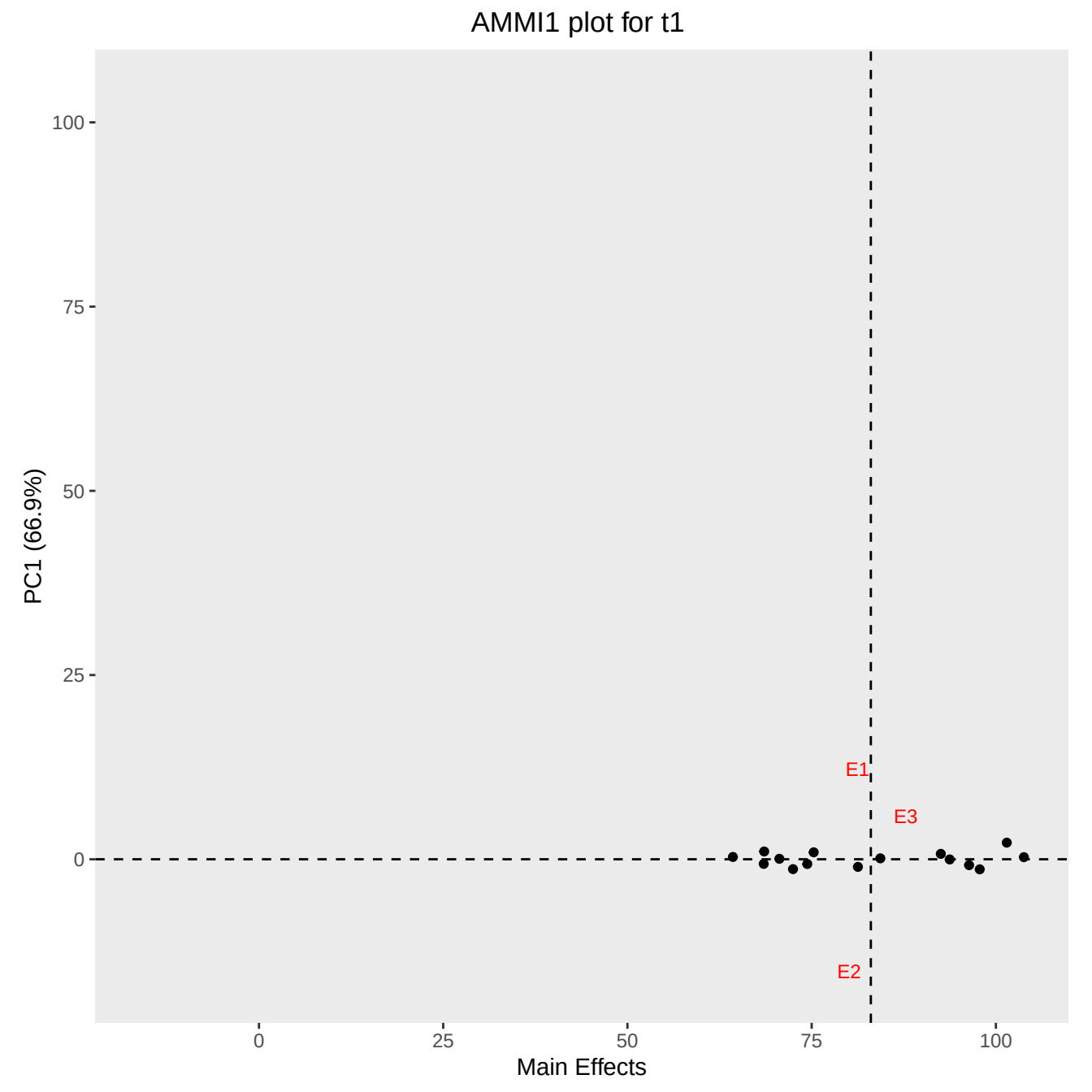
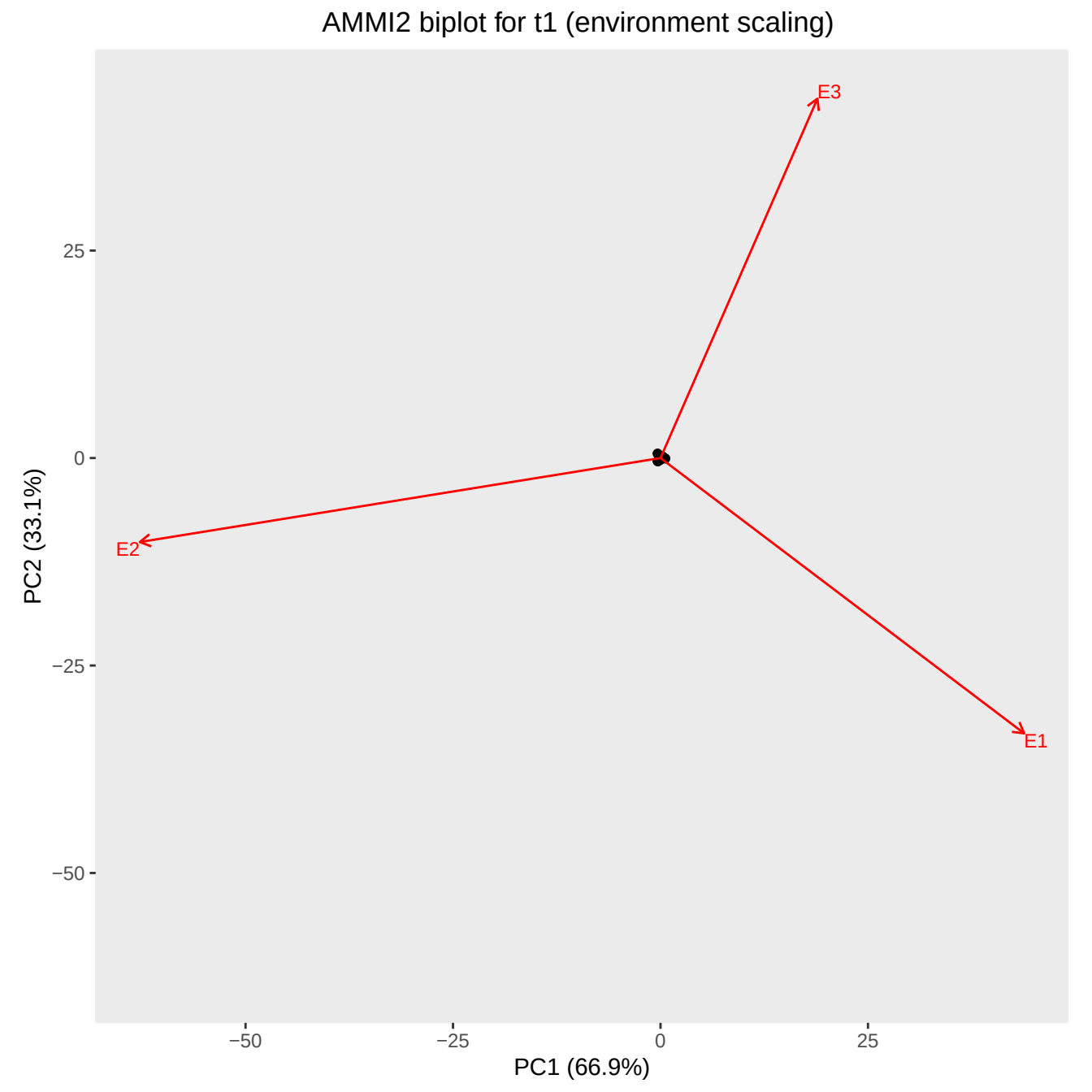
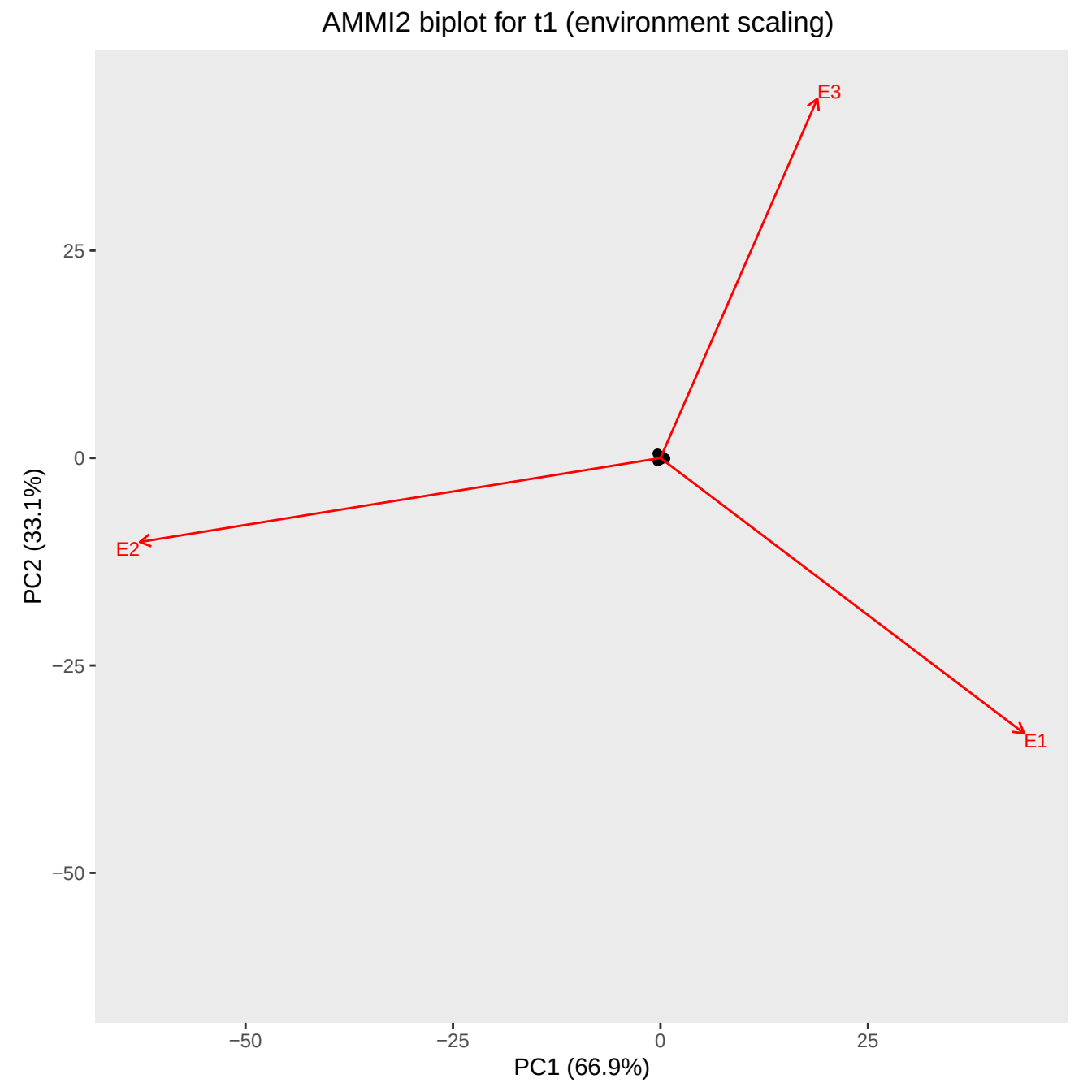
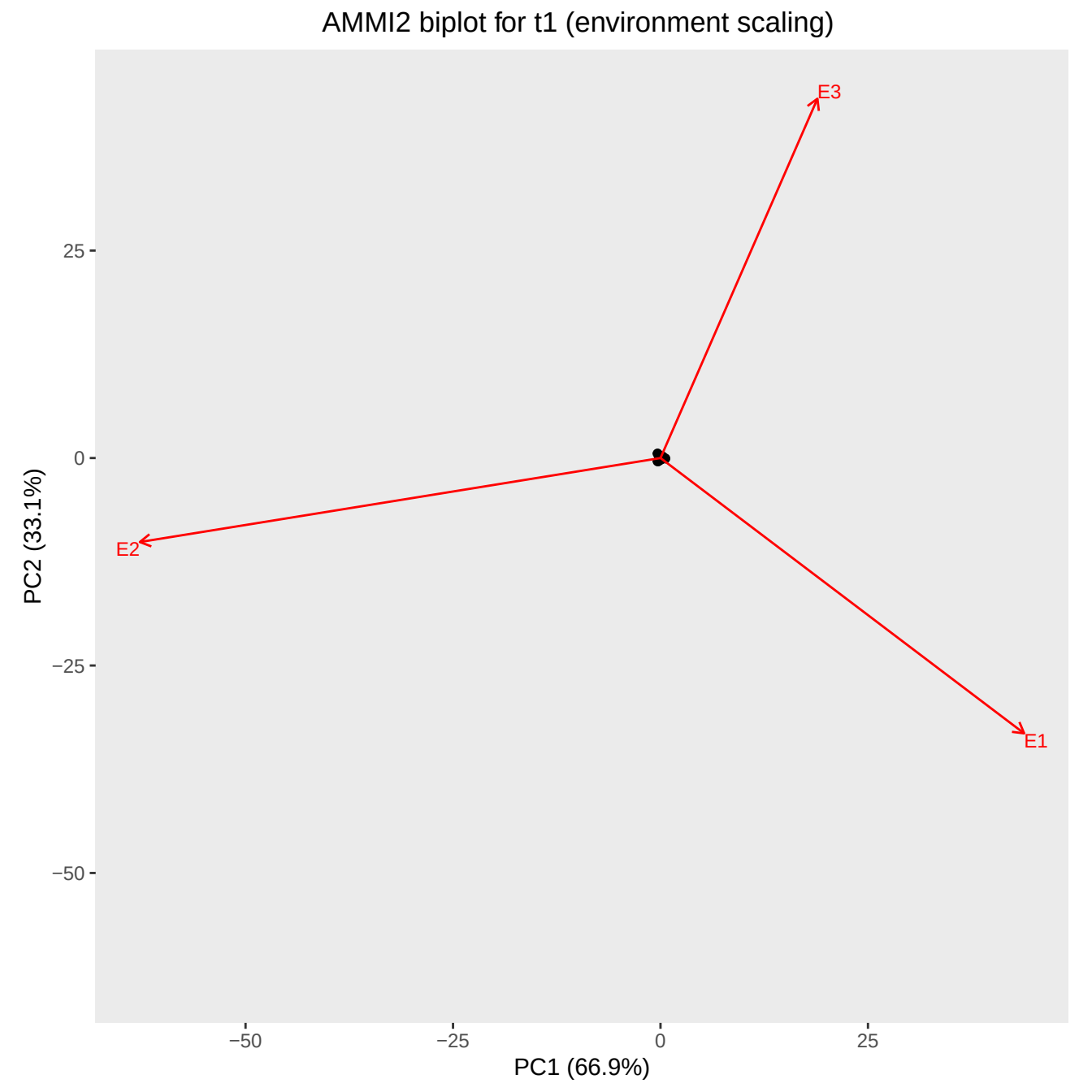
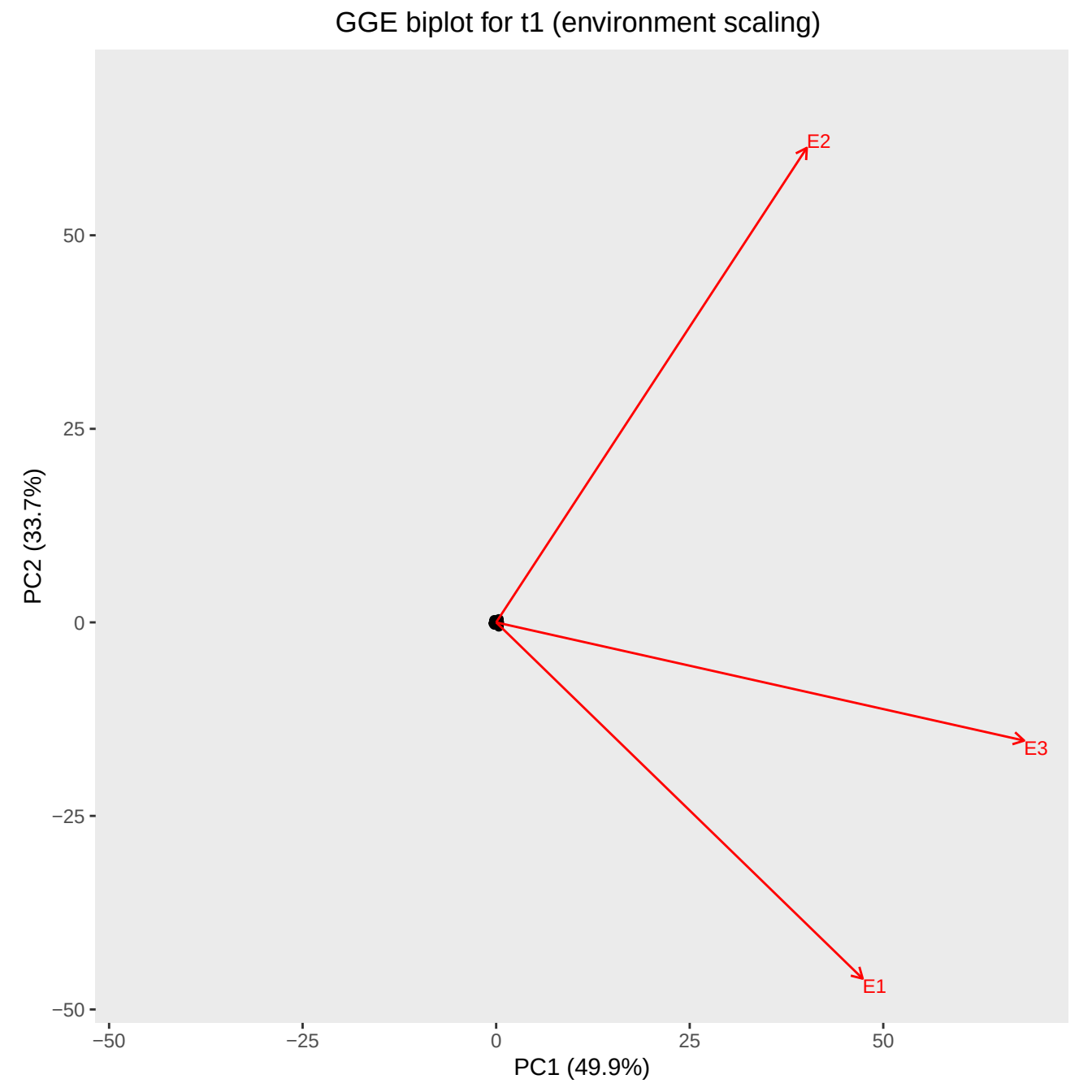
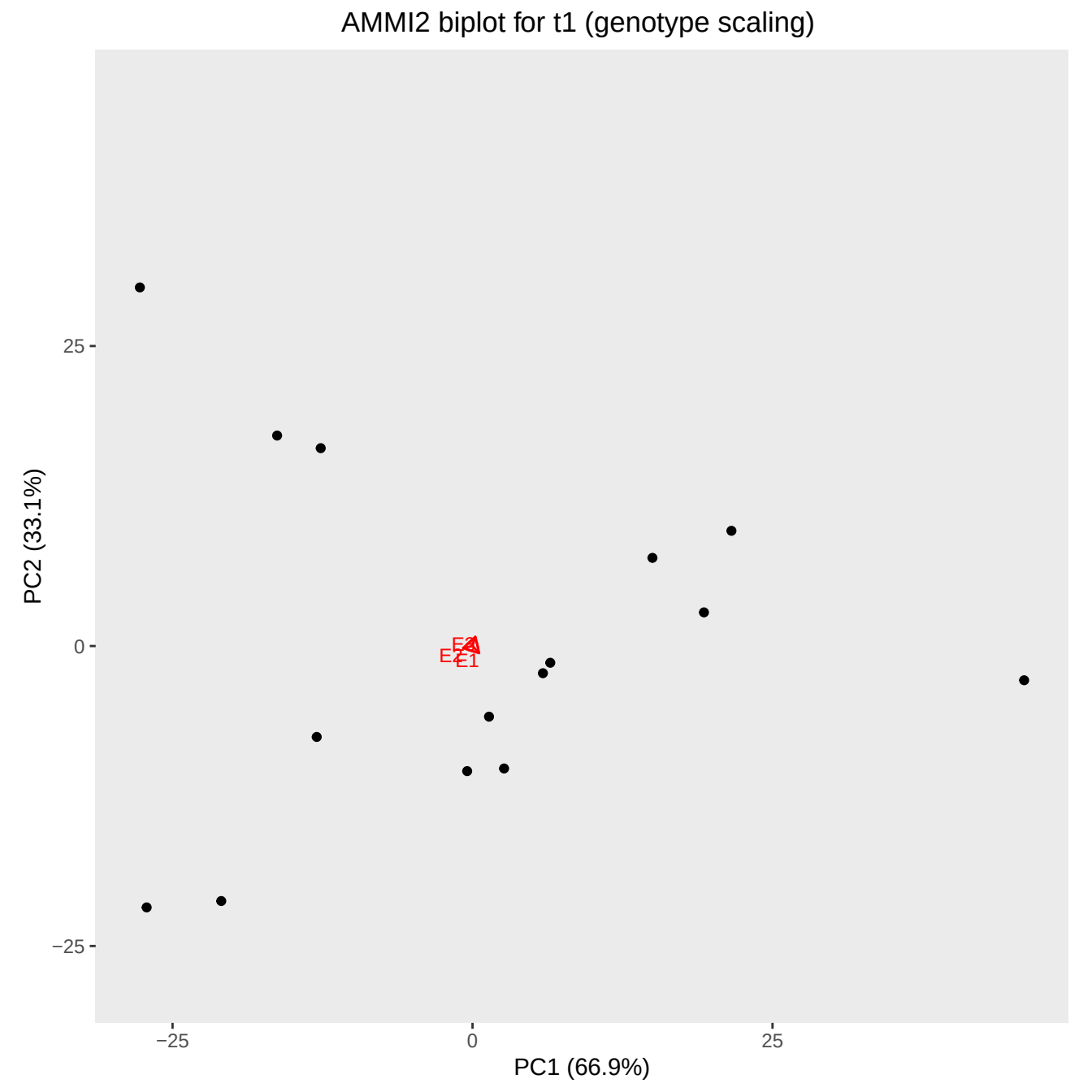

AMMI1 plot for t1
100
75
50
25
0
PC1 (66.9%)
E1
E3
E2
0
25
50
75
100
Main Effects

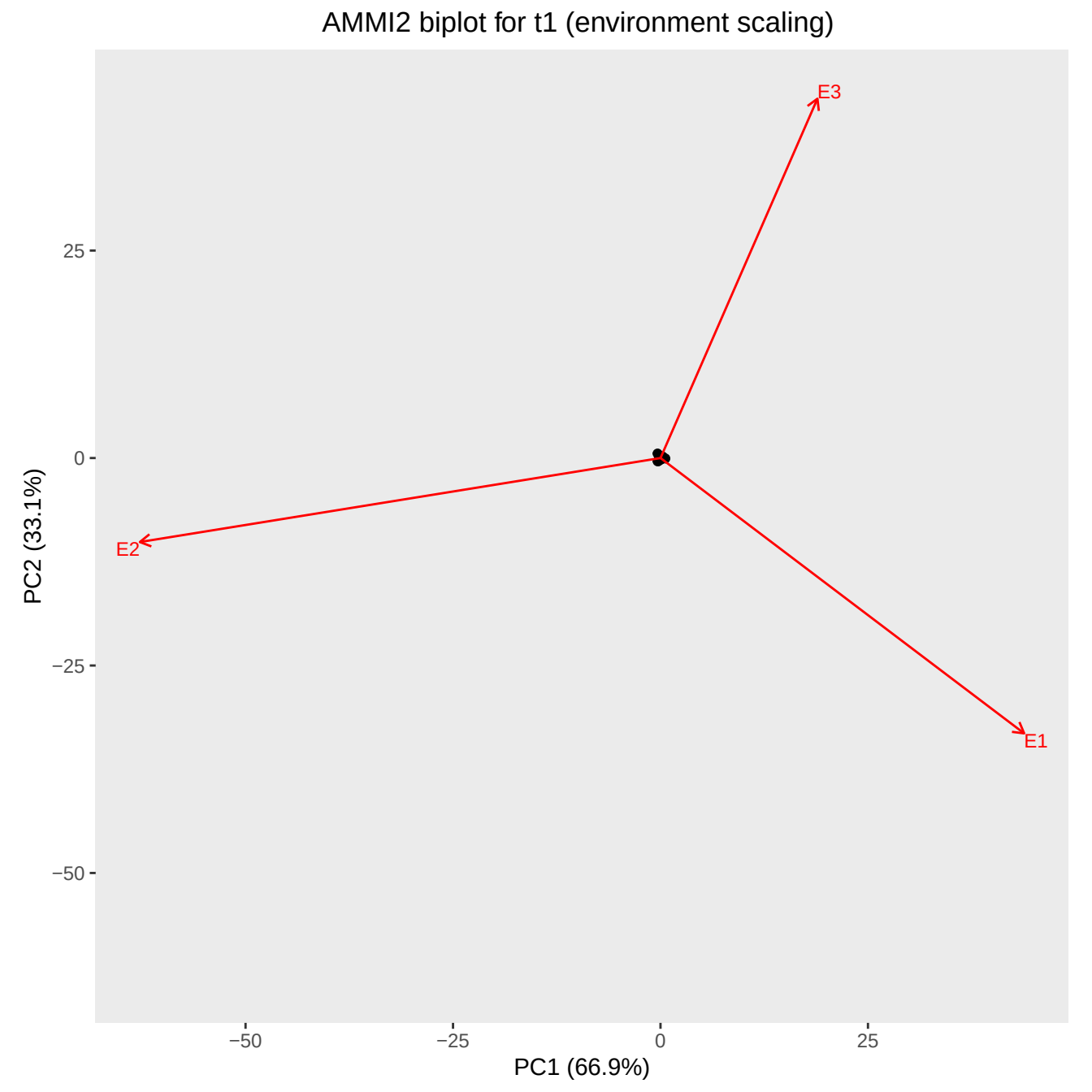

AMMI2 biplot for t1 (environment scaling)
E3
E2
E1
25
0
−25
−50
PC2 (33.1%)
−50
−25
0
25
PC1 (66.9%)

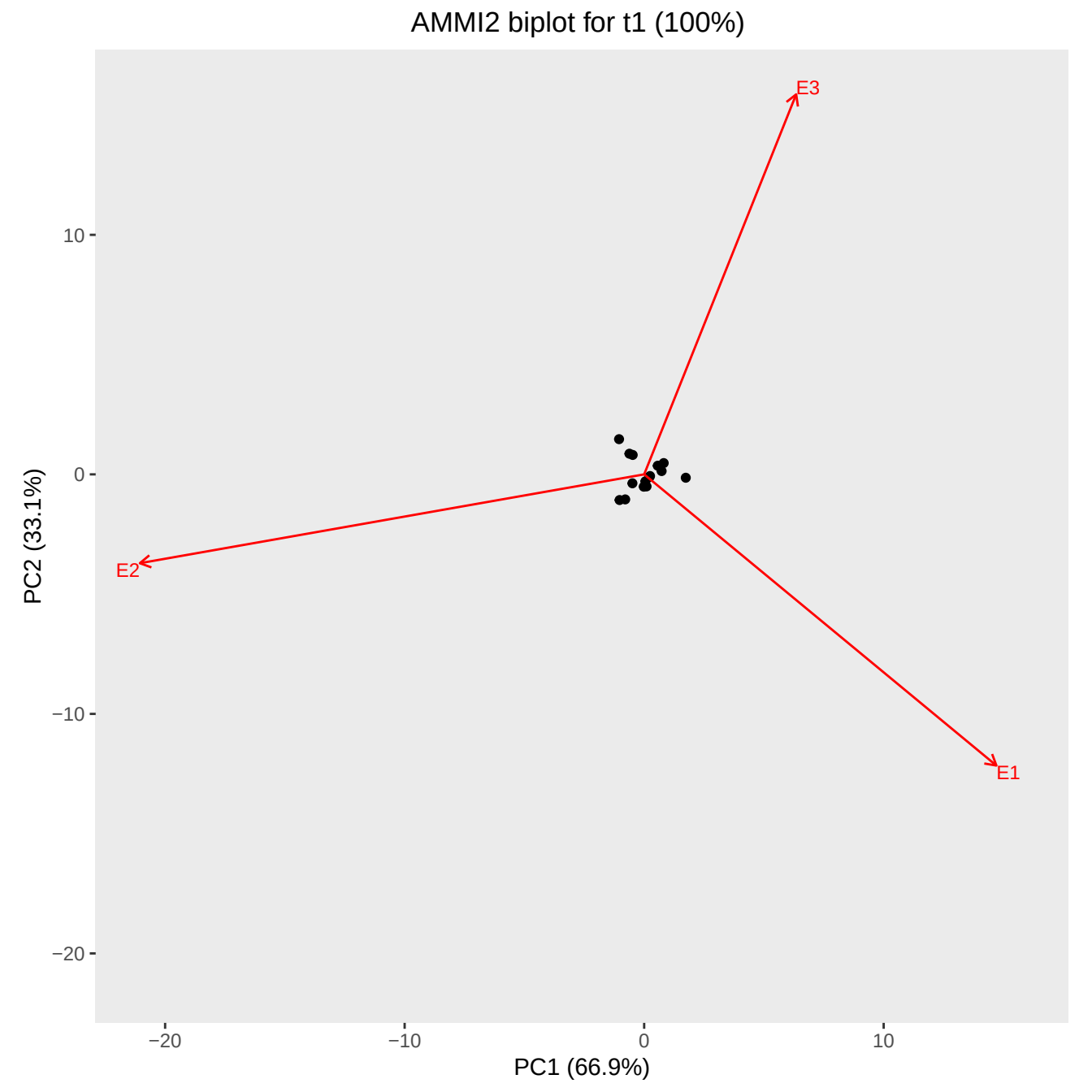

AMMI2 biplot for t1 (environment scaling)
E3
E2
E1
25
0
−25
−50
PC2 (33.1%)
−50
−25
0
25
PC1 (66.9%)

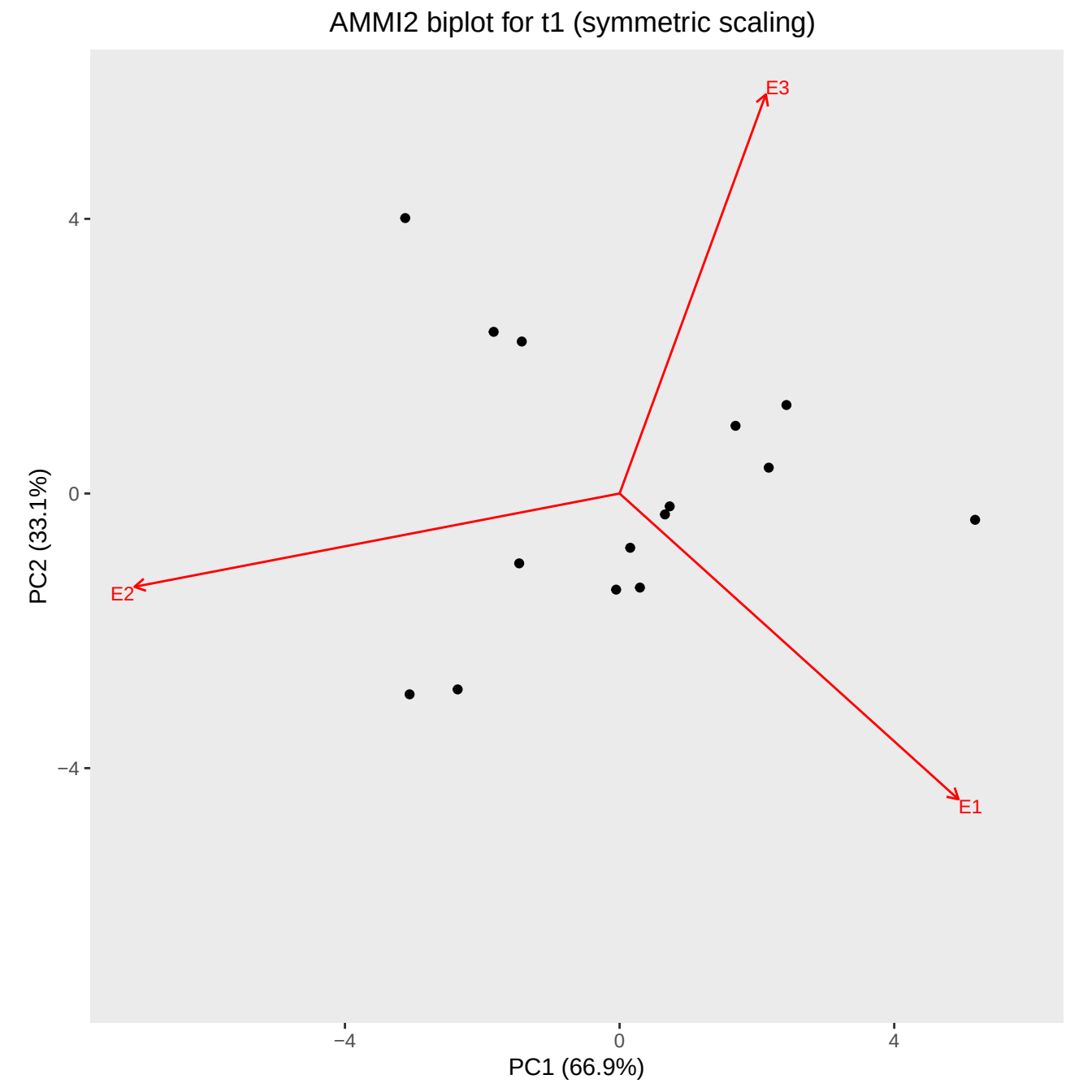

AMMI2 biplot for t1 (environment scaling)
E3
E2
E1
25
0
−25
−50
PC2 (33.1%)
−50
−25
0
25
PC1 (66.9%)

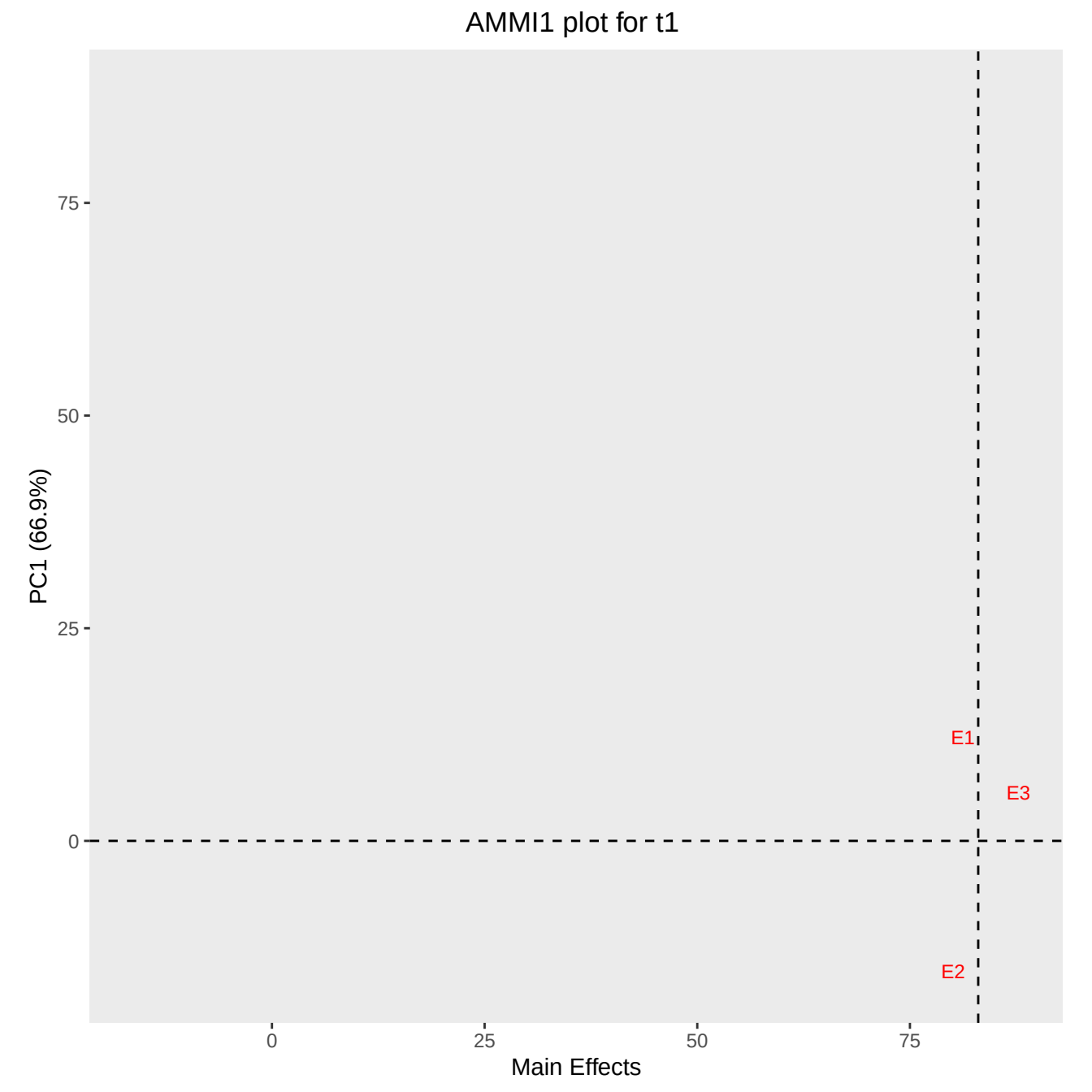

GGE biplot for t1 (environment scaling)
E2
E3
E1
50
25
0
−25
−50
PC2 (33.7%)
−50
−25
0
25
50
PC1 (49.9%)

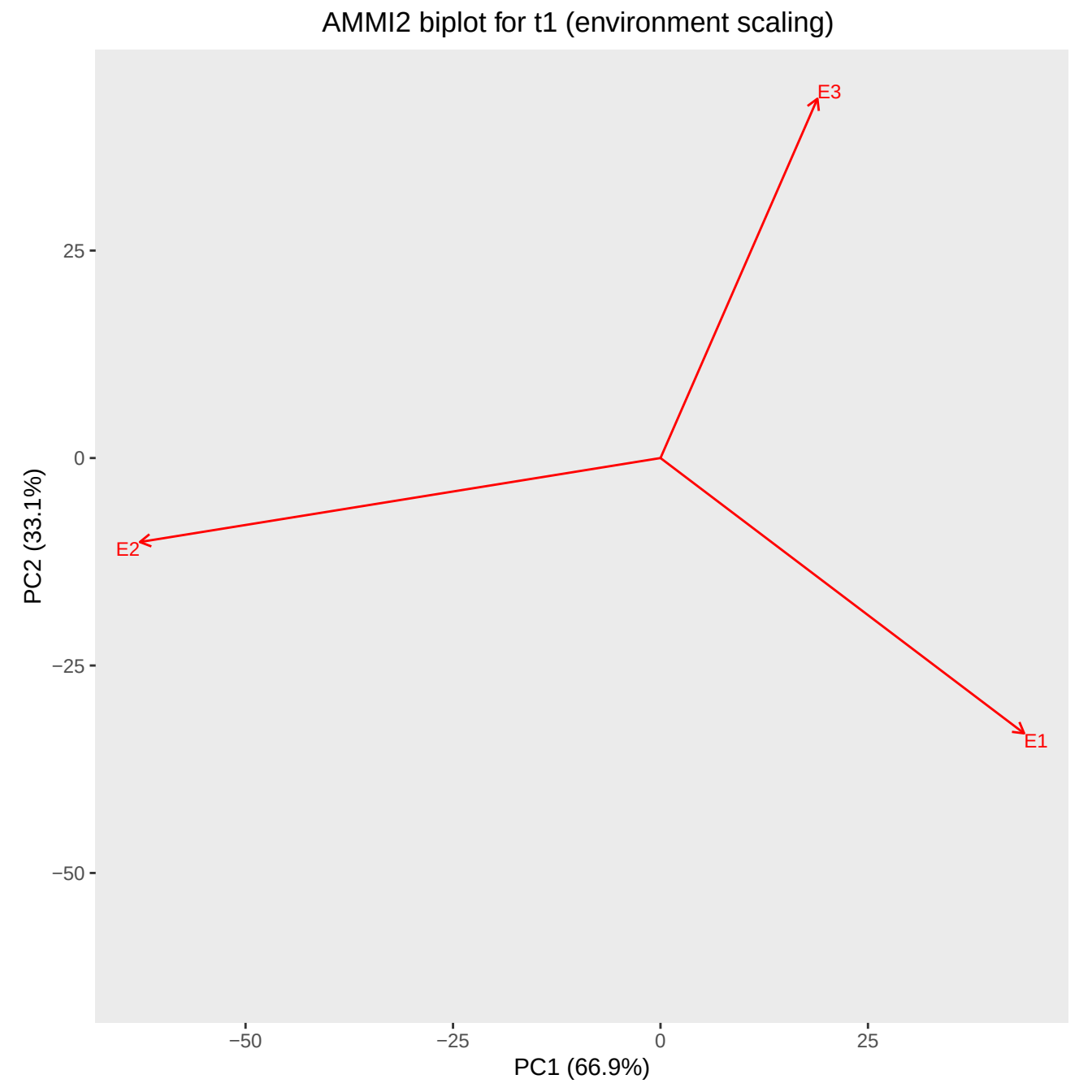

AMMI2 biplot for t1 (genotype scaling)
PC2 (33.1%)
PC1 (66.9%)
25
0
−25
−25
0
25
E4
E3
E1

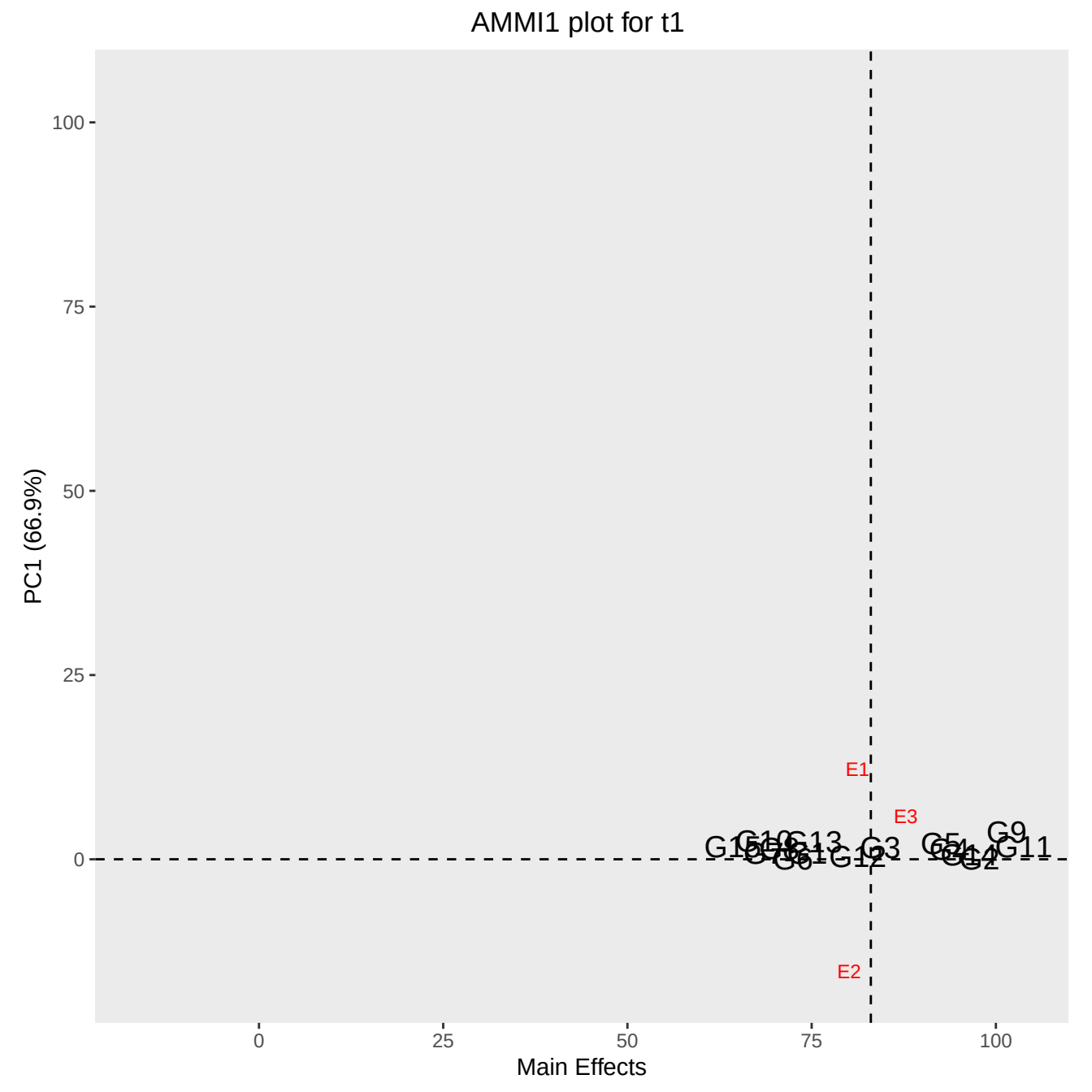

AMMI2 biplot for t1 (environment scaling)
E3
E2
E1
25
0
−25
−50
PC2 (33.1%)
−50
−25
0
25
PC1 (66.9%)

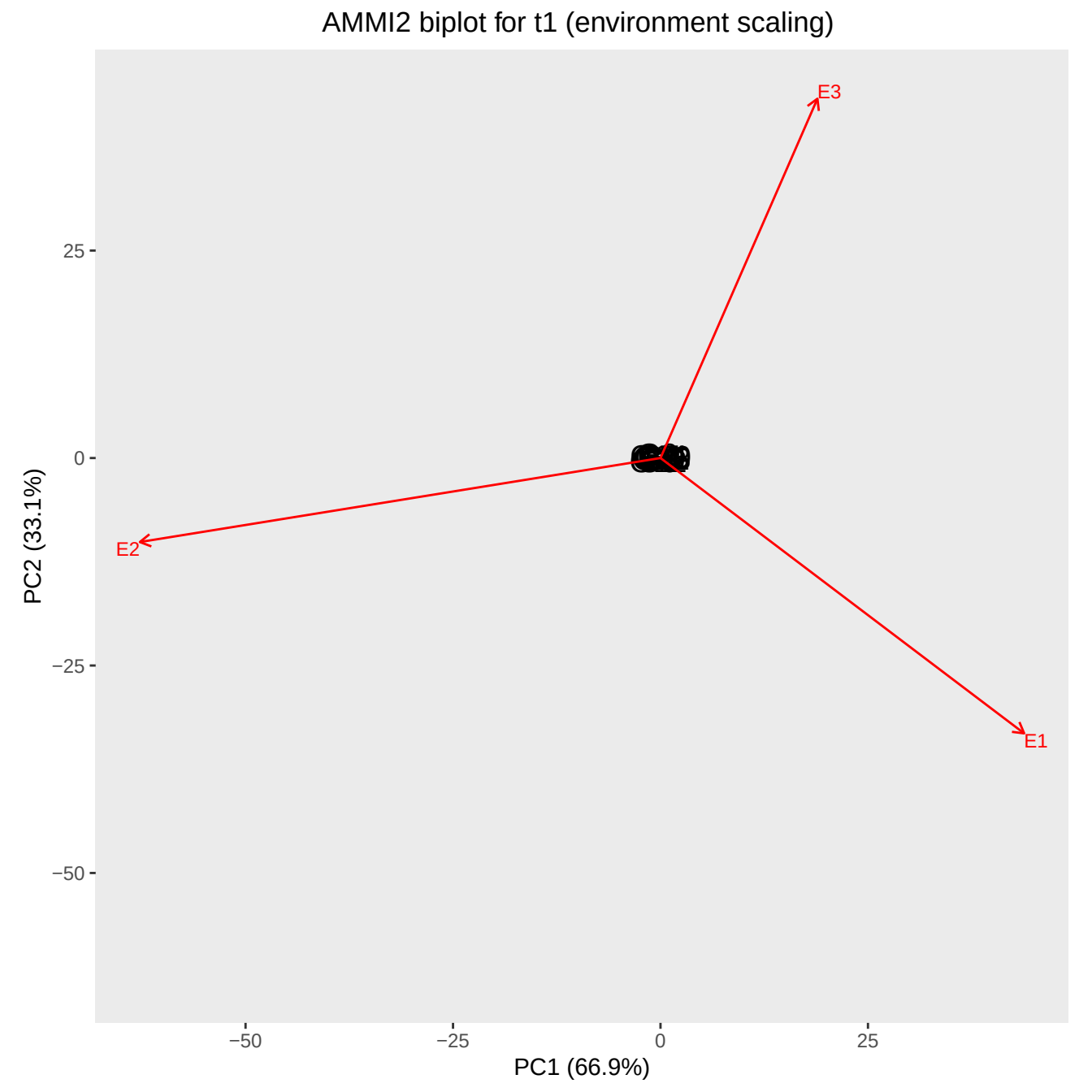

AMMI2 biplot for t1 (100%)
E3
E2
E1
10
0
−10
−20
PC2 (33.1%)
−20
−10
0
10
PC1 (66.9%)

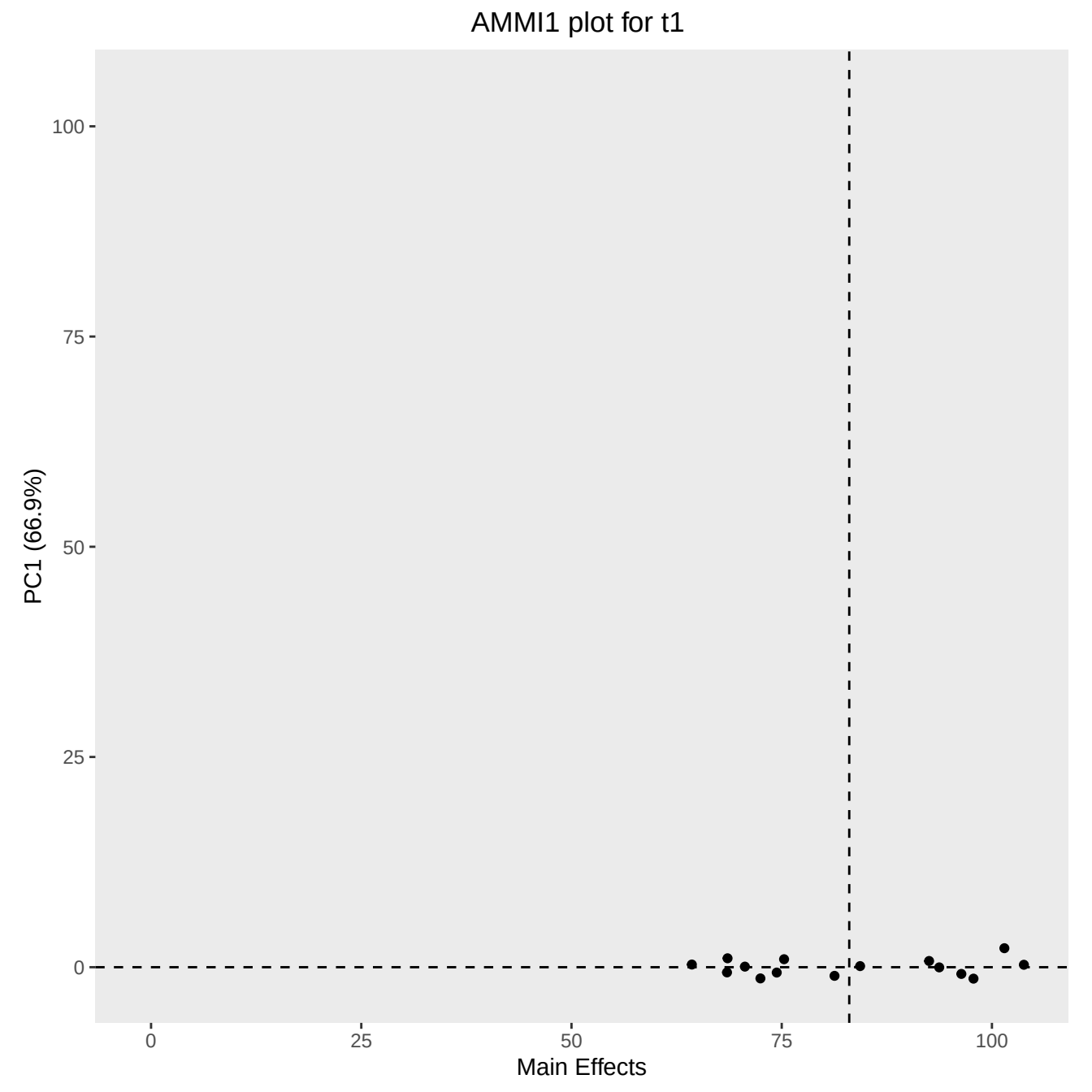

AMMI2 biplot for t1 (symmetric scaling)
E3
E2
E1
4
0
−4
PC2 (33.1%)
−4
0
4
PC1 (66.9%)

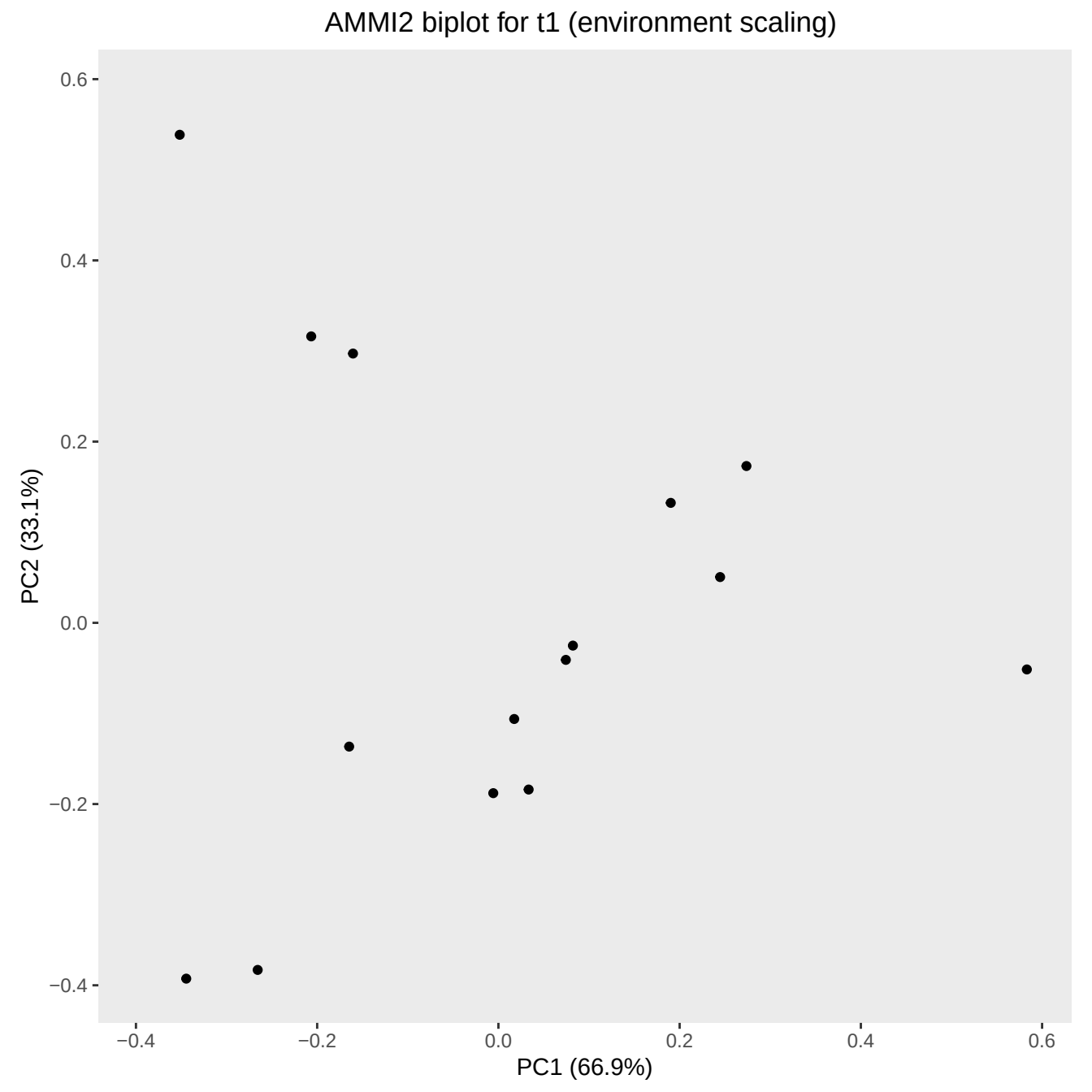

AMMI1 plot for t1
75
50
25
0
PC1 (66.9%)
E1
E3
E2
0
25
50
75
Main Effects

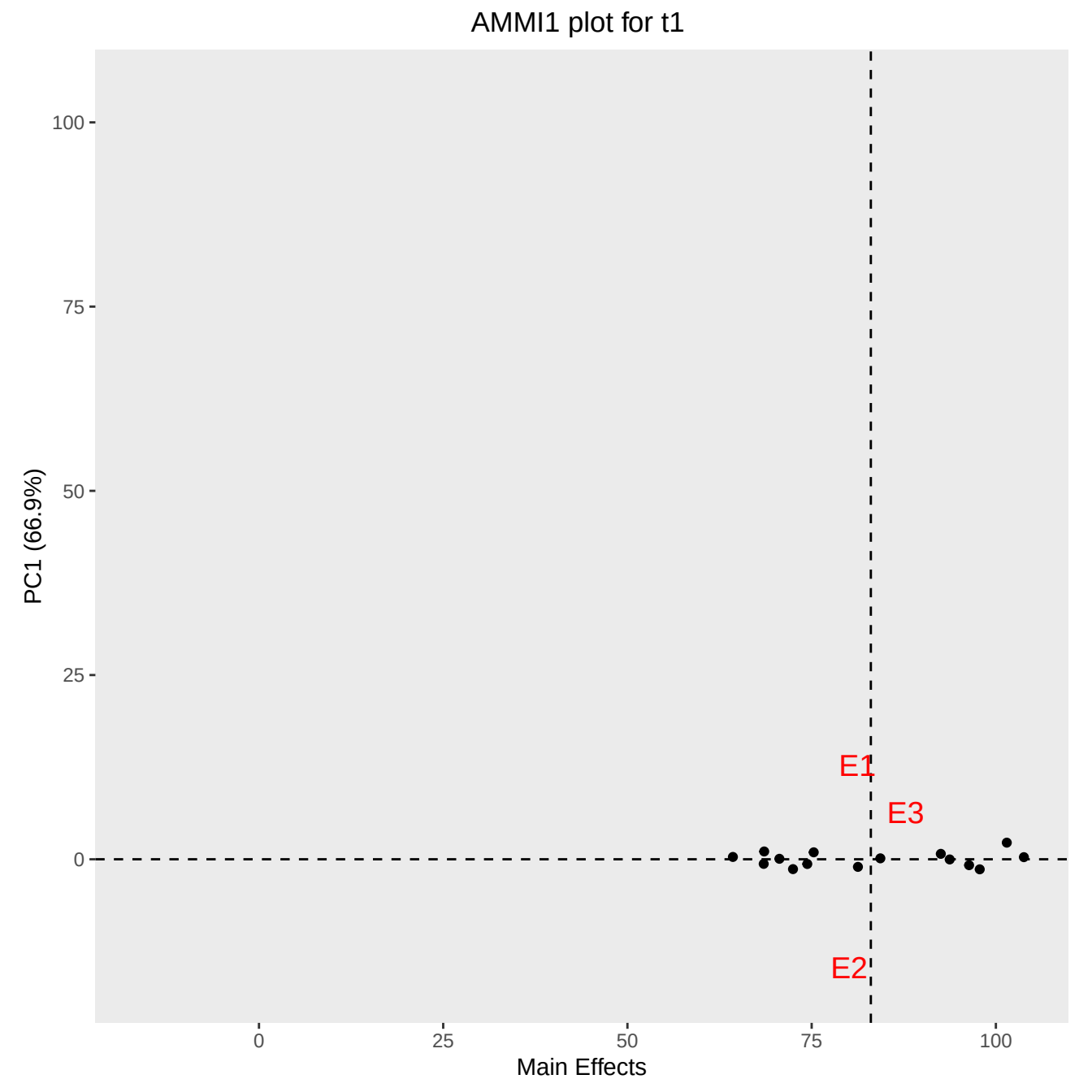

AMMI2 biplot for t1 (environment scaling)
E3
E2
E1
25
0
−25
−50
PC2 (33.1%)
−50
−25
0
25
PC1 (66.9%)

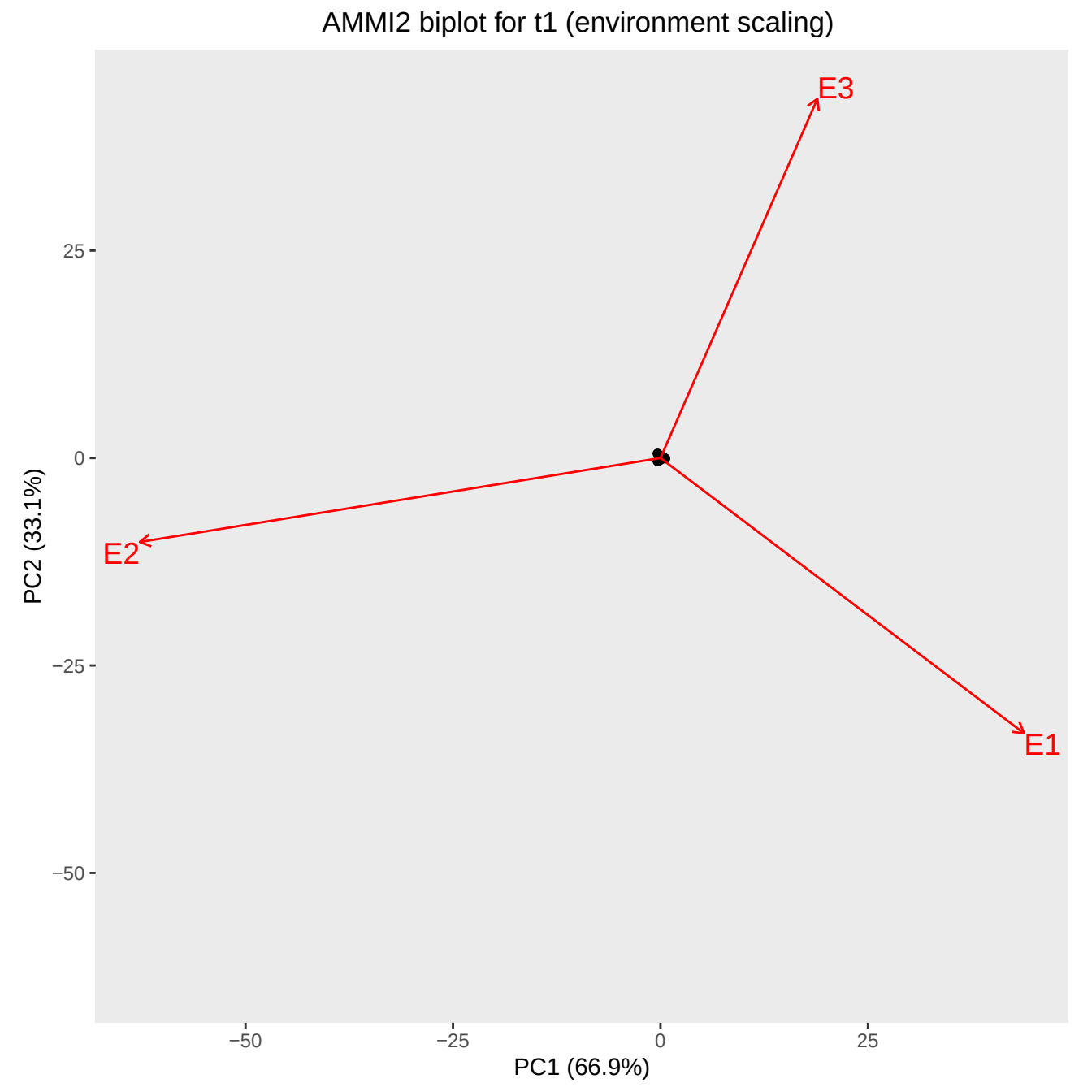

AMMI1 plot for t1
PC1 (66.9%)
Main Effects
100
75
50
25
0
0
25
50
75
100
E1
E2
E3
G9
G11

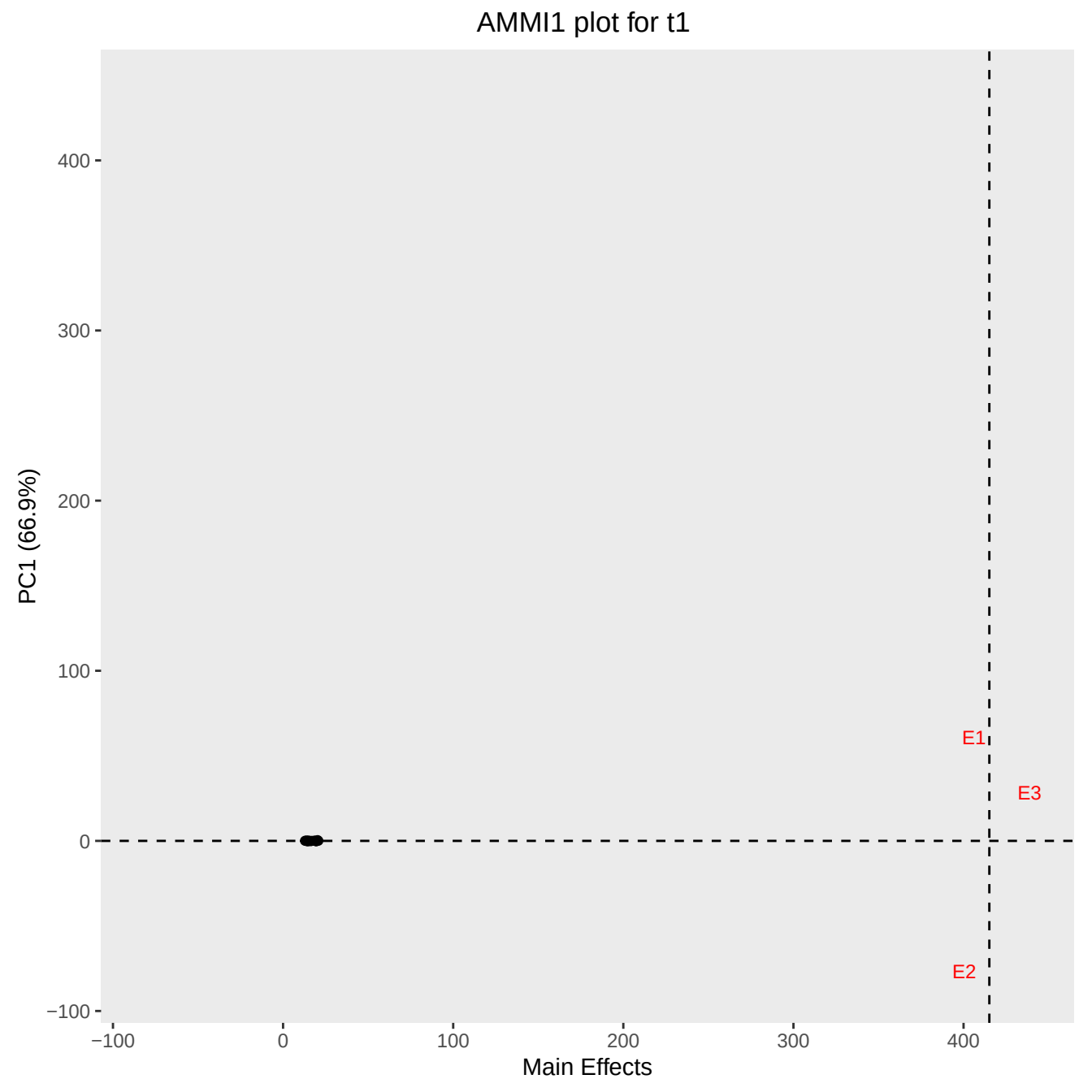

AMMI2 biplot for t1 (environment scaling)
E3
E2
E1
25
0
−25
−50
PC2 (33.1%)
−50
−25
0
25
PC1 (66.9%)

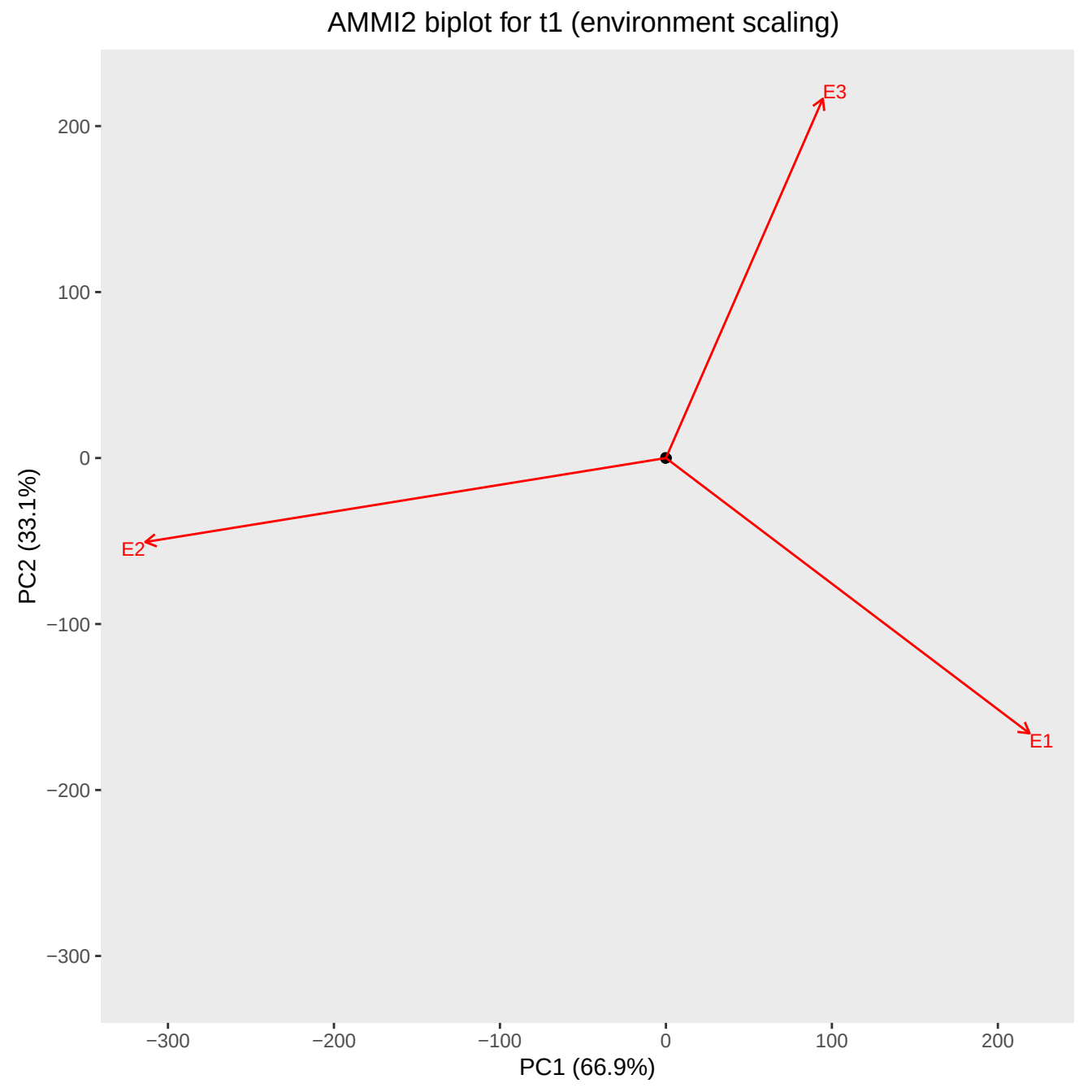

AMMI1 plot for t1
100
75
50
25
0
PC1 (66.9%)
0
25
50
75
100
Main Effects

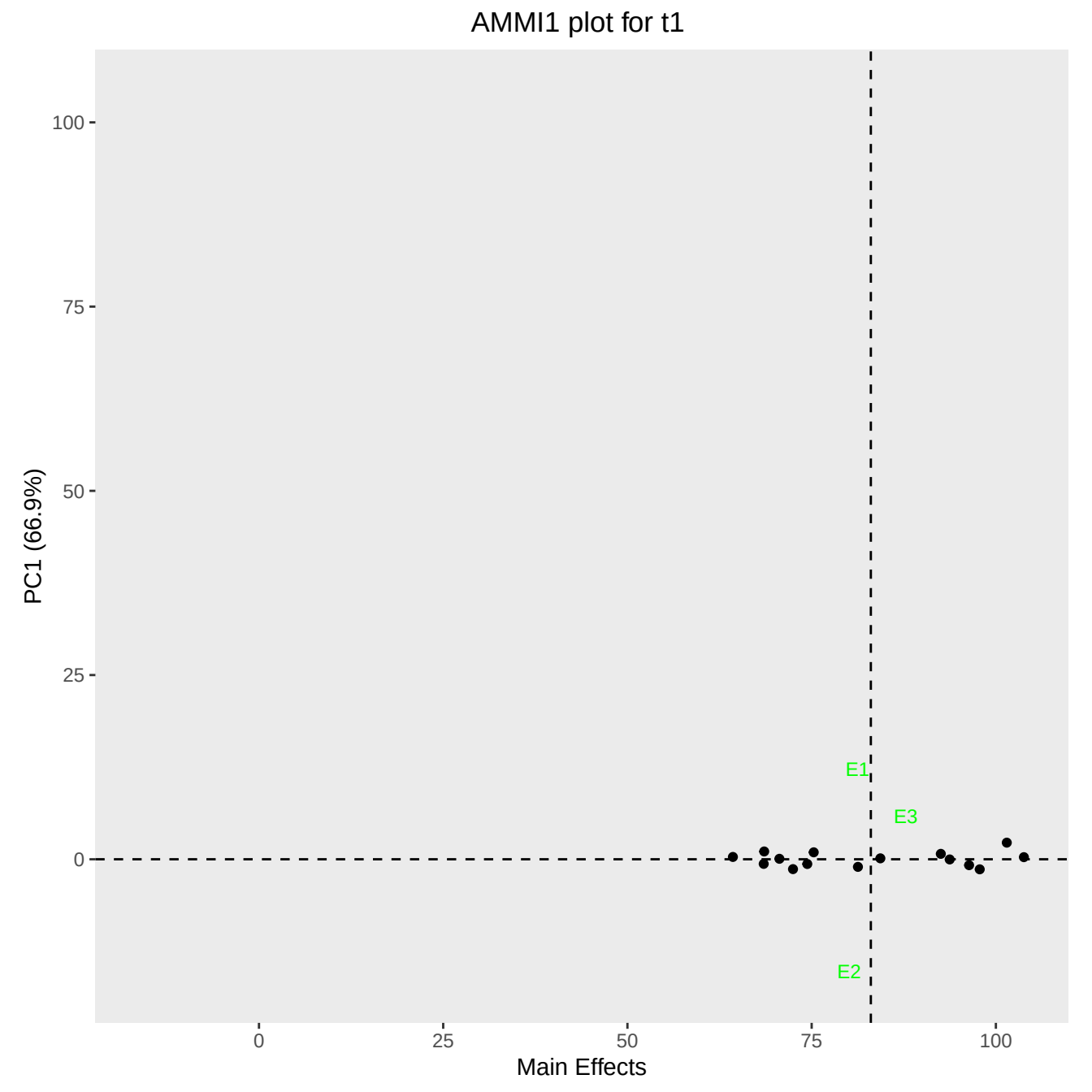

AMMI2 biplot for t1 (environment scaling)
0.6
0.4
0.2
0.0
−0.2
−0.4
PC2 (33.1%)
−0.4
−0.2
0.0
0.2
0.4
0.6
PC1 (66.9%)

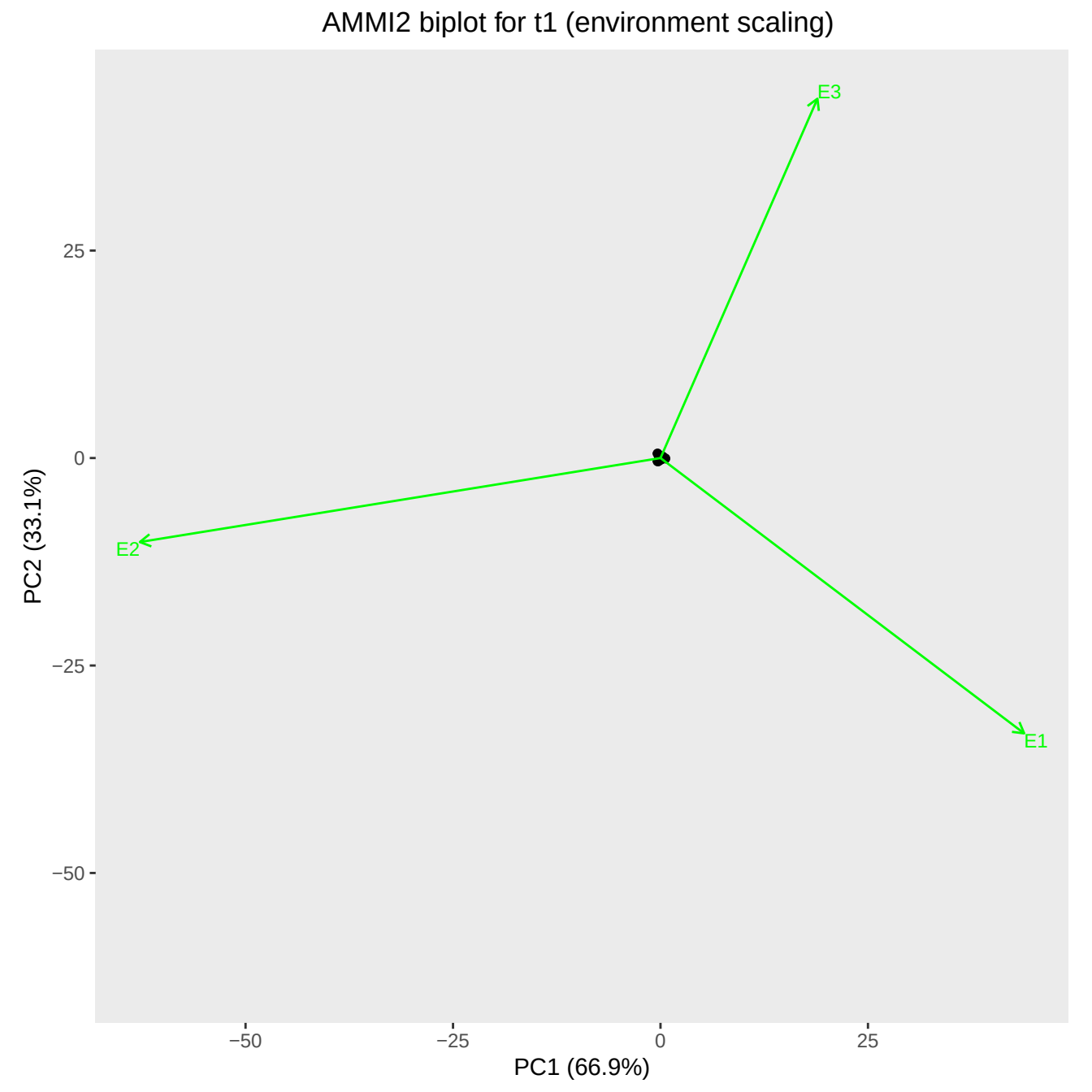

AMMI1 plot for t1
100
75
50
25
0
PC1 (66.9%)
E1
E3
E2
0
25
50
75
100
Main Effects

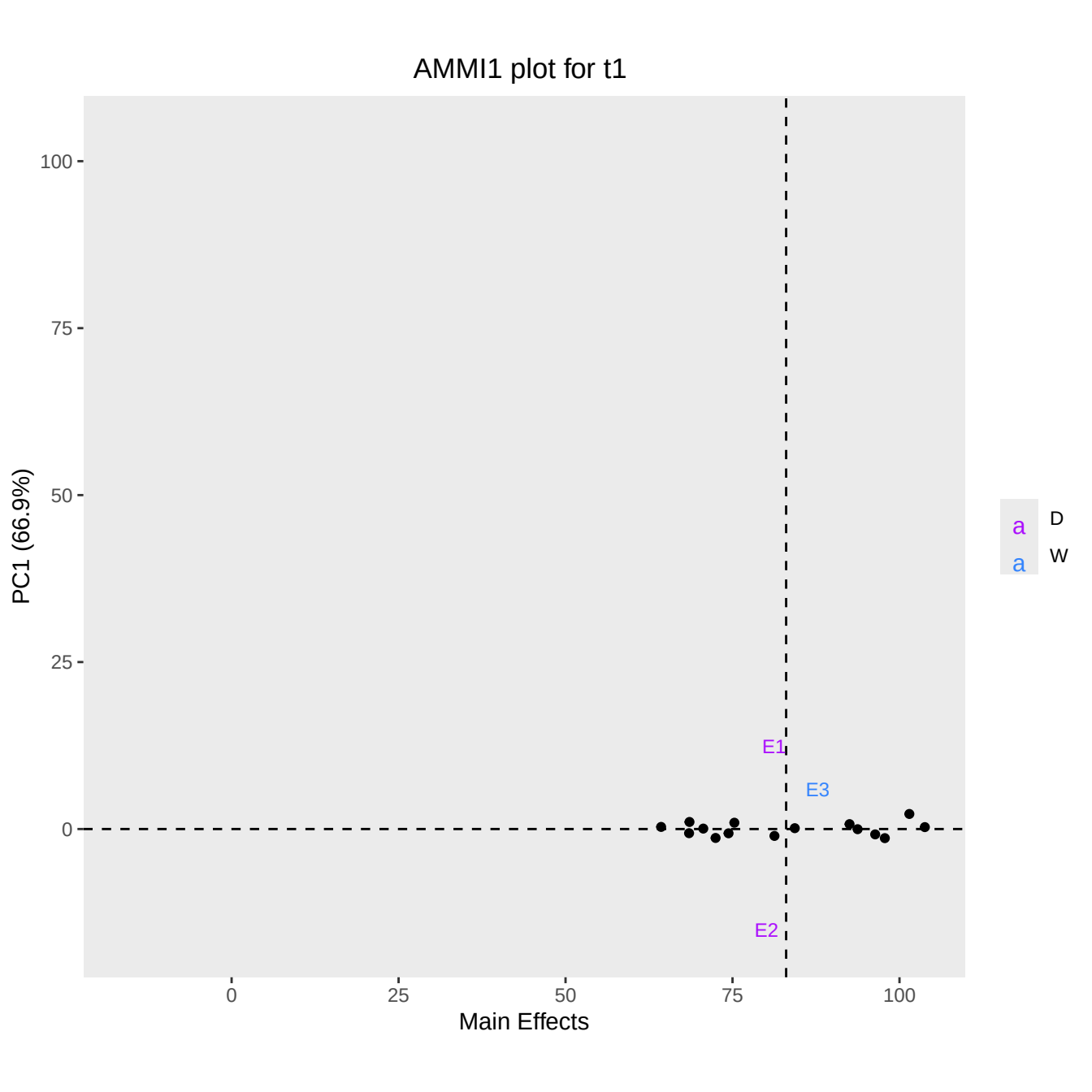

AMMI2 biplot for t1 (environment scaling)
E3
E2
E1
25
0
−25
−50
PC2 (33.1%)
−50
−25
0
25
PC1 (66.9%)

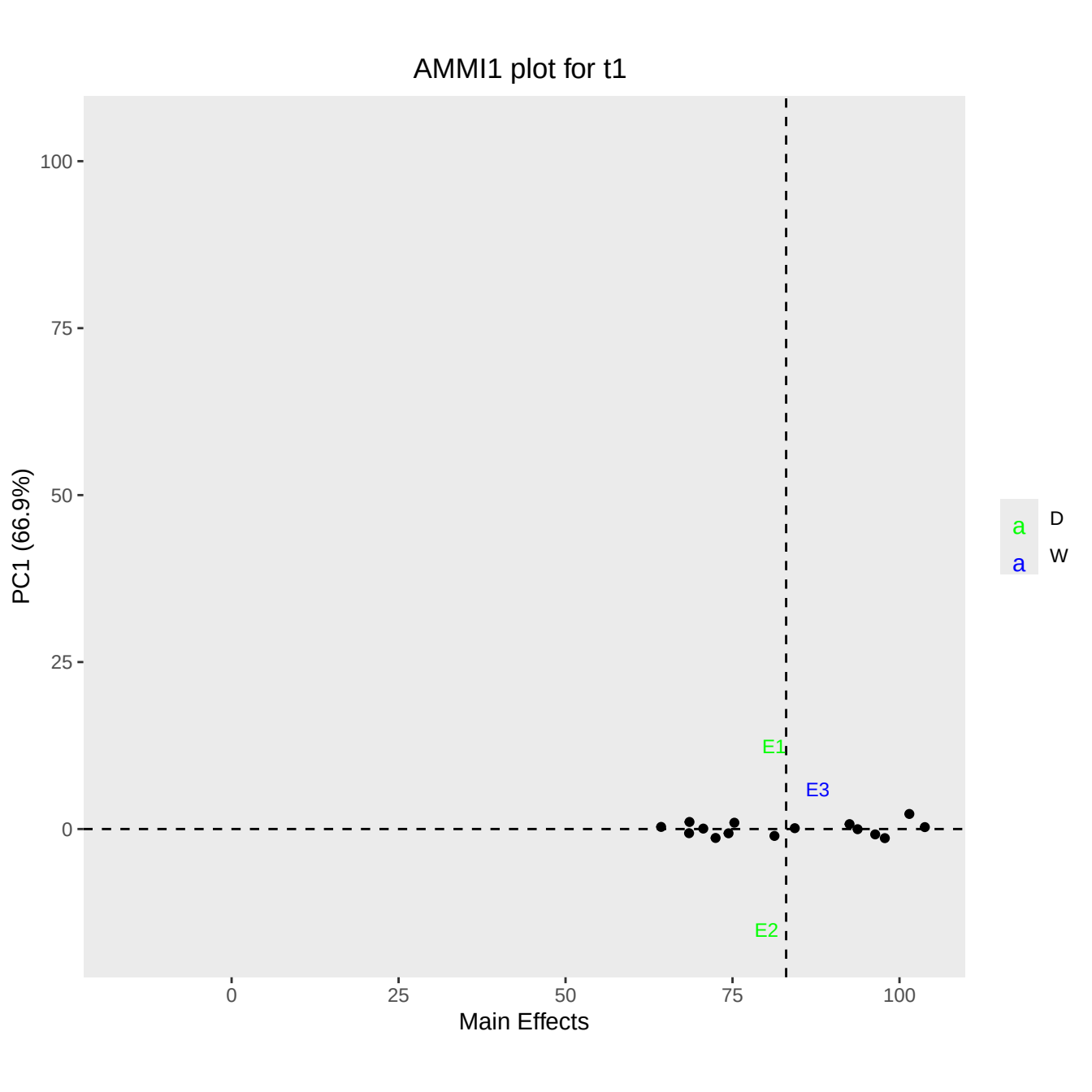

AMMI1 plot for t1
PC1 (66.9%)
Main Effects
400
300
200
100
0
−100
−100
0
100
200
300
400
E1
E3
E2

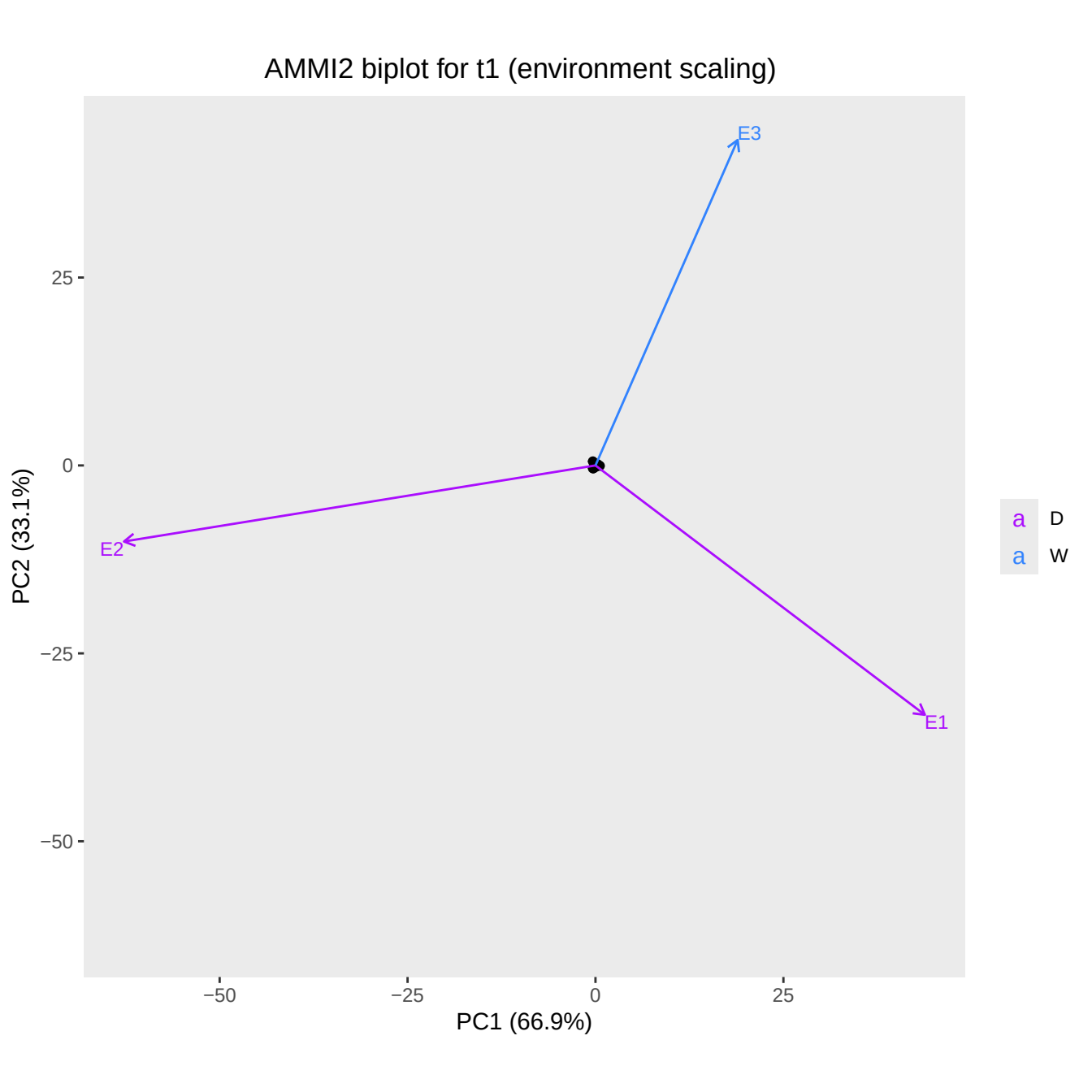

AMMI2 biplot for t1 (environment scaling)
E3
E2
E1
200
100
0
−100
−200
−300
PC2 (33.1%)
−300
−200
−100
0
100
200
PC1 (66.9%)

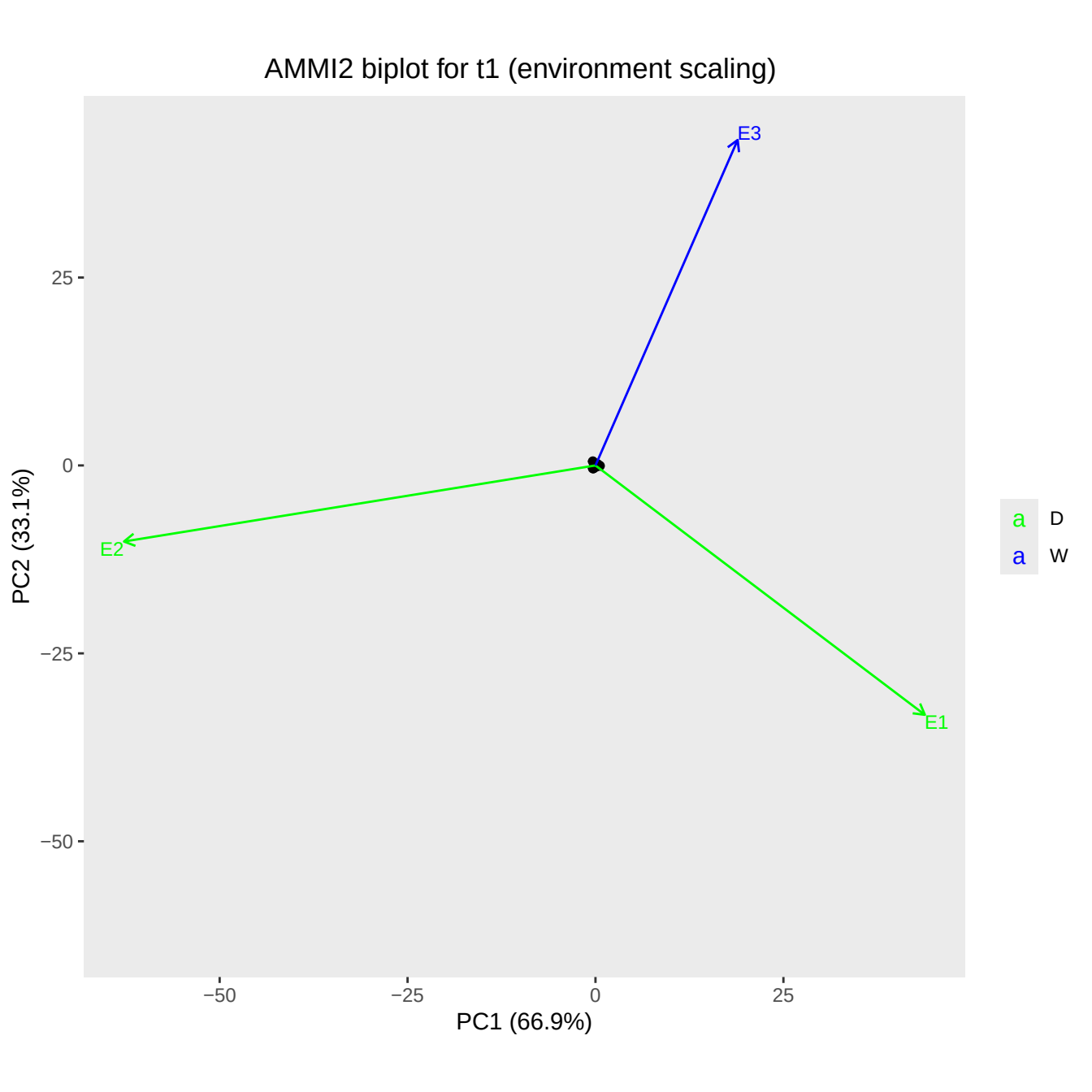

AMMI1 plot for t1
100
75
50
25
0
PC1 (66.9%)
E1
E3
E2
0
25
50
75
100
Main Effects

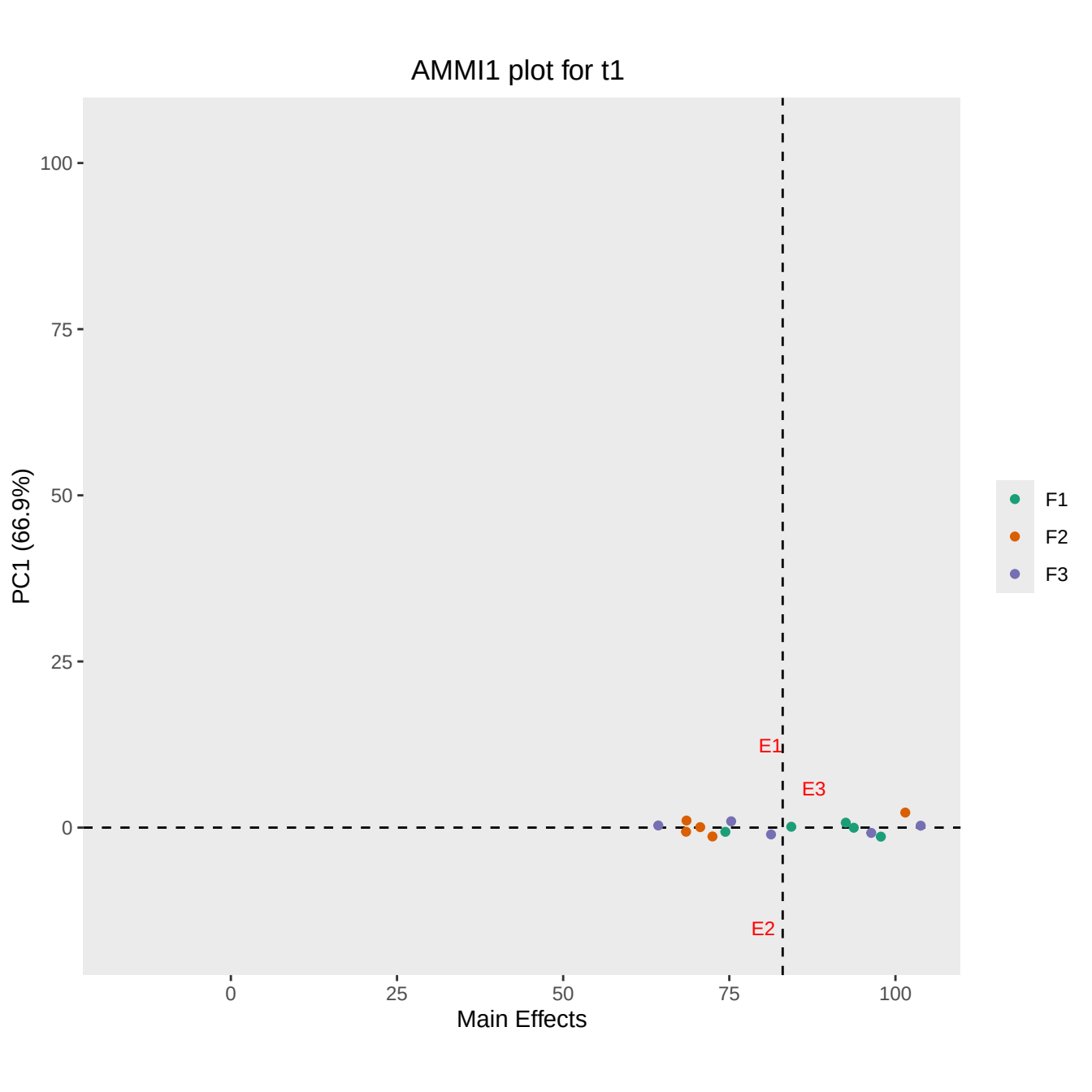

AMMI2 biplot for t1 (environment scaling)
E3
E2
E1
25
0
−25
−50
PC2 (33.1%)
−50
−25
0
25
PC1 (66.9%)

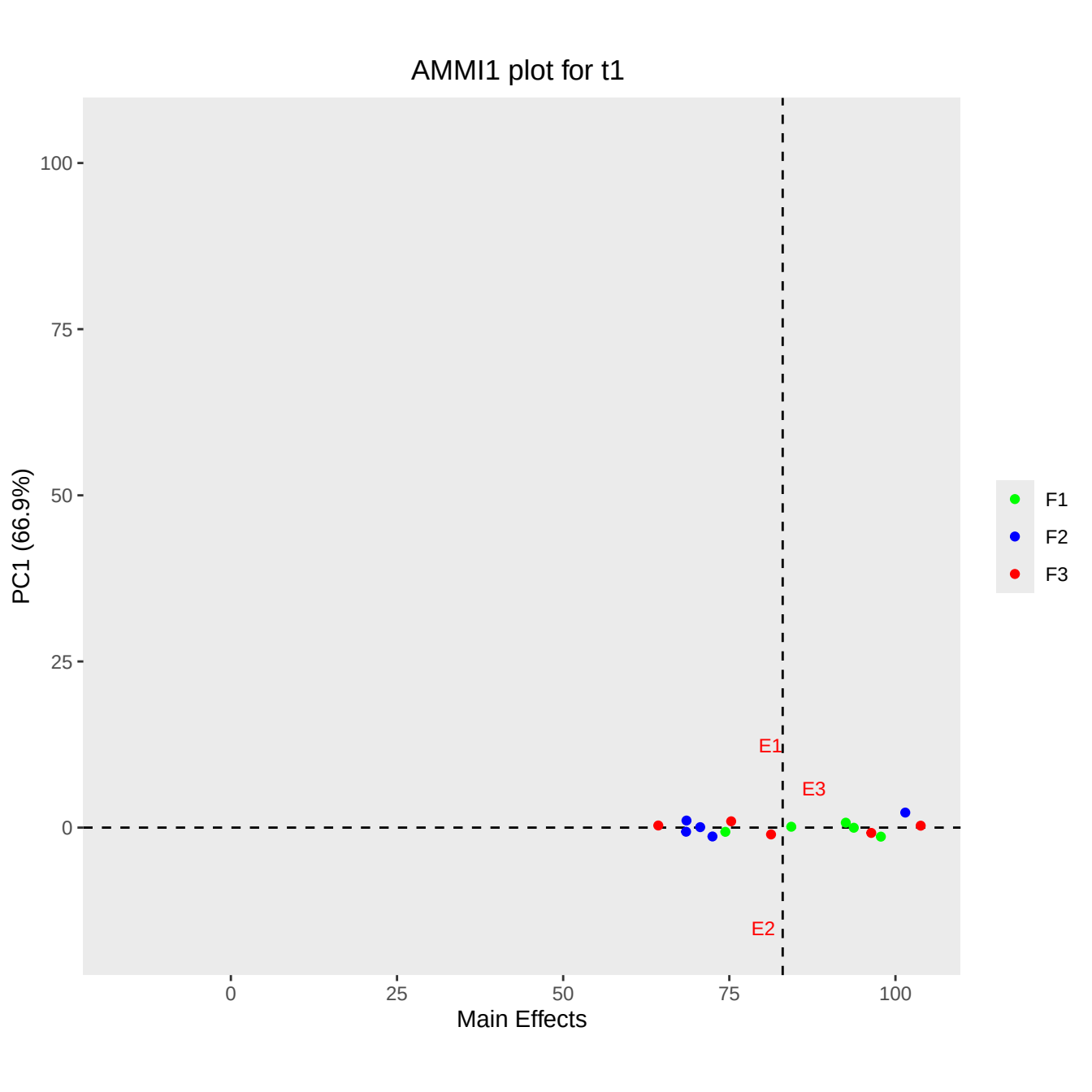

AMMI1 plot for t1
PC1 (66.9%)
100
75
50
25
0
E1
E3
E2
0
25
50
75
100
Main Effects
a
a
D
W

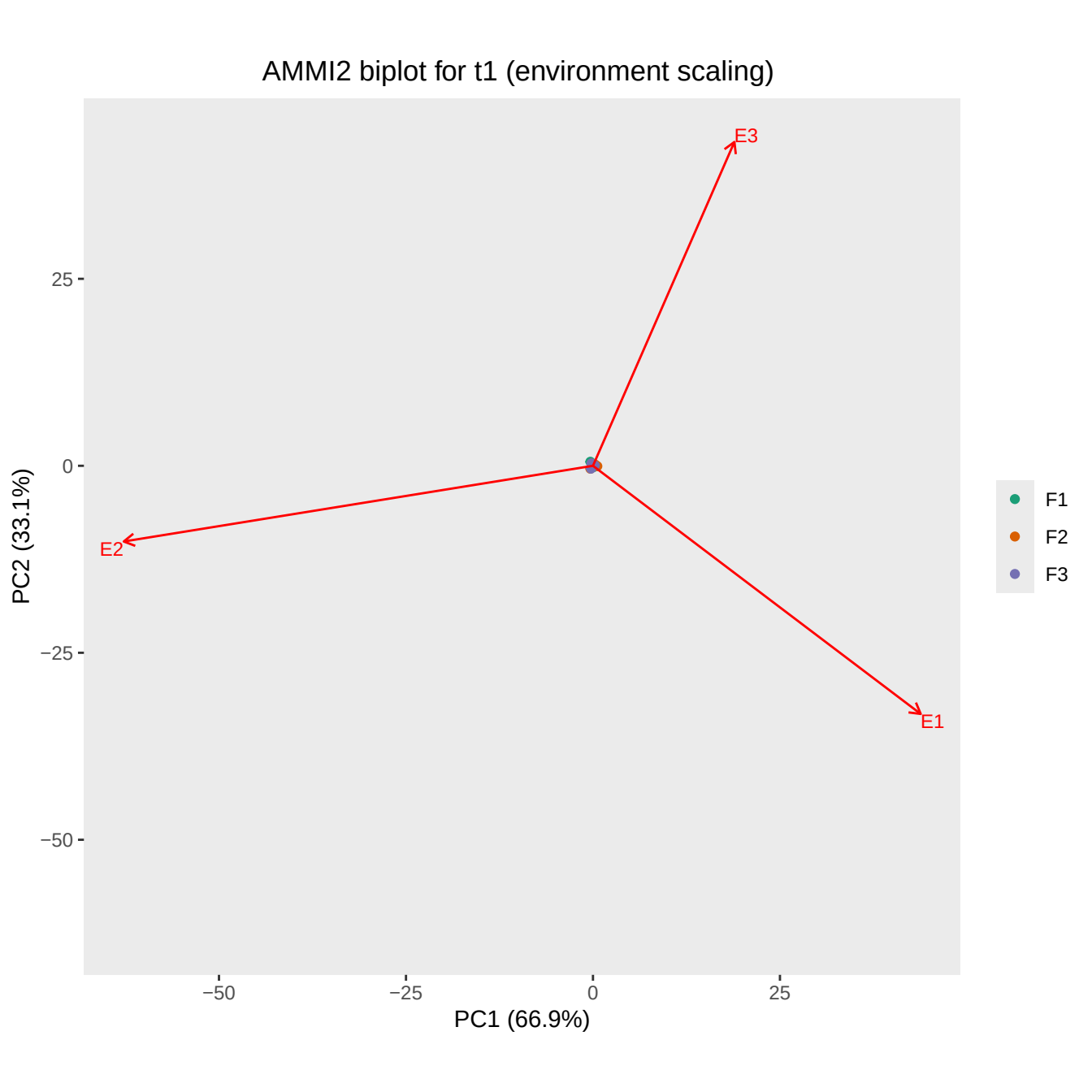

AMMI1 plot for t1
PC1 (66.9%)
100
75
50
25
0
E1
E3
E2
0
25
50
75
100
Main Effects
a
a
D
W

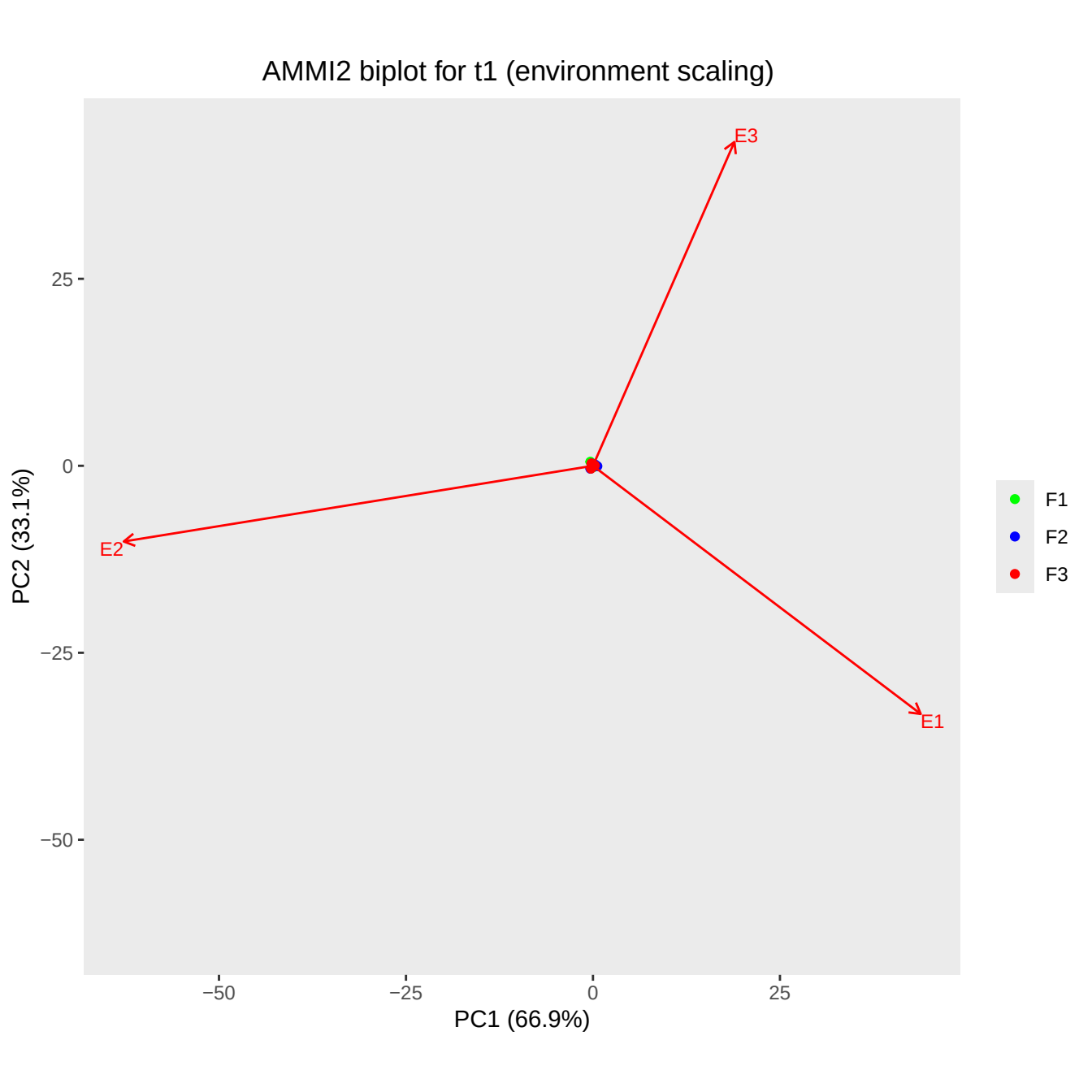

AMMI2 biplot for t1 (environment scaling)
E3
E2
E1
25
0
−25
−50
PC2 (33.1%)
−50
−25
0
25
PC1 (66.9%)
a
D
a
W

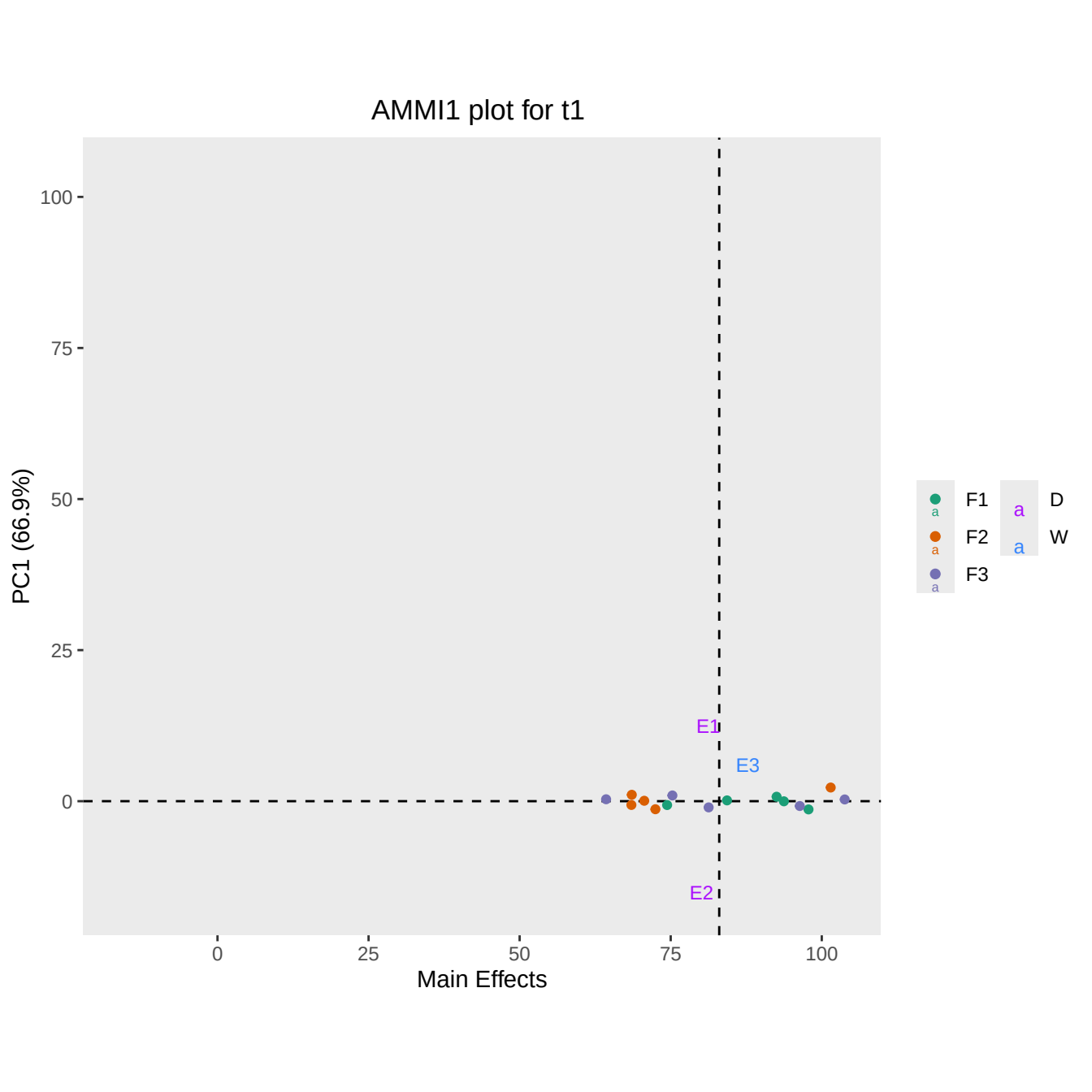

AMMI2 biplot for t1 (environment scaling)
E3
E2
E1
25
0
−25
−50
PC2 (33.1%)
−50
−25
0
25
PC1 (66.9%)
a
D
a
W

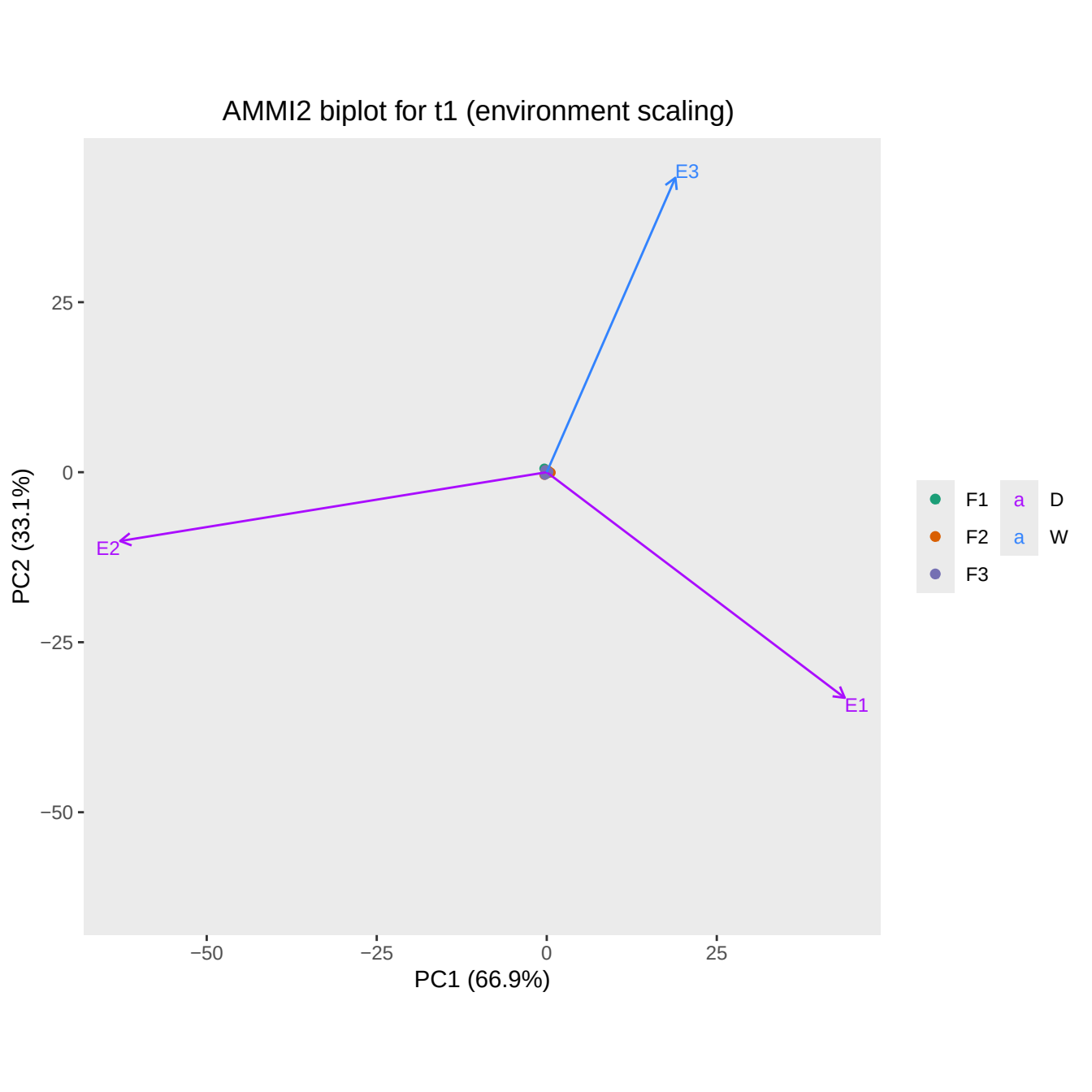

AMMI1 plot for t1
PC1 (66.9%)
Main Effects
100
75
50
25
0
0
25
50
75
100
E1
E2
E3
F1
F2
F3

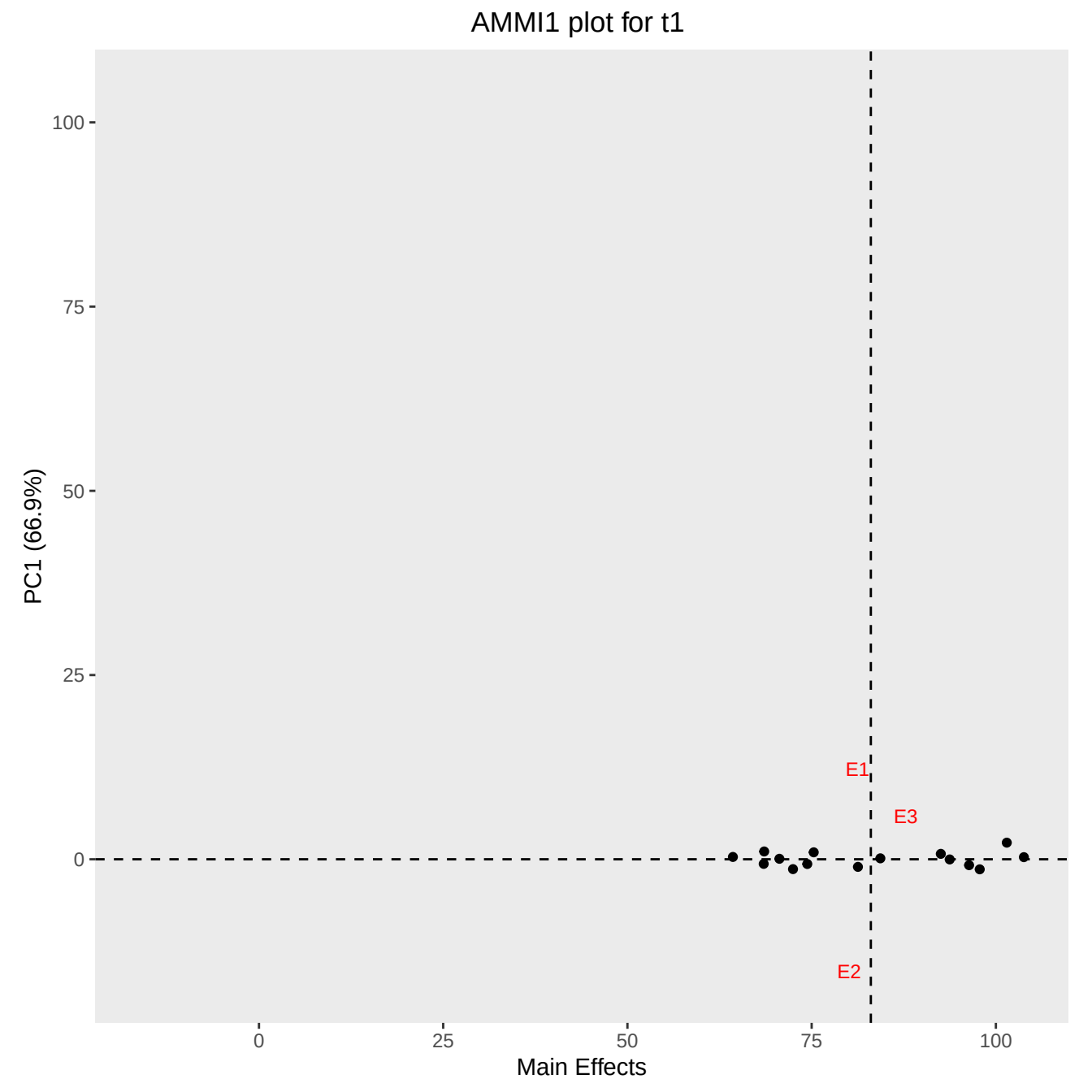

AMMI1 plot for t1
PC1 (66.9%)
Main Effects
100
75
50
25
0
0
25
50
75
100
E1
E2
E3
F1
F2
F3

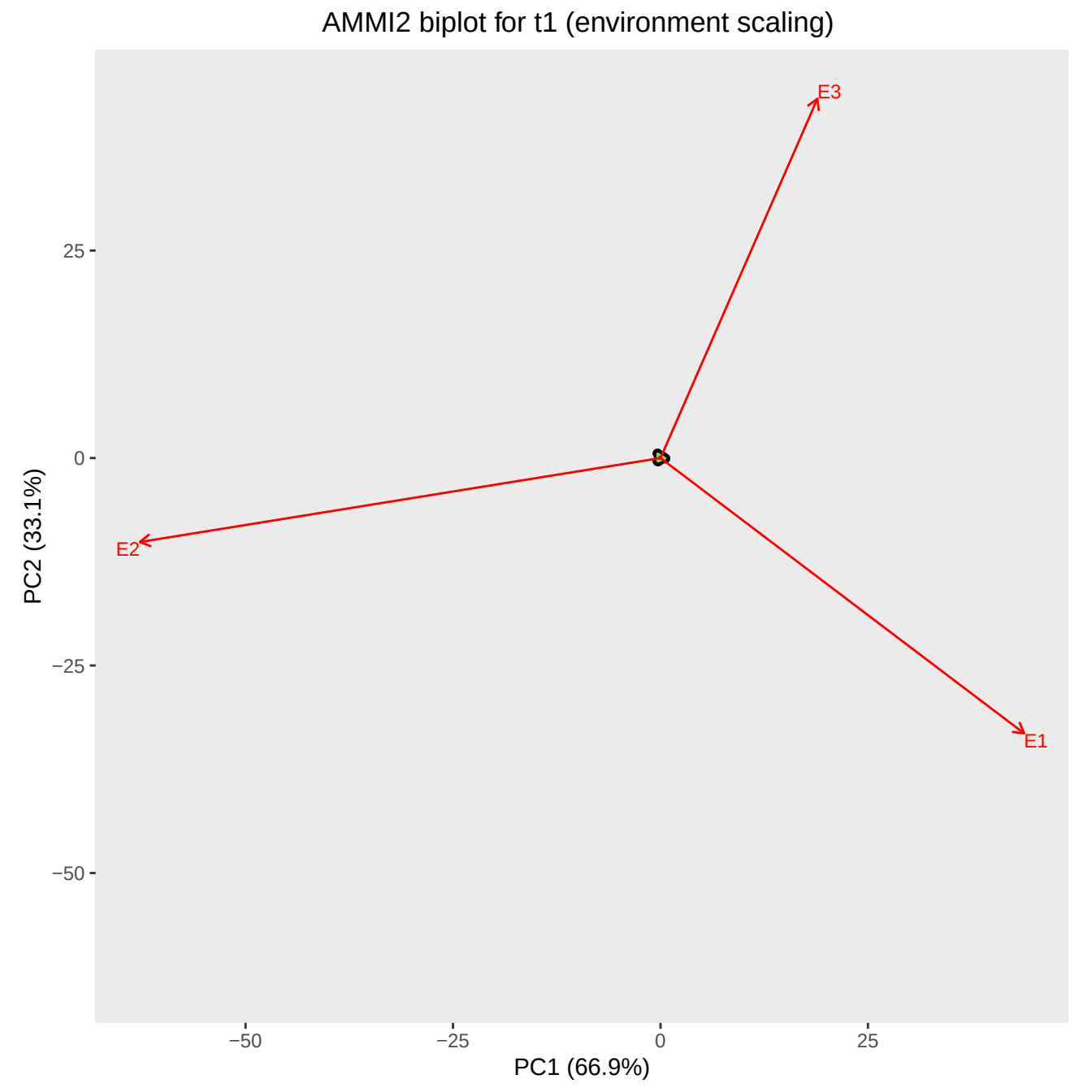

AMMI2 biplot for t1 (environment scaling)
E3
E2
E1
25
0
−25
−50
PC2 (33.1%)
−50
−25
0
25
PC1 (66.9%)
F1
F2
F3

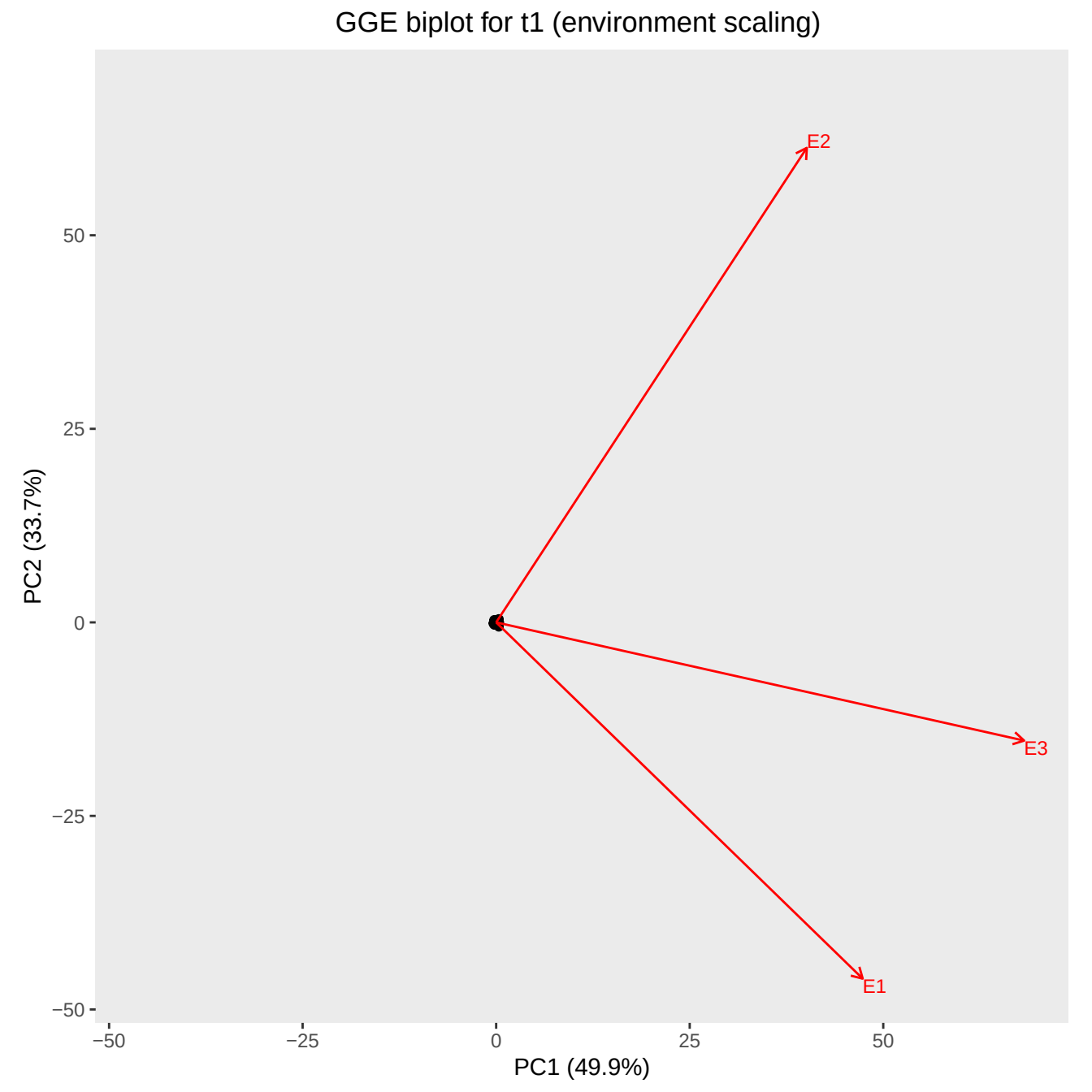

AMMI2 biplot for t1 (environment scaling)
E3
E2
E1
25
0
−25
−50
PC2 (33.1%)
−50
−25
0
25
PC1 (66.9%)
F1
F2
F3

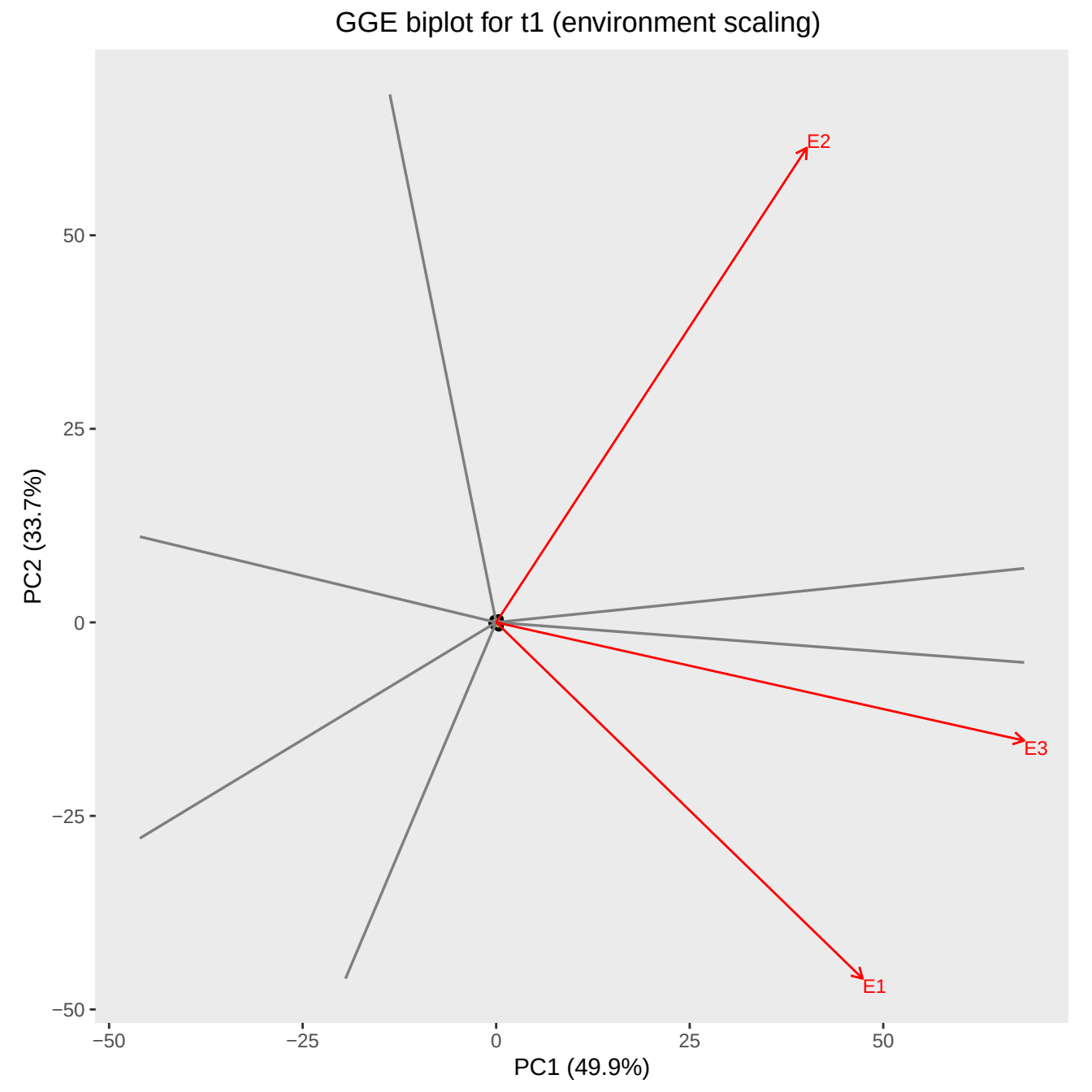

AMMI1 plot for t1
PC1 (66.9%)
Main Effects
100
75
50
25
0
0
25
50
75
100
E1
E3
E2
F1
F2
F3
a
a
a
D
W
a
a

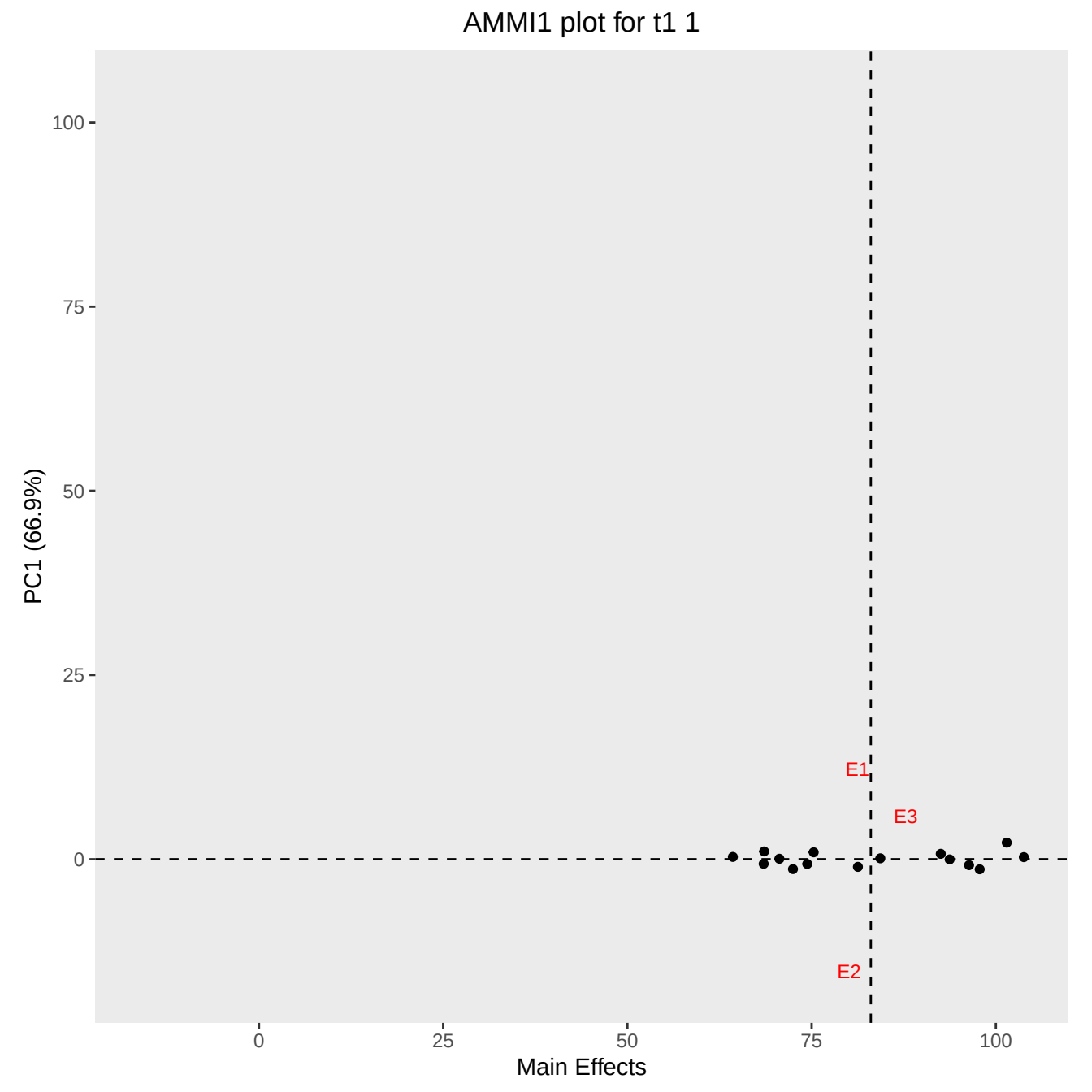

AMMI2 biplot for t1 (environment scaling)
E3
E2
E1
25
0
−25
−50
PC2 (33.1%)
−50
−25
0
25
PC1 (66.9%)
F1
F2
F3
a D
a W

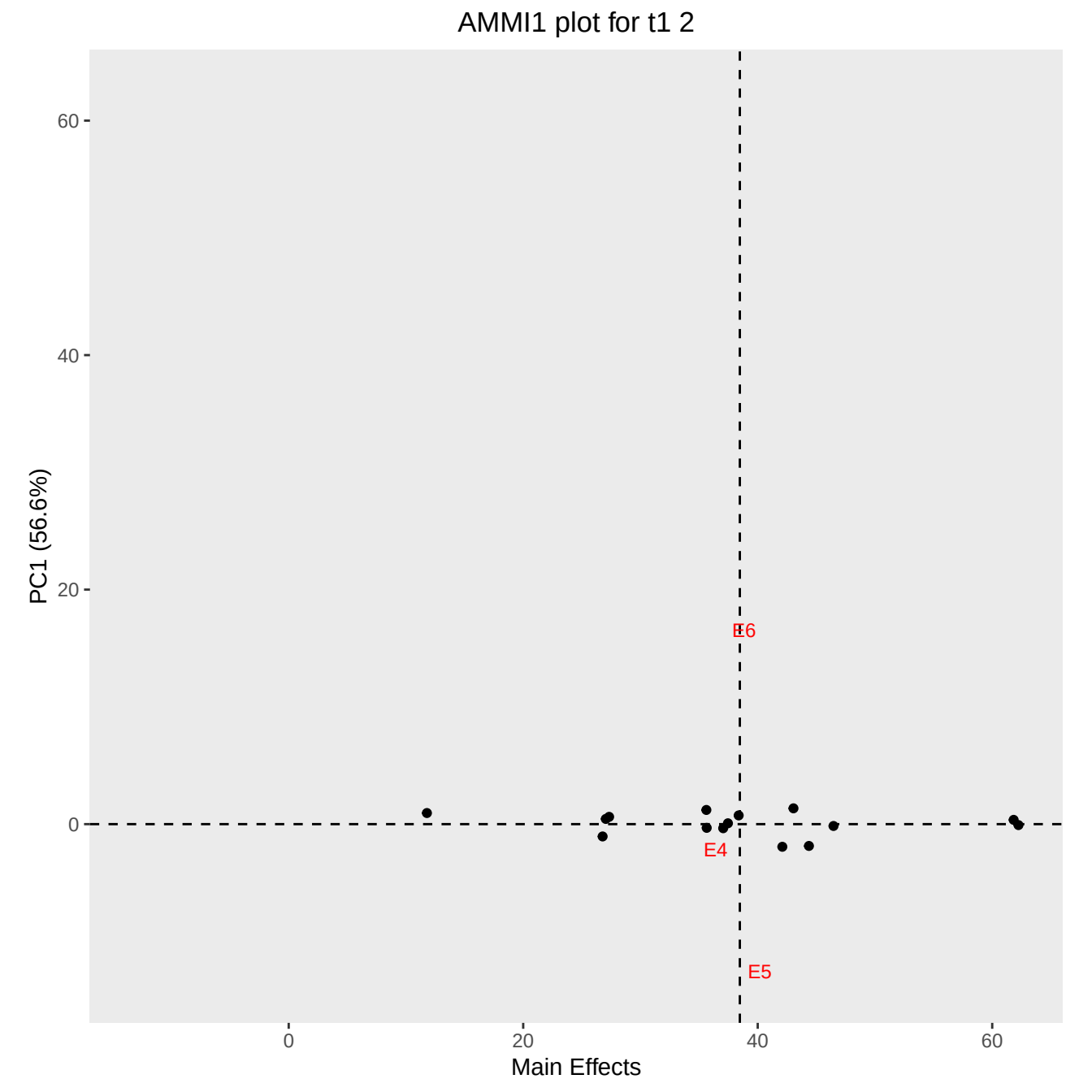

AMMI1 plot for t1
100
75
50
25
0
PC1 (66.9%)
E1
E3
E2
0
25
50
75
100
Main Effects

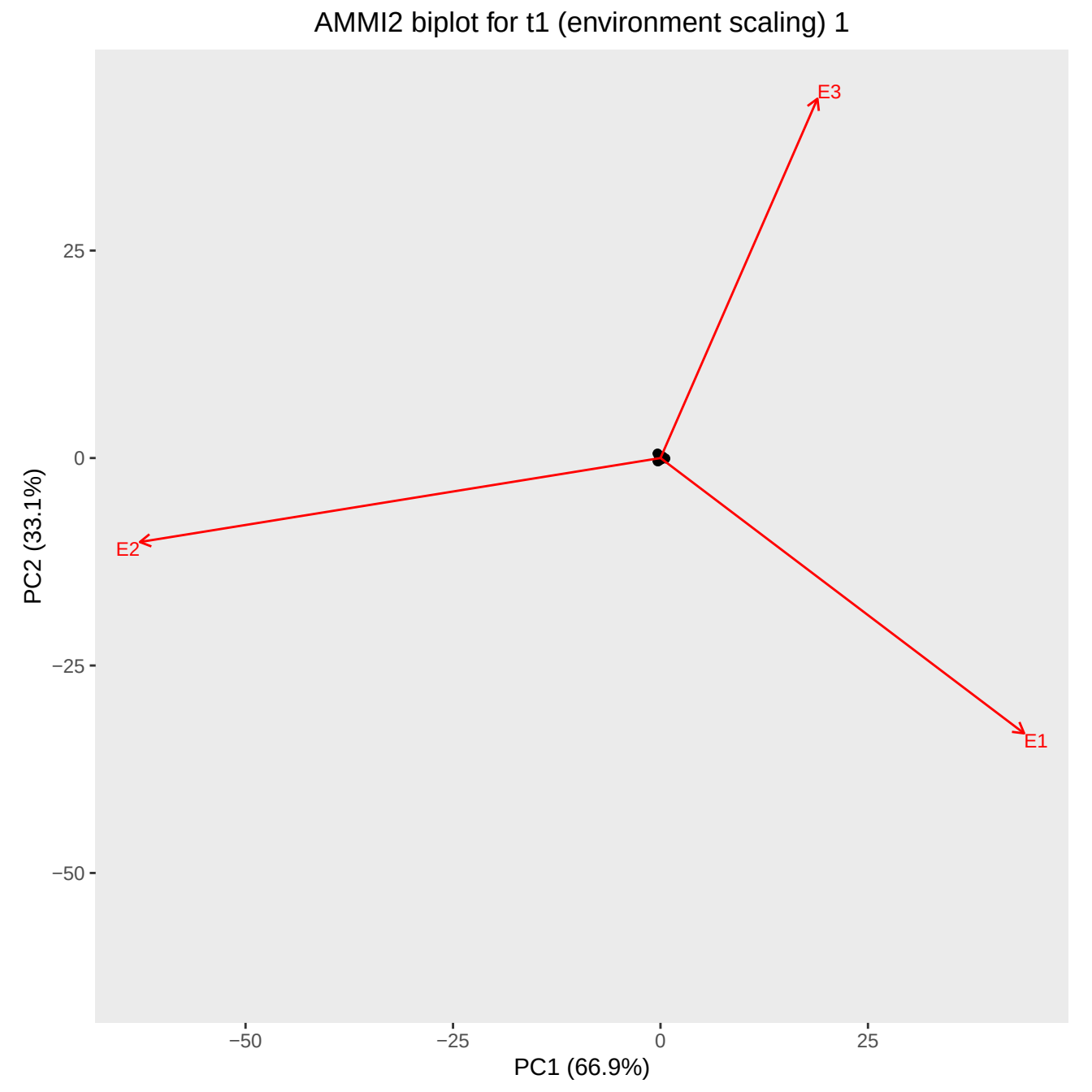

AMMI2 biplot for t1 (environment scaling)
E3
E2
E1
25
0
−25
−50
PC2 (33.1%)
−50
−25
0
25
PC1 (66.9%)

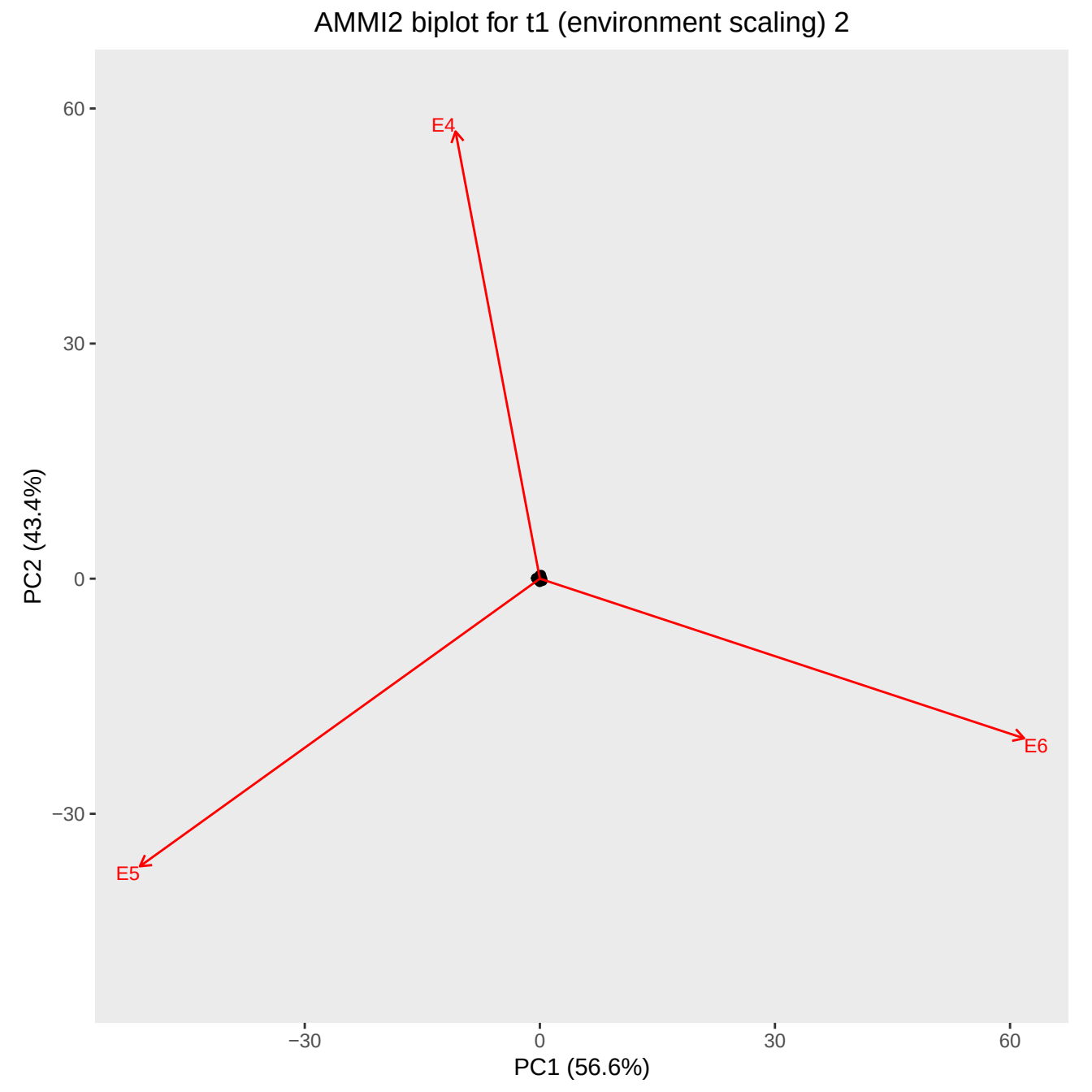

GGE biplot for t1 (environment scaling)
E2
E3
E1
50
25
0
−25
−50
PC2 (33.7%)
−50
−25
0
25
50
PC1 (49.9%)

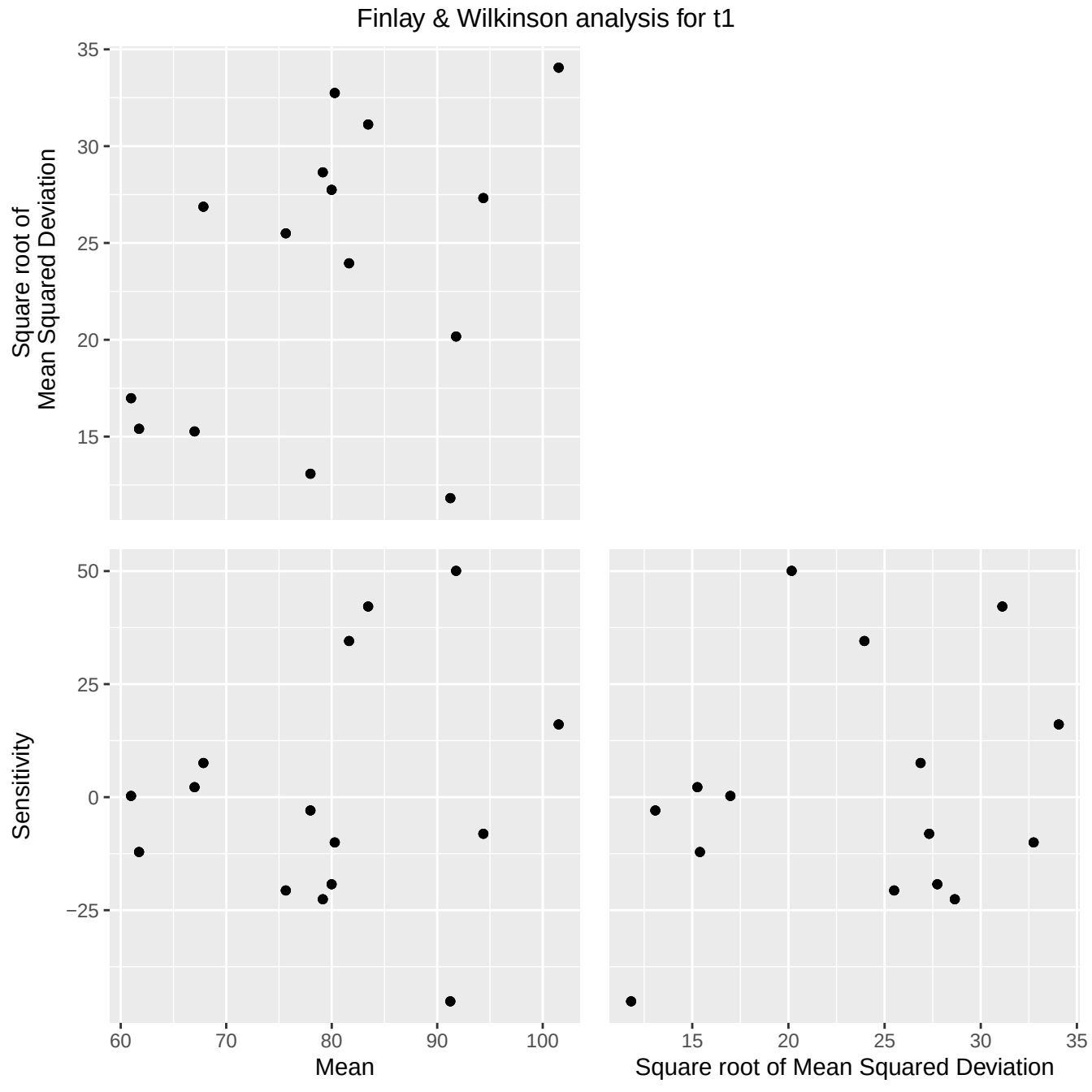

GGE biplot for t1 (environment scaling)
E2
E3
E1
50
25
0
−25
−50
PC2 (33.7%)
−50
−25
0
25
50
PC1 (49.9%)

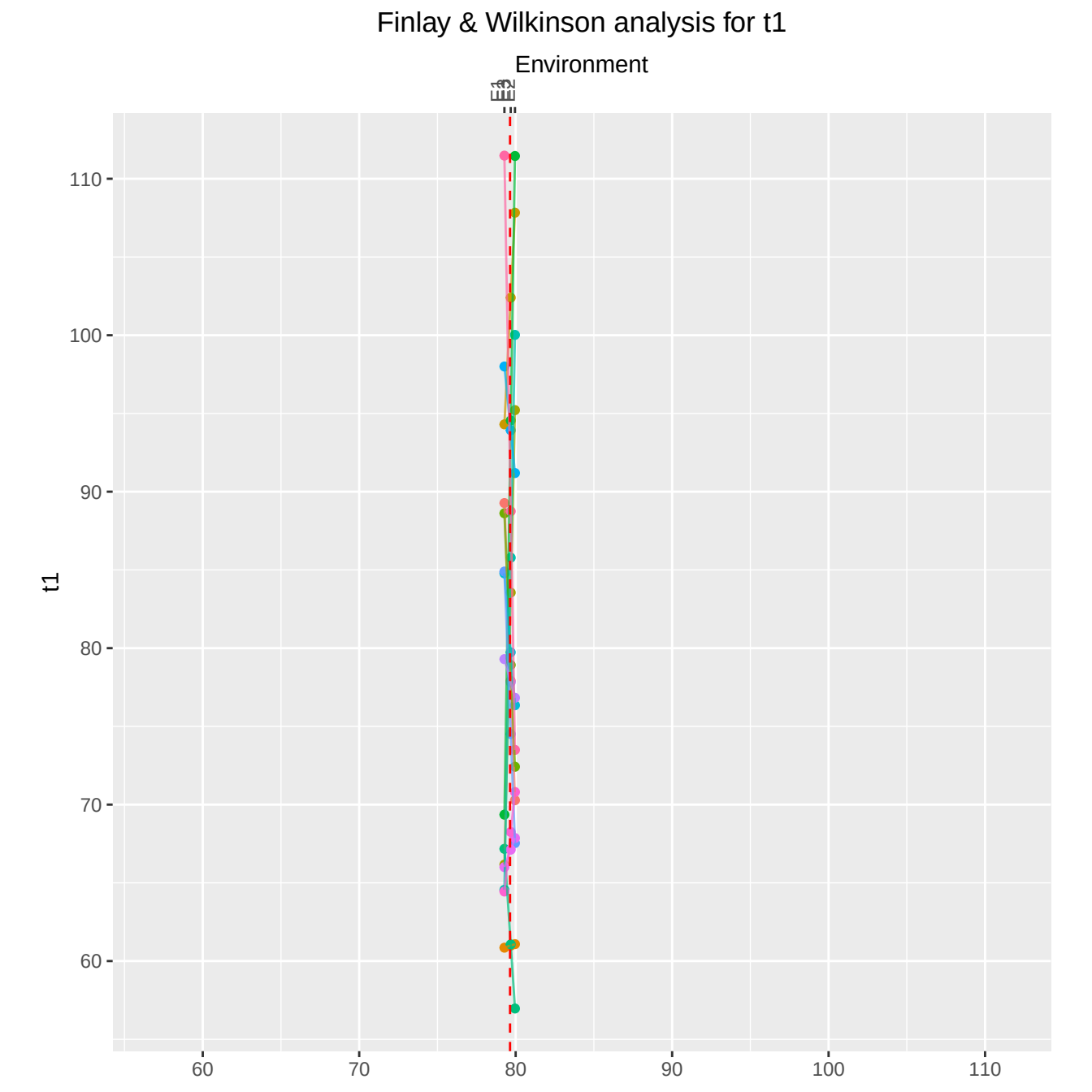

AMMI1 plot for t1 1
PC1 (66.9%)
Main Effects
100
75
50
25
0
0
25
50
75
100
E1
E3
E2

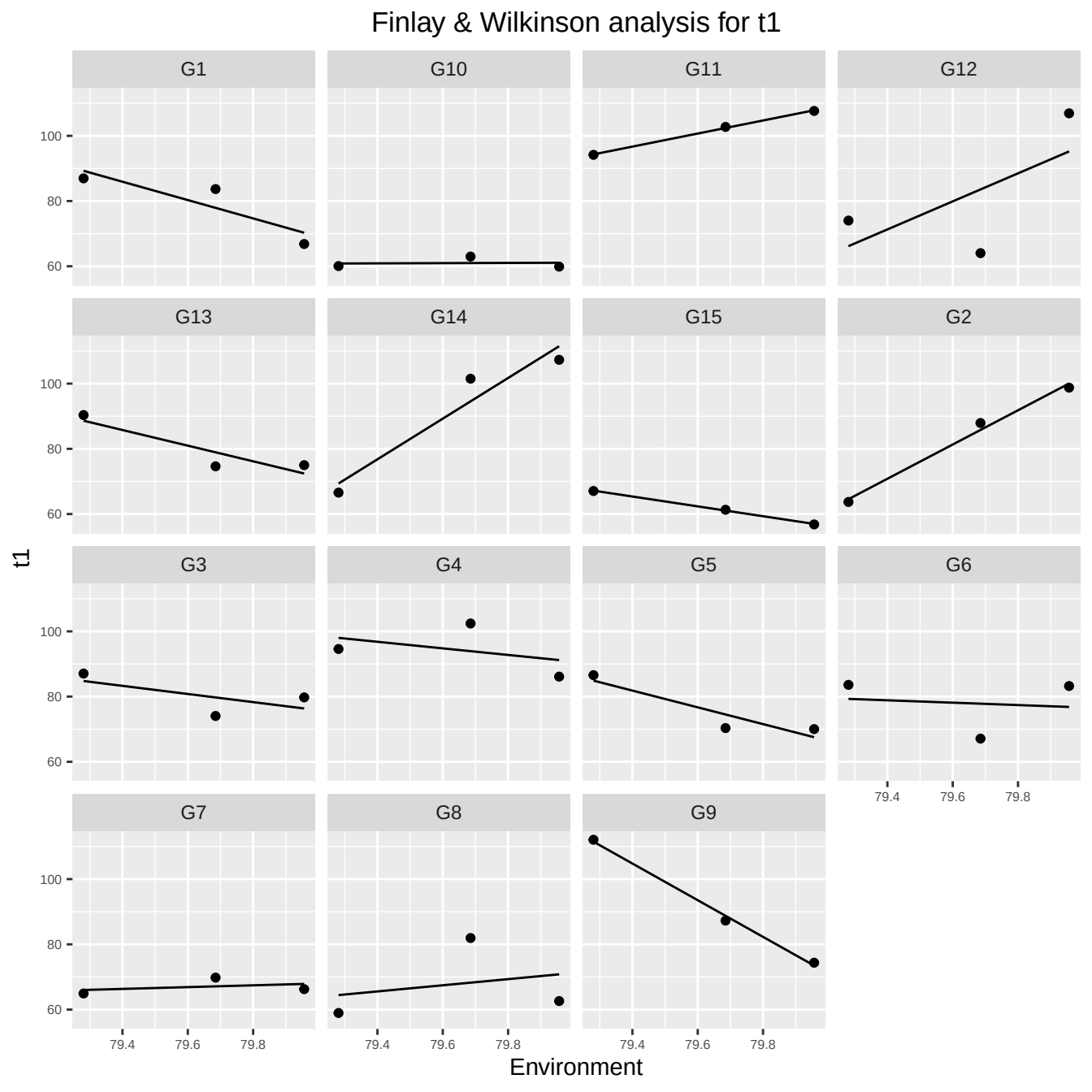

AMMI1 plot for t1 2
60
40
20
0
PC1 (56.6%)
E6
E4
E5
0
20
40
60
Main Effects

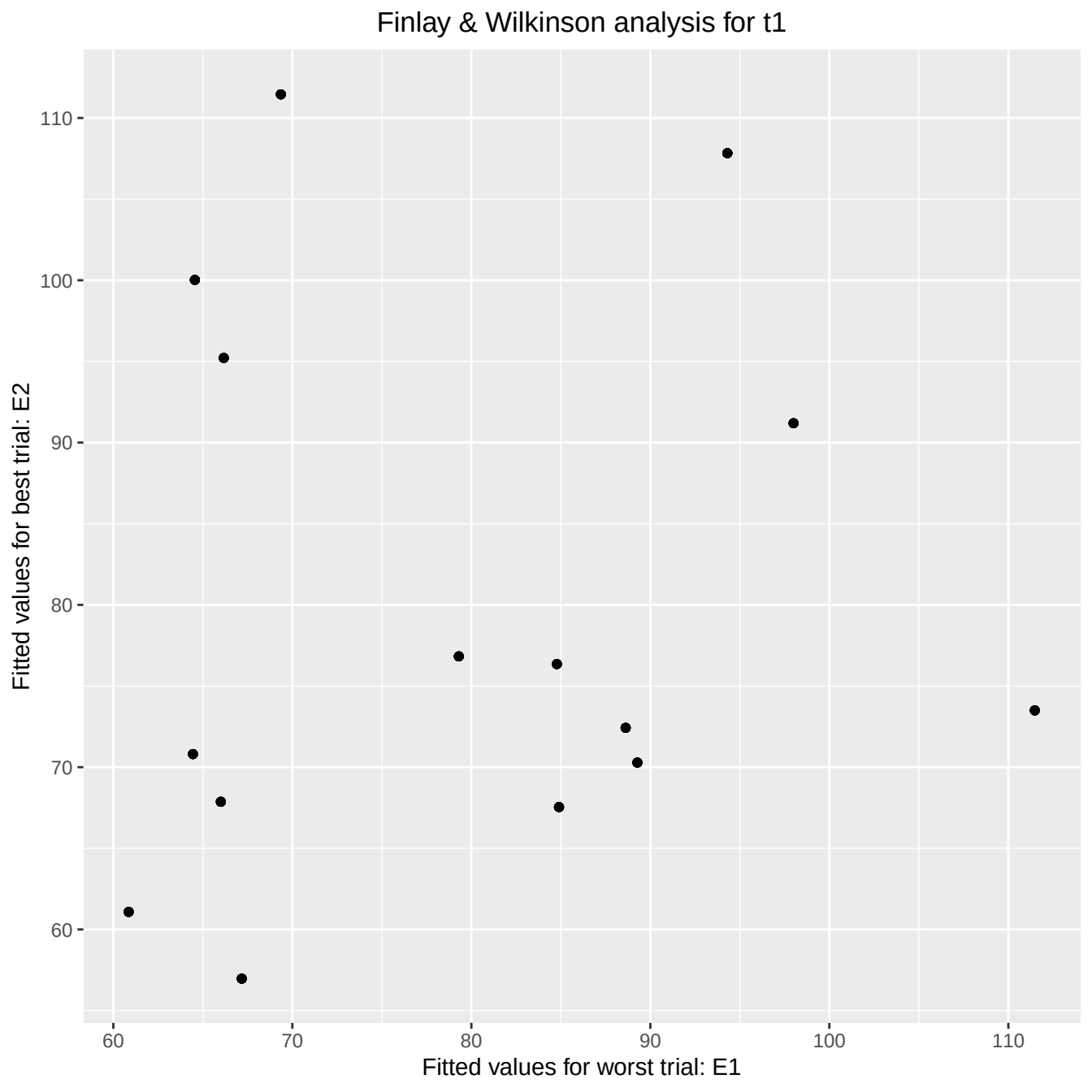

AMMI2 biplot for t1 (environment scaling) 1
E3
E2
E1
25
0
−25
−50
PC2 (33.1%)
−50
−25
0
25
PC1 (66.9%)

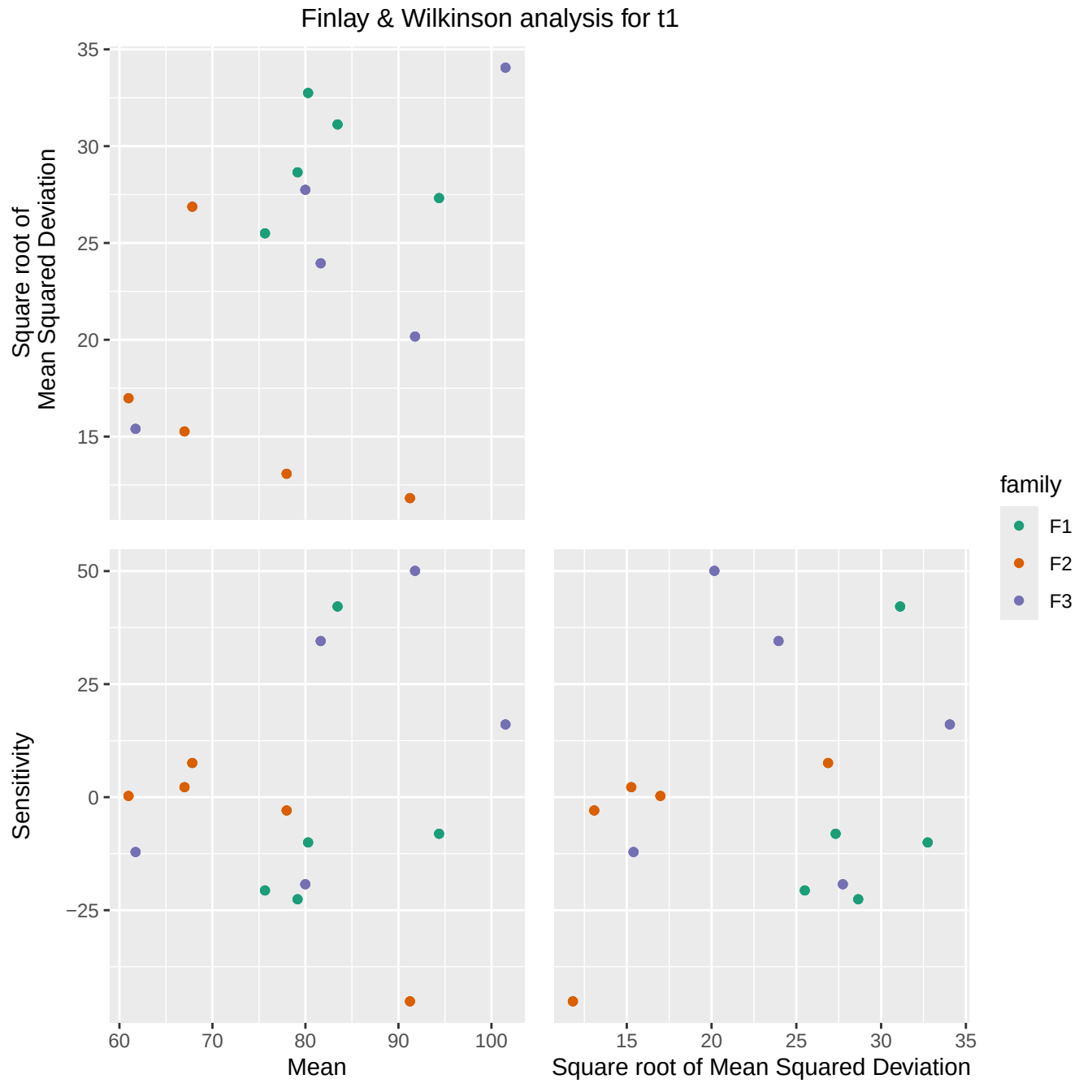

AMMI2 biplot for t1 (environment scaling) 2
E4
E5
E6
60
30
0
−30
PC2 (43.4%)
−30
0
30
60
PC1 (56.6%)

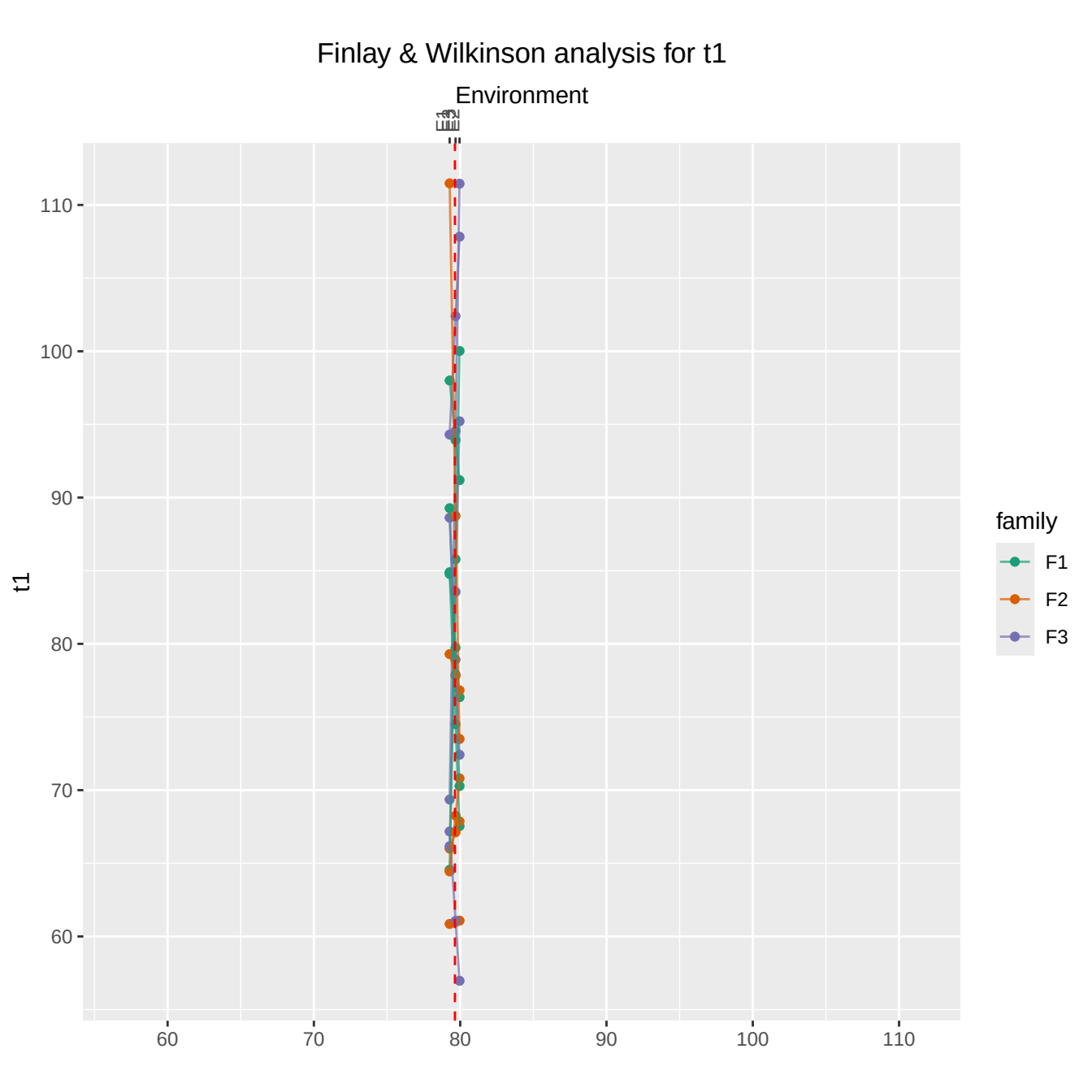

Finlay & Wilkinson analysis for t1
Square root of
Mean Squared Deviation
35
30
25
20
15
Sensitivity
50
25
0
−25
60
70
80
90
100
Mean
15
20
25
30
35
Square root of Mean Squared Deviation

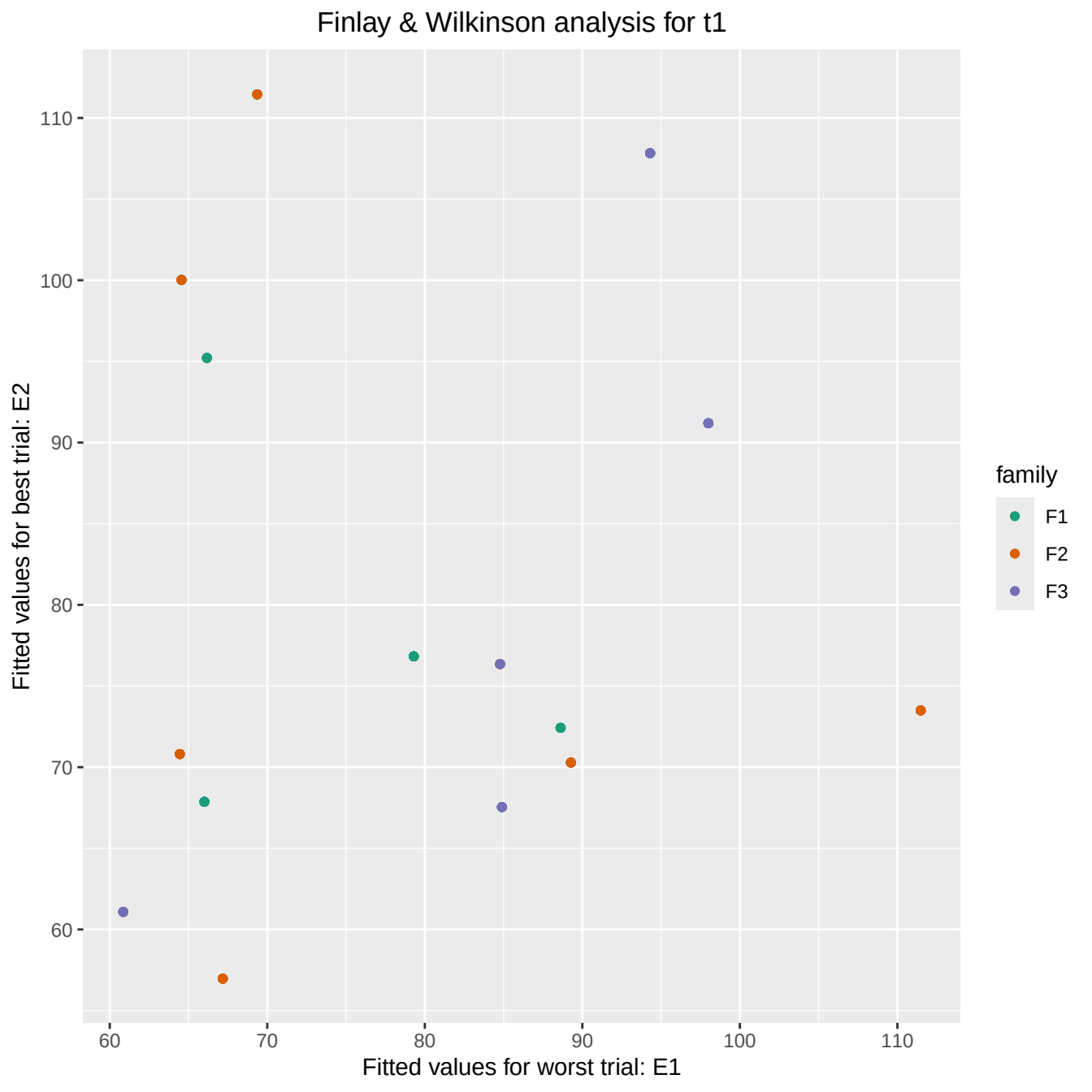

Finlay & Wilkinson analysis for t1
Environment
E1
E2
E3
t1
110
100
90
80
70
60
60
70
80
90
100
110

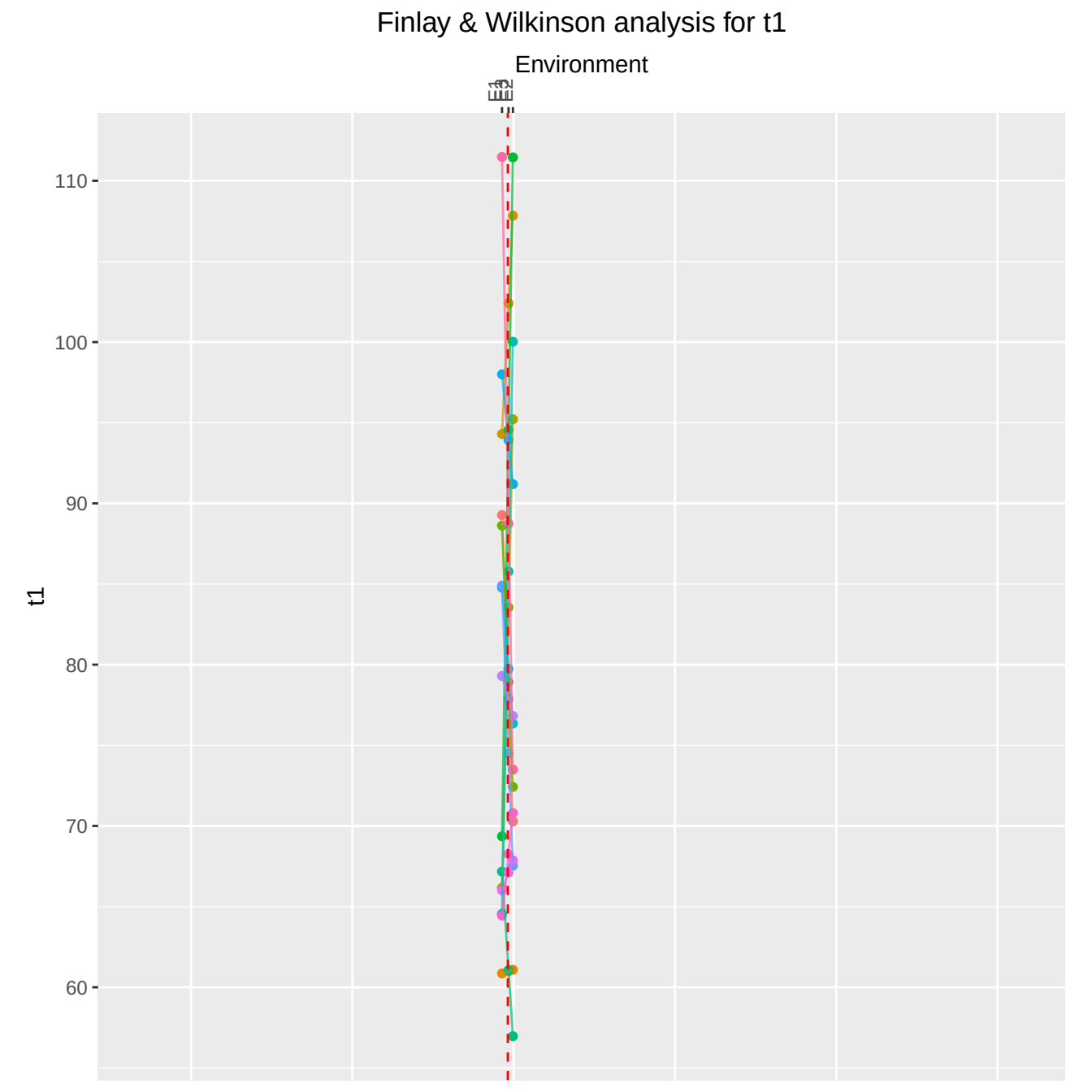

Finlay & Wilkinson analysis for t1
G1
G10
G11
G12
G13
G14
G15
G2
G3
G4
G5
G6
G7
G8
G9
t1
Environment
100
80
60
79.4
79.6
79.8

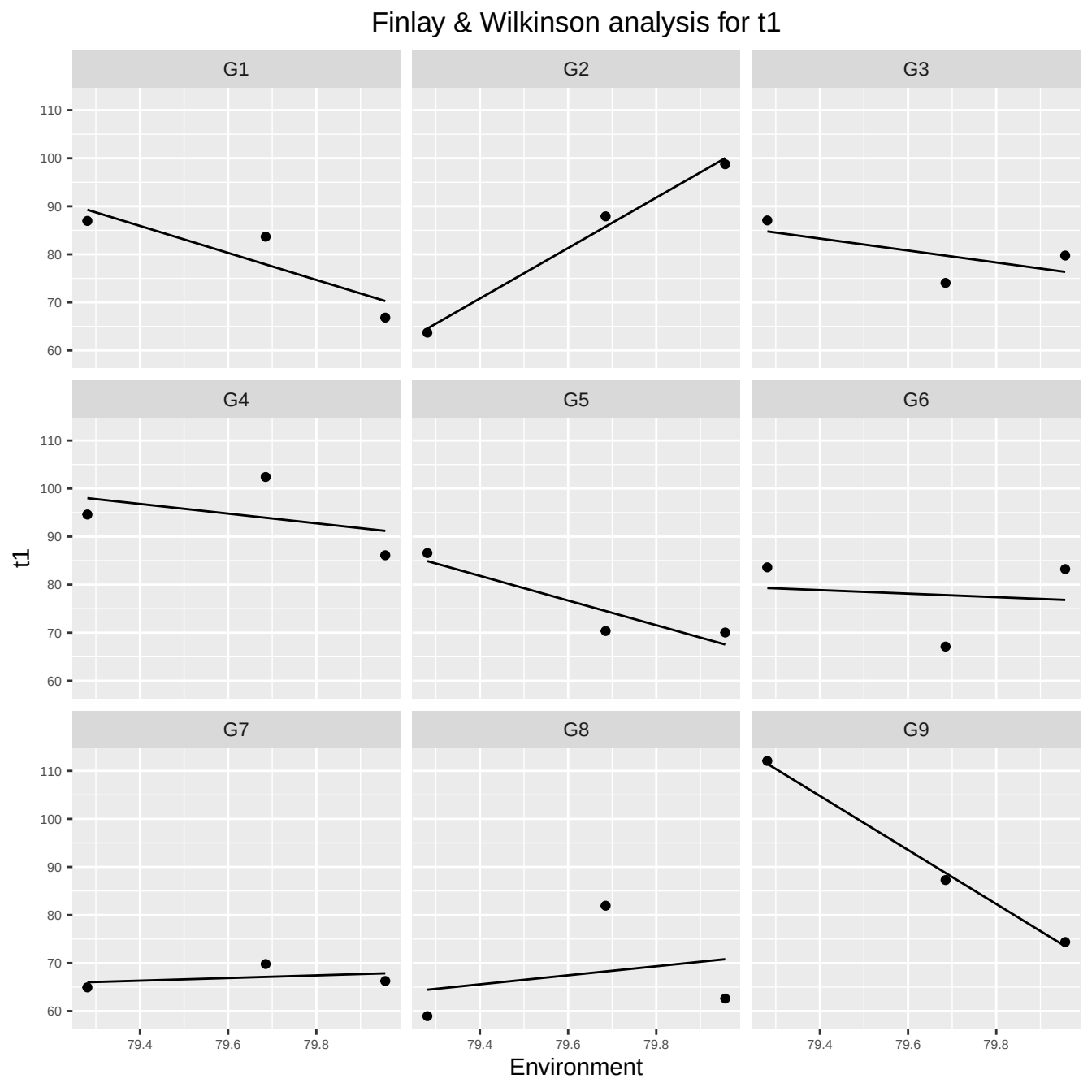

Finlay & Wilkinson analysis for t1
Fitted values for best trial: E2
Fitted values for worst trial: E1
110
100
90
80
70
60
60
70
80
90
100
110


Finlay & Wilkinson analysis for t1
Square root of
Mean Squared Deviation
35
30
25
20
15
Sensitivity
50
25
0
−25
60
70
80
90
100
Mean
15
20
25
30
35
Square root of Mean Squared Deviation
family
F1
F2
F3

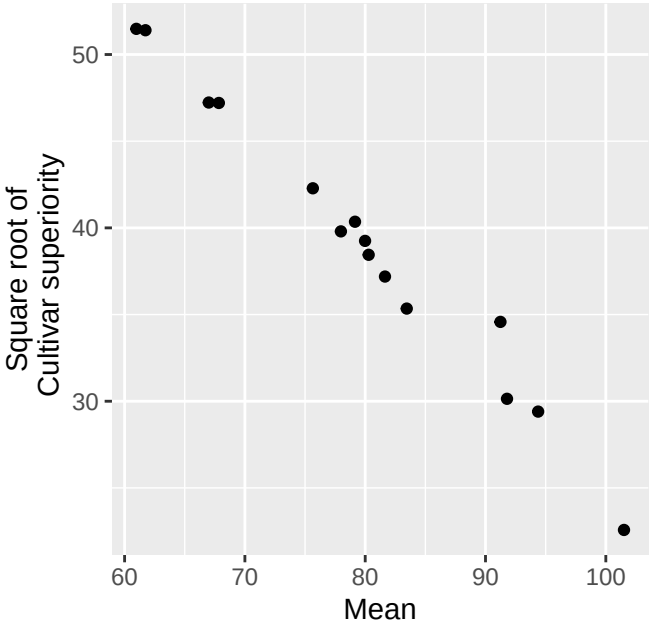

Finlay & Wilkinson analysis for t1
Environment
E1
E2
E3
t1
110
100
90
80
70
60
60
70
80
90
100
110
family
F1
F2
F3

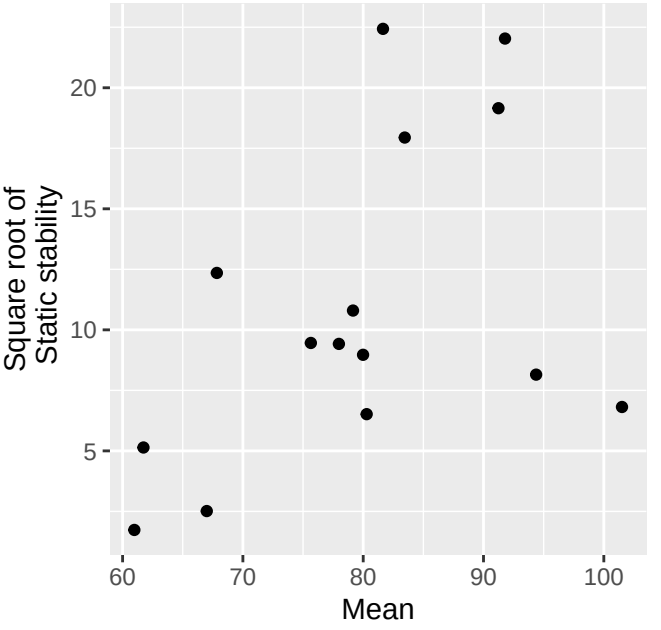

Finlay & Wilkinson analysis for t1
Fitted values for best trial: E2
Fitted values for worst trial: E1
110
100
90
80
70
60
60
70
80
90
100
110
family
F1
F2
F3

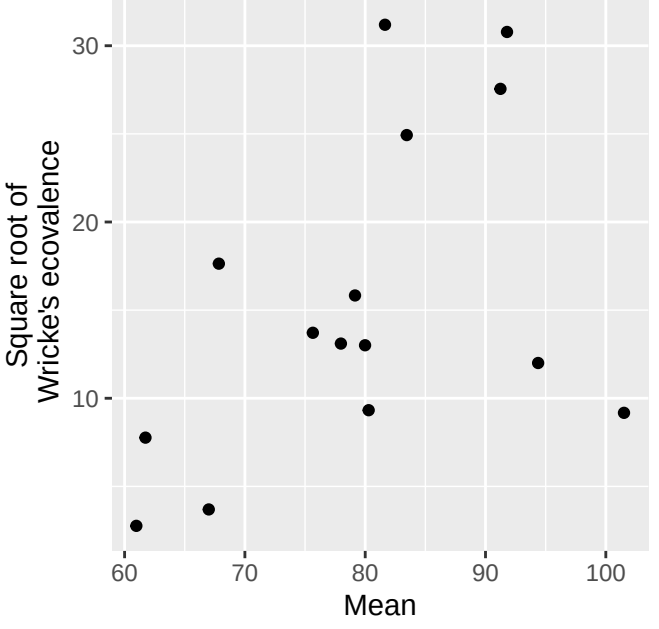

Finlay & Wilkinson analysis for t1
Environment
E1
E2
E3
t1
110
100
90
80
70
60

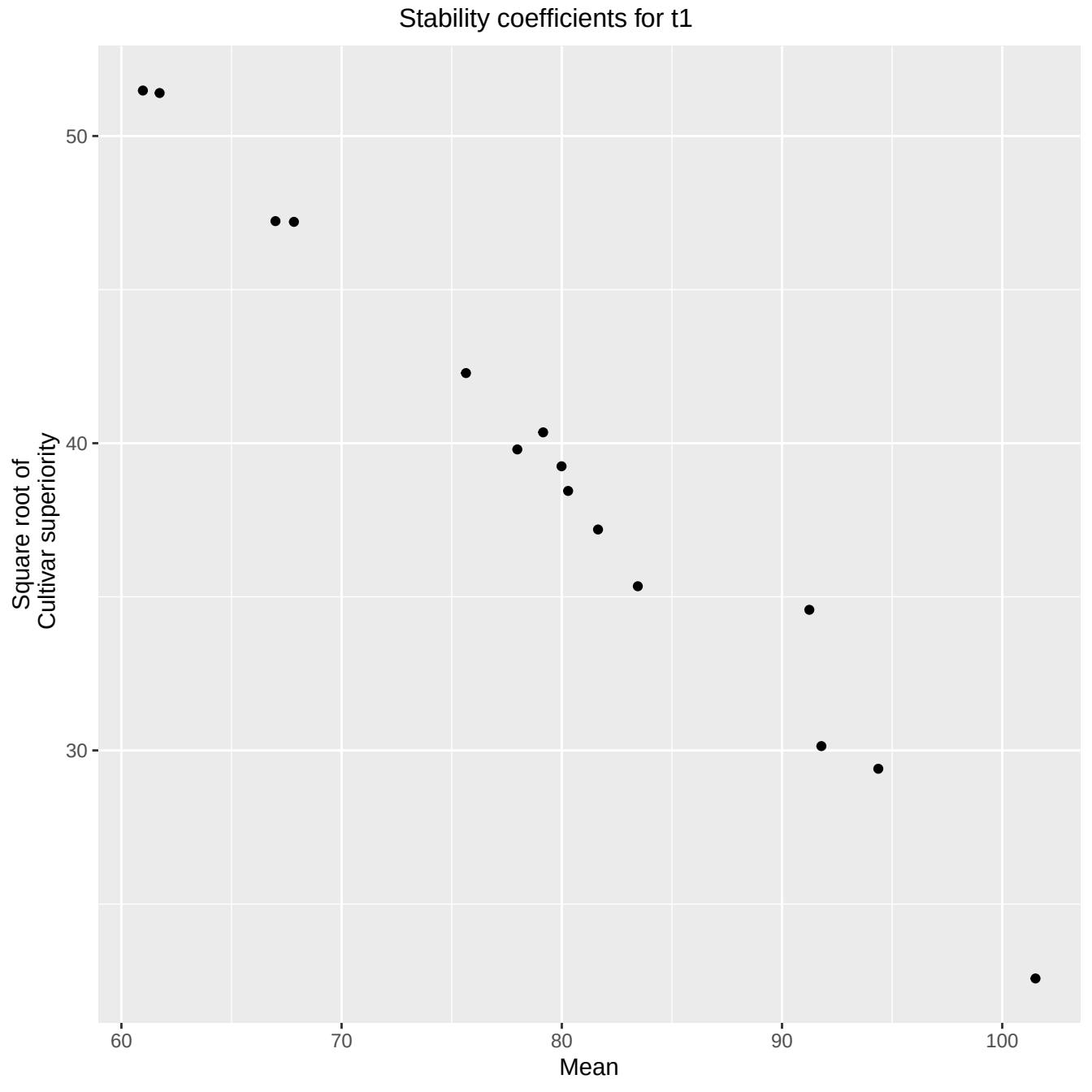

Finlay & Wilkinson analysis for t1
G1
G2
G3
G4
G5
G6
G7
G8
G9
t1
Environment
110
100
90
80
70
60
79.4
79.6
79.8

Stability coefficients for t1

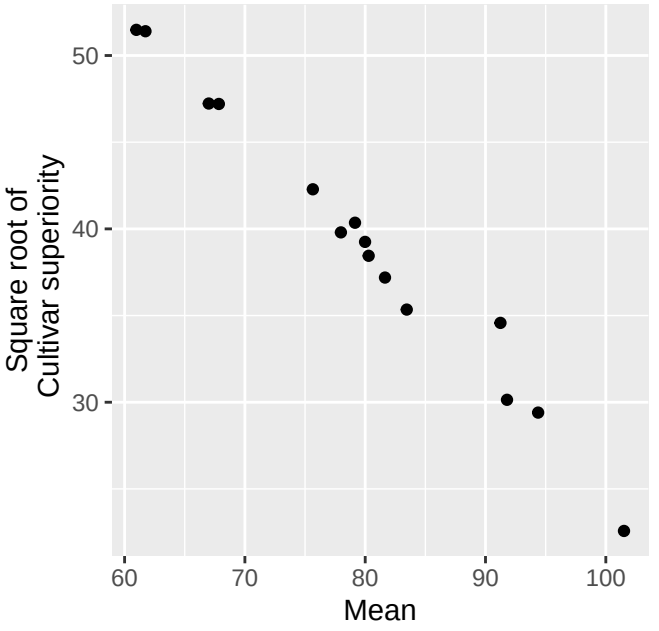


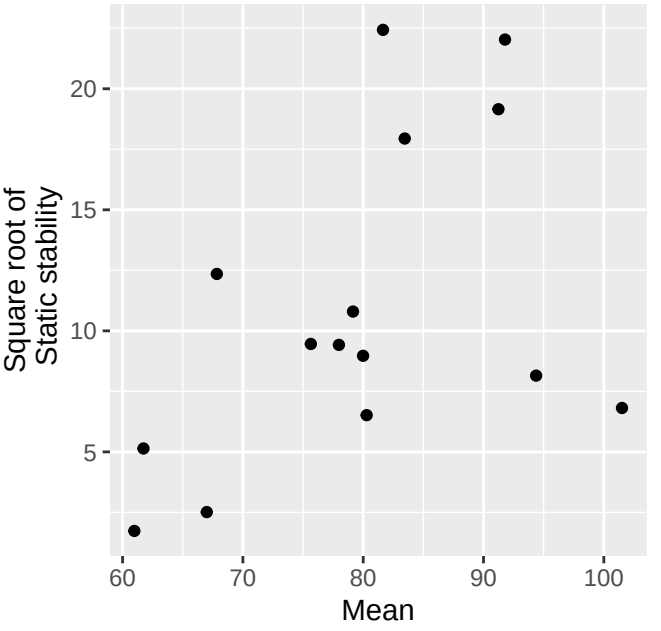


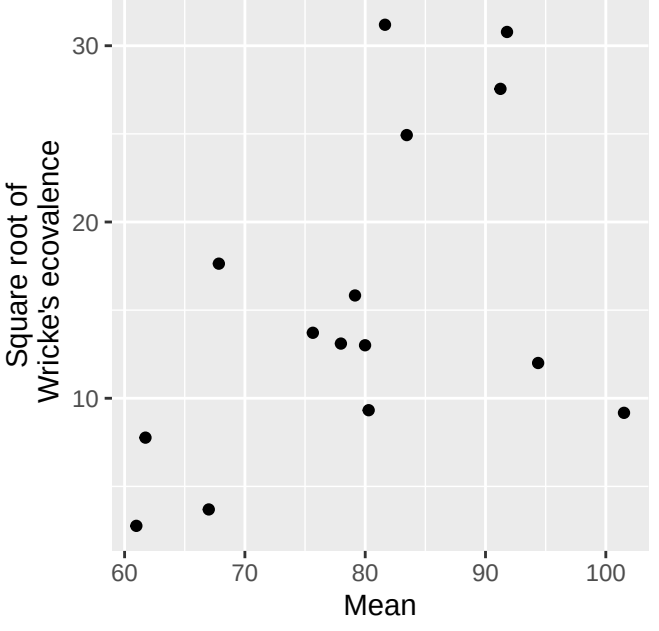



Stability coefficients for t1
Square root of
Cultivar superiority
50
40
30
60
70
80
90
100
Mean

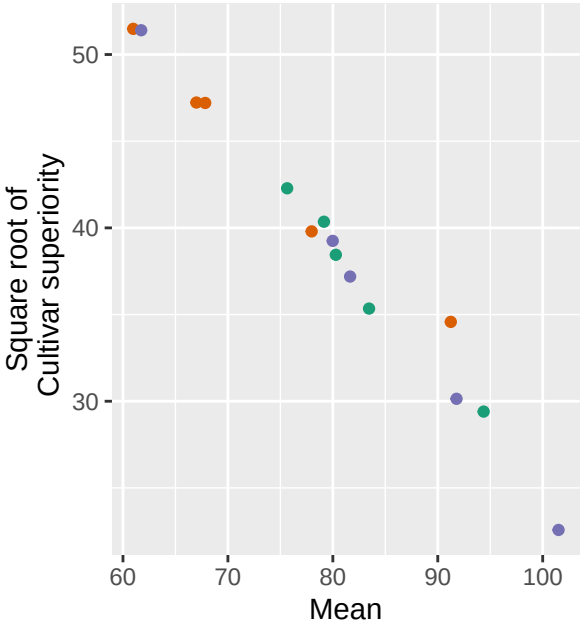
Test

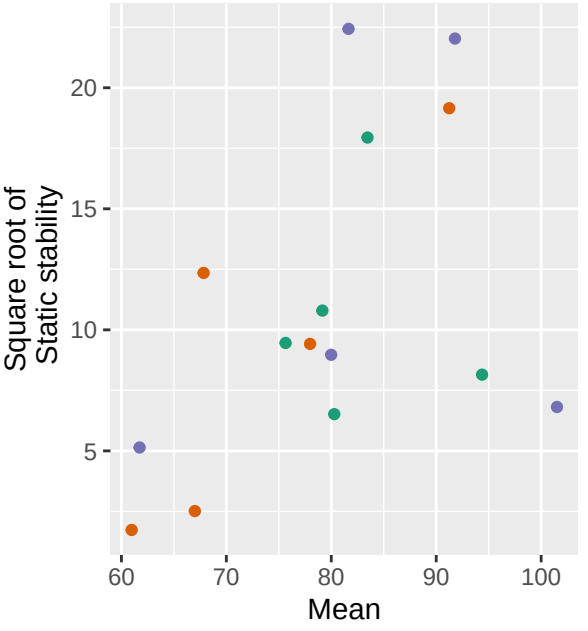

Square root of Cultivar superiority
50
40
30
60
70
80
90
100
Mean

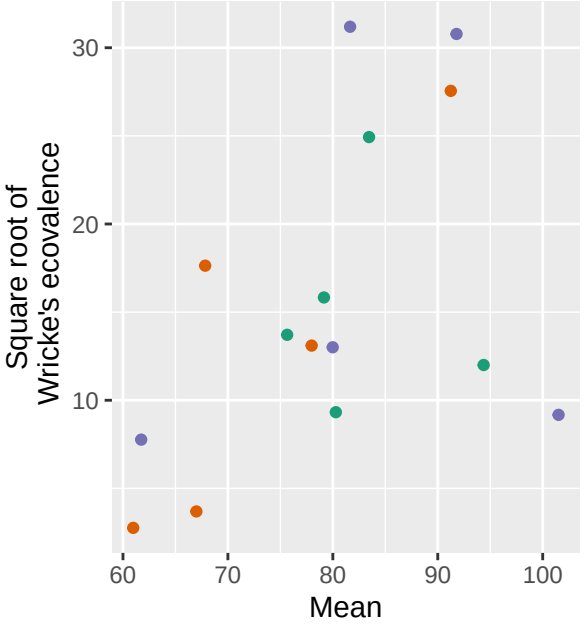

Square root of Static stability
20
15
10
5
60
70
80
90
100
Mean

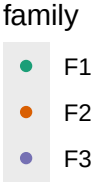

Square root of Wricke's ecovalence
30
20
10
60
70
80
90
100
Mean

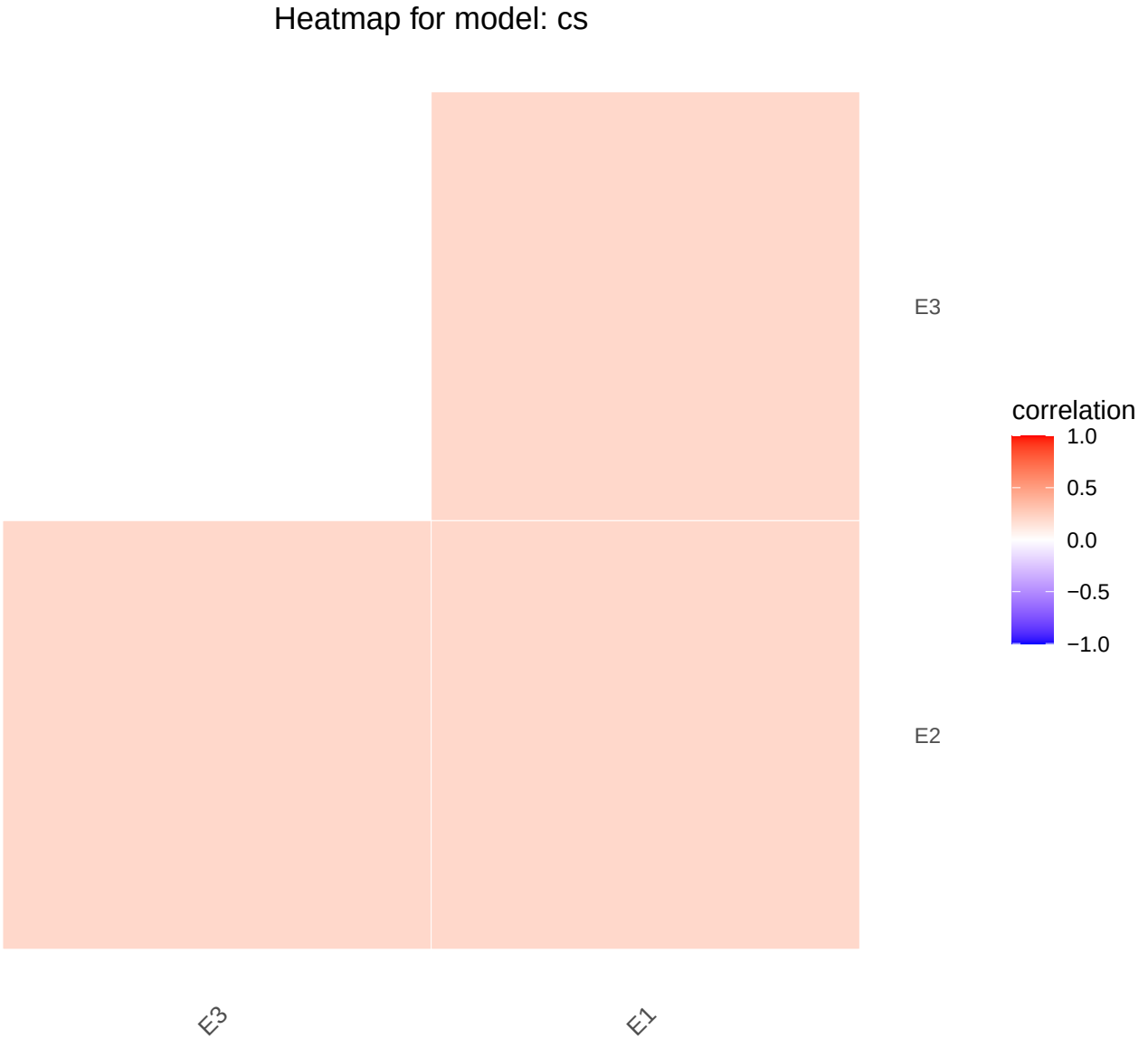
Stability coefficients for t1

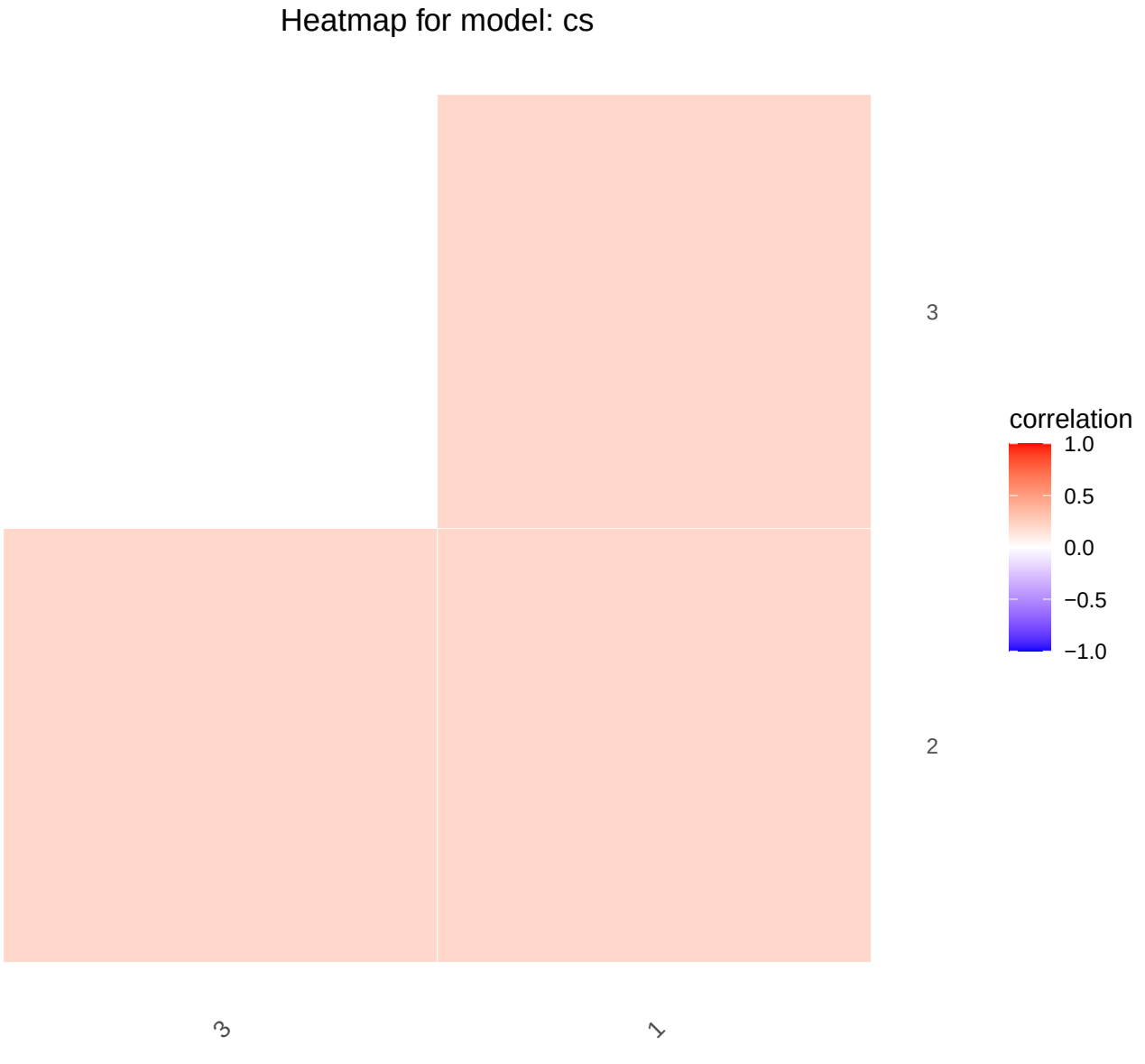


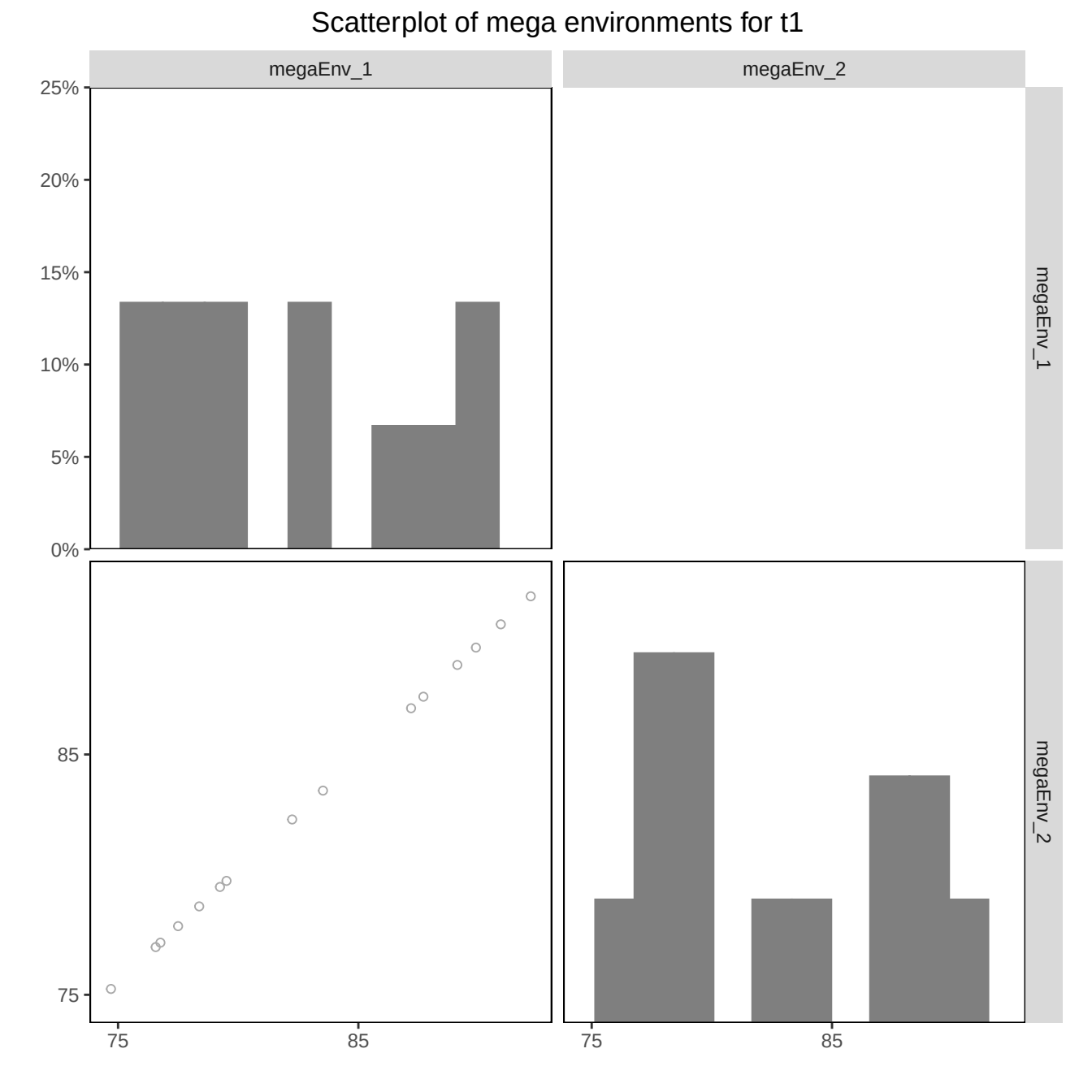


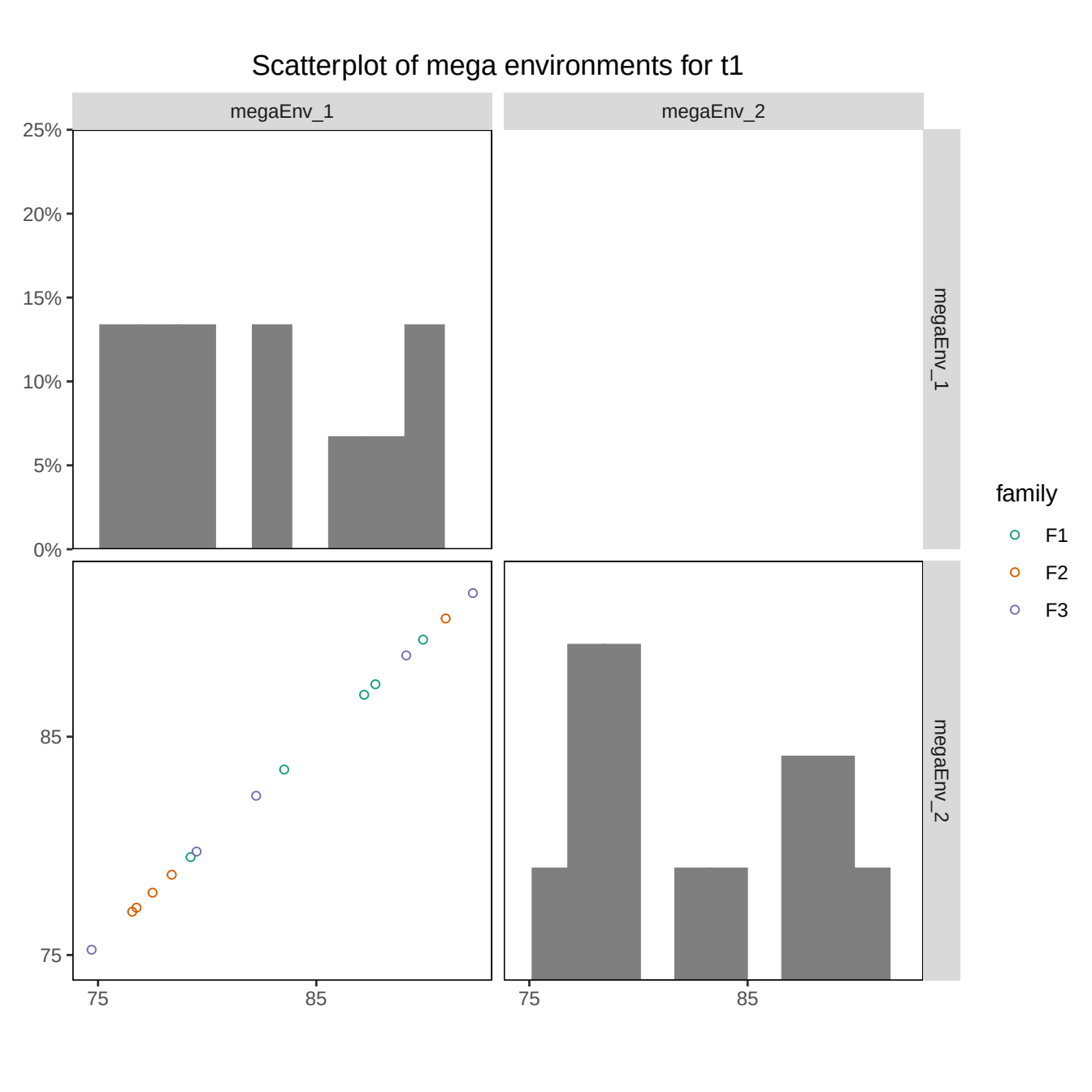


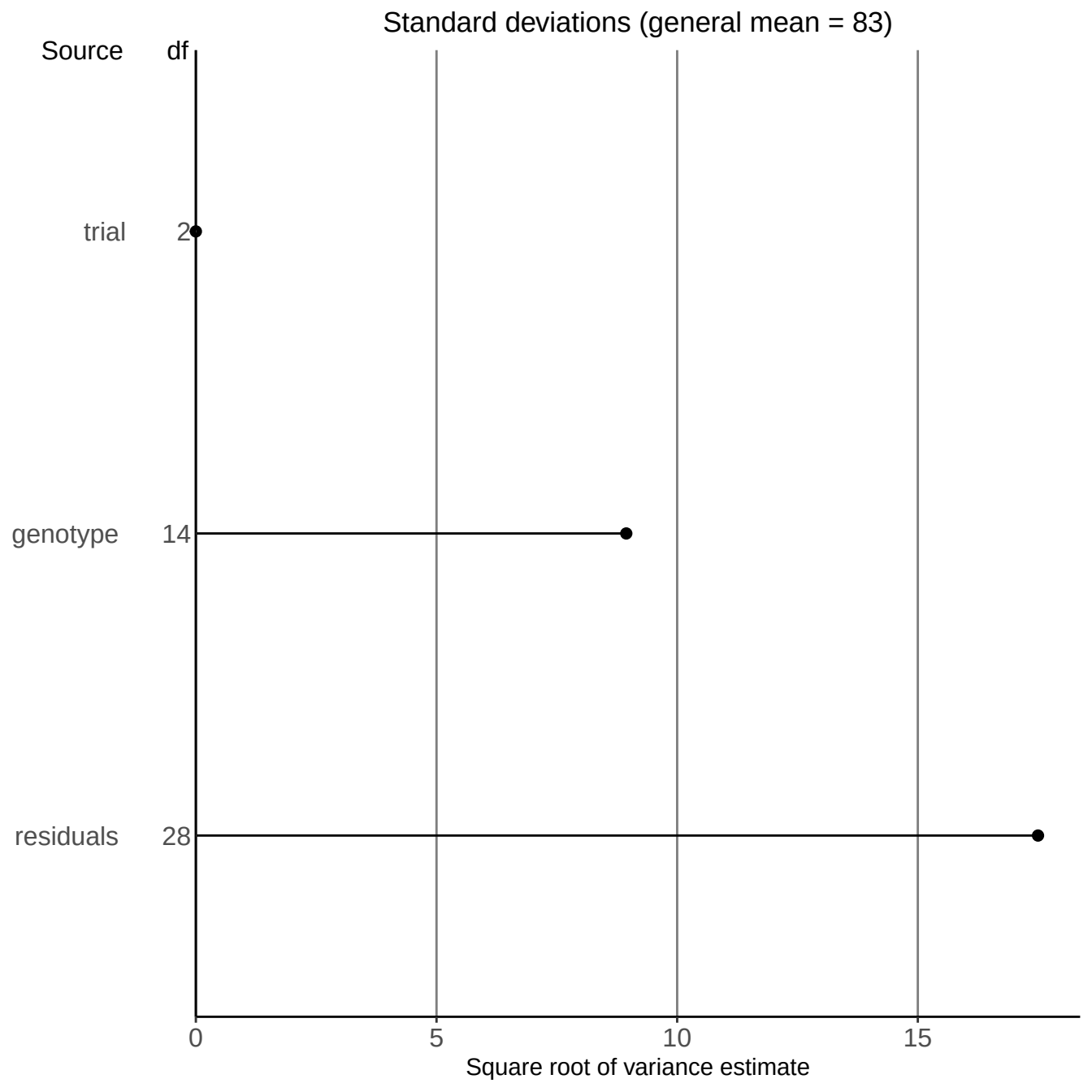


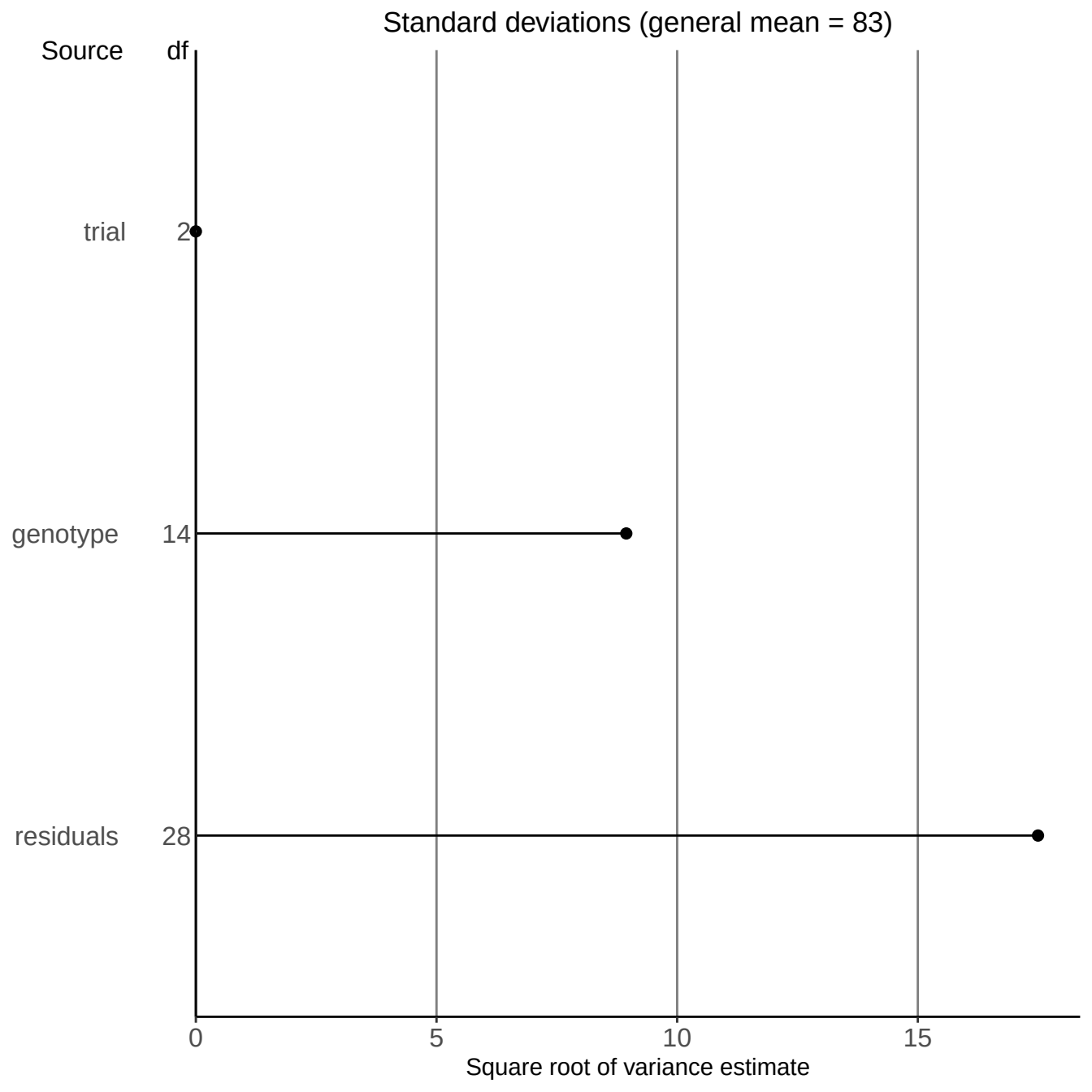

Heatmap for model: cs
E3
E2
correlation
1.0
0.5
0.0
−0.5
−1.0
E3
E1

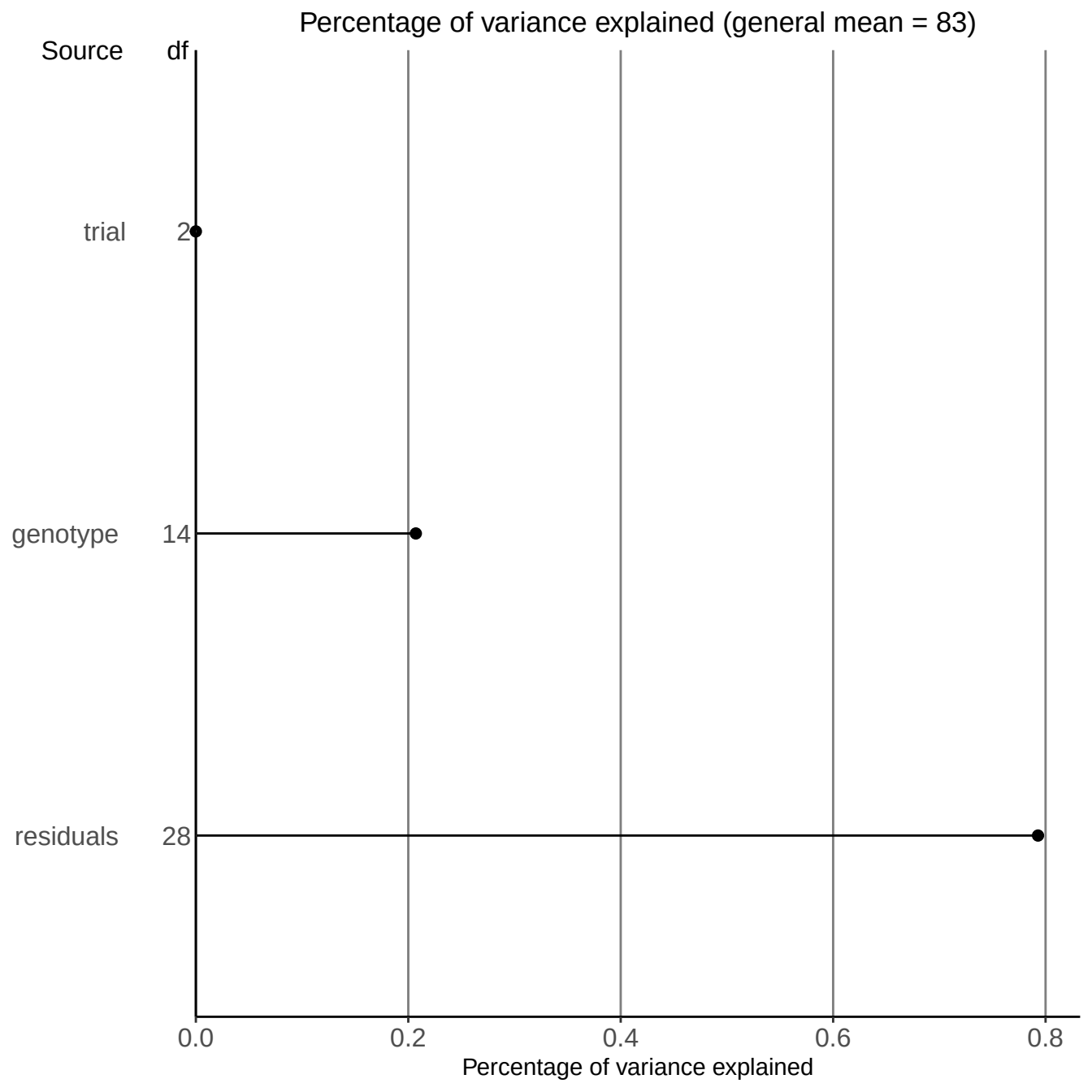

Heatmap for model: cs
3
2
3
1
correlation
1.0
0.5
0.0
−0.5
−1.0


Scatterplot of mega environments for t1
megaEnv_1
megaEnv_2
megaEnv_1
megaEnv_2
25%
20%
15%
10%
5%
0%
85
75
75
85
75
85


Scatterplot of mega environments for t1
megaEnv_1
megaEnv_2
megaEnv_1
megaEnv_2
25%
20%
15%
10%
5%
0%
85
75
75
85
75
85
family
F1
F2
F3


Standard deviations (general mean = 83)
Source
df
trial
2
genotype
14
residuals
28
0
5
10
15
Square root of variance estimate


Standard deviations (general mean = 83)
Source
df
trial
2
genotype
14
residuals
28
0
5
10
15
Square root of variance estimate


Percentage of variance explained (general mean = 83)
Source
df
trial
2
genotype
14
residuals
28
0.0
0.2
0.4
0.6
0.8
Percentage of variance explained