

Supplementary Figure 6

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

colorSet <- c("Dm"="#00FC00", "b1h"="#00FC00", "sw"="#008080", "bml"="darkgreen",
             "Mm"="brown", "MmDREAM"="blue", "Ms"="#F69156",
             "Hs"="#D900D9")

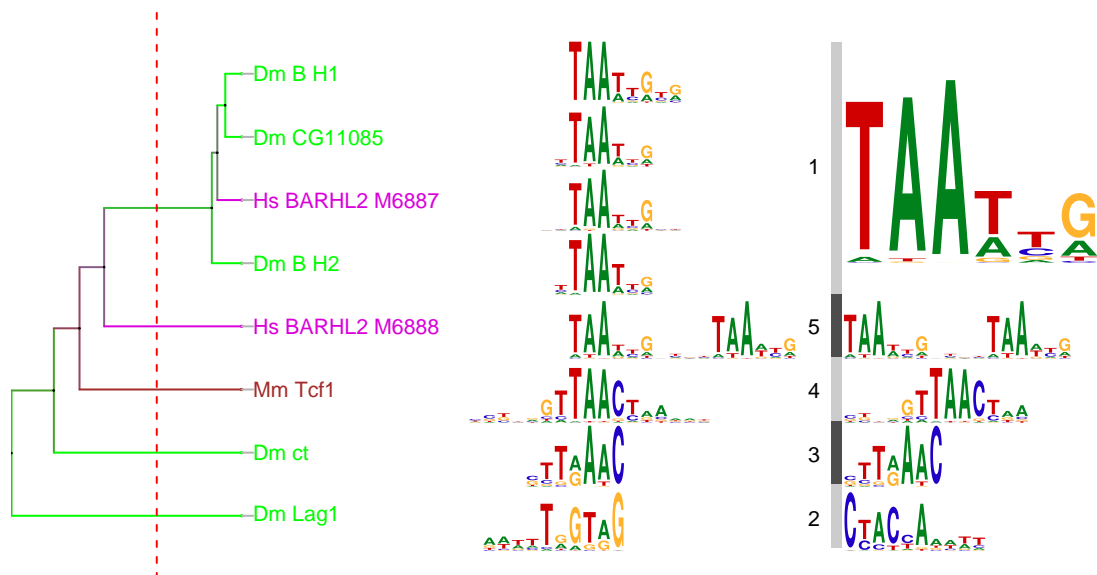
## function to read example data
readDataDoAna <- function(pcmPath, outputPath="output", groupDistance=2.5, trim=0.2){
  pcms <- readPCM(pcmPath)
  pfms<-lapply(pcms,pcm2pfm)
  matalign_path <- "./app/matalign-v4a"
  neighbor_path <- "./app/neighbor.app/Contents/MacOS/neighbor"
  system(paste("perl MatAlign2tree.pl --in . --pcmPath", pcmPath, "--out", outputPath,
              "--matalign", matalign_path, "--neighbor", neighbor_path, "--tree","UPGMA"))
  newickstrUPGMA <- readLines(con=file.path(outputPath, "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, minimalConsensus=3),
             leaves=leaves, unaligned.pfms=motifs))
}

gpDis <- 2.5
samples <- readDataDoAna("pcmsDatasetSamples", groupDistance=gpDis)

attach(samples)
leaveCols <- colorSet[gsub("^((Dm|Mm|Hs)_)ate.*$", "\\1", leaves)]
leaves <- gsub("Dm_cluster", "cluster", leaves)
motifFiles(phylog=phylog, motifs, sig, groupDistance = gpDis,
           col.pfms2 = gpCol, col.pfms2.width = 0.02,
           labels.leaves=leaves, col.leaves=leaveCols, col.tree=leaveCols,
           plotIndex=c(FALSE, TRUE), IndexCex=1.5, clabel.leaves=1.5)

detach(samples)
```



Supplementary Figure 6: Examples of specific motifs for *Drosophila* or human/mouse