

Supplementary Material 4: phylogenetic analysis

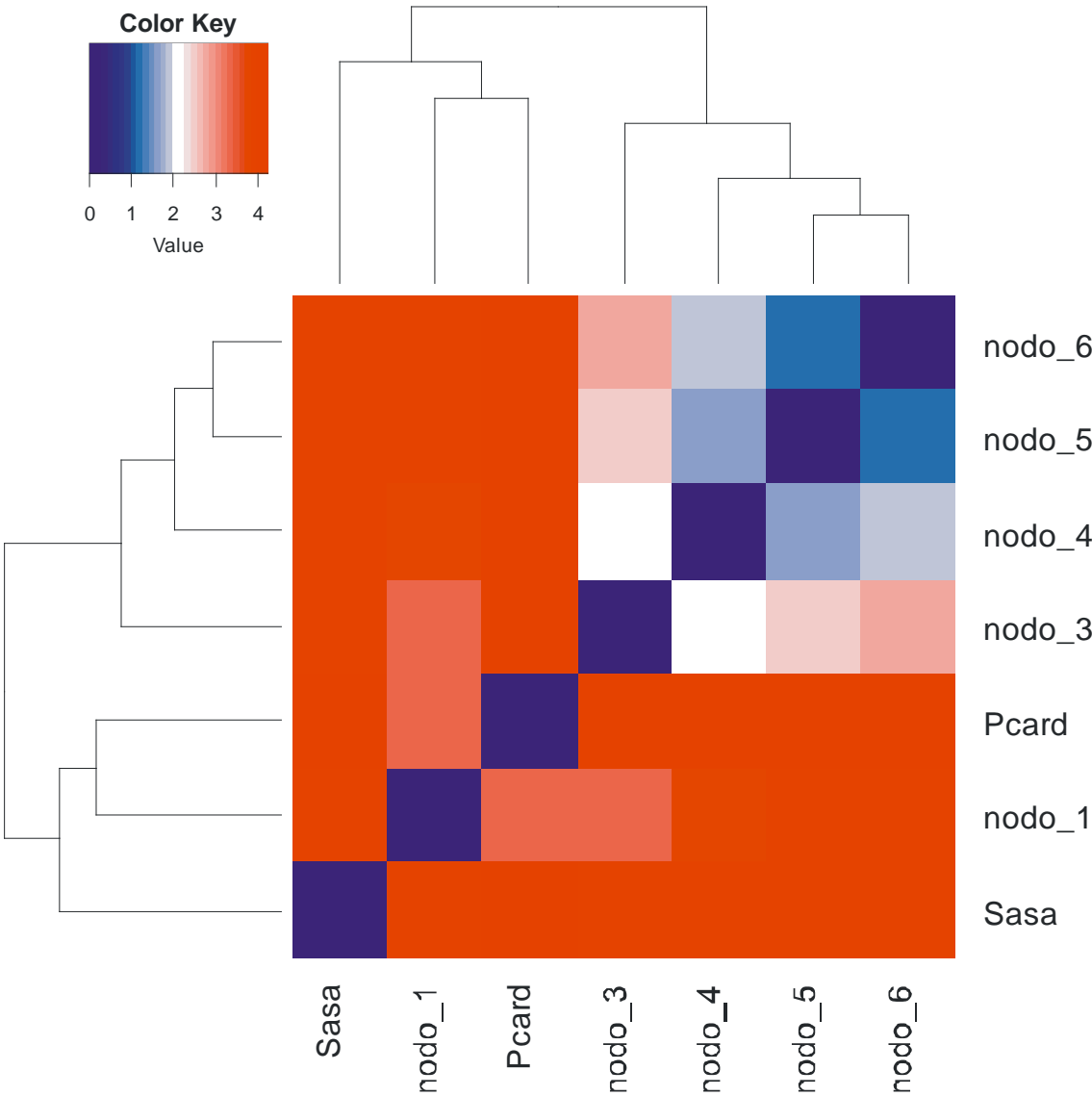
Contents

1. Disparity metrics of main Paucituberculata clades.
2. Heatmaps GED of each time-bin, performed using the command “heatmap.2” of the R package *gplots* (Warnes et al. 2016).
3. Interquartile intervals by jack-knifing.
4. Scree-plots of PCOs.
5. Shapiro-Wilk normality tests, performed using the command “shapiro.test” of the R core package *stats*.
6. Jack-knife script used in this study
7. Comparison of Weighted Mean Pairwise Distance (WMPD; distances weighted by the ratio of comparable characters) based on different distance measurements.

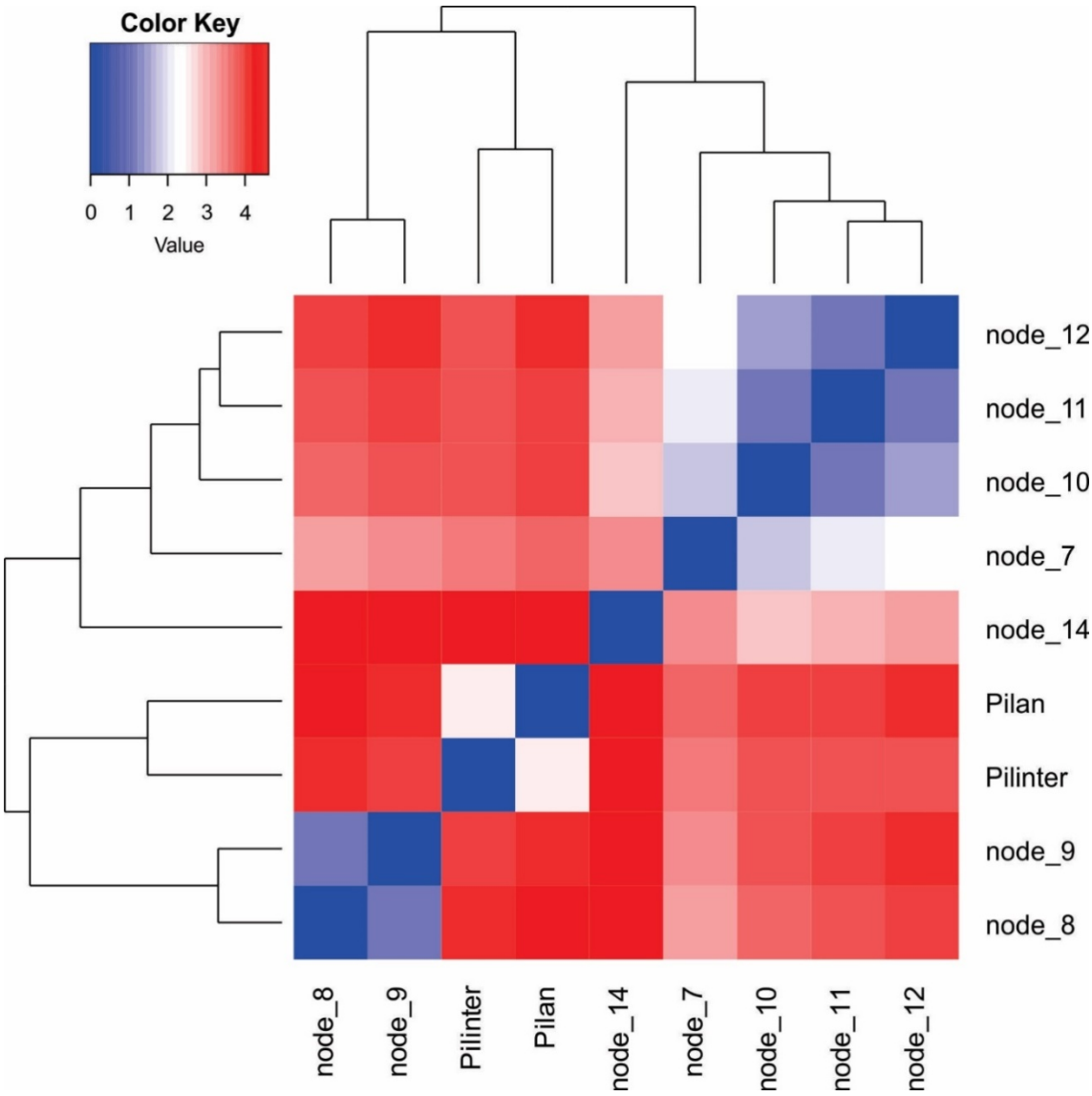
1. Disparity metrics of main Paucituberculata clades

Clade	WMPD	SV	SM
Caenolestidae	3.488108	6.597165	21.18668
Pichipilidae	3.832916	8.387727	19.36744
NPP	3.834038	14.03157	43.3636

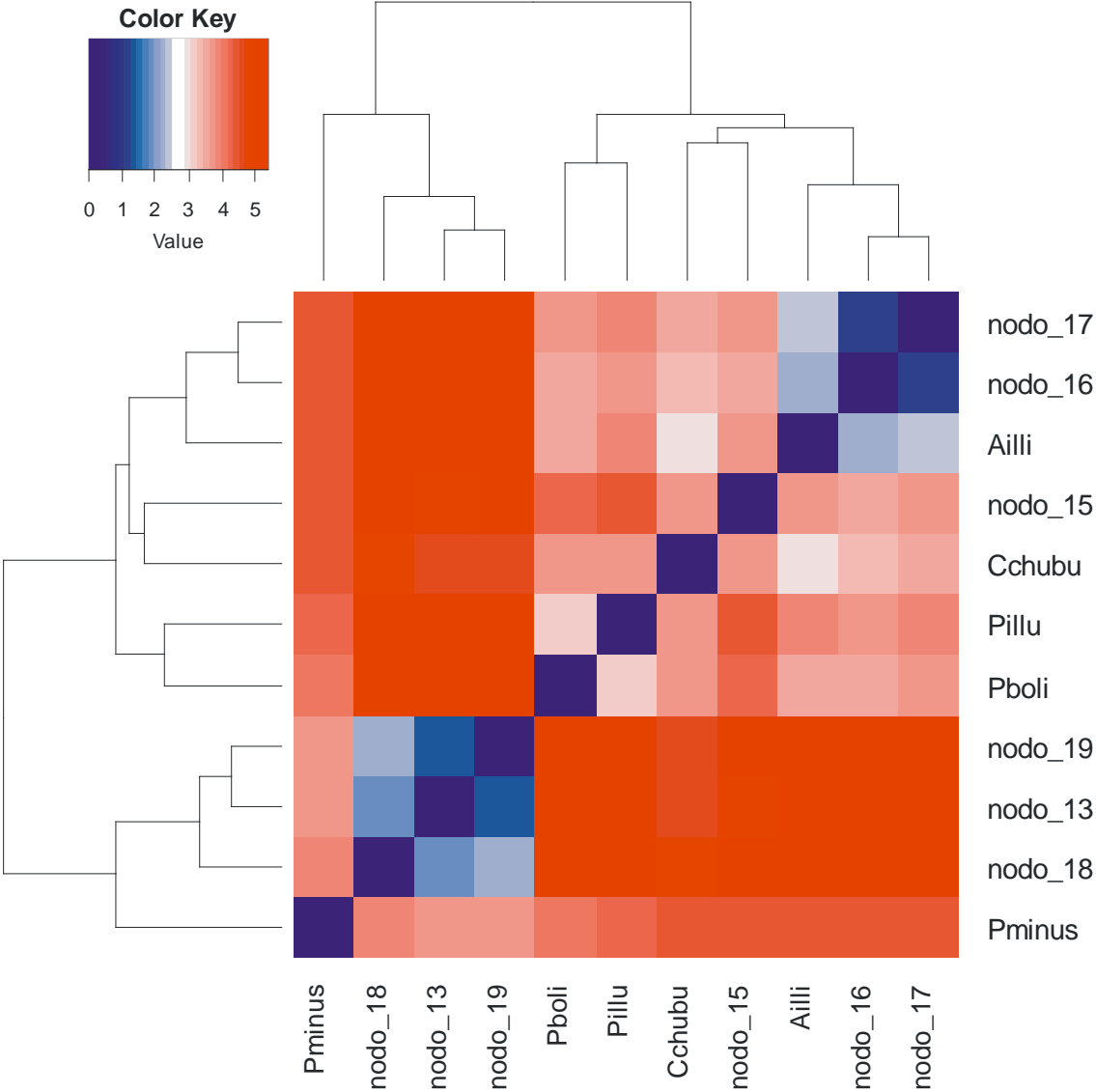
2.1. Heatmap of GED for Eocene



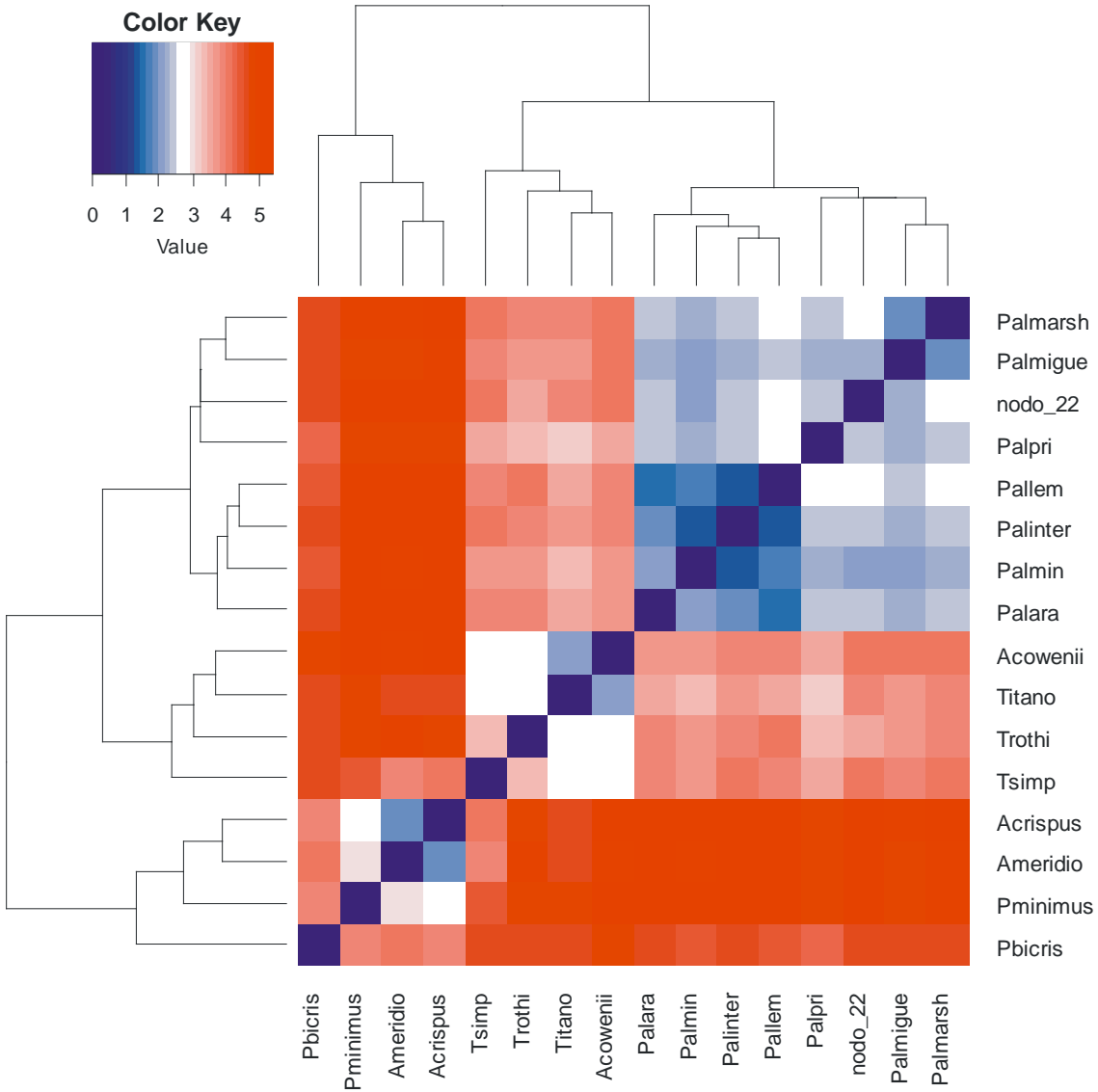
2.2. Heatmap of GED for early Oligocene



2.3. Heatmap of GED for late Oligocene



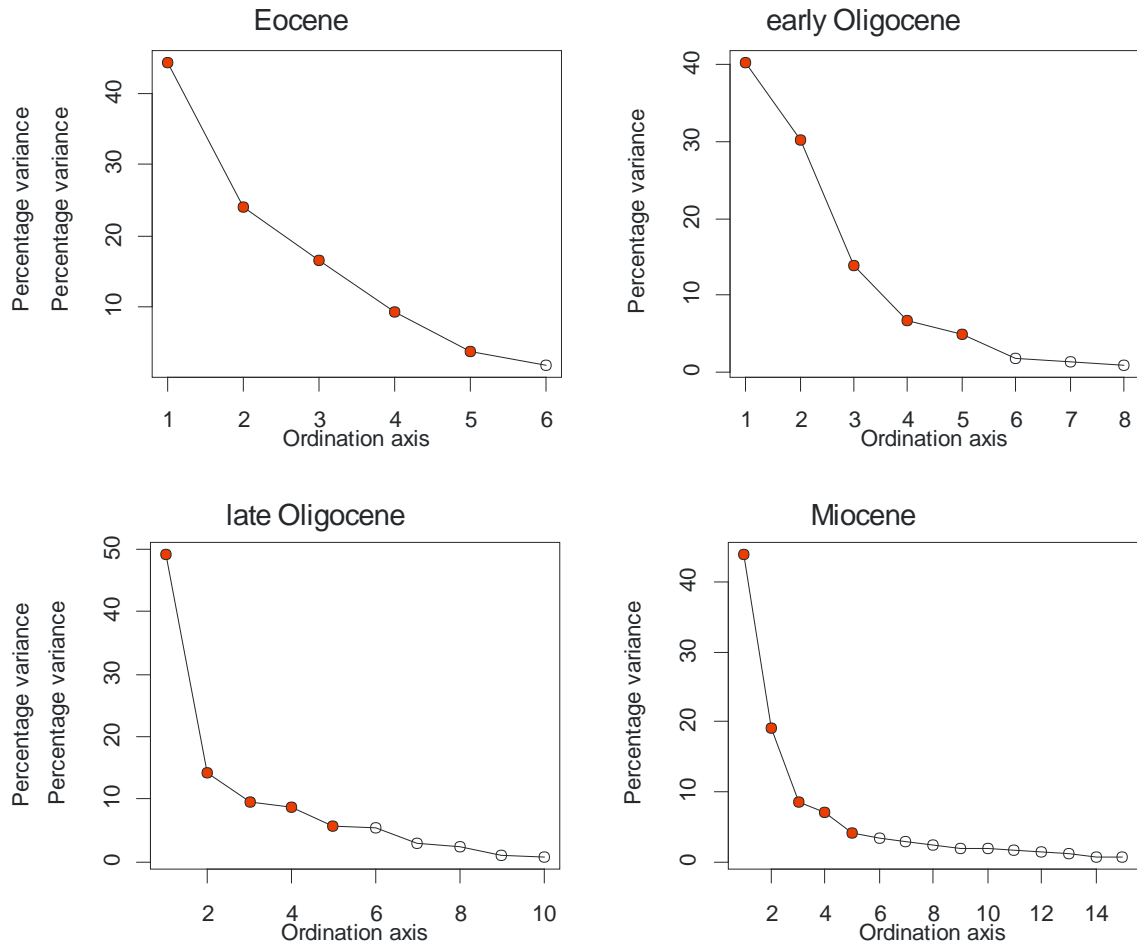
2.4. Heatmap of GED for Miocene



3. Quantile intervals built by jack-knifing on taxa-character matrices.

WMPD	0%	25%	50%	75%	100%
Eocene	2.585720	2.902587	3.299078	3.423777	3.504061
early Oligocene	3.119762	3.195397	3.223932	3.489785	3.515387
late Oligocene	4.005940	4.075391	4.118288	4.192077	4.254889
Miocene	3.542464	3.662801	3.762037	3.816493	3.848884
SV	0%	25%	50%	75%	100%
Eocene	4.400295	5.132765	6.766983	7.112032	7.462206
early Oligocene	5.436537	5.612010	5.713701	6.464700	6.656255
late Oligocene	7.557030	7.881399	8.206596	8.363652	8.558585
Miocene	5.915557	6.355618	6.611127	6.667844	6.826756
SR	0%	25%	50%	75%	100%
Eocene	11.57460	11.69859	14.19544	14.70237	15.07016
early Oligocene	13.22908	14.27064	14.83464	15.37817	15.79938
late Oligocene	16.56091	16.89876	18.02053	18.33581	18.58594
Miocene	14.94396	16.39779	16.58472	16.69301	16.97159

4. Cumulative variance scree-plots of PCOs. Eigenvectors analyzed for disparity are highlighted in red.



5.1 Shapiro-Wilk normality test of GEDs.

	W	p-value
Eocene	0.8020	0.0007
early Oligocene	0.8656	0.0004
late Oligocene	0.9079	0.0004
Miocene	0.9400	0.0000

5.2 Shapiro-Wilk normality test of PCO scores.

	W	p-value
Eocene	0.9865	0.9683
early Oligocene	0.9200	0.0126
late Oligocene	0.9012	0.0057
Miocene	0.9359	0.0114

6. Jack-knife script used in this study.

```
Time.bins=as.numeric(readline(print("number of time-bins:")))

weighted.mean=list(NULL)

sum.var=list(NULL)

sum.range=list(NULL)

for (j in 1: Time.bins)

{

nexus.obs <- ReadMorphNexus(file = file.choose())

dist.obs<- MorphDistMatrix(nexus.obs)

obs.comparable.char <- as.dist(dist.obs$comp.char.matrix)

ged.obs<-dist.obs$GED.dist.matrix

tr.obs<-as.dist(ged.obs)

pco.obs <- cmdscale(d = dist.obs$GED.dist.matrix,k = nrow(dist.obs$GED.dist.matrix)-1,
add = TRUE)$points

weighted.mean.obs<-(sum(obs.comparable.char*tr.obs)/sum(obs.comparable.char))

sum.var.obs<-sum(apply(pco.obs[,1:5], 2, var))

sum.range.obs<-sum(apply(apply(pco.obs[,1:5], 2, range), 2, diff))

nexJACK=nexus.obs

taxa=nrow(nexJACK$matrix)

w.mean.jack<-numeric(0)

sum.var.jack<-numeric(0)

sum.range.jack=numeric(0)

for (i in 1:taxa)

{

jack.m=nexJACK

jack.m$matrix=jack.m$matrix[-i,]

dist.jack <- MorphDistMatrix(jack.m)

Jack.comparable.char <- as.dist(dist.jack $comp.char.matrix)

ged.jack<-dist.jack$GED.dist.matrix

tr.jack<-as.dist(ged.jack)

pco.jack <- cmdscale(d = dist.jack$GED.dist.matrix,k =
nrow(dist.jack$GED.dist.matrix)-1, add = TRUE)$points

w.mean.jack<-
c(w.mean.jack,(sum(Jack.comparable.char*tr.jack)/sum(Jack.comparable.char)))

sum.var.jack<-c(sum.var.jack,sum(apply(pco.jack[,1:5], 2, var)))

sum.range.jack<-c(sum.range.jack,sum(apply(apply(pco.jack[,1:5], 2, range), 2, diff)))

}

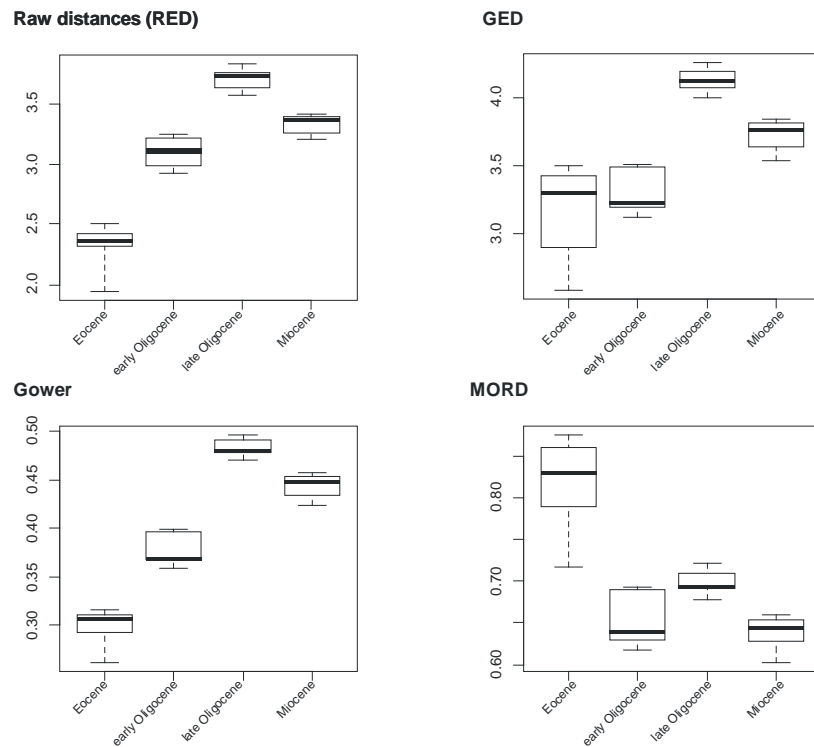
weighted.mean[[j]]=list(weighted.mean.obs,w.mean.jack)

sum.var[[j]]=list(sum.var.obs,sum.var.jack)

sum.range[[j]]=list(sum.range.obs,sum.range.jack)

}
```


7. Comparison of Weighted Mean Pairwise Distance (WMPD; distances weighted by the ratio of comparable characters) based on different distance measurements. WMPD based on GED showed the highest resemblance respect the one based on raw distances (RED), followed by WMPD based on Gower transformation, while that based on MORD showed highest departure, therefore we avoided to use this type of distance.



References

Warnes, GR, Bolker B, Bonebakker L, Gentleman R, Huber W, Liaw A, Lumley T, Maechler M, Magnusson A, Moeller S, Schwartz M & Venables B (2016). gplots: Various R Programming Tools for Plotting Data. R package version 3.0.1. <https://CRAN.R-project.org/package=gplots>