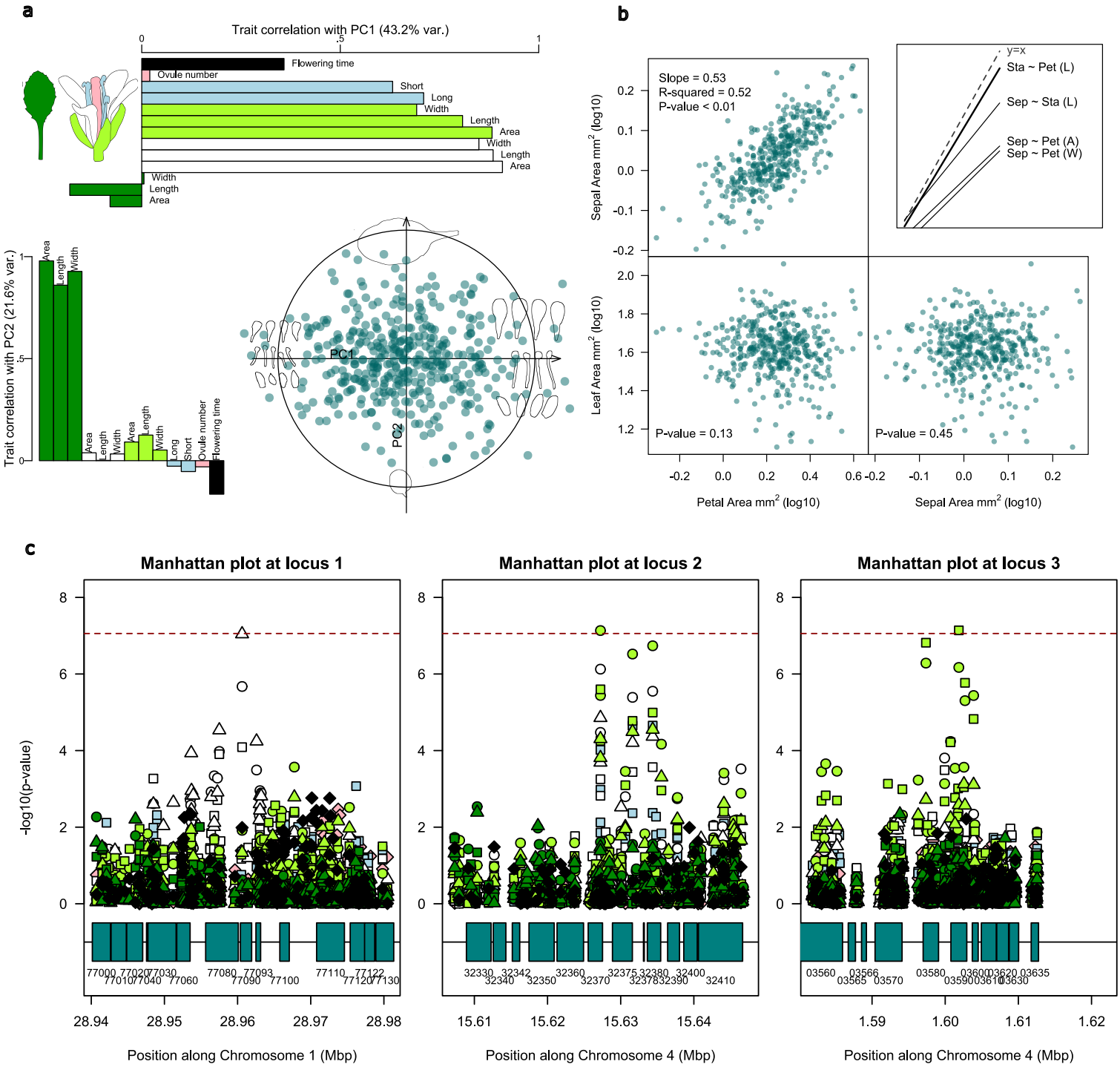
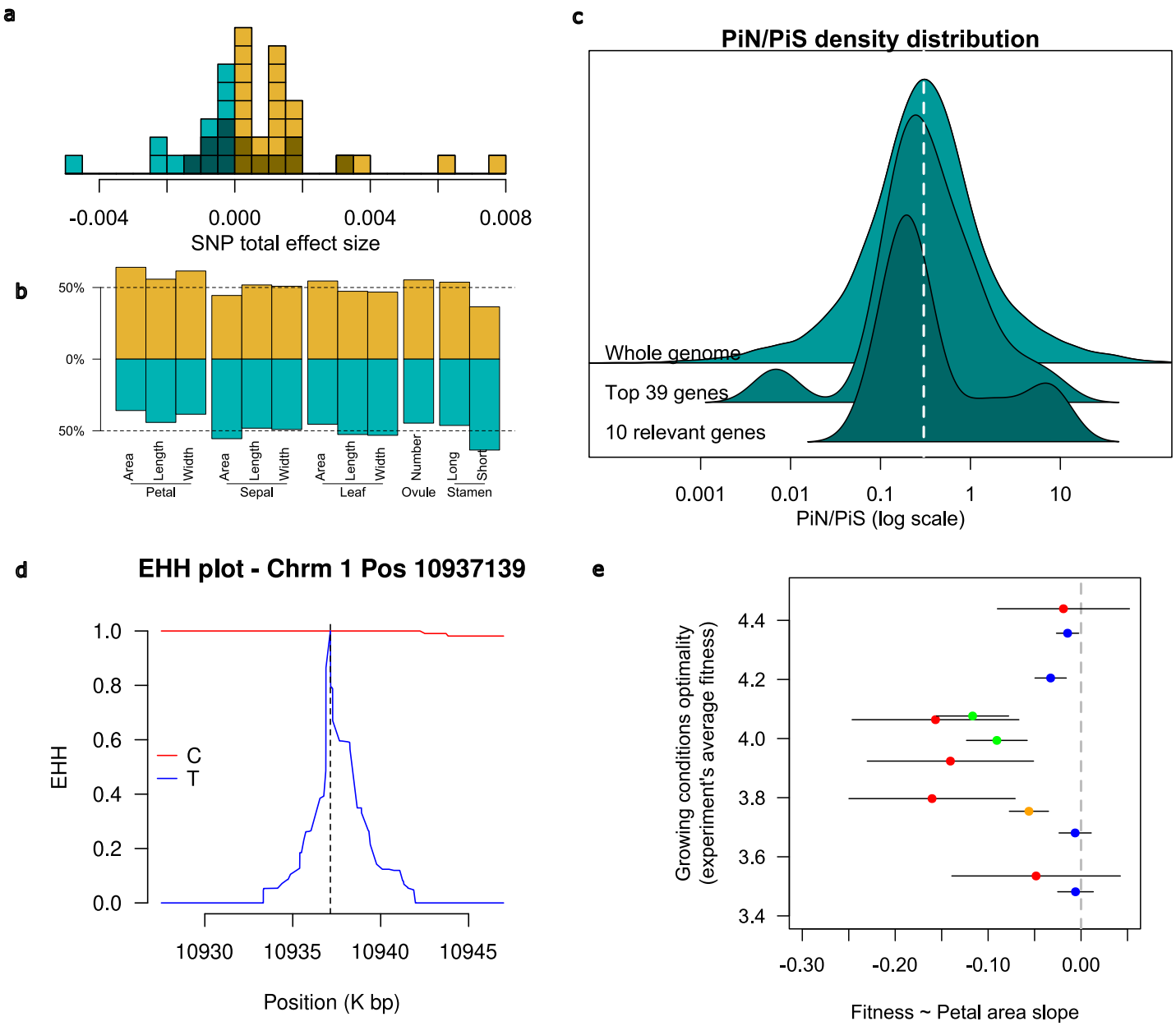
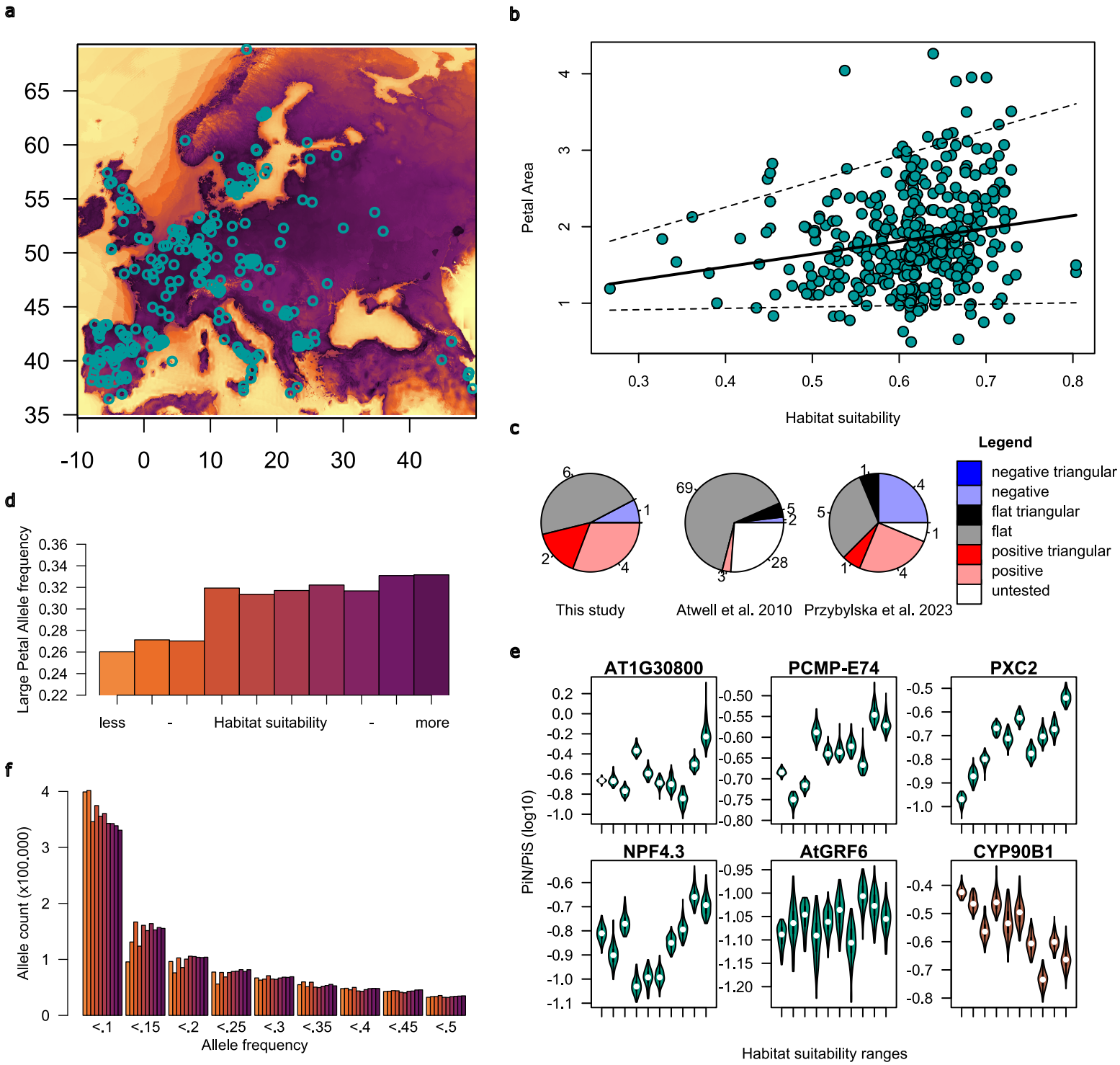

a
Trait correlation with PC1 (43.2% var.)
Flowering time
Ovule number
Short
Long
Width
Length
Area
Width
Length
Area
Width
Length
Area
Trait correlation with PC2 (21.6% var.)
PC1
PC2
b
Slope = 0.53
R-squared = 0.52
P-value < 0.01
y=x
Sta ~ Pet (L)
Sep ~ Sta (L)
Sep ~ Pet (A)
Sep ~ Pet (W)
Sepal Area mm2 (log10)
Leaf Area mm2 (log10)
P-value = 0.13
P-value = 0.45
Petal Area mm2 (log10)
Sepal Area mm2 (log10)
c
Manhattan plot at locus 1
Manhattan plot at locus 2
Manhattan plot at locus 3
-log10(p-value)
Position along Chromosome 1 (Mbp)
Position along Chromosome 4 (Mbp)
Position along Chromosome 4 (Mbp)


a
-0.004
0.000
0.004
0.008
SNP total effect size
b
50%
0%
50%
Area
Length
Width
Petal
Area
Length
Width
Sepal
Area
Length
Width
Leaf
Number
Ovule
Long
Short
Stamen
c
PiN/PiS density distribution
Whole genome
Top 39 genes
10 relevant genes
0.001
0.01
0.1
1
10
PiN/PiS (log scale)
d
EHH plot - Chrm 1 Pos 10937139
EHH
1.0
0.8
0.6
0.4
0.2
0.0
C
T
10930
10935
10940
10945
Position (K bp)
e
Growing conditions optimality
(experiment's average fitness)
4.4
4.2
4.0
3.8
3.6
3.4
-0.30
-0.20
-0.10
0.00
Fitness ~ Petal area slope


a
65
60
55
50
45
40
35
-10
0
10
20
30
40
b
Petal Area
Habitat suitability
c
Legend
negative triangular
negative
flat triangular
flat
positive triangular
positive
untested
This study
Atwell et al. 2010
Przybylska et al. 2023
d
Large Petal Allele frequency
less
Habitat suitability
more
e
AT1G30800
PCMP-E74
PXC2
NPF4.3
AtGRF6
CYP90B1
PiN/PiS (log10)
Habitat suitability ranges
f
Allele count (x100.000)
Allele frequency