

Supplementary material

Supporting information for the manuscript “Life-history trade-offs and the genetic basis of fitness in *Arabidopsis thaliana*” by Thomas Ellis, Froukje M. Postma, Christopher G. Oakley and Jon Ågren.

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Supplementary tables

Table S1: QTL for number of seeds per fruit identified in individual experiments. QTL positions are shown with their 95% Bayesian credible intervals. Effect sizes are given as additive effects and as a percentage of variance among RIL means. Effect sizes are quantified as the least-square mean difference in seeds/fruit between genotypes homozygous for the Swedish and Italian allele, respectively; negative values indicate that the Swedish genotype is associated with fewer seeds/fruit. Names indicated chromosome number and cM position.

| Name | Site | Year | Chr. | Position (cM) | LOD | Effect size | % var. explained |
|--------|--------|------|------|------------------|------|-------------|------------------|
| 1@9.5 | Italy | 2010 | 1 | 9.5 (8.4-12.6) | 9.3 | -1.431 | 8.7 |
| 2@56.0 | Italy | 2010 | 2 | 56.0 (44.3-60.9) | 3.9 | -0.906 | 3.5 |
| 3@18.0 | Italy | 2010 | 3 | 18.0 (14.7-19.7) | 5.9 | -1.130 | 5.4 |
| 5@56.6 | Italy | 2010 | 5 | 56.6 (49.9-58.6) | 6.9 | -1.211 | 6.3 |
| 1@58.6 | Italy | 2011 | 1 | 58.6 (51.5-61.8) | 4.7 | -1.071 | 4.0 |
| 2@32.6 | Italy | 2011 | 2 | 32.6 (26.8-45.6) | 6.3 | -1.246 | 5.3 |
| 5@15.0 | Italy | 2011 | 5 | 15.0 (9.4-22.0) | 4.0 | -1.001 | 3.4 |
| 5@50.2 | Italy | 2011 | 5 | 50.2 (49.9-60.1) | 13.8 | -1.924 | 12.3 |
| 1@22.7 | Sweden | 2010 | 1 | 22.7 (20.8-23.7) | 4.9 | 0.815 | 4.4 |
| 1@75.4 | Sweden | 2010 | 1 | 75.4 (73.2-79.6) | 7.3 | 1.334 | 6.6 |
| 4@41.0 | Sweden | 2010 | 4 | 41.0 (41.0-42.3) | 9.2 | 1.508 | 8.4 |
| 5@70.6 | Sweden | 2010 | 5 | 70.6 (68.7-78.2) | 7.1 | 1.093 | 6.4 |
| 1@61.1 | Sweden | 2011 | 1 | 61.1 (58.8-61.1) | 9.9 | -0.819 | 8.7 |
| 1@77.9 | Sweden | 2011 | 1 | 77.9 (73.2-82.1) | 2.5 | 0.909 | 2.1 |
| 3@21.0 | Sweden | 2011 | 3 | 21.0 (21.0-23.3) | 12.8 | -1.332 | 11.5 |
| 4@50.2 | Sweden | 2011 | 4 | 50.2 (35.8-57.7) | 6.9 | 1.380 | 6.0 |
| 5@74.5 | Sweden | 2011 | 5 | 74.5 (70.1-77.4) | 9.3 | 1.597 | 8.2 |

Table S2: Pairs of significant epistatic QTL detected across traits. QTL names indicated chromosome number and cM position.

| Trait | Site | Year | QTL | LOD | % var. explained |
|----------------|--------|------|-----------------|-------|------------------|
| Fruits/RP | Italy | 2010 | 5@7.5 x 5@70.1 | 0.55 | 0.35 |
| Fruits/RP | Italy | 2011 | 1@58.6 x 5@74.5 | 6.42 | 3.33 |
| Fruits/RP | Sweden | 2011 | 1@61.8 x 3@26.7 | 8.43 | 6.93 |
| Seeds/fruit | Sweden | 2010 | 1@22.7 x 5@70.6 | 2.38 | 2.08 |
| Seeds/fruit | Sweden | 2011 | 1@61.1 x 3@21.0 | 7.41 | 6.45 |
| Seeds/RP | Italy | 2010 | 5@9.4 x 5@71.4 | 1.19 | 0.85 |
| Seeds/RP | Sweden | 2011 | 1@61.1 x 3@24.4 | 10.11 | 8.59 |
| Seeds/seedling | Italy | 2010 | 5@9.4 x 5@71.4 | 0.77 | 0.48 |
| Seeds/seedling | Sweden | 2011 | 1@61.1 x 3@24.4 | 9.07 | 6.49 |
| Seed mass | Sweden | 2011 | 3@55.4 x 5@78.2 | 3.54 | 3.00 |

Table S3: QTL for number of fruits per seedling identified in individual experiments. QTL positions are shown with their 95% Bayesian credible intervals. Effect sizes are given as additive effects, and as a percentage of variance among RIL means. Effect sizes are quantified as the least-square mean difference in fruits/seedling between genotypes homozygous for the Swedish and Italian allele, respectively; negative values indicate that the Swedish genotype is associated with fewer fruits/seedling. Names indicated chromosome number and cM position.

| Name | Site | Year | Chr. | Position (cM) | LOD | Effect size | % var. explained |
|--------|--------|------|------|------------------|------|-------------|------------------|
| 1@10.3 | Italy | 2010 | 1 | 10.3 (8.4-12.0) | 9.9 | -0.774 | 6.2 |
| 1@57.3 | Italy | 2010 | 1 | 57.3 (55.9-57.3) | 11.1 | -0.823 | 7.0 |
| 2@53.4 | Italy | 2010 | 2 | 53.4 (52.5-56.0) | 7.6 | -0.664 | 4.7 |
| 3@54.1 | Italy | 2010 | 3 | 54.1 (53.3-59.2) | 7.2 | -0.646 | 4.4 |
| 4@50.0 | Italy | 2010 | 4 | 50.0 (43.5-57.7) | 4.4 | -0.541 | 2.6 |
| 5@7.5 | Italy | 2010 | 5 | 7.5 (2.6-10.0) | 6.9 | -0.677 | 4.2 |
| 5@60.6 | Italy | 2010 | 5 | 60.6 (53.4-70.1) | 2.9 | -0.465 | 1.7 |
| 5@78.2 | Italy | 2010 | 5 | 78.2 (70.1-78.2) | 4.5 | -0.583 | 2.8 |
| 1@61.8 | Italy | 2011 | 1 | 61.8 (60.2-61.8) | 13.6 | -0.761 | 6.8 |
| 1@77.2 | Italy | 2011 | 1 | 77.2 (77.0-83.8) | 4.4 | -0.421 | 2.1 |
| 2@49.5 | Italy | 2011 | 2 | 49.5 (48.7-50.6) | 14.3 | -0.675 | 7.2 |
| 3@1.7 | Italy | 2011 | 3 | 1.7 (0.0- 8.2) | 3.6 | 0.332 | 1.7 |
| 3@64.9 | Italy | 2011 | 3 | 64.9 (63.1-65.9) | 16.3 | -0.727 | 8.3 |
| 4@55.2 | Italy | 2011 | 4 | 55.2 (51.1-56.6) | 10.6 | -0.593 | 5.2 |
| 5@56.6 | Italy | 2011 | 5 | 56.6 (56.6-57.7) | 8.3 | -0.622 | 4.0 |
| 5@70.1 | Italy | 2011 | 5 | 70.1 (70.1-78.2) | 5.6 | -0.514 | 2.7 |
| 3@10.7 | Sweden | 2010 | 3 | 10.7 (8.2-34.4) | 2.5 | 0.296 | 2.9 |
| 1@62.5 | Sweden | 2011 | 1 | 62.5 (61.0-62.5) | 13.1 | -0.646 | 9.4 |
| 2@58.6 | Sweden | 2011 | 2 | 58.6 (32.6-60.9) | 3.0 | 0.608 | 2.0 |
| 3@29.5 | Sweden | 2011 | 3 | 29.5 (29.5-30.5) | 12.1 | -0.725 | 8.6 |
| 3@66.6 | Sweden | 2011 | 3 | 66.6 (36.1-70.5) | 2.2 | 0.522 | 1.5 |
| 4@53.5 | Sweden | 2011 | 4 | 53.5 (50.0-56.6) | 7.9 | 1.046 | 5.5 |
| 5@1.4 | Sweden | 2011 | 5 | 1.4 (1.4- 4.6) | 4.7 | 0.807 | 3.2 |
| 5@27.1 | Sweden | 2011 | 5 | 27.1 (20.4-34.1) | 2.7 | 0.616 | 1.8 |
| 5@60.6 | Sweden | 2011 | 5 | 60.6 (56.6-62.6) | 3.0 | -0.740 | 2.0 |
| 5@74.5 | Sweden | 2011 | 5 | 74.5 (74.5-74.5) | 18.6 | 1.892 | 13.8 |

Table S4: QTL for number of seeds per seedling identified in individual experiments. QTL positions are shown with their 95% Bayesian credible intervals. Effect sizes are given as additive effects and as a percentage of variance among RIL means. Effect sizes are quantified as the least-square mean difference in seeds/seedling between genotypes homozygous for the Swedish and Italian allele, respectively; negative values indicate that the Swedish genotype is associated with fewer seeds/seedling. Names indicated chromosome number and cM position.

| Name | Site | Year | Chr. | Position (cM) | LOD | Effect size | % var. explained |
|--------|--------|------|------|------------------|------|-------------|------------------|
| 1@10.3 | Italy | 2010 | 1 | 10.3 (7.3-12.0) | 12.5 | -33.121 | 8.3 |
| 1@57.3 | Italy | 2010 | 1 | 57.3 (55.9-61.1) | 9.4 | -28.474 | 6.2 |
| 2@53.4 | Italy | 2010 | 2 | 53.4 (51.0-56.0) | 7.2 | -24.485 | 4.7 |
| 3@19.7 | Italy | 2010 | 3 | 19.7 (14.7-30.5) | 1.2 | -10.411 | 0.8 |
| 3@55.4 | Italy | 2010 | 3 | 55.4 (41.1-66.8) | 3.0 | -16.202 | 1.9 |
| 4@20.7 | Italy | 2010 | 4 | 20.7 (17.1-44.3) | 2.8 | -15.534 | 1.8 |
| 5@9.4 | Italy | 2010 | 5 | 9.4 (4.6-12.0) | 5.9 | -20.793 | 3.8 |
| 5@58.6 | Italy | 2010 | 5 | 58.6 (54.3-61.3) | 3.5 | -20.923 | 2.2 |
| 5@71.4 | Italy | 2010 | 5 | 71.4 (68.7-73.6) | 2.9 | -15.678 | 1.9 |
| 1@61.1 | Italy | 2011 | 1 | 61.1 (57.3-61.8) | 12.5 | -28.327 | 6.7 |
| 1@80.9 | Italy | 2011 | 1 | 80.9 (77.0-83.8) | 3.8 | -15.287 | 1.9 |
| 2@31.7 | Italy | 2011 | 2 | 31.7 (25.6-40.3) | 3.1 | -13.873 | 1.6 |
| 2@49.4 | Italy | 2011 | 2 | 49.4 (45.6-51.0) | 7.5 | -21.523 | 3.9 |
| 3@64.9 | Italy | 2011 | 3 | 64.9 (63.1-65.9) | 7.7 | -19.639 | 4.0 |
| 4@52.0 | Italy | 2011 | 4 | 52.0 (50.0-57.7) | 4.4 | -15.495 | 2.2 |
| 5@18.5 | Italy | 2011 | 5 | 18.5 (1.4-43.0) | 2.7 | -11.992 | 1.3 |
| 5@56.6 | Italy | 2011 | 5 | 56.6 (56.6-57.7) | 11.7 | -29.901 | 6.2 |
| 5@72.1 | Italy | 2011 | 5 | 72.1 (69.4-78.2) | 4.7 | -18.419 | 2.4 |
| 1@13.5 | Sweden | 2010 | 1 | 13.5 (0.0-20.8) | 2.5 | -29.376 | 2.4 |
| 1@22.7 | Sweden | 2010 | 1 | 22.7 (21.9-22.7) | 5.7 | 45.258 | 5.7 |
| 1@75.4 | Sweden | 2010 | 1 | 75.4 (49.8-82.1) | 3.1 | 24.579 | 3.1 |
| 4@41.0 | Sweden | 2010 | 4 | 41.0 (37.4-42.3) | 6.0 | 34.597 | 6.1 |
| 1@61.1 | Sweden | 2011 | 1 | 61.1 (61.0-61.8) | 12.1 | -20.792 | 8.8 |
| 3@24.4 | Sweden | 2011 | 3 | 24.4 (22.3-25.4) | 15.5 | -42.447 | 11.5 |
| 3@66.6 | Sweden | 2011 | 3 | 66.6 (59.2-70.5) | 2.9 | 25.576 | 2.0 |
| 4@50.2 | Sweden | 2011 | 4 | 50.2 (41.0-56.6) | 9.0 | 46.843 | 6.4 |
| 5@1.4 | Sweden | 2011 | 5 | 1.4 (0.0-23.7) | 5.3 | 34.857 | 3.7 |
| 5@74.5 | Sweden | 2011 | 5 | 74.5 (74.5-75.8) | 18.7 | 67.112 | 14.2 |

Table S5: QTL for seed mass identified in individual experiments. QTL positions are shown with their 95% Bayesian credible intervals. Effect sizes are given as additive effects and as a percentage of variance among RIL means. Effect sizes are quantified as the least-square mean difference in seed mass between genotypes homozygous for the Swedish and Italian allele, respectively; negative values indicate that the Swedish genotype is associated with lower seed mass. Names indicated chromosome number and cM position.

| Name | Site | Year | Chr. | Position (cM) | LOD | Effect size | % var. explained |
|--------|--------|------|------|------------------|------|-------------|------------------|
| 1@48.9 | Italy | 2010 | 1 | 48.9 (40.6-61.1) | 3.3 | -0.570 | 3.5 |
| 3@57.1 | Italy | 2010 | 3 | 57.1 (50.2-59.2) | 4.7 | -0.688 | 5.2 |
| 1@16.1 | Italy | 2011 | 1 | 16.1 (7.3-18.9) | 3.7 | 0.768 | 3.7 |
| 1@29.5 | Italy | 2011 | 1 | 29.5 (22.7-61.8) | 3.7 | -0.765 | 3.7 |
| 3@53.3 | Italy | 2011 | 3 | 53.3 (18.0-60.4) | 4.0 | -0.655 | 4.0 |
| 4@9.3 | Italy | 2011 | 4 | 9.3 (4.2-28.0) | 3.5 | -0.612 | 3.5 |
| 5@7.7 | Italy | 2011 | 5 | 7.7 (5.7-13.6) | 3.6 | 0.619 | 3.6 |
| 1@3.9 | Sweden | 2010 | 1 | 3.9 (0.0- 6.1) | 8.9 | 0.749 | 8.1 |
| 1@32.4 | Sweden | 2010 | 1 | 32.4 (20.8-43.5) | 3.4 | -0.454 | 3.0 |
| 2@58.0 | Sweden | 2010 | 2 | 58.0 (50.4-60.9) | 3.1 | -0.413 | 2.7 |
| 3@65.9 | Sweden | 2010 | 3 | 65.9 (45.9-70.5) | 4.8 | -0.514 | 4.3 |
| 5@7.7 | Sweden | 2010 | 5 | 7.7 (2.6- 7.7) | 11.4 | 0.821 | 10.6 |
| 1@11.5 | Sweden | 2011 | 1 | 11.5 (9.9-12.6) | 5.4 | 0.841 | 4.6 |
| 1@21.9 | Sweden | 2011 | 1 | 21.9 (19.6-22.7) | 5.1 | -0.820 | 4.4 |
| 3@55.4 | Sweden | 2011 | 3 | 55.4 (49.1-60.4) | 5.1 | -0.360 | 4.3 |
| 4@15.8 | Sweden | 2011 | 4 | 15.8 (14.4-28.0) | 3.6 | -0.534 | 3.0 |
| 4@57.7 | Sweden | 2011 | 4 | 57.7 (54.5-60.7) | 3.2 | 0.516 | 2.7 |
| 5@2.6 | Sweden | 2011 | 5 | 2.6 (1.4- 7.7) | 10.3 | 0.930 | 9.1 |
| 5@52.4 | Sweden | 2011 | 5 | 52.4 (6.7-71.4) | 2.8 | 0.496 | 2.4 |
| 5@78.2 | Sweden | 2011 | 5 | 78.2 (72.1-78.2) | 4.7 | 0.282 | 4.0 |

Table S6: Pearson correlations between seed mass and number of seeds per fruit.

| Site | Year | r | Deg. freedom | p-value |
|--------|------|-------|--------------|---------|
| Italy | 2010 | 0.02 | 393 | 0.655 |
| Italy | 2011 | 0.02 | 396 | 0.761 |
| Sweden | 2010 | -0.19 | 393 | 0.000 |
| Sweden | 2011 | -0.06 | 392 | 0.266 |

Table S7: QTL for survival to reproduction identified in individual experiments. QTL positions are shown with their 95% Bayesian credible intervals. Effect sizes are given as additive effects, as a percentage of variance among RIL means, and as a percentage of the difference between parental means. Effect sizes are quantified as the least-square mean difference in survival between genotypes homozygous for the Swedish and Italian allele, respectively; negative values indicate that the Swedish genotype is associated with lower survival. Names indicated chromosome number and cM position.

| Name | Site | Year | Chr. | Position (cM) | LOD | Effect size | % var. explained |
|--------|--------|------|------|------------------|------|-------------|------------------|
| 1@40.6 | Italy | 2010 | 1 | 40.6 (2.1-45.1) | 2.9 | -0.024 | 2.1 |
| 1@62.5 | Italy | 2010 | 1 | 62.5 (58.6-64.9) | 5.5 | -0.033 | 3.9 |
| 2@53.4 | Italy | 2010 | 2 | 53.4 (49.4-55.3) | 12.6 | -0.046 | 9.3 |
| 3@59.2 | Italy | 2010 | 3 | 59.2 (37.9-65.9) | 4.6 | -0.027 | 3.2 |
| 5@9.4 | Italy | 2010 | 5 | 9.4 (6.7-10.0) | 10.1 | -0.041 | 7.3 |
| 5@66.1 | Italy | 2010 | 5 | 66.1 (64.1-77.4) | 9.1 | -0.039 | 6.6 |
| 1@40.6 | Italy | 2011 | 1 | 40.6 (36.7-51.5) | 6.7 | -0.027 | 5.8 |
| 1@83.8 | Italy | 2011 | 1 | 83.8 (74.4-83.8) | 4.8 | -0.023 | 4.1 |
| 2@49.5 | Italy | 2011 | 2 | 49.5 (44.3-51.0) | 10.0 | -0.033 | 9.0 |
| 5@57.5 | Italy | 2011 | 5 | 57.5 (53.4-60.1) | 9.2 | -0.032 | 8.1 |
| 4@53.5 | Sweden | 2011 | 4 | 53.5 (39.1-56.6) | 6.2 | 0.037 | 5.1 |
| 5@1.4 | Sweden | 2011 | 5 | 1.4 (0.0- 1.4) | 10.8 | 0.049 | 9.2 |
| 5@73.6 | Sweden | 2011 | 5 | 73.6 (73.6-75.8) | 17.1 | 0.061 | 15.0 |

Table S8: QTL for number of fruits per reproductive plant identified in individual experiments. QTL positions are shown with their 95% Bayesian credible intervals. Effect sizes are given as additive effects and as a percentage of variance among RIL means. Effect sizes are quantified as the least-square mean difference in fruits/RP between genotypes homozygous for the Swedish and Italian allele, respectively; negative values indicate that the Swedish genotype is associated with fewer fruits/RP. Names indicated chromosome number and cM position.

| Name | Site | Year | Chr. | Position (cM) | LOD | Effect size | % var. explained |
|--------|--------|------|------|------------------|------|-------------|------------------|
| 1@10.3 | Italy | 2010 | 1 | 10.3 (8.8-12.0) | 13.2 | -1.576 | 9.0 |
| 1@57.3 | Italy | 2010 | 1 | 57.3 (55.9-57.3) | 9.4 | -1.312 | 6.2 |
| 2@53.4 | Italy | 2010 | 2 | 53.4 (48.7-56.4) | 2.8 | -0.700 | 1.8 |
| 3@8.2 | Italy | 2010 | 3 | 8.2 (3.5- 9.6) | 4.7 | 1.179 | 3.0 |
| 3@19.7 | Italy | 2010 | 3 | 19.7 (18.0-22.3) | 2.2 | -0.846 | 1.4 |
| 3@54.1 | Italy | 2010 | 3 | 54.1 (49.1-65.5) | 4.3 | -0.888 | 2.7 |
| 4@18.3 | Italy | 2010 | 4 | 18.3 (14.4-31.0) | 2.6 | -0.697 | 1.7 |
| 4@50.6 | Italy | 2010 | 4 | 50.6 (44.3-55.9) | 4.3 | -0.967 | 2.8 |
| 5@7.5 | Italy | 2010 | 5 | 7.5 (4.9-12.0) | 4.9 | -0.914 | 3.2 |
| 5@70.1 | Italy | 2010 | 5 | 70.1 (68.7-72.1) | 7.3 | -1.060 | 4.8 |
| 1@58.6 | Italy | 2011 | 1 | 58.6 (57.3-61.1) | 15.1 | -0.916 | 8.2 |
| 1@77.2 | Italy | 2011 | 1 | 77.2 (77.0-83.8) | 4.8 | -0.597 | 2.5 |
| 2@38.2 | Italy | 2011 | 2 | 38.2 (32.0-40.3) | 8.1 | -0.689 | 4.2 |
| 3@5.1 | Italy | 2011 | 3 | 5.1 (1.7- 7.3) | 5.4 | 0.562 | 2.8 |
| 3@57.1 | Italy | 2011 | 3 | 57.1 (54.7-65.9) | 13.3 | -0.903 | 7.2 |
| 4@53.9 | Italy | 2011 | 4 | 53.9 (51.3-55.5) | 12.2 | -0.878 | 6.6 |
| 5@56.6 | Italy | 2011 | 5 | 56.6 (53.4-58.6) | 4.9 | -0.616 | 2.5 |
| 5@74.5 | Italy | 2011 | 5 | 74.5 (72.9-77.4) | 12.5 | -0.676 | 6.7 |
| 1@13.5 | Sweden | 2010 | 1 | 13.5 (3.9-20.8) | 3.4 | -3.414 | 3.6 |
| 1@22.7 | Sweden | 2010 | 1 | 22.7 (21.9-55.6) | 3.7 | 3.559 | 3.8 |
| 1@77.9 | Sweden | 2010 | 1 | 77.9 (74.4-83.8) | 3.3 | -2.487 | 3.4 |
| 2@58.0 | Sweden | 2010 | 2 | 58.0 (49.7-60.9) | 2.1 | 1.956 | 2.2 |
| 3@9.6 | Sweden | 2010 | 3 | 9.6 (8.2-42.6) | 2.4 | 2.115 | 2.5 |
| 1@61.8 | Sweden | 2011 | 1 | 61.8 (61.0-62.5) | 13.4 | -1.934 | 11.3 |
| 2@58.3 | Sweden | 2011 | 2 | 58.3 (50.4-60.9) | 4.2 | 2.065 | 3.4 |
| 3@26.7 | Sweden | 2011 | 3 | 26.7 (25.4-30.5) | 10.7 | -1.754 | 8.9 |
| 4@55.5 | Sweden | 2011 | 4 | 55.5 (37.4-56.6) | 4.1 | 2.073 | 3.3 |
| 5@20.4 | Sweden | 2011 | 5 | 20.4 (15.0-34.1) | 4.7 | 2.186 | 3.8 |
| 5@60.6 | Sweden | 2011 | 5 | 60.6 (50.2-64.1) | 3.3 | -2.166 | 2.7 |
| 5@74.5 | Sweden | 2011 | 5 | 74.5 (74.5-75.8) | 11.0 | 4.043 | 9.2 |

Table S9: QTL for number of seeds per reproductive plant identified in individual experiments. QTL positions are shown with their 95% Bayesian credible intervals. Effect sizes are given as additive effects and as a percentage of variance among RIL means. Effect sizes are quantified as the least-square mean difference in seeds/RP between genotypes homozygous for the Swedish and Italian allele, respectively; negative values indicate that the Swedish genotype is associated with fewer seeds/RP. Names indicated chromosome number and cM position.

| Name | Site | Year | Chr. | Position (cM) | LOD | Effect size | % var. explained |
|--------|--------|------|------|------------------|------|-------------|------------------|
| 1@10.3 | Italy | 2010 | 1 | 10.3 (8.4-10.3) | 12.2 | -58.194 | 9.3 |
| 1@57.3 | Italy | 2010 | 1 | 57.3 (55.2-57.3) | 7.8 | -45.710 | 5.7 |
| 2@53.4 | Italy | 2010 | 2 | 53.4 (48.7-56.4) | 3.2 | -28.643 | 2.3 |
| 3@54.1 | Italy | 2010 | 3 | 54.1 (18.0-60.4) | 4.2 | -32.925 | 3.1 |
| 4@31.0 | Italy | 2010 | 4 | 31.0 (18.3-32.1) | 5.6 | -39.584 | 4.1 |
| 5@9.4 | Italy | 2010 | 5 | 9.4 (2.6-12.0) | 4.5 | -28.700 | 3.3 |
| 5@71.4 | Italy | 2010 | 5 | 71.4 (70.1-73.6) | 7.9 | -39.604 | 5.8 |
| 1@60.2 | Italy | 2011 | 1 | 60.2 (57.3-61.8) | 9.3 | -31.861 | 5.1 |
| 1@79.6 | Italy | 2011 | 1 | 79.6 (77.0-83.8) | 3.5 | -19.123 | 1.9 |
| 2@32.6 | Italy | 2011 | 2 | 32.6 (25.6-40.3) | 2.9 | -17.713 | 1.5 |
| 2@49.4 | Italy | 2011 | 2 | 49.4 (44.3-60.5) | 3.5 | -19.166 | 1.8 |
| 3@5.1 | Italy | 2011 | 3 | 5.1 (4.5- 8.2) | 3.3 | 23.424 | 1.8 |
| 3@14.7 | Italy | 2011 | 3 | 14.7 (13.5-19.7) | 2.0 | -18.386 | 1.0 |
| 3@64.9 | Italy | 2011 | 3 | 64.9 (63.1-65.9) | 8.0 | -26.330 | 4.4 |
| 4@52.8 | Italy | 2011 | 4 | 52.8 (50.0-57.7) | 5.0 | -21.542 | 2.7 |
| 5@18.5 | Italy | 2011 | 5 | 18.5 (2.6-43.0) | 2.8 | -16.171 | 1.5 |
| 5@56.6 | Italy | 2011 | 5 | 56.6 (56.6-57.7) | 11.3 | -35.522 | 6.3 |
| 5@78.2 | Italy | 2011 | 5 | 78.2 (72.1-78.2) | 4.8 | -22.641 | 2.6 |
| 1@13.5 | Sweden | 2010 | 1 | 13.5 (0.0-20.8) | 3.7 | -151.237 | 4.0 |
| 1@22.7 | Sweden | 2010 | 1 | 22.7 (21.9-23.7) | 5.2 | 178.597 | 5.6 |
| 3@30.5 | Sweden | 2010 | 3 | 30.5 (9.6-45.9) | 3.1 | 103.634 | 3.3 |
| 1@61.1 | Sweden | 2011 | 1 | 61.1 (61.0-62.5) | 12.7 | -48.232 | 11.0 |
| 3@24.4 | Sweden | 2011 | 3 | 24.4 (21.0-29.5) | 13.1 | -74.780 | 11.3 |
| 4@50.2 | Sweden | 2011 | 4 | 50.2 (39.1-57.7) | 4.1 | 80.002 | 3.4 |
| 5@20.4 | Sweden | 2011 | 5 | 20.4 (1.4-25.4) | 3.9 | 76.310 | 3.2 |
| 5@74.5 | Sweden | 2011 | 5 | 74.5 (74.5-75.8) | 10.0 | 122.523 | 8.5 |

Supplementary figures

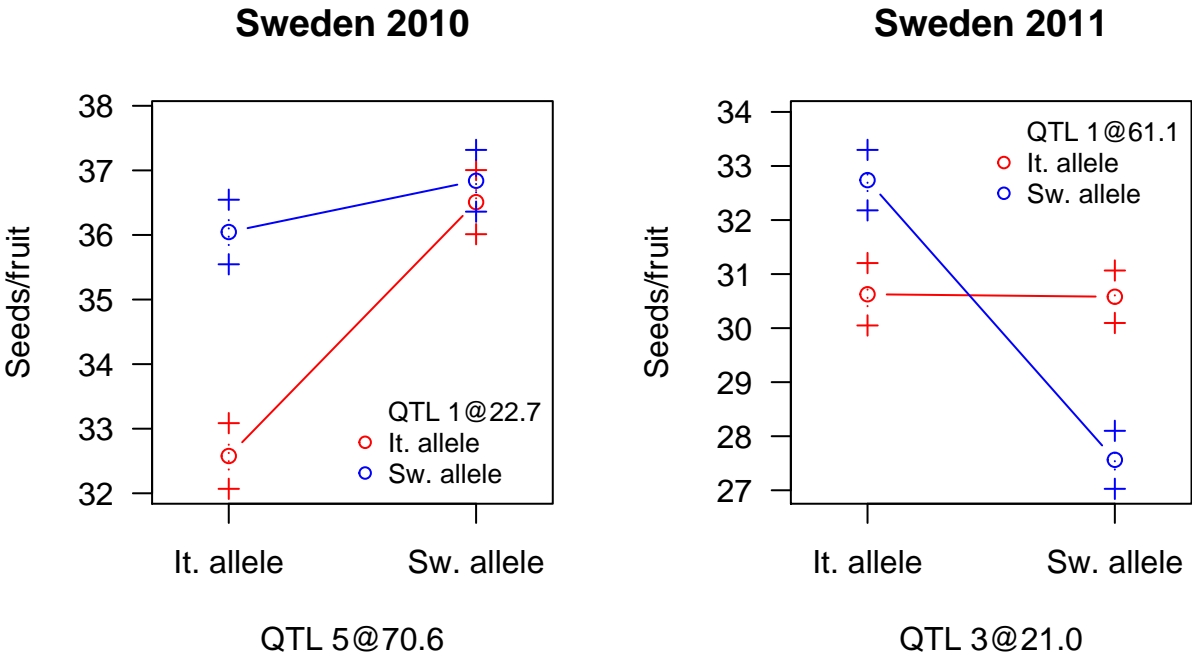


Figure S1: Interaction plots for epistatic interactions detected for number of seeds per fruit, showing mean and standard errors for each genotype-by-genotype combination.

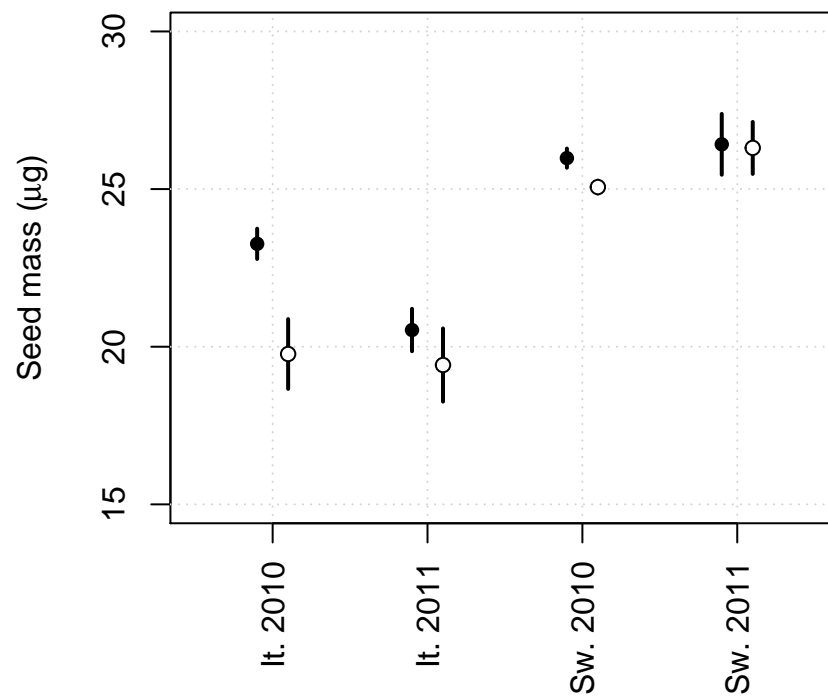


Figure S2: Mean seed mass of the Italian (closed symbols) and Swedish (open symbols) parental ecotypes at the field sites in Italy (It.) and Sweden (Sw.) in 2010 and 2011. Bars indicate standard error.

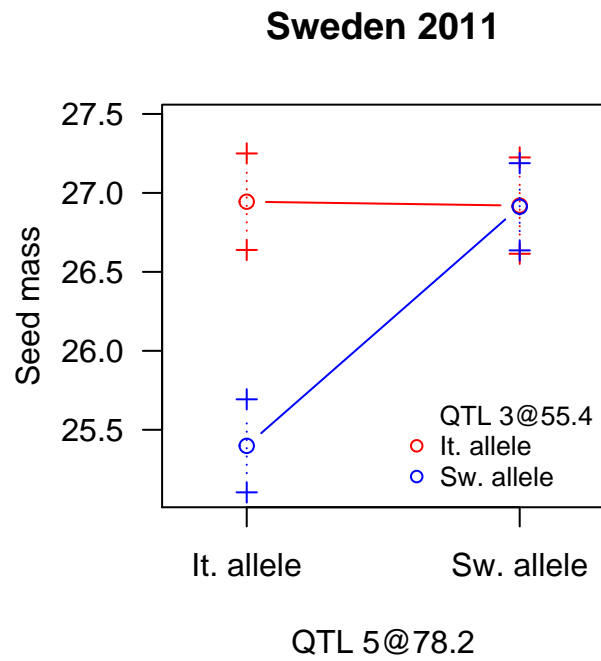


Figure S3: Interaction plots for epistatic interactions detected for seed mass, showing mean and standard errors for each genotype-by-genotype combination.

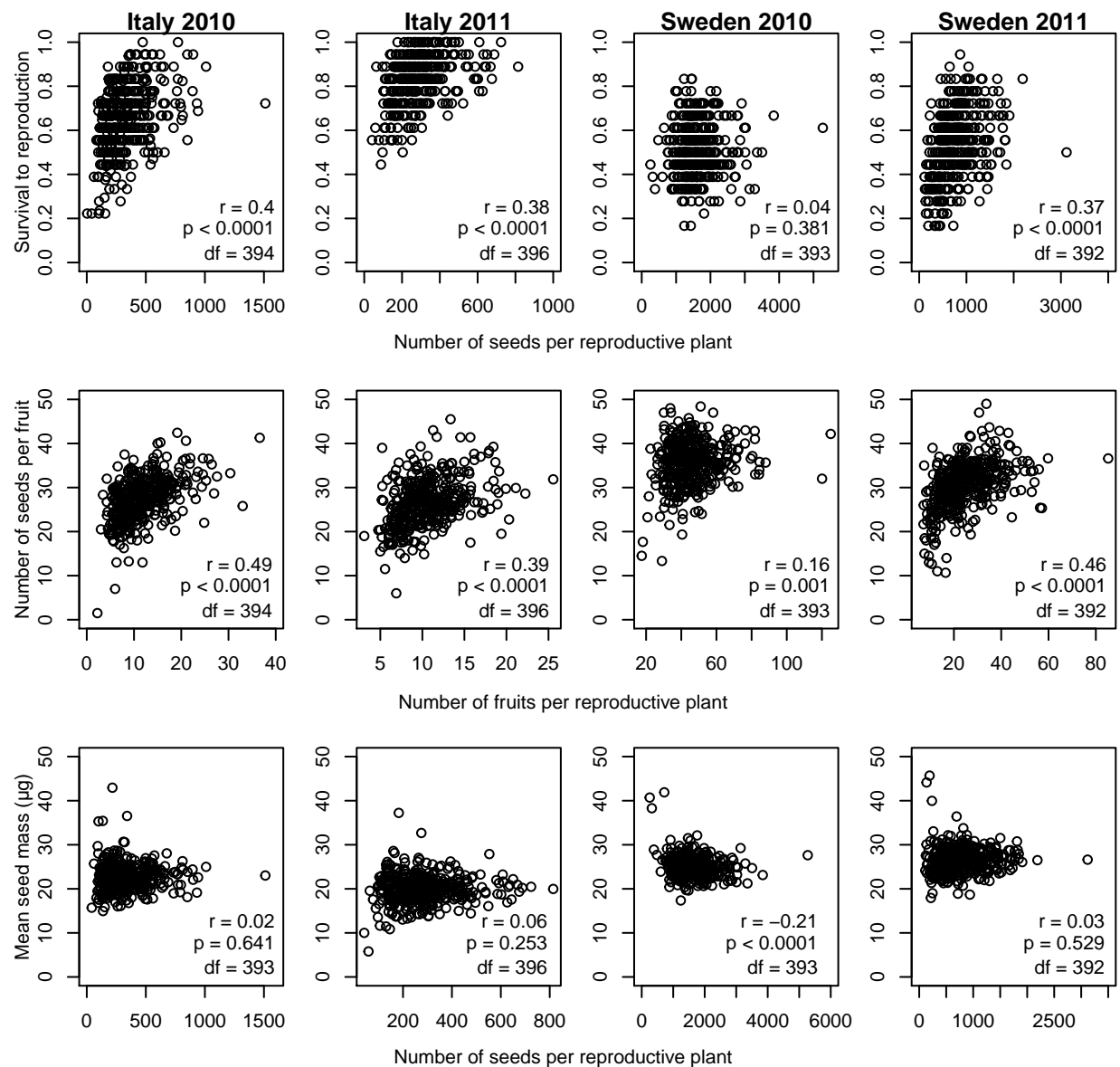


Figure S4: Relationships between RIL-means for survival and fecundity (top), components of fecundity (middle), and between fecundity and seed mass (bottom). Pearson correlation coefficients (r), associated p -values and degrees of freedom (df) are indicated.

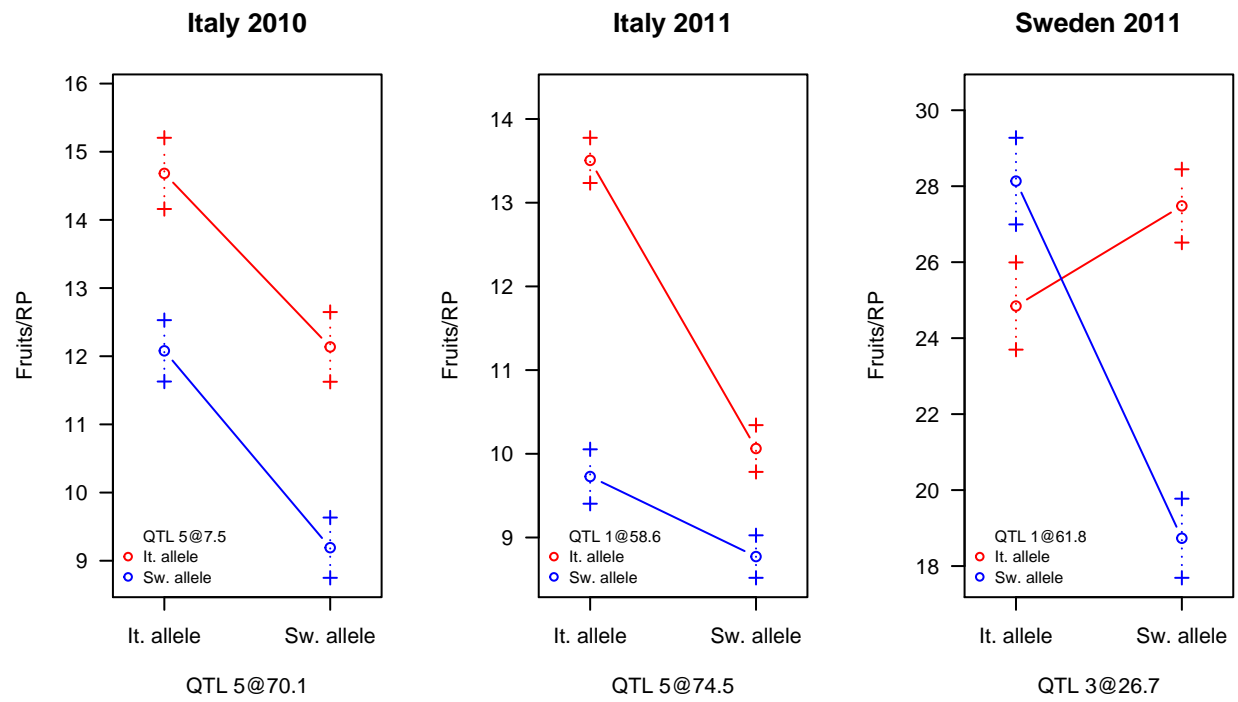


Figure S5: Interaction plots for epistatic interactions detected for number of fruits per reproductive plant (fruits/RP), showing mean and standard errors for each genotype-by-genotype combination.

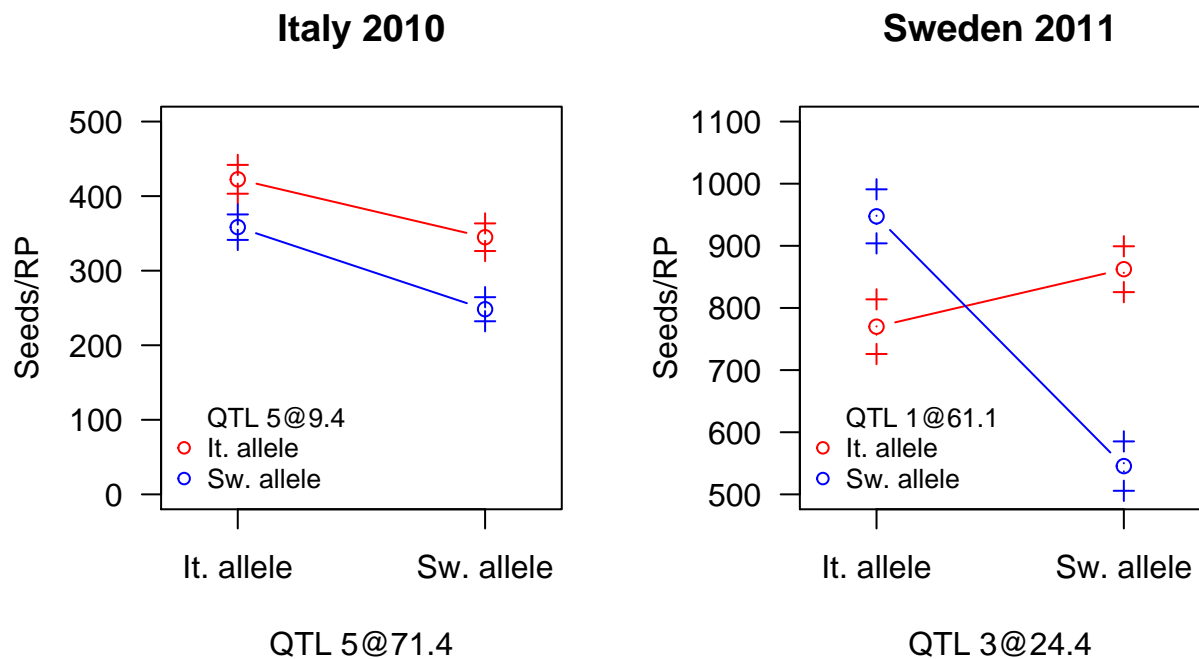


Figure S6: Interaction plots for epistatic interactions detected for number of seeds per reproductive plant, showing mean and standard errors for each genotype-by-genotype combination.

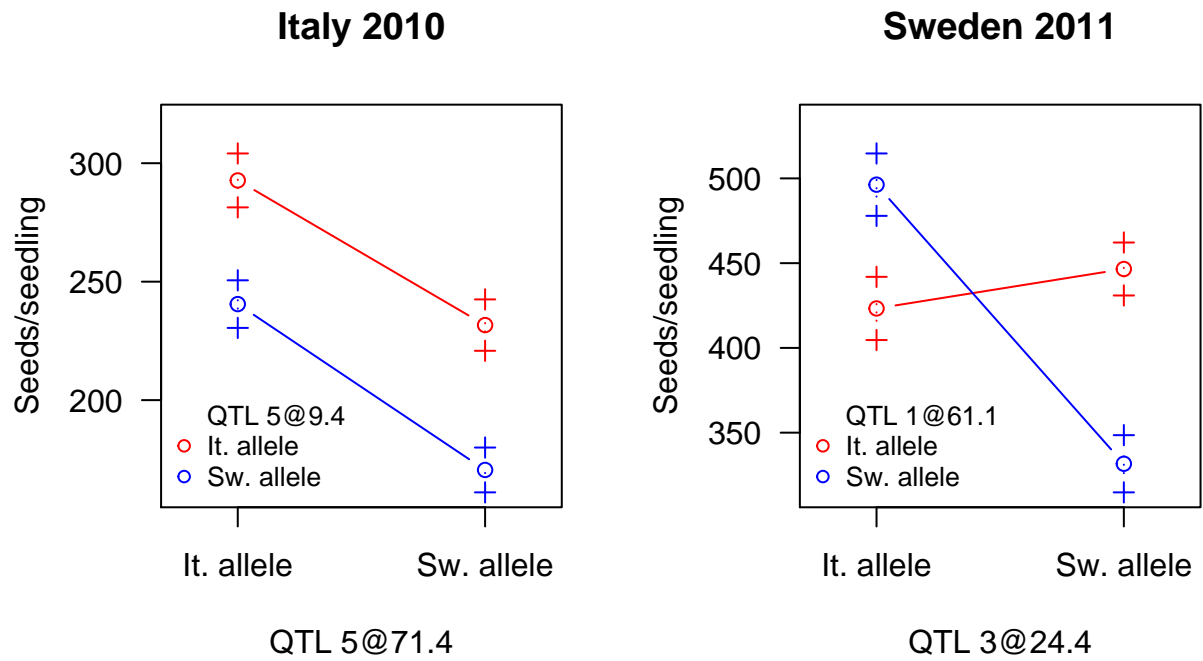


Figure S7: Interaction plots for epistatic interactions detected for number of seeds per seedling, showing mean and standard errors for each genotype-by-genotype combination.

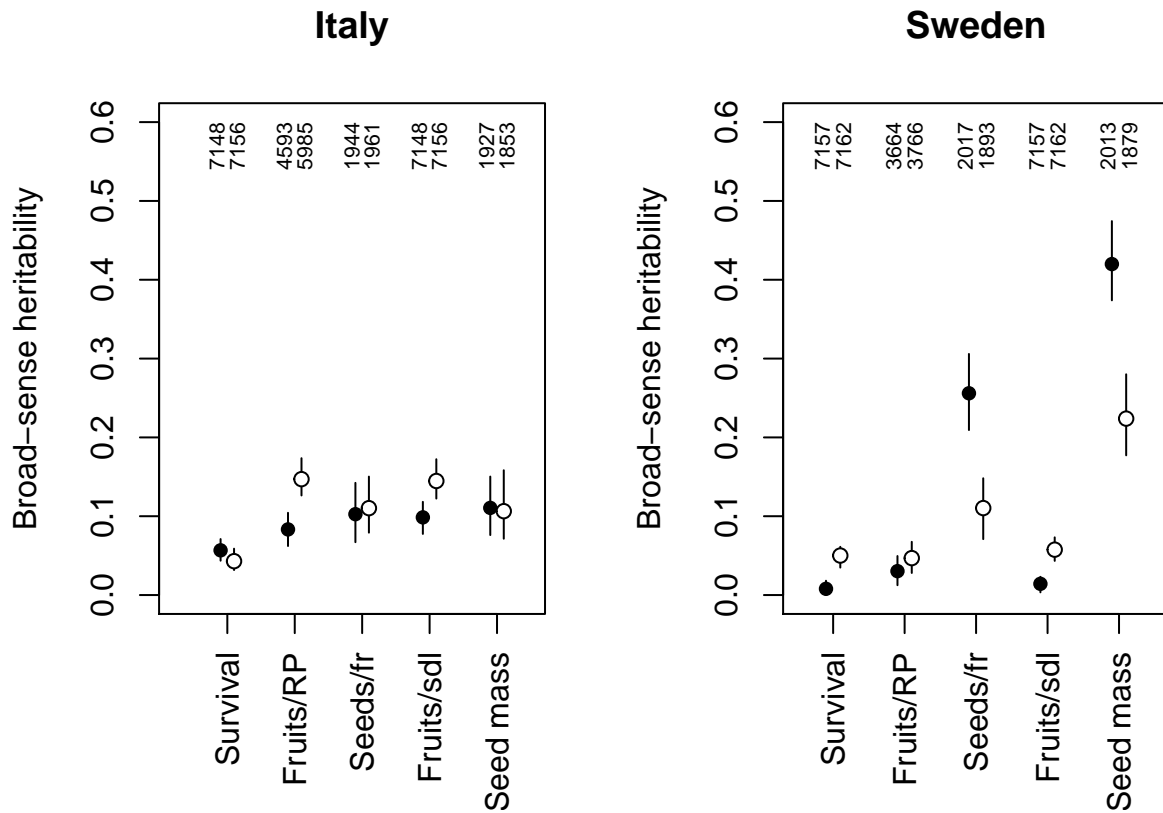


Figure S8: Broad-sense heritability estimates for survival to reproduction, number of fruits per reproductive plants (fruits/RP), number of seeds per fruit (Seeds/fr), number of fruits per seedling (Fruits/sdl), and seed mass. Open and closed symbols show values in 2010 and 2011 respectively. Error bars show 95% parametric bootstrap confidence intervals. Numbers indicate the number of individuals each estimate is based on.