

Supplementary Table 1. Molecular genetic description of the early flowering mutant collection.

| Mutant genotype | Dominance | Allelic group | T2 parental line | Kan R/S segregation | T-DNA linkage | Identified locus | FST characterized | FST genomic localization | Known or putative function | Reference |
|-----------------|-----------|-----------------|------------------|---------------------|----------------|---------------------|-------------------|----------------------------------------------------------------------------------|--------------------------------------------------------------------|-----------------------------|
| eav1 | R | no | COV22 | nd | no | | | | | |
| eav2 | SemiD | no | CPV20 | 3/1 | no | | | | | |
| eav4 | SemiD | no | CPX11 | 2/1 | no | | | | | |
| eav5 | R | eav11 | CSD15 | 2/1 | no | | | | | |
| eav6 | R | no | CSE15 | 3/1 | d<1% | | Southern | | | |
| eav7 | R | no | CSH2 | 15% S | no | | | | | |
| eav8 | R | no | CSR6 | 3/1 | no | | | | | |
| eav9 | SemiD | eav12 | CTA14 | 13% S | no | | | | | |
| eav10 | R | <i>elf4</i> | CTK2 | 3/1 | d<1% | ELF4 (At2g40080) | | | regulator of circadian clock | Doyle et al., 2002 |
| eav11 | R | eav5 | CUA18 | 3/1 | no | | | | | |
| eav12 | SemiD | eav9 | CUQ17 | 3/1 | no | | | | | |
| eav13 | R | no | CUS13 | 3/1 | d<1% | | Southern | | | |
| eav14 | R | no | CUX8 | 15/1 | d<1% | | | | | |
| eav15 | R | eav37, eav42 | DEK224 | 2/1 | d<1% | | 048C04 | into gene CPR5/HYS1 (At5g64930) | regulator of expression of PR genes | Yoshida et al., 2002 |
| eav17 | SemiD | no | DFO10 | 2/1 | no (d=6.3%) | | | | | |
| eav18 | R | no | DFQ16 | 3/1 | no | | | | | |
| eav19 | R | no | DFS16 | 3/1 | no | | | | | |
| eav21 | R | <i>lhp1-1</i> | DGU13 | 3/1 | d<1% | LHP1 (At5g17690) | | | chromatin protein | Gaudin et al., 2001 |
| eav22 | R | no | DTP49 | 17% S | nd (d<20%) | | 193H07 | into At1g34250; 7557 bp upstream of At1g34245 ; 4252 bp downstream of At1g34260 | At1g34250 : transposable element | none |
| eav23 | R | <i>lhp1-2</i> | DXT72 | 2/1 | no | LHP1 (At5g17690) | | | chromatin protein | Gaudin et al., 2001 |
| eav24 | R | no | DXW4 | 2/1 | no | | | | | |
| eav25 | R | no | DXX1 | 3/1 | no | | | | | |
| eav28 | R | no | DYA37 | 15/1 | d<1% | | 104B01 | 585 bp downstream of At4g08360 (GTA02-like gene) ; 4369 bp upstream of At4g08370 | GTA02-like : KOW-domain SPT5-like transcription elongation protein | none |
| eav29 | R | no | DYA100 | 3/1 | no | | | | | |
| eav30 | SemiD | no | DYB43 | 3/1 | d<1% | | lab | into last intron of AGL27/FLM/MAF1 | MADS-box transcription factor | Werner et al., 2005 ; Oh et |

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|-------|-------|-----------------|--------|-------|-----------------|-------------------------|-------------------|---------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------|--------------------------|
| | | | | | | | (At1g77080) | | | al., 2004 |
| eav31 | R | no | DYB271 | 3/1 | d<1.9% | | | | | |
| eav32 | R | eav33, eav46 | DYC203 | 3/1 | no | | | | | |
| eav33 | R | eav32, eav46 | DYE15 | 15/1 | d<1% | | 192B06/ 193A08 | into gene XTH3 (At3g25050) | xyloglucan endotransglucosylase | Yokoyama et al., 2001 |
| eav34 | R | no | DYE164 | 63/1 | no | | | | | |
| eav35 | R | no | DYH67 | 2/1 | no | | | | | |
| eav37 | R | eav15, eav42 | DYJ8 | 15/1 | no | | | | | |
| eav38 | R | no | DYK121 | 3/1 | no | | | | | |
| eav39 | R | no | DYN78 | 15/1 | d<1% | | 122H12/ 128E03 | into gene At3g09190 | pseudogene, receptor-like protein kinase like | none |
| eav40 | R | no | DYO7 | 15/1 | d<1% | | Southern | | | |
| eav41 | SemiD | no | DYP95 | 3/1 | no | | | | | |
| eav42 | R | eav15, eav37 | DYR43 | 3/1 | d<1% | | 194A02/ 195F11 | 377 bp downstream of At5g65870 (ATPSK5) ; 286 bp upstream of At5g65880 (hypothetical protein) | ATPSK5 : phyto­sulfokine 5 precursor, peptide growth factor | Yoshida et al., 2002 |
| eav43 | SemiD | no | DZE80 | 63/1 | nd | | 195G06 | into first intron of gene At5g51930 | glucose-methanol-choline (GMC) oxidoreductase | none |
| eav46 | R | eav32, eav33 | DZT11 | 17% S | no | | | | | |
| eav47 | nd | no | DZZ92 | 80% S | nd | | | | | |
| eav49 | R | no | DZZ232 | 2/1 | no | | | | | |
| eav50 | R | no | EAB21 | 3/1 | no | | | | | |
| eav51 | SemiD | no | EAB60 | 16% S | nd (d<33.3%) | | 017B05 | 1606 bp downstream of At3g51080 (GATA6) ; 1864 bp upstream of At3g51090 (hypothetical protein) | GATA6 : zinc finger (GATA type) transcription factor | Manfield et al., 2007 |
| eav52 | R | no | EAB68 | 15/1 | d<10% | | | | | |
| eav53 | R | no | EAC59 | 63/1 | nd | | | | | |
| eav54 | R | <i>elf3</i> | EAF41 | 15/1 | no | ELF3 (near At2g6845) | | | regulator of circadian clock | Hicks et al., 2001 |
| eav55 | R | no | EAF72 | 15/1 | nd (d<25%) | | | | | |
| eav56 | R | no | EAH7 | 2/1 | no | | | | | |

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|-------|-------|-------------|--------|------|---------------|---------------------|-------------------|---------------------------------------------------------------------------------------------------|------------------------------------------|--------------------------|
| eav57 | SemiD | no | EAI164 | 3/1 | d<10% | | 194F11/ 204H08 | 1752 bp downstream of At3g57390 (AGL18) ; 711 bp upstream of At3g57400 (unknown protein) | AGL18 : MADS-box transcription factor | Adamczyk et al., 2007 |
| eav58 | SemiD | no | EAI247 | 15/1 | nd (d<20%) | | | | | |
| eav59 | R | no | EAI285 | 3/1 | no | | | | | |
| eav60 | R | no | EAI353 | 3/1 | d<2.1% | | | | | |
| eav61 | R | <i>elf4</i> | EAI439 | nd | no | ELF4 (At2g40080) | | | regulator of circadian clock | Doyle et al., 2002 |

The eav mutants were obtained from T2 parental lines of the Versailles collection, INRA, France (Bechtold et al., 1993; <http://dbsgap.versailles.inra.fr/portail/>). Recessive (R) and semi-dominant (SemiD) alleles were determined. Complementation analyses identified 5 allelic groups each comprising 2 or 3 alleles (as indicated by similarly coloured cells). Segregations of the kanamycin resistance marker (KanaR/S: kanamycin resistant/sensitive) in the parental lines are described in the dbsgap database. The linkage between early flowering phenotypes and T-DNA insertions (T-DNA linkage) was analyzed and specific loci were identified based on genetic crosses or by cloning. For mutations linked to a T-DNA insertion, preliminary molecular analysis was conducted by characterizing T-DNA flanking sequences. For three mutants, Southern analyses revealed complex insertions. Codes for FSTs available in the FLAGdb++ database are indicated.