1   **Supplementary Figures**

2   **Genome-wide differentiation corresponds to climatic niche in two species of lichen-forming fungi**

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Figure legends

Supp. Figure 1. Genome-wide differentiation among populations along each of the five analysed gradients

12 - PCA of each gradient using SNPs with 100% allele frequency change between topmost and bottommost

13 populations. IT, ESi and ESii are gradient identifiers for *U. pustulata*; SN and MJ are gradient identifiers for

14 *U. phaea*.

15

16 **Supp. Figure 2**. Bioclimatic variables fitted to each gradient. Black curves represent *U. pustulata* clines and

17 grey curves represent *U. phaea* clines. Dotted lines denote the average cline centre of each gradient and

18 their corresponding bioclimatic variable values. The order of gradients based on the lowest population's

19 elevation is as follows: *U.* pustulata: IT, ESi, ESii; *U. phaea*: SN, MJ.

20

21 **Supp. Figure 3**. Number of SNPs in each allele frequency change category in *U. phaea* and *U. pustulata*.

22

23 **Supp. Figure 4.** Combined clines of alleles driven to fixation common among all gradients of the same

24 species for elevation (meter above sea level). Sample size (number of SNPs) of *U. phaea* is 3,301 and that

25 of *U. pustulata* is 138.

26

27 **Supp. Figure 5**. Boxplot for cline centres of alleles driven to fixation common among all gradients of the

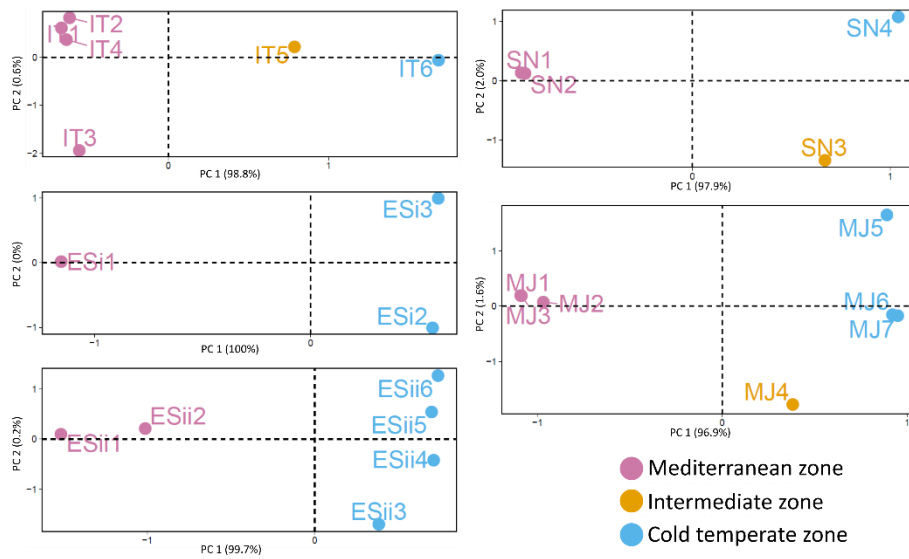28 same species for elevation (meter above sea level).

29

30 **Supp. Figure 6**. Number of transitions and transversions among the alleles driven to fixation within each

31 of the species.

32

33 **Supp. Figure 7**. Results of the outlier scan from RAiSD and various polymorphism statistics for temperate

34 and Mediterranean climate populations of *U. phaea.*
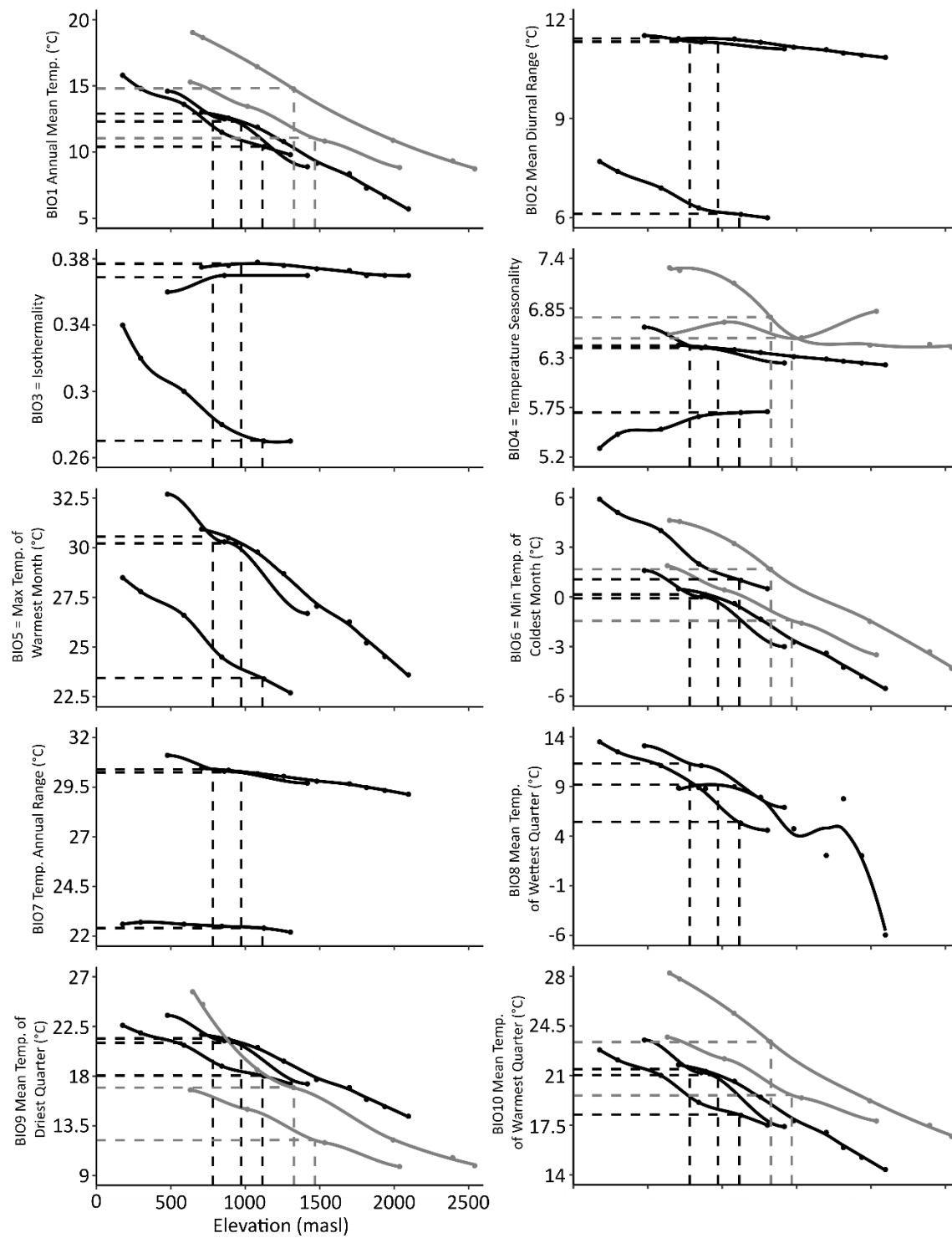
35 **Supp. Figure 8**. Results of the outlier scan from RAiSD and various polymorphism statistics for temperate

36 and Mediterranean populations of *U. pustulata.*
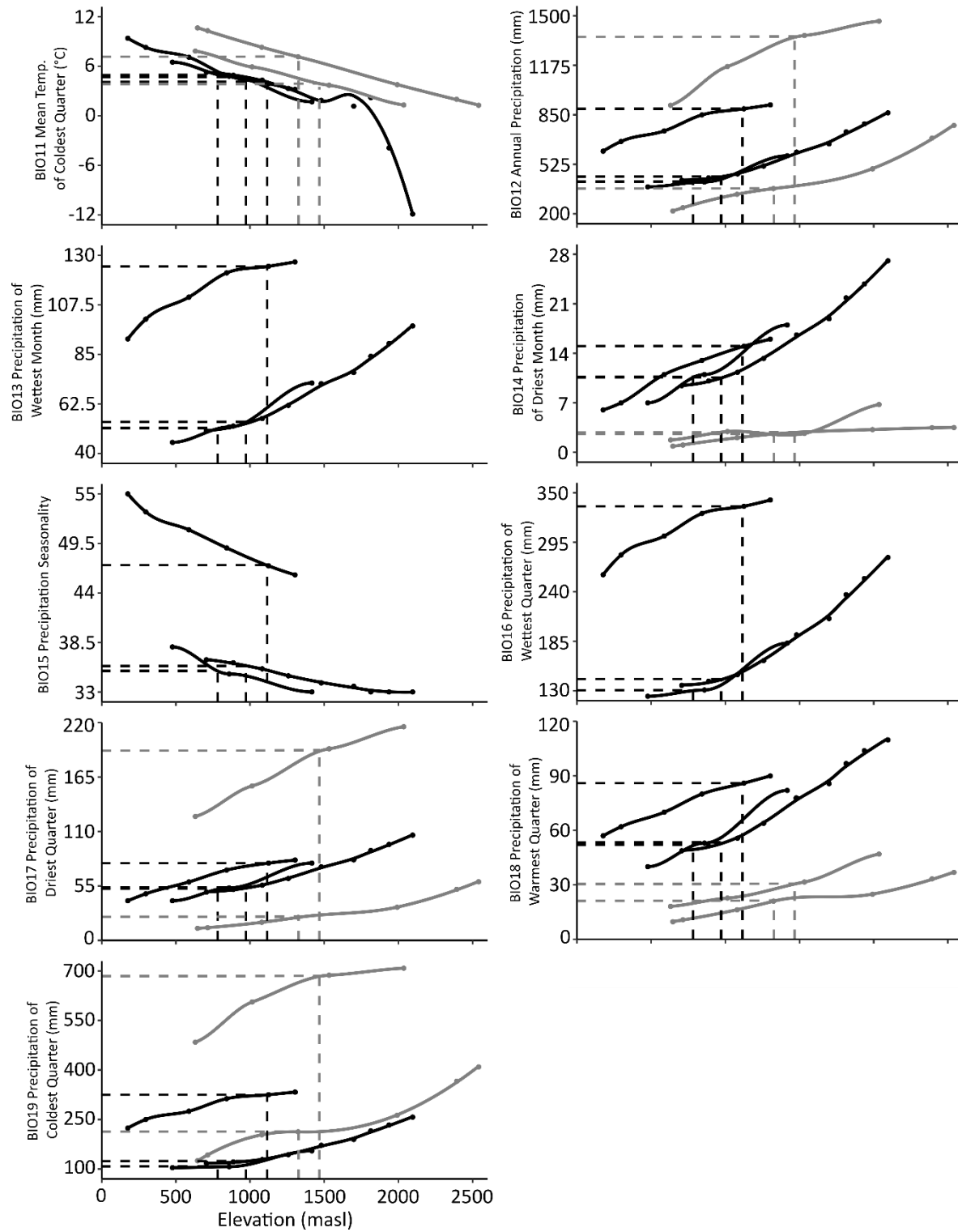
37

38 **Supp. Figure 9**. Genome-wide recombination landscape inferred using *ReLERNN* for one gradient in each

39 species. (a-c) *U. pustulata* IT populations; (d-f) *U. phaea* SN populations. Alternate back and grey regions

40 denote consecutive scaffolds in the genome assembly. Mutation rate was set to 2×10^{-10} and generation

41 time was set to 20 for all runs. Population 1 in both cases (a, d) represents the lowest sampled elevation

42 and population 6 in both cases (c, f) represents the highest sampled elevation. All panels have the same

43 y-scale.

44

45 **Supp. Figure 10**. Genome-wide recombination landscape inferred using *ReLERNN* for *U. pustulata* IT

46 population 6, with different mutation rates. Please note that the y-scale between (a) and (b) have a 30-
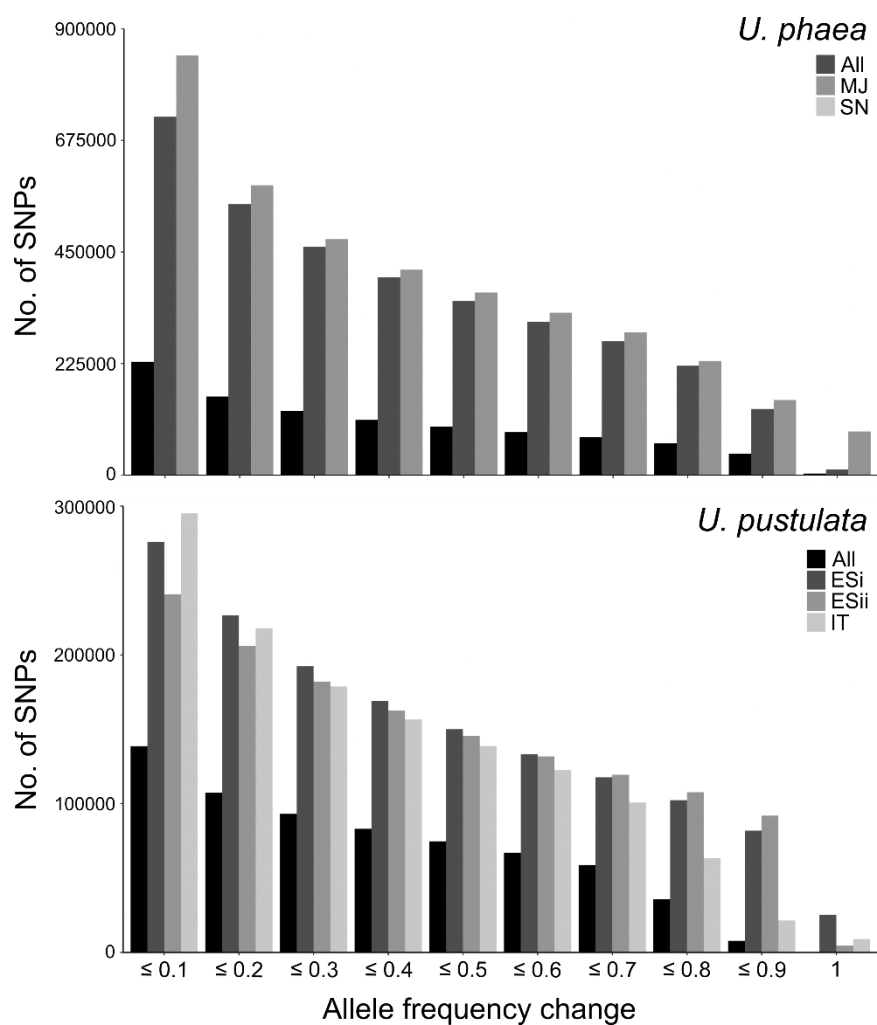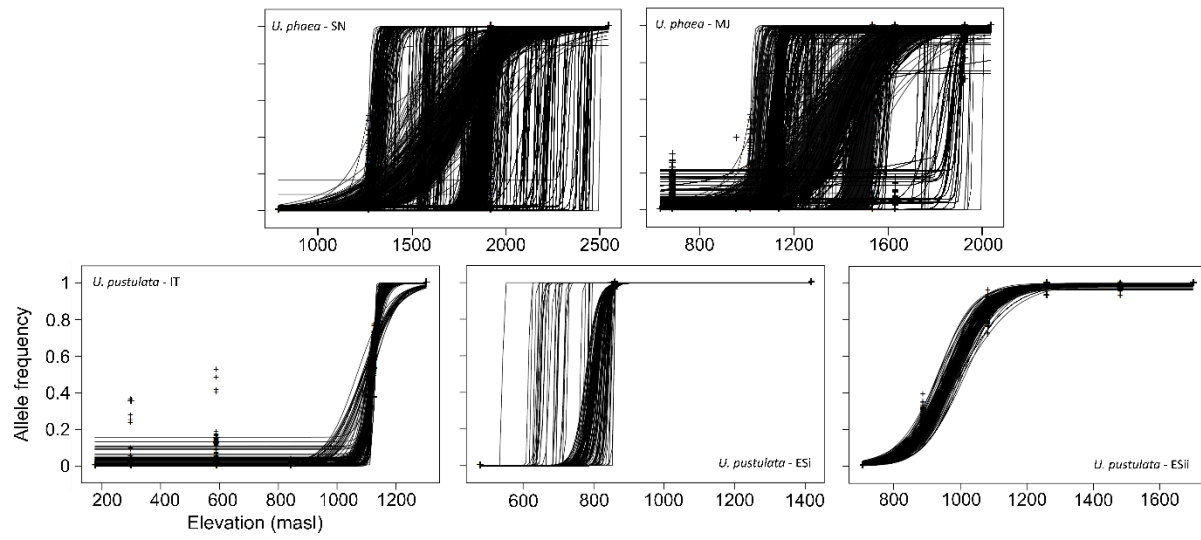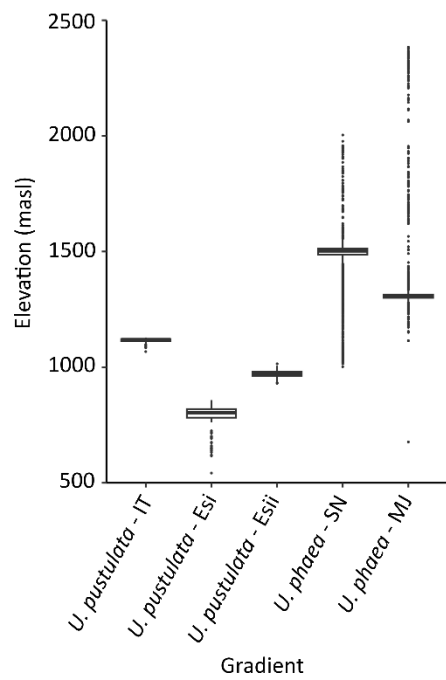
47 fold difference.
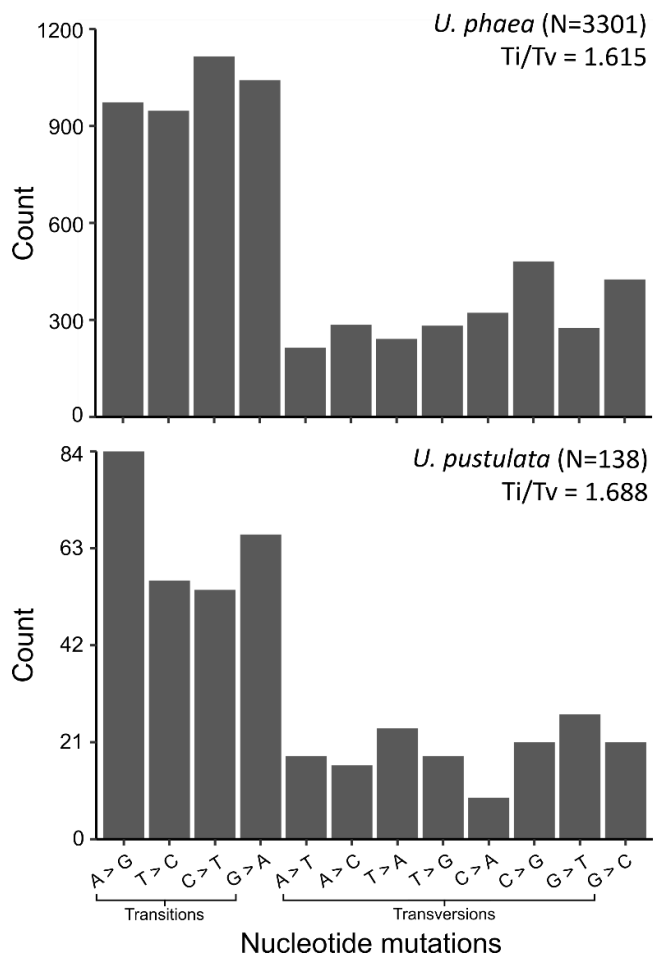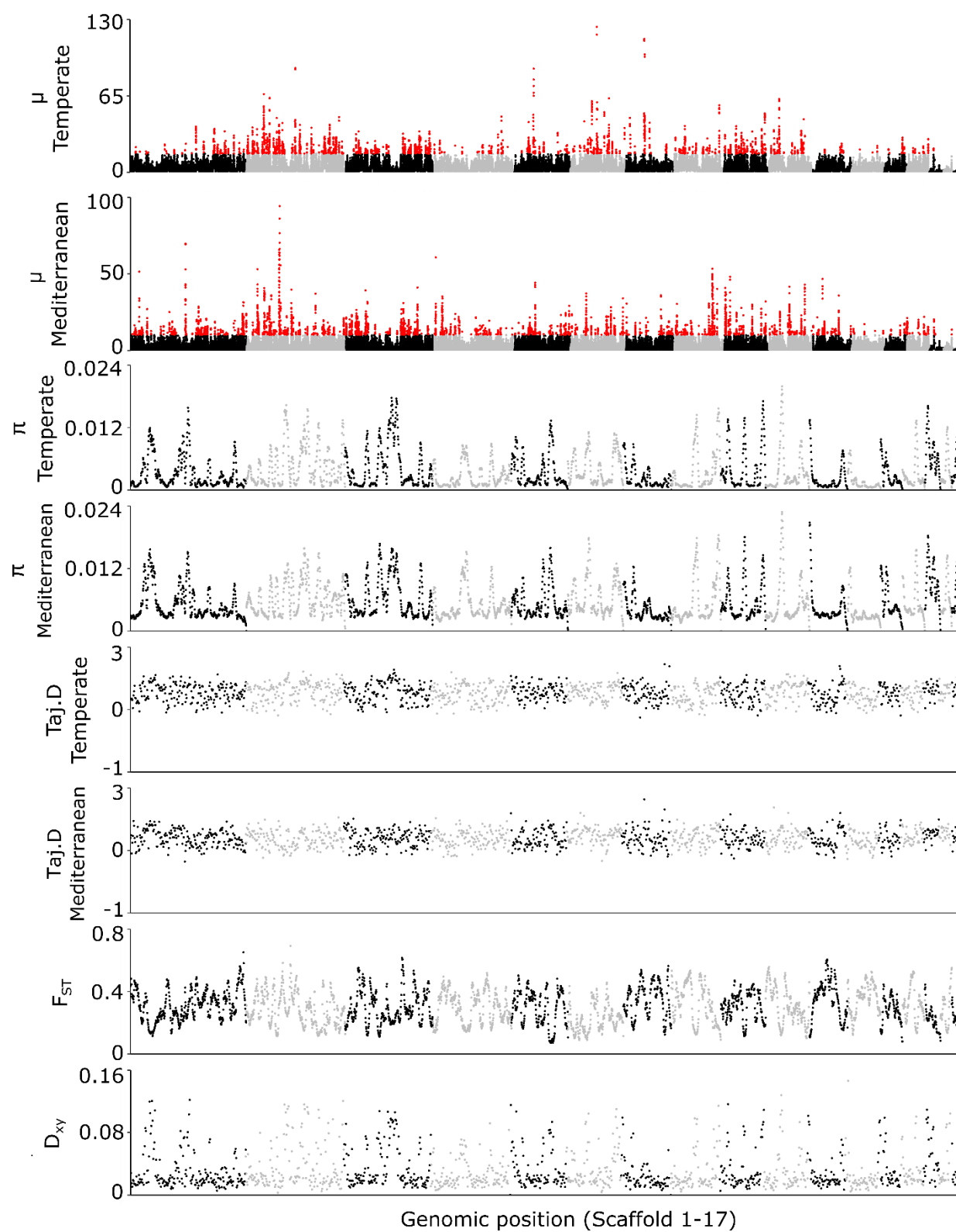
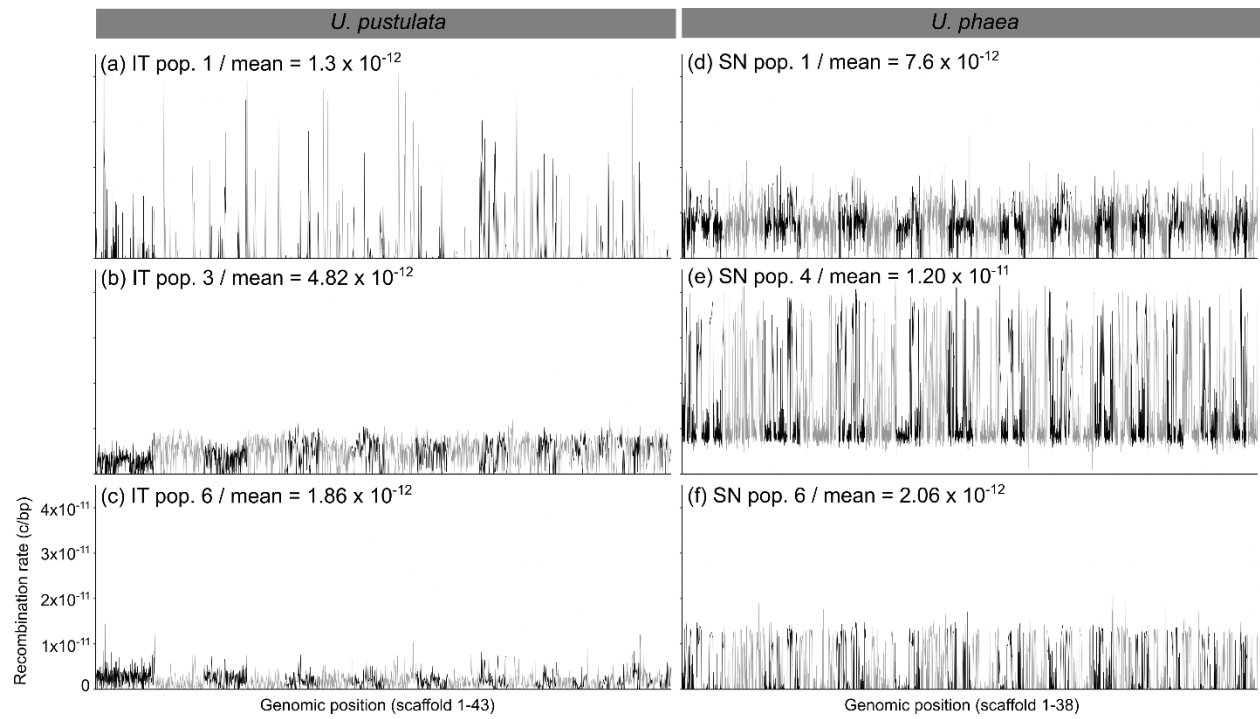48   Supp. Figure 1

51   Supp. Figure 3

52   Supp. Figure 4

53   Supp. Figure 5

54   Supp. Figure 6

U. phaea

Genomic position (Scaffold 1-17)

55   Supp. Figure 7

U. pustulata

	U. pustulata	*U. phaea*
	(a) IT pop. 1 / mean = 1.3×10^{-12}	(d) SN pop. 1 / mean = 7.6×10^{-12}
	(b) IT pop. 3 / mean = 4.82×10^{-12}	(e) SN pop. 4 / mean = 1.20×10^{-11}
Recombination rate (c/bp)	(c) IT pop. 6 / mean = 1.86×10^{-12}	(f) SN pop. 6 / mean = 2.06×10^{-12}
	Genomic position (scaffold 1-43)	Genomic position (scaffold 1-38)

57   Supp. Figure 9

(a) μ = 1 x 10⁻¹⁰

(b) μ = 2 x 10⁻¹⁰

Recombination rate (c/bp)

Genomic position (scaffold 1-43)

58   Supp. Table 10