Are environmental and geographic effective surrogates for genetic variation in conservation planning?

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Abstract

Insert abstract here.

Contents

Introduction

Methods

Study area

To address the aims of this study, we utilized species distribution and genomic data collected by the IntraBioDiv project (Figure S1; Meirmans *et al.* 2011). As part of this project, data for 27 alpine plant species were collected across the European Alps using a regular grid (22.3 km × 25 km; see Gugerli *et al.* 2008 for methodological details). In every second cell, plant samples were collected from three individiduals for each species present inside the cell. Samples were genotyped using amplified fragment length polymorphisms (AFLP; Vos *et al.* 1995). Matrices denoting the presence/absence of polymorphisms at loci were consutrcted independently for each species. This dataset was well suited for the purposes of this study, because it provides spatially explicit genomic data for a multitude of species. Additionally, the study area spans across broad-scale environmental gradients–ranging from lowlands to snow-caped peaks–that have been found to correlate with genetic variation for some of these species [].

Surrogate data

We explored the effectiveness of environmental and geographic surrogates. To describe variation in the location of each grid, we projected the grids to an equal-area coordinate system (ESRI:102014) and determined the centroid of each cell. To describe the climatic variation among each cell, we obtained twenty-one bioclimatic variables (Hijmans *et al.* 2005). These layers were clipped to the extent of the grid and subject to a principle components analysis (PCA; Table S1). The first two principle components (PCs) cumulatively explained 97.2% of the variation and were used to generate two new layers. The average value of each PC layer in each grid was used to characterise the climatic conditions in the grid cell (Figure S2).

Outlier locus detection

To investigate the effectiveness of the surrogates for adaptive and neutral genetic variation, we first identifed which of the sampled loci for each species for each species were under selection. We used an outlier locus detection method (evaluated in Pérez-Figueroa *et al.* 2010) to avoid circularity issues. The basic premise underpinning this method is that neutral loci are expected to have a specific level of variation among populations (F_{st}), and loci that deviate from this expectation are under selection. Previously, Bothwell *et al.* (2013) applied such detection methods to one of the species (*Getiana nivalis*) in this dataset. Here, we applied their methods to each of the twenty-seven species in the dataset.

Breifly, we grouped individuals into genetic lineages (Figure S2). The purpose of this step was to avoid confounding variation between populations with due to genetic history with variation attributed to selection pressures. We used the Bayesian clustering method implemented in Structure (version 2.3.4) assuming admixture and an independent alleles model. For each species, we identified the most plausible number of populations (K = 1–10; 4 runs for each K; model with lowest mean posterior negative log likelihood; Figure S3), and estimated the probability that each individual belonged to each population (10 burn-in; 10 iterations). Individuals with ≥ 0.75 probability of

belonging to a single population were assigned accordingly (Figure S4), and used for subseqent detection methods.

We used Bayescan (version 2.1; Foll and Gaggiotti 2008) to identify the sampled loci under selection for each species (Table S2). For each species, Bayescan was run using the population memberships identified using Structure (1:1 prior odds, 3 pilot runs, and 10 iterations thinned by 1 iterations with a 40 burn-in). Following guidelines in the Bayescan manual, we omitted loci where the global frequency of the minor allele was ≥ 0.05 to avoid false-positives. To ensure convergence, we ran 2 replicates per species using a false discovery rate (FDR) ≤ 0.5.

After classifying the loci as adaptive or neutral for each species, we mapped the main gradients of adaptive and/or neutral genetic variation for each species (Figures S4–S29). For each species, we used Gower distances to express the difference in adaptive and/or neutral polymorphisms between individuals (using the cluster R package; Maechler *et al.* 2015). These distances were subject to a non metric multi-dimensional scaling analysis (implemented in the vegan R package using K=2 and 2 random starts; Table S3; Oksanen *et al.* 2015). The ordinated variables were then associated with the grid cells were each species was sampled.

Prioritisations

Results

Single species prioritisations

```
# prepare data for plotting
single.spp.PDF <- expand.grid(
    Prioritisation=unique(single.spp.SDF$Prioritisation),
    Metric=unique(single.spp.SDF$Metric))
single.spp.PDF <- cbind(single.spp.PDF,
    as.data.frame(predict(single.spp.GLM, single.spp.PDF,
        type='response', se.fit=TRUE))) %>%
    mutate(lower=fit-se.fit, upper=fit+se.fit,
        letters=toupper(cld(single.spp.MCP)$mcletters$Letters),
        letter_pos=upper+0.05)
# make plot
ggplot(aes(x=Metric,y=fit,fill=Prioritisation),
    data=single.spp.PDF) +
    geom_bar(position=position_dodge(0.9),
        stat='identity') +
    geom_errorbar(
        aes(ymin=lower,ymax=upper),
        position=position_dodge(0.9), width=0.6) +
    geom_text(aes(x=Metric, y=letter_pos,
        label=letters), position=position_dodge(0.9)) +
    scale_fill_manual(name='Prioritisation',
        values=c('grey80','grey50','grey20')) +
    ylab('Proportion genetic\nvariation secured (%)') +
```

```
    xlab('') +
    theme_classic()
```

```
## ymax not defined: adjusting position using y instead
```
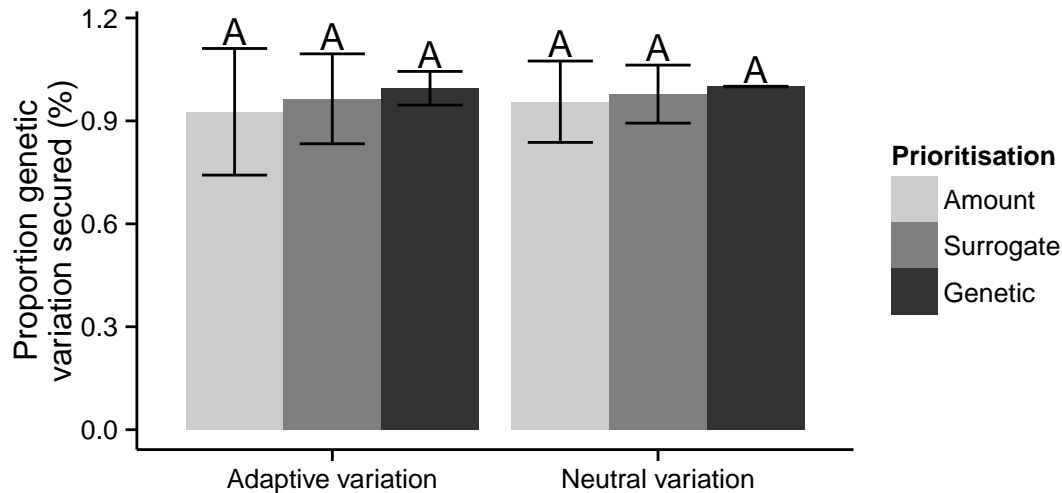

Figure 1 Summary of single species prioritisations. Single species prioritisations were generated using amount-based targets, amount-based and surrogate-based targets, and amount-based and genetic-based targets for each species. Data shows the performance of prioritisations generated using these three sets of targets. Bars denote means and standard errors.

Multi-species prioritisations

```
# download basemap
data(countriesHigh)
countries.FPLY <- countriesHigh[
    countriesHigh$ADMIN %in% c(
        'Italy', 'Switzerland', 'France', 'Austria',
        'Germany', 'Slovenia', 'Croatia', 'Hungary',
        'Monaco', 'Germany'
    )
,] %>% spFortify
# prepare data for plotting
multi.spp.grid.FPLY <- grid.PLY
for (i in seq_along(multi.spp.prioritisations))
    multi.spp.grid.FPLY@data[[paste0('v',i)]] <- selections(multi.spp.prioritisations[[i]])
multi.spp.grid.FPLY <- spFortify(multi.spp.grid.FPLY)
# make maps
do.call(
```

```
    grid.arrange,
    append(
        llply(
            seq_along(multi.spp.prioritisations),
            function(i) {
                ggplot() +
                    geom_polygon(data=countries.FPLY, aes(x=long, y=lat, group=group),
                        fill='grey20', color='grey80') +
                    geom_polygon(data=multi.spp.grid.FPLY, aes_string(x='long', y='lat',
                        group='group', fill=paste0('v',i)),
                        alpha=0.8, color='grey10') +
                    guides(fill=guide_legend(title=' ')) +
                    theme_classic() +
                    theme(axis.ticks=element_blank(), axis.text=element_blank(),
                        plot.margin=unit(c(0,0,0,0),'cm'), axis.line=element_blank(),
                        legend.position='none') +
                    coord_cartesian(
                        xlim=buffered.range(multi.spp.grid.FPLY$long, 0.05),
                        ylim=buffered.range(multi.spp.grid.FPLY$lat, 0.05)
                    ) +
                    xlab('') +
                    ylab('') +
                    annotate('text',
                        x=min(multi.spp.grid.FPLY$long)+diff(range(multi.spp.grid.FPLY$long)*0
                        y=min(multi.spp.grid.FPLY$lat)+diff(range(multi.spp.grid.FPLY$lat)*1.0
                        label=letters[i], hjust=1, vjust=1, color='white', size=8)
            }
        ),
        list(nrow=1)
    )
)
```
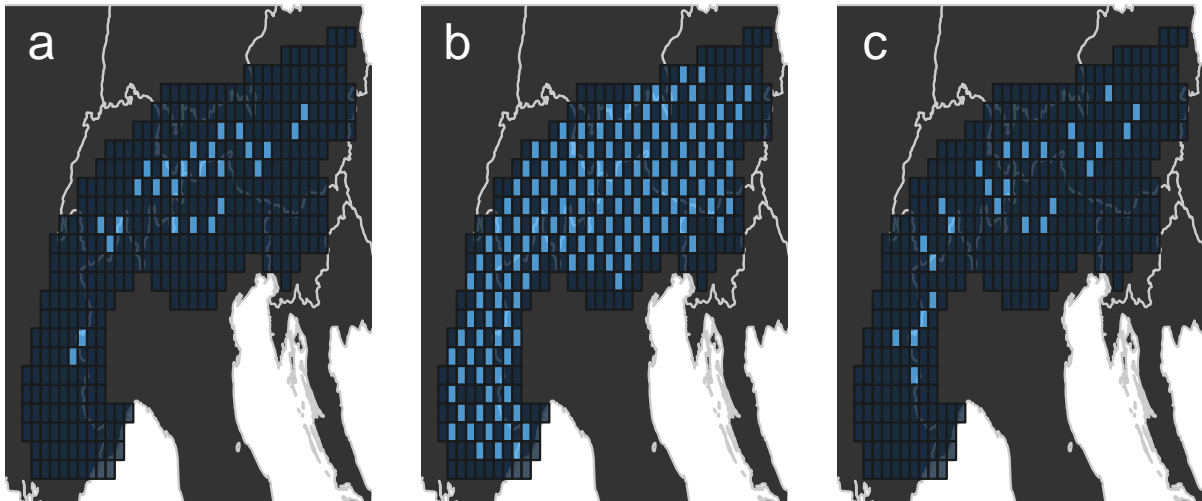
Figure 2 Multi-species prioritisations. Panel (a) shows the prioritisation generated for using just amount-based targets. Panel (b) shows the prioritisation generated using amount-based and surrogate based targets. Panel (c) shows the prioritisation generated using amount-based and genetic-based targets

```r
# prepare data for plotting
multi.spp.PDF <- expand.grid(
    Prioritisation=unique(multi.spp.SDF$Prioritisation),
    Metric=unique(multi.spp.SDF$Metric))
multi.spp.PDF <- cbind(multi.spp.PDF,
    as.data.frame(predict(multi.spp.GLM, multi.spp.PDF,
        type='response', se.fit=TRUE))) %>%
    mutate(lower=fit-se.fit, upper=fit+se.fit,
        letters=toupper(cld(multi.spp.MCP)$mcletters$Letters),
        letter_pos=upper+0.05)
# make plot
ggplot(aes(x=Metric,y=fit,fill=Prioritisation),
    data=multi.spp.PDF) +
    geom_bar(position=position_dodge(0.9),
        stat='identity') +
    geom_errorbar(
        aes(ymin=lower,ymax=upper),
        position=position_dodge(0.9), width=0.6) +
    geom_text(aes(x=Metric, y=letter_pos,
        label=letters), position=position_dodge(0.9)) +
    scale_fill_manual(name='Prioritisation',
        values=c('grey80','grey50','grey20')) +
    ylab('Proportion genetic\nvariation secured (%)') +
    xlab('') +
    theme_classic()
```

```
## ymax not defined: adjusting position using y instead
```
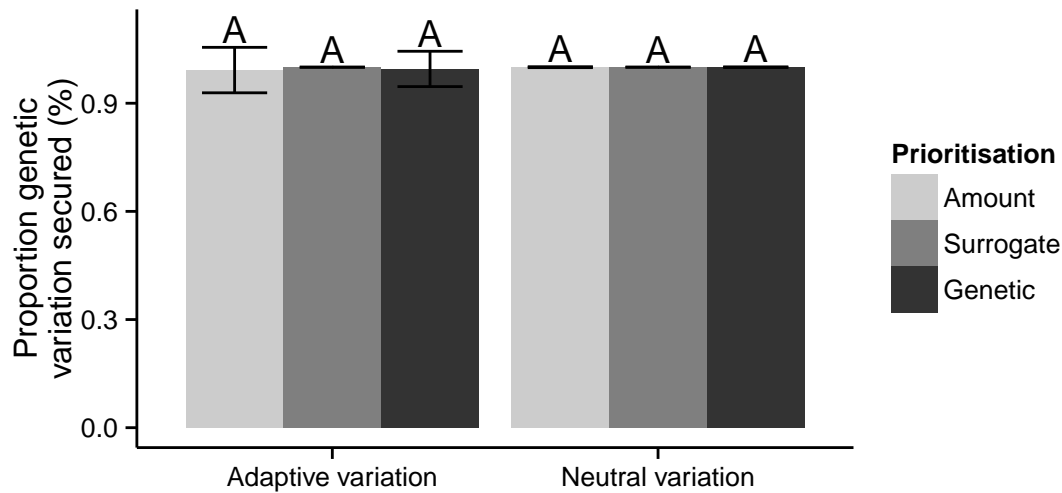
Figure 3 Summary of multi-species prioritisations. Three prioritisations were generated using amount-based targets, amount-based and surrogate-based targets, and amount-based and genetic-based targets for each species. Data shows the performance of these prioritisations based on how much genetic variation they explain. Bars denote means and standard errors.

Pareo-frontier analysis

```r
# make plots
p1 <- ggplot(data=env.pareto.DF) +
    geom_line(aes(x=Surrogate.target,y=adaptive.held,group=Species),
        alpha=0.5) +
    xlab('Environmental variation secured (%)') +
    ylab('Adaptive genetic\nvariation secured (%)') +
    theme_classic()
p2 <- ggplot(data=geo.pareto.DF) +
    geom_line(aes(x=Surrogate.target,y=neutral.held,group=Species),
        alpha=0.5) +
    xlab('Geographic variation secured (%)') +
    ylab('Neutral genetic\nvariation secured (%)') +
    theme_classic()
grid.arrange(p1, p2, nrow=1)
```
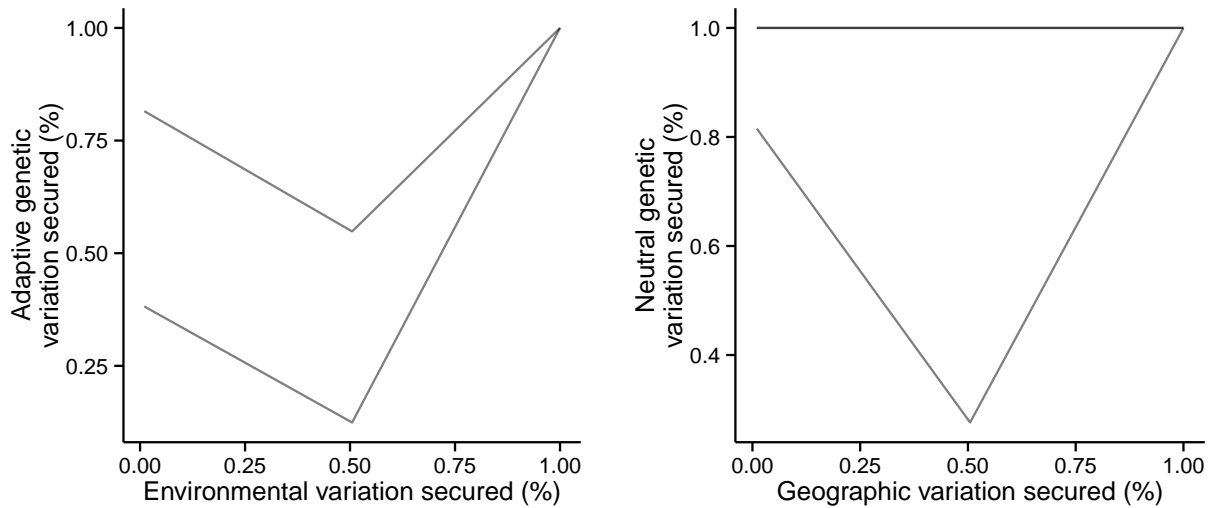
Figure 4 The relationship between surrogates and genetic variation secured in prioritisations.

Discussion

Acknowledgements

References

Figures

Tables

Supporting Information

Figure S1: Species distributions

```
## plot map of species distributions
# fortify data
grid.FPLY <- spFortify(grid.PLY)
spp.grid.FPLY <- ldply(unique(spp.samples.DF$species), function(x) {
        z <- grid.FPLY[,c('long', 'lat', 'group', x),drop=FALSE]
        names(z)[4] <- 'presence'
        z$species <- gsub('\\_', ' ', x)
```

```
        return(z)
    }
)
# plot species data
ggplot() +
    geom_polygon(data=countries.FPLY, aes(x=long, y=lat, group=group),
        fill='grey20', color='grey80') +
    geom_polygon(data=spp.grid.FPLY, aes(x=long, y=lat,
        group=group, fill=presence), alpha=0.8, color='grey10') +
    theme_classic() +
    guides(fill=guide_legend(title='Presence')) +
    theme(axis.ticks=element_blank(), axis.text=element_blank(),
        axis.line=element_blank()) +
    coord_cartesian(
        xlim=buffered.range(grid.FPLY$long, 0.05),
        ylim=buffered.range(grid.FPLY$lat, 0.05)
    ) +
    xlab('') +
    ylab('') +
    facet_wrap(~ species, ncol=4)
```
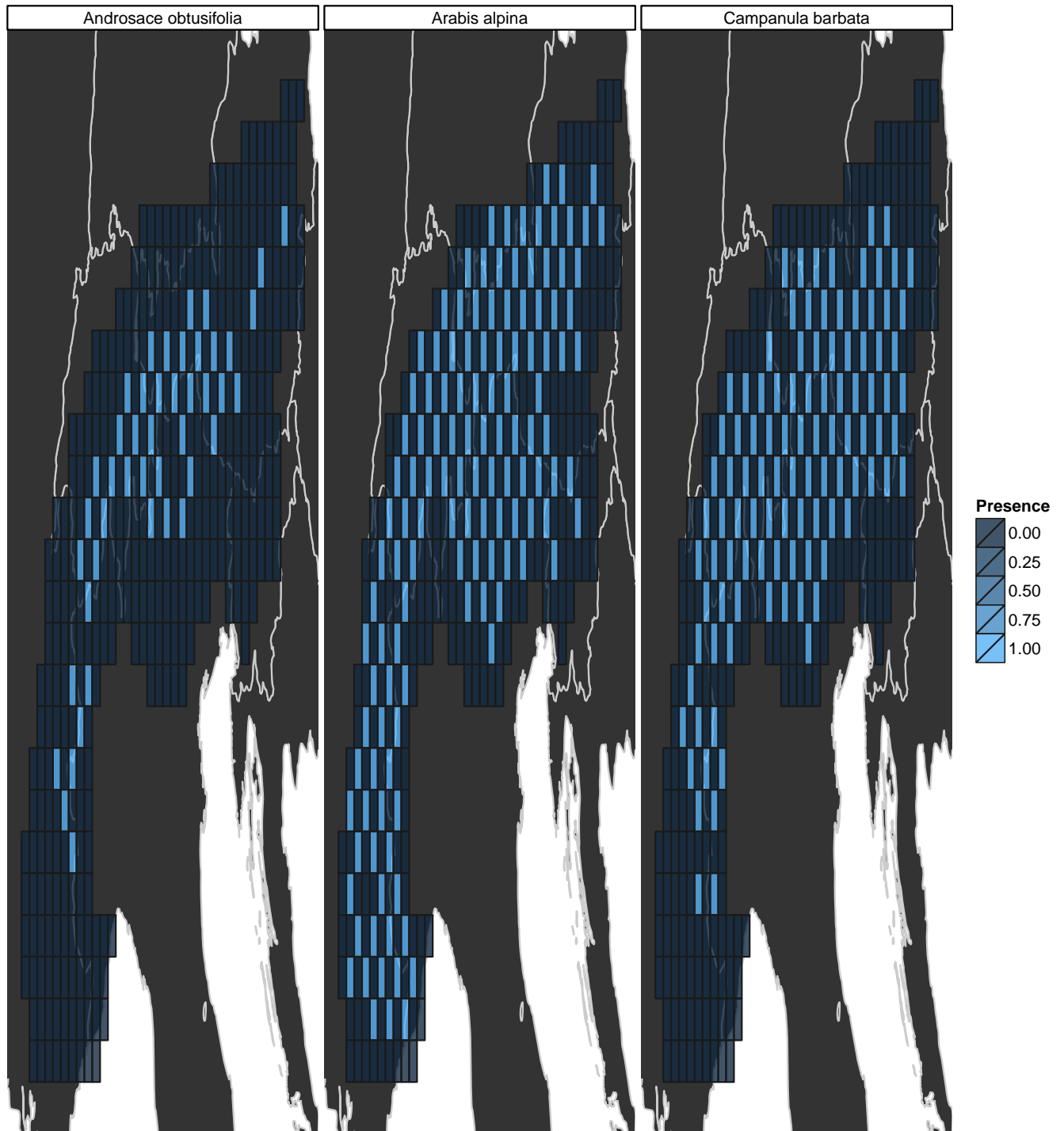
Figure 5 Species distributions. Squares represent planning units. For a given species, planning units that were found to be inhabited are denoted with bright blue.

```
# calculate species richness
grid.PLY$Species_richness <- grid.PLY@data %>%
    select(5:(4+n.spp)) %>% as.matrix() %>% rowSums()

# plot species richness
ggplot() +
    geom_polygon(data=countries.FPLY, aes(x=long, y=lat, group=group),
        fill='grey20', color='grey80') +
    geom_polygon(data=spFortify(grid.PLY), aes(x=long, y=lat,
        group=group, fill=Species_richness), alpha=0.8, color='grey10') +
    guides(fill=guide_legend(title='Count (#)')) +
    theme_classic() +
    theme(axis.ticks=element_blank(), axis.text=element_blank(),
        axis.line=element_blank()) +
    coord_cartesian(
        xlim=buffered.range(grid.FPLY$long, 0.05),
        ylim=buffered.range(grid.FPLY$lat, 0.05)
    ) +
    xlab('') +
    ylab('') +
    ggtitle('Species richness')
```
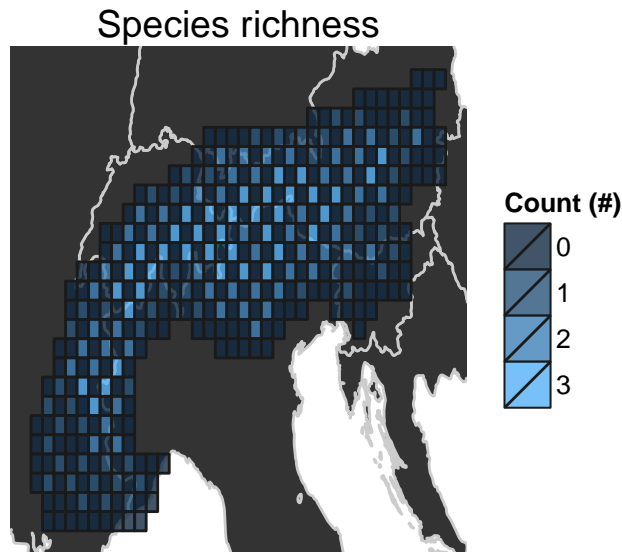

Figure 6 Species richness. Squares denote planning units. Planning units with a brighter color are inhabited by more species.

Figure S2: Maps of climatic variation

```
do.call(
    grid.arrange,
        append(
        llply(grep('^env\\_.*$', names(grid.DF), value=TRUE), function(x) {
            ggplot() +
                geom_polygon(data=countries.FPLY, aes(x=long, y=lat, group=group),
                    fill='grey20', color='grey80') +
                geom_polygon(data=grid.FPLY, aes_string(x='long', y='lat',
                    group='group', fill=x),
                    alpha=0.8, color='grey10') +
                guides(fill=guide_legend(title=' ')) +
                theme_classic() +
                theme(axis.ticks=element_blank(), axis.text=element_blank(),
                    plot.margin=unit(c(0,0,0,0),'cm'), axis.line=element_blank()) +
                coord_cartesian(
                    xlim=buffered.range(grid.FPLY$long, 0.05),
                    ylim=buffered.range(grid.FPLY$lat, 0.05)
                ) +
                xlab('') +
                ylab('') +
                ggtitle(paste0('PC ', substr(x, nchar(x), nchar(x))))
        }),
        list(ncol=2)
    )
)
```
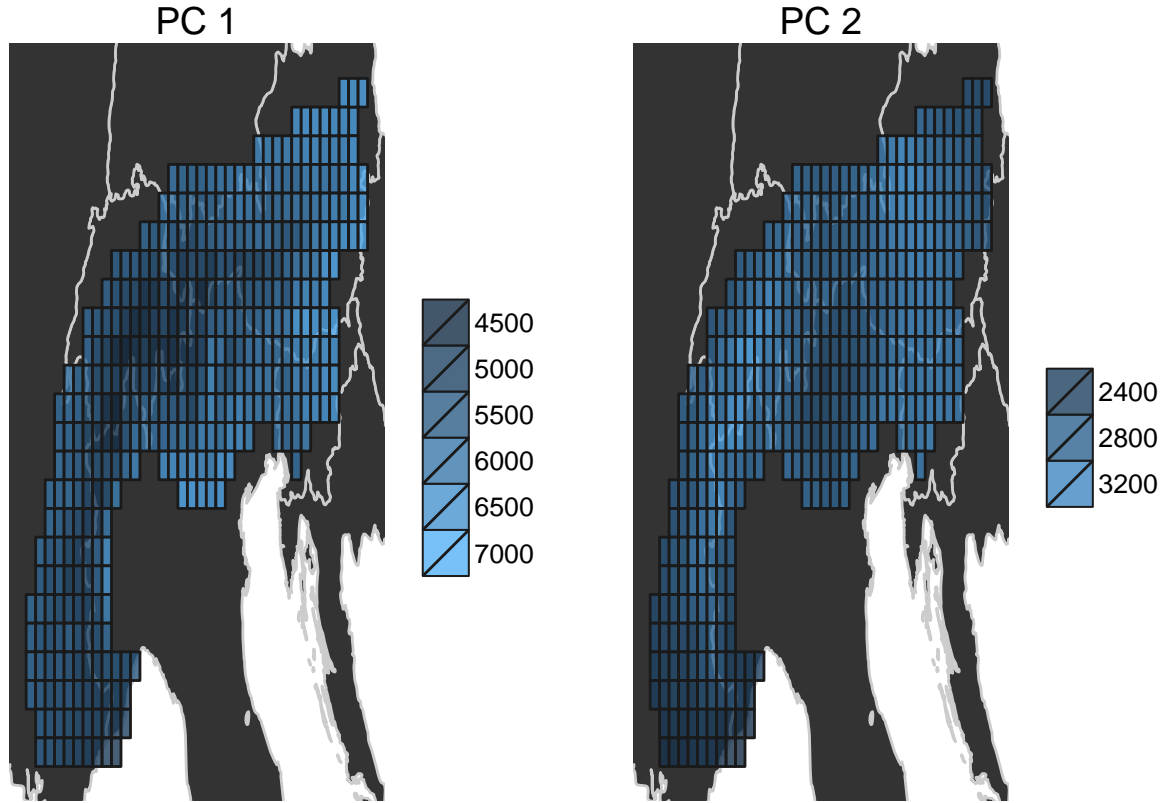
Figure 7 Climatic variation. Each panel depicts variation based on a different principle component (PC). Sqaures represent planning units. The color of each planning unit denotes the average priciniple component value of pixels inside it. Planning units with more similar colors have more similar climates regimes.

Figure S3. Number populations in each species.

Figure S4. Distribution of populations for each species.

```
plot.spp.mds <- function(i) {
    # define function
    make.mds.plot <- function(j,k) {
        ggplot() +
            geom_polygon(data=countries.FPLY, aes(x=long, y=lat, group=group),
                fill='grey20', color='grey80') +
            geom_polygon(data=grid.FPLY, aes_string(x='long', y='lat',
                group='group', fill=paste0(unique(spp.samples.DF$species)[i], '_', j, '_d',k))
                alpha=0.8, color='grey10') +
            guides(fill=guide_legend(title=' ')) +
            theme_classic() +
            theme(axis.ticks=element_blank(), axis.text=element_blank(),
                plot.margin=unit(c(0,0,0,0),'cm'), axis.line=element_blank()) +
            coord_cartesian(
```

```r
                xlim=buffered.range(grid.FPLY$long, 0.05),
                ylim=buffered.range(grid.FPLY$lat, 0.05)
            ) +
            xlab('') +
            ylab('') +
            ggtitle(paste0(j,' (',k,')'))
    }
    # init
    adapt.col <- paste0(unique(spp.samples.DF$species)[i], '_adaptive_d1')
    neutral.col <- paste0(unique(spp.samples.DF$species)[i], '_neutral_d1')
    plotLST <- list()
    # make adaptive plot
    if (adapt.col %in% names(grid.FPLY)) {
        for (k in seq_len(mds.k))
            plotLST <- append(plotLST, list(make.mds.plot('adaptive', k)))
    }
    # make neutral plot
    if (neutral.col %in% names(grid.FPLY)) {
        for (k in seq_len(mds.k))
            plotLST <- append(plotLST, list(make.mds.plot('neutral', k)))
    }
    # make plot
    do.call(
        grid.arrange,
        append(
            plotLST,
            list(ncol=6)
        )
    )
}
```

Figures S

```r
plot.spp.mds(1)
```
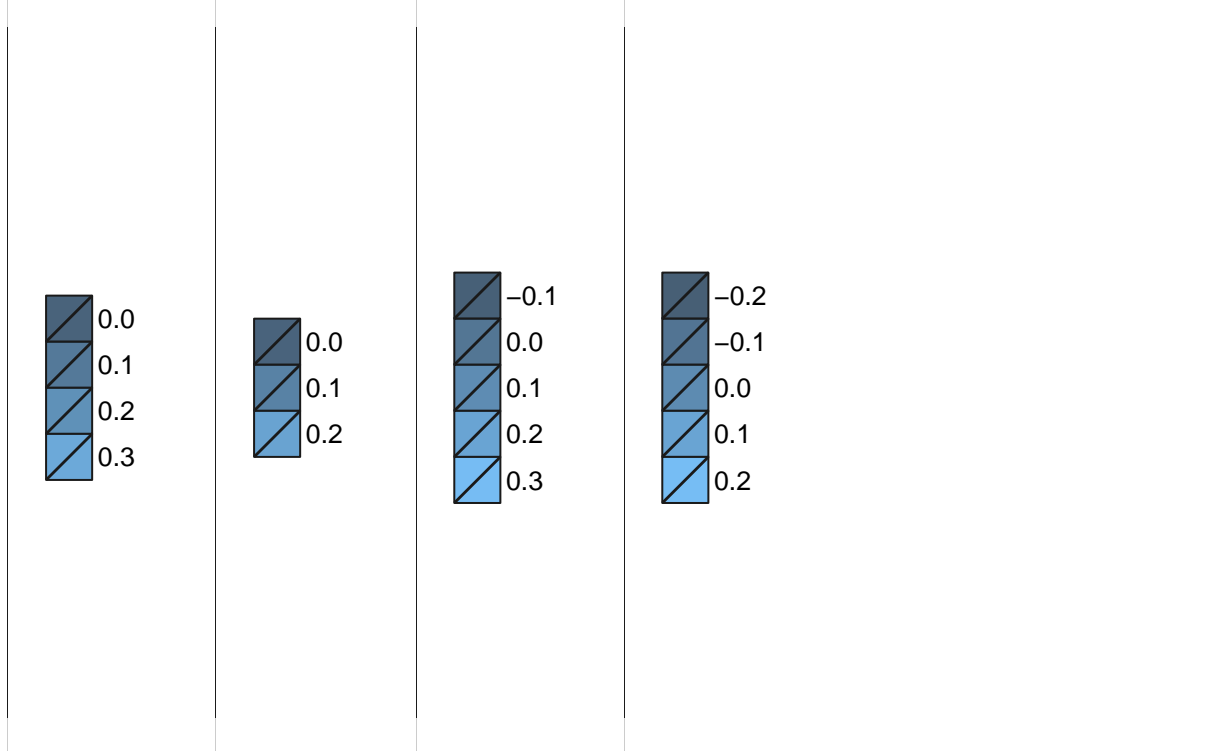
Figure 8 Distribution of adaptive and neutral genetic variation in *Androsace obtusifolia*. Each square represents a planning unit. The color of each planning unit panel corresponds to ordination values. Planning units with similar colors contain individiduals with similar genetic variation.

```
plot.spp.mds(2)
```

utral (1)   neutral (2)
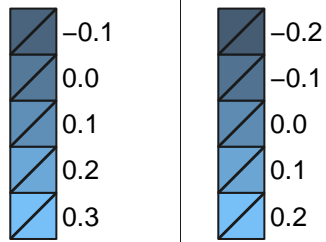
Figure 9 Distribution of adaptive and neutral genetic variation in *Arabis alpina*. See Figure XX caption for conventions.

```
plot.spp.mds(3)
```
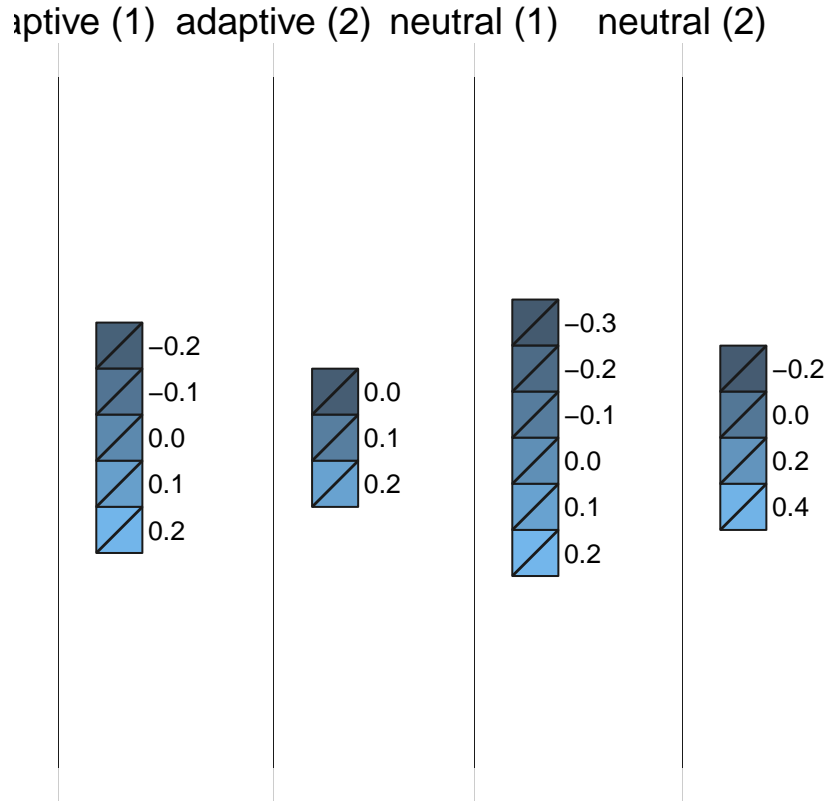
Figure 10 Distribution of adaptive and neutral genetic variation in *Campanula barbata*. See Figure XX caption for conventions.

Table S1: Principle components analysis on climatic variation

```
## make results table showing Eigen values
knitr::kable(
    pca.DF,
    digits=2,
    caption='Summary of principle components analysis (PCA) on bioclimatic variation across the
    align=c('l', 'c', 'c', 'c')
)
```

Principle Component	Eigen Value	Variation explained (%)	Accumulative variation explained (%)
1	216765.14	82.67	82.67
2	38177.84	14.56	97.23
3	5356.75	2.04	99.27
4	1216.67	0.46	99.73
5	700.39	0.27	100.00

Principle Component	Eigen Value	Variation explained (%)	Accumulative variation explained (%)

Table 1 Summary of principle components analysis (PCA) on bioclimatic variation across the study area. The first two principle components (PCs) were used for subsequent analysis.

Table S2: BayeScan Results

```
knitr::kable(
    format.table(
        ldply(
            seq_along(unique(spp.samples.DF$species)),
            function(i) {
                data.frame(
                    Species=paste0('\\textit{',gsub('\\_', ' ', unique(spp.samples.DF$species)
                    Primer=spp.BayeScan.sample.loci.subset.LST[[i]]@data@primers,
                    Probability=spp.BayeScan.sample.loci.subset.LST[[i]]@results@summary[[2]],
                    qval=spp.BayeScan.sample.loci.subset.LST[[i]]@results@summary[[4]],
                    alpha=spp.BayeScan.sample.loci.subset.LST[[i]]@results@summary[[5]],
                    fst=spp.BayeScan.sample.loci.subset.LST[[i]]@results@summary[[6]],
                    Type=spp.BayeScan.sample.loci.subset.LST[[i]]@results@summary[[7]]
                )
            }
        ),
        omit='Type'
    ),
    digits=2,
    col.names=c('Species', 'Primer', 'Probability', 'q-value', '$\\alpha$', '$F_{ST}$', 'Type')
    align=c('l', 'c', 'c', 'c', 'c', 'c', 'c')
)
```

Species	Primer	Probability	q-value	α	F_{ST}	Type
Androsace obtusifolia	AAC_CAN_83.0	0.00	0.87	0.00	0.14	neutral
	AAC_CAN_85.0	0.00	0.87	0.00	0.14	neutral
	AAC_CAN_89.0	0.04	0.83	0.04	0.14	neutral
	AAC_CAN_91.0	0.07	0.77	-0.04	0.13	neutral
	AAC_CAN_100.0	0.07	0.77	0.01	0.14	neutral
	AAC_CAN_102.0	0.30	0.55	0.20	0.16	neutral
	AAC_CAN_108.0	0.04	0.83	0.04	0.14	neutral
	AAC_CAN_124.0	0.33	0.57	-0.46	0.10	neutral
	AAC_CAN_125.0	0.07	0.78	0.00	0.14	neutral

Species	Primer	Probability	q-value	α	F_{ST}	Type
	AAC_CAN_128.0	0.33	0.58	-0.11	0.13	neutral
	AAC_CAN_130.0	0.19	0.59	NaN	NaN	neutral
	AAC_CAN_132.0	0.30	0.55	0.05	0.14	neutral
	AAC_CAN_133.0	0.00	0.87	0.00	0.14	neutral
	AAC_CAN_136.0	0.07	0.77	0.00	0.14	neutral
	AAC_CAN_137.0	0.19	0.59	0.14	0.16	neutral
	AAC_CAN_146.0	0.22	0.61	0.15	0.16	neutral
	AAC_CAN_151.0	0.56	0.17	0.33	0.24	adaptive
	AAC_CAN_152.0	0.19	0.59	NaN	NaN	neutral
	AAC_CAN_153.0	0.11	0.68	0.02	0.14	neutral
	AAC_CAN_182.0	0.15	0.65	-0.26	0.12	neutral
	AAC_CAN_195.0	0.07	0.78	0.02	0.14	neutral
	AAC_CAN_211.0	0.04	0.83	0.01	0.14	neutral
	AAC_CAN_220.0	0.00	0.87	0.00	0.14	neutral
	AAC_CAN_231.0	0.48	0.37	-0.18	0.12	neutral
	AAC_CAN_239.0	0.37	0.54	-0.56	0.10	neutral
	AAC_CAN_272.0	0.04	0.82	-0.01	0.14	neutral
	AAC_CAN_319.0	0.07	0.77	0.05	0.14	neutral
	ACA_CAT_81.0	0.04	0.82	-0.01	0.14	neutral
	ACA_CAT_85.0	0.37	0.52	0.18	0.17	neutral
	ACA_CAT_90.0	0.15	0.61	0.03	0.14	neutral
	ACA_CAT_97.0	0.07	0.73	-0.04	0.13	neutral
	ACA_CAT_99.0	0.15	0.65	0.16	0.17	neutral
	ACA_CAT_100.0	0.07	0.76	0.02	0.14	neutral
	ACA_CAT_102.0	0.07	0.76	-0.04	0.13	neutral
	ACA_CAT_103.0	0.00	0.87	0.00	0.14	neutral
	ACA_CAT_108.0	0.15	0.64	-0.10	0.13	neutral
	ACA_CAT_120.0	0.11	0.67	-0.05	0.13	neutral
	ACA_CAT_124.0	0.04	0.82	-0.04	0.13	neutral
	ACA_CAT_126.0	0.04	0.82	0.05	0.15	neutral
	ACA_CAT_129.0	0.33	0.58	0.00	0.14	neutral
	ACA_CAT_131.0	0.19	0.59	-0.12	0.13	neutral

Species	Primer	Probability	q-value	α	F_{ST}	Type
	ACA_CAT_133.0	0.70	0.24	-0.35	0.12	neutral
	ACA_CAT_135.0	0.07	0.73	-0.04	0.13	neutral
	ACA_CAT_140.0	0.04	0.82	0.02	0.14	neutral
	ACA_CAT_148.0	0.04	0.82	0.03	0.14	neutral
	ACA_CAT_152.0	0.07	0.78	-0.05	0.13	neutral
	ACA_CAT_153.0	0.04	0.82	0.00	0.14	neutral
	ACA_CAT_155.0	0.07	0.76	0.01	0.14	neutral
	ACA_CAT_157.0	0.37	0.54	-0.16	0.12	neutral
	ACA_CAT_159.0	0.11	0.70	0.18	0.17	neutral
	ACA_CAT_162.0	0.07	0.73	0.01	0.14	neutral
	ACA_CAT_168.0	0.19	0.60	-0.05	0.13	neutral
	ACA_CAT_173.0	0.33	0.58	0.20	0.17	neutral
	ACA_CAT_177.0	0.00	0.87	0.00	0.14	neutral
	ACA_CAT_178.0	0.19	0.58	0.07	0.14	neutral
	ACA_CAT_187.0	0.04	0.81	-0.02	0.14	neutral
	ACA_CAT_192.0	0.19	0.59	0.09	0.15	neutral
	ACA_CAT_196.0	0.00	0.87	0.00	0.14	neutral
	ACA_CAT_199.0	0.04	0.83	0.00	0.14	neutral
	ACA_CAT_200.0	0.04	0.83	-0.02	0.14	neutral
	ACA_CAT_204.0	0.00	0.87	0.00	0.14	neutral
	ACA_CAT_205.0	0.07	0.77	-0.02	0.13	neutral
	ACA_CAT_210.0	0.15	0.61	-0.03	0.13	neutral
	ACA_CAT_214.0	0.33	0.58	0.03	0.14	neutral
	ACA_CAT_219.0	0.11	0.68	-0.03	0.13	neutral
	ACA_CAT_229.0	0.15	0.61	-0.04	0.13	neutral
	ACA_CAT_237.0	0.15	0.65	-0.07	0.13	neutral
	ACA_CAT_243.0	0.04	0.82	-0.02	0.14	neutral
	ACA_CAT_246.0	0.04	0.82	-0.01	0.14	neutral
	ACA_CAT_248.0	0.04	0.83	-0.02	0.13	neutral
	ACA_CAT_282.0	0.00	0.87	0.00	0.14	neutral
	ACA_CAT_300.0	0.04	0.81	-0.02	0.14	neutral
	ACA_CAT_390.0	0.41	0.49	-0.02	0.15	neutral

Species	Primer	Probability	q-value	α	F_{ST}	Type
	ACA_CAT_391.0	0.04	0.81	0.03	0.14	neutral
	ACA_CAT_393.0	0.04	0.83	-0.01	0.14	neutral
	AGG_CAA_82.3	0.04	0.83	-0.03	0.13	neutral
	AGG_CAA_83.0	0.15	0.65	-0.02	0.14	neutral
	AGG_CAA_84.2	0.41	0.45	-0.05	0.13	neutral
	AGG_CAA_86.9	0.07	0.77	0.00	0.14	neutral
	AGG_CAA_90.9	0.11	0.65	-0.02	0.14	neutral
	AGG_CAA_94.8	0.04	0.81	0.01	0.14	neutral
	AGG_CAA_95.6	0.07	0.71	0.05	0.15	neutral
	AGG_CAA_100.0	0.07	0.78	-0.01	0.14	neutral
	AGG_CAA_101.0	0.07	0.73	-0.13	0.13	neutral
	AGG_CAA_109.3	0.07	0.78	0.04	0.14	neutral
	AGG_CAA_110.2	0.00	0.87	0.00	0.14	neutral
	AGG_CAA_113.5	0.04	0.81	0.04	0.14	neutral
	AGG_CAA_115.9	0.11	0.68	-0.02	0.14	neutral
	AGG_CAA_117.4	0.33	0.58	-0.31	0.12	neutral
	AGG_CAA_118.2	0.04	0.82	-0.02	0.14	neutral
	AGG_CAA_122.9	0.33	0.58	-0.11	0.13	neutral
	AGG_CAA_129.5	0.37	0.42	0.43	0.23	neutral
	AGG_CAA_130.1	0.48	0.29	0.17	0.16	adaptive
	AGG_CAA_135.5	0.37	0.52	-0.10	0.13	neutral
	AGG_CAA_137.9	0.26	0.57	-0.12	0.13	neutral
	AGG_CAA_144.9	0.37	0.53	-0.03	0.14	neutral
	AGG_CAA_145.8	0.37	0.52	-0.36	0.11	neutral
	AGG_CAA_150.9	0.00	0.87	0.00	0.14	neutral
	AGG_CAA_152.8	0.07	0.74	0.04	0.15	neutral
	AGG_CAA_155.4	0.04	0.83	0.02	0.14	neutral
	AGG_CAA_164.0	0.22	0.61	-0.08	0.13	neutral
	AGG_CAA_175.9	0.41	0.49	-0.17	0.13	neutral
	AGG_CAA_181.6	0.04	0.83	0.00	0.14	neutral
	AGG_CAA_182.1	0.00	0.87	0.00	0.14	neutral
	AGG_CAA_188.1	0.07	0.73	0.01	0.14	neutral

Species	Primer	Probability	q-value	α	F_{ST}	Type
	AGG_CAA_191.3	0.07	0.77	0.01	0.14	neutral
	AGG_CAA_193.9	0.04	0.83	0.02	0.14	neutral
	AGG_CAA_196.8	0.11	0.70	0.02	0.14	neutral
	AGG_CAA_201.7	0.07	0.77	-0.04	0.14	neutral
	AGG_CAA_212.4	0.07	0.76	-0.02	0.14	neutral
	AGG_CAA_215.6	0.15	0.65	-0.05	0.13	neutral
	AGG_CAA_219.0	0.04	0.83	0.00	0.14	neutral
	AGG_CAA_225.2	0.04	0.83	-0.02	0.13	neutral
	AGG_CAA_253.2	0.07	0.76	0.01	0.14	neutral
	AGG_CAA_256.7	0.04	0.82	0.02	0.14	neutral
	AGG_CAA_262.5	0.30	0.54	-0.02	0.14	neutral
	AGG_CAA_263.6	0.11	0.67	-0.09	0.13	neutral
	AGG_CAA_264.8	0.04	0.81	-0.01	0.14	neutral
	AGG_CAA_267.9	0.41	0.49	0.28	0.17	neutral
	AGG_CAA_269.8	0.04	0.83	0.03	0.14	neutral
	AGG_CAA_270.8	0.11	0.72	0.05	0.14	neutral
	AGG_CAA_276.8	0.07	0.78	-0.06	0.13	neutral
	AGG_CAA_299.0	0.26	0.55	0.11	0.15	neutral
	AGG_CAA_305.1	0.11	0.69	-0.06	0.13	neutral
	AGG_CAA_312.1	0.04	0.82	0.01	0.14	neutral
	AGG_CAA_313.2	0.04	0.81	-0.03	0.13	neutral
	AGG_CAA_316.0	0.00	0.87	0.00	0.14	neutral
	AGG_CAA_319.0	0.00	0.87	0.00	0.14	neutral
	AGG_CAA_324.1	0.04	0.81	-0.06	0.13	neutral
	AGG_CAA_359.4	0.11	0.70	-0.02	0.14	neutral
	AGG_CAA_360.5	0.19	0.60	-0.05	0.14	neutral
	AGG_CAA_363.2	0.07	0.73	-0.05	0.14	neutral
	AGG_CAA_364.1	0.07	0.78	0.03	0.14	neutral
	AGG_CAA_376.2	0.11	0.68	0.05	0.14	neutral
	AGG_CAA_376.7	0.00	0.87	0.00	0.14	neutral
	AGG_CAA_396.0	0.30	0.54	-0.25	0.11	neutral
	AGG_CAA_403.4	0.07	0.73	0.05	0.14	neutral

Species	Primer	Probability	q-value	α	F_{ST}	Type
	AGG_CAA_420.5	0.07	0.78	-0.06	0.13	neutral
Arabis alpina	AAT_CAC_51.9	0.30	0.57	0.51	0.26	neutral
	AAT_CAC_54.7	0.00	0.86	0.00	0.17	neutral
	AAT_CAC_69.0	0.22	0.52	0.03	0.17	neutral
	AAT_CAC_73.6	0.04	0.81	-0.03	0.17	neutral
	AAT_CAC_77.9	0.37	0.53	0.25	0.21	neutral
	AAT_CAC_86.9	0.15	0.64	0.08	0.18	neutral
	AAT_CAC_90.5	0.04	0.80	0.01	0.17	neutral
	AAT_CAC_95.3	0.00	0.86	0.00	0.17	neutral
	AAT_CAC_97.0	0.07	0.76	-0.08	0.16	neutral
	AAT_CAC_97.1	0.07	0.76	0.02	0.17	neutral
	AAT_CAC_100.3	0.00	0.86	0.00	0.17	neutral
	AAT_CAC_105.4	0.33	0.57	0.13	0.19	neutral
	AAT_CAC_118.4	0.04	0.82	0.01	0.17	neutral
	AAT_CAC_121.3	0.00	0.86	0.00	0.17	neutral
	AAT_CAC_128.0	0.37	0.50	-0.45	0.16	neutral
	AAT_CAC_130.0	0.15	0.62	0.09	0.18	neutral
	AAT_CAC_147.4	0.33	0.57	0.07	0.19	neutral
	AAT_CAC_156.9	0.11	0.70	0.03	0.18	neutral
	AAT_CAC_175.1	0.07	0.78	-0.02	0.17	neutral
	AAT_CAC_177.9	0.04	0.81	-0.02	0.17	neutral
	AAT_CAC_179.6	0.11	0.72	0.03	0.18	neutral
	AAT_CAC_188.6	0.07	0.75	-0.01	0.17	neutral
	AAT_CAC_190.0	0.37	0.54	0.22	0.21	neutral
	AAT_CAC_195.5	0.26	0.43	-0.04	0.17	neutral
	AAT_CAC_197.1	0.00	0.86	0.00	0.17	neutral
	AAT_CAC_200.6	0.04	0.81	-0.02	0.17	neutral
	AAT_CAC_201.8	0.11	0.66	0.05	0.18	neutral
	AAT_CAC_209.2	0.11	0.68	0.01	0.18	neutral
	AAT_CAC_213.1	0.04	0.80	0.00	0.17	neutral
	AAT_CAC_215.0	0.07	0.78	-0.01	0.17	neutral
	AAT_CAC_216.2	0.00	0.86	0.00	0.17	neutral

Species	Primer	Probability	q-value	α	F_{ST}	Type
	AAT_CAC_217.0	0.30	0.55	0.13	0.20	neutral
	AAT_CAC_218.1	0.11	0.68	-0.06	0.17	neutral
	AAT_CAC_219.1	0.00	0.86	0.00	0.17	neutral
	AAT_CAC_225.5	0.00	0.86	0.00	0.17	neutral
	AAT_CAC_227.1	0.37	0.54	-0.15	0.16	neutral
	AAT_CAC_229.1	0.44	0.40	0.39	0.24	neutral
	AAT_CAC_231.4	0.04	0.82	-0.03	0.17	neutral
	AAT_CAC_249.7	0.07	0.76	0.01	0.17	neutral
	AAT_CAC_259.3	0.33	0.58	-0.05	0.17	neutral
	AAT_CAC_277.3	0.04	0.80	-0.01	0.17	neutral
	AAT_CAC_298.1	0.11	0.71	-0.01	0.17	neutral
	AAT_CAC_315.9	0.19	0.58	NaN	NaN	neutral
	AAT_CAC_330.4	0.07	0.76	0.02	0.17	neutral
	AAT_CAC_334.8	0.00	0.86	0.00	0.17	neutral
	AAT_CAC_336.6	0.11	0.72	-0.07	0.17	neutral
	AAT_CAC_353.0	0.04	0.82	0.00	0.17	neutral
	AAT_CAC_359.2	0.07	0.76	-0.08	0.16	neutral
	AAT_CAC_399.9	0.04	0.82	0.02	0.18	neutral
	AAT_CAC_410.5	0.00	0.86	0.00	0.17	neutral
	AAT_CAC_412.4	0.33	0.58	0.12	0.19	neutral
	AAT_CAC_458.1	0.15	0.59	-0.03	0.17	neutral
	AAT_CAC_488.6	0.04	0.82	0.03	0.18	neutral
	AGT_CAC_53.8	0.07	0.72	0.01	0.17	neutral
	AGT_CAC_56.3	0.04	0.80	-0.01	0.17	neutral
	AGT_CAC_98.2	0.44	0.43	-0.44	0.13	neutral
	AGT_CAC_104.9	0.41	0.47	-0.16	0.16	neutral
	AGT_CAC_114.8	0.07	0.75	-0.05	0.16	neutral
	AGT_CAC_145.8	0.07	0.75	0.00	0.17	neutral
	AGT_CAC_154.2	0.04	0.80	0.01	0.17	neutral
	AGT_CAC_158.1	0.07	0.76	0.01	0.17	neutral
	AGT_CAC_169.0	0.04	0.81	-0.02	0.17	neutral
	AGT_CAC_171.1	0.11	0.68	0.03	0.18	neutral

Species	Primer	Probability	q-value	α	F_{ST}	Type
	AGT_CAC_181.1	0.15	0.62	-0.04	0.17	neutral
	AGT_CAC_183.0	0.33	0.57	0.21	0.20	neutral
	AGT_CAC_184.4	0.11	0.72	0.00	0.17	neutral
	AGT_CAC_191.2	0.04	0.81	0.03	0.18	neutral
	AGT_CAC_195.0	0.15	0.61	-0.05	0.17	neutral
	AGT_CAC_200.9	0.19	0.58	0.08	0.19	neutral
	AGT_CAC_203.8	0.07	0.75	0.01	0.17	neutral
	AGT_CAC_205.8	0.11	0.67	-0.02	0.17	neutral
	AGT_CAC_210.0	0.04	0.82	0.01	0.17	neutral
	AGT_CAC_230.8	0.41	0.44	-0.20	0.15	neutral
	AGT_CAC_241.0	0.41	0.44	0.00	0.17	neutral
	AGT_CAC_245.6	0.07	0.76	-0.05	0.17	neutral
	AGT_CAC_264.7	0.04	0.82	-0.04	0.17	neutral
	AGT_CAC_266.9	0.00	0.86	0.00	0.17	neutral
	AGT_CAC_269.4	0.04	0.82	0.04	0.18	neutral
	AGT_CAC_274.0	0.11	0.68	0.04	0.18	neutral
	AGT_CAC_285.6	0.07	0.78	0.02	0.18	neutral
	AGT_CAC_291.5	0.07	0.71	-0.01	0.17	neutral
	AGT_CAC_295.6	0.07	0.78	0.02	0.17	neutral
	AGT_CAC_315.2	0.44	0.38	0.29	0.23	neutral
	AGT_CAC_332.1	0.48	0.31	0.72	0.31	neutral
	AGT_CAC_347.8	0.11	0.72	-0.07	0.16	neutral
	AGT_CAC_355.2	0.00	0.86	0.00	0.17	neutral
	AGT_CAC_360.2	0.15	0.65	0.08	0.19	neutral
	AGT_CAC_386.5	0.04	0.82	0.02	0.17	neutral
	AGT_CAC_418.5	0.15	0.64	0.05	0.19	neutral
	AGT_CAC_420.2	0.37	0.47	-0.08	0.16	neutral
	AGT_CAC_444.3	0.04	0.82	-0.04	0.17	neutral
	AGT_CAC_453.4	0.11	0.68	-0.04	0.17	neutral
	AGT_CAC_458.5	0.15	0.57	-0.01	0.17	neutral
	AGT_CAC_489.1	0.07	0.75	-0.06	0.16	neutral
	ATC_CAC_52.4	0.15	0.65	0.00	0.17	neutral

Species	Primer	Probability	q-value	α	F_{ST}	Type
	ATC_CAC_56.7	0.15	0.65	0.06	0.18	neutral
	ATC_CAC_61.5	0.15	0.65	-0.06	0.16	neutral
	ATC_CAC_64.3	0.07	0.75	0.04	0.18	neutral
	ATC_CAC_91.9	0.07	0.76	-0.02	0.17	neutral
	ATC_CAC_96.2	0.41	0.42	-0.54	0.13	neutral
	ATC_CAC_99.5	0.00	0.86	0.00	0.17	neutral
	ATC_CAC_100.6	0.11	0.68	-0.02	0.17	neutral
	ATC_CAC_102.0	0.11	0.66	0.02	0.17	neutral
	ATC_CAC_111.9	0.37	0.53	-0.35	0.15	neutral
	ATC_CAC_113.5	0.41	0.48	0.30	0.23	neutral
	ATC_CAC_123.5	0.00	0.86	0.00	0.17	neutral
	ATC_CAC_139.7	0.07	0.71	-0.05	0.17	neutral
	ATC_CAC_140.8	0.26	0.55	-0.15	0.16	neutral
	ATC_CAC_142.9	0.41	0.47	-0.07	0.16	neutral
	ATC_CAC_144.1	0.15	0.64	0.21	0.21	neutral
	ATC_CAC_148.6	0.07	0.76	0.02	0.17	neutral
	ATC_CAC_149.8	0.07	0.72	-0.06	0.17	neutral
	ATC_CAC_151.8	0.07	0.75	0.03	0.18	neutral
	ATC_CAC_156.1	0.04	0.80	0.00	0.17	neutral
	ATC_CAC_162.5	0.19	0.60	0.31	0.23	neutral
	ATC_CAC_181.9	0.00	0.86	0.00	0.17	neutral
	ATC_CAC_186.4	0.07	0.76	-0.02	0.17	neutral
	ATC_CAC_189.9	0.00	0.86	0.00	0.17	neutral
	ATC_CAC_194.8	0.07	0.75	0.00	0.17	neutral
	ATC_CAC_198.3	0.00	0.86	0.00	0.17	neutral
	ATC_CAC_199.4	0.22	0.55	-0.15	0.15	neutral
	ATC_CAC_204.2	0.37	0.53	0.14	0.20	neutral
	ATC_CAC_207.3	0.04	0.81	-0.02	0.17	neutral
	ATC_CAC_215.8	0.00	0.86	0.00	0.17	neutral
	ATC_CAC_220.7	0.41	0.44	0.18	0.21	neutral
	ATC_CAC_223.7	0.07	0.76	0.02	0.17	neutral
	ATC_CAC_229.1	0.00	0.86	0.00	0.17	neutral

Species	Primer	Probability	q-value	α	F_{ST}	Type
	ATC_CAC_230.7	0.04	0.80	0.00	0.17	neutral
	ATC_CAC_233.7	0.56	0.23	-0.14	0.16	neutral
	ATC_CAC_235.8	0.37	0.54	-0.05	0.16	neutral
	ATC_CAC_258.7	0.07	0.78	-0.03	0.17	neutral
	ATC_CAC_266.2	0.04	0.82	-0.04	0.17	neutral
	ATC_CAC_270.8	0.41	0.44	-0.51	0.12	neutral
	ATC_CAC_273.6	0.07	0.78	-0.01	0.17	neutral
	ATC_CAC_274.9	0.07	0.76	-0.05	0.17	neutral
	ATC_CAC_276.4	0.33	0.58	0.44	0.26	neutral
	ATC_CAC_277.8	0.11	0.67	-0.08	0.17	neutral
	ATC_CAC_287.8	0.07	0.75	0.06	0.18	neutral
	ATC_CAC_288.7	0.04	0.82	0.00	0.17	neutral
	ATC_CAC_332.4	0.52	0.30	0.26	0.22	neutral
	ATC_CAC_347.9	0.19	0.58	NaN	NaN	neutral
	ATC_CAC_370.4	0.07	0.75	0.01	0.17	neutral
	ATC_CAC_373.3	0.07	0.78	0.05	0.18	neutral
	ATC_CAC_378.0	0.00	0.86	0.00	0.17	neutral
	ATC_CAC_387.7	0.33	0.58	0.15	0.20	neutral
	ATC_CAC_401.5	0.22	0.53	0.27	0.22	neutral
	ATC_CAC_405.7	0.04	0.82	0.00	0.17	neutral
	ATC_CAC_430.5	0.00	0.86	0.00	0.17	neutral
	ATC_CAC_442.2	0.37	0.53	-0.19	0.16	neutral
	ATC_CAC_445.2	0.00	0.86	0.00	0.17	neutral
	ATC_CAC_456.3	0.00	0.86	0.00	0.17	neutral
Campanula barbata	ACA_CTA_55.8	0.07	0.78	-0.03	0.12	neutral
	ACA_CTA_69.2	0.00	0.87	0.00	0.12	neutral
	ACA_CTA_101.6	0.19	0.55	0.03	0.13	neutral
	ACA_CTA_114.7	0.33	0.54	-0.14	0.11	neutral
	ACA_CTA_122.8	0.04	0.78	-0.01	0.12	neutral
	ACA_CTA_132.9	0.07	0.78	0.01	0.12	neutral
	ACA_CTA_153.4	0.33	0.55	-0.24	0.11	neutral
	ACA_CTA_155.4	0.04	0.83	0.00	0.12	neutral

Species	Primer	Probability	q-value	α	F_{ST}	Type
	ACA_CTA_164.8	0.41	0.48	-0.45	0.09	neutral
	ACA_CTA_169.4	0.07	0.78	-0.09	0.12	neutral
	ACA_CTA_174.3	0.07	0.77	-0.06	0.12	neutral
	ACA_CTA_178.0	0.04	0.78	-0.05	0.12	neutral
	ACA_CTA_179.5	0.00	0.87	0.00	0.12	neutral
	ACA_CTA_183.6	0.15	0.61	-0.09	0.11	neutral
	ACA_CTA_186.8	0.19	0.59	-0.15	0.11	neutral
	ACA_CTA_187.9	0.07	0.78	-0.02	0.12	neutral
	ACA_CTA_194.5	0.15	0.60	0.07	0.13	neutral
	ACA_CTA_195.9	0.11	0.72	0.04	0.13	neutral
	ACA_CTA_197.7	0.04	0.82	0.01	0.12	neutral
	ACA_CTA_203.8	0.56	0.20	-0.30	0.13	adaptive
	ACA_CTA_213.5	0.15	0.64	0.02	0.13	neutral
	ACA_CTA_254.3	0.04	0.83	0.02	0.12	neutral
	ACA_CTA_284.5	0.04	0.82	-0.01	0.12	neutral
	ACA_CTA_289.0	0.07	0.77	-0.08	0.12	neutral
	ACA_CTA_296.4	0.00	0.87	0.00	0.12	neutral
	ACA_CTA_311.1	0.00	0.87	0.00	0.12	neutral
	ACA_CTA_347.7	0.00	0.87	0.00	0.12	neutral
	ACA_CTA_368.6	0.07	0.75	-0.01	0.12	neutral
	ACA_CTA_378.8	0.04	0.78	0.00	0.12	neutral
	ACA_CTA_382.7	0.19	0.56	-0.08	0.12	neutral
	ACA_CTA_393.5	0.07	0.75	0.03	0.12	neutral
	ACA_CTA_415.5	0.11	0.70	-0.01	0.12	neutral
	ACA_CTA_489.5	0.37	0.55	0.57	0.22	neutral
	ACA_CTA_491.1	0.07	0.78	0.01	0.13	neutral
	AGA_CAC_84.2	0.11	0.68	-0.10	0.11	neutral
	AGA_CAC_89.4	0.00	0.87	0.00	0.12	neutral
	AGA_CAC_91.6	0.00	0.87	0.00	0.12	neutral
	AGA_CAC_102.6	0.04	0.82	-0.02	0.12	neutral
	AGA_CAC_106.2	0.00	0.87	0.00	0.12	neutral
	AGA_CAC_107.0	0.22	0.50	-0.05	0.12	neutral

Species	Primer	Probability	q-value	α	F_{ST}	Type
	AGA_CAC_109.0	0.11	0.70	0.01	0.12	neutral
	AGA_CAC_116.9	0.04	0.78	-0.04	0.12	neutral
	AGA_CAC_130.4	0.07	0.75	-0.07	0.12	neutral
	AGA_CAC_133.3	0.37	0.55	-0.11	0.12	neutral
	AGA_CAC_135.7	0.07	0.77	0.03	0.13	neutral
	AGA_CAC_141.4	0.04	0.83	-0.09	0.12	neutral
	AGA_CAC_168.9	0.00	0.87	0.00	0.12	neutral
	AGA_CAC_170.2	0.41	0.48	-0.09	0.12	neutral
	AGA_CAC_180.6	0.04	0.82	0.01	0.12	neutral
	AGA_CAC_183.6	0.41	0.48	0.21	0.15	neutral
	AGA_CAC_196.1	0.00	0.87	0.00	0.12	neutral
	AGA_CAC_202.0	0.52	0.26	0.10	0.14	adaptive
	AGA_CAC_204.8	0.04	0.83	-0.02	0.12	neutral
	AGA_CAC_214.4	0.07	0.74	-0.06	0.11	neutral
	AGA_CAC_218.3	0.11	0.68	-0.18	0.11	neutral
	AGA_CAC_227.1	0.07	0.74	0.06	0.13	neutral
	AGA_CAC_231.4	0.00	0.87	0.00	0.12	neutral
	AGA_CAC_245.4	0.07	0.78	-0.03	0.12	neutral
	AGA_CAC_247.3	0.11	0.68	0.01	0.12	neutral
	AGA_CAC_250.2	0.07	0.75	0.04	0.13	neutral
	AGA_CAC_251.1	0.04	0.83	0.00	0.12	neutral
	AGA_CAC_269.0	0.00	0.87	0.00	0.12	neutral
	AGA_CAC_279.6	0.04	0.82	0.04	0.13	neutral
	AGA_CAC_283.4	0.00	0.87	0.00	0.12	neutral
	AGA_CAC_285.4	0.15	0.64	-0.09	0.11	neutral
	AGA_CAC_286.8	0.11	0.69	0.03	0.13	neutral
	AGA_CAC_294.8	0.04	0.83	0.00	0.12	neutral
	AGA_CAC_299.4	0.41	0.46	-0.11	0.11	neutral
	AGA_CAC_308.2	0.33	0.57	-0.23	0.11	neutral
	AGA_CAC_314.3	0.19	0.54	-0.13	0.12	neutral
	AGA_CAC_316.2	0.04	0.82	0.04	0.13	neutral
	AGA_CAC_318.3	0.37	0.54	0.13	0.14	neutral

Species	Primer	Probability	q-value	α	F_{ST}	Type
	AGA_CAC_321.0	0.11	0.65	0.01	0.12	neutral
	AGA_CAC_324.2	0.33	0.58	0.12	0.14	neutral
	AGA_CAC_326.2	0.00	0.87	0.00	0.12	neutral
	AGA_CAC_338.4	0.04	0.82	-0.05	0.12	neutral
	AGA_CAC_356.5	0.04	0.78	0.00	0.12	neutral
	AGA_CAC_441.7	0.04	0.82	-0.03	0.12	neutral
	AGA_CAC_445.1	0.07	0.77	-0.01	0.12	neutral
	AGA_CAC_475.7	0.37	0.54	0.06	0.13	neutral
	AGA_CAC_477.9	0.67	0.29	-0.25	0.13	neutral
	AGA_CAC_487.7	0.04	0.82	-0.01	0.12	neutral
	AGT_CTG_85.2	0.33	0.57	-0.13	0.11	neutral
	AGT_CTG_109.9	0.11	0.66	0.01	0.13	neutral
	AGT_CTG_127.9	0.00	0.87	0.00	0.12	neutral
	AGT_CTG_130.9	0.11	0.66	-0.03	0.12	neutral
	AGT_CTG_135.5	0.07	0.75	-0.06	0.12	neutral
	AGT_CTG_144.4	0.19	0.56	0.06	0.13	neutral
	AGT_CTG_151.4	0.07	0.70	-0.02	0.12	neutral
	AGT_CTG_152.8	0.15	0.64	-0.05	0.12	neutral
	AGT_CTG_181.2	0.07	0.78	-0.01	0.12	neutral
	AGT_CTG_191.2	0.33	0.58	-1.05	0.09	neutral
	AGT_CTG_196.4	0.37	0.55	-0.28	0.10	neutral
	AGT_CTG_202.3	0.04	0.82	0.00	0.12	neutral
	AGT_CTG_218.5	0.07	0.78	0.00	0.12	neutral
	AGT_CTG_221.0	0.04	0.82	0.03	0.13	neutral
	AGT_CTG_226.4	0.11	0.69	-0.08	0.12	neutral
	AGT_CTG_228.9	0.00	0.87	0.00	0.12	neutral
	AGT_CTG_230.8	0.11	0.68	0.13	0.14	neutral
	AGT_CTG_234.9	0.04	0.82	0.02	0.13	neutral
	AGT_CTG_245.4	0.07	0.75	-0.01	0.12	neutral
	AGT_CTG_262.1	0.04	0.82	-0.01	0.12	neutral
	AGT_CTG_266.2	0.48	0.29	-0.21	0.12	neutral
	AGT_CTG_297.5	0.00	0.87	0.00	0.12	neutral

Species	Primer	Probability	q-value	α	F_{ST}	Type
	AGT_CTG_336.5	0.00	0.87	0.00	0.12	neutral
	AGT_CTG_344.2	0.33	0.58	-0.23	0.10	neutral
	AGT_CTG_359.0	0.44	0.44	-0.47	0.10	neutral
	AGT_CTG_363.4	0.04	0.82	0.00	0.12	neutral
	AGT_CTG_392.1	0.37	0.49	-0.28	0.10	neutral
	AGT_CTG_415.3	0.00	0.87	0.00	0.12	neutral
	AGT_CTG_443.5	0.04	0.83	0.02	0.12	neutral
	AGT_CTG_452.7	0.00	0.87	0.00	0.12	neutral
	AGT_CTG_459.7	0.37	0.55	0.25	0.16	neutral
	AGT_CTG_488.9	0.07	0.70	0.02	0.12	neutral

Table S3: Genomic MDS results

```r
knitr::kable(
    format.table(
        filter(
            ldply(
                seq_along(unique(spp.samples.DF$species)),
                function(i) {
                    ldply(
                        seq_along(spp.mds.LST[[i]]),
                        function(j) {
                        data.frame(
                            Species=paste0('\\textit{',gsub('\\_', ' ', unique(spp.samples.DF$s
                            Loci=names(spp.mds.LST[[i]])[j],
                            Stress=ifelse(is.null(spp.mds.LST[[i]][[j]]), NA_real_, spp.mds.LST
                            Converged=ifelse(is.null(spp.mds.LST[[i]][[j]]), NA_real_, spp.mds
                        )
                    })
                }
            ),
            !is.na(Stress)
        ),
        omit=c('Loci','Converged')
    ),
    digits=2,
    caption='Summary of non-metric multi-dimensional scaling (MDS) analyses on genetic variatio
    col.names=c('Species', 'Loci Type', 'NMDS Stress', 'Converged'),
    align=c('l', 'c', 'c', 'c')
)
```

Species	Loci Type	NMDS Stress	Converged
Androsace obtusifolia	adaptive	0.00	0
	neutral	0.22	0
Arabis alpina	neutral	0.24	0
Campanula barbata	adaptive	0.00	0
	neutral	0.20	0

Table 3 Summary of non-metric multi-dimensional scaling (MDS) analyses on genetic variation for each species.

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