*Extended mixed model for association mapping with growth response curve*

Recall that the salt stress induced growth response is measured as the square root transformed ratio of the projected shoot area (PSA) of plants under salt stress over that of plants under normal growth situations. For each single SNP, the mean response curve of a specific genotype *k* (1or 2 for the two alleles) is modeled as a decreasing logistic function:

$$f_k(t) = \gamma + \frac{(1+\beta_k)(1-\gamma_k)}{1+\beta_k e^{\alpha_k t}}$$

where *t* is the time, α, β and γ are regression coefficients. Note that this function is nonincreasing, it is 1 at time zero, and it will flatten out as time becomes really long. These are reasonable assumptions for the salt response curve as all plants are under normal growing conditions at time zero, the salt stress has a detrimental effect on the growth on average, and growth will slow for all plants near the end of the growing period.

The growth response for line *i* with genotype *k* at time *t* (day 0 to day 17) is then designated as

$$y_{it} = f_k(t) + \varepsilon_{it}.$$

Here $\varepsilon_{it}$ is the error term that incorporates the correlation structure both through time and between lines (kinship). Let $\varepsilon_i = (\varepsilon_{i0}, ..., \varepsilon_{i17})$ be the vector of responses for line *i*, then

$$Cor(\varepsilon_i) = \begin{bmatrix} 1 & \rho & ... & \rho^{17} \\ \rho & 1 & ... & \rho^{16} \\ ... & ... & ... & ... \\ \rho^{16} & \rho^{15} & ... & 1 \end{bmatrix}.$$

Thus, for a single line, the model reduces to a nonlinear mixed model with a first order auto regressive covariance structure. On the other hand, let $\varepsilon_t = (\varepsilon_{1t}, ..., \varepsilon_{360t})$ be the vector of the response of all lines at time *t*, we have

$$Cov(\varepsilon_t) = \sigma_g^2 K + \sigma_e^2 I$$

where *K* is the kinship matrix between lines, *I* is a 360 by 360 identity matrix, $\sigma_g^2$ is the genotype variance component, and $\sigma_e^2$ is the error variance component. Thus, considering a single time point, we have exactly the same model used by other researchers in plant association mapping studies.

To consider correlation both across time and across lines, let

$$\varepsilon = vec([\varepsilon_{it}])$$

where the vec operator stacks columns of a matrix into a single vector. We assume that the covariance matrix

$$\Sigma = Cov(\varepsilon) = Cov(\varepsilon_t) \otimes Cor(\varepsilon_i)$$

with $\otimes$ being the kronecker product. Further, we assume that the response $y_{it}$ has a normal distribution with the mean defined by the function $f_k(t)$ and the variance matrix given by $\Sigma$. As a result, the likelihood ratio test on whether $f_k(t)$ is the same for $k$=1,2 can be carried out as usual with the likelihood defined by the normal distribution.

*Statistical analysis of phenotypic data*

Data derived from fluorescence and RGB/VIS images were combined across experiments, and a linear model was fit to calculate the adjusted means for each individual accession using the `'lsmeans'` function in the LSMeans package in R (R Core Team, 2014; Lenth and Hervé, 2015). The linear model included experiment and treatment as fixed effects, and accession as a random effect. The adjusted means were used for phenotypic analysis and GWA of fluorescence traits, as well as phenotypic analysis of PSA.

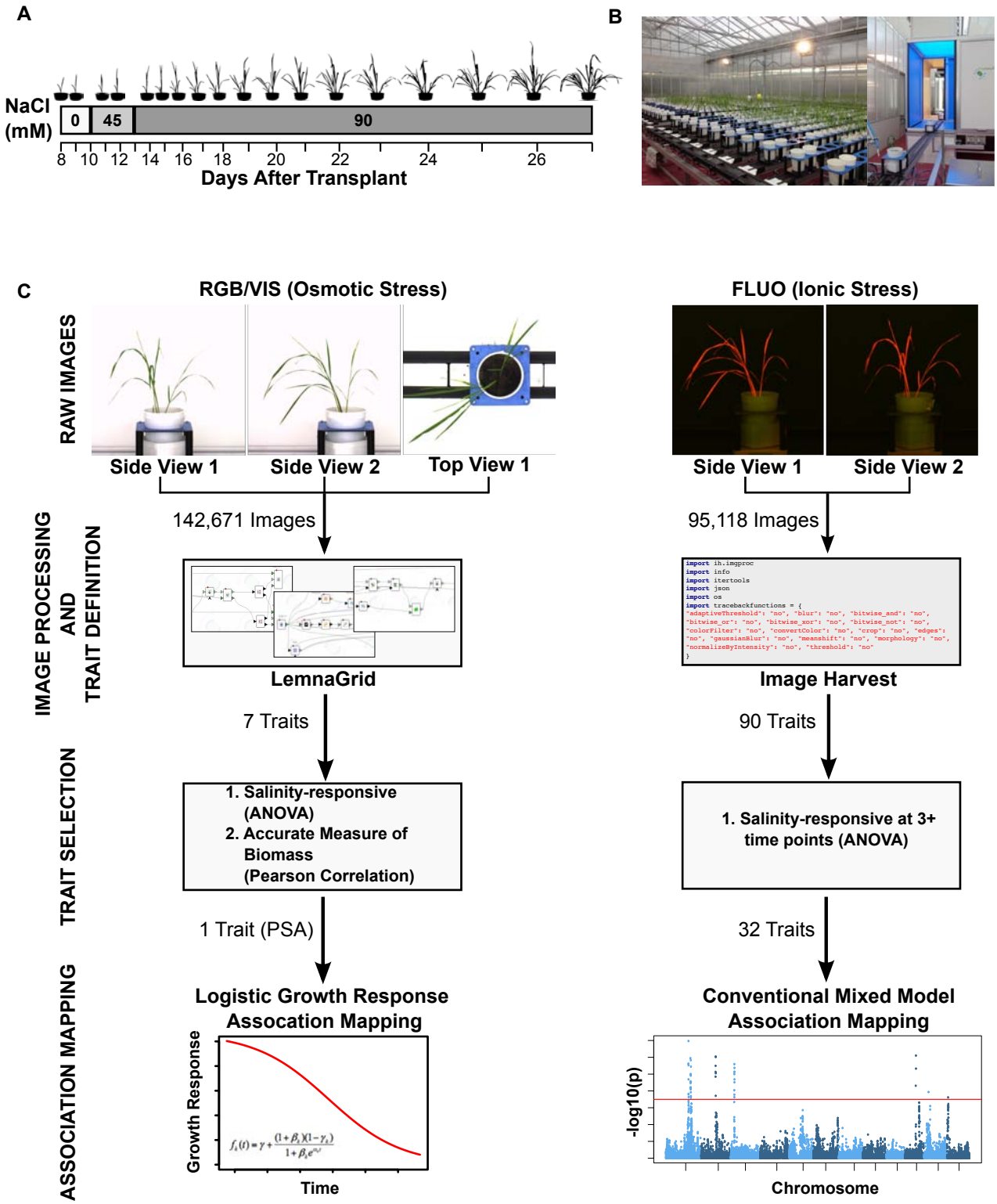



**Fig S1:** Schematic illustrating the experimental design and pipeline for the analysis of high-throughput phenotyping data. (A) Implementation of 90 mM NaCl. (B) High-throughput phenotyping of rice plants at the early-tillering stage using the LemnaTec system at the Plant Accelerator. (C) Workflow for image acquisition, processing and analysis (see Materials and Methods for a complete description).

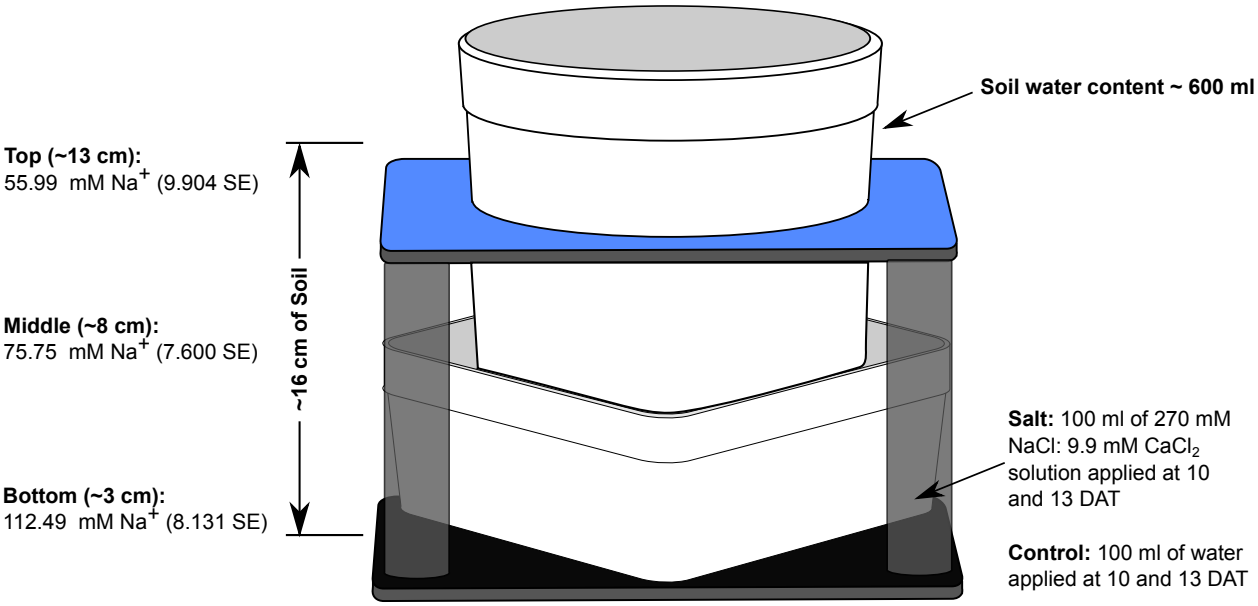



**Figure S2. Schematic illustrating NaCl application.** The salt treatment was applied by adding 100 ml of NaCl solution (270 mM NaCl: 9.9 mM $CaCl_2$) the square dish beneath the pot. The treatment was applied in two steps of 45 mM to reach a final concentration of 90 mM, at 10 and 13 DAT. Soil sodium concentration throughout the soil profile is listed on the left. DAT: Days after transplant.

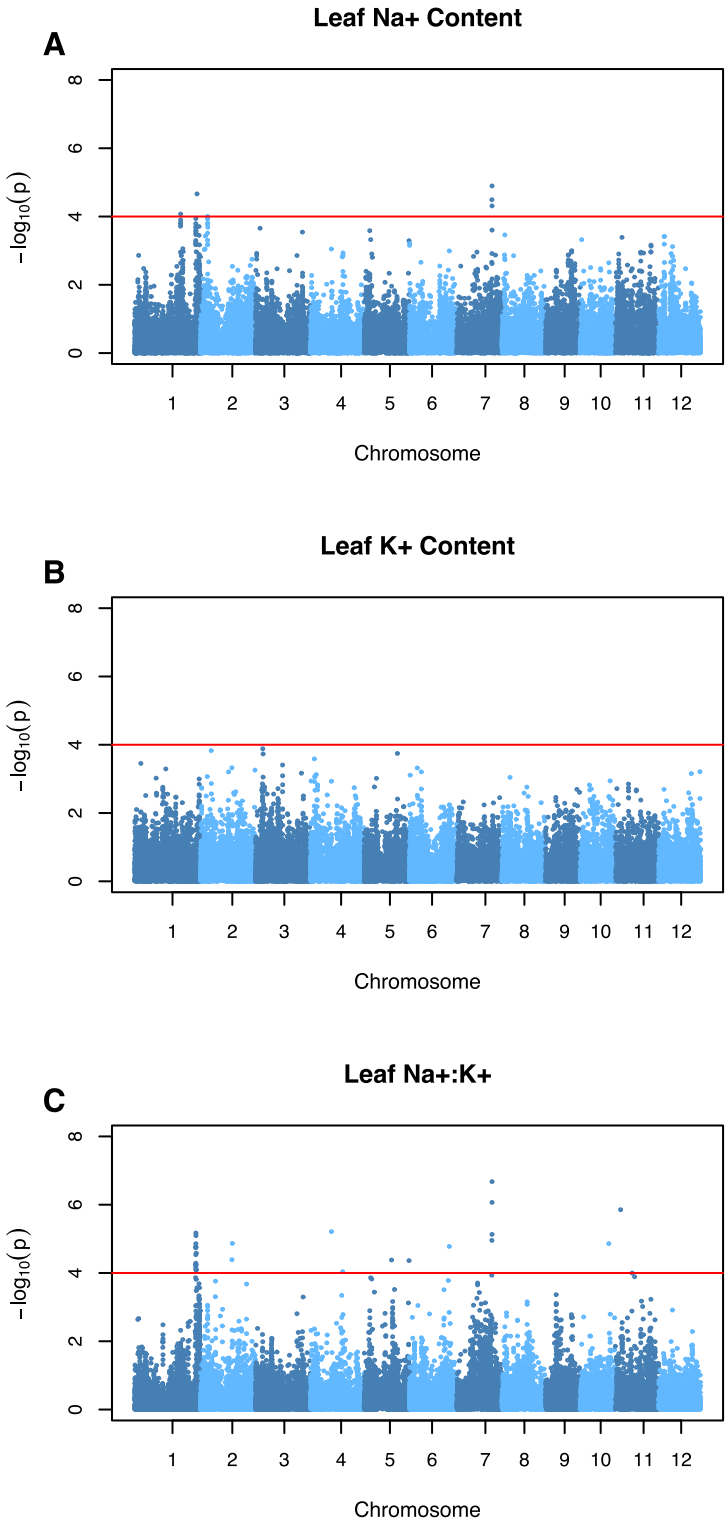



**Fig S3:** GWA analysis of leaf $Na^+$ (A), $K^+$ (B) and $Na^+$:$K^+$ content (C). The third leaf was collected at day 15 after 90 mM NaCl. The red horizontal line indicates statistical significance ($p < 10^{-4}$).

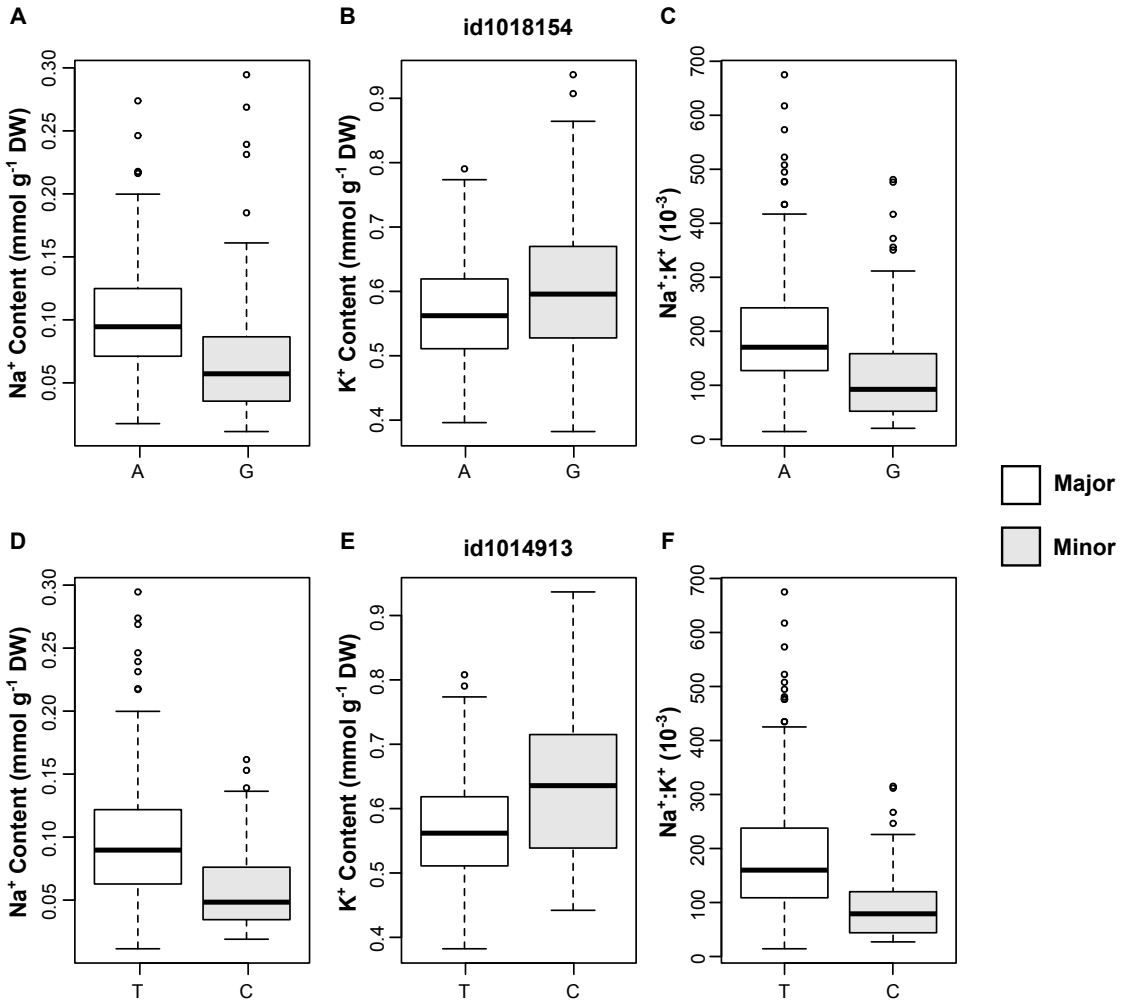
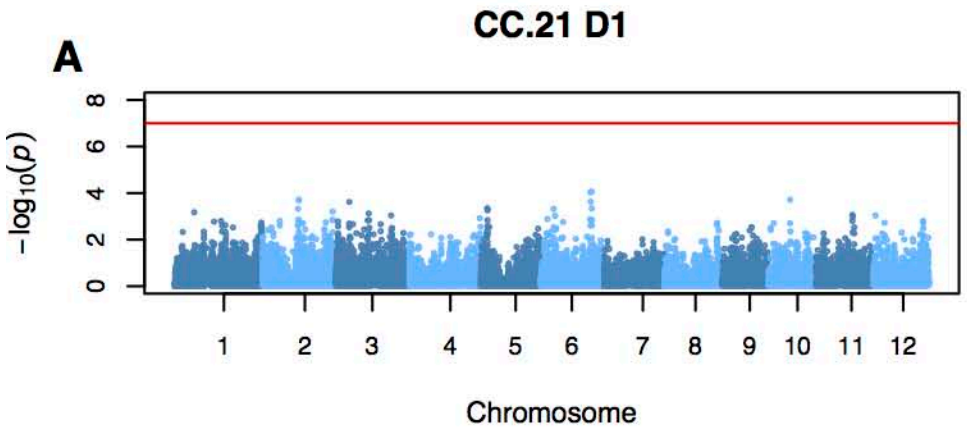
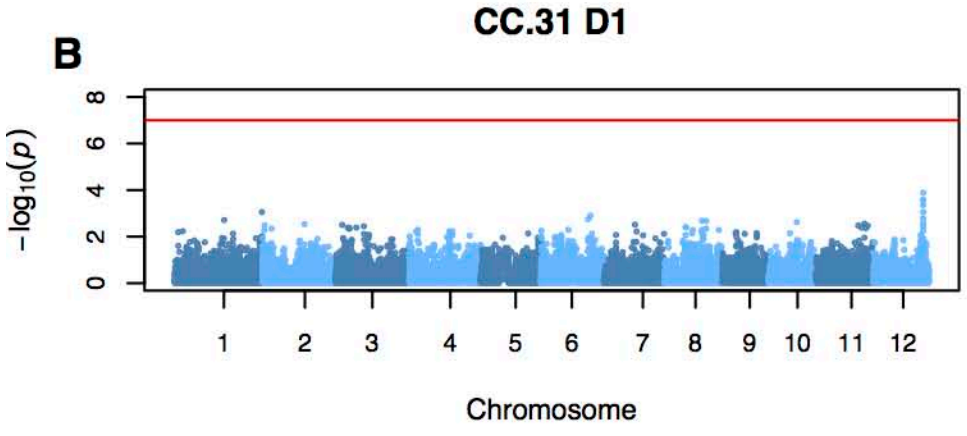
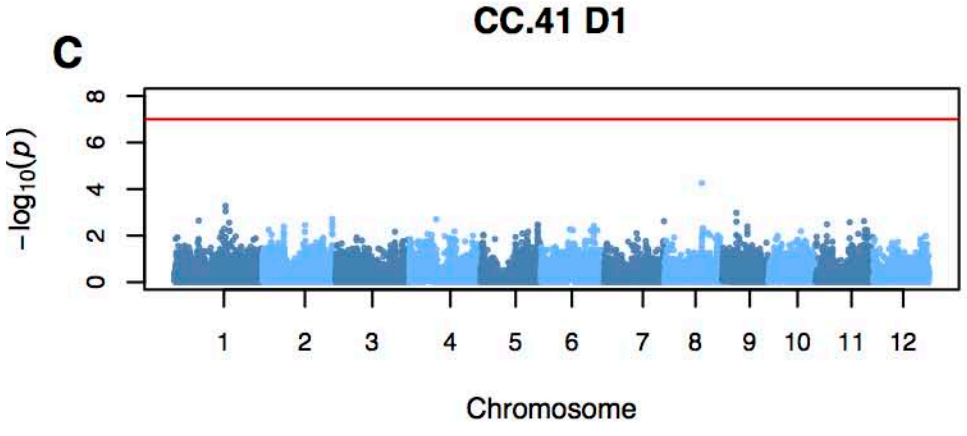


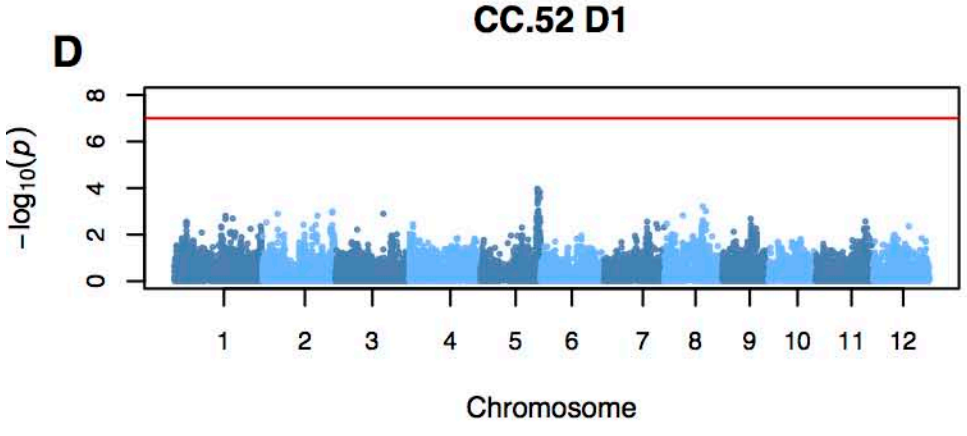

**Fig S4:** Distribution of leaf ion content observed between allelic groups at id1018154 (A-C) and id1014913 (D-F). (A) The minor allelic group at id1018154 is indicated by “G” where *n*=147, while “A” represents the major allelic group where *n*=173. (B) “C” indicates the minor allelic group at id1014913 where *n*=69, and “T” represents the major allelic group where *n*=263.

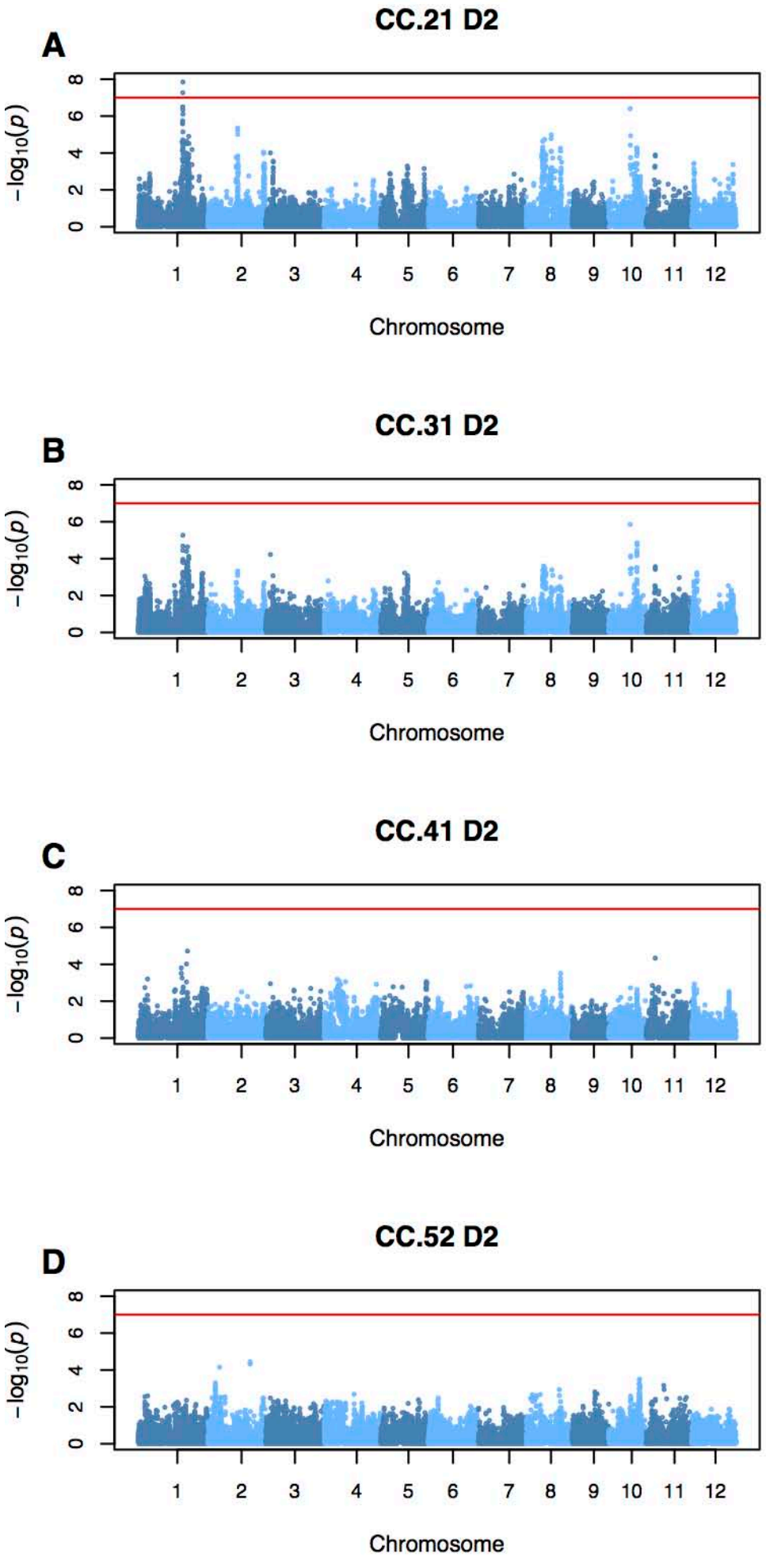
**Fig S5-18:** (A-D) GWA analysis of fluorescence color classes CC.21 (A), CC.31 (B), CC.41 (C) and CC.52 (D) at day 1-14 after 90 mM NaCl. Red horizontal line indicates statistical significance ($p < 10^{-7}$).

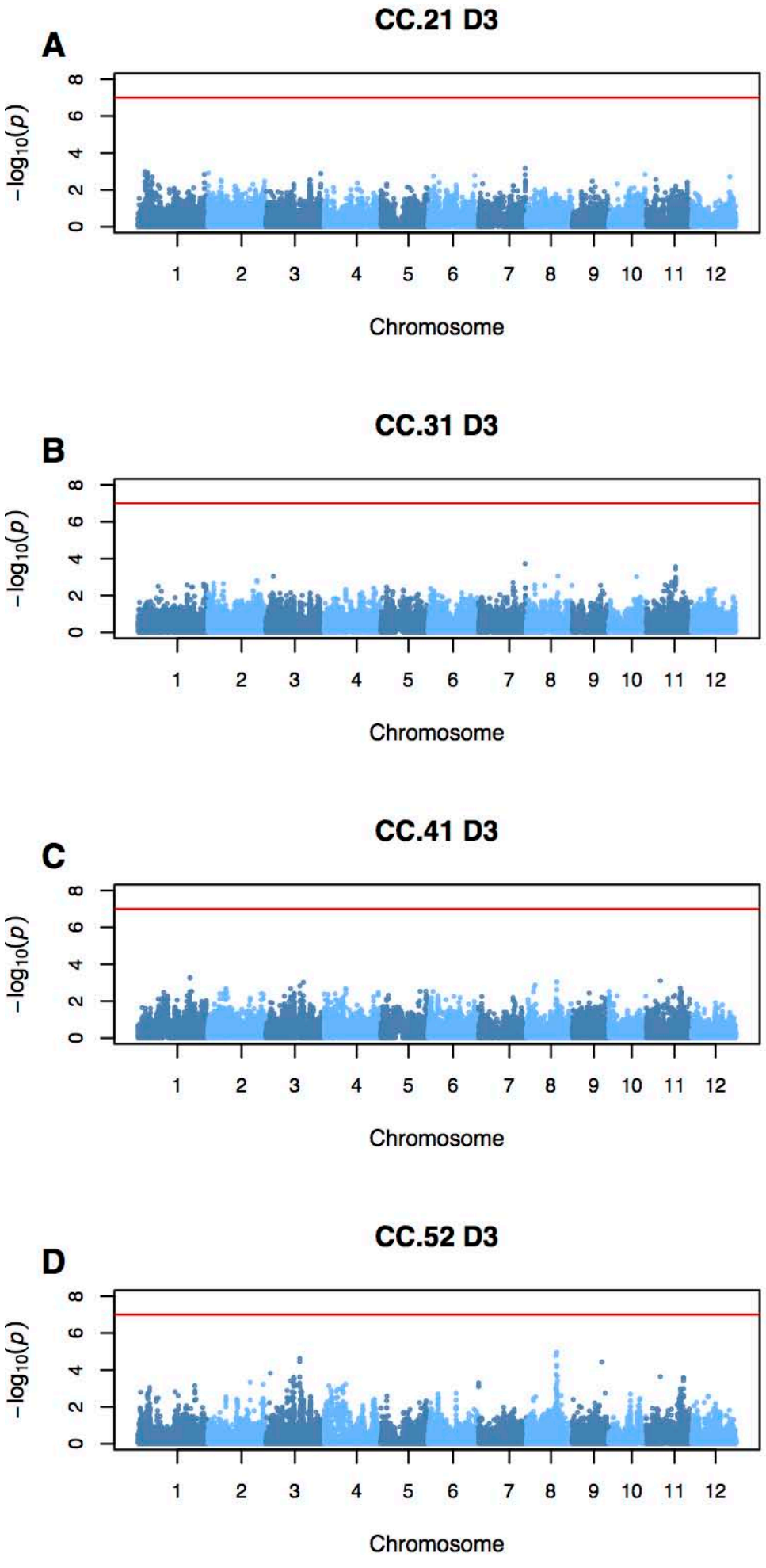

CC.21 D1
A
−log10(p)
0
2
4
6
8
1
2
3
4
5
6
7
8
9
10
11
12
Chromosome

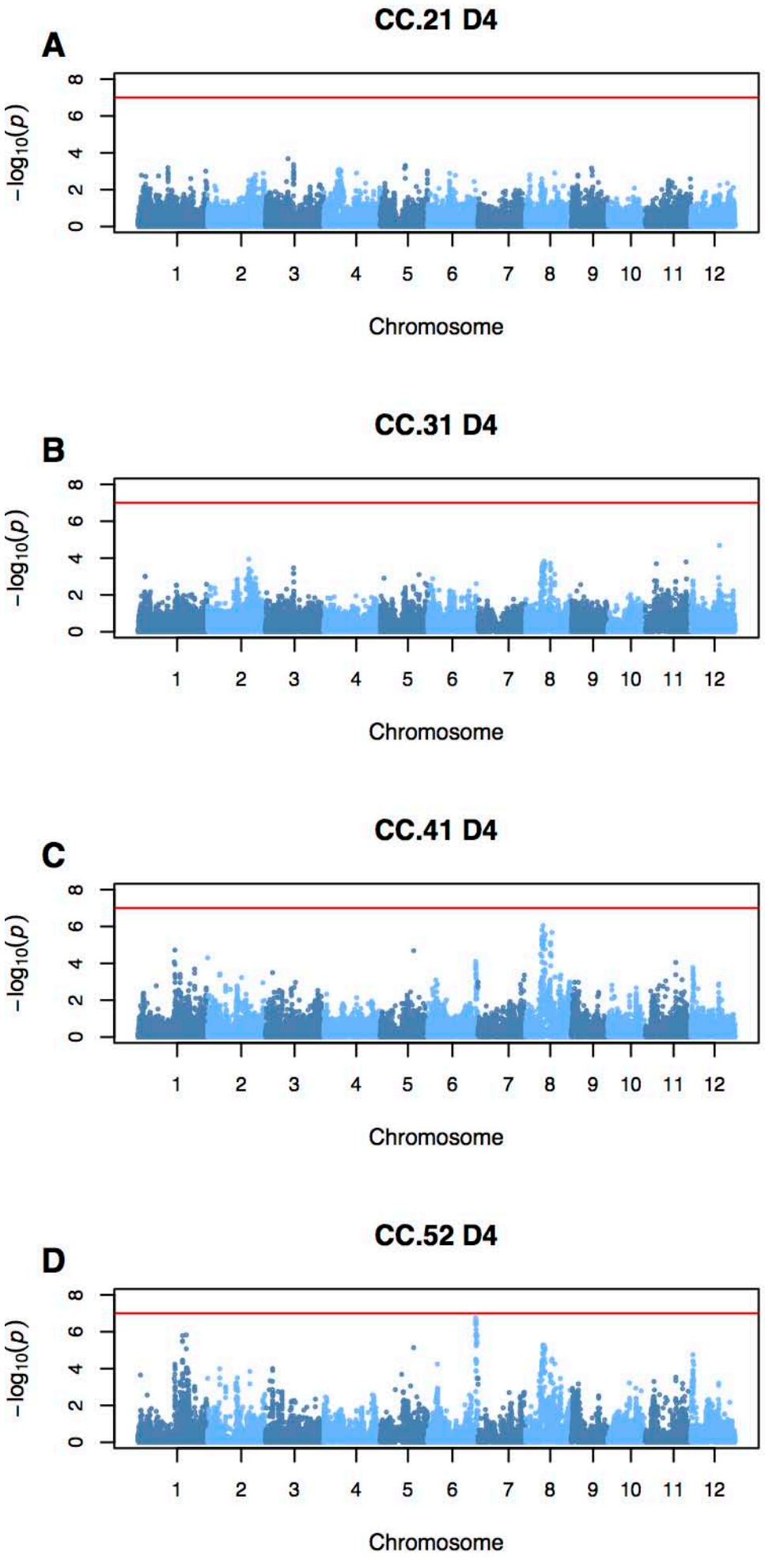

CC.31 D1
B
−log10(p)
0
2
4
6
8
1
2
3
4
5
6
7
8
9
10
11
12
Chromosome

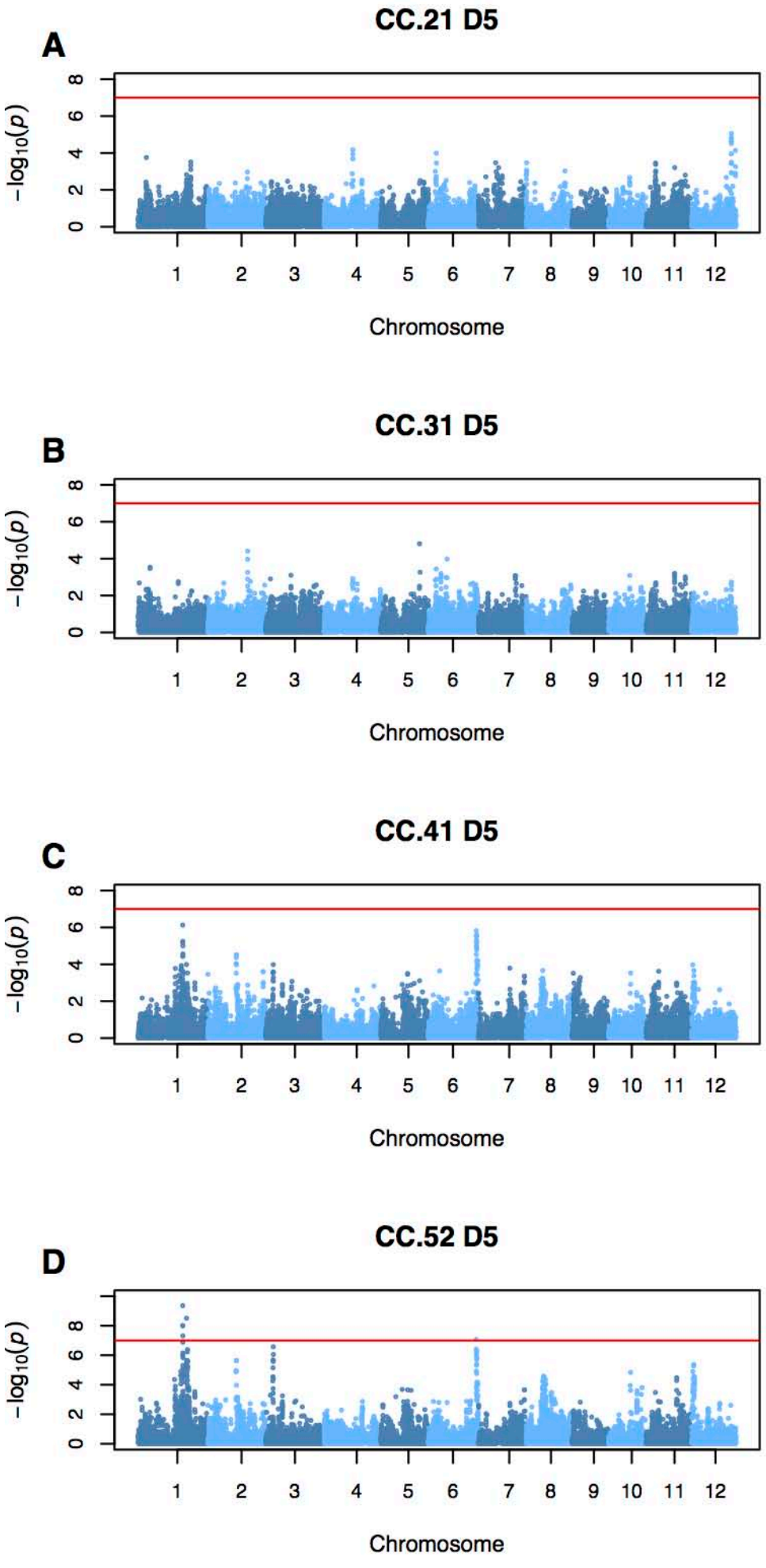

CC.41 D1
C
−log10(p)
0
2
4
6
8
1
2
3
4
5
6
7
8
9
10
11
12
Chromosome

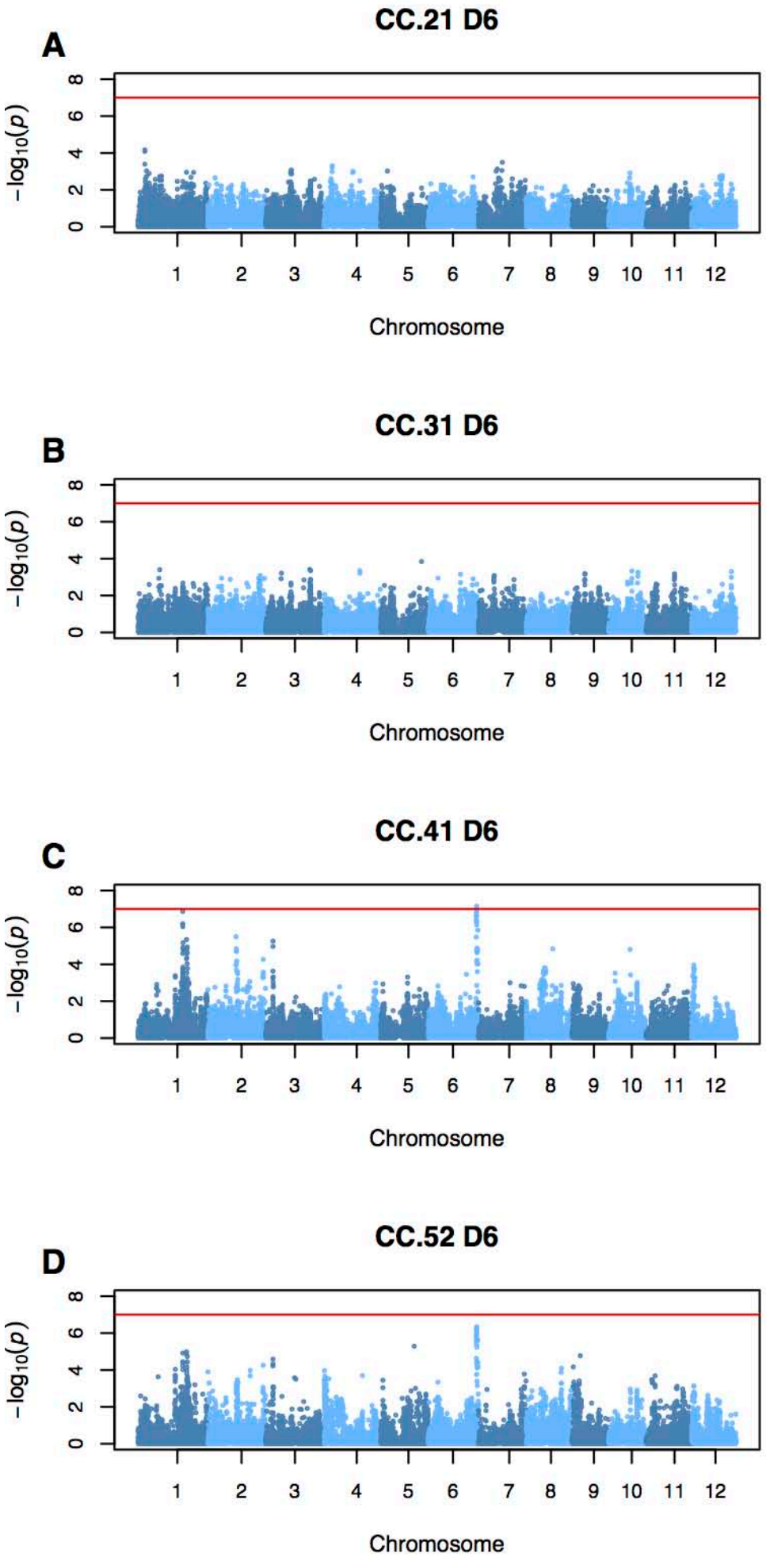

CC.52 D1
D
−log10(p)
0
2
4
6
8
1
2
3
4
5
6
7
8
9
10
11
12
Chromosome

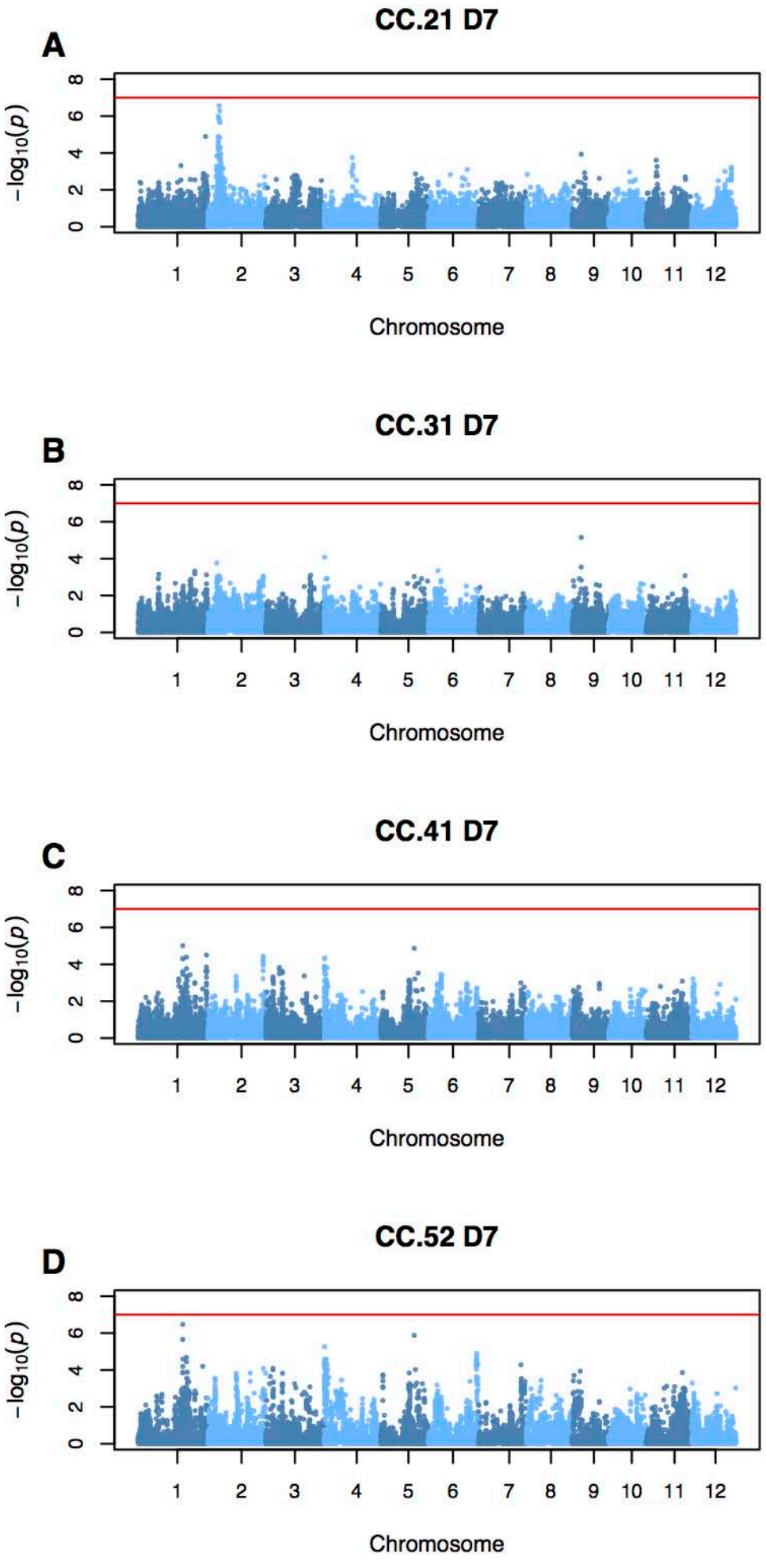

A
CC.21 D2
B
CC.31 D2
C
CC.41 D2
D
CC.52 D2
−log10(p)
0
2
4
6
8
1
2
3
4
5
6
7
8
9
10
11
12
Chromosome

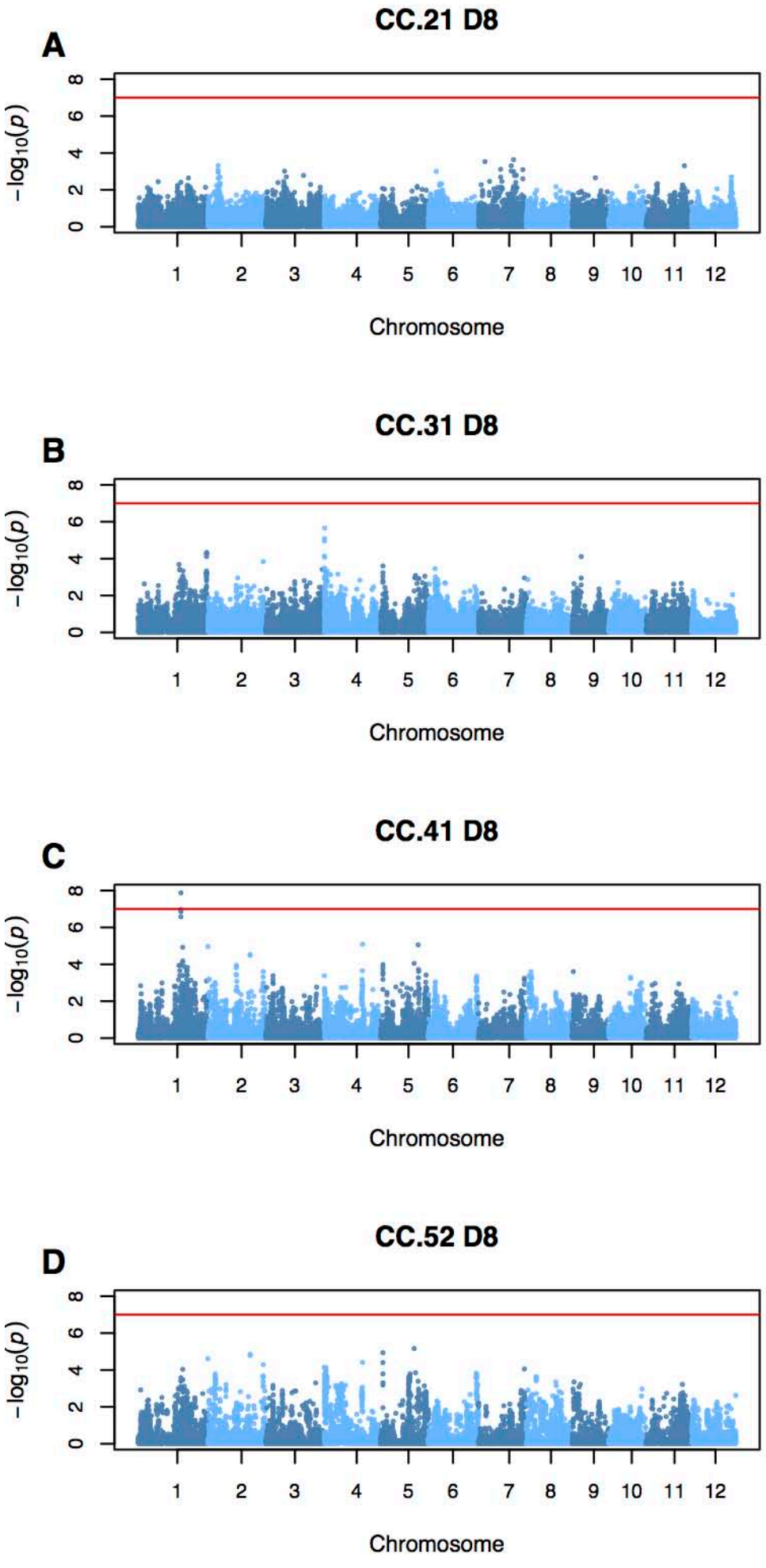

A
CC.21 D3
B
CC.31 D3
C
CC.41 D3
D
CC.52 D3
−log10(p)
0 2 4 6 8
1 2 3 4 5 6 7 8 9 10 11 12
Chromosome

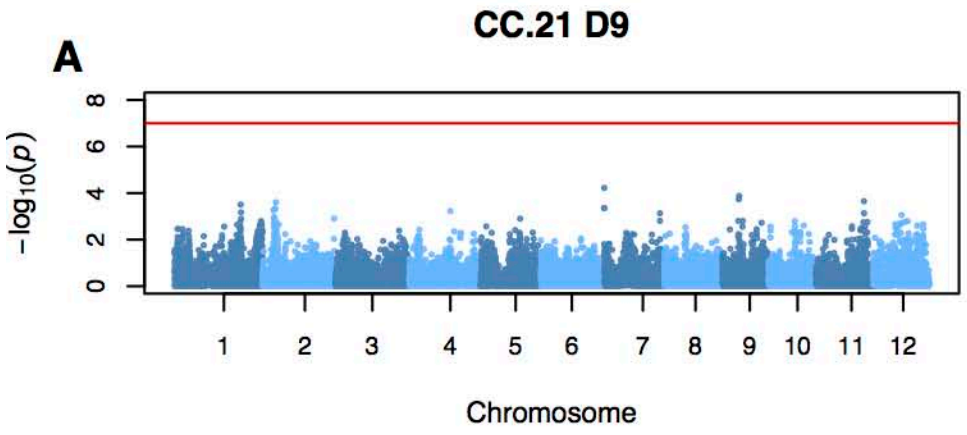

CC.21 D4
A
$-\log_{10}(p)$
0 2 4 6 8
1 2 3 4 5 6 7 8 9 10 11 12
Chromosome
CC.31 D4
B
$-\log_{10}(p)$
0 2 4 6 8
1 2 3 4 5 6 7 8 9 10 11 12
Chromosome
CC.41 D4
C
$-\log_{10}(p)$
0 2 4 6 8
1 2 3 4 5 6 7 8 9 10 11 12
Chromosome
CC.52 D4
D
$-\log_{10}(p)$
0 2 4 6 8
1 2 3 4 5 6 7 8 9 10 11 12
Chromosome

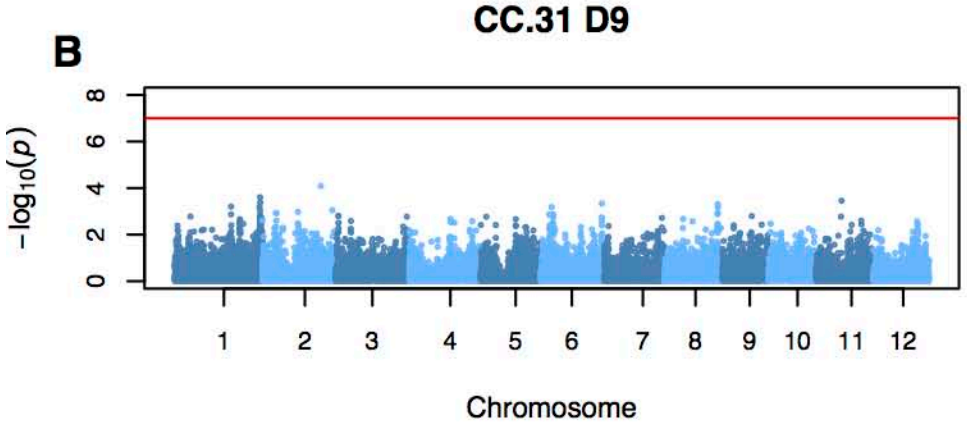

A
CC.21 D5
B
CC.31 D5
C
CC.41 D5
D
CC.52 D5
−log10(p)
0 2 4 6 8
1 2 3 4 5 6 7 8 9 10 11 12
Chromosome

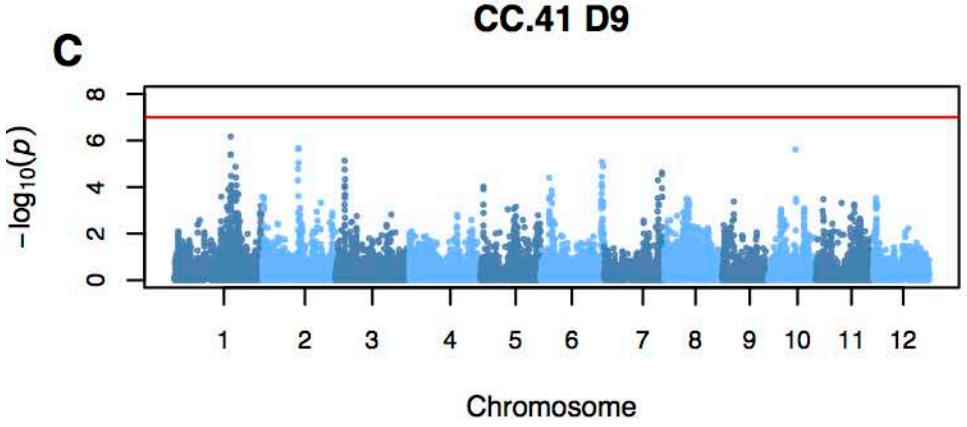

CC.21 D6
A
$-\log_{10}(p)$
0 2 4 6 8
1 2 3 4 5 6 7 8 9 10 11 12
Chromosome
CC.31 D6
B
$-\log_{10}(p)$
0 2 4 6 8
1 2 3 4 5 6 7 8 9 10 11 12
Chromosome
CC.41 D6
C
$-\log_{10}(p)$
0 2 4 6 8
1 2 3 4 5 6 7 8 9 10 11 12
Chromosome
CC.52 D6
D
$-\log_{10}(p)$
0 2 4 6 8
1 2 3 4 5 6 7 8 9 10 11 12
Chromosome

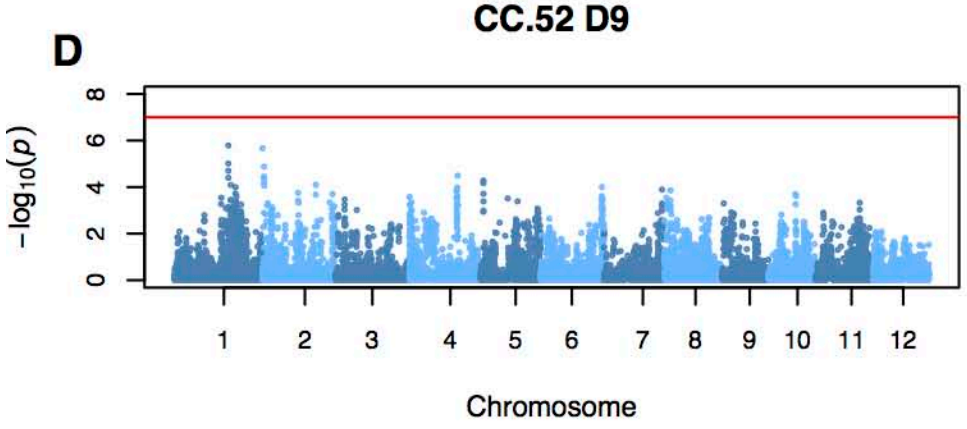

A
CC.21 D7
B
CC.31 D7
C
CC.41 D7
D
CC.52 D7
−log10(p)
0 2 4 6 8
1 2 3 4 5 6 7 8 9 10 11 12
Chromosome


CC.21 D8
A
$-\log_{10}(p)$
0 2 4 6 8
1 2 3 4 5 6 7 8 9 10 11 12
Chromosome
CC.31 D8
B
$-\log_{10}(p)$
0 2 4 6 8
1 2 3 4 5 6 7 8 9 10 11 12
Chromosome
CC.41 D8
C
$-\log_{10}(p)$
0 2 4 6 8
1 2 3 4 5 6 7 8 9 10 11 12
Chromosome
CC.52 D8
D
$-\log_{10}(p)$
0 2 4 6 8
1 2 3 4 5 6 7 8 9 10 11 12
Chromosome


CC.21 D9
A
−log10(p)
0
2
4
6
8
1
2
3
4
5
6
7
8
9
10
11
12
Chromosome


CC.31 D9
B
−log10(p)
0
2
4
6
8
1
2
3
4
5
6
7
8
9
10
11
12
Chromosome


CC.41 D9
C
−log10(p)
0
2
4
6
8
1
2
3
4
5
6
7
8
9
10
11
12
Chromosome


CC.52 D9
D
−log10(p)
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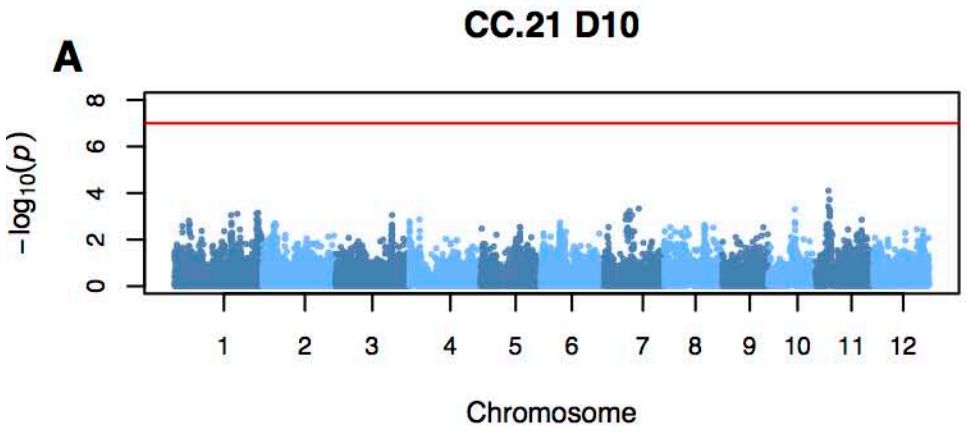
2
4
6
8
1
2
3
4
5
6
7
8
9
10
11
12
Chromosome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A
−log10(p)
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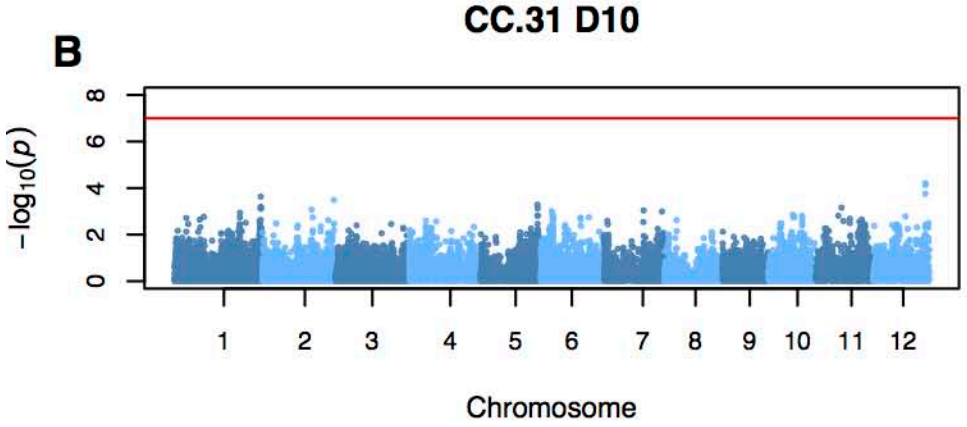
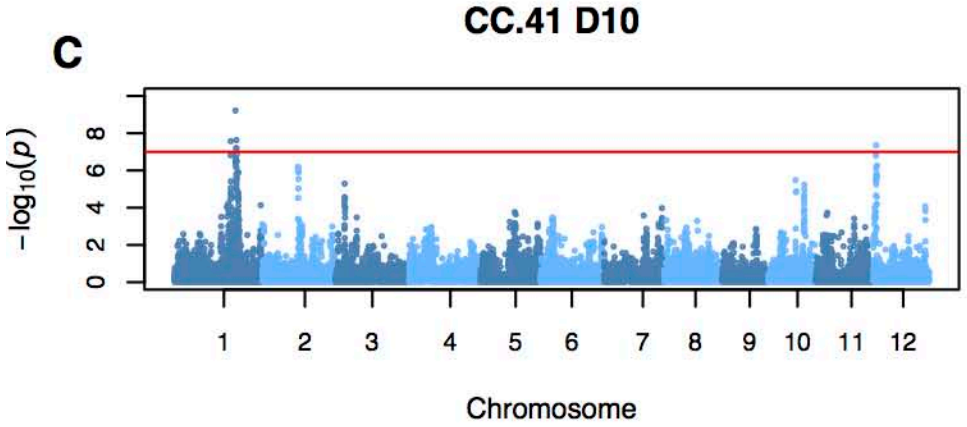
4
6
8
1
2
3
4
5
6
7
8
9
10
11
12
Chromosome


CC.31 D10
B
−log10(p)
0
2
4
6
8
1
2
3
4
5
6
7
8
9
10
11
12
Chromosome


CC.41 D10
C
−log10(p)
0
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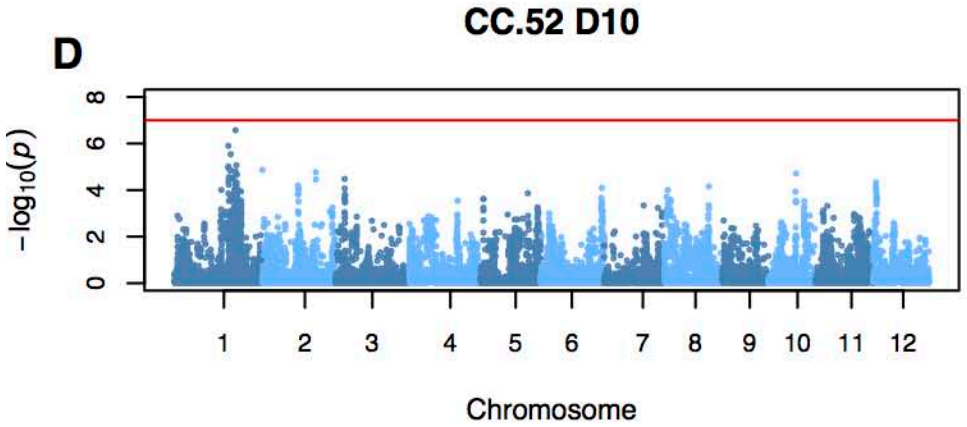
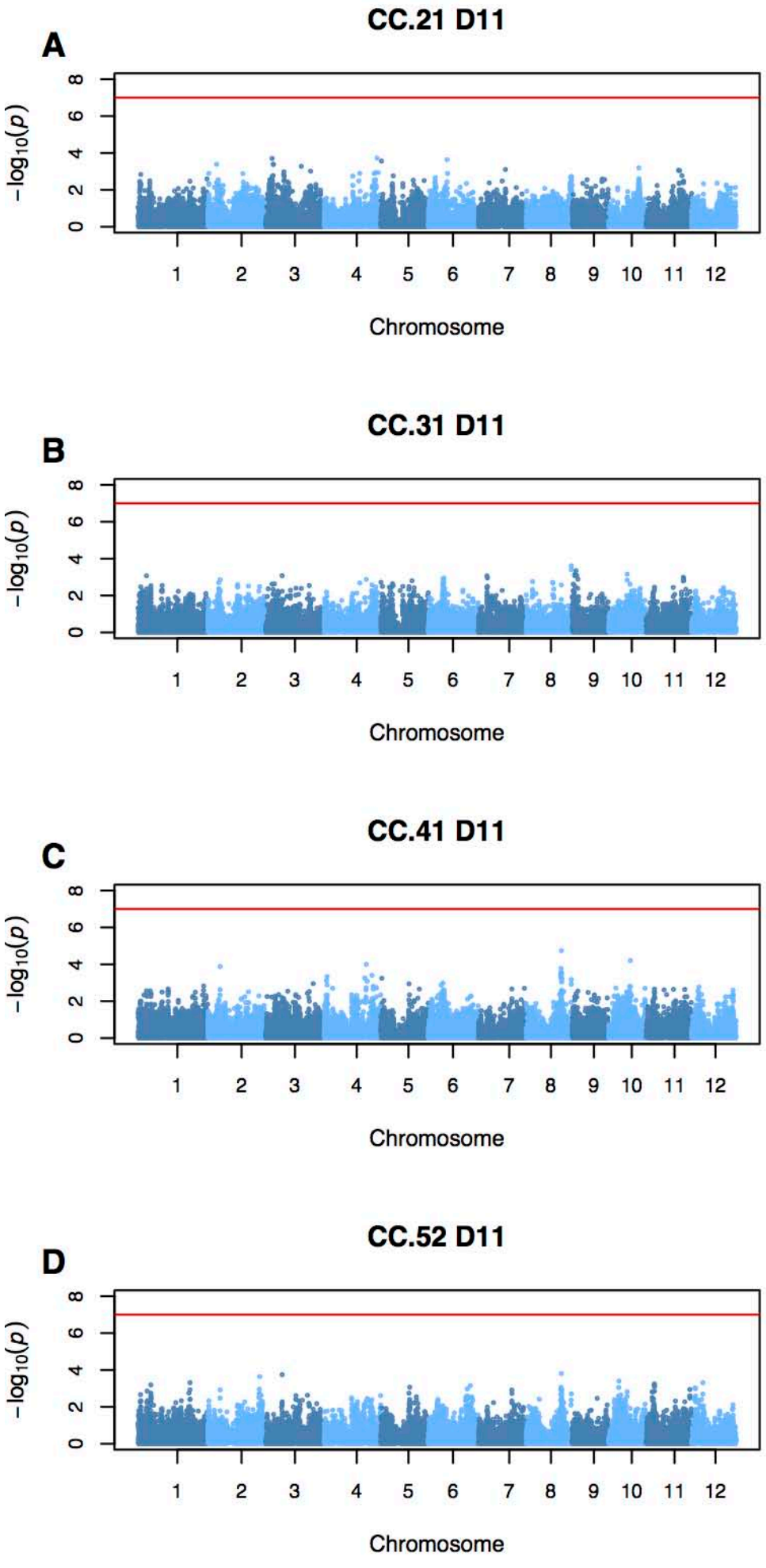
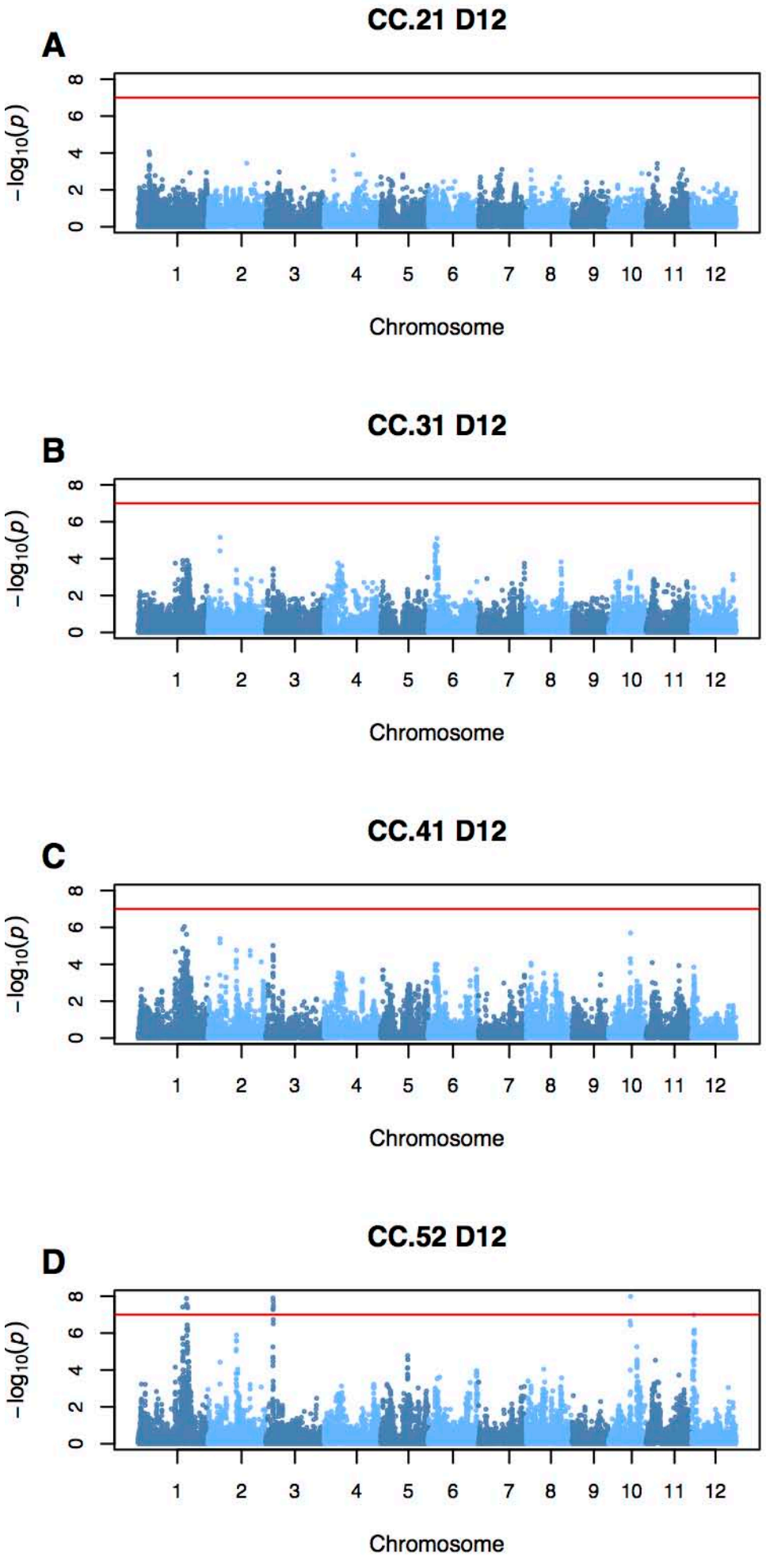
4
6
8
1
2
3
4
5
6
7
8
9
10
11
12
Chromosome


CC.52 D10
D
−log10(p)
0
2
4
6
8
1
2
3
4
5
6
7
8
9
10
11
12
Chromosome


A
CC.21 D11
−log10(p)
0 2 4 6 8
1 2 3 4 5 6 7 8 9 10 11 12
Chromosome
B
CC.31 D11
−log10(p)
0 2 4 6 8
1 2 3 4 5 6 7 8 9 10 11 12
Chromosome
C
CC.41 D11
−log10(p)
0 2 4 6 8
1 2 3 4 5 6 7 8 9 10 11 12
Chromosome
D
CC.52 D11
−log10(p)
0 2 4 6 8
1 2 3 4 5 6 7 8 9 10 11 12
Chromosome


A
CC.21 D12
−log10(p)
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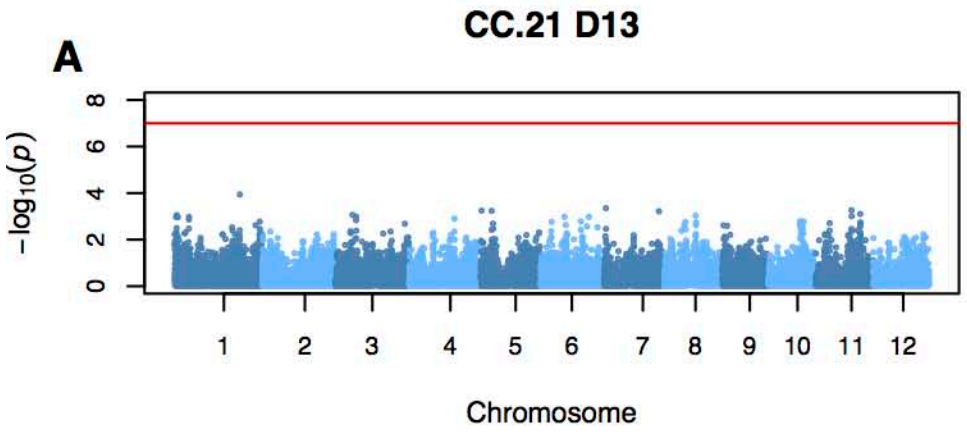
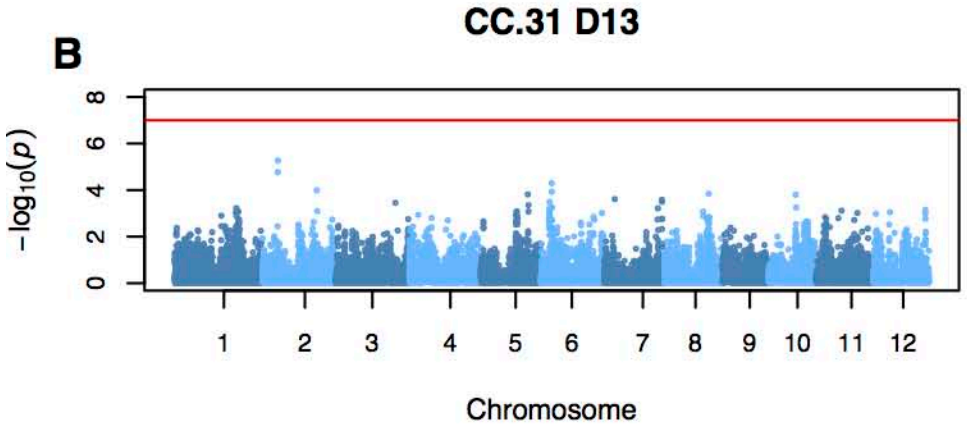
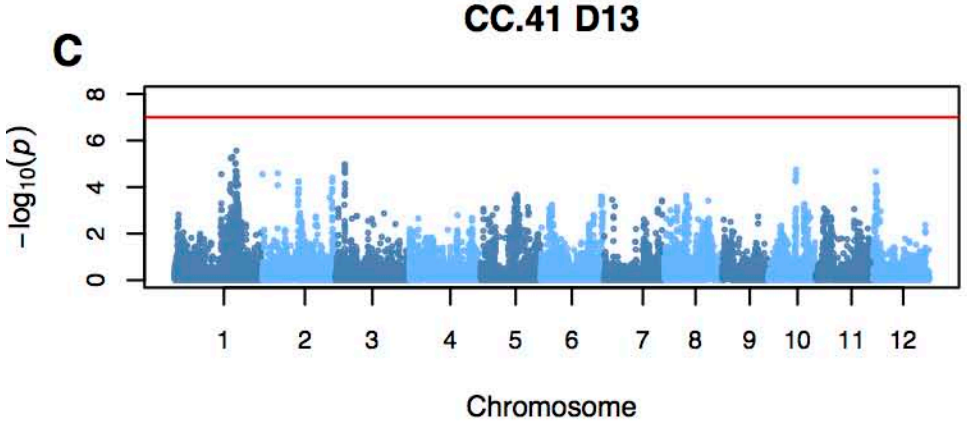
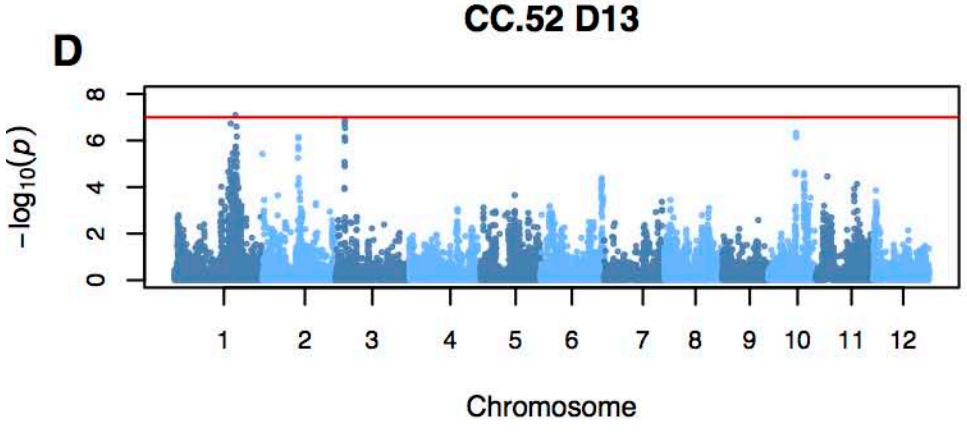
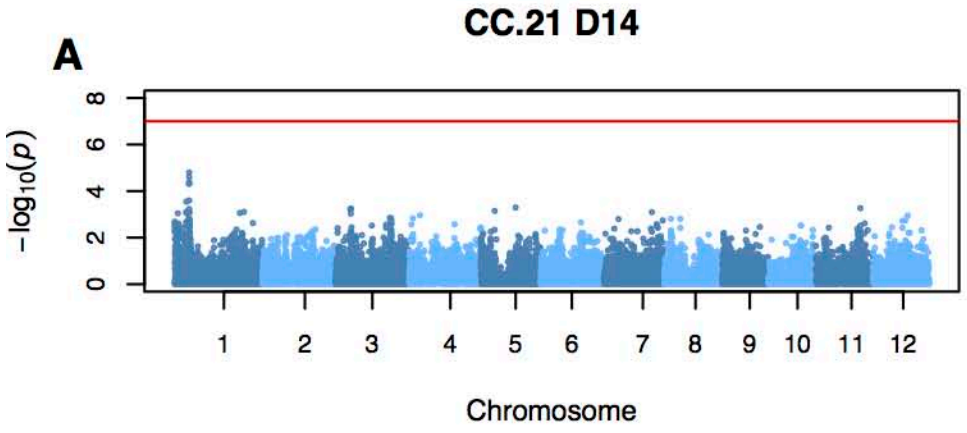
1 2 3 4 5 6 7 8 9 10 11 12
Chromosome
B
CC.31 D12
−log10(p)
0 2 4 6 8
1 2 3 4 5 6 7 8 9 10 11 12
Chromosome
C
CC.41 D12
−log10(p)
0 2 4 6 8
1 2 3 4 5 6 7 8 9 10 11 12
Chromosome
D
CC.52 D12
−log10(p)
0 2 4 6 8
1 2 3 4 5 6 7 8 9 10 11 12
Chromosome

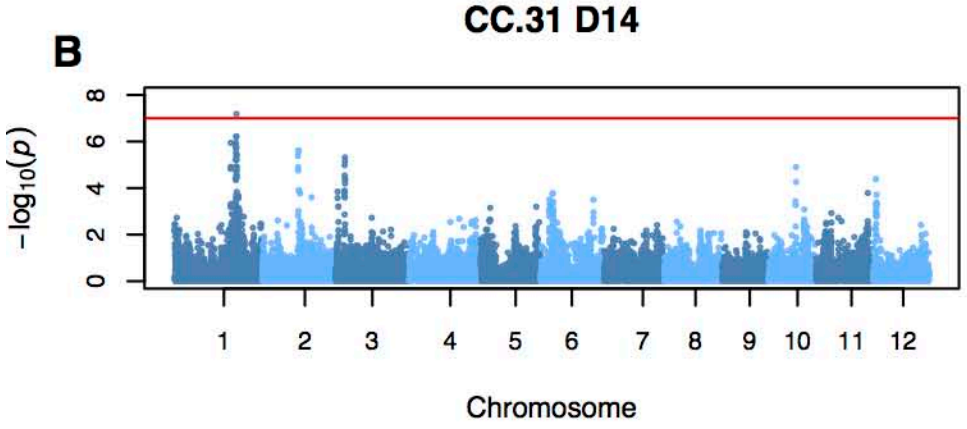

CC.21 D13
A
$-\log_{10}(p)$
0 2 4 6 8
1 2 3 4 5 6 7 8 9 10 11 12
Chromosome

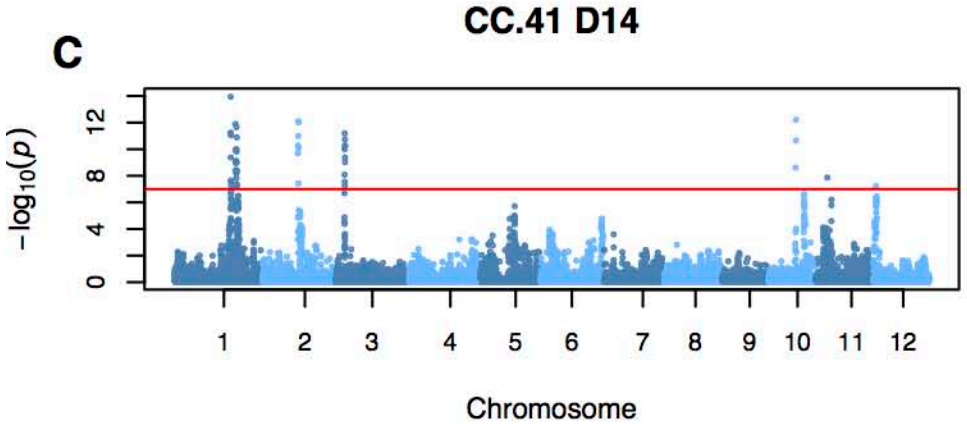

CC.31 D13
B
$-\log_{10}(p)$
0 2 4 6 8
1 2 3 4 5 6 7 8 9 10 11 12
Chromosome


CC.41 D13
C
$-\log_{10}(p)$
0 2 4 6 8
1 2 3 4 5 6 7 8 9 10 11 12
Chromosome


CC.52 D13
D
$-\log_{10}(p)$
0 2 4 6 8
1 2 3 4 5 6 7 8 9 10 11 12
Chromosome


CC.21 D14
A
−log10(p)
0
2
4
6
8
1
2
3
4
5
6
7
8
9
10
11
12
Chromosome


CC.31 D14
B
−log10(p)
0
2
4
6
8
1
2
3
4
5
6
7
8
9
10
11
12
Chromosome


CC.41 D14
C
−log10(p)
0
4
8
12
1
2
3
4
5
6
7
8
9
10
11
12
Chromosome

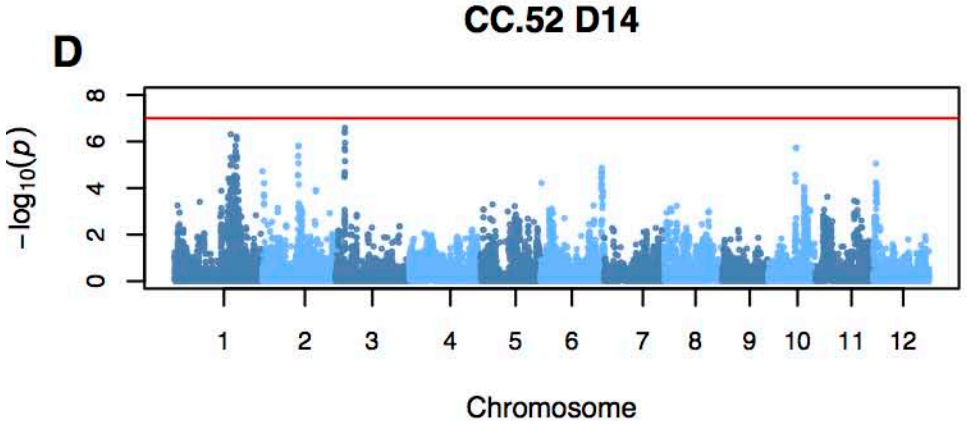
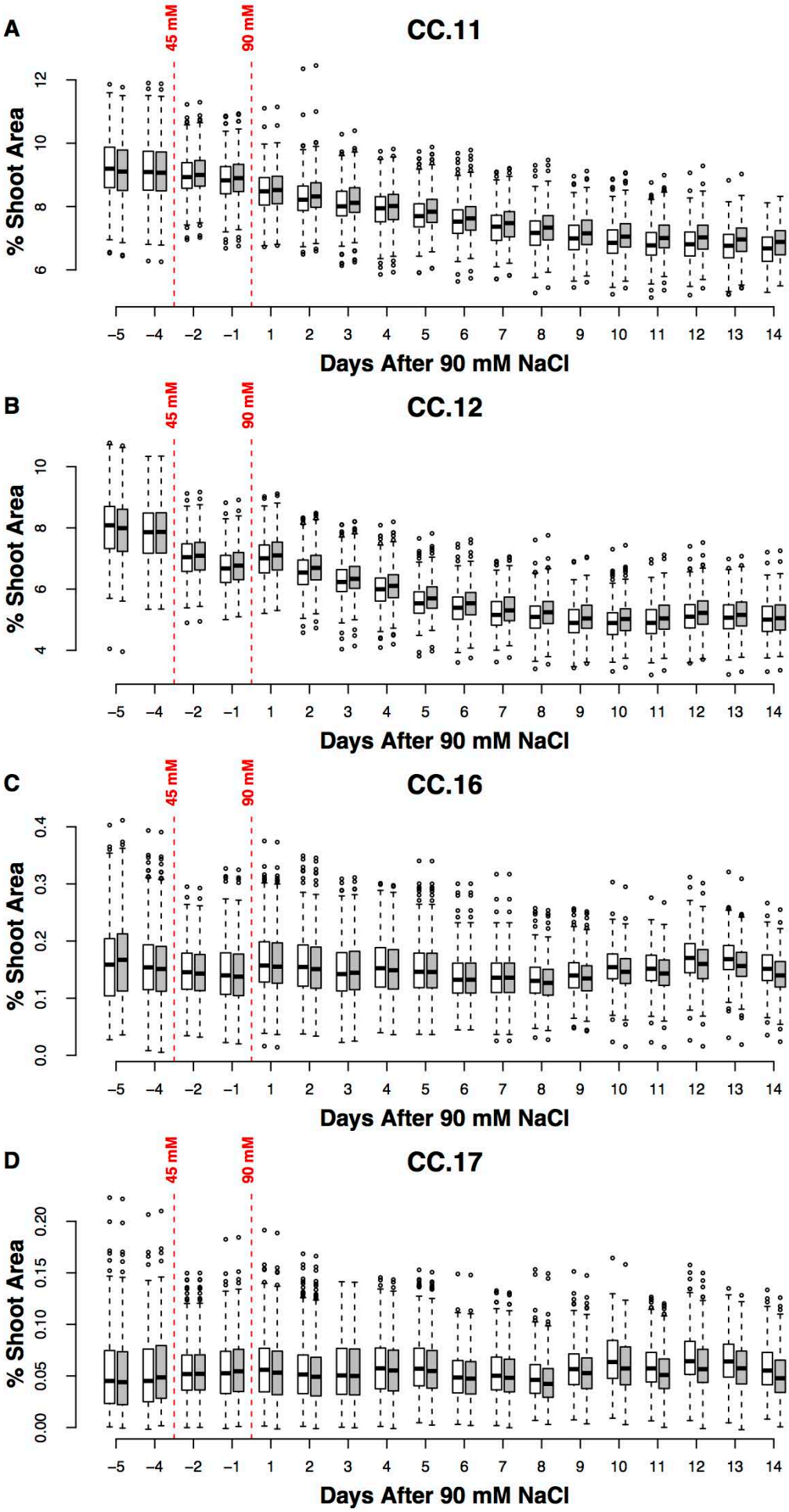
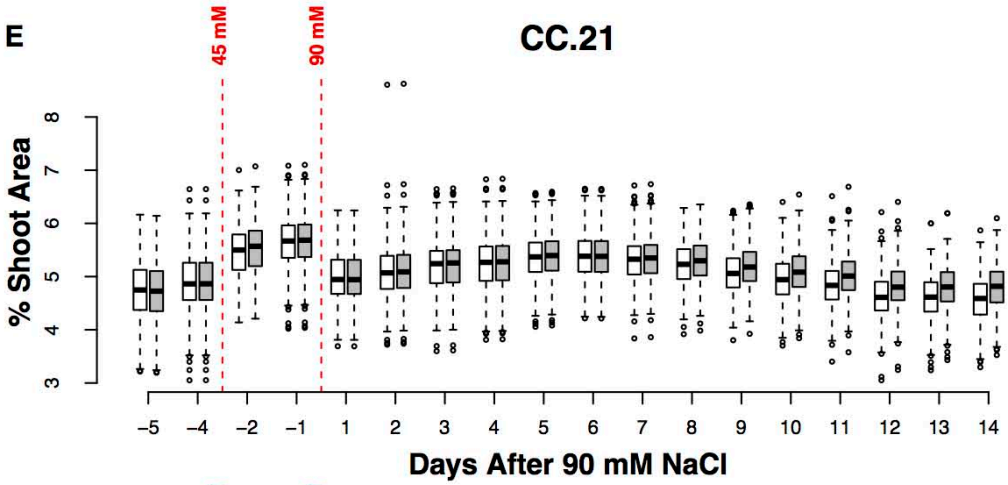
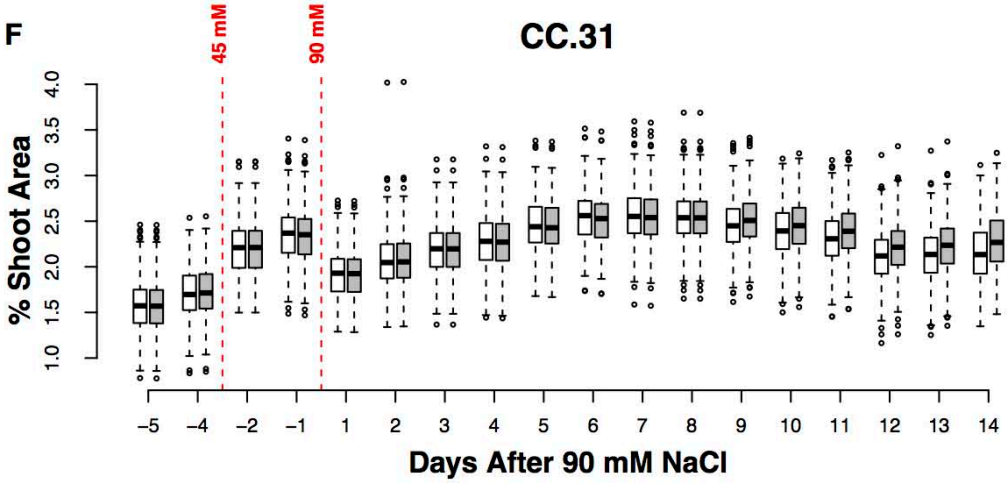
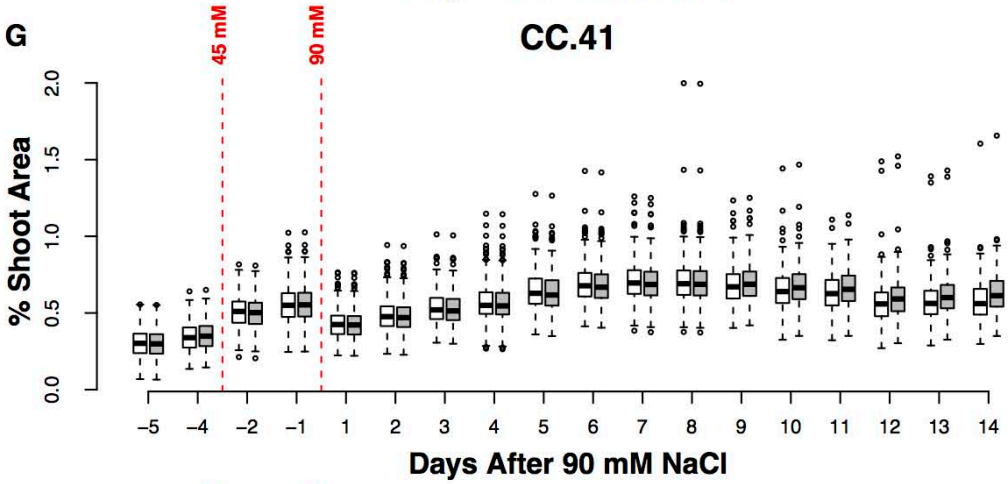

CC.52 D14
D
−log10(p)
0
2
4
6
8
1
2
3
4
5
6
7
8
9
10
11
12
Chromosome

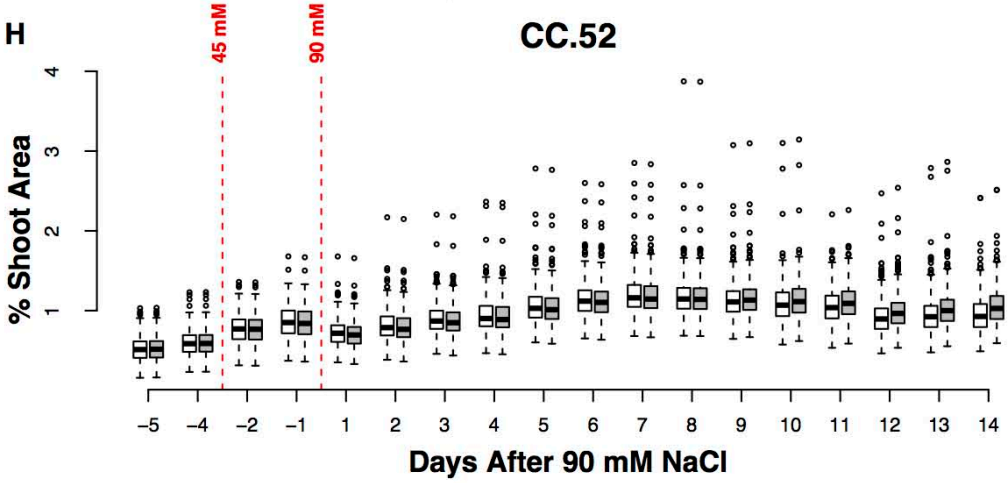
**Fig S19:** (A-AF) Trajectories of the 32 salinity-responsive fluorescence color classes. Control plants are indicated by white bars, while plants in saline conditions are indicated by grey bars. Values are expressed as a percentage of total pixels from two side view fluorescence images.

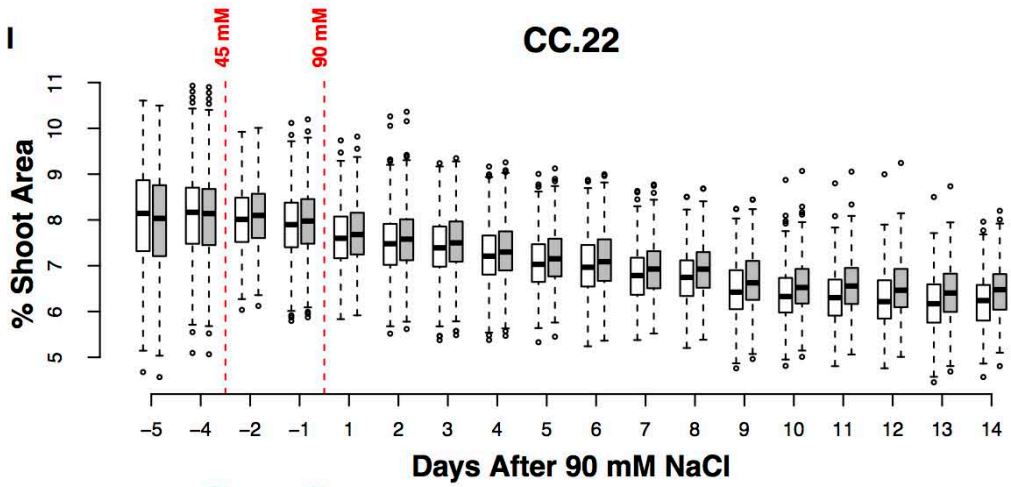

A
CC.11
45 mM
90 mM
% Shoot Area
6
8
10
12
−5
−4
−2
−1
1
2
3
4
5
6
7
8
9
10
11
12
13
14
Days After 90 mM NaCl
B
CC.12
45 mM
90 mM
% Shoot Area
4
6
8
10
−5
−4
−2
−1
1
2
3
4
5
6
7
8
9
10
11
12
13
14
Days After 90 mM NaCl
C
CC.16
45 mM
90 mM
% Shoot Area
0.0
0.1
0.2
0.3
0.4
−5
−4
−2
−1
1
2
3
4
5
6
7
8
9
10
11
12
13
14
Days After 90 mM NaCl
D
CC.17
45 mM
90 mM
% Shoot Area
0.00
0.05
0.10
0.15
0.20
−5
−4
−2
−1
1
2
3
4
5
6
7
8
9
10
11
12
13
14
Days After 90 mM NaCl

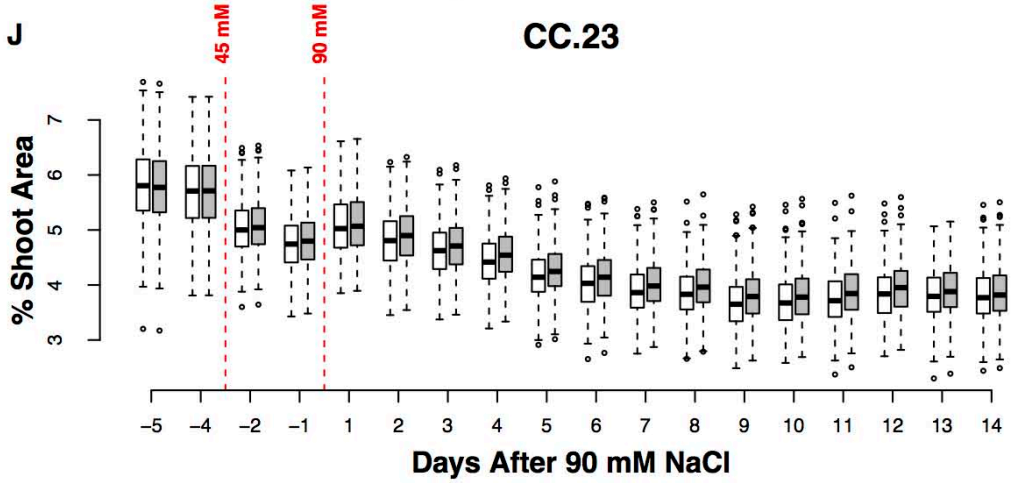

E
CC.21
45 mM
90 mM
% Shoot Area
3
4
5
6
7
8
−5
−4
−2
−1
1
2
3
4
5
6
7
8
9
10
11
12
13
14
Days After 90 mM NaCl

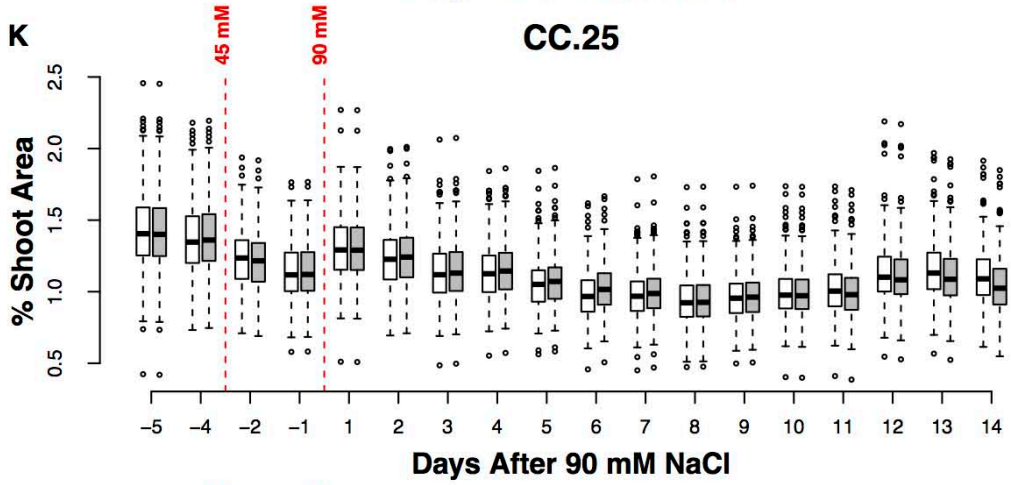

F
CC.31
45 mM
90 mM
% Shoot Area
1.0
1.5
2.0
2.5
3.0
3.5
4.0
−5
−4
−2
−1
1
2
3
4
5
6
7
8
9
10
11
12
13
14
Days After 90 mM NaCl

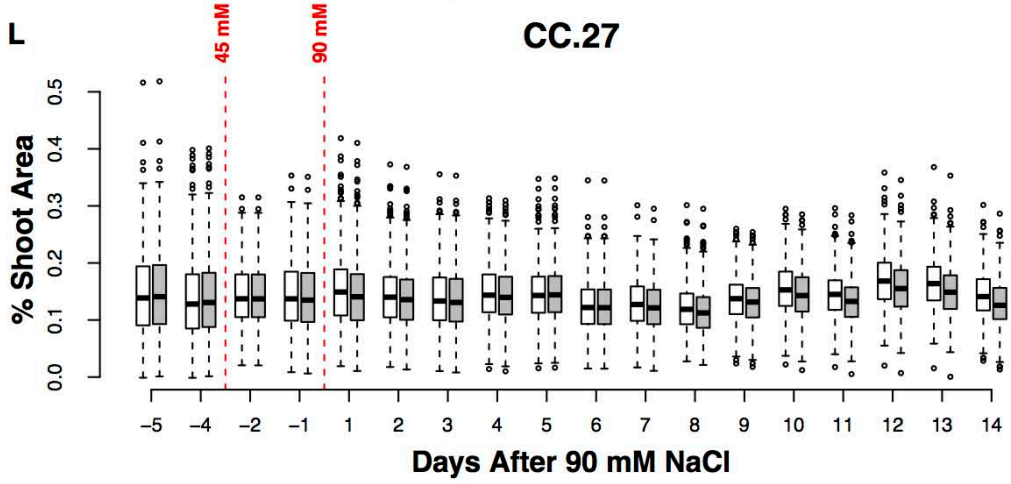

G
CC.41
45 mM
90 mM
% Shoot Area
0.0
0.5
1.0
1.5
2.0
−5
−4
−2
−1
1
2
3
4
5
6
7
8
9
10
11
12
13
14
Days After 90 mM NaCl

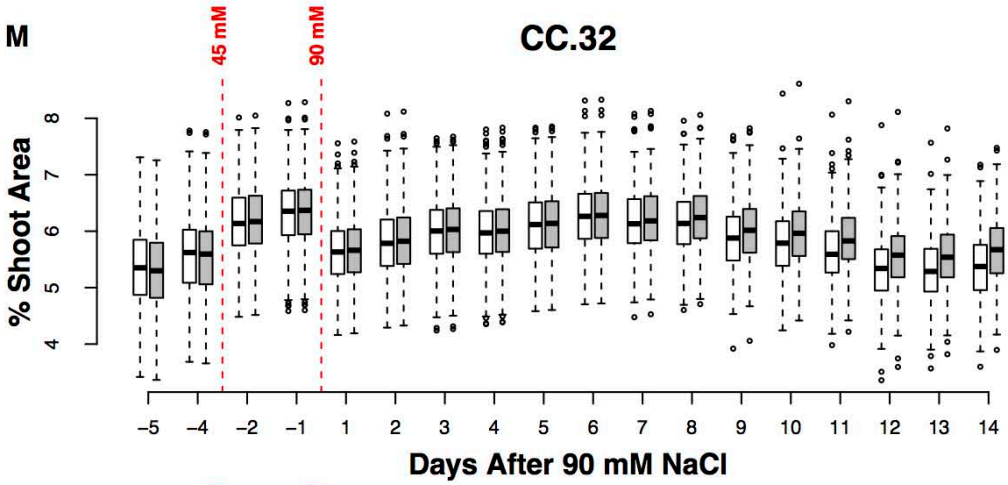

H
CC.52
45 mM
90 mM
% Shoot Area
1
2
3
4
−5
−4
−2
−1
1
2
3
4
5
6
7
8
9
10
11
12
13
14
Days After 90 mM NaCl

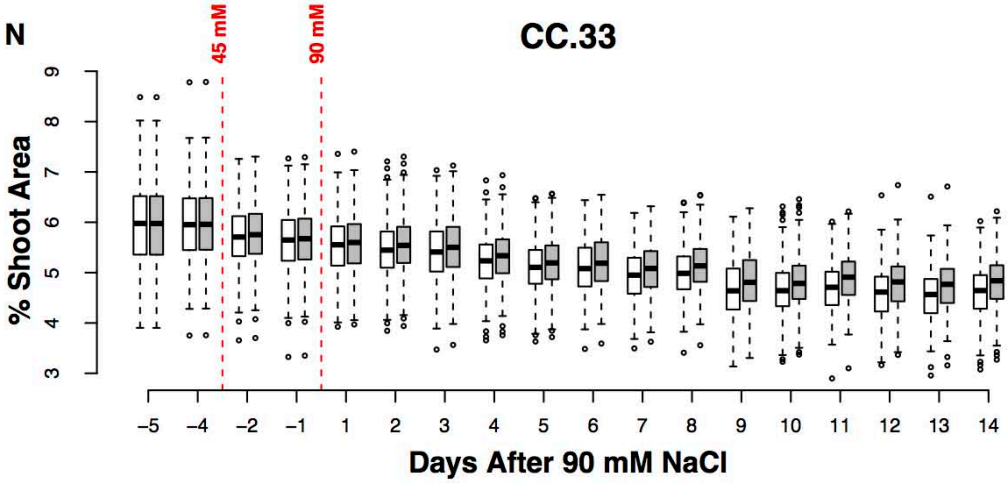

I
CC.22
45 mM
90 mM
% Shoot Area
5 6 7 8 9 10 11
−5 −4 −2 −1 1 2 3 4 5 6 7 8 9 10 11 12 13 14
Days After 90 mM NaCl

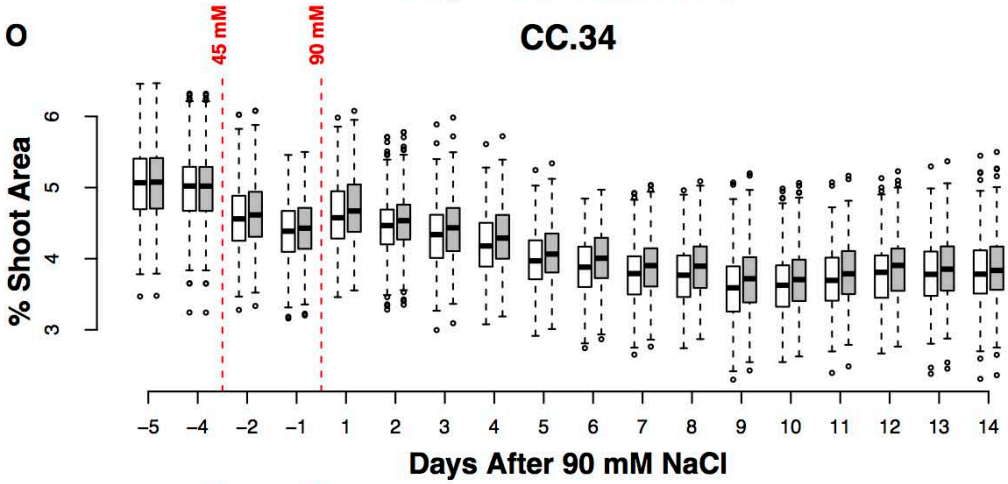

J
CC.23
45 mM
90 mM
% Shoot Area
3 4 5 6 7
−5 −4 −2 −1 1 2 3 4 5 6 7 8 9 10 11 12 13 14
Days After 90 mM NaCl

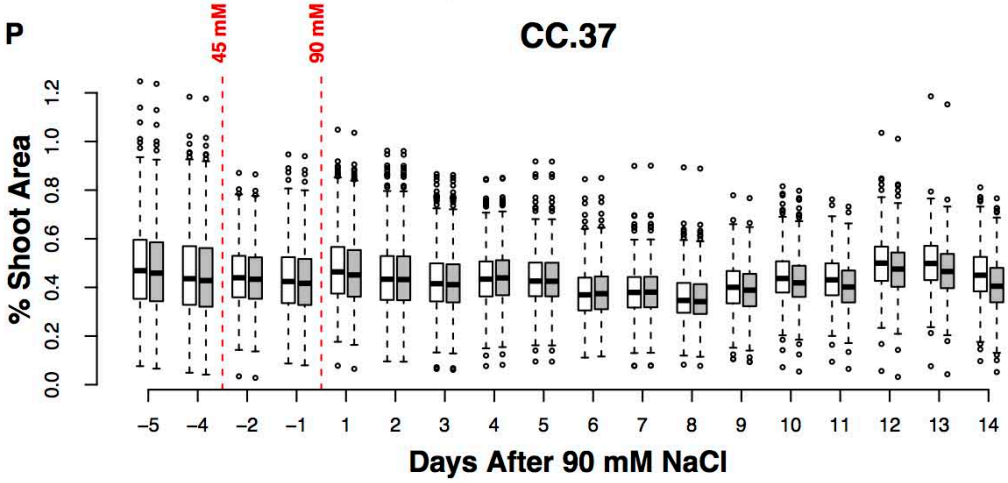

K
CC.25
45 mM
90 mM
% Shoot Area
0.5 1.0 1.5 2.0 2.5
−5 −4 −2 −1 1 2 3 4 5 6 7 8 9 10 11 12 13 14
Days After 90 mM NaCl

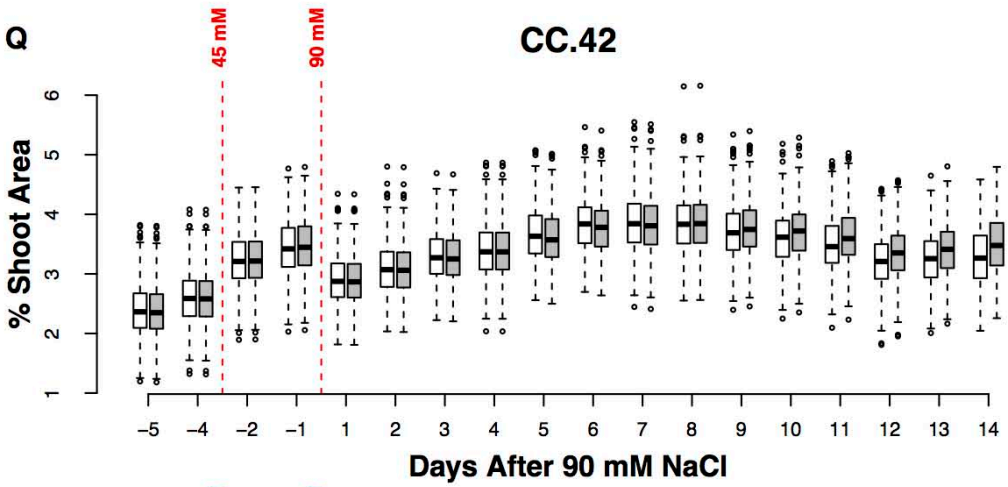

L
CC.27
45 mM
90 mM
% Shoot Area
0.0 0.1 0.2 0.3 0.4 0.5
−5 −4 −2 −1 1 2 3 4 5 6 7 8 9 10 11 12 13 14
Days After 90 mM NaCl

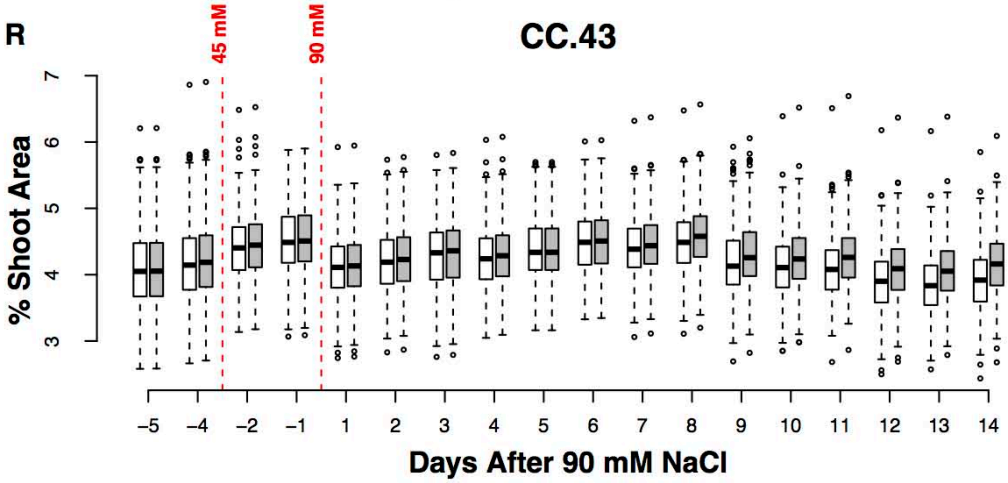

M
CC.32
45 mM
90 mM
% Shoot Area
4 5 6 7 8
−5 −4 −2 −1 1 2 3 4 5 6 7 8 9 10 11 12 13 14
Days After 90 mM NaCl

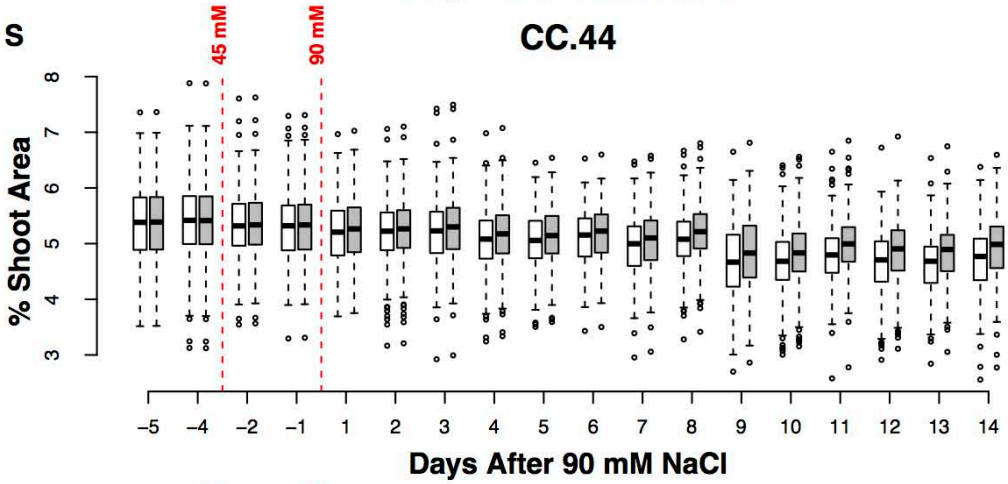

N
CC.33
45 mM
90 mM
% Shoot Area
3 4 5 6 7 8 9
−5 −4 −2 −1 1 2 3 4 5 6 7 8 9 10 11 12 13 14
Days After 90 mM NaCl

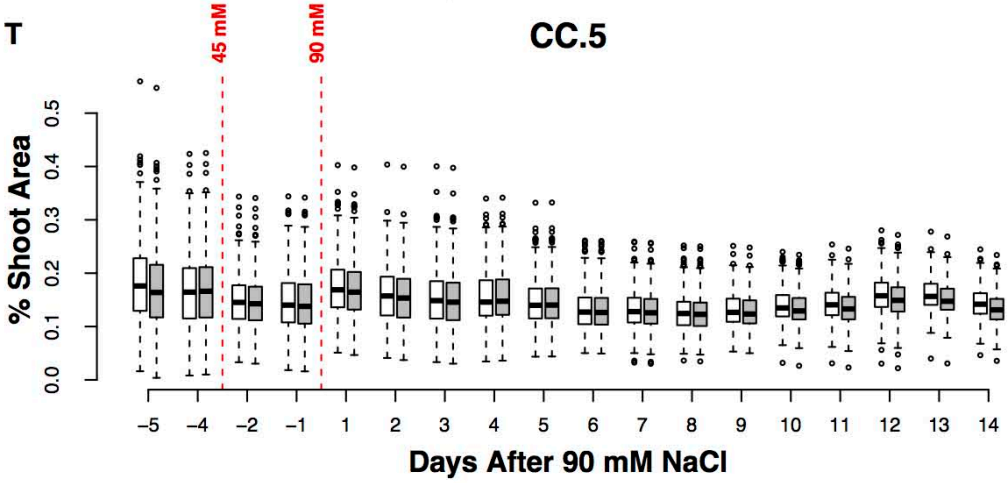

O
CC.34
45 mM
90 mM
% Shoot Area
3 4 5 6
−5 −4 −2 −1 1 2 3 4 5 6 7 8 9 10 11 12 13 14
Days After 90 mM NaCl

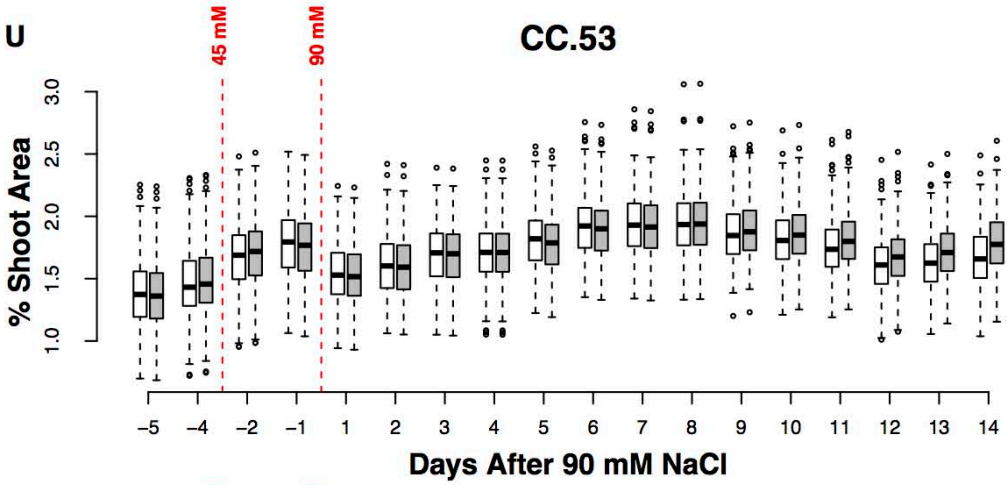

P
CC.37
45 mM
90 mM
% Shoot Area
0.0 0.2 0.4 0.6 0.8 1.0 1.2
−5 −4 −2 −1 1 2 3 4 5 6 7 8 9 10 11 12 13 14
Days After 90 mM NaCl

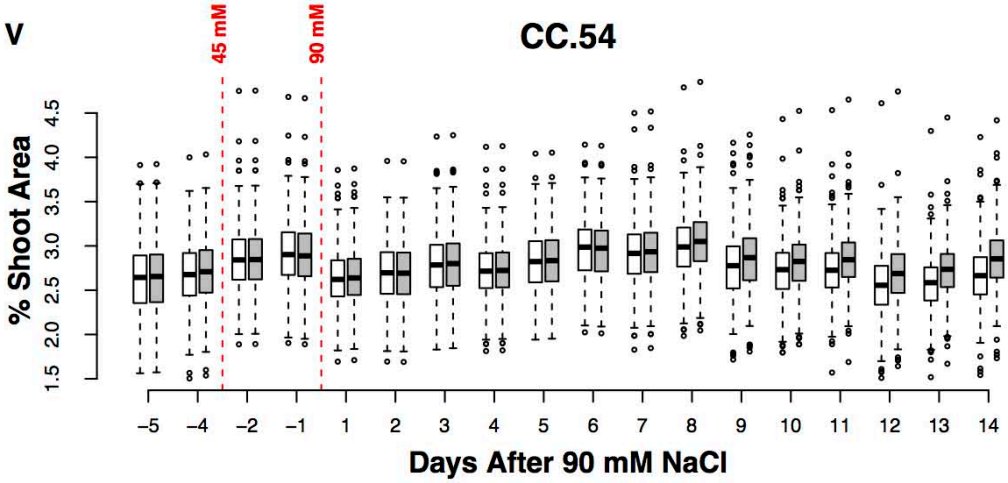

Q
CC.42
45 mM
90 mM
% Shoot Area
Days After 90 mM NaCl

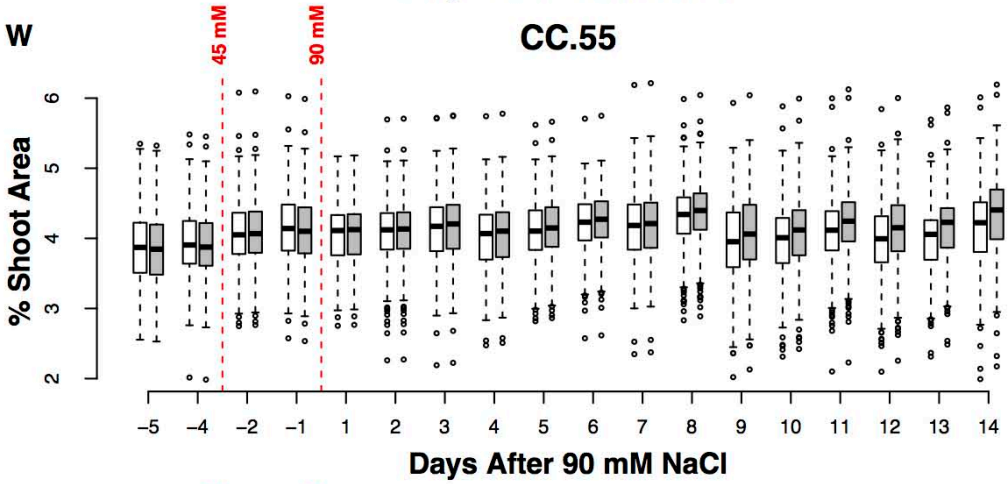

R
CC.43
45 mM
90 mM
% Shoot Area
Days After 90 mM NaCl

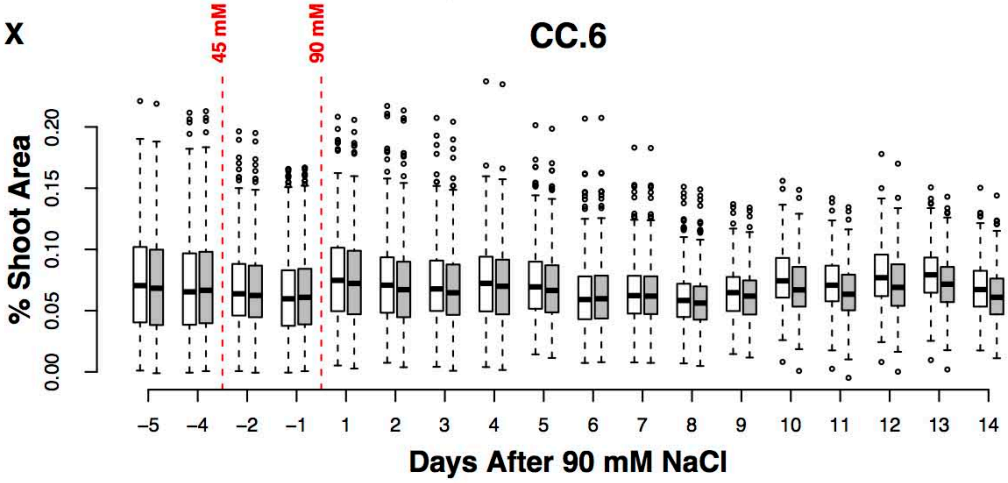

S
CC.44
45 mM
90 mM
% Shoot Area
Days After 90 mM NaCl

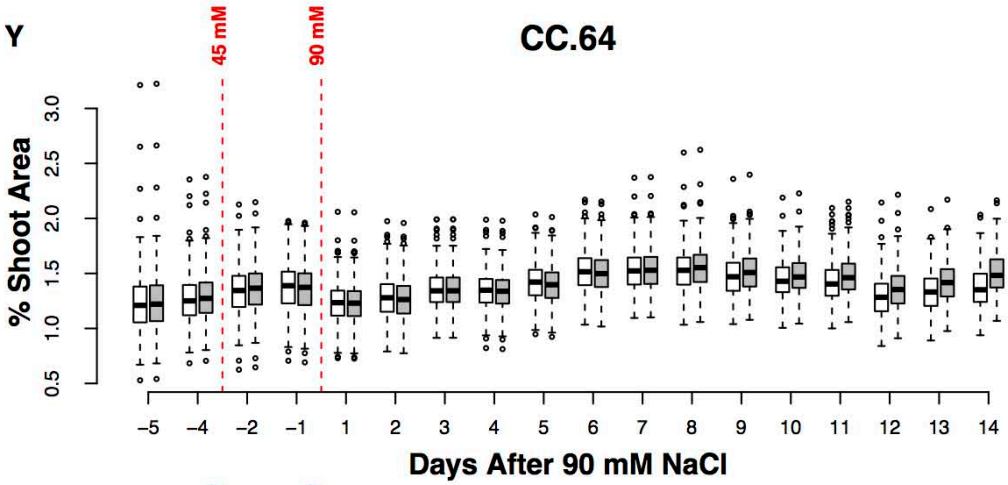

T
CC.5
45 mM
90 mM
% Shoot Area
Days After 90 mM NaCl

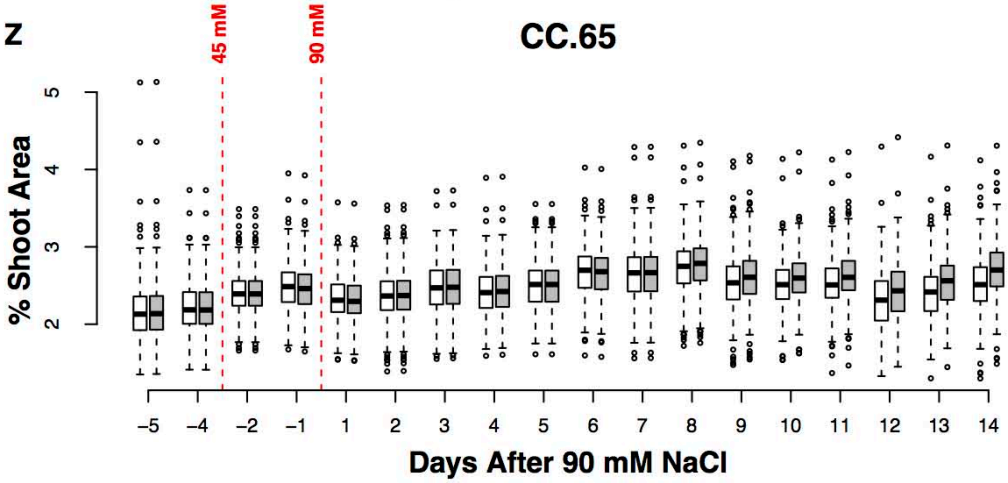

U
CC.53
45 mM
90 mM
% Shoot Area
1.0
1.5
2.0
2.5
3.0
−5
−4
−2
−1
1
2
3
4
5
6
7
8
9
10
11
12
13
14
Days After 90 mM NaCl

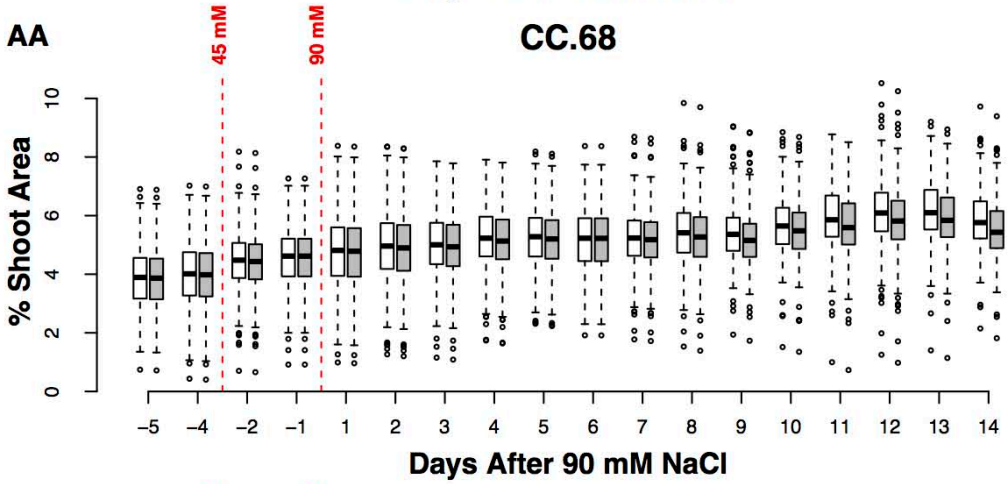

V
CC.54
45 mM
90 mM
% Shoot Area
1.5
2.0
2.5
3.0
3.5
4.0
4.5
−5
−4
−2
−1
1
2
3
4
5
6
7
8
9
10
11
12
13
14
Days After 90 mM NaCl

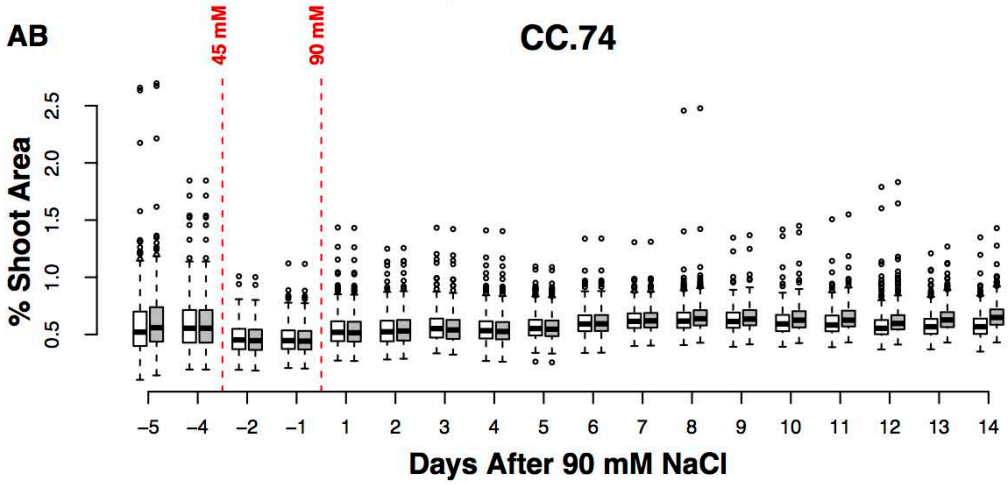

W
CC.55
45 mM
90 mM
% Shoot Area
2
3
4
5
6
−5
−4
−2
−1
1
2
3
4
5
6
7
8
9
10
11
12
13
14
Days After 90 mM NaCl

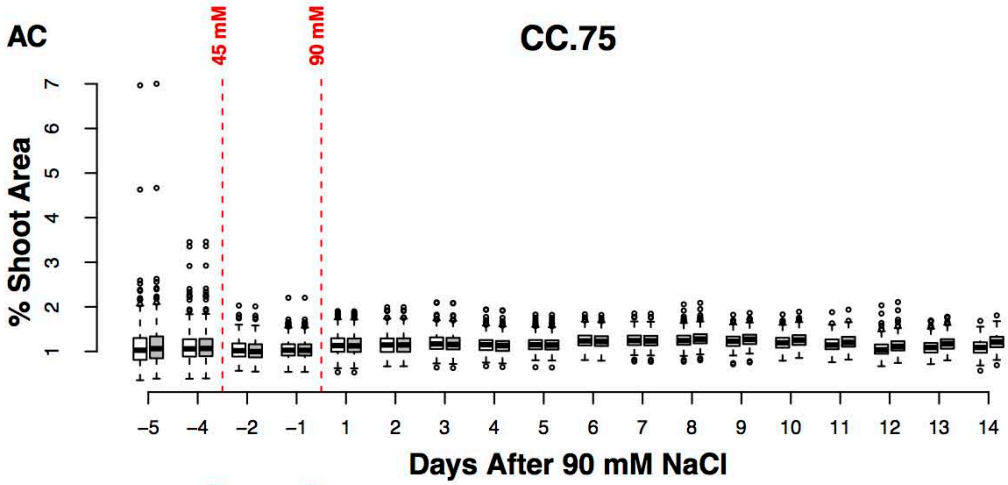

X
CC.6
45 mM
90 mM
% Shoot Area
0.00
0.05
0.10
0.15
0.20
−5
−4
−2
−1
1
2
3
4
5
6
7
8
9
10
11
12
13
14
Days After 90 mM NaCl

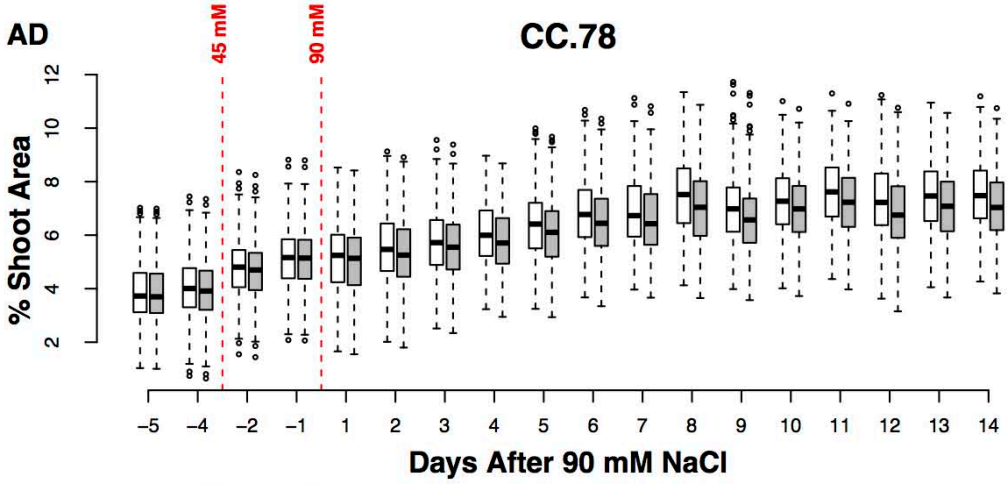

Y
CC.64
45 mM
90 mM
% Shoot Area
0.5
1.0
1.5
2.0
2.5
3.0
−5 −4 −2 −1 1 2 3 4 5 6 7 8 9 10 11 12 13 14
Days After 90 mM NaCl

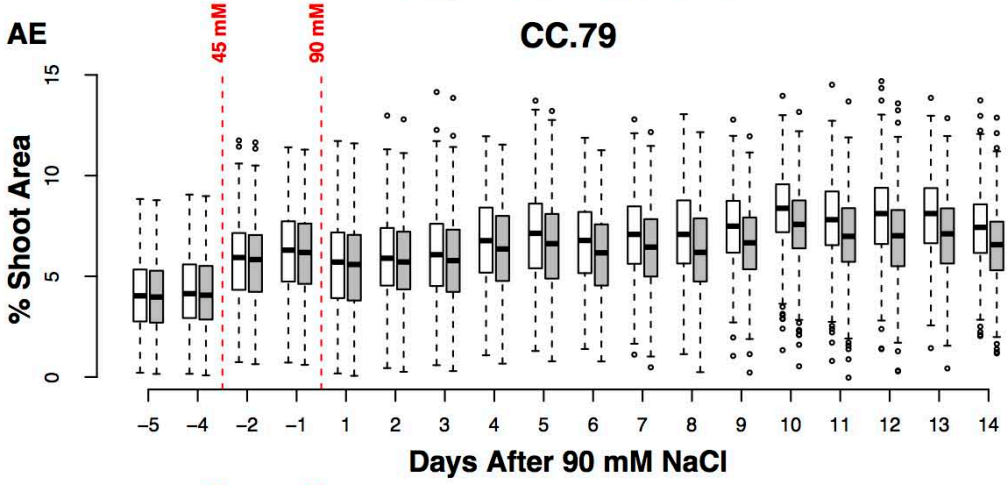

Z
CC.65
45 mM
90 mM
% Shoot Area
2
3
4
5
−5 −4 −2 −1 1 2 3 4 5 6 7 8 9 10 11 12 13 14
Days After 90 mM NaCl


AA
CC.68
45 mM
90 mM
% Shoot Area
0
2
4
6
8
10
−5 −4 −2 −1 1 2 3 4 5 6 7 8 9 10 11 12 13 14
Days After 90 mM NaCl


AB
CC.74
45 mM
90 mM
% Shoot Area
0.5
1.0
1.5
2.0
2.5
−5 −4 −2 −1 1 2 3 4 5 6 7 8 9 10 11 12 13 14
Days After 90 mM NaCl


AC
CC.75
45 mM
90 mM
% Shoot Area
1 2 3 4 5 6 7
−5 −4 −2 −1 1 2 3 4 5 6 7 8 9 10 11 12 13 14
Days After 90 mM NaCl


AD
CC.78
45 mM
90 mM
% Shoot Area
2 4 6 8 10 12
−5 −4 −2 −1 1 2 3 4 5 6 7 8 9 10 11 12 13 14
Days After 90 mM NaCl


AE
CC.79
45 mM
90 mM
% Shoot Area
0 5 10 15
−5 −4 −2 −1 1 2 3 4 5 6 7 8 9 10 11 12 13 14
Days After 90 mM NaCl

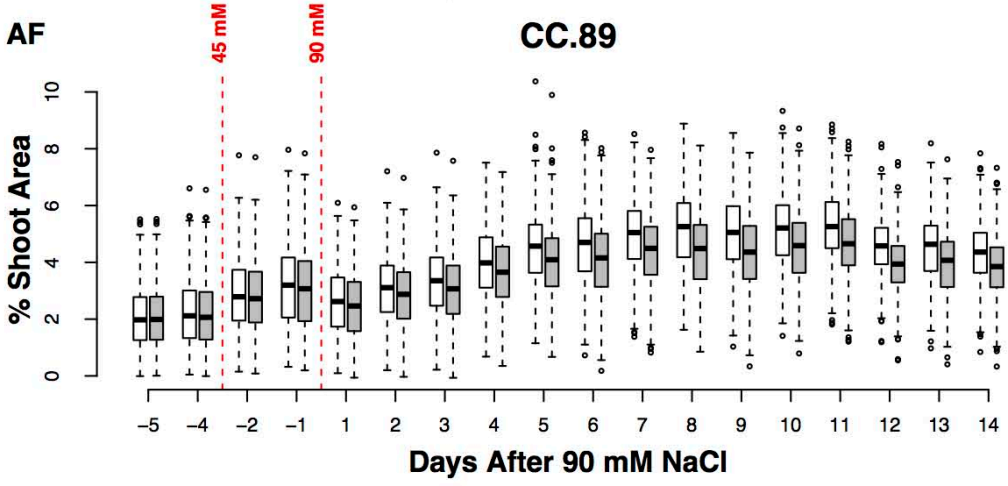
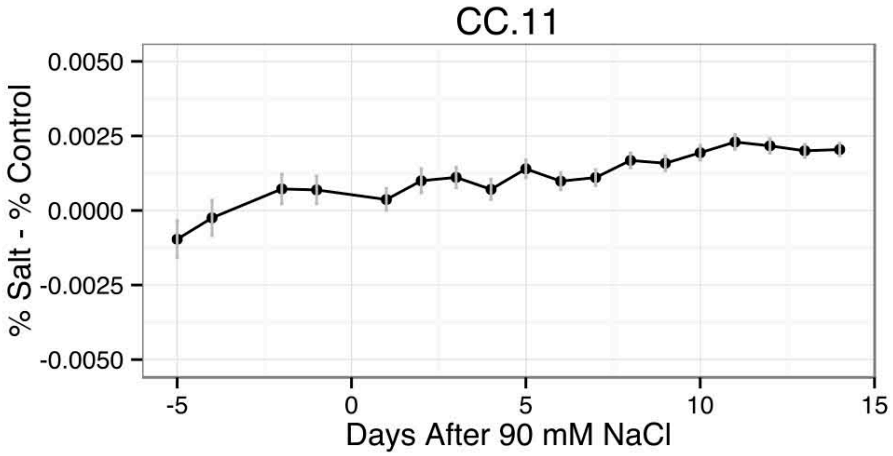
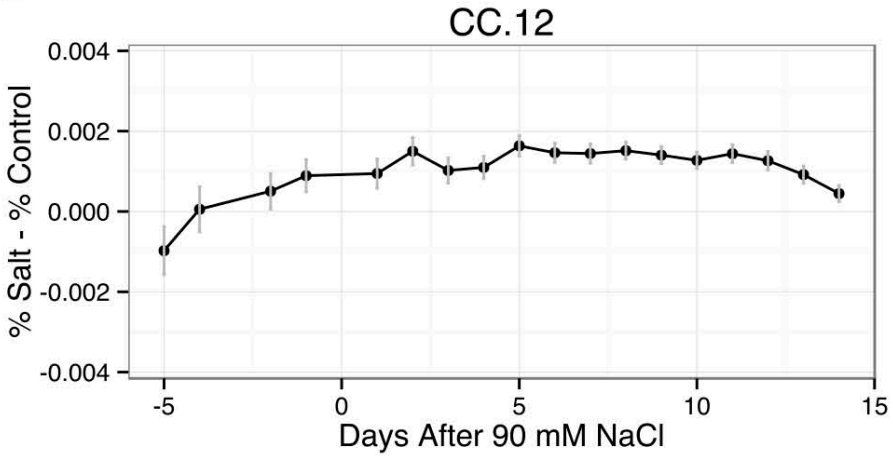

AF
CC.89
45 mM
90 mM
% Shoot Area
0 2 4 6 8 10
−5 −4 −2 −1 1 2 3 4 5 6 7 8 9 10 11 12 13 14
Days After 90 mM NaCl

**Fig S20:** (A-AF) Mean temporal trends of the 32 salinity-responsive fluorescence color classes. For each color class and accession we calculated the salinity response, which is defined as the percent of total pixels from two side-view images accounted for by the color class in saline conditions minus the percent of total pixels accounted by the class in control conditions. Error bars represent standard error.

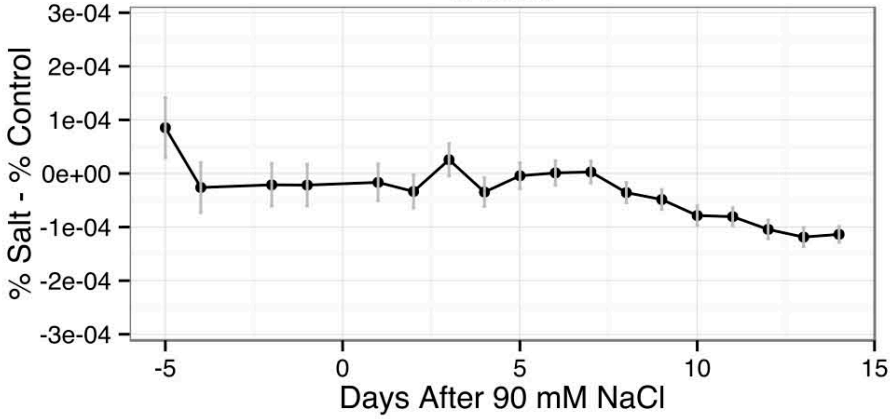
A


CC.11
% Salt - % Control
0.0050
0.0025
0.0000
-0.0025
-0.0050
-5
0
5
10
15
Days After 90 mM NaCl

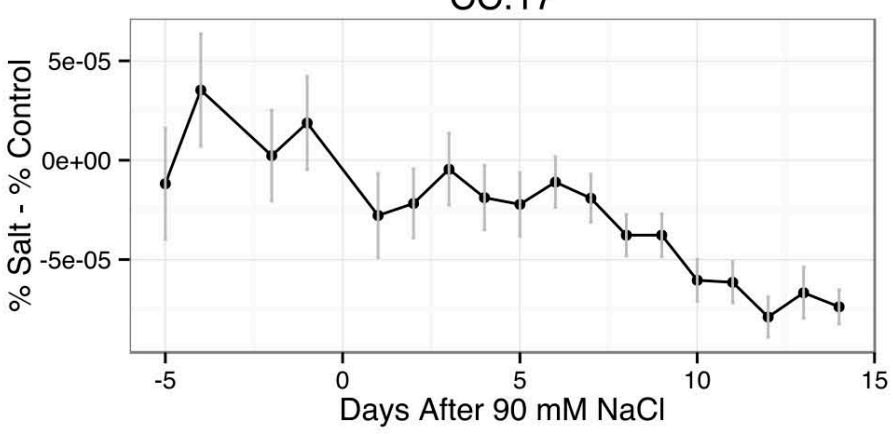
B

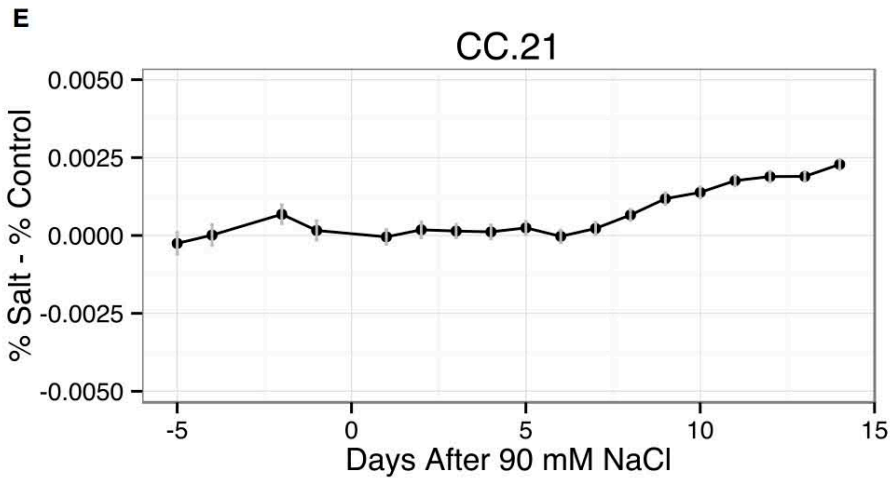

CC.12
% Salt - % Control
0.004
0.002
0.000
-0.002
-0.004
-5
0
5
10
15
Days After 90 mM NaCl

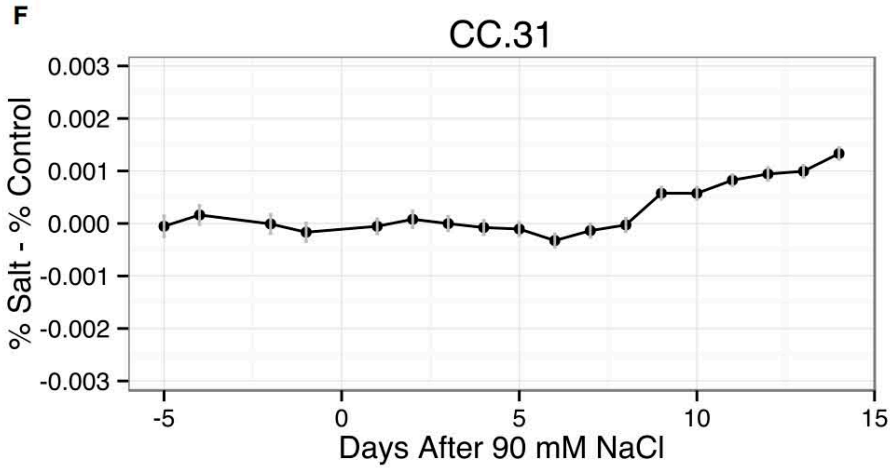
C

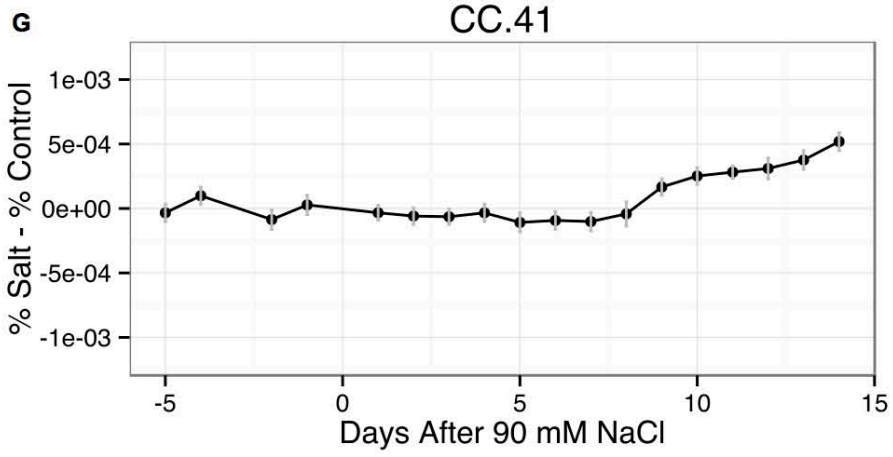

CC.16
% Salt - % Control
3e-04
2e-04
1e-04
0e+00
-1e-04
-2e-04
-3e-04
-5
0
5
10
15
Days After 90 mM NaCl

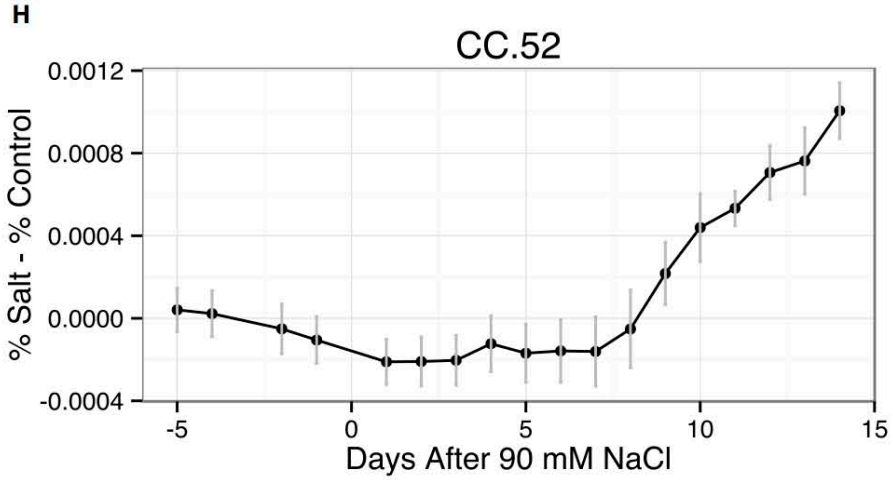
D


CC.17
% Salt - % Control
5e-05
0e+00
-5e-05
-5
0
5
10
15
Days After 90 mM NaCl

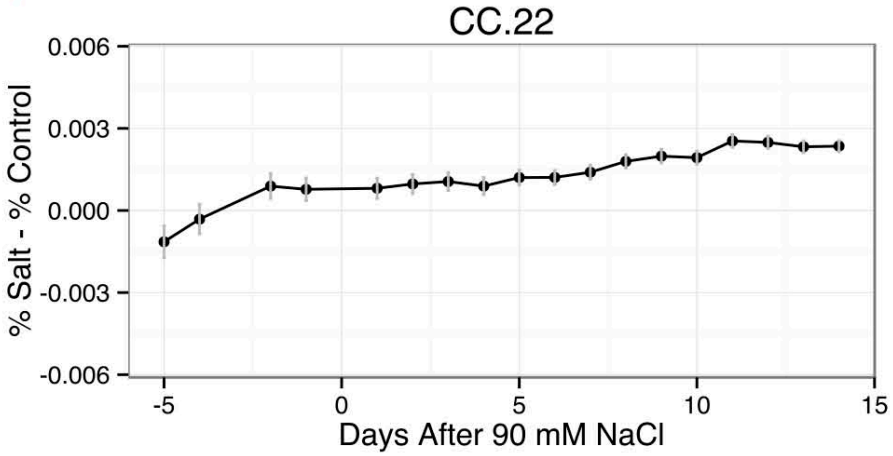

E
CC.21
0.0050
0.0025
0.0000
-0.0025
-0.0050
% Salt - % Control
-5
0
5
10
15
Days After 90 mM NaCl


F
CC.31
0.003
0.002
0.001
0.000
-0.001
-0.002
-0.003
% Salt - % Control
-5
0
5
10
15
Days After 90 mM NaCl

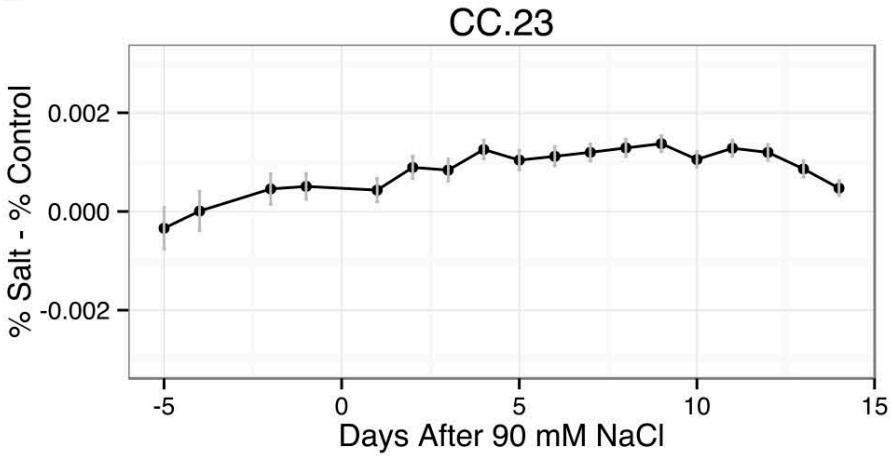

G
CC.41
1e-03
5e-04
0e+00
-5e-04
-1e-03
% Salt - % Control
-5
0
5
10
15
Days After 90 mM NaCl


H
CC.52
0.0012
0.0008
0.0004
0.0000
-0.0004
% Salt - % Control
-5
0
5
10
15
Days After 90 mM NaCl

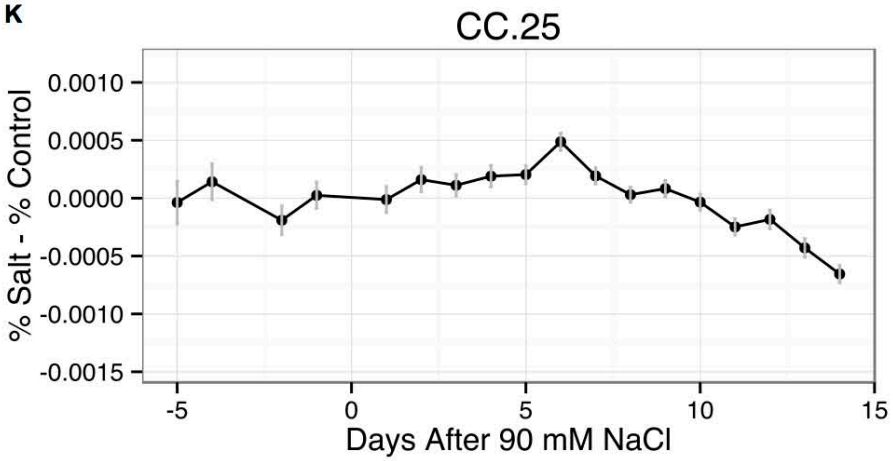
I


CC.22
0.006
0.003
0.000
-0.003
-0.006
% Salt - % Control
-5
0
5
10
15
Days After 90 mM NaCl

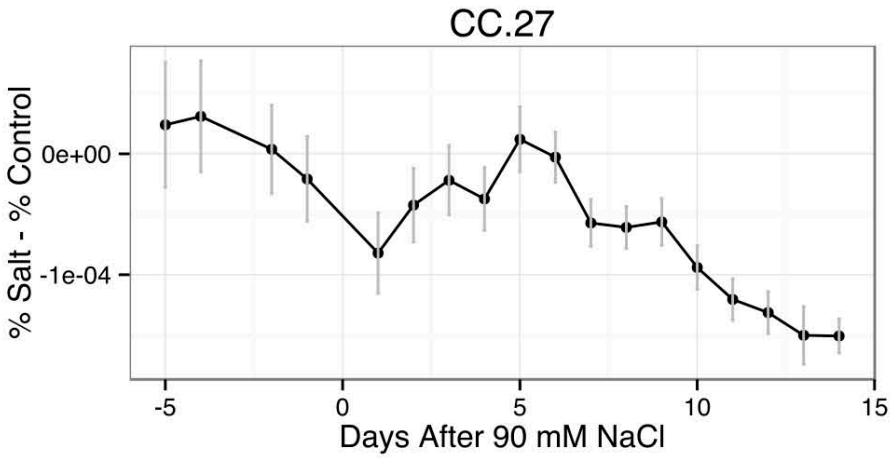
J


CC.23
0.002
0.000
-0.002
% Salt - % Control
-5
0
5
10
15
Days After 90 mM NaCl

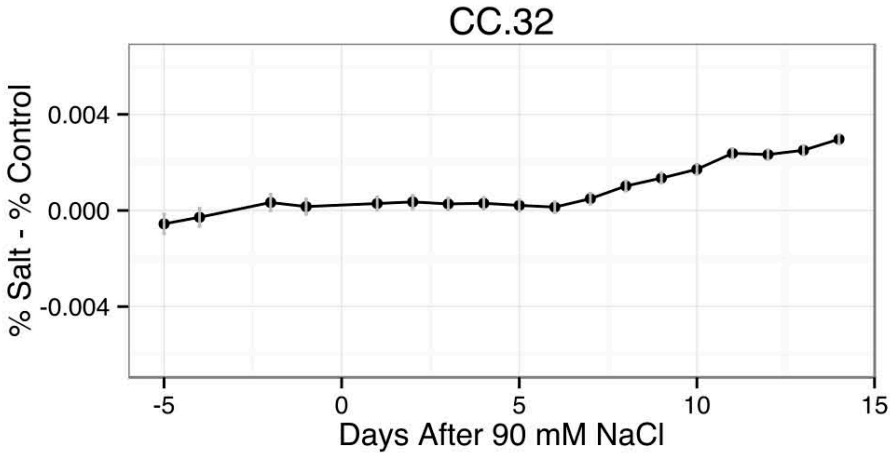
K


CC.25
0.0010
0.0005
0.0000
-0.0005
-0.0010
-0.0015
% Salt - % Control
-5
0
5
10
15
Days After 90 mM NaCl

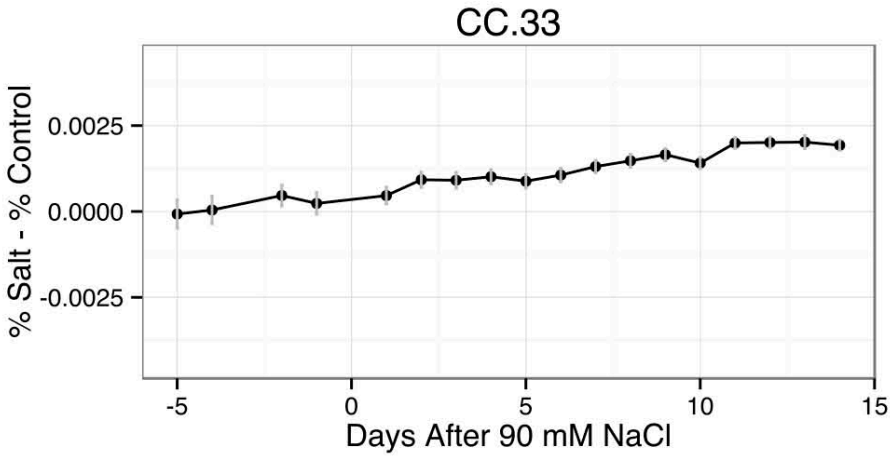
L


CC.27
0e+00
-1e-04
% Salt - % Control
-5
0
5
10
15
Days After 90 mM NaCl

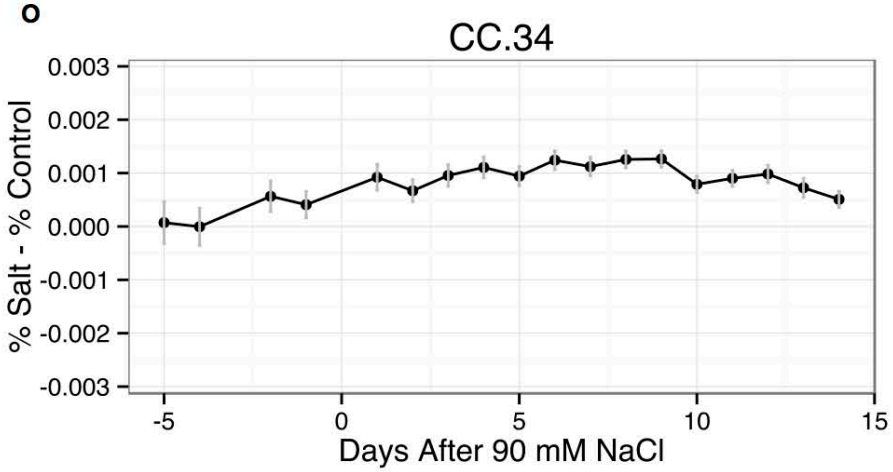
M


CC.32
% Salt - % Control
0.004
0.000
-0.004
-5
0
5
10
15
Days After 90 mM NaCl

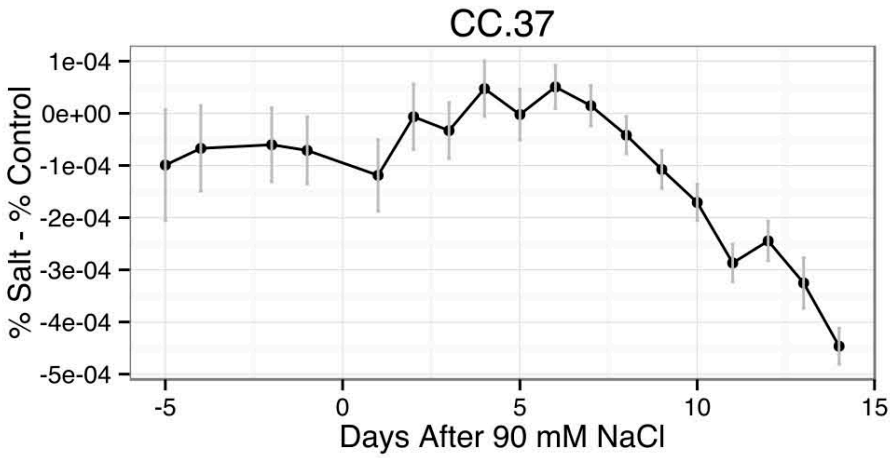
N


CC.33
% Salt - % Control
0.0025
0.0000
-0.0025
-5
0
5
10
15
Days After 90 mM NaCl

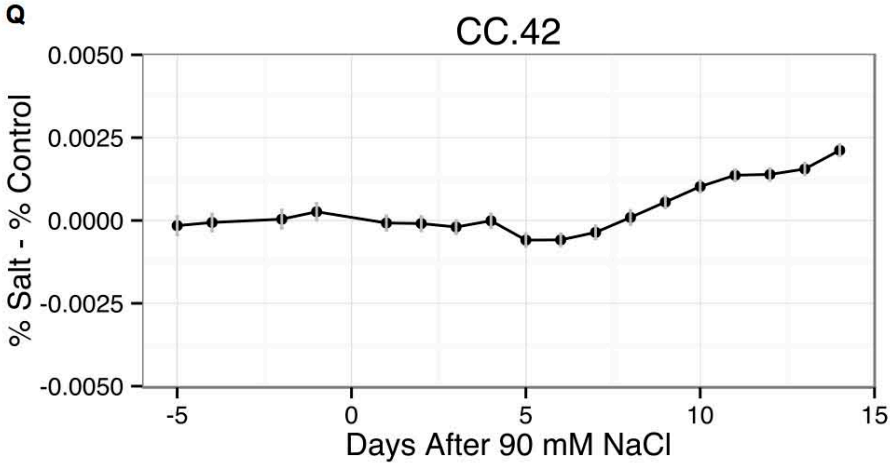
O


CC.34
% Salt - % Control
0.003
0.002
0.001
0.000
-0.001
-0.002
-0.003
-5
0
5
10
15
Days After 90 mM NaCl

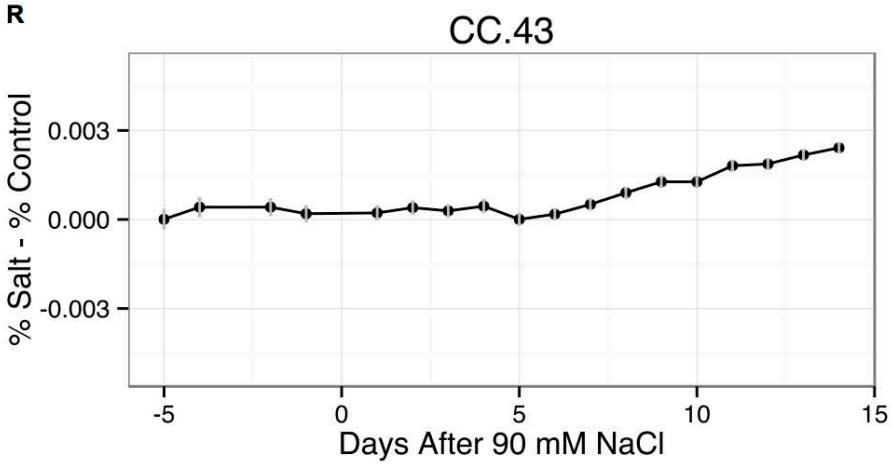
P


CC.37
% Salt - % Control
1e-04
0e+00
-1e-04
-2e-04
-3e-04
-4e-04
-5e-04
-5
0
5
10
15
Days After 90 mM NaCl

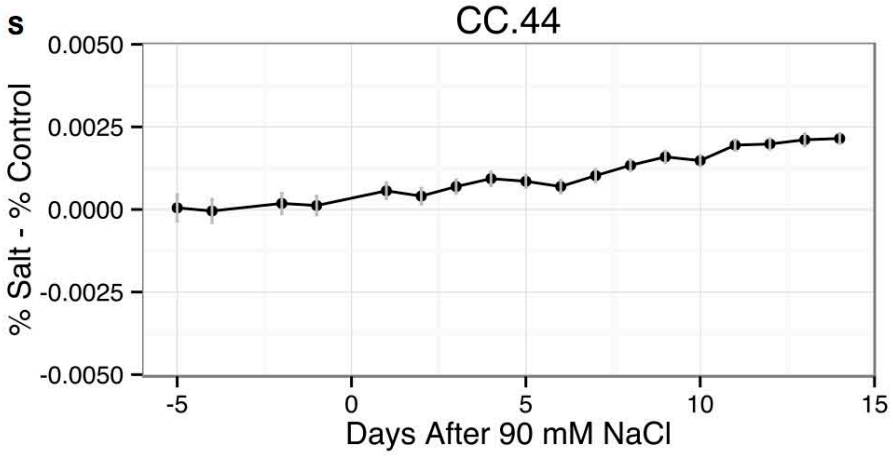
Q


CC.42
0.0050
0.0025
0.0000
-0.0025
-0.0050
% Salt - % Control
-5
0
5
10
15
Days After 90 mM NaCl

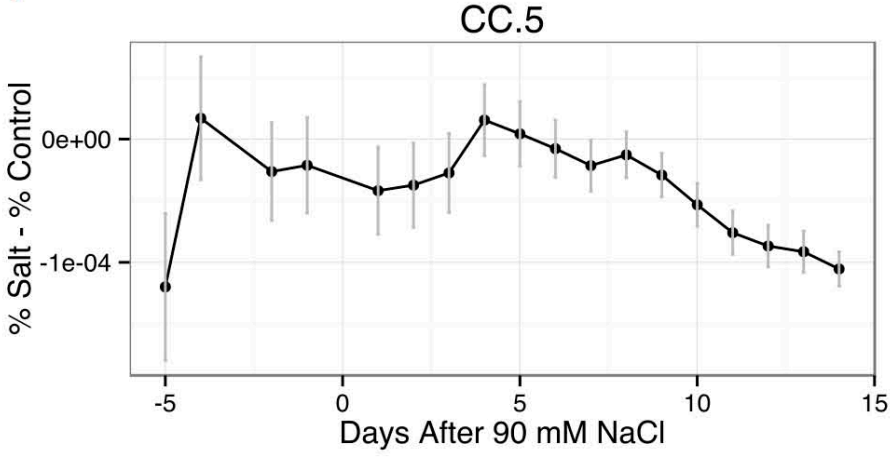
R


CC.43
0.003
0.000
-0.003
% Salt - % Control
-5
0
5
10
15
Days After 90 mM NaCl

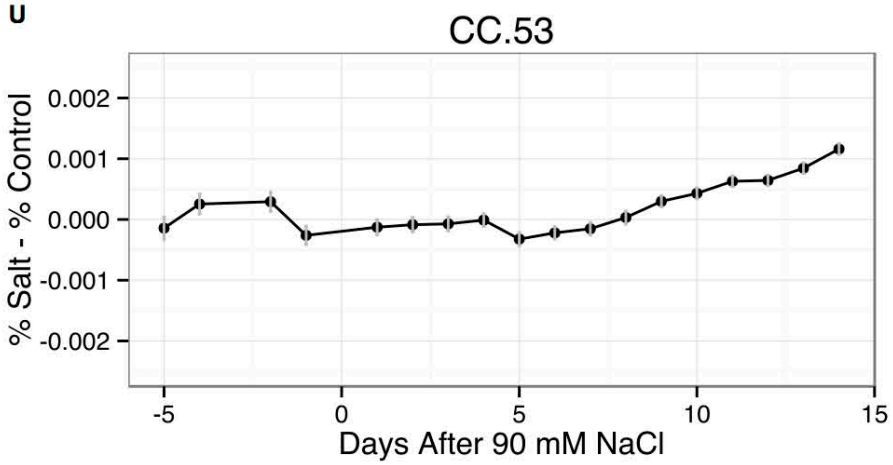
S


CC.44
0.0050
0.0025
0.0000
-0.0025
-0.0050
% Salt - % Control
-5
0
5
10
15
Days After 90 mM NaCl

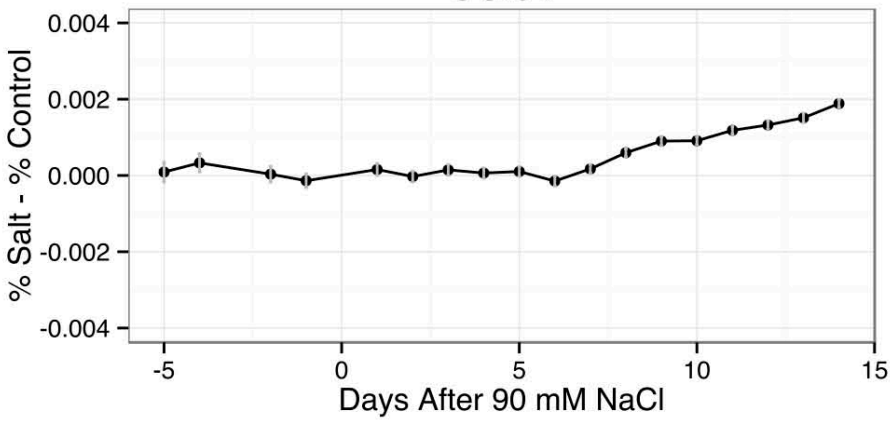
T


CC.5
0e+00
-1e-04
% Salt - % Control
-5
0
5
10
15
Days After 90 mM NaCl

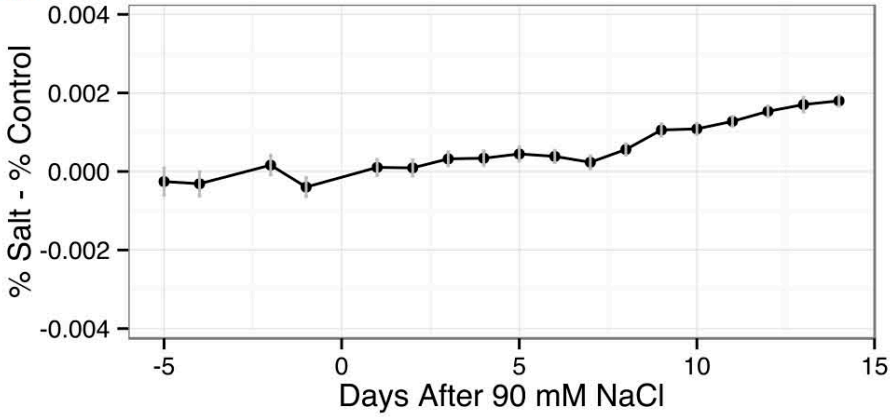
u


CC.53
% Salt - % Control
0.002
0.001
0.000
-0.001
-0.002
-5
0
5
10
15
Days After 90 mM NaCl

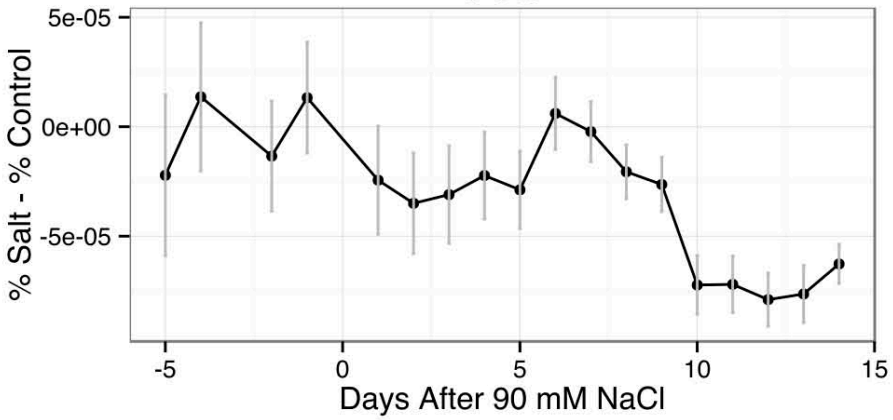
v


CC.54
% Salt - % Control
0.004
0.002
0.000
-0.002
-0.004
-5
0
5
10
15
Days After 90 mM NaCl

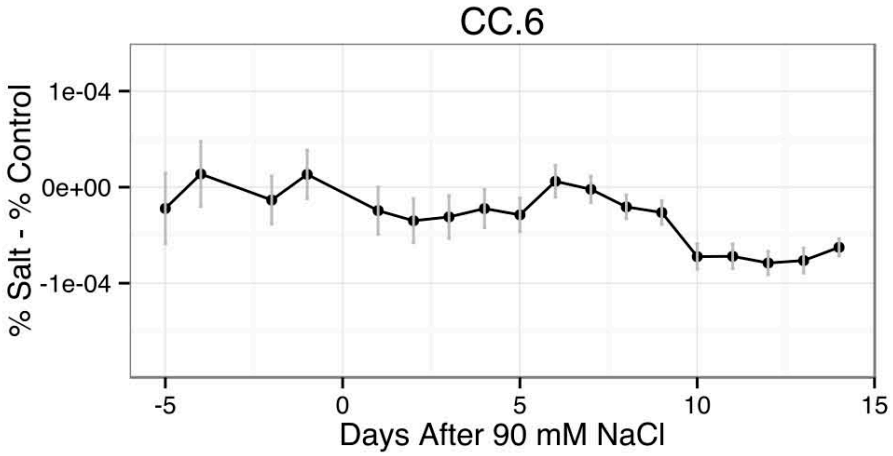
w


CC.55
% Salt - % Control
0.004
0.002
0.000
-0.002
-0.004
-5
0
5
10
15
Days After 90 mM NaCl

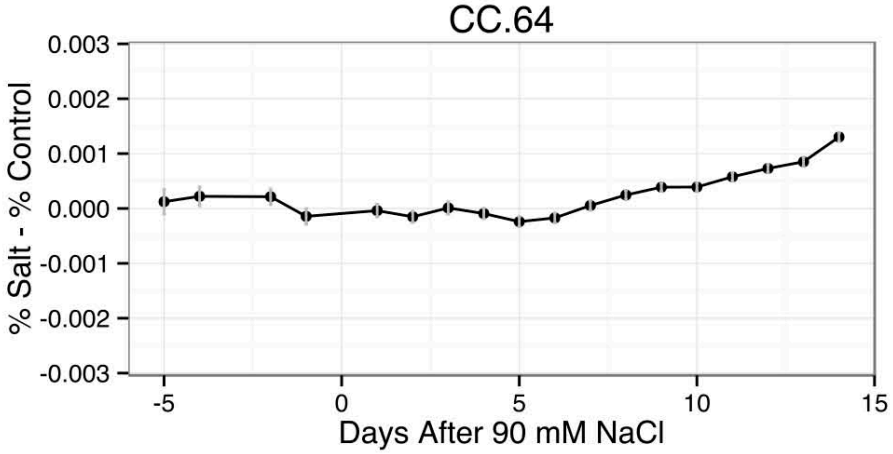
x


CC.6
% Salt - % Control
5e-05
0e+00
-5e-05
-5
0
5
10
15
Days After 90 mM NaCl

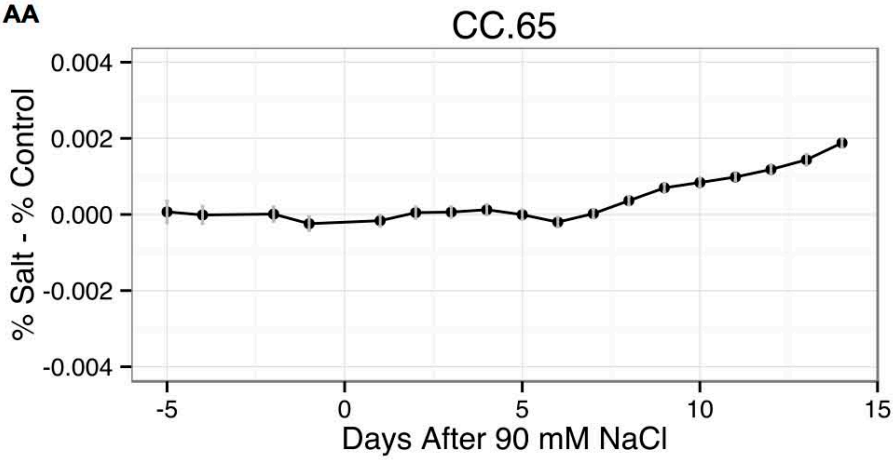
Y


CC.6
% Salt - % Control
1e-04
0e+00
-1e-04
-5
0
5
10
15
Days After 90 mM NaCl

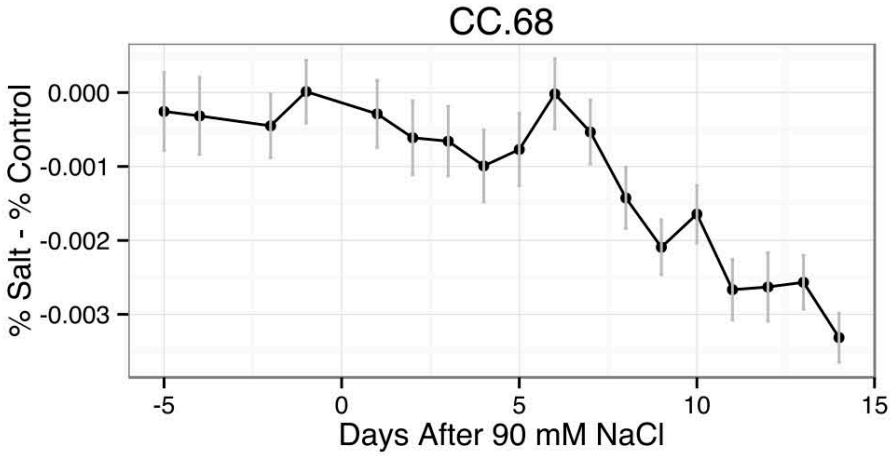
Z


CC.64
% Salt - % Control
0.003
0.002
0.001
0.000
-0.001
-0.002
-0.003
-5
0
5
10
15
Days After 90 mM NaCl

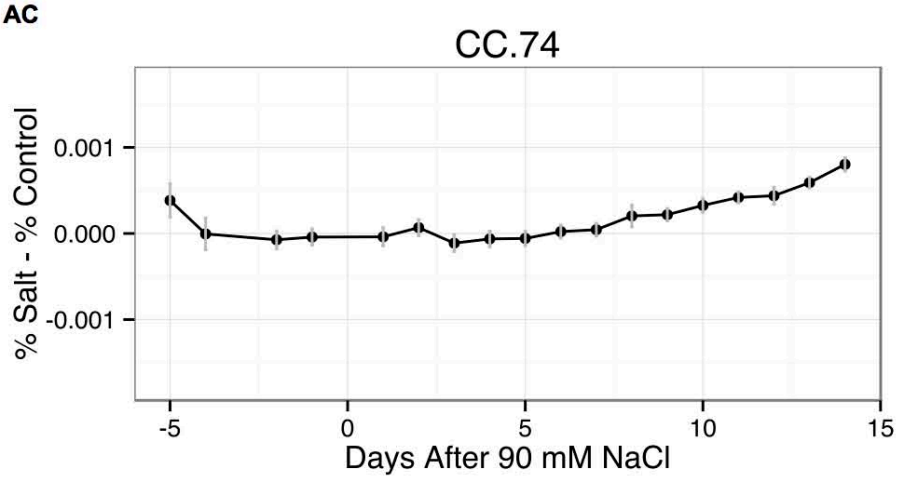
AA


CC.65
% Salt - % Control
0.004
0.002
0.000
-0.002
-0.004
-5
0
5
10
15
Days After 90 mM NaCl

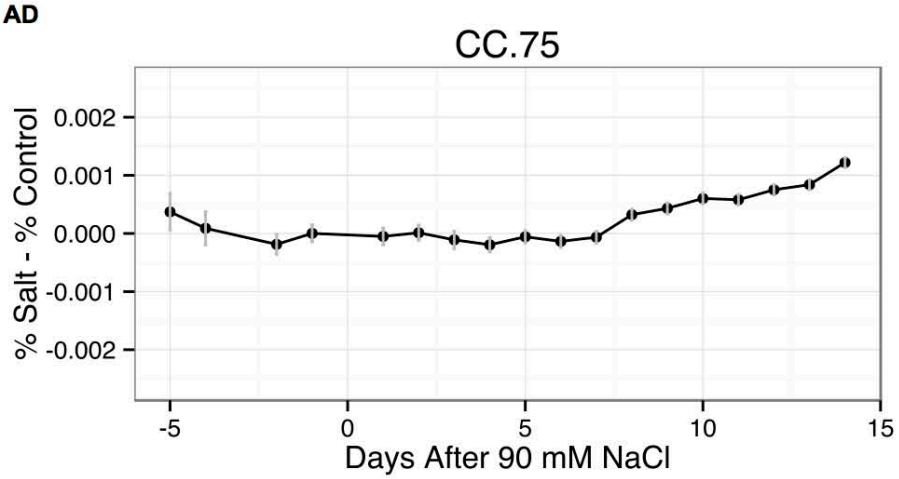
AB


CC.68
% Salt - % Control
0.000
-0.001
-0.002
-0.003
-5
0
5
10
15
Days After 90 mM NaCl

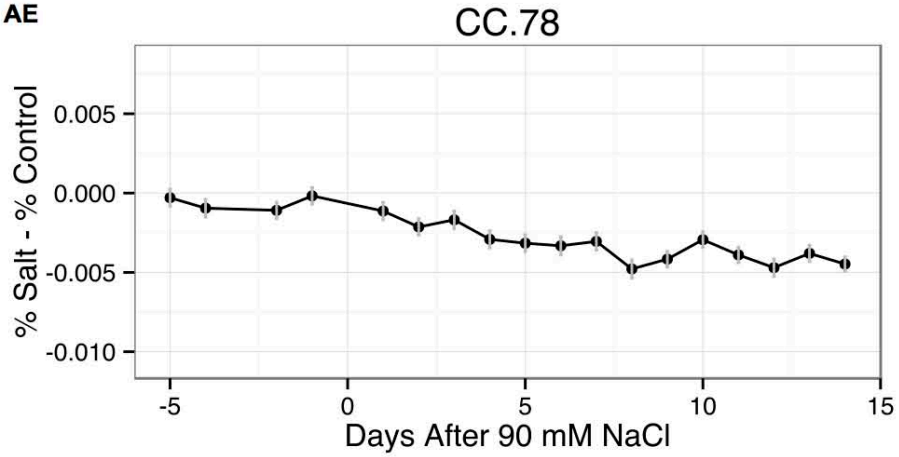
**AC**


CC.74
% Salt - % Control
0.001
0.000
-0.001
-5
0
5
10
15
Days After 90 mM NaCl

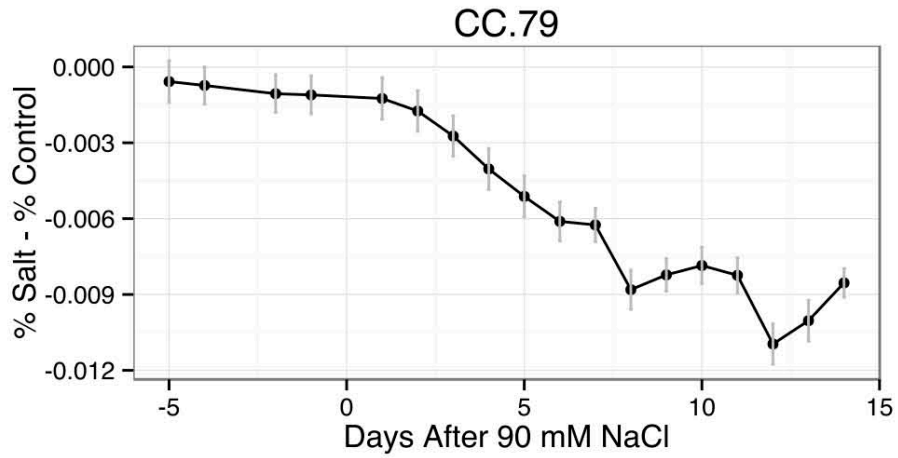
**AD**


CC.75
% Salt - % Control
0.002
0.001
0.000
-0.001
-0.002
-5
0
5
10
15
Days After 90 mM NaCl

**AE**


CC.78
% Salt - % Control
0.005
0.000
-0.005
-0.010
-5
0
5
10
15
Days After 90 mM NaCl

**AF**


CC.79
% Salt - % Control
0.000
-0.003
-0.006
-0.009
-0.012
-5
0
5
10
15
Days After 90 mM NaCl

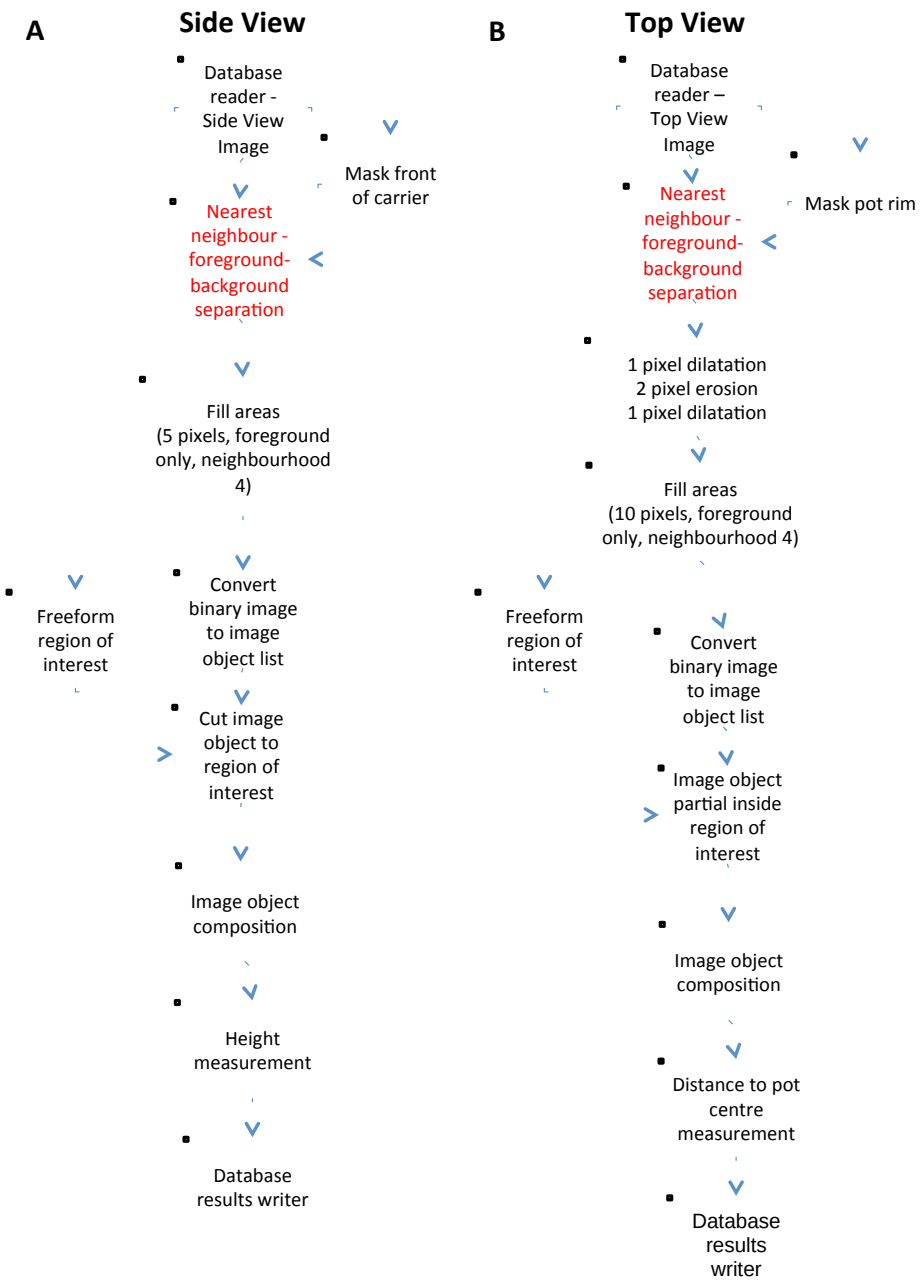



**Figure S21. LemnaGrid pipeline used to process RGB side (A) and top (B) view images.**

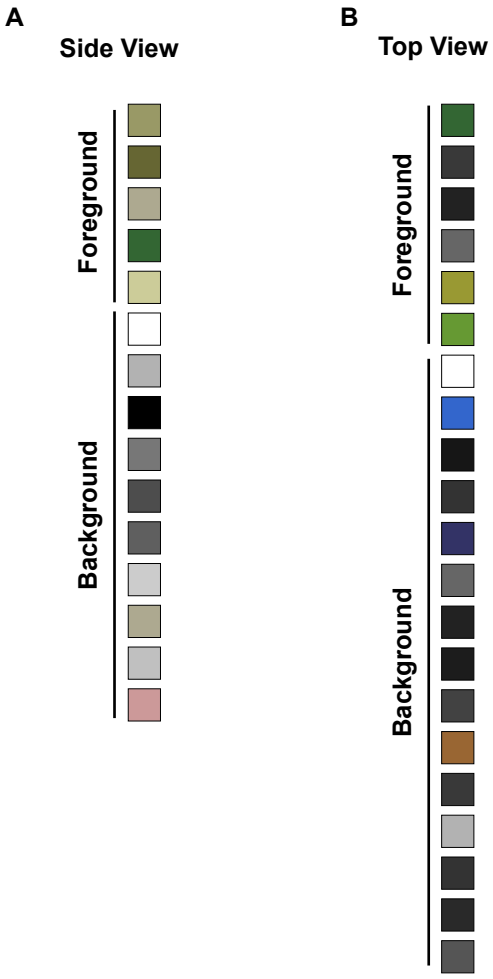



**Figure S22. Color classes used to define foreground and background pixels from RGB side view (A) and top view (B) images for the LemnaGrid Nearest Neighbor foreground-background colour separation method.**

**S1 Table:** Seven digital traits used to describe plant growth responses.

| Abbreviation | Image Type | Processing Platform | View | Definition |
|---|---|---|---|---|
| **MinR SV** | RGB (Visable) | LemnaGrid | SV1 + SV2 | The area of the minimum-enclosing rectangle enclosing the object. |
| **MinC SV** | RGB (Visable) | LemnaGrid | SV1 + SV2 | The diameter of the minimum enclosing circle enclosing the object. |
| **ConC SV** | RGB (Visable) | LemnaGrid | SV1 + SV2 | Circumference of the convex hull for the object. |
| **ConA SV** | RGB (Visable) | LemnaGrid | SV1 + SV2 | Area of the convex hull for the object. |
| **Ci SV** | RGB (Visable) | LemnaGrid | SV1 + SV2 | The circumference of the minimum circle that encloses the plant. |
| **CL SV** | RGB (Visable) | LemnaGrid | SV1 + SV2 | The greatest distance between any of the points within the convex hull. |
| **PSA** | RGB (Visable) | LemnaGrid | SV1 + SV2 + TV | Projected Surface Area. Sum of plant pixels from each view. |

The convex hull is the smallest shape that encloses a set of points *X*, so that any line drawn between points of *X* is enclosed within the shape.

**Table S2. Accuracy of digital traits for describing biomass and shoot area.** Pearson correlation analysis of seven growth-related digital metrics and three manual measurements. Asterisks indicate statistical significance ($p < 0.001$).

| | Plant Area | Fresh Wt. | Dry Wt. | PSA | CL SV | Ci SV | ConA SV | ConC SV | MinC SV | MinR SV |
|---|---|---|---|---|---|---|---|---|---|---|
| **MinR SV** | -0.04 | -0.11 | -0.09 | -0.04 | -0.44* | -0.41* | -0.5* | -0.46* | 0.96* | 1 |
| **MinC SV** | -0.1 | -0.16 | -0.13 | -0.11 | -0.36 | -0.46* | -0.47* | -0.42* | 1 | |
| **ConC SV** | 0.35 | 0.43* | 0.4* | 0.43* | 0.95* | 0.44* | 0.97* | 1 | | |
| **ConA SV** | 0.38 | 0.47* | 0.43* | 0.46* | 0.89* | 0.4* | 1 | | | |
| **Ci SV** | 0.34 | 0.36 | 0.35 | 0.38* | 0.41* | 1 | | | | |
| **CL SV** | 0.25 | 0.32 | 0.3 | 0.32 | 1 | | | | | |
| **PSA** | 0.96* | 0.95* | 0.95* | 1 | | | | | | |
| **Dry Wt.** | 0.96* | 0.97* | 1 | | | | | | | |
| **Fresh Wt.** | 0.96* | 1 | | | | | | | | |
| **Plant Area** | 1 | | | | | | | | | |

**Table S3. Candidate genes underlying significant SNPs.** All genes within 200kb of a significant SNP were considered as possible candidates. A significance threshold of $p < 10^{-8}$ was used for logistic growth-response association analysis, and $p < 10^{-7}$ for GWA of salinity-induced fluorescence responses. SNP positions are based on MSU build 7.

| Trait(s) | Chr. | SNP Position | SNP ID | p-value | Rice Gene | Rice Annotation | Arabidopsis Annotation | | Reference(s) |
|---|---|---|---|---|---|---|---|---|---|
| Growth | 1 | 7447351 | dd1001171 | 1.89E-11 | LOC_Os01g13460 | Helix-loop-helix DNA-binding domain containing protein | AT2G46510 | AIB | (Li et al., 2007) |
| Growth | 2 | 32258316 | id2014363 | 5.79E-10 | LOC_Os02g52780 | bZIP transcription factor | AT3G19290 | ABF4 | (Choi et al., 2005) |
| Growth | 3 | 11079914 | id3005794 | 2.25E-10 | LOC_Os03g19720 | EF hand family protein | AT5G49480 | AtCP1 | (Jang et al., 1998) |
| Growth | 3 | 16293444 | id3008139 | 1.11E-16 | LOC_Os03g28120 | Potassium channel protein | AT2G26650 | AKT1 | (Hirsch et al., 1998) |
| Growth | 6 | 27647390 | id6015813 | 2.81E-09 | LOC_Os06g45940 | Potassium transporter | AT2G30070 | AtKT1 | - |
| Growth | 7 | 26461039 | id7005111 | 9.45E-09 | LOC_Os07g44290 | CAMK-KIN1/SNF1/Nim1-like.29 | AT3G17510 | CIPK1 | (D'Angelo et al., 2006) |
| Growth | 9 | 879018 | ud9000038 | 7.15E-09 | LOC_Os09g02214 | Citrate transporter protein | AT3G19490 | AtNHD1 | (Müller et al., 2014) |
| Growth | 9 | 16562832 | id9005164 | 2.05E-11 | LOC_Os09g27580 | Potassium transporter | AT2G30070 | AtKT1 | - |
| Growth | 12 | 25277179 | id12009128 | 1.17E-10 | LOC_Os12g40830 | PFKB kinase family | AT5G37850 | AtSOS4 | (Shi et al., 2002) |
| Growth | 1 | 25003341 | id1014913 | 3.18E-11 | LOC_Os01g43410 | CAMK-like.9 | AT4G23650 | CDPK6 | (Latz et al., 2013) |
| FLUO (cc.41) | 1 | 27738377 | id1016079 | 2.57E-08 | LOC_Os01g48680 | Two pore calcium channel protein 1 | AT4G03560 | AtCCH1 | (Choi et al., 2014) |
| FLUO (cc.41, cc.52) | 1 | 29950678 | id1017845 | 4.11E-09 | LOC_Os01g52070 | Potassium channel AKT1 | AT4G32650 | AtKC1 | (Geiger et al., 2009) |
| FLUO (cc.31, cc.41, cc.52) | 1 | 30454089 | id1018311 | 6.52E-08 | LOC_Os01g53294 | Respiratory burst oxidase protein B | AT1G64060 | RBOH F | (Ma et al., 2012) |

**Table S4. LemnaGrid devices used for processing RGB images and corresponding ImageHarvest/OpenCV functions.**

| LemnaGrid Device | LemnaGrid Parameters | Definition | ImageHarvest Function(s)* |
|---|---|---|---|
| Nearest Neighbor foreground-background colour separation | 5 foreground colors, 10 background colors (see Fig. S21 for colors) | A set of colours are selected in that represent background and foreground objects. Each pixel in the image is assigned to background or foreground class using nearest neighbour method. | knn(self, k labels)<br>self: class containing image<br>k: number of forground colors classes<br>labels: List of BGR (blue, green, red) ranges that define the plant/foreground object |
| Fill Holes | Five pixels (foreground only); neighborhood 4 | A hole, which is defined as a background area that is completely surrounded by the foreground object, is filled using the user-defined parameters and is added to the foreground object. | cv2.findContours(img,cv2.RETR_CCOMP,cv2.CHAIN_APPROX_SIMPLE)<br>img: An 8-bit single-channel image<br>cv2.RETR_CCOMP: Contour retrieval mode (see OpenCV documentation for complete description)<br><br>cv2.CHAIN_APPROX_SIMPLE: Contour approximation method (see OpenCV documentation for complete description)<br>cv2.drawContours(img,contour)<br>img: An 8-bit single-channel image |
| Morphological Filter | 1 pixel dilation, 2 pixel erosion, 1 pixel dilation | This device performs a defined series of pixel size reduction steps on a binary image to eliminate small noise from the foreground object. | cv.Erode(src, dst, element=None, iterations=1)<br>cv.Dilate(src, dst, element=None, iterations=1)<br>src: source image<br>dst: output image of the same size as src<br>element: a structuring element used for erosion/dilation |

*LemnaGrid is a proprietary software, and while these functions may be related to LemnaGrid devices they are not exact replicates.

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