Maerl Whole Genome Genotyping Supplementary Material

Jenkins et al.
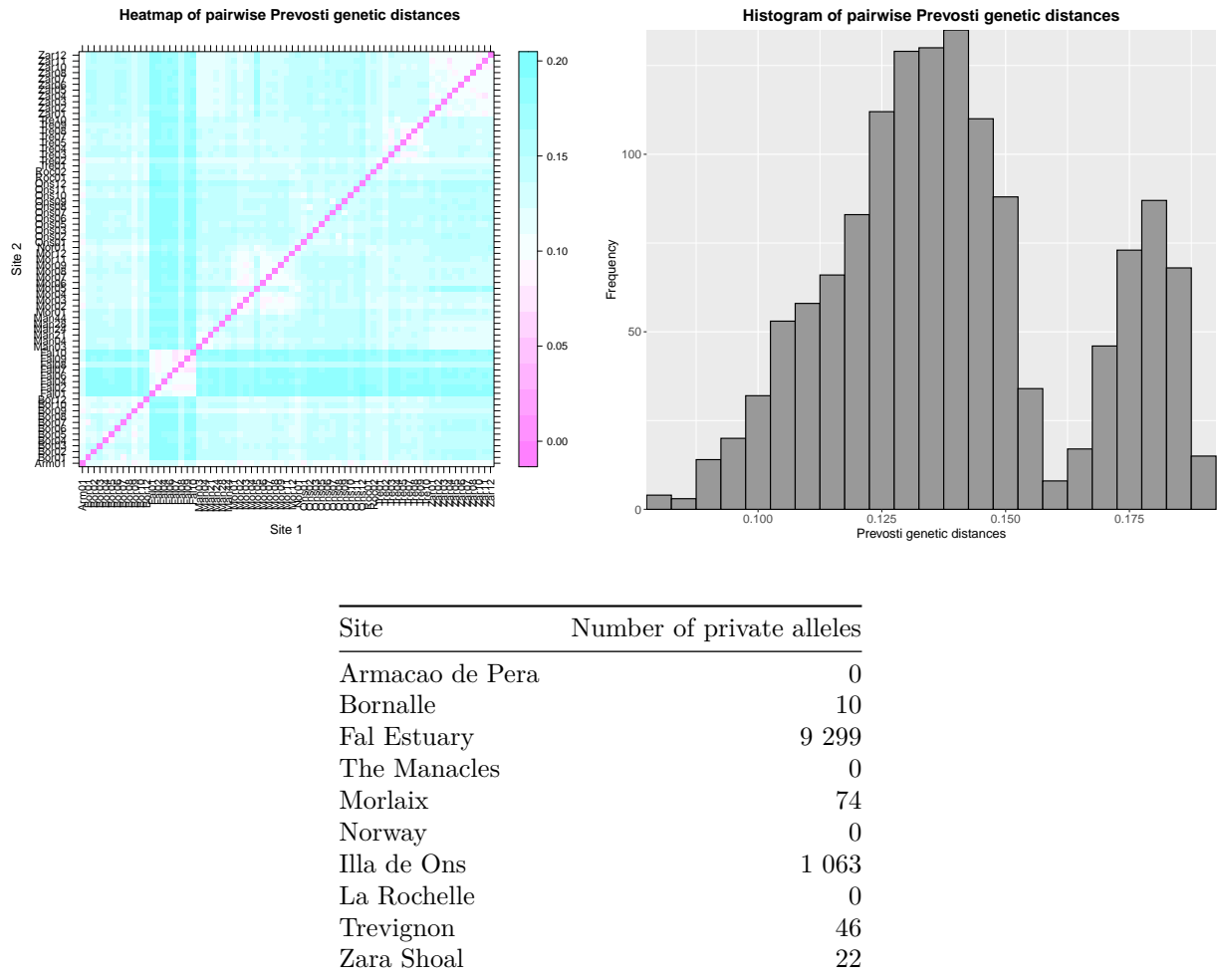
Heatmap of pairwise Prevosti genetic distances

Histogram of pairwise Prevosti genetic distances

Site	Number of private alleles
Armacao de Pera	0
Bornalle	10
Fal Estuary	9 299
The Manacles	0
Morlaix	74
Norway	0
Illa de Ons	1 063
La Rochelle	0
Trevignon	46
Zara Shoal	22

Figure S1. Distribution of Prevosti genetic distances visualised with a heatmap (top-left) and a histogram (top-right). The heatmap shows that the highest pairwise genetic distances are between individuals from the Fal Estuary and all other individuals. The histogram shows no individuals with a pairwise distance of zero and that no clear gap is present between individuals of low genetic distances, the presence of which can be indicative of clones in the data set. The table shows the number of private alleles found at each site.
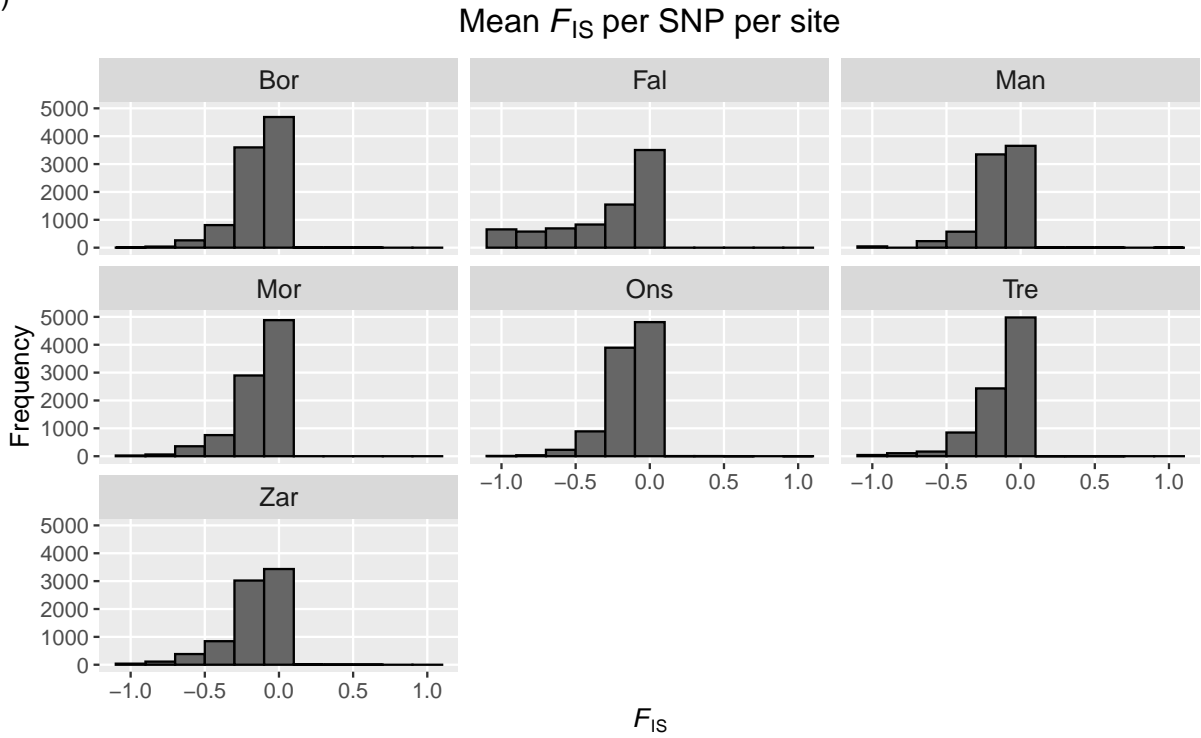
(a)

Mean observed heterozygosity per SNP per site

(b)

Mean F_{IS} per SNP per site
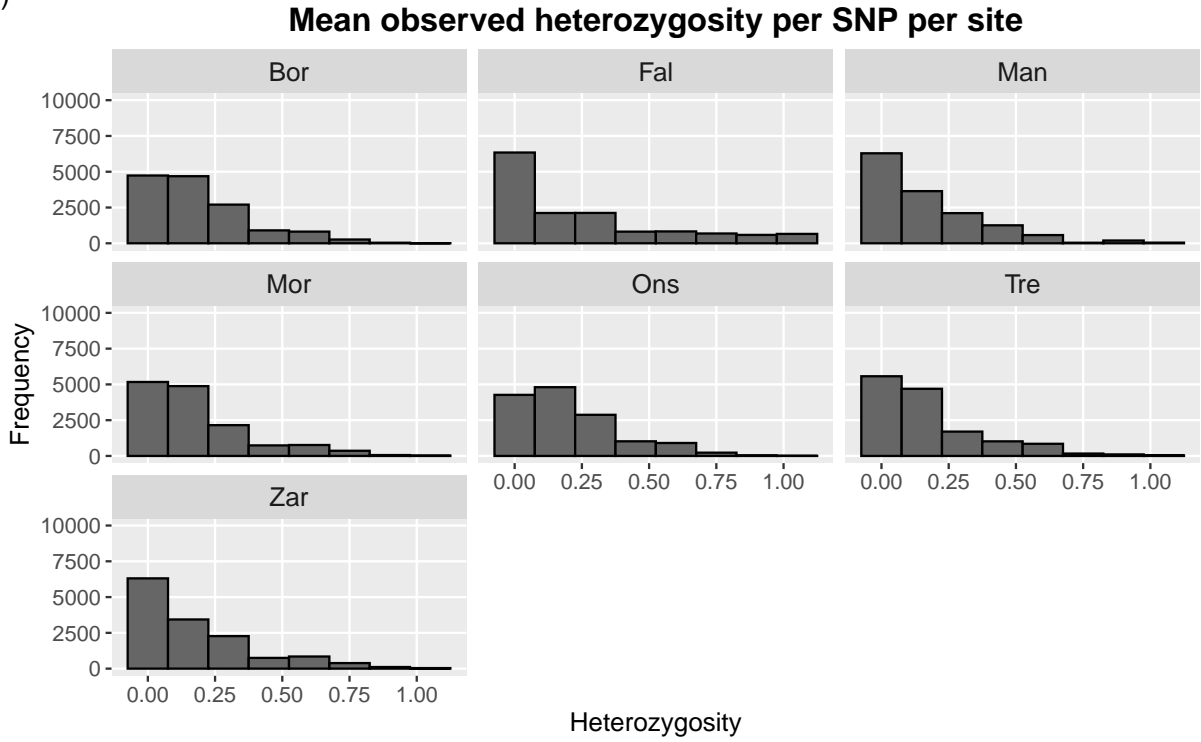
Figure S2. (a) Mean observed heterozygosity per SNP per site and (b) mean F_{IS} per SNP per site. Site codes are explained in Table 1.
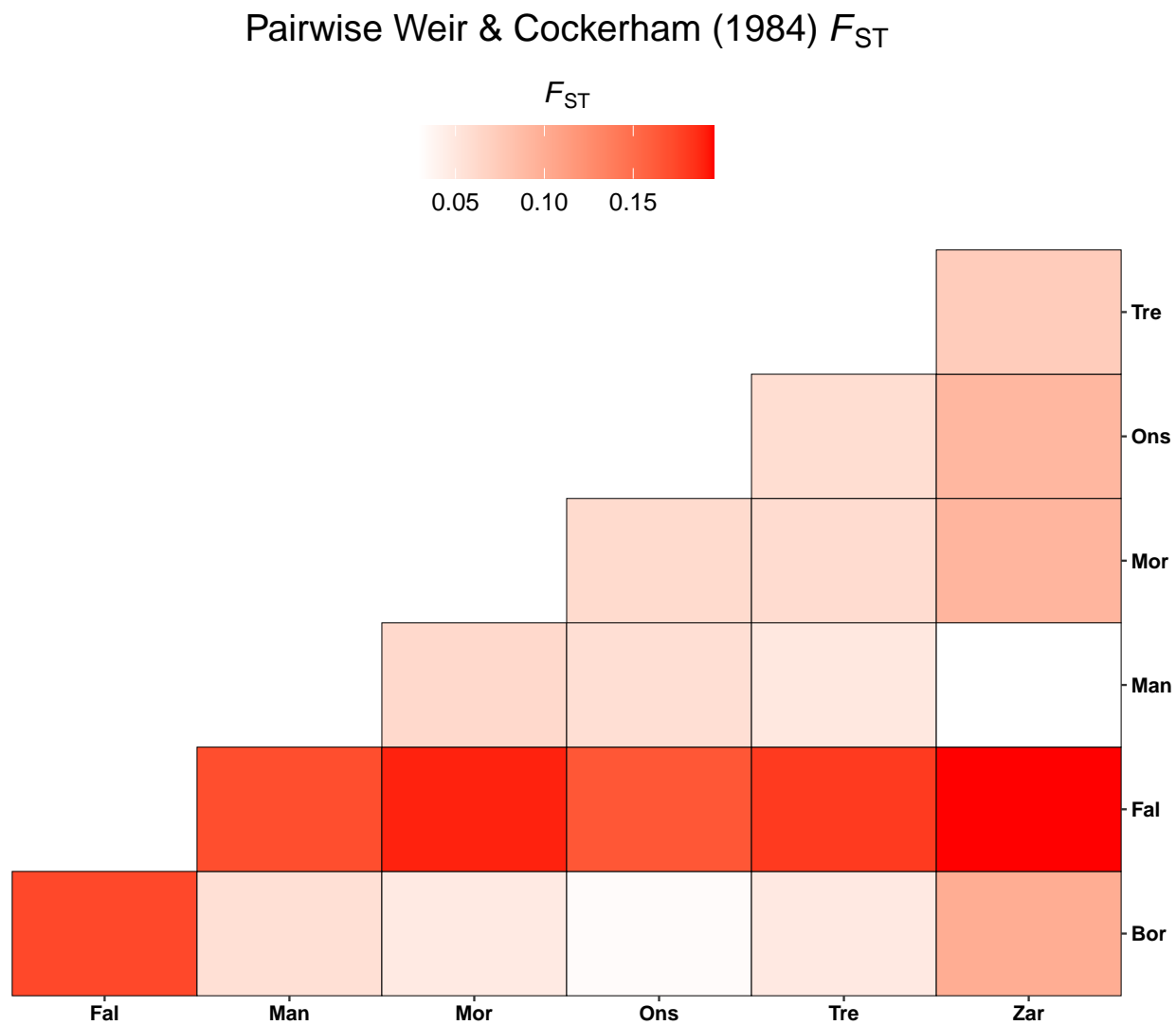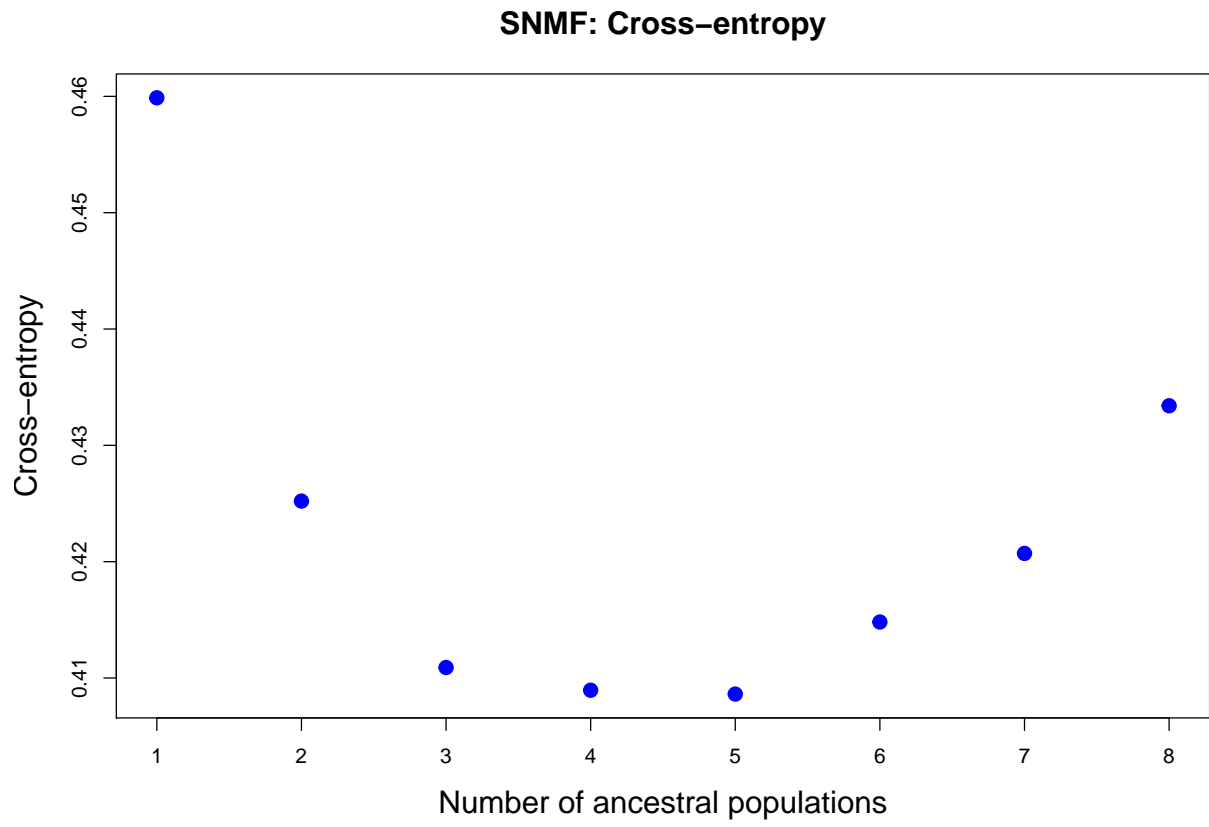
Pairwise Weir & Cockerham (1984) F_{ST}

Figure S3. Heatmap of pairwise F_{ST} (Weir & Cockerham 1984). Site codes are explained in Table 1.
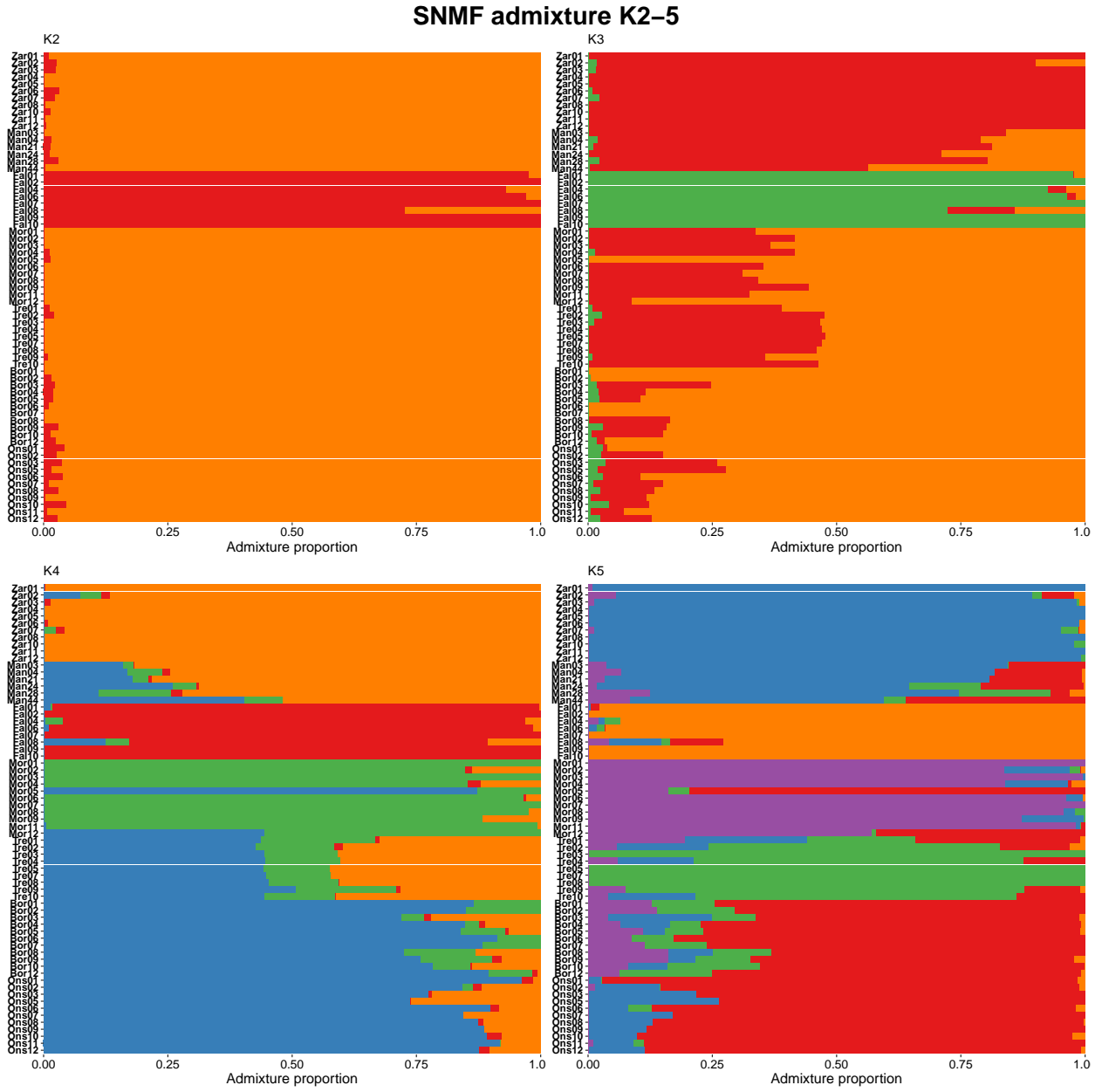
(a)

SNMF: Cross−entropy
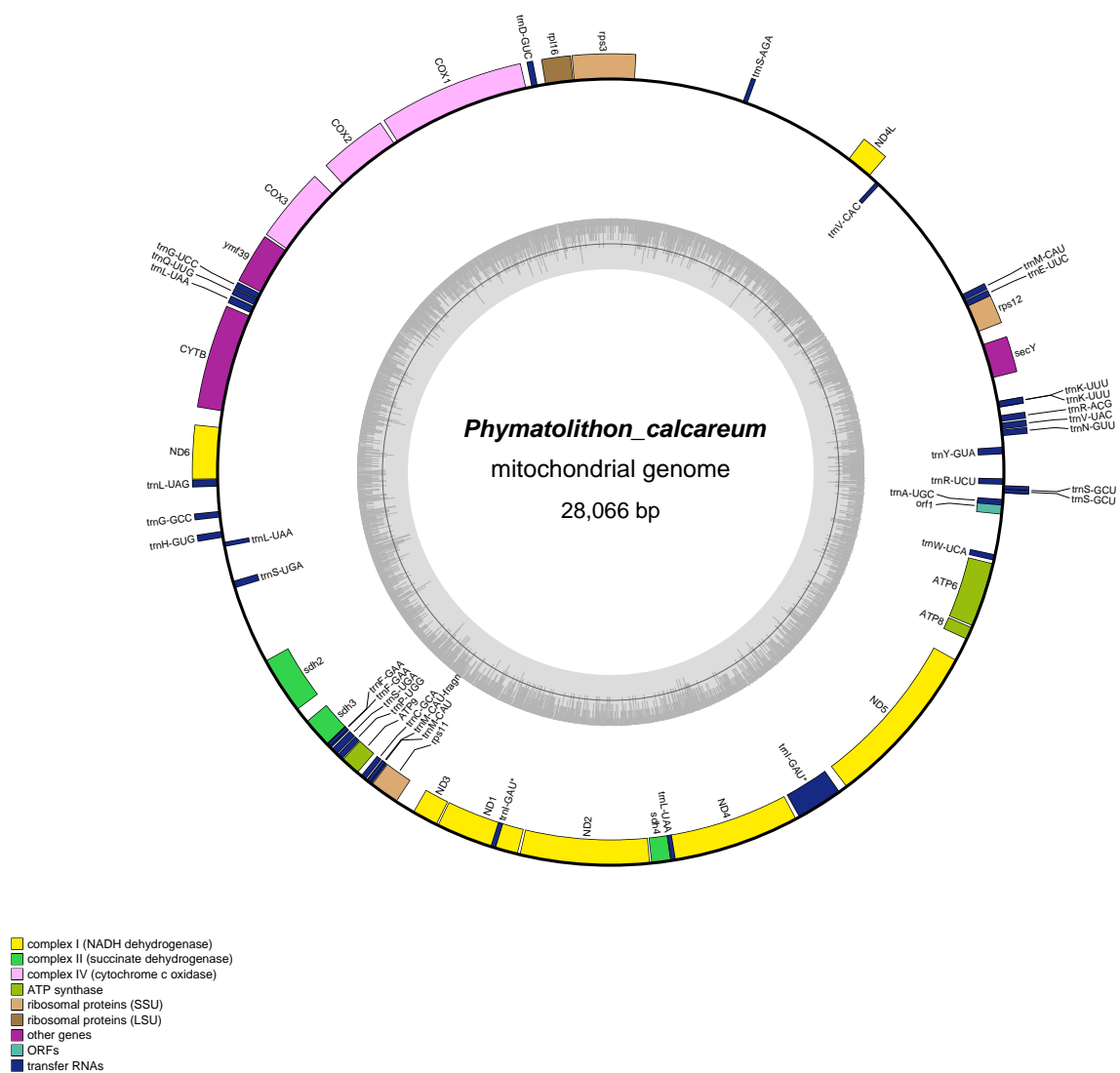
(b)

Figure S4. (a) Cross-entropy analysis. (b) Sparse non-negative matrix factorisation (SNMF) analysis. Admixture results are shown for K2-5.

Figure S5a. Tre04 mitogenome annotation. GeSeq was used for gene prediction and annotation using The Mold, Protozoan, and Coelenterate Mitochondrial Code and the Mycoplasma/Spiroplasma Code. ARWEN 1.2.3 was used to annotate tRNAs.

Figure S5b. Tre04 plastome annotation. GeSeq was used for gene prediction and annotation using The Bacterial, Archaeal and Plant Plastid Code. ARWEN 1.2.3 was used to annotate tRNAs.

Figure S5c. Sco01 mitogenome annotation. GeSeq was used for gene prediction and annotation using The Mold, Protozoan, and Coelenterate Mitochondrial Code and the Mycoplasma/Spiroplasma Code. ARWEN 1.2.3 was used to annotate tRNAs.
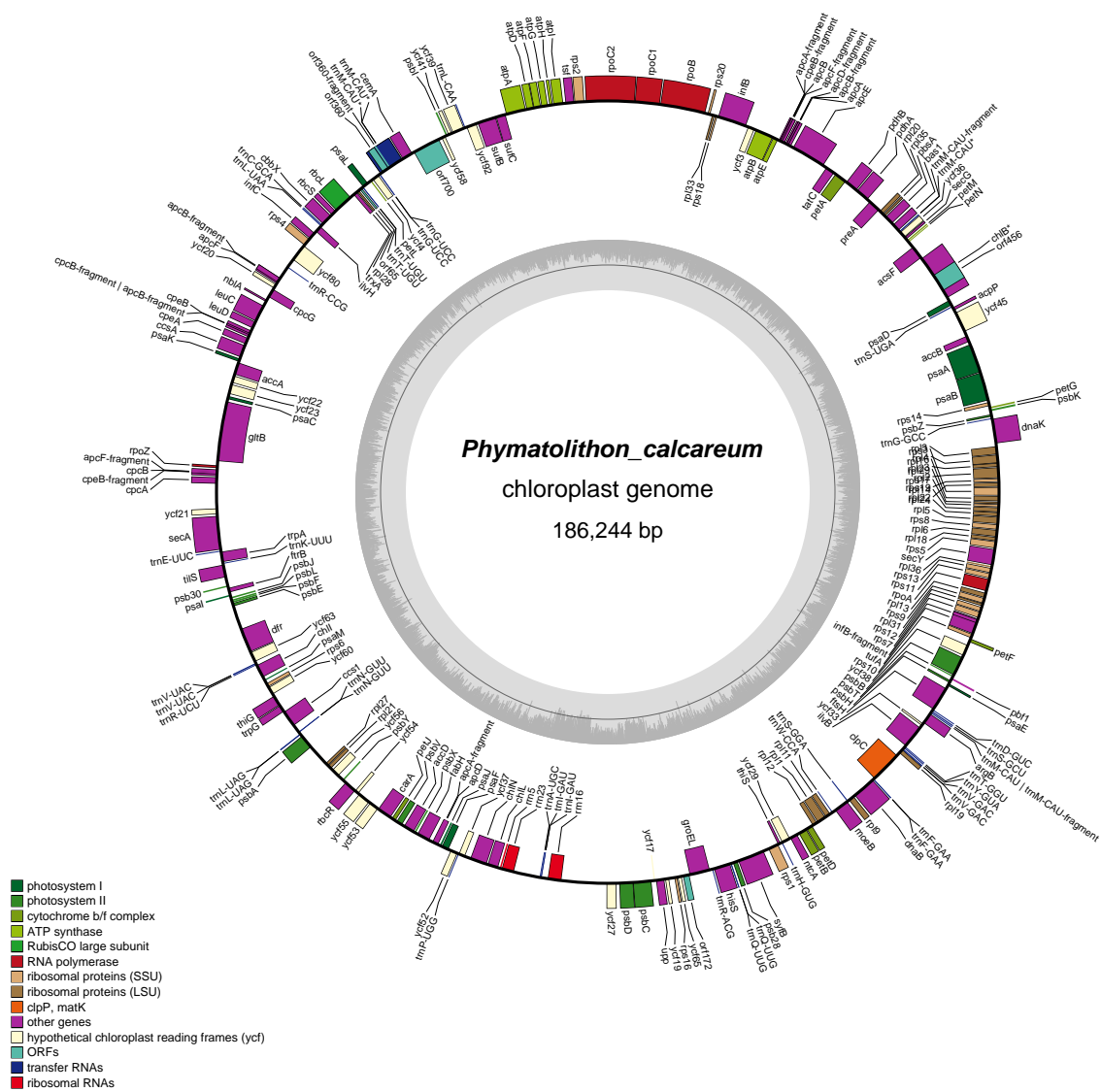
Figure S5d. Sco01 plastome annotation. GeSeq was used for gene prediction and annotation using The Bacterial, Archaeal and Plant Plastid Code. ARWEN 1.2.3 was used to annotate tRNAs.
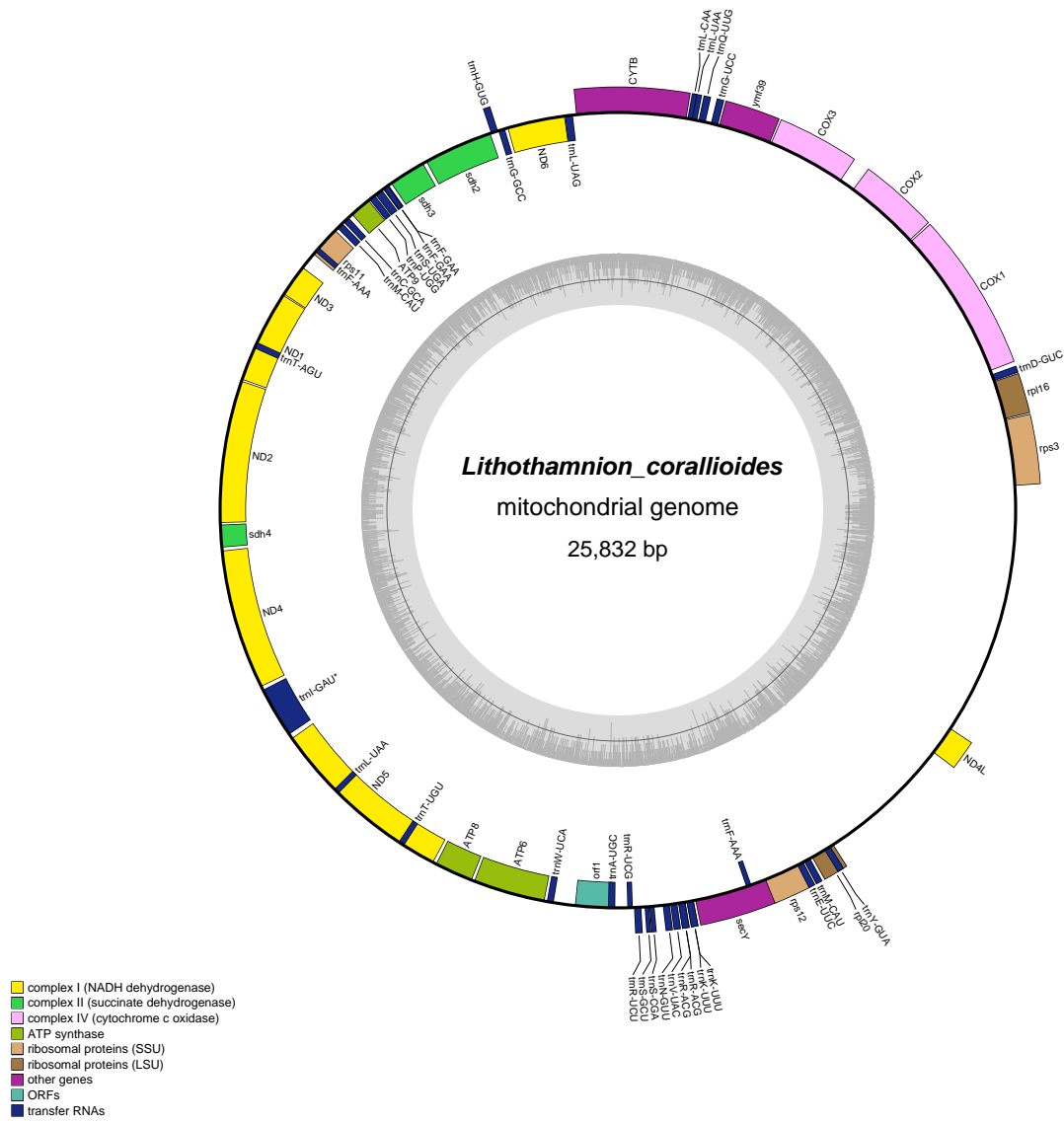
Figure S5e. Lcor09 mitogenome annotation. GeSeq was used for gene prediction and annotation using The Mold, Protozoan, and Coelenterate Mitochondrial Code and the Mycoplasma/Spiroplasma Code. ARWEN 1.2.3 was used to annotate tRNAs.

Figure S5f. Lcor09 plastome annotation. GeSeq was used for gene prediction and annotation using The Bacterial, Archaeal and Plant Plastid Code. ARWEN 1.2.3 was used to annotate tRNAs.
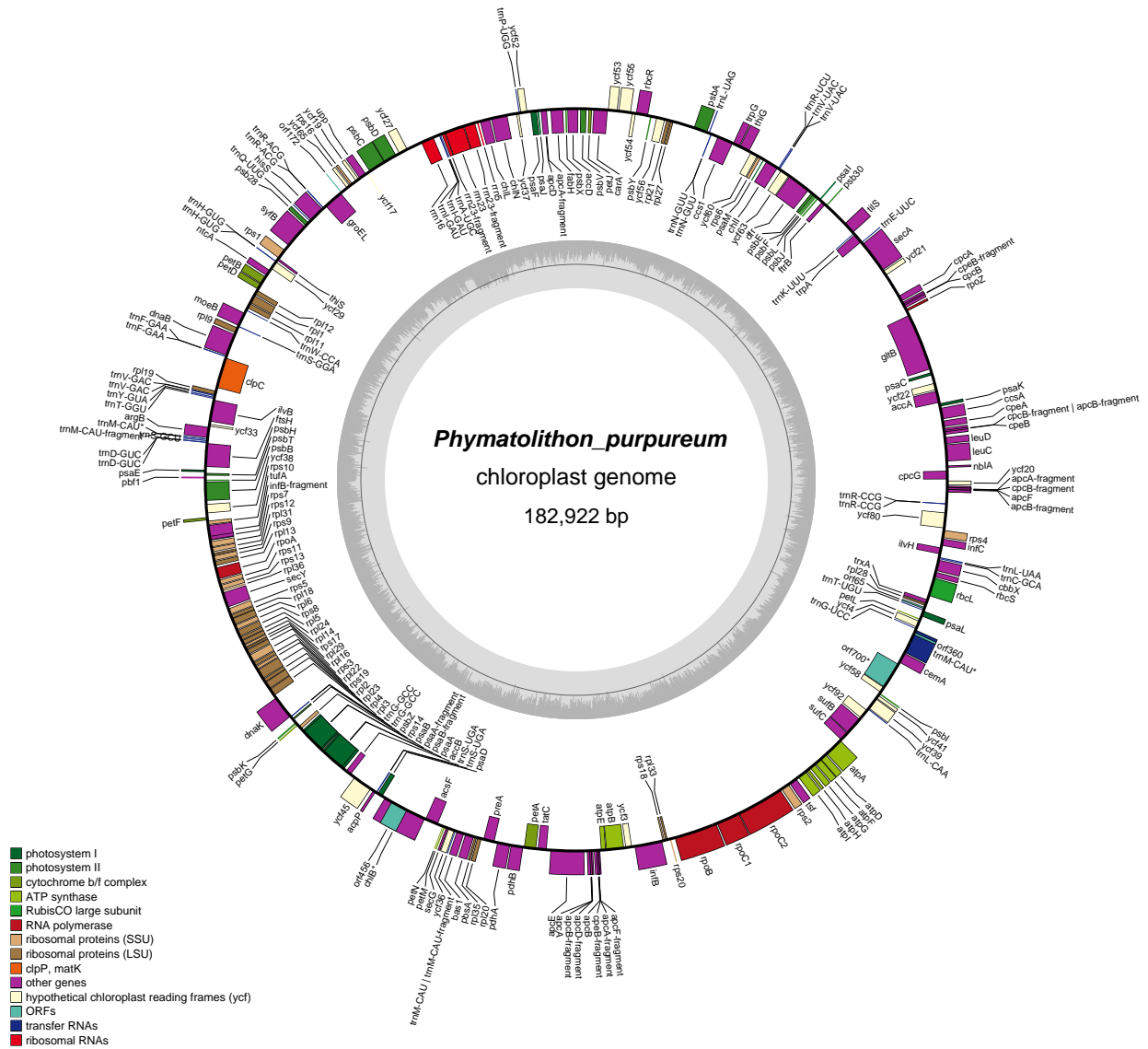
(a)

Maerl species mitogenome CDS alignment

(60.9 % of sites were invariant)

(b)

Maerl species plastome CDS alignment

(73.1 % of sites were invariant)

Figure S6. Hierarchical clustering analysis using Tamura and Nei (1993) pairwise genetic distances. (a) Analysis conducted using an alignment of 23 concatenated mitochondrial coding sequences from 69 *Phymatolithon calcareum* individuals, seven *P. purpureum* individuals, and two *Lithothamnion corallioides* individuals. (b) Analysis conducted using an alignment of 212 concatenated chloroplast coding sequences from 75 *Phymatolithon calcareum* individuals, nine *P. purpureum* individuals, and four *Lithothamnion corallioides* individuals. See Table 1 for code translation and sampling site information.