

Supplementary Figure 4

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Supplementary Figure 4A. Align motifs from fly by MatAlign

Supplementary Figure 4B. Alignment motifs from fly using MotIV

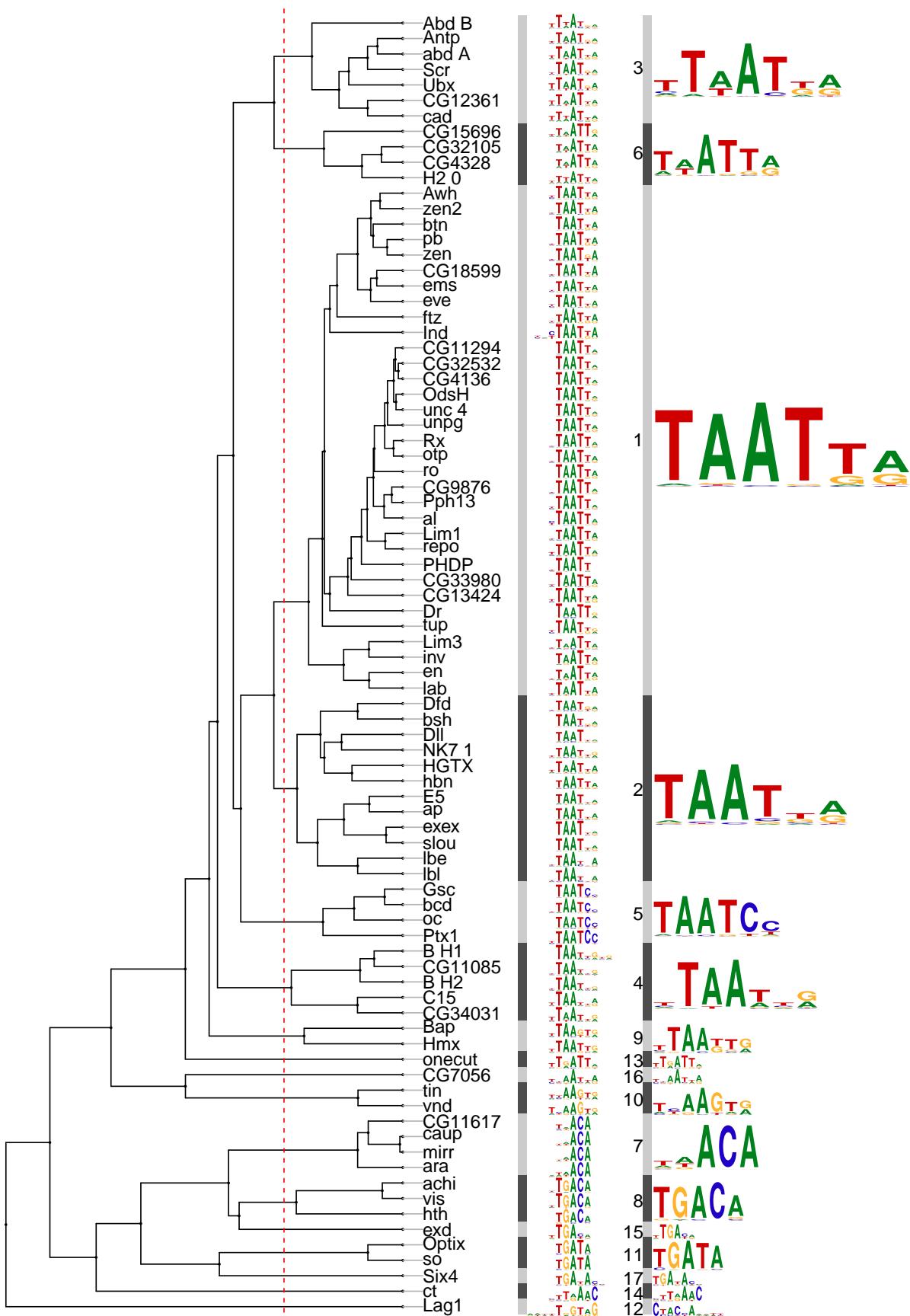
Supplementary Figure 4C. Align motifs from fly and mouse using MatAlign

Supplementary Figure 4D. Align motifs from fly and human using MatAlign

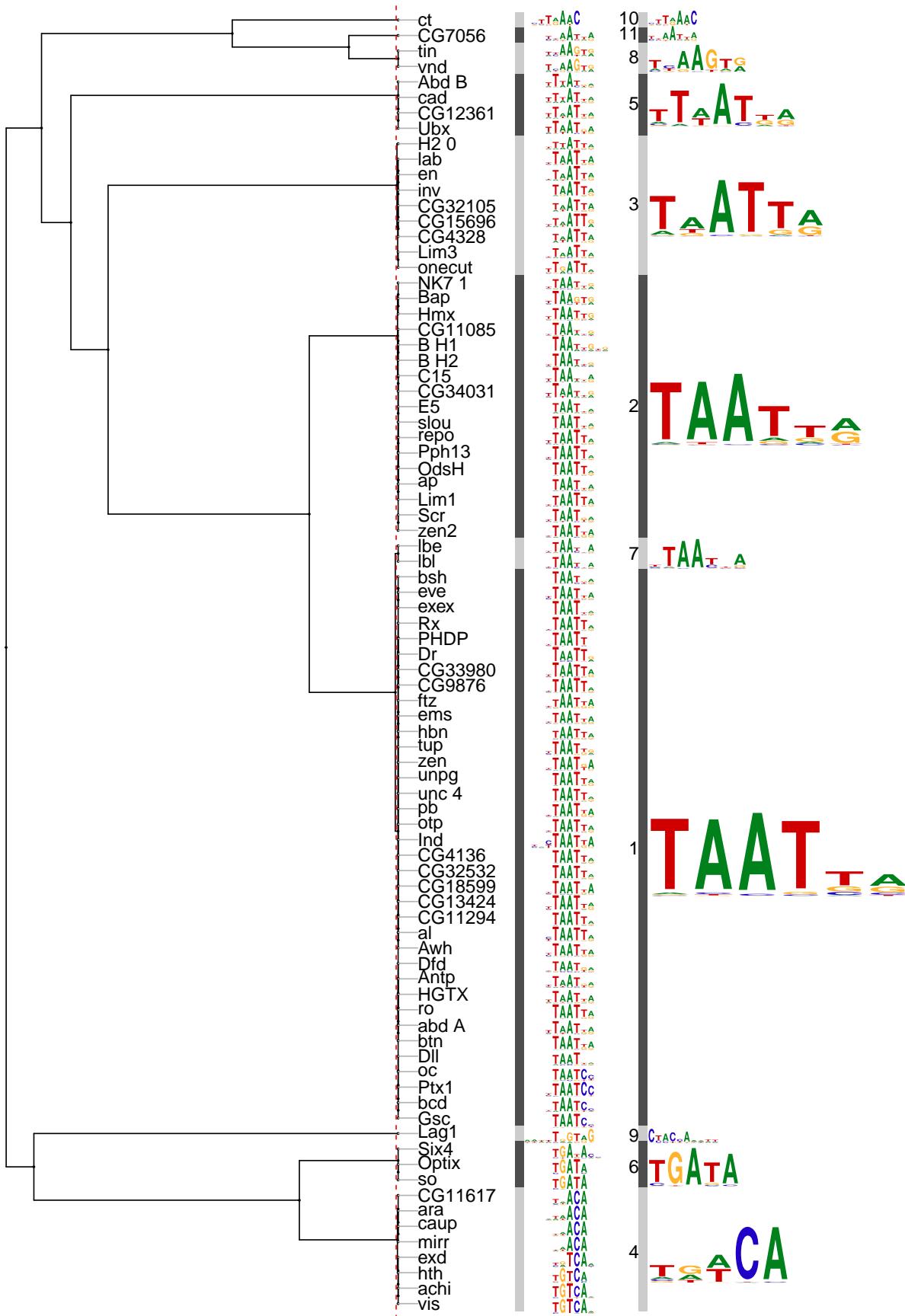
Supplementary Figure 4E. Align motifs from mouse generated by different methods (SELEX, PBM-SW and PBM-dream5) using MatAlign

```
gpDis <- 2
MmPBM_SELEX <- getMatAlignOut("pcmsDatasetMmPBM_SELEX", groupDistance=gpDis)
attach(MmPBM_SELEX)

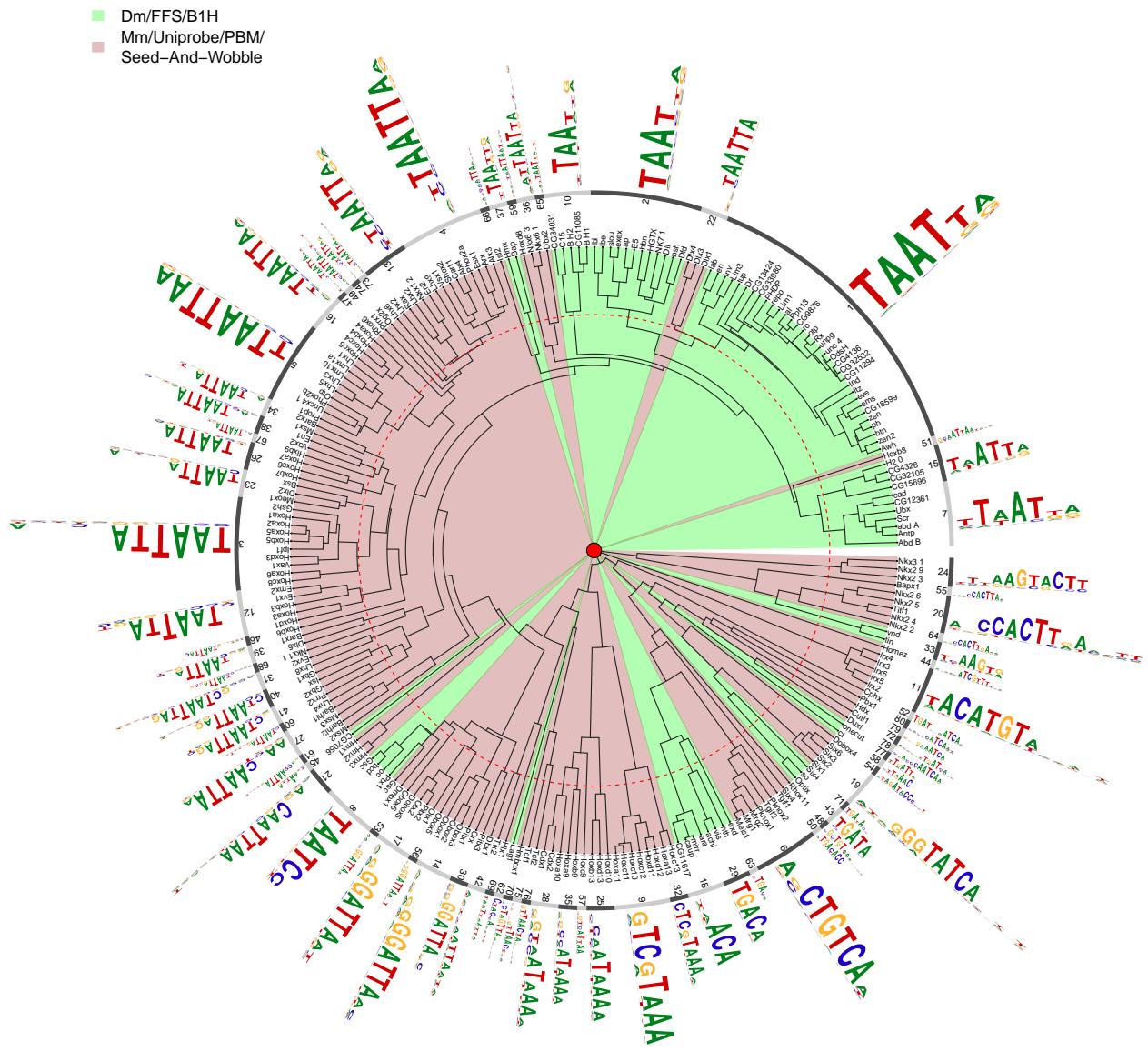
##set methods color
methods <- factor(grep("_SELEX", leaves) + grep("_M\\d{4}", leaves))
```



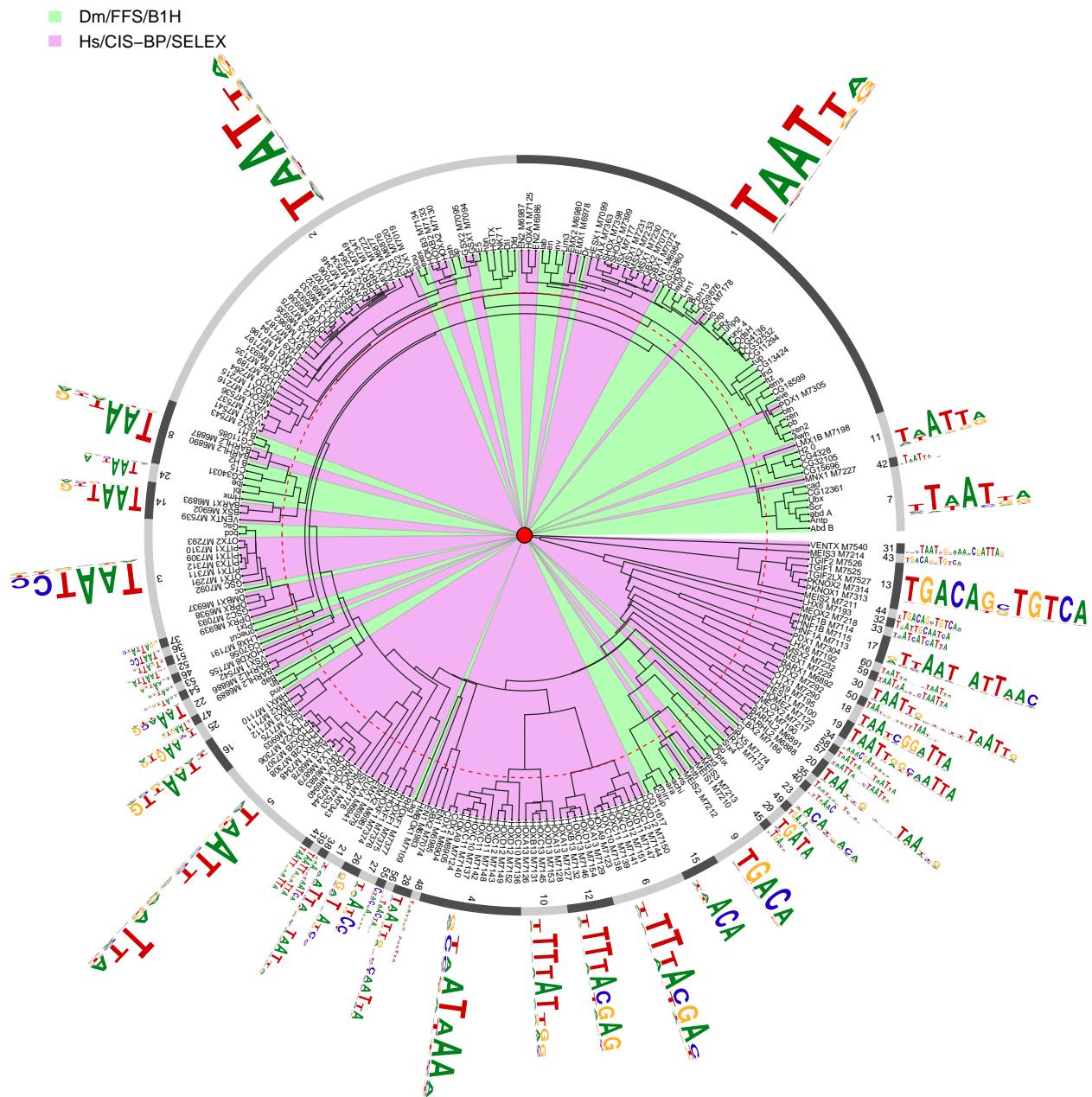
Supplementary Figure 4A: Alignment of fly motifs using MatAlign



Supplementary Figure 4B: Alignment of fly motifs using MotIF



Supplementary Figure 4C: Alignment of motifs of fly and mouse using MatAlign



```

levels(methods) <- c("Mm", "MmDREAM", "Ms")
##c("PBM/Uniprobe/Seed-And-Wobble", "PBM/CIS-BP/DREAM5", "SELEX/CIS-BP")
levels(methods) <- colorSet[levels(methods)]
methods <- as.character(methods)

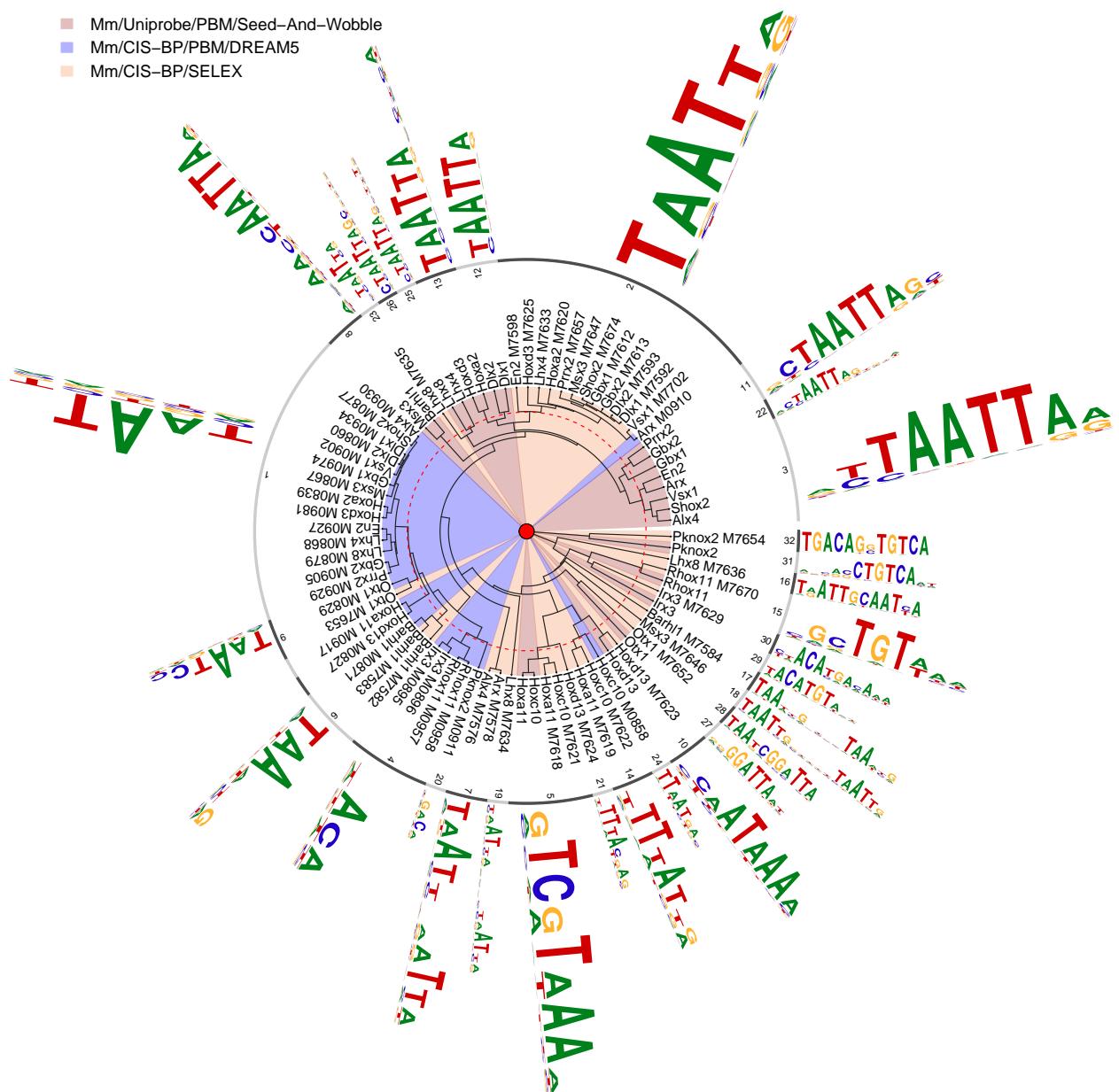
leaveNames <- gsub("_ (SELEX|PBM)", "", gsub("_ (Jolma|Berger)", "", leaves))

## calculate average of top 8 position information content for each motif
icgp <- sapply(sapply(unaligned.pfms, getIC), function(.ele)
  mean(sort(.ele, decreasing=TRUE)[1:min(8, length(.ele))]))
icgp.ranges <- range(icgp)
icgp <- cut(icgp, 10, labels=colorRampPalette(c("green", "black", "red"))(10))
icgp.image <- as.raster(matrix(rev(levels(icgp)), ncol=1))
icgp <- as.character(icgp)

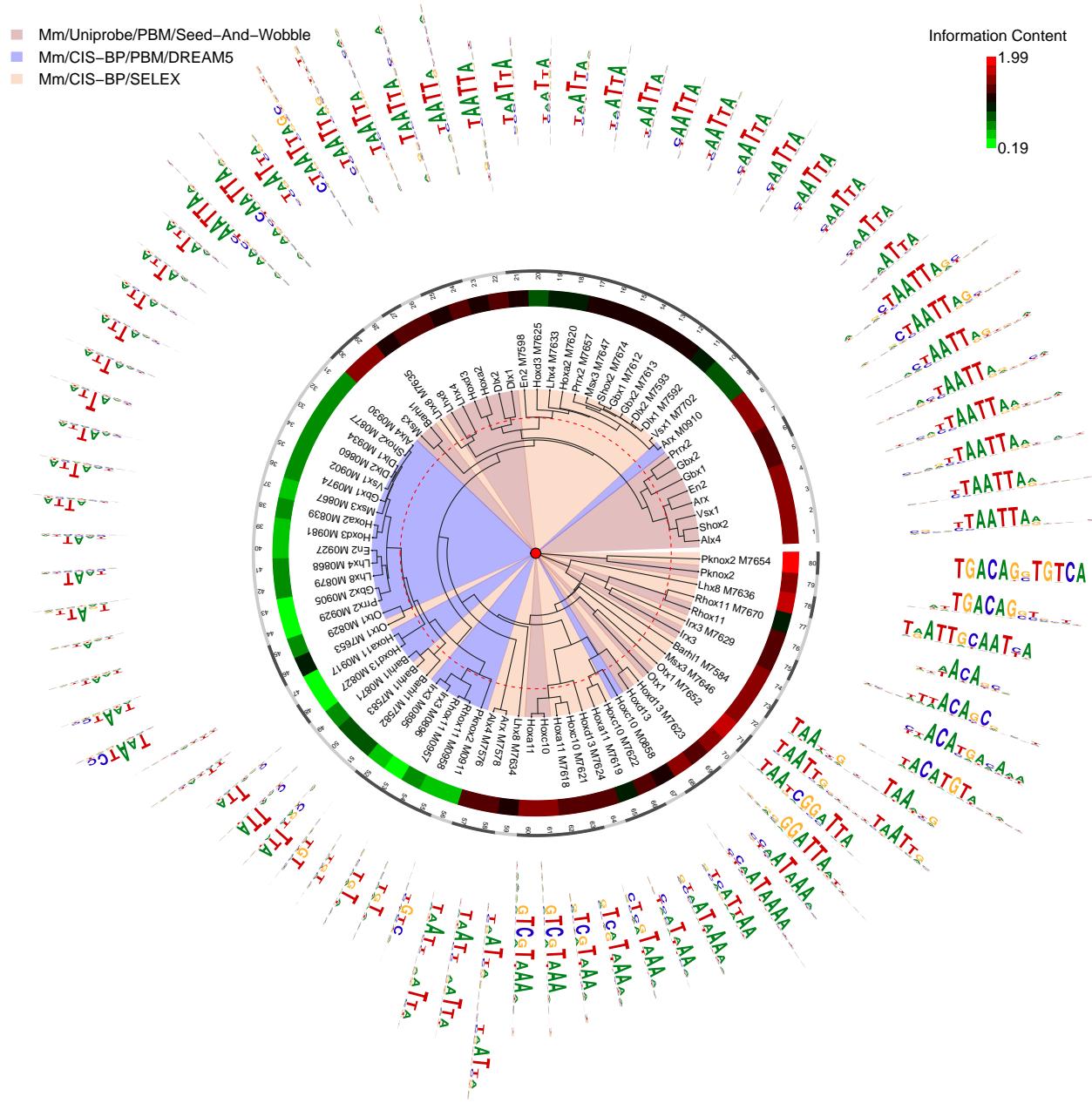
plotMotifStackWithRadialPhylog(phylog=phylog, pfms=sig,
                                col.bg=methods, col.bg.alpha=.3,
                                col.inner.label.circle=gpCol,
                                inner.label.circle.width=0.02,
                                labels.leaves=leaveNames, cleaves=.1,
                                circle=.95, circle.motif=1.8, clabel.leaves=.8,
                                motifScale="logarithmic", angle=358,
                                plotIndex=TRUE, IndexCex=.6, groupDistance=gpDis)

legend(-2, 2.2, legend=c("Mm/Uniprobe/PBM/Seed-And-Wobble",
                        "Mm/CIS-BP/PBM/DREAM5", "Mm/CIS-BP/SELEX"),
       fill=highlightCol(colorSet[c("Mm", "MmDREAM", "Ms")], .3),
       border="white", lty=NULL, bty = "n")

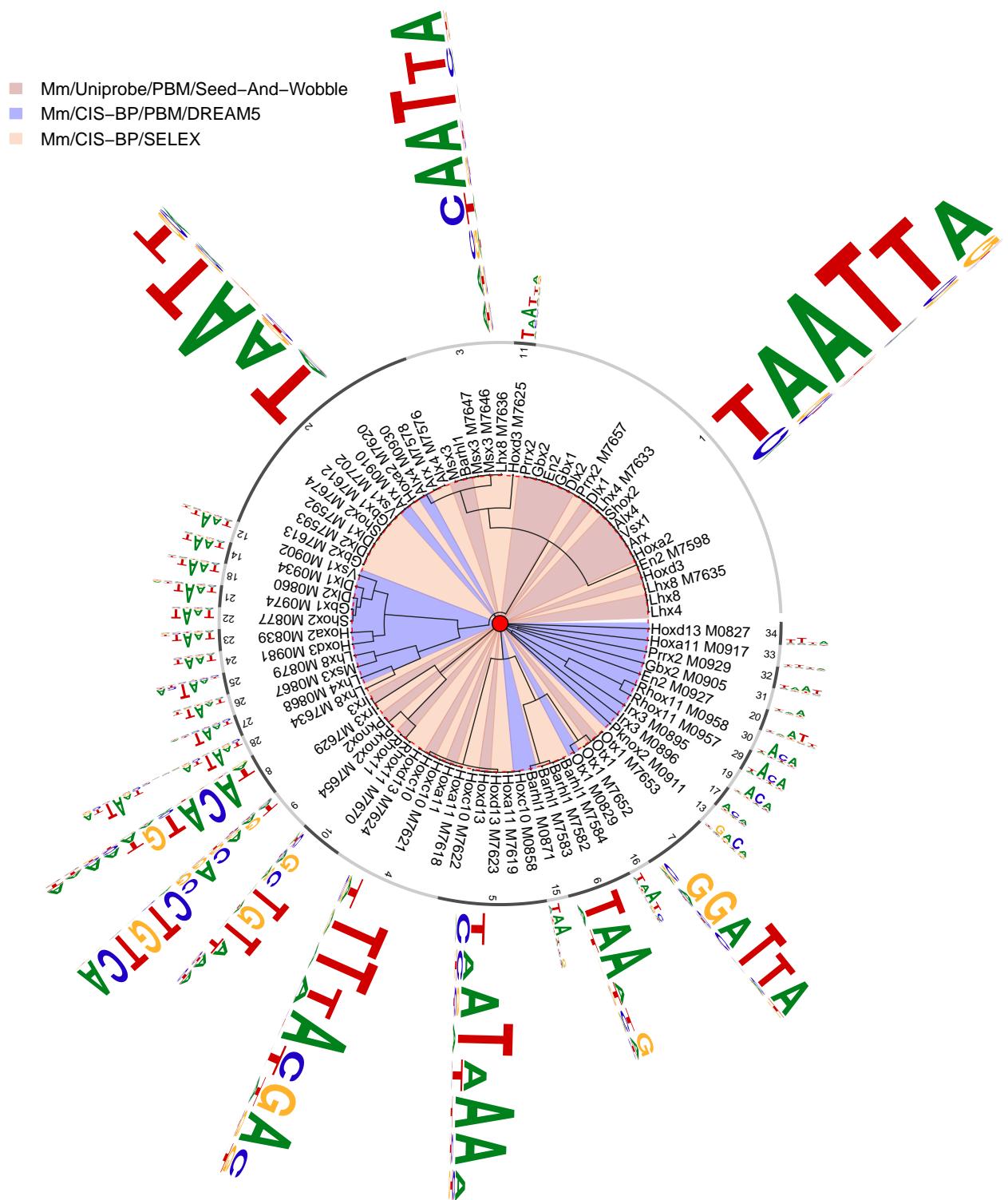
```



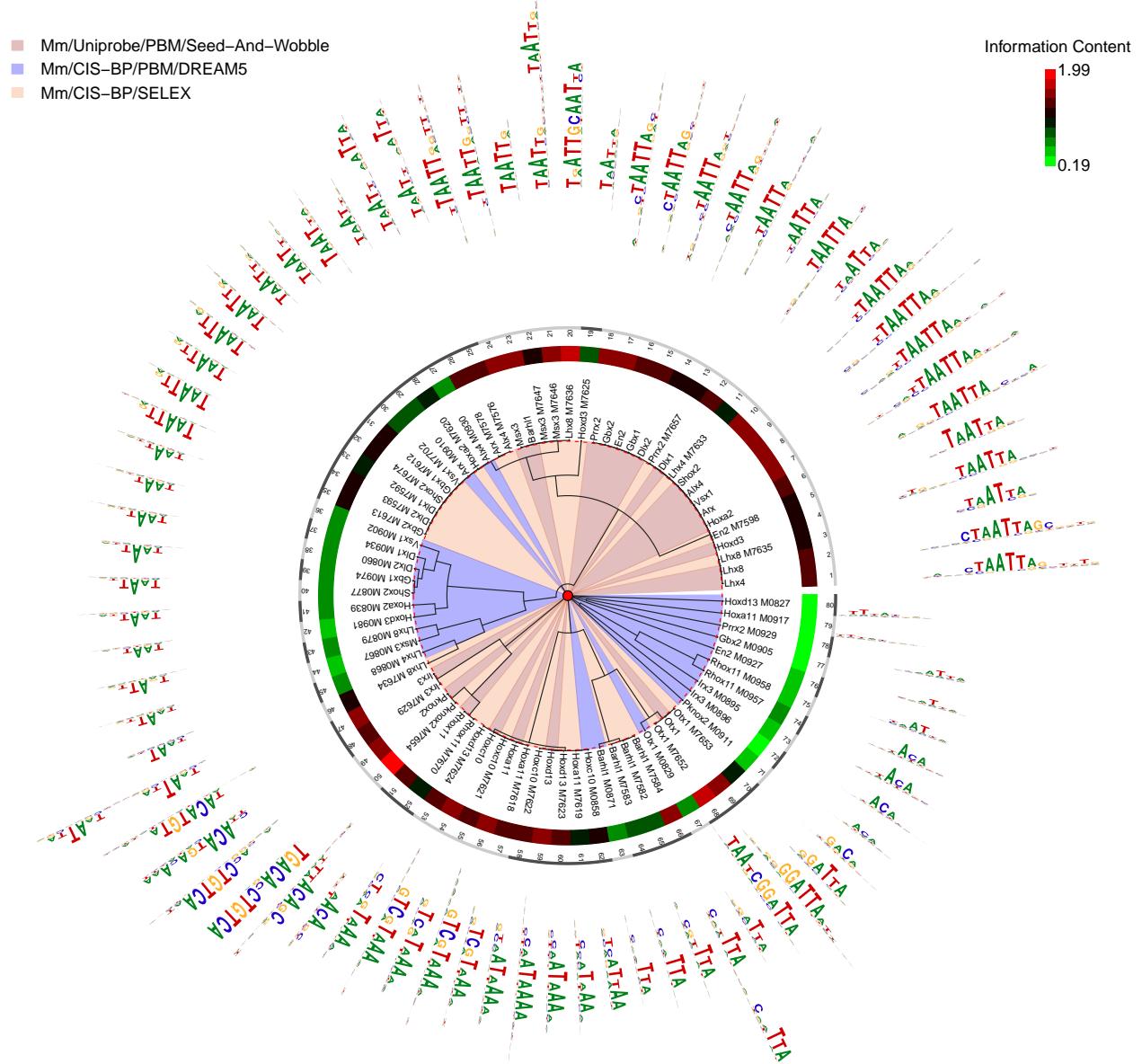
Supplementary Figure 4E.a: Alignment of ouse data generated by different methods using MatAlign



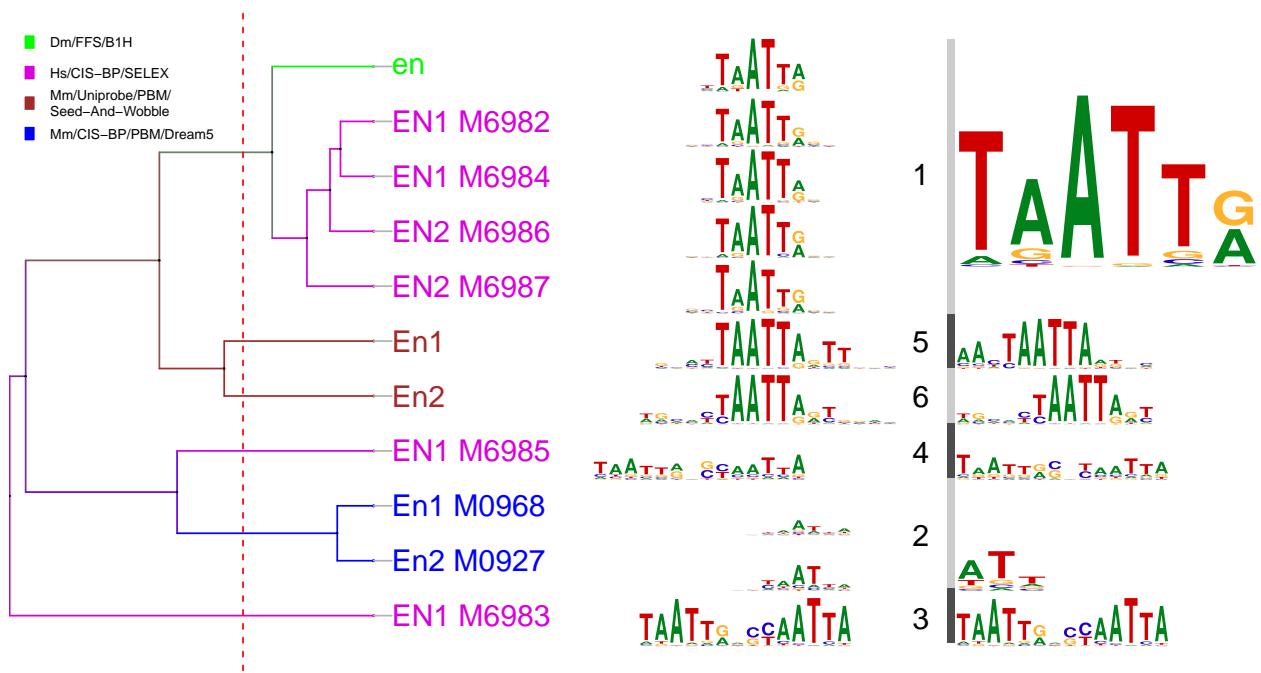
Supplementary Figure 4E.b: Alignment of mouse motifs from different methods



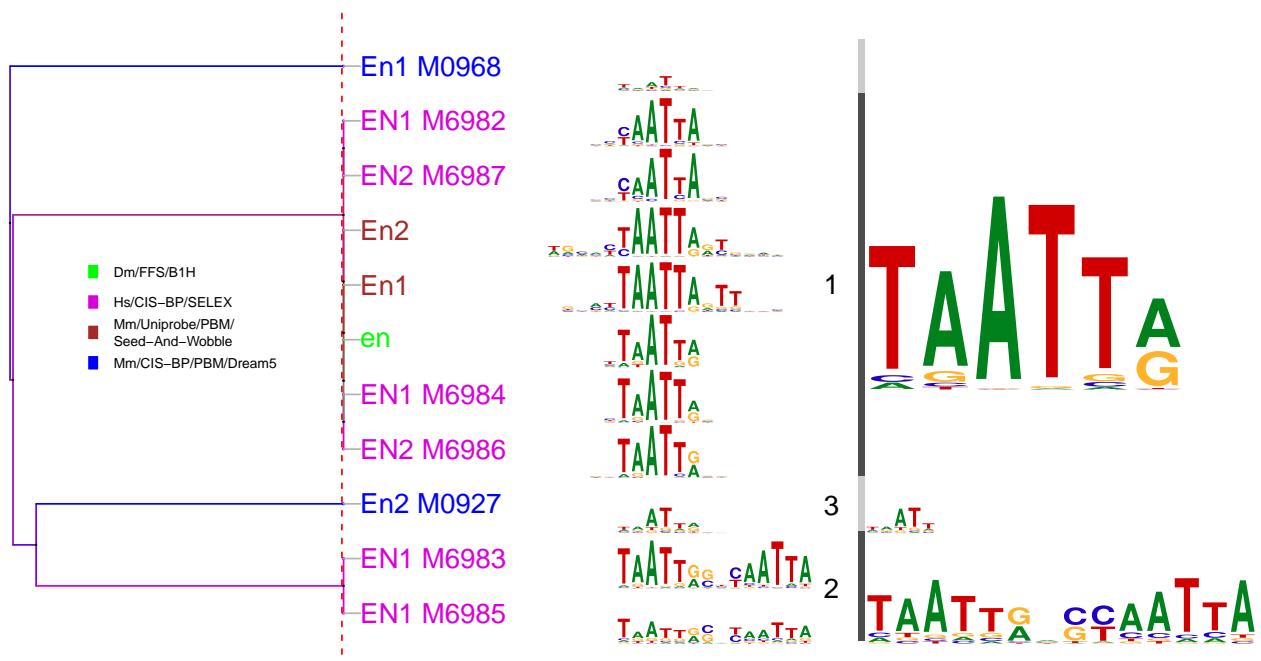
Supplementary Figure 4F.a: Alignment of mouse data generated by different methods using MotIV



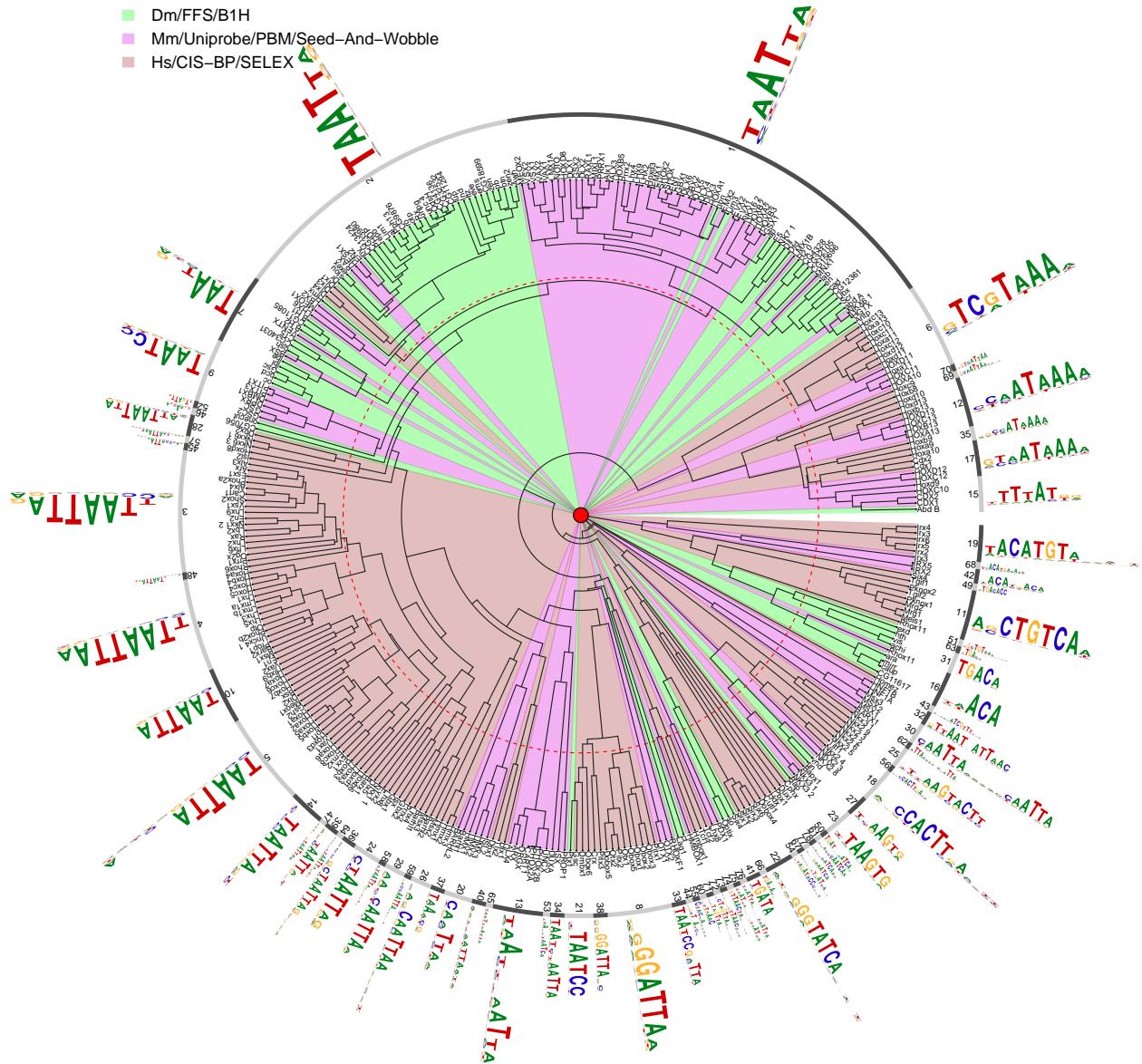
Supplementary Figure 4F.b: Alignment of mouse motifs generated by different methods using MotIV



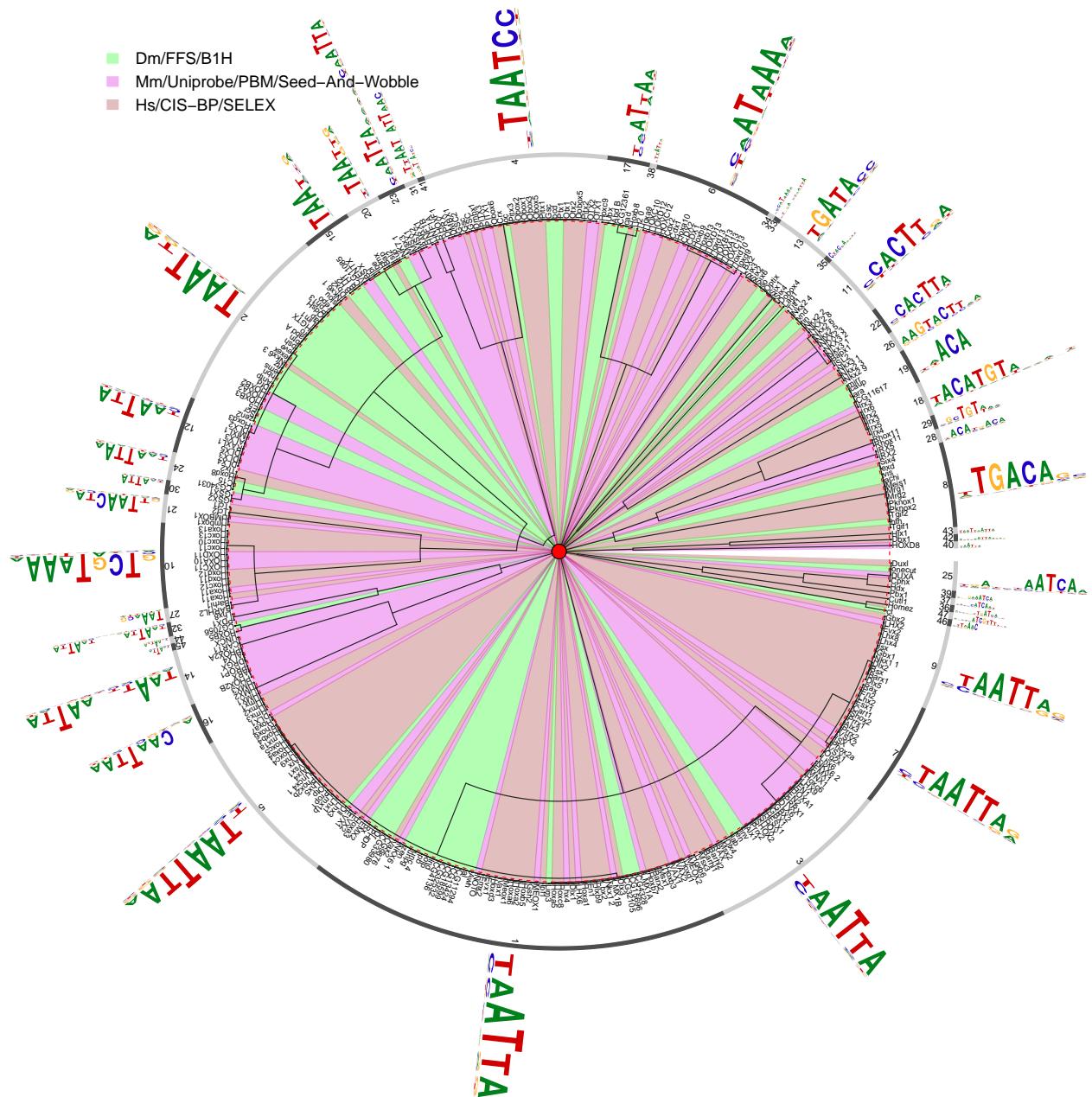
Supplementary Figure 4G: Alignment of engrailed orthologs using MatAlign



Supplementary Figure 4H: Alignment of engrailed orthologs using MotIV



Supplementary Figure 4I: Alignment of motifs from fly, mouse and human using MatAlign



Supplementary Figure 4J: Alignment of motifs from fly, mouse and human using MotIV

Supplementary Figure 4F. Align motifs from mouse generated by different platforms (SELEX, PBM-SW and PBM-dream5) using MotIV

Supplementary Figure 4G. Align motifs of engrailed orthologs using MatAlign

Supplementary Figure 4H. Align motifs of engrailed orthologs using MotIV

Supplementary Figure 4I. Align motifs from fly, mouse and human using MatAlign

Supplementary Figure 4J. Align motifs from fly vs mouse and human using MotIV

```
sessionInfo()

## R version 3.4.1 (2017-06-30)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: OS X El Capitan 10.11.6
##
## Matrix products: default
## BLAS: /Library/Frameworks/R.framework/Versions/3.4/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.4/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats4     parallel   grid       stats      graphics   grDevices utils
## [8] datasets   methods    base
##
## other attached packages:
## [1] motifStack_1.20.1    Biostrings_2.44.2    XVector_0.16.0
## [4] IRanges_2.10.2       S4Vectors_0.14.3    ade4_1.7-6
## [7] MotIV_1.32.0        BiocGenerics_0.22.0 grImport_0.9-0
## [10] XML_3.98-1.9
##
## loaded via a namespace (and not attached):
## [1] Rcpp_0.12.12           highr_0.6
## [3] plyr_1.8.4             compiler_3.4.1
## [5] GenomeInfoDb_1.12.2    bitops_1.0-6
## [7] tools_3.4.1            zlibbioc_1.22.0
## [9] digest_0.6.12          evaluate_0.10.1
## [11] lattice_0.20-35        BSgenome_1.44.0
## [13] Matrix_1.2-10          DelayedArray_0.2.7
```

```
## [15] yaml_2.1.14                  seqLogo_1.42.0
## [17] GenomeInfoDbData_0.99.0      rtracklayer_1.36.4
## [19] stringr_1.2.0                 knitr_1.16
## [21] htmlwidgets_0.9                rprojroot_1.2
## [23] Biobase_2.36.2                 BiocParallel_1.10.1
## [25] rGADEM_2.24.0                 rmarkdown_1.6
## [27] magrittr_1.5                   scales_0.4.1
## [29] backports_1.1.0                Rsamtools_1.28.0
## [31] htmltools_0.3.6                matrixStats_0.52.2
## [33] GenomicRanges_1.28.4          GenomicAlignments_1.12.1
## [35] SummarizedExperiment_1.6.3    colorspace_1.3-2
## [37] stringi_1.1.5                 munsell_0.4.3
## [39] RCurl_1.95-4.8
```