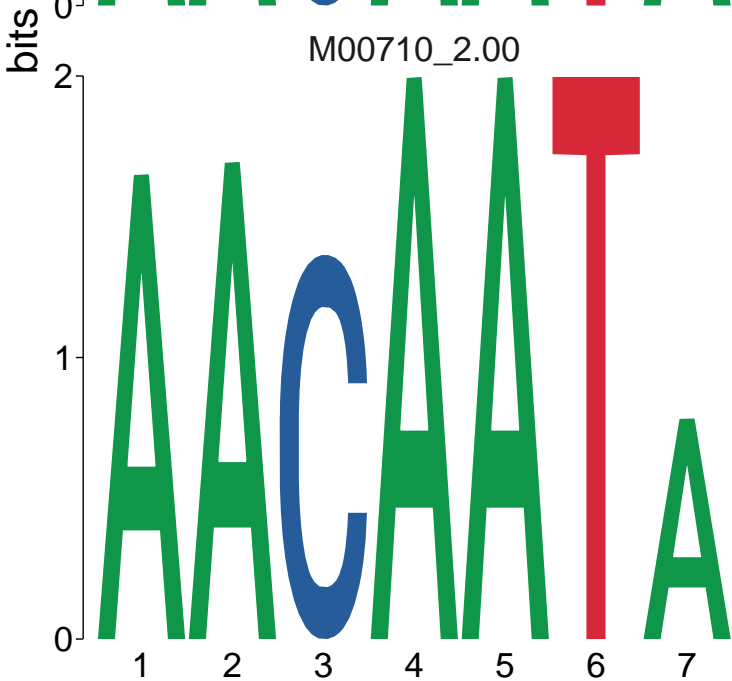
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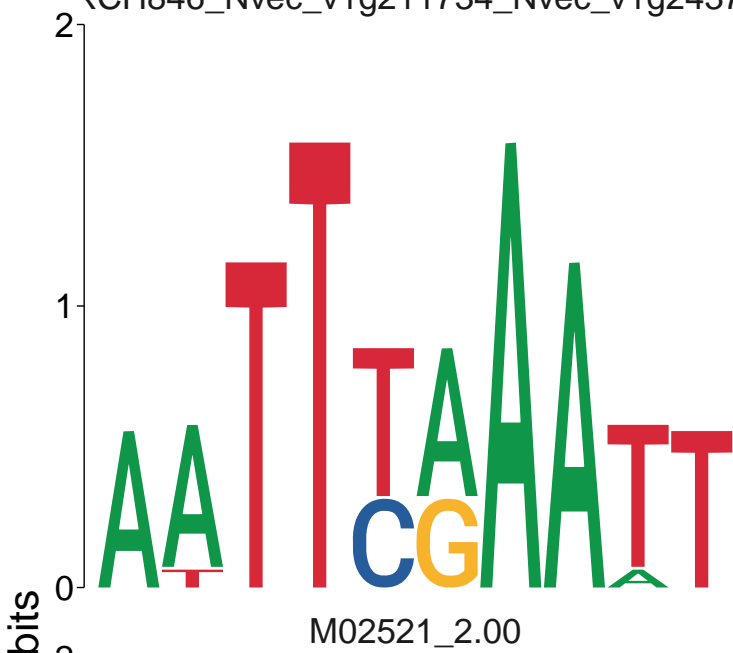
ARCH816_HMGbox_Sox



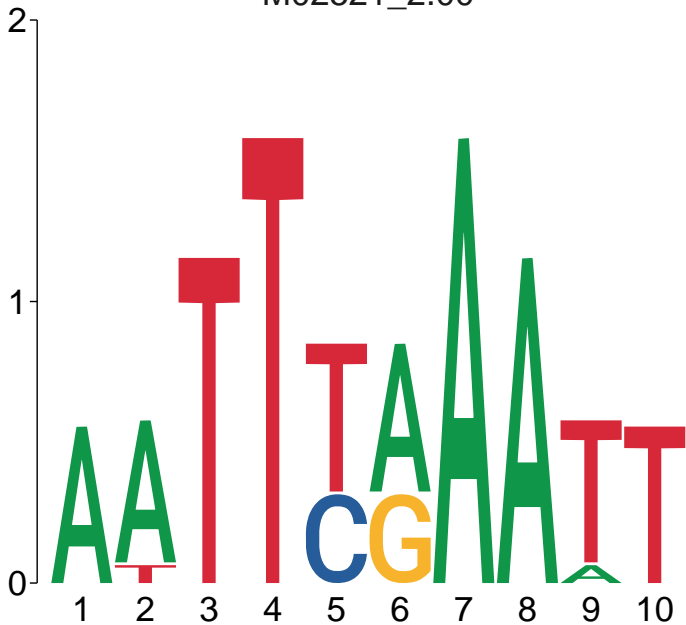
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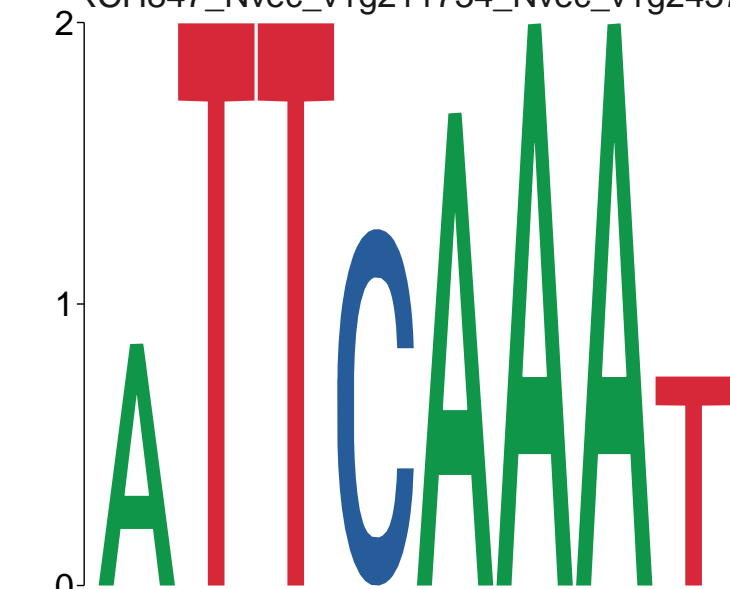
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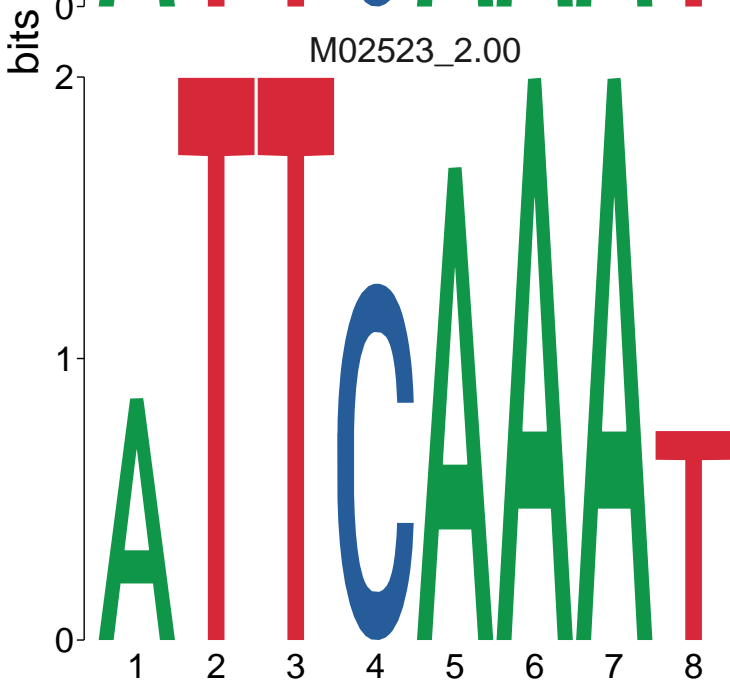
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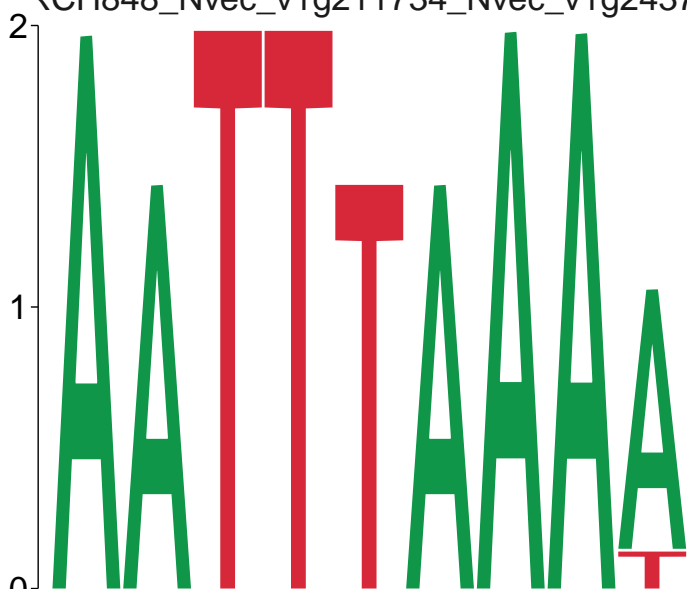
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M02523_2.00



RCH848_Nvec_v1g211734_Nvec_v1g2437:



M02524_2.00

