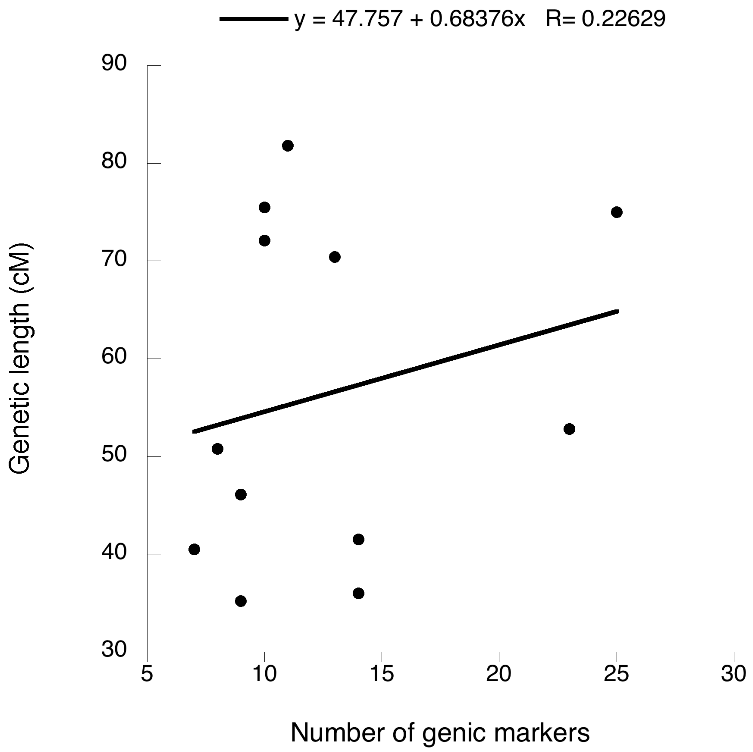
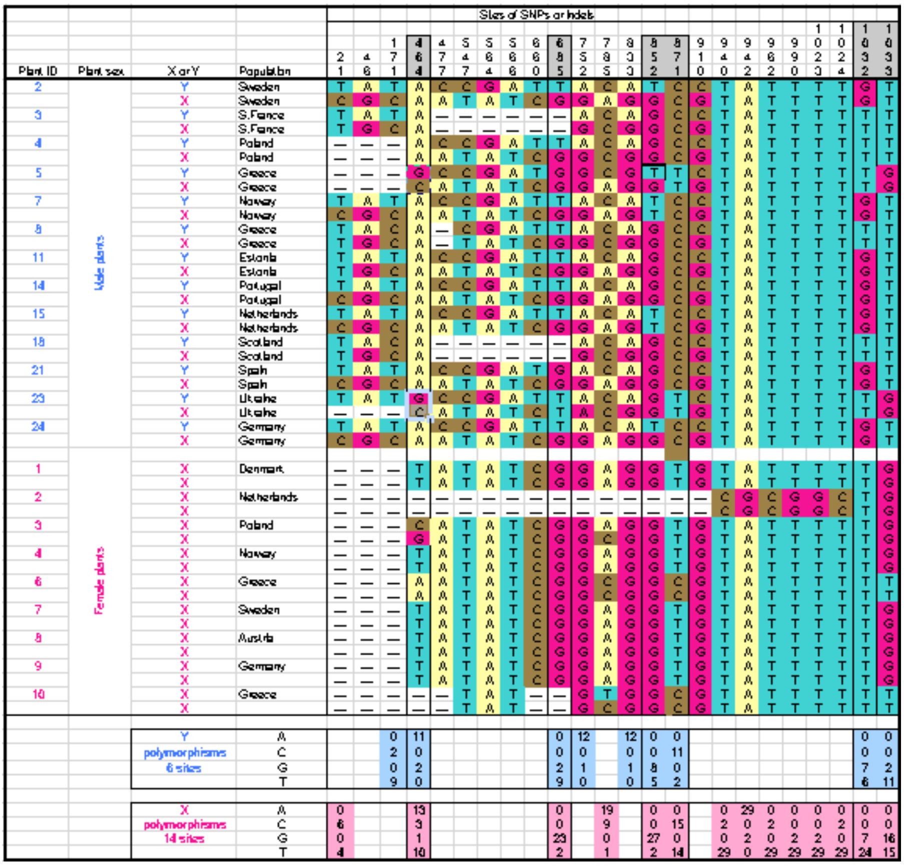


**Figure S1** Genetic lengths of linkage groups and numbers of genic markers.

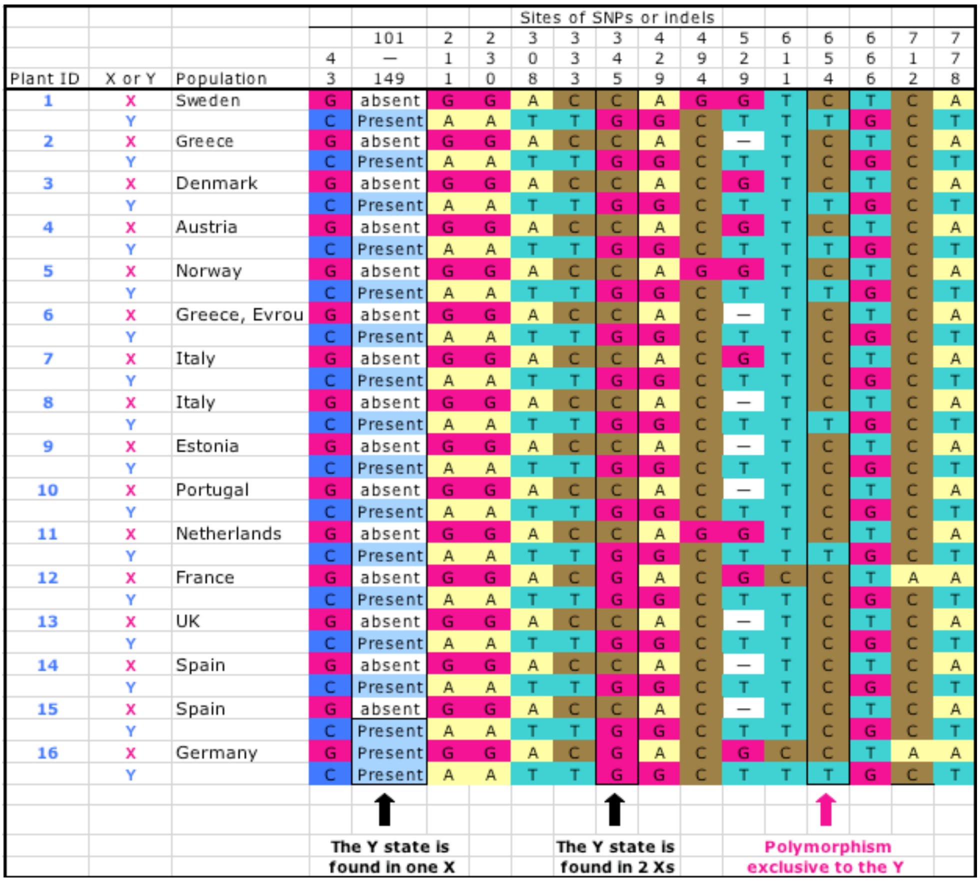
# Gene *E559*



| | | | | Sites of SNPs or Indels | | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Plant ID | Plant sex | X or Y | Population | 21 | 46 | 171 | 464 | 477 | 547 | 564 | 566 | 660 | 685 | 752 | 785 | 833 | 852 | 871 | 910 | 940 | 942 | 962 | 990 | 1023 | 1024 | 1032 | 1033 |
| 2 | Male plants | Y | Sweden | T | A | T | A | C | C | G | A | T | T | A | C | A | T | C | C | T | A | T | T | T | T | G | T |
| | | X | Sweden | C | G | C | A | A | T | A | T | C | G | G | A | G | G | C | G | T | A | T | T | T | T | G | T |
| 3 | | Y | S.France | T | A | T | A | — | — | — | — | — | — | A | C | A | G | C | C | T | A | T | T | T | T | T | T |
| | | X | S.France | T | G | C | A | — | — | — | — | — | — | G | C | G | G | C | G | T | A | T | T | T | T | T | T |
| 4 | | Y | Poland | — | — | — | A | C | C | G | A | T | T | A | C | A | G | C | C | T | A | T | T | T | T | T | T |
| | | X | Poland | — | — | — | A | A | T | A | T | C | G | G | C | G | G | C | G | T | A | T | T | T | T | T | T |
| 5 | | Y | Greece | — | — | — | G | C | C | G | A | T | G | G | C | G | T | T | C | T | A | T | T | T | T | T | G |
| | | X | Greece | — | — | — | C | A | T | A | T | C | G | G | A | G | G | T | G | T | A | T | T | T | T | T | G |
| 7 | | Y | Norway | T | A | T | A | C | C | G | A | T | T | A | C | A | T | C | C | T | A | T | T | T | T | G | T |
| | | X | Norway | C | G | C | A | A | T | A | T | C | G | G | A | G | T | C | G | T | A | T | T | T | T | G | T |
| 8 | | Y | Greece | T | A | C | A | — | C | G | A | T | T | A | C | A | G | C | C | T | A | T | T | T | T | T | T |
| | | X | Greece | T | G | C | A | — | T | A | T | C | G | G | C | G | G | C | G | T | A | T | T | T | T | T | T |
| 11 | | Y | Estonia | T | A | T | A | C | C | G | A | T | T | A | C | A | G | C | C | T | A | T | T | T | T | G | T |
| | | X | Estonia | T | G | C | A | A | T | A | T | C | G | G | A | G | G | C | G | T | A | T | T | T | T | G | T |
| 14 | | Y | Portugal | T | A | T | A | C | C | G | A | T | T | A | C | A | G | C | C | T | A | T | T | T | T | G | T |
| | | X | Portugal | C | G | C | A | A | T | A | T | C | G | G | A | G | G | C | G | T | A | T | T | T | T | G | T |
| 15 | | Y | Netherlands | T | A | T | A | C | C | G | A | T | T | A | C | A | T | C | C | T | A | T | T | T | T | G | T |
| | | X | Netherlands | C | G | C | A | A | T | A | T | C | G | G | A | G | T | C | G | T | A | T | T | T | T | G | T |
| 18 | | Y | Scotland | T | A | C | A | — | — | — | — | — | — | A | C | A | G | C | C | T | A | T | T | T | T | T | T |
| | | X | Scotland | T | G | C | A | — | — | — | — | — | — | G | C | G | G | C | G | T | A | T | T | T | T | T | T |
| 21 | | Y | Spain | T | A | T | A | C | C | G | A | T | G | A | C | A | G | C | C | T | A | T | T | T | T | G | T |
| | | X | Spain | C | G | C | A | A | T | A | T | C | G | G | A | G | G | C | G | T | A | T | T | T | T | G | T |
| 23 | | Y | Ukraine | T | A | T | G | C | C | G | A | T | T | A | C | A | G | T | C | T | A | T | T | T | T | T | G |
| | | X | Ukraine | — | — | — | C | A | T | A | T | C | T | A | C | G | G | T | G | T | A | T | T | T | T | T | G |
| 24 | | Y | Germany | T | A | T | A | C | C | G | A | T | T | A | C | A | T | C | C | T | A | T | T | T | T | G | T |
| | | X | Germany | C | G | C | A | A | T | A | T | C | G | G | A | G | G | C | G | T | A | T | T | T | T | G | T |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 1 | Female plants | X | Denmark | — | — | — | T | A | T | A | T | C | G | G | A | G | G | T | G | T | A | T | T | T | T | T | G |
| | | X | | — | — | — | T | A | T | A | T | C | G | G | A | G | G | T | G | T | A | T | T | T | T | T | G |
| 2 | | X | Netherlands | — | — | — | — | — | — | — | — | — | — | — | — | — | — | — | — | C | G | C | G | G | C | T | G |
| | | X | | — | — | — | — | — | — | — | — | — | — | — | — | — | — | — | — | C | G | C | G | G | C | T | G |
| 3 | | X | Poland | — | — | — | C | A | T | A | T | C | G | G | A | G | G | T | G | T | A | T | T | T | T | T | G |
| | | X | | — | — | — | G | A | T | A | T | C | G | G | C | G | G | T | G | T | A | T | T | T | T | T | G |
| 4 | | X | Norway | — | — | — | T | A | T | A | T | C | G | G | A | G | G | T | G | T | A | T | T | T | T | T | G |
| | | X | | — | — | — | T | A | T | A | T | C | G | G | A | G | G | T | G | T | A | T | T | T | T | T | G |
| 6 | | X | Greece | — | — | — | A | A | T | A | T | C | G | G | C | G | G | C | G | T | A | T | T | T | T | T | T |
| | | X | | — | — | — | A | A | T | A | T | C | G | G | C | G | G | C | G | T | A | T | T | T | T | T | T |
| 7 | | X | Sweden | — | — | — | T | A | T | A | T | C | G | G | A | G | G | T | G | T | A | T | T | T | T | T | G |
| | | X | | — | — | — | T | A | T | A | T | C | G | G | A | G | G | T | G | T | A | T | T | T | T | T | G |
| 8 | | X | Austria | — | — | — | T | A | T | A | T | C | G | G | A | G | G | T | G | T | A | T | T | T | T | T | G |
| | | X | | — | — | — | T | A | T | A | T | C | G | G | A | G | G | T | G | T | A | T | T | T | T | T | G |
| 9 | | X | Germany | — | — | — | T | A | T | A | T | C | G | G | A | G | G | T | G | T | A | T | T | T | T | T | G |
| | | X | | — | — | — | T | A | T | A | T | C | G | G | A | G | G | T | G | T | A | T | T | T | T | T | G |
| 10 | | X | Greece | — | — | — | — | — | T | A | T | — | — | G | T | G | G | C | G | T | A | T | T | T | T | T | T |
| | | X | | — | — | — | — | — | T | A | T | — | — | G | C | G | G | C | G | T | A | T | T | T | T | T | T |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | Y | A | | | 0 | 11 | | | | | | 0 | 12 | | 12 | 0 | 0 | | | | | | | | 0 | 0 |
| | | polymorphisms | C | | | 2 | 0 | | | | | | 0 | 0 | | 0 | 0 | 11 | | | | | | | | 0 | 0 |
| | | 6 sites | G | | | 0 | 2 | | | | | | 2 | 1 | | 1 | 8 | 0 | | | | | | | | 7 | 2 |
| | | | T | | | 9 | 0 | | | | | | 9 | 0 | | 0 | 5 | 2 | | | | | | | | 6 | 11 |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | X | A | 0 | | | 13 | | | | | | 0 | | 19 | | 0 | 0 | | 0 | 29 | 0 | 0 | 0 | 0 | 0 | 0 |
| | | polymorphisms | C | 6 | | | 3 | | | | | | 0 | | 9 | | 0 | 15 | | 2 | 0 | 2 | 0 | 0 | 2 | 0 | 0 |
| | | 14 sites | G | 0 | | | 1 | | | | | | 23 | | 0 | | 27 | 0 | | 0 | 2 | 0 | 2 | 2 | 0 | 7 | 16 |
| | | | T | 4 | | | 10 | | | | | | 2 | | 1 | | 2 | 14 | | 29 | 0 | 29 | 29 | 29 | 29 | 24 | 15 |

]

# Gene *E523*



| | | | Sites of SNPs or indels | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Plant ID | X or Y | Population | 43 | 101 – 149 | 211 | 230 | 308 | 333 | 345 | 429 | 494 | 529 | 611 | 654 | 666 | 712 | 778 |
| 1 | X | Sweden | G | absent | G | G | A | C | C | A | G | G | T | C | T | C | A |
| | Y | | C | Present | A | A | T | T | G | G | C | T | T | T | G | C | T |
| 2 | X | Greece | G | absent | G | G | A | C | C | A | C | — | T | C | T | C | A |
| | Y | | C | Present | A | A | T | T | G | G | C | T | T | C | G | C | T |
| 3 | X | Denmark | G | absent | G | G | A | C | C | A | C | G | T | C | T | C | A |
| | Y | | C | Present | A | A | T | T | G | G | C | T | T | T | G | C | T |
| 4 | X | Austria | G | absent | G | G | A | C | C | A | C | G | T | C | T | C | A |
| | Y | | C | Present | A | A | T | T | G | G | C | T | T | T | G | C | T |
| 5 | X | Norway | G | absent | G | G | A | C | C | A | G | G | T | C | T | C | A |
| | Y | | C | Present | A | A | T | T | G | G | C | T | T | T | G | C | T |
| 6 | X | Greece, Evrou | G | absent | G | G | A | C | C | A | C | — | T | C | T | C | A |
| | Y | | C | Present | A | A | T | T | G | G | C | T | T | C | G | C | T |
| 7 | X | Italy | G | absent | G | G | A | C | C | A | C | G | T | C | T | C | A |
| | Y | | C | Present | A | A | T | T | G | G | C | T | T | C | G | C | T |
| 8 | X | Italy | G | absent | G | G | A | C | C | A | C | — | T | C | T | C | A |
| | Y | | C | Present | A | A | T | T | G | G | C | T | T | T | G | C | T |
| 9 | X | Estonia | G | absent | G | G | A | C | C | A | C | — | T | C | T | C | A |
| | Y | | C | Present | A | A | T | T | G | G | C | T | T | C | G | C | T |
| 10 | X | Portugal | G | absent | G | G | A | C | C | A | C | — | T | C | T | C | A |
| | Y | | C | Present | A | A | T | T | G | G | C | T | T | C | G | C | T |
| 11 | X | Netherlands | G | absent | G | G | A | C | C | A | G | G | T | C | T | C | A |
| | Y | | C | Present | A | A | T | T | G | G | C | T | T | T | G | C | T |
| 12 | X | France | G | absent | G | G | A | C | G | A | C | G | C | C | T | A | A |
| | Y | | C | Present | A | A | T | T | G | G | C | T | T | C | G | C | T |
| 13 | X | UK | G | absent | G | G | A | C | C | A | C | — | T | C | T | C | A |
| | Y | | C | Present | A | A | T | T | G | G | C | T | T | C | G | C | T |
| 14 | X | Spain | G | absent | G | G | A | C | C | A | C | — | T | C | T | C | A |
| | Y | | C | Present | A | A | T | T | G | G | C | T | T | C | G | C | T |
| 15 | X | Spain | G | absent | G | G | A | C | C | A | C | — | T | C | T | C | A |
| | Y | | C | Present | A | A | T | T | G | G | C | T | T | C | G | C | T |
| 16 | X | Germany | G | Present | G | G | A | C | G | A | C | G | C | C | T | A | A |
| | Y | | C | Present | A | A | T | T | G | G | C | T | T | T | G | C | T |
| | | | | ↑ | | | | | ↑ | | | | | ↑ | | | |
| | | | | The Y state is found in one X | | | | | The Y state is found in 2 Xs | | | | | Polymorphism exclusive to the Y | | | |

**Figure S2** Variants in the Y- and X-linked haplotypes of the *E559* (part A of the figure) and *E523* (part B of the figure) genes.

**Table S1** The mapping family and three other families used to score genotypes of autosomal genes, putative PAR genes and sex-linked genes, and to estimate recombination fractions. One *S.vulgaris* family was used for comparative mapping.

| Family | Parental plants | | | |
|---|---|---|---|---|
| | Identity of ♀ parent | Population of origin | Identity of pollen donor | Population of origin |
| H2005-1 (F2 family)<br>(the "mapping family") [1] | H2005-1/9 [2] | F1 | H2005-1/4 | F1 |
| G2008-3 | K2005-12/2 | Germany | K2005-4/2 | Heiligenstadt, Austria |
| D2009-2 | | | G2005-5/1 | Loanninon, Greece |
| G2008-9 | K2005-4/3 | Heiligenstadt, Austria | K2005-5B/1 | Oland, Grasgard Sweden |
| J2010-1 (F2 family) | Family F2009-1 female plant | F1 [3] | Family F2009-1 male plant | F1 (as for female parent) |
| *S. vulgaris* SV2 | E2000-5/9 (female) | Dijon, France | 99K-10/4 (hermaphrodite) | Sussex, England |

[1] The mapping family is an F2 generated by crossing sibling plants descended from an F1 cross (family H2005-1) made by pollinating plant E2004-11/1 from Canche (Northern France) with E2004-17/1 (from River Waal, Netherlands). The other families from this study were obtained by crossing adult plants obtained from field-collected seeds.

[2] Identity of plants within families are indicated by the family name followed by the individual number (e.g. H2005-1/9 is individual 9 from family H2005-1).

[3] Female from the mapping family H2005-1 x male 11/5 from Madrid.

**Table S2** List of genes mapped to the 10 *S. latifolia* autosomes (denoted by LG1 to LG11) and sex chromosomes (LG12 and LG13). GenBank accession numbers are listed for sequences from Sanger sequencing of *S. latifolia* cDNA clones, and those for sequences from 454 sequencing and RNA-Seq are in the Transcriptome Shotgun Assembly (TSA) Database at DDBJ/EMBL/GenBank under the accession number GAKC00000000. The version described in this paper is the first version, GAKC01000000. Individual gene sequences are visible under this accession number. Three sequences of less than 200 bp are not in database (see below); primers and these sequences are available from the authors on request.

| Contig name | Source | Accession numbers of putative *A. thaliana* orthologues | *S.latifolia* linkage group | *S.latifolia* GenBank accession numbers |
|---|---|---|---|---|
| Autosomal genes | | | | |
| *E72* | cDNA clone | AT1G02150 | LG1 | KF034810 |
| *E246* | 454 sequencing | AT5G19485 | LG1 | |
| *E269* | 454 sequencing | AT1G36980 | LG1 | |
| *E271* | 454 sequencing | AT2G30410 | LG1 | |
| *E310* | 454 sequencing | AT3G11945 | LG1 | |
| *E312* | 454 sequencing | AT3G51130 | LG1 | |
| *E522* | 454 sequencing | AT4G17600 | LG1 | |
| *E546* | 454 sequencing | AT3G51240 | LG1 | |
| *E561* | 454 sequencing | AT4G08150 | LG1 | |
| *E568* | 454 sequencing | AT2G35920 | LG1 | |
| *E599* | 454 sequencing | AT4G10140 | LG1 | |
| *RB9* | cDNA clone | AT1G36980 | LG1 | KF034808 |
| *2A10* | cDNA clone | AT1G03900 | LG2 | KF034809 |
| *E98* | cDNA clone | AT4G10930 | LG2 | KF034811 |

| | | | | |
|---|---|---|---|---|
| *E154* | 454 sequencing | AT2G33040 | LG2 | |
| *E221* | 454 sequencing | AT4G17050 | LG2 | |
| *E253* | 454 sequencing | AT4G02030 | LG2 | |
| *E277* | 454 sequencing | AT3G27180 | LG2 | |
| *E380* | 454 sequencing | AT4G02220 | LG2 | |
| *E515* | 454 sequencing | AT4G17830 | LG2 | |
| *E565* | 454 sequencing | AT4G01100 | LG2 | |
| *E585* | 454 sequencing | AT1G80920 | LG2 | |
| *E603* | 454 sequencing | AT1G71270 | LG2 | |
| *1H12* | cDNA clone | AT4G37930 | LG3 | KF034813 |
| *E39* | cDNA clone | AT5G56090 | LG3 | KF034812 |
| *E166* | 454 sequencing | AT2G39080 | LG3 | |
| *E261* | 454 sequencing | AT4G14570 | LG3 | |
| *E285* | 454 sequencing | AT5G14140 | LG3 | |
| *E304* | 454 sequencing | AT5G13420 | LG3 | |
| *E363* | 454 sequencing | AT3G52040 | LG3 | |
| *E503* | 454 sequencing | AT1G67060 | LG3 | |
| *E569* | 454 sequencing | AT5G14420 | LG3 | |
| *E574* | 454 sequencing | AT3G04240 | LG3 | |
| *E278* | 454 sequencing | AT1G04080 | LG4 | |
| *E517* | 454 sequencing | AT2G40730 | LG4 | |

| | | | | |
|---|---|---|---|---|
| *E532* | 454 sequencing | AT5G01990 | LG4 | |
| *E536* | 454 sequencing | AT1G03250 | LG4 | |
| *E578* | 454 sequencing | AT3G48425 | LG4 | |
| *E354* | 454 sequencing | AT2G39990 | LG4 | |
| *2C10* | cDNA clone | AT3G55440 | LG4 | KF034815 |
| *RB14* | cDNA clone | AT3G46430 | LG4 | KF034814 |
| E106 | cDNA clone | AT2G05170 | LG5 | KF034816 |
| E155 | 454 sequencing | AT3G10300 | LG5 | |
| E218 | 454 sequencing | AT1G16210 | LG5 | |
| E227 | 454 sequencing | AT4G33210 | LG5 | |
| E359 | 454 sequencing | AT4G35250 | LG5 | |
| E554 | 454 sequencing | AT5G22830 | LG5 | |
| E587 | 454 sequencing | AT3G18940 | LG5 | |
| E634 | 454 sequencing | AT3G55440 | LG5 | |
| E645 | 454 sequencing | AT2G25737 | LG5 | |
| *E224* | 454 sequencing | AT4G13430 | LG6 | |
| *E231* | 454 sequencing | AT5G27560 | LG6 | |
| *E233* | 454 sequencing | AT5G63620 | LG6 | |
| *E261b* | 454 sequencing | AT4G14570 | LG6 | |
| *E341* | 454 sequencing | AT5G22580 | LG6 | |
| *E388* | 454 sequencing | AT2G48070 | LG6 | |

| | | | | |
|---|---|---|---|---|
| *E391* | 454 sequencing | AT5G54770 | LG6 | |
| *E514* | 454 sequencing | AT3G15520 | LG6 | |
| *E528* | 454 sequencing | AT1G08200 | LG6 | |
| *E547* | 454 sequencing | AT1G63900 | LG6 | |
| *E579* | 454 sequencing | AT1G08370 | LG6 | |
| *E584* | 454 sequencing | ATG55640 | LG6 | |
| *E605* | 454 sequencing | AT5G10920 | LG6 | |
| *E612* | 454 sequencing | AT3G20390 | LG6 | |
| *E203* | 454 sequencing | AT4G29830 | LG7 | |
| *E336* | 454 sequencing | AT4G15180 | LG7 | |
| *E360* | 454 sequencing | AT5G51150 | LG7 | |
| *E382* | 454 sequencing | AT1G21065 | LG7 | |
| *E386* | 454 sequencing | AT1G12230 | LG7 | |
| *E548* | 454 sequencing | AT3G17210 | LG7 | |
| *E575* | 454 sequencing | AT2G25730 | LG7 | |
| *E614* | 454 sequencing | AT2G04550 | LG7 | |
| *RB7* | cDNA clone | AT3G26070 | LG7 | KF034817 |
| *E272* | 454 sequencing | AT4G27600 | LG8 | |
| *E393* | 454 sequencing | AT4G12800 | LG8 | |
| *E502* | 454 sequencing | AT2G33255 | LG8 | |
| *E519* | 454 sequencing | AT1G08520 | LG8 | |

| | | | | |
|---|---|---|---|---|
| *E572* | 454 sequencing | AT1G66730 | LG8 | |
| *E577* | 454 sequencing | AT3G27460 | LG8 | |
| *E611* | 454 sequencing | AT2G45290 | LG8 | |
| *3C8* | cDNA clone | AT5G14030 | LG9 | KF034819 |
| *NAP* | cDNA clone | AT2G35110 | LG9 | Short sequence not in database |
| *E157* | 454 sequencing | AT1G1400 | LG9 | |
| *E165* | 454 sequencing | AT2G25110 | LG9 | |
| *E167* | 454 sequencing | AT4G34450 | LG9 | Short sequence not in database |
| *E215* | 454 sequencing | AT1G24310 | LG9 | |
| *E229* | 454 sequencing | AT1G80410 | LG9 | |
| *E344* | 454 sequencing | AT4G33640 | LG9 | |
| *E242* | 454 sequencing | AT3G47460 | LG9 | |
| *E252* | 454 sequencing | AT1G27530 | LG9 | |
| *E279* | 454 sequencing | AT5G11490 | LG9 | |
| *E281* | 454 sequencing | AT5G24710 | LG9 | |
| *E344* | 454 sequencing | AT4G33640 | LG9 | |
| *E351* | 454 sequencing | AT3G10940 | LG9 | |
| *E373* | 454 sequencing | AT2G03420 | LG9 | |
| *E513* | 454 sequencing | AT3G58140 | LG9 | |
| *E526* | 454 sequencing | AT1G30970 | LG9 | |
| *E534* | 454 sequencing | AT2G21280 | LG9 | |

| | | | | |
|---|---|---|---|---|
| *E30* | cDNA clone | AT2G45670 | LG10 | KF034821 |
| *E83* | cDNA clone | AT4G01560 | LG10 | KF034822 |
| *E160* | 454 sequencing | AT5G67590 | LG10 | |
| *E239* | 454 sequencing | AT5G58030 | LG10 | |
| *E249* | 454 sequencing | AT4G01560 | LG10 | |
| *E288* | 454 sequencing | AT3G23490 | LG10 | |
| *E314* | 454 sequencing | AT1G34000 | LG10 | |
| *E323* | 454 sequencing | AT5G61510 | LG10 | |
| *E504* | 454 sequencing | AT1G64850 | LG10 | |
| *RB16* | cDNA clone | AT2G06520 | LG10 | KF034820 |
| *E151* | 454 sequencing | AT1G30580 | LG11 | |
| *E213* | 454 sequencing | AT3G24530 | LG11 | |
| *E234* | 454 sequencing | AT1G01860 | LG11 | |
| *E266* | 454 sequencing | AT3G23620 | LG11 | |
| *E287* | 454 sequencing | AT2G45990 | LG11 | |
| *E308* | 454 sequencing | AT5G09650 | LG11 | |
| *E327* | 454 sequencing | AT5G11980 | LG11 | |
| *E356* | 454 sequencing | AT1G47640 | LG11 | |
| *E505* | 454 sequencing | AT1G20810 | LG11 | |
| *E506* | 454 sequencing | AT4G04930 | LG11 | |
| *E560* | 454 sequencing | AT5G25760 | LG11 | |

| | | | | |
|---|---|---|---|---|
| *RB15* | cDNA clone | AT5G20240 | LG11 | KF034823 |
| Sex chromosomes, fully sex-linked | | | | |
| *E247* | 454 sequencing | AT2G01490 | LG12 | |
| *E316* | 454 sequencing | AT3G63140 | LG12 | |
| *E330* | 454 sequencing | AT3G32930 | LG12 | |
| *E521* | 454 sequencing | AT4G27450 | LG12 | |
| *E523* | 454 sequencing | AT5G55220 | LG12 | |
| *SlCypX* | cDNA clone | AT3G44600 | LG12 | DV768216 |
| *SlCytX* | cDNA clone | AT1G26340 | LG12 | Short sequence not in database |
| *SlX3* | cDNA clone | AT5G66210 | LG12 | ACB86624 |
| *SlX4* | cDNA clone | AT3G26780 | LG12 | ACB86605 |
| *SlX6A* | cDNA clone | AT2G34570 | LG12 | DV768271 |
| *SlX6B* | cDNA clone | AT2G34570 | LG12 | DV768271 |
| *SlX7* | cDNA clone | AT5G48020 | LG12 | DV768352 |
| *SlX9* | cDNA clone | AT1G08380 | LG12 | HM141608–HM141717 |
| *E707X* | 454 sequencing | AT3G27090 | LG12 | |
| *E711X* | 454 sequencing | AT4G35770 | LG12 | |
| *E713X* | 454 sequencing | AT5G42190 | LG12 | |
| *E378X* | 454 sequencing | AT4G30600 | LG12 | |
| *E777X* | RNAseq | AT2G29690 | LG12 | |
| *E779X* | RNAseq | AT3G46980 | LG12 | |

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|---|---|---|---|
| *E780X* | RNAseq | AT1G79620 | LG12 |
| *E799X* | RNAseq | AT3G49880 | LG12 |
| *E807X* | RNAseq | AT1G65950 | LG12 |
| *E559X* | 454 sequencing | AT3G21865 | LG12 |
| *E162* | 454 sequencing | AT1G78900 | LG13 |
| Partially sex-linked | | | |
| *E352* | 454 sequencing | AT2G43640 | LG12 |
| *E200* | 454 sequencing | AT5G06160 | LG12 |
| *E241* | 454 sequencing | AT4G27700 | LG12 |
| *E284* | 454 sequencing | AT5G52440 | LG12 |
| *E219* | 454 sequencing | AT2G13360 | LG12 |
| *E592* | 454 sequencing | AT3G22960 | LG12 |