

Supplementary Figure 7

```
##load the library
library(motifStack)

getMatAlignOut <- function(pcmppath, outpath="output",
                           groupDistance=NA, trim=0.2){
  pcms <- readPCM(pcmppath)
  pfms<-lapply(pcms,pcm2pfm)
  matalign_path <- "./app/matalign-v4a"
  neighbor_path <- "./app/neighbor.app/Contents/MacOS/neighbor"
  system(paste("perl MatAlign2tree.pl --in . --pcmppath", pcmppath,
               "--out", outpath,
               "--matalign", matalign_path,
               "--neighbor", neighbor_path,
               "--tree","UPGMA"))
  newickstrUPGMA <-
    readLines(con=file.path(outpath, "NJ.matalign.distMX.nwk"))
  phylog <- newick2phylog(newickstrUPGMA, FALSE)
  leaves <- names(phylog$leaves)
  motifs <- pfms[leaves]
  if(!is.na(groupDistance)){
    motifSig <-
      motifSignature(motifs, phylog,
                    groupDistance=groupDistance,
                    min.freq=1, trim=trim)
    sig <- signatures(motifSig)
    gpCol <- sigColor(motifSig)
  }else{
    motifSig <- NA
    sig <- NA
    gpCol <- NA
  }

  return(list(phylog=phylog, sig=sig, gpCol=gpCol,
             motifs=DNAmotifAlignment(motifs),
             leaves=leaves,
             unaligned.pfms=motifs))
}

pcmppath <- dir("pcmsUni", include.dirs=TRUE)
matAlignOut <- lapply(file.path("pcmsUni", pcmppath),
                      getMatAlignOut, groupDistance=4)

description <- c("## Dimeric motifs separated from monomeric motifs from the same TF\n\nFor most dimeric
colorSet <- c("Dm"="#00FC00",
              "Mm"="brown", "Ms"="#F69156",
              "Hs"="#D900D9")

## kexpand is function to extend knitr.
# kexpand<-function(.ele, id, cap, figheight, des){
#   text <- paste("{{des}}\n``{r {{cap}}},fig.cap='{{cap}}',fig.height={{figheight}},echo=",
#   ifelse(id==1,"TRUE","FALSE"),
#   "}\n
```

```

# leaveNames <- gsub('^(Dm|Mm|Ms|Hs)_', '', .ele$leaves)\n
# species <- colorSet[gsub(\"^(Dm|Mm|Ms|Hs).*$\", \"\\\\1\", .ele$leaves)]\n
# motifPiles(phylog=.ele$phylog, .ele$motifs,
#             .ele$sig,
#             col.tree=species, col.leaves=species,
#             col.pfms2=.ele$gpCol,
#             col.pfms2.width=.01, labels.leaves=leaveNames,
#             plotIndex=c(FALSE,TRUE), IndexCex=1.5,
#             groupDistance=4, clabel.leaves=3)\n
# ```\n\", sep="")
#   cat(knit(text=knit_expand(text=text)))
# }

sta <- mapply(function(.ele, name, ID, des){
  kexpand(.ele, id=ID, cap=paste0("Supplementary Figure 7.", name),
    figheight=ceiling(.25*length(.ele$leaves)), des)
}, matAlignOut, pcmpath, 1:length(pcmpath), description)

```

Dimeric motifs separated from monomeric motifs from the same TF

For most dimeric clusters, one or more monomeric motifs cluster with a Drosophilar motif, suggesting that the absence of a fly TF in a dimeric cluster may be a methological difference rather than a biological one.

```

leaveNames <- gsub('^(Dm|Mm|Ms|Hs)_', '', .ele$leaves)

species <- colorSet[gsub(\"^(Dm|Mm|Ms|Hs).*$\", \"\\\\1\", .ele$leaves)]

motifPiles(phylog=.ele$phylog, .ele$motifs,
            .ele$sig,
            col.tree=species, col.leaves=species,
            col.pfms2=.ele$gpCol,
            col.pfms2.width=.01, labels.leaves=leaveNames,
            plotIndex=c(FALSE,TRUE), IndexCex=1.5,
            groupDistance=4, clabel.leaves=3)

```

There is no monomeric motif in mammals.

The dimeric motif cluster is different from the above clusters. There are overlaps for the subunits of monomeric motif.

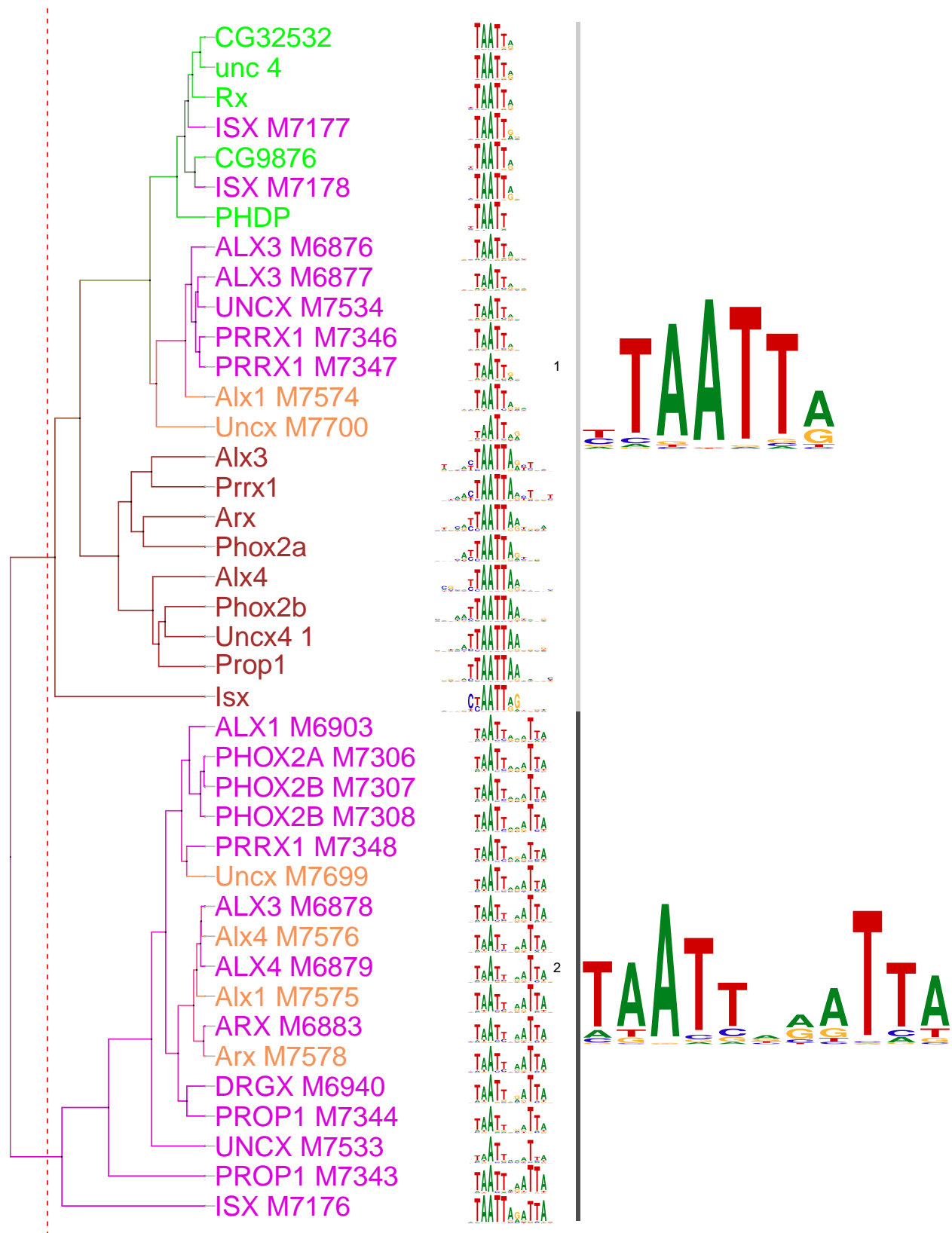
For MEOX/LHX cluster, there are some exceptions like LHX6_M7193 and Lhx_M7636. The subunit of both has stong G after TAATT comparing to other monomeric motifs with stong A after TAATT.

Difference by platform.

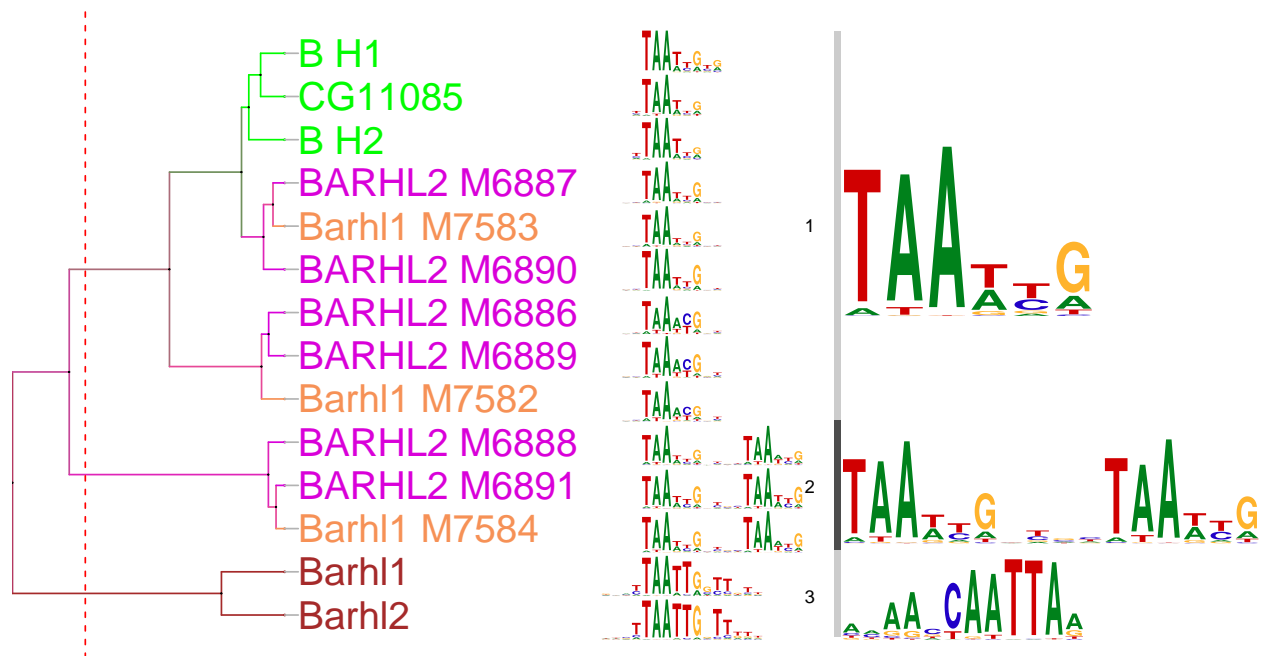
The absence of a fly TF in a dimeric cluster may be a methological difference rather than a biological one.

Unique clusters

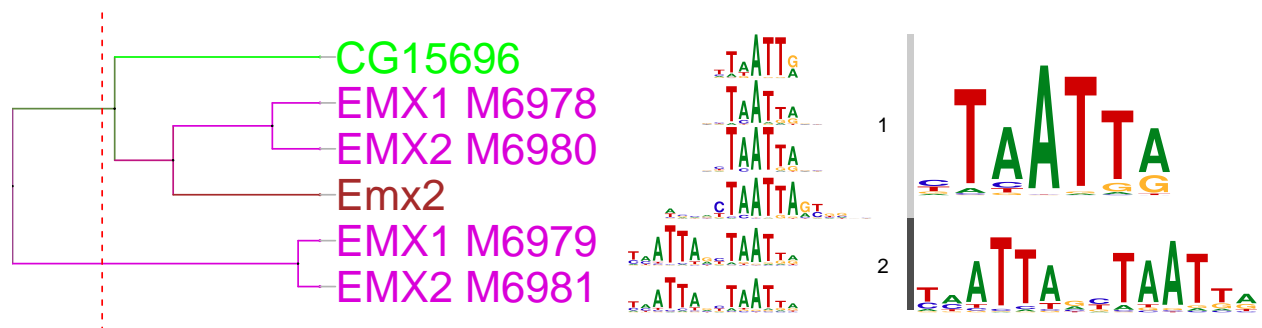
Cleaned unique clusters



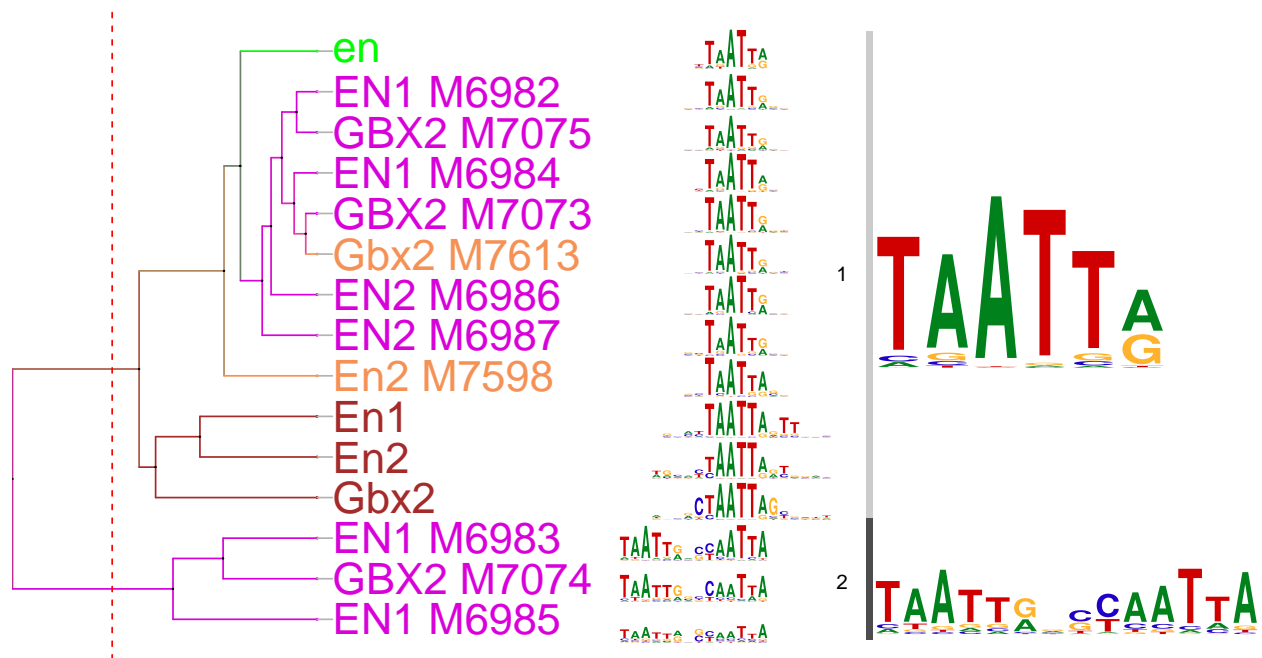
Supplementary Figure 7.01.DimerClusterALX



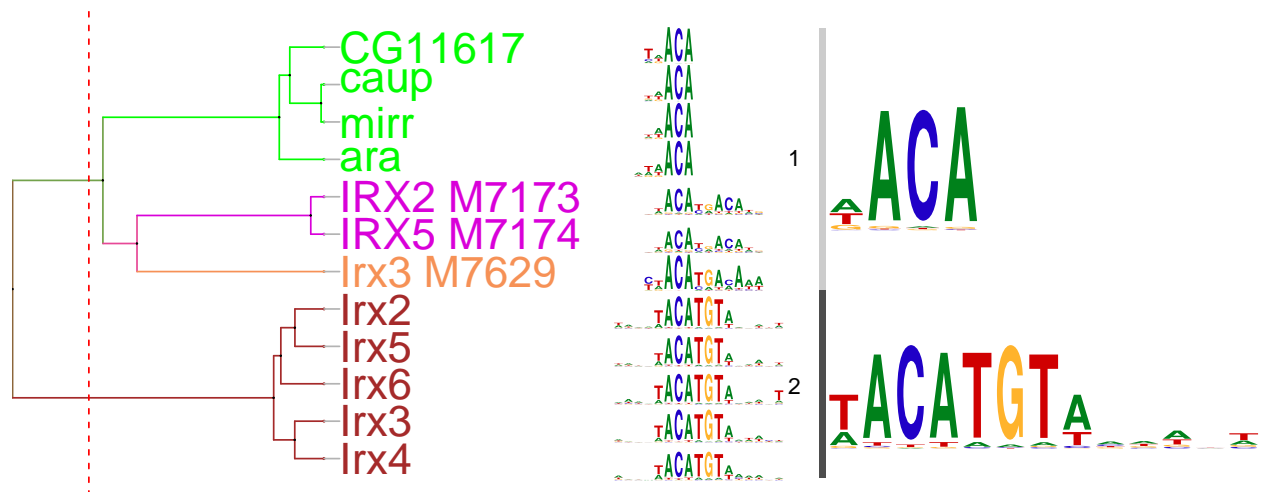
Supplementary Figure 7.02.DimerClusterBARHL



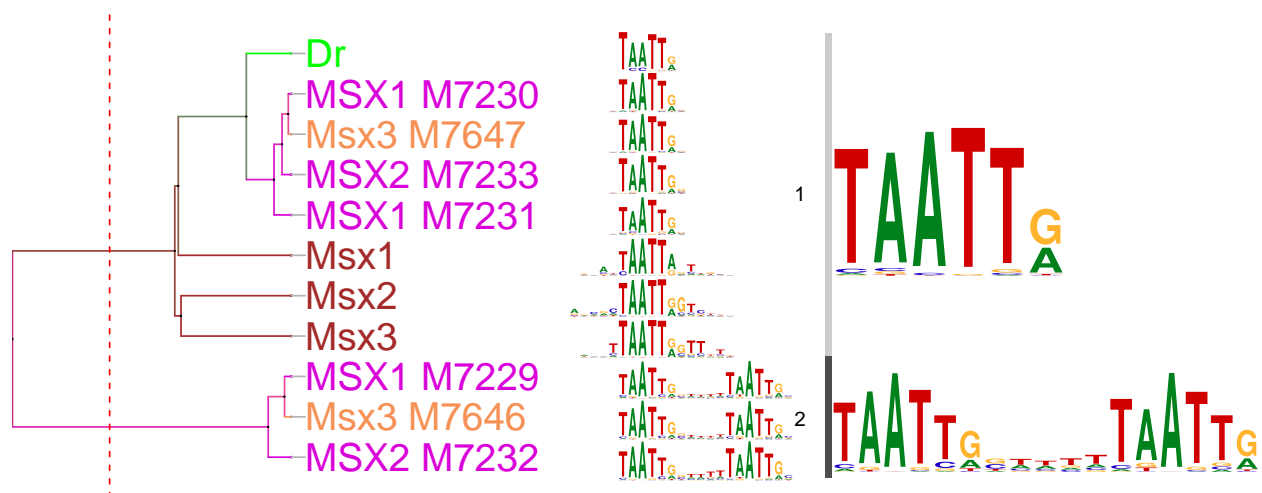
Supplementary Figure 7.03.DimerClusterEMX



Supplementary Figure 7.04.DimerClusterEN



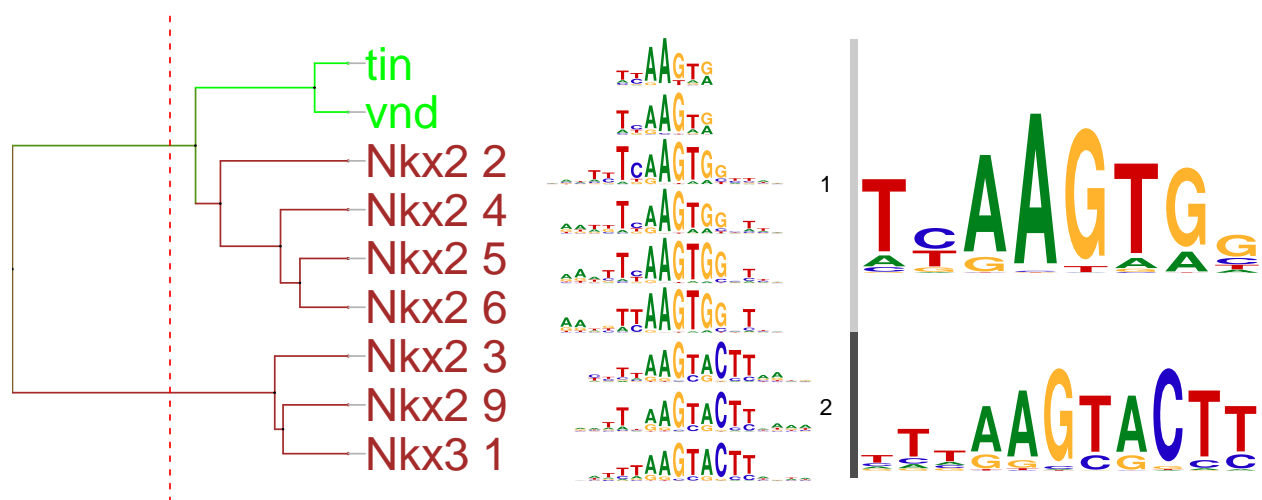
Supplementary Figure 7.05.DimerClusterIrx



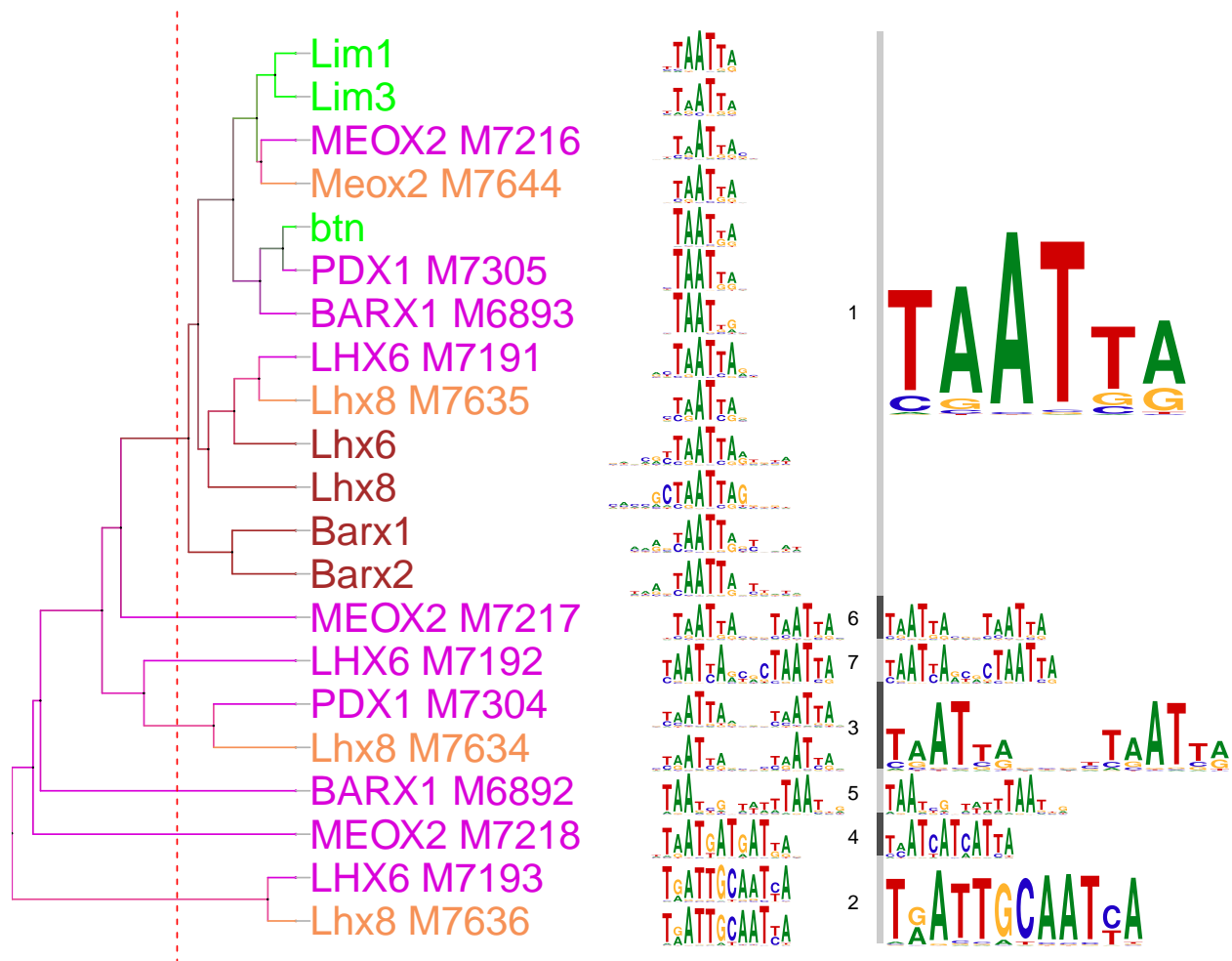
Supplementary Figure 7.06.DimerClusterMSX



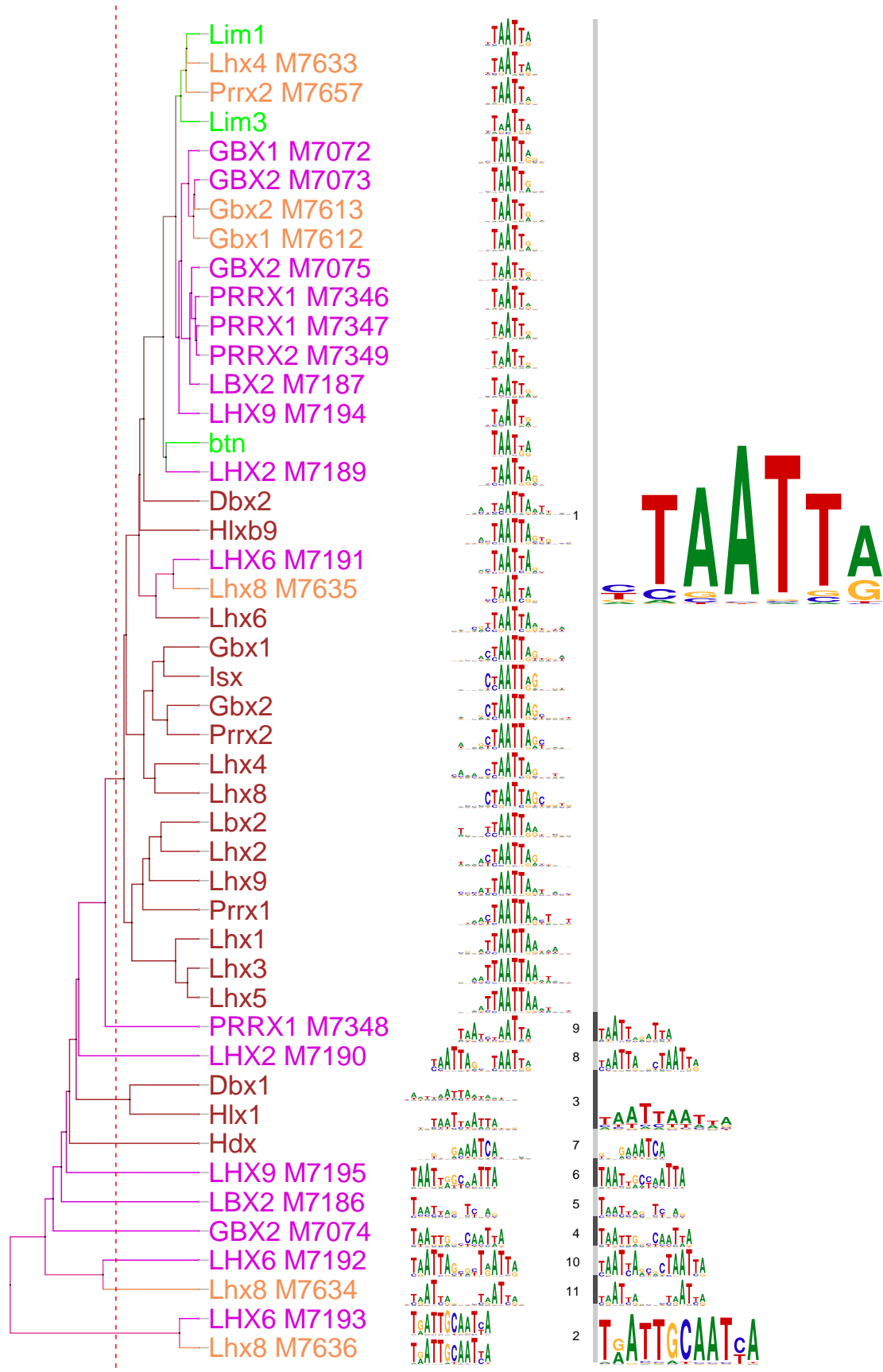
Supplementary Figure 7.07.DimerClusterCphx



Supplementary Figure 7.08.DimerClusterNkx



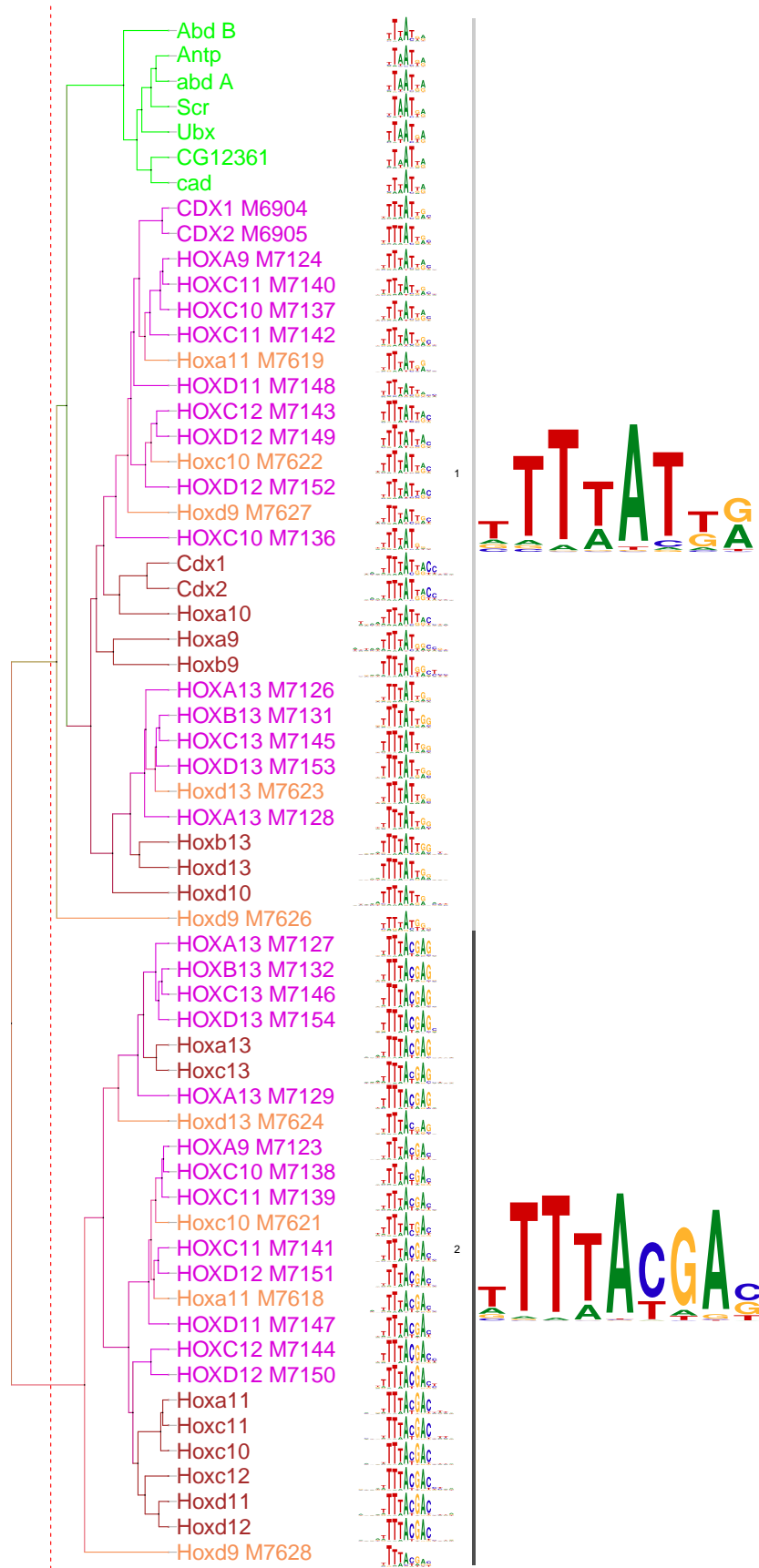
Supplementary Figure 7.09.DimerClusterLHX



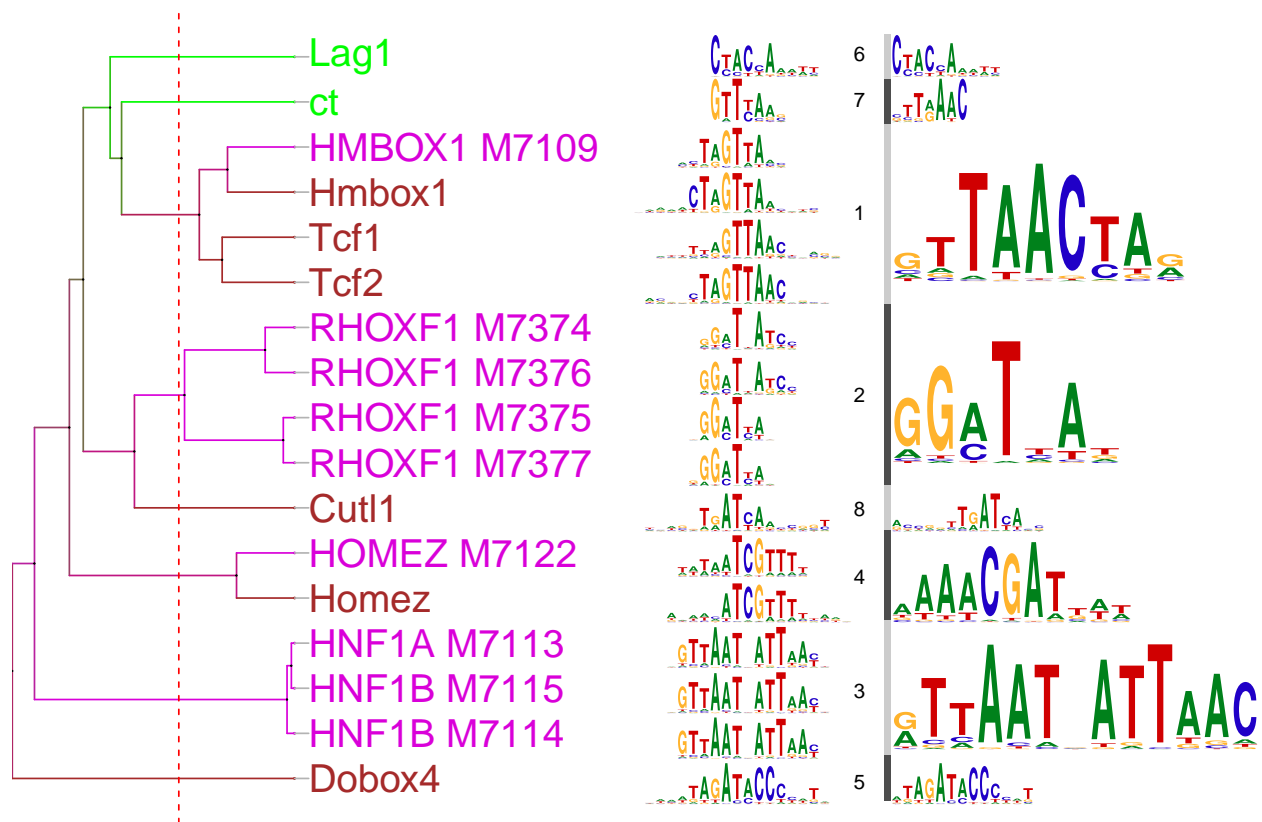
Supplementary Figure 7.10.PlatformClusterLHXCluster



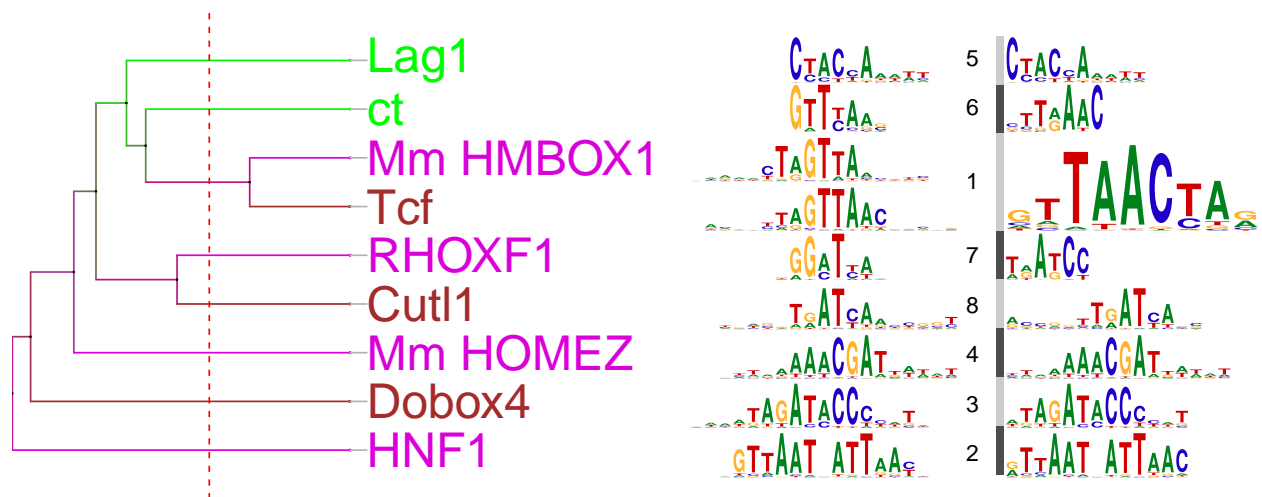
Supplementary Figure 7.11.PlatformClusterHmxCluster



Supplementary Figure 7.12.PlatformClusterHoxCluster



Supplementary Figure 7.13.UniqueCluster



Supplementary Figure 7.14.UniqueCleanCluster