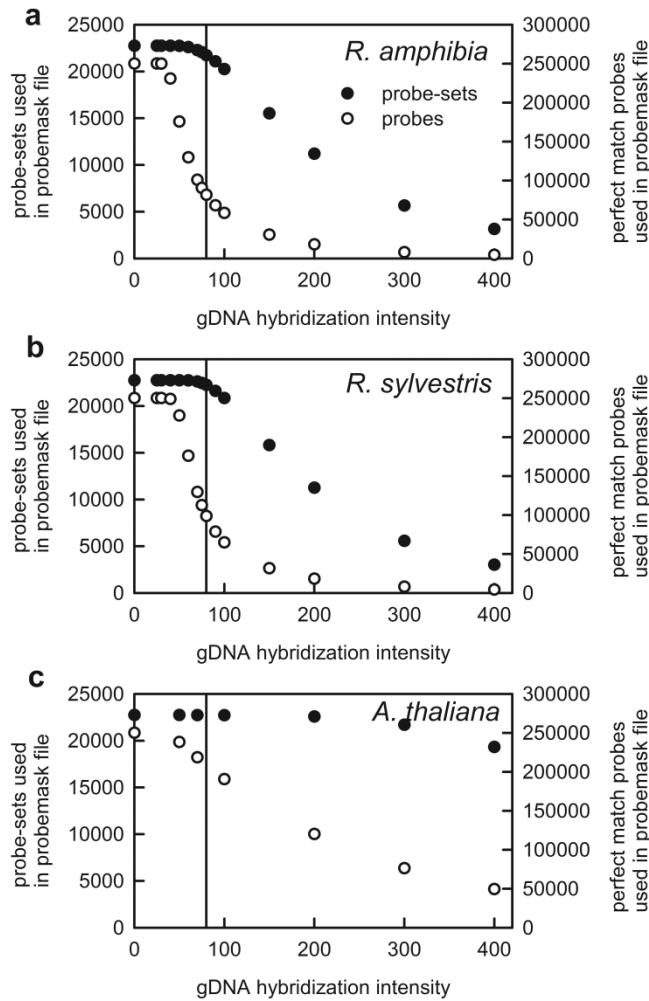


# 1 Supplemental information



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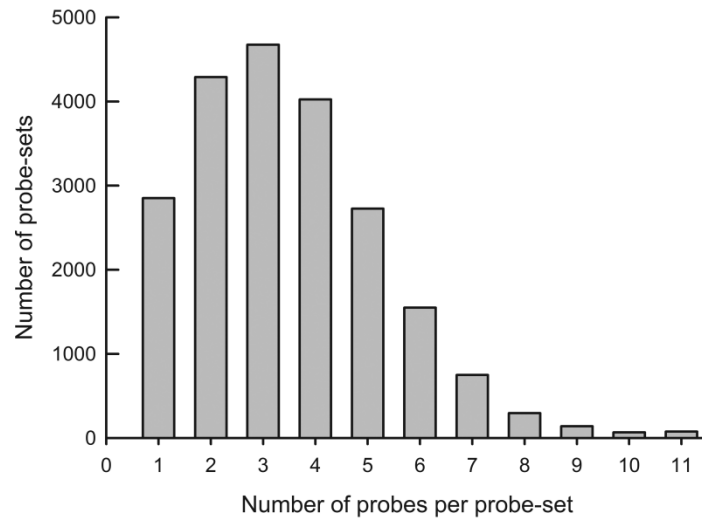
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5 **Figure S1.** *Rorippa* genomic DNA (gDNA) hybridisation based probe selection of Ath  
6 GeneChips.

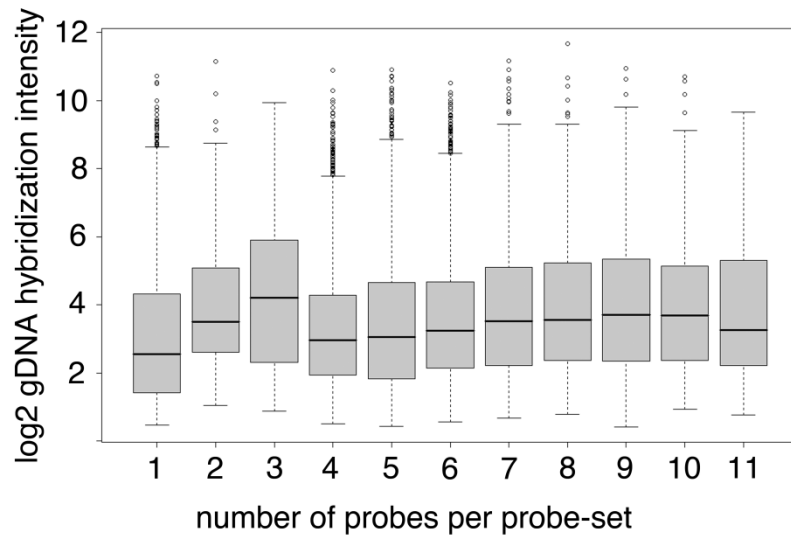
7 (a) *R. amphibia* and (b) *R. sylvestris* gDNA was hybridized to the Affymetrix Ath1  
8 GeneChip. Within a probe-set of 11 probes interrogating one gene, probes were removed  
9 if their hybridisation intensity was below a given threshold and a probe mask (a CDF file)  
10 was created containing the remaining probes and probe-sets. When all 11 probes of a set  
11 were removed, that set was also removed. Shown are numbers of probes and probe-sets  
12 as affected by applying a probe mask based on gDNA hybridisation intensity. (c) Same  
13 procedure applied to gDNA of *Arabidopsis thaliana* shown for comparison.

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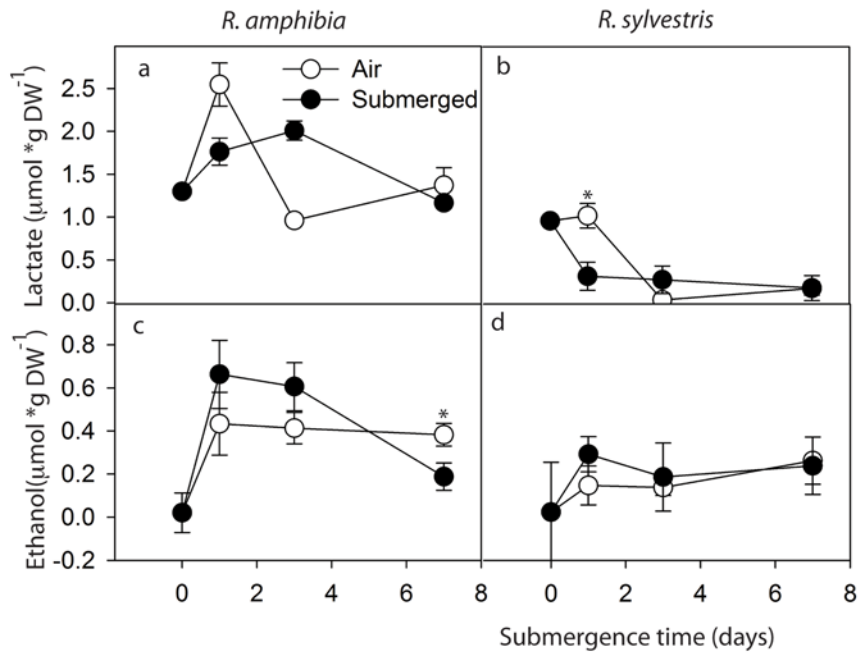
**Figure S2.** Histogram of number of probes per probe-set.



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3 **Figure S3.** Boxplots showing the average of *R. amphibius* and *R. sylvestrus* gDNA  
4 hybridization intensity by the number of probes per probe-set.

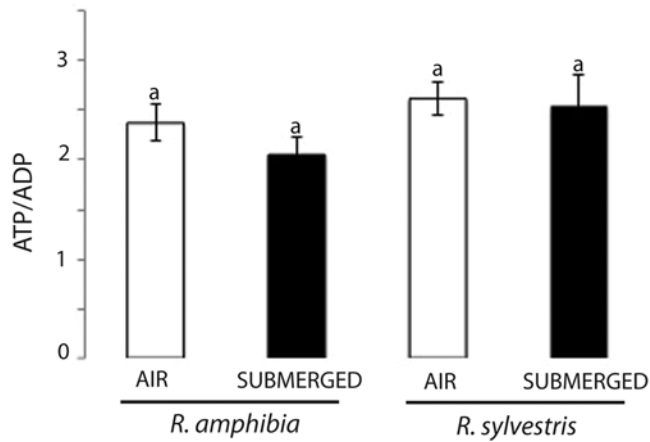
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**Figure S4.** Submergence-induced changes in fermentation end products in *Rorippa* roots. (a, b) Ethanol and (c, d) lactate content in the roots of *R. amphibia* (a, c) and *R. sylvestris* (b, d) plants that were completely submerged (black circles) or kept in air (white circles) for 1, 3 and 7 days. Values are means of 5 biological replicates  $\pm$  SE. Asterisks indicate significant differences between air and submerged values at that time-point ( $P < 0.05$ ; Student's *t*-test). A significant (ANOVA) species effect was found for both ethanol ( $F = 13.2$ ;  $P < 0.05$ ) and lactate ( $F = 61.8$ ;  $P < 0.05$ ). Values are express on a dry weight (DW) basis.

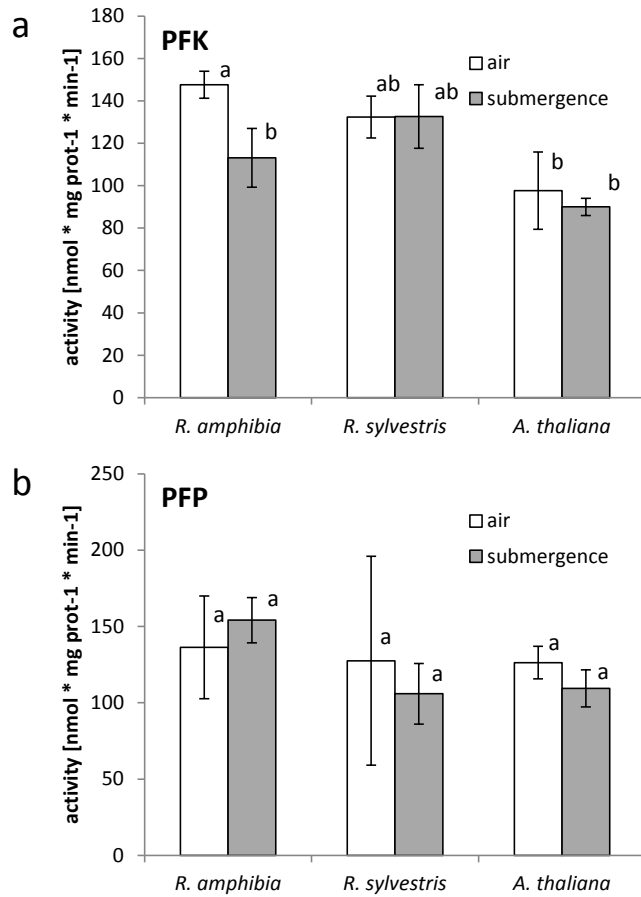
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4 **Figure S5.** Submergence-induced changes in the ATP/ADP ratio in *Rorippa*. The energy  
5 charge ATP/ADP was calculated from measurements of ATP and ADP (Figure 6) in the  
6 roots of *Rorippa* plants exposed to 24h of complete submergence or control (air)  
7 conditions. Data are means  $\pm$  SE (n=8). Different letters above bars denote statistically  
8 significant differences (P<0.05) (Tukey's "Honest Significant Difference" test).

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**Figure S6.** Enzyme activities in roots of *Rorippa* or *Arabidopsis* plants that were submerged (gray bars) for 24 h, or were kept in aerated soil (white bars). (a) Phosphofructokinase (ATP-dependent) (PFK) (b) Pyrophosphate-Fructose-6-Phosphate-phosphotransferase (PFP). Values are means of 5 biological replicates  $\pm$  SD. Different letters indicate significant differences from an Tukey's “Honest Significant Difference” test at  $P < 0.05$ .

1 **Table S5:** Sequences of primer combinations (5'-3') for the *Arabidopsis* and *Rorippa*  
 2 genes studied using real-time RT-PCR. \* Sequences from Akman et al. 2011

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| Gene name                          | AGI code  | Forward Primer                  | Reverse Primer                   |
|------------------------------------|-----------|---------------------------------|----------------------------------|
| <b><i>Arabidopsis thaliana</i></b> |           |                                 |                                  |
| <i>PFK6</i>                        | At4g32840 | GGGAGATCGTGTGGTCTT              | TGTCACTCACAGTCTTCGGC             |
| <i>ADH1</i>                        | At1g77120 | GGTCTTGGTGCTGTTGGTTT            | CTCAGCGATCACCTGTTGAA             |
| <i>CXXS1</i>                       | At1g11530 | GCGATGCCAACTTTCTTGTT            | ACTGAACGAAACCATCGACC             |
| <i>GH</i>                          | At2g43610 | CACAAAAGCCTACTGTGGCA            | GTACCACGAGGACCAGCATT             |
| <i>PFPB2</i>                       | At1g76550 | ATGACGGTTAAGCGTTGGTC            | TGCGCGTTTTGTCTCAATAG             |
| <i>PFPA2</i>                       | At4g04040 | GATGAAGAAGGCCAATGGAA            | AGCTCGGTTTCAACCATTTG             |
| <i>PAO</i>                         | At3g44880 | ATCACCAAATCCCAATCCAA            | GCGTAAAGGGTTGTGGAAAA             |
| <i>AGT3</i>                        | At2g38400 | GAATTGGGAATGGGTTTCCT            | CATTGAGAACAGCGAGACCA             |
| <i>HEMF1</i>                       | At1g03475 | TCAGATTCTCCCGTCCAATC            | ACACTGTCTTGAGCAGCCCT             |
| <i>PPDK</i>                        | At4g15530 | TTCGAACTGAGACAAGCCCT            | ACACGAATCTCGGAACAACC             |
| <i>UBQ10</i>                       | At4g05320 | GGCCTTGTATAATCCCTGATGAA<br>TAAG | AAAGAGATAACAGGAACGGAAA<br>CATAGT |
| <b><i>Rorippa spec.</i></b>        |           |                                 |                                  |
| <i>PFK6</i>                        | At4g32840 | GAAAACGGCATTGGACTTGT            | CATGTGGCCACTTTYTCTGA             |
| <i>ADH1*</i>                       | At1g77120 | GGACTTGGTGCTGTTGGTTTAG          | CTGGTTTGTGTCATGCTCTCGCG          |
| <i>CXXS1<sup>§</sup></i>           | At1g11530 | CGCTCATTTCACAGCATCAT            | AGTCTGTTCCGCACTTCCTG             |
| <i>GH</i>                          | At2g43610 | TCGTGGTACCATAGCGAGTG            | TTTAGCGACGGTTCCTTTGT             |
| <i>PFPB2</i>                       | At1g76550 | TAGAAACCAGGGTGGGTTTG            | TGCTTTTCAAGTCACCATCG             |
| <i>PFPA2<sup>§</sup></i>           | At4g04040 | CCTTTGGCTCACTTCCTCAG            | CTTAGCGTTGTGCACYTTRA             |
| <i>PAO</i>                         | At3g44880 | CGAATCGAGGAAGATTACGG            | TTCCGATCAAACCAGAGGAC             |
| <i>HEMF1</i>                       | At1g03475 | GGATGCTCCAAAGGGTAACA            | ACCGAATGGAAATGCTTGAC             |
| <i>PPDK</i>                        | At4g15530 | ACCATATCAACGGAGGCTTG            | GCGAGAGAAGCTCCAATGTC             |
| <i>SUS4</i>                        | At3g43190 | GTTCTTGGCATGATCCGTCT            | TGACCACCAGTGTGAGGGTA             |
| <i>SUS1*</i>                       | At5g20830 | GGAGAGTTTGCTTCCATTGC            | TCCGCTTTCCTCAAGATGTG             |
| <i>LDH1</i>                        | At4g17260 | GGCATTTATTGTGGGAGAGC            | CATAAGCGCTACGAACGACA             |
| <i>PDC2</i>                        | At5g54960 | GAGAAGCAATCATCGTGCAA            | TGGGACAAAGATCCTGTGGT             |
| <i>HB1</i>                         | At2g16060 | GAGATTGCACCAACAGCAA             | GCTCCAAGTCTCTTCAAAGTTGT          |
| <i>ACTIN2</i>                      |           | GTTGGGATGAACCAGAAGGA            | AGCAATACGGAGCTCATTGTAG<br>A      |

- 1 \*Sequences from Akman et al. 2011; §Primers were designed based on *R. sylvestris*
- 2 sequence only; §Primers fit to both isoforms, PFPA1 and PFPA2
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