

SUPPLEMENTAL EXPERIMENTAL PROCEDURES

Generation of the *RAD51pro::GFP* transgene

The *RAD51pro::GFP* strain was created using the standard agrobacterium-mediated floral dip transformation on *atxr5/6* mutants [1]. The GFP protein [1] was fused to sequence corresponding to the upstream region (1 kb of sequence 5' of the start codon) of the *RAD51* gene. The resulting transgene also carried a hygromycin resistance marker that allowed for plant selection. Primer sequence used to amplify this sequence is found in below.

DNA-seq analysis

The flower, cotyledon, and 16C sorted nuclei libraries presented in Fig 1 and 2 were all sequenced at 100 bp length. Due to poor quality of the 3' end of these reads, the flower and cotyledon reads were trimmed to 50 bp in length while the 16C libraries were trimmed to 80 bp in length for downstream analysis. Flower/cotyledon reads were mapped to the TAIR10 genome using Bowtie [2] allowing for 1 mismatch, while 16C reads were allowed 2 mismatches given their greater length. For all mappings, only uniquely mapping reads were retained. RPKM of genes/TEs was calculated as (((# of reads overlapping a feature)/(total aligning reads for that library))/length of the feature)*1000000*1000. For generation of chromosomal views, 100 kb regions of low coverage (coverage below the 5th percentile) in either library of the comparison were excluded from analysis. As the sum of log2 ratios between any library should total to 0, we chose to center the log2 ratio on the average ratio of any two compared libraries on the first 5 Mbp of chromosome 1. This avoids the computational artifact of giving a negative ratio of coverage for *atxr5/6* mutants compared to Col over euchromatic regions, something we do not believe is biologically relevant.

RNA-seq analysis

All RNA-seq reads were mapped to the TAIR10 genome build using Tophat2 [3], allowing for 1 mismatch and retaining only uniquely mapping reads. RPKM values were calculated as (((# of reads overlapping a feature)/(total aligning reads for that library which overlap with mRNA encoding regions))/length of the feature)*1000000*1000. To call genes or TEs as up-regulated in a given RNA-seq library, that library must have had two biological replicates and the gene or TE must have shown 4-fold up-regulation as compared to Col in both biological replicates at a False Discovery Rate (FDR) less than 0.01. FDRs were estimated using a Benjamani-Hochberg adjustment of P-values calculated using a Fisher Exact Test (FET).

EMS-induced mutation mapping via RNA-seq or DNA-seq analysis

Mapping of EMS-induced genetic lesions was carried out under the operating assumption that EMS treatment would induce a large number of unique mutations in each line sequenced. Following backcross of the EMS mutant to an *atxr5/6* plant and resegregation of the EMS mutants in the F2 generation, any given EMS mutation would be expected to be present at the level of 25% in a population of the F2 mutants. This hypothesis would fail to hold true for mutations linked to the causal EMS mutation, which would therefore be over-represented in the sequencing data at levels exceeding 25% of the reads for a given position.

To identify these over-represented mutations, we first identified candidate mutations in the RNA-seq or DNA-seq data by considering any bp position that had at least 2 mismatches. The candidate mutations were then compared to candidate mutations called for all the RNA-seq or DNA-seq libraries generated from EMS lines as well as control RAD51pro::GFP and Col lines. A candidate mutation was considered unique if it had >=4 mismatches for only

one library. These unique candidate mutations were considered significantly enriched in a library, if the mismatched base pair was present at a level greater than 25% of all base pairs sequenced at that position ($P < 0.01$, Binomial Test). The resulting significantly enriched unique mutations were then visually assessed via chromosomal view plots for clusters that might be indicative of regions of linkage. Following identification of these regions, mutations were scanned for mutations that fell within gene coding regions that were predicted to cause splice site/nonsense/ or missense mutations. These candidate mutations were then chosen for downstream RNA-seq and complementation analysis.

Whole-genome bisulfite sequencing analysis

DMRs were identified for the newly identified suppressors of *atxr5/6* following alignment of the whole-genome bisulfite sequencing reads to the TAIR10 genome [4]. To identify DMRs, we used methods as previously described [5] with the following modifications: 1) Minimum coverage for a cytosine to be considered in DMR calling was 5X, 2) At least 5 cytosines of a given context must be present in a DMR for that context, 3) Minimum absolute difference in percent methylation to be considered a DMR for CG, CHG, and CHH contexts was 50%, 25%, and 15%, respectively. A Benjamani-Hochberg estimated FDR of < 0.01 based on a FET P-value was required to be called as a DMR. Comparisons between the mutant libraries and three Col (wild type) libraries were carried out. To be retained for downstream analysis, a DMR must have been called for a given mutant library in comparison to all three of the Col libraries. The Col samples used included one library generated in parallel and two previously published Col methylomes (GEO samples: GSM1193638 and GSM881756). For the analysis of *met1* in Figure 6, a previously published whole-genome bisulfite sequencing library was used (GSM981031), although the reads from this library were downsampled (to ~ 50 million reads) to match the coverage of libraries generated in this study, and were realigned and processed using the same parameters as described above.

Primers Used to Amplify the *RAD51* promoter sequence for the *RAD51pro::GFP* transgene.

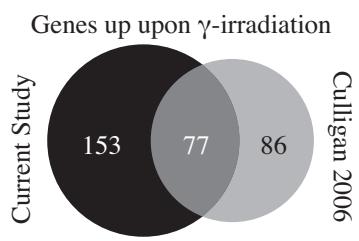
| Primer Name | Sequence | Description |
|--------------------|-----------------------------------|---|
| JP7488 | CTGGGTTTCTTCATCGTCTTG | Reverse primer directly upstream of RAD51 start codon |
| JP7515 | CACCGTTGACATTCAAACACCTAGGTA TC | Forward primer ~1kb upstream of RAD51, with CACC tag added for Gateway Cloning into P-ENTR D TOPO (Life Technologies) |

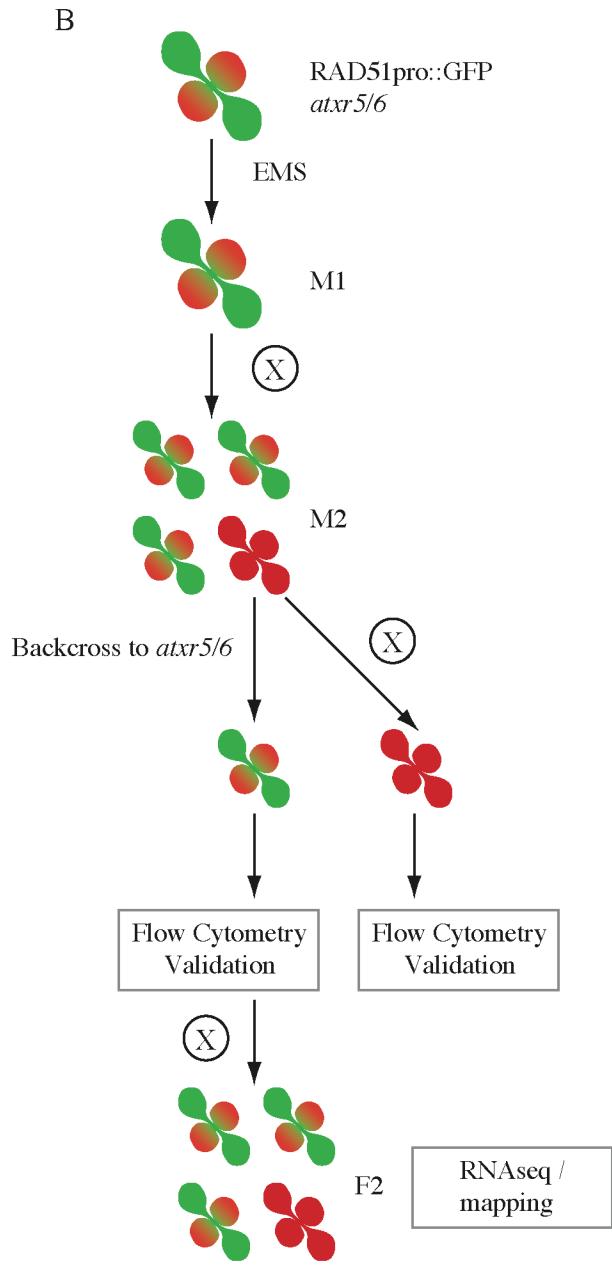
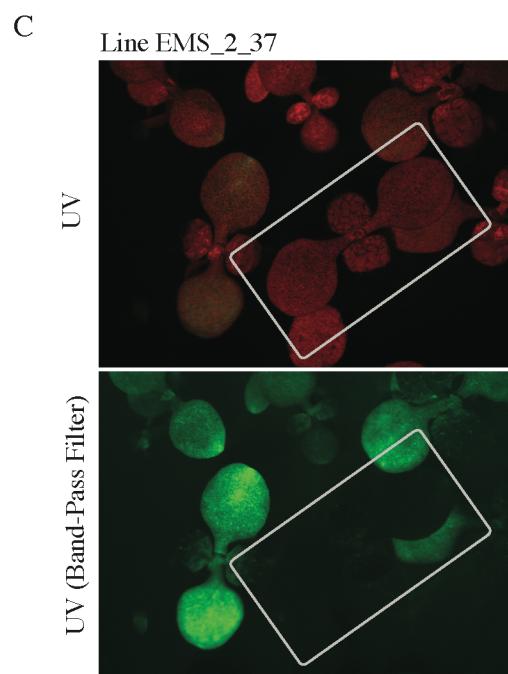
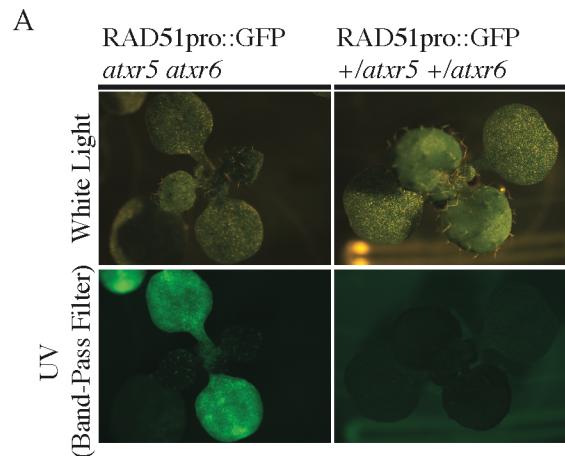
Genetic stocks used in this study

| Allele | EMS/T-DNA identifier | Gene Target | Ecotype |
|--------------------------|----------------------|----------------------------|---------|
| <i>atxr5</i> | SALK_130607 | <i>AT5G09790</i> (ATXR5) | Col |
| <i>atxr6</i> | SAIL_240_H01 | <i>AT5G24330</i> (ATXR6) | Col |
| <i>atbrca1-1</i> | SALK_014731 | <i>AT4G21070</i> (AtBRCA1) | Col |
| <i>atsac3b-3</i> | SALK_065672 | <i>AT3G06290</i> (AtSAC3B) | Col |
| <i>atsac3b-4</i> | ems_2_37 | <i>AT3G06290</i> (AtSAC3B) | Col |
| <i>atsac3b-5</i> | ems_2_209 | <i>AT3G06290</i> (AtSAC3B) | Col |
| <i>atthp1-1</i> | SAIL_82_A02 | <i>AT2G19560</i> (AtTHP1) | Col |
| <i>atthp1-5</i> | ems_2_300 | <i>AT2G19560</i> (AtTHP1) | Col |
| <i>bru1-4</i> | SALK_034207 | <i>AT3G18730</i> (BRU1) | Col |
| <i>fas2</i> | SALK_033228 | <i>AT5G64630</i> (FAS2) | Col |
| <i>mbd9-3</i> | SALK_039302 | <i>AT3G01460</i> (MBD9) | Col |
| <i>mbd9-4</i> | ems_2_129 | <i>AT3G01460</i> (MBD9) | Col |
| <i>atstUBL2-1</i> | ems_2_325 | <i>AT1G67180</i> (STUBL2) | Col |
| <i>atstUBL2-2</i> | 430E03 (FCA227) | <i>AT1G67180</i> (STUBL2) | Ws |
| <i>met1-3</i> | CS16394 | <i>AT5G49160</i> (MET1) | Col |

REFERENCES

1. Moissiard G, Cokus SJ, Cary J, Feng S, Billi AC, Stroud H, et al. MORC family ATPases required for heterochromatin condensation and gene silencing. *Science*. 2012;336: 1448–51. doi:10.1126/science.1221472
2. Langmead B, Trapnell C, Pop M, Salzberg SL. Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. *Genome Biol*. Nature Publishing Group, a division of Macmillan Publishers Limited. All Rights Reserved.; 2009;10: R25. doi:10.1186/gb-2009-10-3-r25
3. Kim D, Pertea G, Trapnell C, Pimentel H, Kelley R, Salzberg SL. TopHat2: accurate alignment of transcriptomes in the presence of insertions, deletions and gene fusions. *Genome Biol*. 2013;14: R36. doi:10.1186/gb-2013-14-4-r36
4. Xi Y, Li W. BSMAP: whole genome bisulfite sequence MAPping program. *BMC Bioinformatics*. 2009;10: 232. doi:10.1186/1471-2105-10-232
5. Stroud H, Greenberg MVC, Feng S, Bernatavichute Y V, Jacobsen SE. Comprehensive analysis of silencing mutants reveals complex regulation of the Arabidopsis methylome. *Cell*. 2013;152: 352–64. doi:10.1016/j.cell.2012.10.054

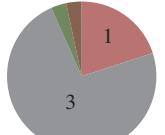




A Genome (119 Mbp)



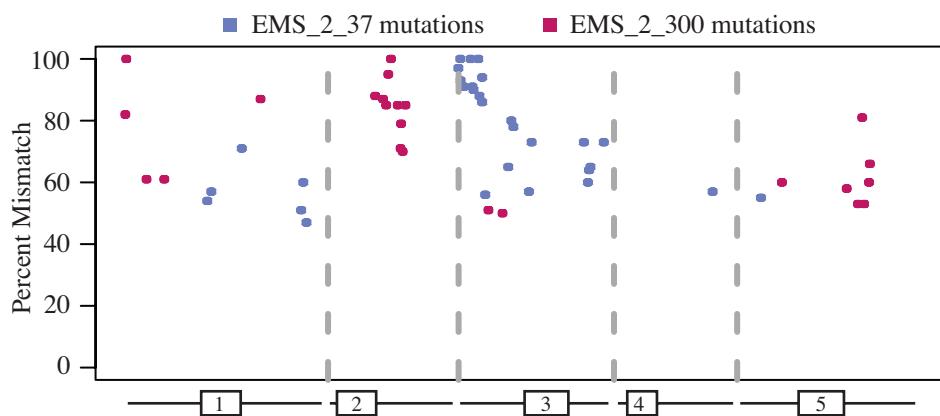
EMS_2_37(n=30)



EMS_2_300(n=22)

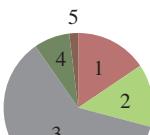


B

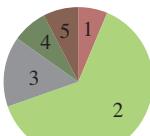


D

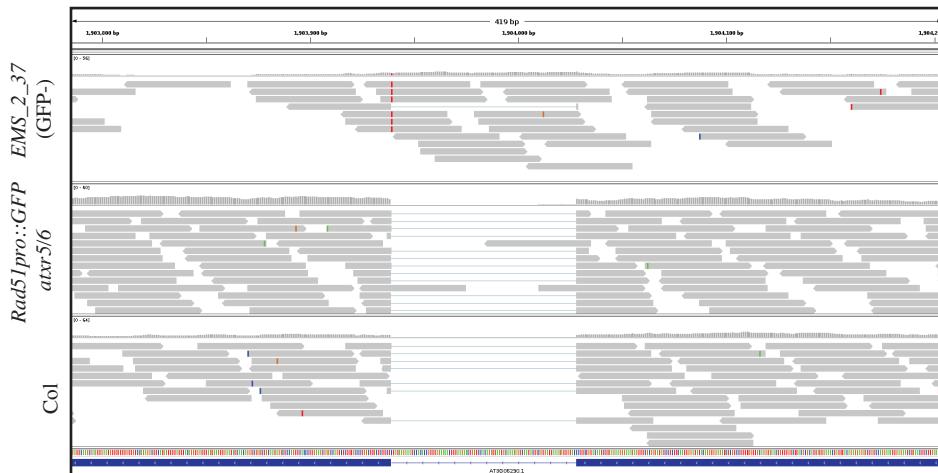
EMS_2_37(n=103)



EMS_2_300(n=79)

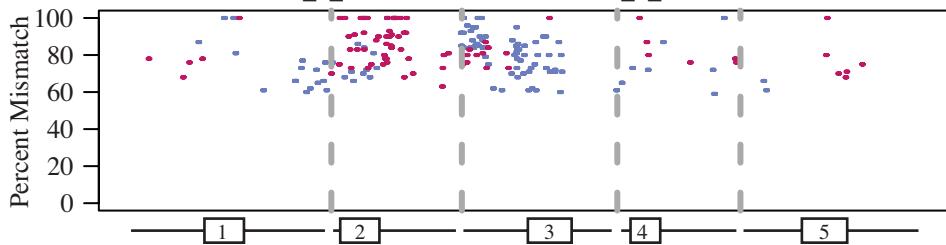


C



E

ems_2_37 mutations ems_2_300 mutations

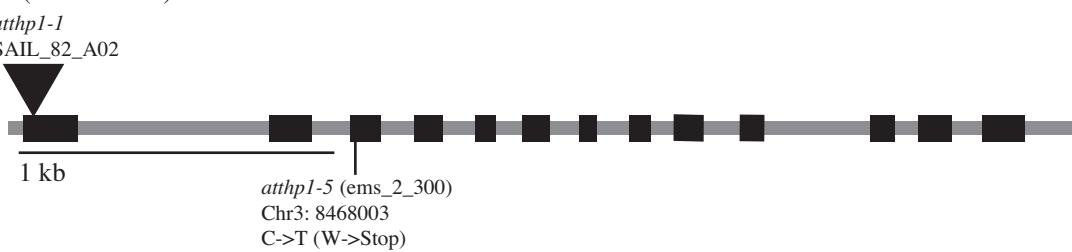


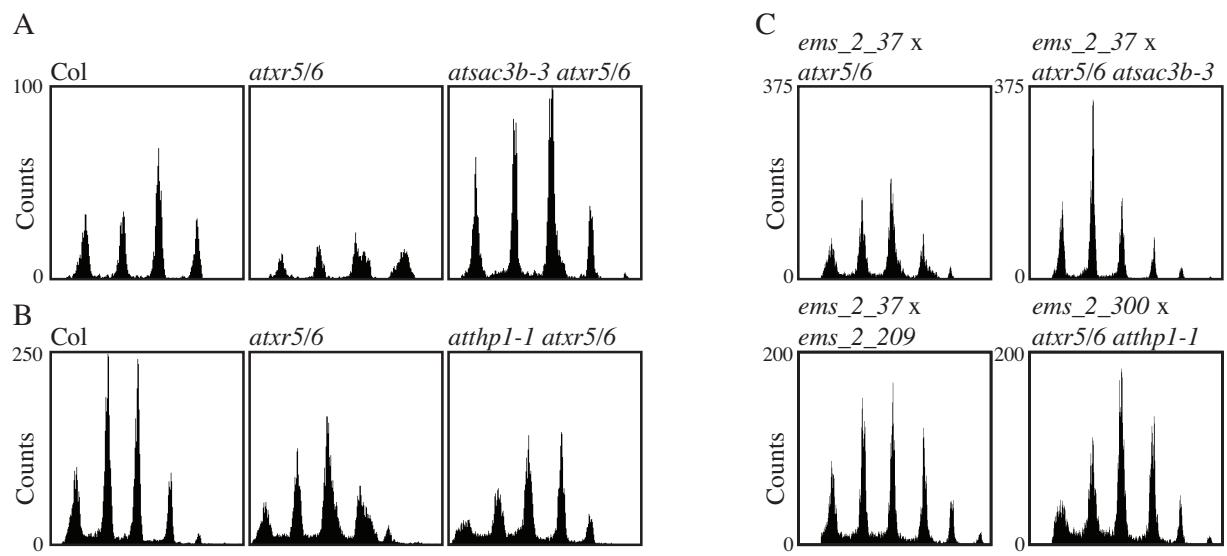
F

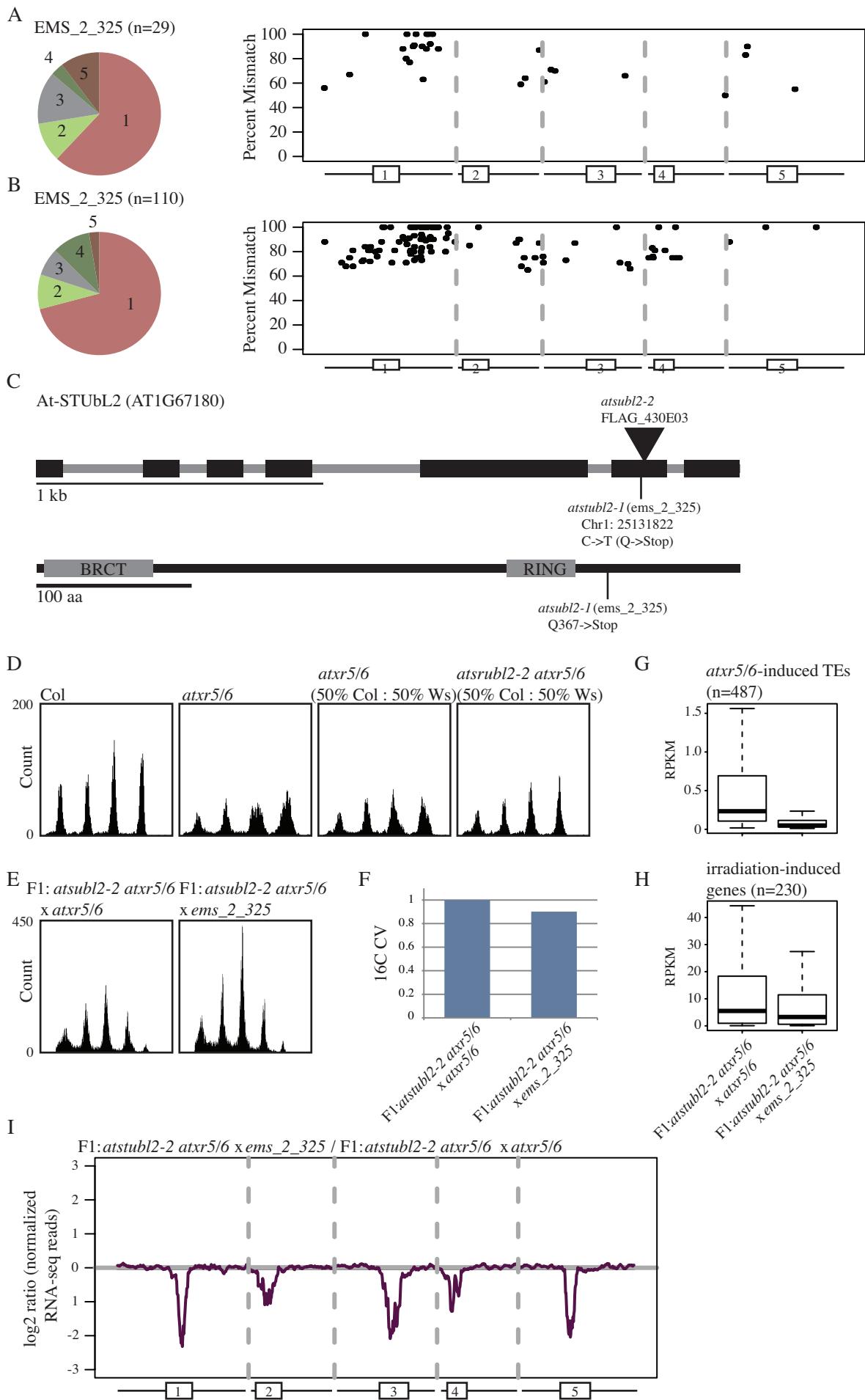
AtSAC3B (AT3G06290)



AtTHP1 (AT2G19560)







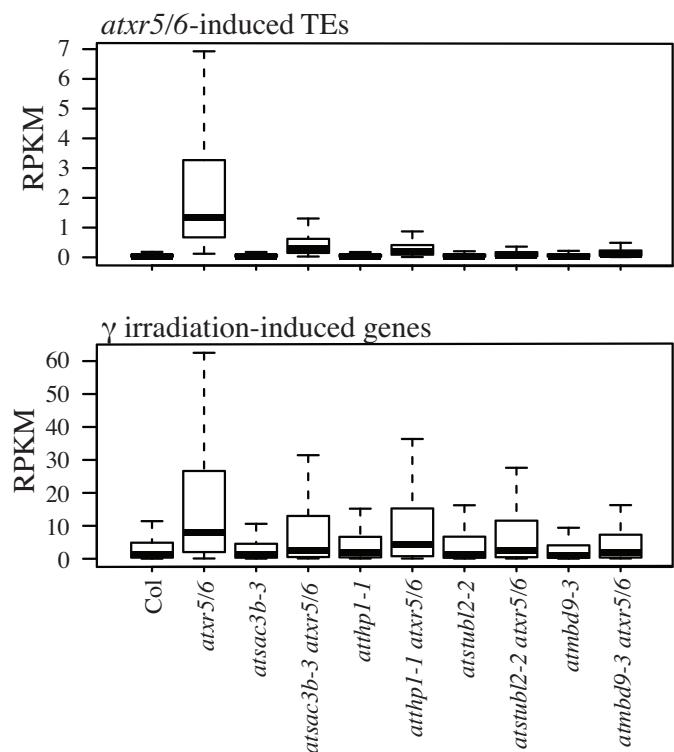


Table S1. Genes and transposons upregulated compared to wild type in atxr5/6 cotyledons. (> 4-fold increase)

| Chromosome | Start | Stop | Gene | Strand |
|------------|----------|----------|-----------|--------|
| Chr1 | 1618601 | 1623452 | AT1G05490 | - |
| Chr1 | 2304765 | 2305031 | AT1G07500 | - |
| Chr1 | 2929216 | 2931841 | AT1G09080 | - |
| Chr1 | 2965022 | 2965972 | AT1G09180 | + |
| Chr1 | 3230449 | 3233109 | AT1G09932 | - |
| Chr1 | 3390321 | 3392571 | AT1G10340 | - |
| Chr1 | 4567934 | 4570598 | AT1G13330 | + |
| Chr1 | 4569447 | 4571118 | AT1G13340 | - |
| Chr1 | 4620227 | 4621580 | AT1G13470 | - |
| Chr1 | 5365664 | 5366497 | AT1G15580 | - |
| Chr1 | 6975387 | 6977264 | AT1G20120 | + |
| Chr1 | 7043712 | 7044592 | AT1G20350 | + |
| Chr1 | 7203301 | 7208998 | AT1G20750 | - |
| Chr1 | 7853083 | 7854963 | AT1G22240 | + |
| Chr1 | 8402045 | 8404301 | AT1G23760 | + |
| Chr1 | 9126736 | 9128528 | AT1G26380 | - |
| Chr1 | 9141566 | 9143304 | AT1G26420 | - |
| Chr1 | 10606250 | 10607784 | AT1G30160 | + |
| Chr1 | 10607887 | 10609618 | AT1G30170 | - |
| Chr1 | 10786978 | 10788683 | AT1G30473 | + |
| Chr1 | 10788225 | 10789943 | AT1G30475 | - |
| Chr1 | 11776855 | 11777557 | AT1G32570 | + |
| Chr1 | 12346231 | 12348513 | AT1G33960 | + |
| Chr1 | 12448725 | 12451287 | AT1G34180 | + |
| Chr1 | 12917148 | 12917763 | AT1G35230 | + |
| Chr1 | 13227323 | 13229796 | AT1G35730 | - |
| Chr1 | 13867567 | 13869490 | AT1G36675 | + |
| Chr1 | 14170350 | 14172040 | AT1G37140 | - |
| Chr1 | 16787507 | 16789318 | AT1G44130 | - |
| Chr1 | 19274657 | 19278528 | AT1G51890 | - |
| Chr1 | 19963213 | 19964712 | AT1G53480 | - |
| Chr1 | 19963266 | 19966952 | AT1G53490 | + |
| Chr1 | 21345638 | 21346157 | AT1G57630 | + |
| Chr1 | 21564110 | 21565171 | AT1G58225 | + |
| Chr1 | 22059423 | 22059822 | AT1G59920 | - |
| Chr1 | 22061082 | 22061481 | AT1G59930 | - |
| Chr1 | 22291581 | 22293964 | AT1G60500 | + |
| Chr1 | 25562117 | 25563948 | AT1G68200 | + |
| Chr1 | 26226865 | 26228580 | AT1G69720 | + |
| Chr1 | 28423895 | 28424931 | AT1G75700 | + |
| Chr2 | 1337385 | 1339270 | AT2G04050 | - |
| Chr2 | 1564165 | 1565106 | AT2G04495 | + |
| Chr2 | 2806624 | 2807368 | AT2G06904 | + |
| Chr2 | 2996775 | 2997889 | AT2G07215 | - |
| Chr2 | 3704576 | 3705594 | AT2G09840 | - |
| Chr2 | 4724035 | 4724143 | AT2G11773 | - |
| Chr2 | 4728071 | 4728239 | AT2G11778 | + |

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|------|----------|----------|-----------|---|
| Chr2 | 6241703 | 6242463 | AT2G14610 | - |
| Chr2 | 6877773 | 6880898 | AT2G15790 | - |
| Chr2 | 7682382 | 7684083 | AT2G17690 | + |
| Chr2 | 7829034 | 7830580 | AT2G18000 | + |
| Chr2 | 7914304 | 7915872 | AT2G18190 | - |
| Chr2 | 7917504 | 7919277 | AT2G18193 | - |
| Chr2 | 8090657 | 8091656 | AT2G18660 | - |
| Chr2 | 8595819 | 8600757 | AT2G19910 | - |
| Chr2 | 10143645 | 10144511 | AT2G23830 | + |
| Chr2 | 10582829 | 10585216 | AT2G24850 | - |
| Chr2 | 12936978 | 12938834 | AT2G30360 | - |
| Chr2 | 13099335 | 13101413 | AT2G30750 | - |
| Chr2 | 13859768 | 13862614 | AT2G32680 | - |
| Chr2 | 17880614 | 17882636 | AT2G43000 | - |
| Chr2 | 18736838 | 18741841 | AT2G45460 | - |
| Chr3 | 229170 | 231105 | AT3G01600 | + |
| Chr3 | 1053365 | 1055163 | AT3G04060 | - |
| Chr3 | 3946035 | 3946960 | AT3G12410 | - |
| Chr3 | 8090653 | 8093248 | AT3G22860 | - |
| Chr3 | 8227221 | 8229576 | AT3G23120 | - |
| Chr3 | 9195502 | 9197124 | AT3G25250 | + |
| Chr3 | 9887947 | 9889705 | AT3G26830 | + |
| Chr3 | 10231115 | 10231418 | AT3G27630 | - |
| Chr3 | 10694443 | 10696123 | AT3G28540 | + |
| Chr3 | 10715622 | 10717329 | AT3G28580 | + |
| Chr3 | 11478731 | 11479749 | AT3G29639 | - |
| Chr3 | 12349046 | 12349832 | AT3G30720 | + |
| Chr3 | 12593958 | 12600432 | AT3G30842 | - |
| Chr3 | 14940113 | 14945291 | AT3G42850 | - |
| Chr3 | 14946187 | 14948167 | AT3G42860 | - |
| Chr3 | 15828176 | 15829088 | AT3G44070 | - |
| Chr3 | 16863400 | 16866041 | AT3G45860 | - |
| Chr3 | 16922752 | 16923247 | AT3G46080 | - |
| Chr3 | 17322118 | 17323545 | AT3G47030 | + |
| Chr3 | 18021649 | 18022324 | AT3G48640 | - |
| Chr3 | 18078473 | 18086817 | AT3G48770 | - |
| Chr3 | 18393746 | 18396816 | AT3G49620 | + |
| Chr3 | 18873957 | 18874780 | AT3G50770 | + |
| Chr3 | 19326332 | 19328323 | AT3G52115 | + |
| Chr3 | 21188516 | 21189859 | AT3G57260 | - |
| Chr3 | 21575886 | 21577845 | AT3G58270 | - |
| Chr4 | 1049956 | 1054065 | AT4G02390 | + |
| Chr4 | 1529445 | 1531780 | AT4G03450 | - |
| Chr4 | 2765961 | 2767957 | AT4G05475 | - |
| Chr4 | 4808634 | 4809352 | AT4G07965 | + |
| Chr4 | 5147699 | 5150966 | AT4G08150 | - |
| Chr4 | 5469344 | 5470466 | AT4G08593 | + |
| Chr4 | 5555315 | 5556616 | AT4G08691 | - |
| Chr4 | 7148245 | 7149921 | AT4G11890 | + |

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|------|----------|----------|-----------|---|
| Chr4 | 10466476 | 10469092 | AT4G19130 | - |
| Chr4 | 11248077 | 11252724 | AT4G21070 | + |
| Chr4 | 11591115 | 11592238 | AT4G21850 | - |
| Chr4 | 12030019 | 12033137 | AT4G22960 | + |
| Chr4 | 12121382 | 12124205 | AT4G23140 | + |
| Chr4 | 12125730 | 12128332 | AT4G23150 | + |
| Chr4 | 12129484 | 12134187 | AT4G23160 | + |
| Chr4 | 12957833 | 12958714 | AT4G25330 | + |
| Chr4 | 13236447 | 13238487 | AT4G26120 | + |
| Chr4 | 16491795 | 16493418 | AT4G34510 | + |
| Chr4 | 17621885 | 17624285 | AT4G37490 | - |
| Chr4 | 18366949 | 18368359 | AT4G39500 | - |
| Chr5 | 999101 | 1001029 | AT5G03780 | - |
| Chr5 | 2406067 | 2407330 | AT5G07610 | + |
| Chr5 | 2882426 | 2884229 | AT5G09290 | + |
| Chr5 | 3400341 | 3402207 | AT5G10760 | - |
| Chr5 | 3638430 | 3639883 | AT5G11410 | - |
| Chr5 | 4670778 | 4672072 | AT5G14490 | - |
| Chr5 | 6040918 | 6042938 | AT5G18270 | - |
| Chr5 | 7070585 | 7072951 | AT5G20850 | - |
| Chr5 | 7478929 | 7479527 | AT5G22520 | + |
| Chr5 | 8251377 | 8262154 | AT5G24280 | - |
| Chr5 | 8752683 | 8754485 | AT5G25260 | + |
| Chr5 | 9147175 | 9148128 | AT5G26170 | - |
| Chr5 | 10201270 | 10203335 | AT5G28235 | - |
| Chr5 | 10824432 | 10826575 | AT5G28810 | + |
| Chr5 | 11190542 | 11191963 | AT5G29560 | - |
| Chr5 | 13386851 | 13387175 | AT5G35120 | - |
| Chr5 | 15573504 | 15575618 | AT5G38900 | - |
| Chr5 | 15883178 | 15884067 | AT5G39670 | + |
| Chr5 | 16359429 | 16363792 | AT5G40840 | - |
| Chr5 | 18095712 | 18097585 | AT5G44820 | - |
| Chr5 | 18260440 | 18264346 | AT5G45150 | + |
| Chr5 | 19758880 | 19761721 | AT5G48720 | + |
| Chr5 | 20952441 | 20953393 | AT5G51580 | - |
| Chr5 | 21386823 | 21387703 | AT5G52760 | + |
| Chr5 | 22478711 | 22481148 | AT5G55490 | - |
| Chr5 | 22974519 | 22975992 | AT5G56810 | + |
| Chr5 | 24252157 | 24254849 | AT5G60250 | + |
| Chr5 | 24498466 | 24501494 | AT5G60900 | - |
| Chr5 | 24571170 | 24574372 | AT5G61070 | - |
| Chr5 | 24808483 | 24812597 | AT5G61740 | + |
| Chr5 | 25633535 | 25635781 | AT5G64060 | - |
| Chr5 | 26434063 | 26437222 | AT5G66130 | + |

e ; FDR of 1e-2 using a Benjamini-Hochberg correction of Fisher's Exact Test)

Table S1. Genes and transposons upregulated compared to wild type in atxr5/6 cotyledons. (> 4-fold increase)

| Chromosome | Start | Stop | Gene | Strand |
|------------|----------|----------|-----------|--------|
| Chr1 | 7203301 | 7208998 | AT1G20750 | - |
| Chr1 | 19963213 | 19964712 | AT1G53480 | - |
| Chr1 | 19963266 | 19966952 | AT1G53490 | + |
| Chr3 | 229170 | 231105 | AT3G01600 | + |
| Chr3 | 10231115 | 10231418 | AT3G27630 | - |
| Chr4 | 9856295 | 9859288 | AT4G17710 | - |
| Chr4 | 12957833 | 12958714 | AT4G25330 | + |
| Chr4 | 18366949 | 18368359 | AT4G39500 | - |
| Chr5 | 4670778 | 4672072 | AT5G14490 | - |

e ; FDR of 1e-2 using a Benjamini-Hochberg correction of Fisher's Exact Test)

Table S1. Genes and transposons upregulated compared to wild type in atxr5/6 cotyledons. (> 4-fold increase)

| Chromosome | Start | Stop | Gene | Strand |
|------------|----------|----------|------------|--------|
| Chr1 | 8927732 | 8933058 | AT1TE28830 | - |
| Chr1 | 12016038 | 12020227 | AT1TE38940 | - |
| Chr1 | 12172517 | 12177219 | AT1TE39515 | - |
| Chr1 | 12406709 | 12410000 | AT1TE40355 | + |
| Chr1 | 12626457 | 12630547 | AT1TE41230 | + |
| Chr1 | 12664497 | 12673969 | AT1TE41345 | - |
| Chr1 | 12949835 | 12953875 | AT1TE42225 | + |
| Chr1 | 13127113 | 13128014 | AT1TE42875 | - |
| Chr1 | 13131405 | 13140006 | AT1TE42890 | + |
| Chr1 | 13180946 | 13181769 | AT1TE43030 | - |
| Chr1 | 13181965 | 13186591 | AT1TE43040 | - |
| Chr1 | 13230993 | 13235723 | AT1TE43225 | - |
| Chr1 | 13263763 | 13276157 | AT1TE43355 | + |
| Chr1 | 13417658 | 13421489 | AT1TE43880 | - |
| Chr1 | 13439444 | 13448530 | AT1TE43975 | + |
| Chr1 | 13507780 | 13515964 | AT1TE44230 | - |
| Chr1 | 13559846 | 13564825 | AT1TE44380 | + |
| Chr1 | 13573425 | 13576126 | AT1TE44450 | - |
| Chr1 | 13576127 | 13581525 | AT1TE44455 | - |
| Chr1 | 13625190 | 13632772 | AT1TE44630 | - |
| Chr1 | 13644552 | 13648938 | AT1TE44670 | - |
| Chr1 | 13711059 | 13712501 | AT1TE44905 | + |
| Chr1 | 13734680 | 13743201 | AT1TE45020 | - |
| Chr1 | 13777611 | 13785849 | AT1TE45145 | - |
| Chr1 | 13786685 | 13795195 | AT1TE45175 | + |
| Chr1 | 13840025 | 13840159 | AT1TE45375 | - |
| Chr1 | 13840160 | 13840729 | AT1TE45380 | - |
| Chr1 | 13840762 | 13840830 | AT1TE45385 | - |
| Chr1 | 13841052 | 13841405 | AT1TE45390 | - |
| Chr1 | 13842619 | 13847118 | AT1TE45395 | - |
| Chr1 | 13871158 | 13871383 | AT1TE45510 | + |
| Chr1 | 13968111 | 13979022 | AT1TE45855 | - |
| Chr1 | 14033278 | 14038199 | AT1TE46095 | - |
| Chr1 | 14044362 | 14045934 | AT1TE46140 | + |
| Chr1 | 14070822 | 14075427 | AT1TE46235 | + |
| Chr1 | 14109014 | 14112560 | AT1TE46330 | - |
| Chr1 | 14196923 | 14206946 | AT1TE46635 | - |
| Chr1 | 14214747 | 14225656 | AT1TE46665 | - |
| Chr1 | 14277551 | 14282138 | AT1TE46830 | - |
| Chr1 | 14280175 | 14281809 | AT1TE46835 | - |
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| Chr1 | 14368381 | 14375118 | AT1TE47280 | + |
| Chr1 | 14379072 | 14379255 | AT1TE47300 | + |
| Chr1 | 14424725 | 14424908 | AT1TE47520 | + |
| Chr1 | 14427922 | 14449178 | AT1TE47540 | + |
| Chr1 | 14432223 | 14442952 | AT1TE47550 | + |
| Chr1 | 14449179 | 14451469 | AT1TE47570 | + |

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| Chr1 | 14481779 | 14481962 AT1TE47705 | + |
| Chr1 | 14590168 | 14598729 AT1TE48035 | - |
| Chr1 | 14837664 | 14845083 AT1TE48730 | - |
| Chr1 | 14865439 | 14874995 AT1TE48765 | - |
| Chr1 | 14875416 | 14885131 AT1TE48775 | + |
| Chr1 | 14891977 | 14897732 AT1TE48830 | - |
| Chr1 | 14897776 | 14908757 AT1TE48835 | - |
| Chr1 | 15061271 | 15069809 AT1TE49300 | - |
| Chr1 | 15074170 | 15076081 AT1TE49325 | - |
| Chr1 | 15139696 | 15142452 AT1TE49675 | + |
| Chr1 | 15209312 | 15215968 AT1TE49955 | + |
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| Chr1 | 15398356 | 15406124 AT1TE50810 | + |
| Chr1 | 15412724 | 15420826 AT1TE50860 | + |
| Chr1 | 15455488 | 15486506 AT1TE51040 | + |
| Chr1 | 15610627 | 15615403 AT1TE51360 | - |
| Chr1 | 15703960 | 15715037 AT1TE51735 | - |
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| Chr1 | 16097901 | 16099192 AT1TE52990 | - |
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| Chr1 | 16659688 | 16664330 AT1TE54925 | - |
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| Chr1 | 17023916 | 17029257 AT1TE56390 | - |
| Chr1 | 18154505 | 18163494 AT1TE60180 | + |
| Chr1 | 18846375 | 18854882 AT1TE62470 | - |
| Chr1 | 19675549 | 19680353 AT1TE65060 | + |
| Chr1 | 28515062 | 28516118 AT1TE93275 | + |
| Chr2 | 31445 | 42029 AT2TE00030 | + |
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| Chr2 | 566757 | 582571 AT2TE02465 | + |
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| Chr2 | 1557070 | 1562055 AT2TE07175 | - |
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| Chr2 | 1758540 | 1766569 AT2TE08135 | - |
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| Chr2 | 2110084 | 2114697 AT2TE09640 | - |
| Chr2 | 2134453 | 2137255 AT2TE09735 | + |

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| Chr2 | 2401125 | 2402966 AT2TE10985 | - |
| Chr2 | 2416281 | 2423558 AT2TE11040 | + |
| Chr2 | 2418614 | 2423173 AT2TE11050 | + |
| Chr2 | 2436994 | 2442260 AT2TE11110 | - |
| Chr2 | 2618649 | 2618894 AT2TE11755 | - |
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| Chr2 | 2638832 | 2648149 AT2TE11815 | + |
| Chr2 | 2660936 | 2664200 AT2TE11890 | + |
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| Chr2 | 2691572 | 2693140 AT2TE11955 | + |
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| Chr2 | 3876712 | 3878306 AT2TE16585 | - |
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| Chr2 | 3922475 | 3925831 AT2TE16725 | + |
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| Chr2 | 3948282 | 3949277 AT2TE16820 | + |
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| Chr2 | 4035772 | 4044425 AT2TE17110 | + |
| Chr2 | 4148680 | 4149237 AT2TE17550 | + |
| Chr2 | 4149396 | 4153427 AT2TE17565 | - |
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| Chr2 | 4162311 | 4169555 AT2TE17600 | + |
| Chr2 | 4175505 | 4183067 AT2TE17625 | + |
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| Chr2 | 4381396 | 4397150 AT2TE18410 | + |

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| Chr2 | 4407946 | 4412568 AT2TE18455 | - |
| Chr2 | 4425637 | 4428291 AT2TE18545 | + |
| Chr2 | 4452530 | 4457022 AT2TE18695 | + |
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| Chr2 | 4570281 | 4583000 AT2TE19005 | - |
| Chr2 | 4626896 | 4631843 AT2TE19200 | - |
| Chr2 | 4635952 | 4641165 AT2TE19240 | - |
| Chr2 | 4715985 | 4723844 AT2TE19590 | + |
| Chr2 | 4724593 | 4725018 AT2TE19595 | - |
| Chr2 | 4725035 | 4726100 AT2TE19600 | - |
| Chr2 | 4728862 | 4729352 AT2TE19610 | + |
| Chr2 | 4729404 | 4737545 AT2TE19615 | - |
| Chr2 | 4731189 | 4731232 AT2TE19620 | + |
| Chr2 | 4731233 | 4732460 AT2TE19625 | + |
| Chr2 | 4852584 | 4856562 AT2TE20105 | + |
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| Chr2 | 4925171 | 4933931 AT2TE20255 | - |
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| Chr2 | 4978469 | 4990075 AT2TE20435 | + |
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| Chr2 | 5105901 | 5110242 AT2TE20965 | + |
| Chr2 | 5148283 | 5153752 AT2TE21105 | + |
| Chr2 | 5149572 | 5151199 AT2TE21110 | + |
| Chr2 | 5220790 | 5227189 AT2TE21345 | - |
| Chr2 | 5338033 | 5346285 AT2TE21710 | - |
| Chr2 | 5353714 | 5362152 AT2TE21745 | - |
| Chr2 | 5365116 | 5381127 AT2TE21760 | - |
| Chr2 | 5367815 | 5377537 AT2TE21765 | - |
| Chr2 | 5440527 | 5444575 AT2TE22040 | + |
| Chr2 | 5453328 | 5456816 AT2TE22075 | - |
| Chr2 | 5517609 | 5520081 AT2TE22315 | - |
| Chr2 | 5523654 | 5527606 AT2TE22335 | - |
| Chr2 | 5729798 | 5732119 AT2TE23185 | + |
| Chr2 | 5780103 | 5786739 AT2TE23510 | - |
| Chr2 | 5808801 | 5814890 AT2TE23670 | - |
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| Chr2 | 5886322 | 5900126 AT2TE23965 | - |
| Chr2 | 5886607 | 5888004 AT2TE23970 | + |
| Chr2 | 5984986 | 5996552 AT2TE24385 | + |
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| Chr2 | 6070846 | 6082356 AT2TE24735 | + |
| Chr2 | 6263279 | 6271099 AT2TE25540 | - |
| Chr2 | 6306615 | 6307823 AT2TE25740 | + |
| Chr2 | 6351159 | 6353252 AT2TE25875 | - |
| Chr2 | 6433987 | 6439754 AT2TE26275 | + |

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| Chr2 | 6700893 | 6706745 AT2TE27390 | + |
| Chr2 | 6837289 | 6843328 AT2TE27870 | + |
| Chr2 | 6880749 | 6880917 AT2TE28015 | + |
| Chr2 | 6881261 | 6884610 AT2TE28020 | + |
| Chr2 | 6884611 | 6885154 AT2TE28025 | - |
| Chr2 | 6885155 | 6885238 AT2TE28030 | - |
| Chr2 | 6886557 | 6887874 AT2TE28035 | + |
| Chr2 | 6979262 | 6980308 AT2TE28430 | + |
| Chr2 | 7006420 | 7007823 AT2TE28555 | + |
| Chr2 | 14407884 | 14412426 AT2TE63800 | + |
| Chr3 | 8537355 | 8543559 AT3TE35825 | + |
| Chr3 | 10477962 | 10483743 AT3TE43550 | - |
| Chr3 | 10917704 | 10922777 AT3TE45385 | - |
| Chr3 | 11176821 | 11181607 AT3TE46520 | - |
| Chr3 | 11404273 | 11413061 AT3TE47555 | + |
| Chr3 | 11513764 | 11521912 AT3TE47975 | + |
| Chr3 | 11560702 | 11569513 AT3TE48120 | - |
| Chr3 | 11570287 | 11575315 AT3TE48135 | + |
| Chr3 | 11575522 | 11577530 AT3TE48150 | + |
| Chr3 | 11793559 | 11798454 AT3TE49090 | + |
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| Chr3 | 12025064 | 12040032 AT3TE50125 | - |
| Chr3 | 12105506 | 12121576 AT3TE50375 | - |
| Chr3 | 12170727 | 12174172 AT3TE50550 | - |
| Chr3 | 12175457 | 12187368 AT3TE50570 | + |
| Chr3 | 12187386 | 12191386 AT3TE50595 | - |
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| Chr3 | 12374068 | 12381768 AT3TE51250 | + |
| Chr3 | 12409273 | 12414048 AT3TE51325 | + |
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| Chr3 | 12535720 | 12539729 AT3TE51660 | + |
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| Chr3 | 12581068 | 12582803 AT3TE51810 | - |
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| Chr3 | 12607223 | 12608295 AT3TE51900 | - |
| Chr3 | 12705155 | 12708553 AT3TE52305 | - |
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| Chr3 | 12853595 | 12861862 AT3TE52805 | + |
| Chr3 | 12919569 | 12927696 AT3TE53045 | - |
| Chr3 | 13165706 | 13169990 AT3TE53850 | + |
| Chr3 | 13168135 | 13169292 AT3TE53860 | + |
| Chr3 | 13169991 | 13170667 AT3TE53865 | + |
| Chr3 | 13198082 | 13205284 AT3TE53985 | + |

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| Chr3 | 13205326 | 13209008 AT3TE53995 | + |
| Chr3 | 13209957 | 13212639 AT3TE54005 | + |
| Chr3 | 13282293 | 13287570 AT3TE54330 | - |
| Chr3 | 13333284 | 13343593 AT3TE54500 | - |
| Chr3 | 13399896 | 13403142 AT3TE54690 | - |
| Chr3 | 13405033 | 13412098 AT3TE54705 | - |
| Chr3 | 13412099 | 13421909 AT3TE54710 | - |
| Chr3 | 13510317 | 13512924 AT3TE55005 | - |
| Chr3 | 13603229 | 13609413 AT3TE55340 | + |
| Chr3 | 13619468 | 13628948 AT3TE55360 | - |
| Chr3 | 13628949 | 13632998 AT3TE55365 | - |
| Chr3 | 13643231 | 13654839 AT3TE55395 | + |
| Chr3 | 13806245 | 13809268 AT3TE56640 | + |
| Chr3 | 13816427 | 13821632 AT3TE56700 | - |
| Chr3 | 13870712 | 13877563 AT3TE57050 | + |
| Chr3 | 13884028 | 13894235 AT3TE57085 | + |
| Chr3 | 13899550 | 13900332 AT3TE57100 | + |
| Chr3 | 13902135 | 13905745 AT3TE57110 | + |
| Chr3 | 13918896 | 13919443 AT3TE57160 | + |
| Chr3 | 13919444 | 13924434 AT3TE57165 | + |
| Chr3 | 13954901 | 13959339 AT3TE57275 | - |
| Chr3 | 13960450 | 13962975 AT3TE57310 | - |
| Chr3 | 13979547 | 13988266 AT3TE57395 | - |
| Chr3 | 13993596 | 14001823 AT3TE57445 | - |
| Chr3 | 14051728 | 14060628 AT3TE57645 | - |
| Chr3 | 14097290 | 14111363 AT3TE57780 | + |
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| Chr3 | 14272908 | 14285452 AT3TE58655 | - |
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| Chr3 | 14348303 | 14350633 AT3TE58900 | + |
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| Chr3 | 14495505 | 14497162 AT3TE59450 | - |
| Chr3 | 14497163 | 14497511 AT3TE59455 | - |
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| Chr3 | 14500039 | 14501564 AT3TE59470 | + |
| Chr3 | 14503142 | 14513418 AT3TE59480 | + |
| Chr3 | 14504215 | 14509015 AT3TE59490 | - |
| Chr3 | 14549334 | 14551093 AT3TE59605 | + |
| Chr3 | 14563702 | 14574067 AT3TE59660 | + |
| Chr3 | 14656779 | 14662773 AT3TE59985 | + |
| Chr3 | 14738726 | 14741751 AT3TE60280 | - |
| Chr3 | 14749400 | 14750294 AT3TE60310 | - |
| Chr3 | 14773640 | 14783116 AT3TE60410 | - |
| Chr3 | 14788099 | 14789519 AT3TE60425 | - |
| Chr3 | 14789522 | 14789998 AT3TE60430 | - |
| Chr3 | 14795320 | 14804954 AT3TE60460 | + |
| Chr3 | 14827631 | 14830228 AT3TE60550 | - |

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| Chr3 | 14830402 | 14836116 AT3TE60560 | - |
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| Chr3 | 15104978 | 15108146 AT3TE61525 | + |
| Chr3 | 15299629 | 15307268 AT3TE62215 | - |
| Chr3 | 15422161 | 15430585 AT3TE62595 | + |
| Chr3 | 15455636 | 15468075 AT3TE62685 | - |
| Chr3 | 15493534 | 15499327 AT3TE62785 | - |
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| Chr3 | 15711476 | 15722693 AT3TE63540 | - |
| Chr3 | 15813075 | 15814056 AT3TE63935 | - |
| Chr3 | 15919028 | 15924078 AT3TE64435 | - |
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| Chr3 | 16635837 | 16647479 AT3TE67445 | + |
| Chr3 | 16957465 | 16962731 AT3TE68730 | - |
| Chr3 | 17106151 | 17115098 AT3TE69350 | + |
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| Chr4 | 1016803 | 1021368 AT4TE05190 | + |
| Chr4 | 1459720 | 1462422 AT4TE07420 | + |
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| Chr4 | 1669366 | 1680248 AT4TE08445 | - |
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| Chr4 | 1919524 | 1925047 AT4TE09315 | + |
| Chr4 | 1943751 | 1955321 AT4TE09385 | + |
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| Chr4 | 2001189 | 2010958 AT4TE09560 | + |
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| Chr4 | 2016444 | 2018942 AT4TE09580 | + |
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| Chr4 | 2076982 | 2077353 AT4TE09845 | + |
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| Chr4 | 2151851 | 2164191 AT4TE10210 | + |
| Chr4 | 2205875 | 2214904 AT4TE10345 | + |
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| Chr4 | 2245569 | 2256834 AT4TE10490 | + |
| Chr4 | 2297640 | 2300477 AT4TE10675 | + |
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| Chr4 | 2786670 | 2788434 AT4TE13035 | + |
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| Chr4 | 2886333 | 2888605 AT4TE13485 | + |
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| Chr4 | 3087019 | 3097887 AT4TE14295 | - |
| Chr4 | 3173943 | 3184236 AT4TE14540 | - |
| Chr4 | 3263245 | 3265514 AT4TE14990 | + |
| Chr4 | 3263585 | 3264171 AT4TE14995 | + |
| Chr4 | 3266373 | 3288504 AT4TE15005 | - |
| Chr4 | 3273949 | 3285542 AT4TE15025 | - |

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| Chr4 | 3364998 | 3369465 AT4TE15365 | + |
| Chr4 | 3374813 | 3376091 AT4TE15400 | + |
| Chr4 | 3376092 | 3378542 AT4TE15405 | + |
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| Chr4 | 3455687 | 3469254 AT4TE15670 | + |
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| Chr4 | 3945017 | 3950541 AT4TE17205 | - |
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| Chr4 | 4269500 | 4279994 AT4TE18315 | - |
| Chr4 | 4281762 | 4288696 AT4TE18330 | + |
| Chr4 | 4320822 | 4333493 AT4TE18435 | + |
| Chr4 | 4328378 | 4328695 AT4TE18440 | + |
| Chr4 | 4328696 | 4332395 AT4TE18445 | + |
| Chr4 | 4335932 | 4345859 AT4TE18470 | + |
| Chr4 | 4356088 | 4373281 AT4TE18500 | + |
| Chr4 | 4385361 | 4388910 AT4TE18610 | + |
| Chr4 | 4414370 | 4416095 AT4TE18705 | + |
| Chr4 | 4416096 | 4416803 AT4TE18715 | + |

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| Chr4 | 4761470 | 4768681 AT4TE19910 | + |
| Chr4 | 4768682 | 4782141 AT4TE19915 | + |
| Chr4 | 4777191 | 4778739 AT4TE19925 | + |
| Chr4 | 4830280 | 4836765 AT4TE20120 | + |
| Chr4 | 4836766 | 4838847 AT4TE20125 | + |
| Chr4 | 4891843 | 4892018 AT4TE20385 | + |
| Chr4 | 4892325 | 4903536 AT4TE20400 | - |
| Chr4 | 4980246 | 4984203 AT4TE20800 | - |
| Chr4 | 5485146 | 5494752 AT4TE22970 | - |
| Chr4 | 5952037 | 5961596 AT4TE25065 | - |
| Chr4 | 6914662 | 6919511 AT4TE29830 | - |
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| Chr5 | 9561935 | 9571088 AT5TE34730 | - |
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| Chr5 | 9949205 | 9954436 AT5TE36230 | + |
| Chr5 | 10050547 | 10056385 AT5TE36620 | + |
| Chr5 | 10139892 | 10146964 AT5TE36940 | + |
| Chr5 | 10146965 | 10148456 AT5TE36945 | + |
| Chr5 | 10398777 | 10400370 AT5TE37965 | + |
| Chr5 | 10547747 | 10553606 AT5TE38495 | - |
| Chr5 | 10582666 | 10586640 AT5TE38635 | + |
| Chr5 | 10738786 | 10740791 AT5TE39090 | - |
| Chr5 | 10755541 | 10760142 AT5TE39140 | - |
| Chr5 | 10785803 | 10790577 AT5TE39230 | - |
| Chr5 | 10816631 | 10820541 AT5TE39315 | + |
| Chr5 | 10846170 | 10853863 AT5TE39425 | + |
| Chr5 | 10869381 | 10873247 AT5TE39485 | + |
| Chr5 | 10945834 | 10954123 AT5TE39830 | - |
| Chr5 | 10958669 | 10958894 AT5TE39850 | + |
| Chr5 | 11170950 | 11175204 AT5TE40425 | - |
| Chr5 | 11192674 | 11193130 AT5TE40505 | - |
| Chr5 | 11194168 | 11194435 AT5TE40510 | - |
| Chr5 | 11195537 | 11197049 AT5TE40520 | + |
| Chr5 | 11197050 | 11198434 AT5TE40525 | + |
| Chr5 | 11198435 | 11202846 AT5TE40530 | + |
| Chr5 | 11211365 | 11213107 AT5TE40565 | + |
| Chr5 | 11213190 | 11218091 AT5TE40575 | + |
| Chr5 | 11218403 | 11222907 AT5TE40580 | + |
| Chr5 | 11320501 | 11331866 AT5TE41070 | - |
| Chr5 | 11428657 | 11437942 AT5TE41355 | + |
| Chr5 | 11441661 | 11452121 AT5TE41395 | + |
| Chr5 | 11454992 | 11460346 AT5TE41420 | + |
| Chr5 | 11555596 | 11562653 AT5TE41795 | + |
| Chr5 | 11577183 | 11587287 AT5TE41865 | + |
| Chr5 | 11587292 | 11592676 AT5TE41870 | + |

| | | | |
|------|----------|---------------------|---|
| Chr5 | 11621550 | 11635002 AT5TE41975 | - |
| Chr5 | 11623257 | 11631509 AT5TE41980 | - |
| Chr5 | 11641247 | 11643340 AT5TE42010 | - |
| Chr5 | 11643341 | 11651273 AT5TE42015 | - |
| Chr5 | 11686006 | 11697352 AT5TE42135 | - |
| Chr5 | 11711929 | 11723225 AT5TE42190 | - |
| Chr5 | 11742799 | 11753141 AT5TE42265 | - |
| Chr5 | 11777537 | 11782793 AT5TE42355 | + |
| Chr5 | 11782795 | 11785054 AT5TE42360 | - |
| Chr5 | 11782971 | 11784600 AT5TE42365 | - |
| Chr5 | 11810265 | 11821593 AT5TE42440 | - |
| Chr5 | 11830762 | 11851813 AT5TE42470 | + |
| Chr5 | 11935195 | 11945566 AT5TE42710 | + |
| Chr5 | 11980611 | 11983005 AT5TE42850 | + |
| Chr5 | 12138054 | 12150833 AT5TE43260 | - |
| Chr5 | 12151734 | 12160420 AT5TE43275 | + |
| Chr5 | 12199587 | 12207543 AT5TE43385 | + |
| Chr5 | 12225103 | 12227283 AT5TE43435 | - |
| Chr5 | 12269311 | 12272892 AT5TE43580 | + |
| Chr5 | 12289069 | 12297594 AT5TE43665 | + |
| Chr5 | 12307822 | 12315770 AT5TE43705 | - |
| Chr5 | 12335501 | 12338654 AT5TE43805 | - |
| Chr5 | 12353643 | 12361416 AT5TE43855 | - |
| Chr5 | 12371307 | 12373510 AT5TE43915 | - |
| Chr5 | 12381357 | 12389681 AT5TE43940 | + |
| Chr5 | 12396084 | 12403525 AT5TE43975 | + |
| Chr5 | 12403540 | 12415223 AT5TE43980 | + |
| Chr5 | 12517297 | 12522612 AT5TE44355 | - |
| Chr5 | 12631168 | 12636386 AT5TE44750 | - |
| Chr5 | 12639602 | 12650823 AT5TE44770 | + |
| Chr5 | 12710658 | 12720096 AT5TE45005 | + |
| Chr5 | 12744146 | 12751391 AT5TE45060 | - |
| Chr5 | 12746198 | 12747967 AT5TE45065 | + |
| Chr5 | 12754604 | 12764996 AT5TE45090 | - |
| Chr5 | 12966769 | 12968156 AT5TE46155 | - |
| Chr5 | 12968300 | 12968626 AT5TE46160 | - |
| Chr5 | 12991095 | 12996437 AT5TE46210 | + |
| Chr5 | 12996438 | 13012738 AT5TE46215 | + |
| Chr5 | 13004467 | 13009799 AT5TE46220 | + |
| Chr5 | 13021860 | 13027035 AT5TE46280 | + |
| Chr5 | 13261021 | 13272510 AT5TE47115 | - |
| Chr5 | 13317244 | 13328540 AT5TE47200 | - |
| Chr5 | 13328543 | 13331829 AT5TE47205 | - |
| Chr5 | 13564022 | 13573335 AT5TE48190 | - |
| Chr5 | 13644714 | 13651105 AT5TE48550 | - |
| Chr5 | 14379336 | 14383621 AT5TE51685 | + |
| Chr5 | 14574599 | 14580412 AT5TE52400 | + |
| Chr5 | 18193410 | 18202051 AT5TE65540 | - |

e ; FDR of 1e-2 using a Benjamini-Hochberg correction of Fisher's Exact Test)

Table S2. Genes and transposons upregulated upon irradiation (100Gy treatment) in wild type seedlings as c

| Chromosome | Start | Stop | Gene | Strand |
|------------|----------|----------|-----------|--------|
| Chr1 | 202135 | 204189 | AT1G01560 | + |
| Chr1 | 529794 | 534677 | AT1G02530 | + |
| Chr1 | 911435 | 911759 | AT1G03660 | - |
| Chr1 | 1618601 | 1623452 | AT1G05490 | - |
| Chr1 | 1701115 | 1702749 | AT1G05675 | - |
| Chr1 | 1775642 | 1778553 | AT1G05880 | + |
| Chr1 | 2304765 | 2305031 | AT1G07500 | - |
| Chr1 | 2590943 | 2606892 | AT1G08260 | + |
| Chr1 | 2606268 | 2607507 | AT1G08270 | - |
| Chr1 | 2964151 | 2964604 | AT1G09176 | + |
| Chr1 | 2965022 | 2965972 | AT1G09180 | + |
| Chr1 | 3275890 | 3278697 | AT1G10040 | - |
| Chr1 | 4257267 | 4259300 | AT1G12480 | - |
| Chr1 | 4567934 | 4570598 | AT1G13330 | + |
| Chr1 | 4622633 | 4624070 | AT1G13480 | - |
| Chr1 | 4631777 | 4633248 | AT1G13520 | - |
| Chr1 | 4974066 | 4975705 | AT1G14540 | - |
| Chr1 | 5365664 | 5366497 | AT1G15580 | - |
| Chr1 | 5872144 | 5873086 | AT1G17180 | + |
| Chr1 | 5998813 | 6002716 | AT1G17460 | + |
| Chr1 | 6180895 | 6183806 | AT1G17960 | - |
| Chr1 | 6389410 | 6391267 | AT1G18570 | + |
| Chr1 | 7043712 | 7044592 | AT1G20350 | + |
| Chr1 | 7203301 | 7208998 | AT1G20750 | - |
| Chr1 | 7395227 | 7396773 | AT1G21120 | - |
| Chr1 | 7542829 | 7543077 | AT1G21528 | - |
| Chr1 | 8350792 | 8352791 | AT1G23550 | + |
| Chr1 | 8536044 | 8537387 | AT1G24140 | - |
| Chr1 | 9078139 | 9079576 | AT1G26240 | - |
| Chr1 | 9126736 | 9128528 | AT1G26380 | - |
| Chr1 | 9138674 | 9140439 | AT1G26410 | - |
| Chr1 | 9648140 | 9649073 | AT1G27730 | - |
| Chr1 | 9714135 | 9715044 | AT1G27890 | - |
| Chr1 | 9733596 | 9738129 | AT1G27940 | - |
| Chr1 | 10606250 | 10607784 | AT1G30160 | + |
| Chr1 | 10607887 | 10609618 | AT1G30170 | - |
| Chr1 | 10719168 | 10720758 | AT1G30370 | - |
| Chr1 | 10788225 | 10789943 | AT1G30475 | - |
| Chr1 | 11181710 | 11185344 | AT1G31280 | + |
| Chr1 | 11776855 | 11777557 | AT1G32570 | + |
| Chr1 | 12393494 | 12396006 | AT1G34050 | + |
| Chr1 | 13853170 | 13853687 | AT1G36640 | - |
| Chr1 | 16933791 | 16934511 | AT1G44830 | + |
| Chr1 | 18939276 | 18941704 | AT1G51130 | - |
| Chr1 | 19481187 | 19482674 | AT1G52315 | + |
| Chr1 | 20011428 | 20011925 | AT1G53620 | - |
| Chr1 | 20014409 | 20014923 | AT1G53625 | - |

| | | | | |
|------|----------|----------|-----------|---|
| Chr1 | 20987287 | 20993072 | AT1G56120 | - |
| Chr1 | 21056231 | 21057577 | AT1G56240 | - |
| Chr1 | 21061599 | 21062995 | AT1G56250 | - |
| Chr1 | 21167588 | 21173632 | AT1G56510 | + |
| Chr1 | 21564110 | 21565171 | AT1G58225 | + |
| Chr1 | 21701184 | 21704255 | AT1G58410 | - |
| Chr1 | 21924692 | 21929424 | AT1G59660 | + |
| Chr1 | 22291581 | 22293964 | AT1G60500 | + |
| Chr1 | 24873290 | 24874758 | AT1G66700 | - |
| Chr1 | 24909212 | 24911485 | AT1G66780 | + |
| Chr1 | 24927612 | 24928803 | AT1G66810 | - |
| Chr1 | 25562117 | 25563948 | AT1G68200 | + |
| Chr1 | 25574863 | 25576129 | AT1G68240 | - |
| Chr1 | 25661500 | 25662239 | AT1G68450 | - |
| Chr1 | 26334249 | 26335558 | AT1G69920 | - |
| Chr1 | 26423873 | 26425356 | AT1G70170 | + |
| Chr1 | 26548951 | 26550520 | AT1G70440 | - |
| Chr1 | 27394746 | 27396799 | AT1G72790 | + |
| Chr1 | 27855698 | 27857534 | AT1G74080 | + |
| Chr1 | 28423895 | 28424931 | AT1G75700 | + |
| Chr1 | 28766749 | 28767517 | AT1G76650 | - |
| Chr1 | 29502581 | 29503241 | AT1G78410 | + |
| Chr1 | 29979972 | 29982773 | AT1G79680 | - |
| Chr2 | 592358 | 593602 | AT2G02240 | - |
| Chr2 | 606181 | 607839 | AT2G02300 | - |
| Chr2 | 1564165 | 1565106 | AT2G04495 | + |
| Chr2 | 6761634 | 6763500 | AT2G15490 | + |
| Chr2 | 7829034 | 7830580 | AT2G18000 | + |
| Chr2 | 7914304 | 7915872 | AT2G18190 | - |
| Chr2 | 7917504 | 7919277 | AT2G18193 | - |
| Chr2 | 8073199 | 8074982 | AT2G18600 | - |
| Chr2 | 8114919 | 8116811 | AT2G18720 | - |
| Chr2 | 9254458 | 9255625 | AT2G21640 | + |
| Chr2 | 9903214 | 9903845 | AT2G23270 | + |
| Chr2 | 10143645 | 10144511 | AT2G23830 | + |
| Chr2 | 10315514 | 10317353 | AT2G24255 | - |
| Chr2 | 11263962 | 11265684 | AT2G26480 | + |
| Chr2 | 11293768 | 11295806 | AT2G26560 | - |
| Chr2 | 11720293 | 11721081 | AT2G27389 | + |
| Chr2 | 11720483 | 11720888 | AT2G27390 | - |
| Chr2 | 12903235 | 12905198 | AT2G30250 | - |
| Chr2 | 12936978 | 12938834 | AT2G30360 | - |
| Chr2 | 13353820 | 13359728 | AT2G31320 | - |
| Chr2 | 13549998 | 13553843 | AT2G31870 | - |
| Chr2 | 13631061 | 13631768 | AT2G32020 | - |
| Chr2 | 13655626 | 13657175 | AT2G32140 | - |
| Chr2 | 15417489 | 15419154 | AT2G36780 | - |
| Chr2 | 15706356 | 15707224 | AT2G37430 | + |
| Chr2 | 16018356 | 16019500 | AT2G38250 | + |

| | | | | |
|------|----------|----------|-----------|---|
| Chr2 | 16067395 | 16068291 | AT2G38340 | - |
| Chr2 | 16108360 | 16110766 | AT2G38470 | + |
| Chr2 | 16527791 | 16529407 | AT2G39650 | - |
| Chr2 | 16848437 | 16850487 | AT2G40340 | - |
| Chr2 | 17685804 | 17689928 | AT2G42480 | - |
| Chr2 | 17880614 | 17882636 | AT2G43000 | - |
| Chr2 | 18400645 | 18401326 | AT2G44578 | - |
| Chr2 | 18736838 | 18741841 | AT2G45460 | - |
| Chr2 | 19084133 | 19085704 | AT2G46495 | - |
| Chr2 | 19136565 | 19138762 | AT2G46610 | - |
| Chr2 | 19543990 | 19544806 | AT2G47670 | - |
| Chr2 | 19545827 | 19550905 | AT2G47680 | - |
| Chr2 | 19568463 | 19569507 | AT2G47770 | + |
| Chr3 | 229170 | 231105 | AT3G01600 | + |
| Chr3 | 489829 | 491587 | AT3G02400 | + |
| Chr3 | 573779 | 574626 | AT3G02670 | - |
| Chr3 | 1172745 | 1174467 | AT3G04420 | + |
| Chr3 | 2489386 | 2491087 | AT3G07800 | - |
| Chr3 | 2753306 | 2754621 | AT3G09020 | + |
| Chr3 | 2894811 | 2897674 | AT3G09405 | - |
| Chr3 | 3420129 | 3420832 | AT3G10930 | - |
| Chr3 | 3896530 | 3899019 | AT3G12220 | - |
| Chr3 | 3946035 | 3946960 | AT3G12410 | - |
| Chr3 | 3967094 | 3967822 | AT3G12510 | + |
| Chr3 | 5133605 | 5135902 | AT3G15240 | + |
| Chr3 | 5692737 | 5694127 | AT3G16720 | + |
| Chr3 | 6045001 | 6048488 | AT3G17690 | + |
| Chr3 | 6258066 | 6258417 | AT3G18250 | - |
| Chr3 | 6616351 | 6617696 | AT3G19150 | - |
| Chr3 | 6652744 | 6658938 | AT3G19210 | - |
| Chr3 | 6814965 | 6815403 | AT3G19615 | - |
| Chr3 | 7153538 | 7156536 | AT3G20490 | - |
| Chr3 | 7581958 | 7582793 | AT3G21520 | + |
| Chr3 | 8116334 | 8119388 | AT3G22910 | - |
| Chr3 | 8289646 | 8290066 | AT3G23230 | - |
| Chr3 | 9195502 | 9197124 | AT3G25250 | + |
| Chr3 | 10231115 | 10231418 | AT3G27630 | - |
| Chr3 | 10520508 | 10521532 | AT3G28210 | + |
| Chr3 | 10685523 | 10687364 | AT3G28510 | + |
| Chr3 | 10715622 | 10717329 | AT3G28580 | + |
| Chr3 | 11005778 | 11006414 | AT3G29000 | + |
| Chr3 | 11259586 | 11262440 | AT3G29340 | - |
| Chr3 | 14940113 | 14945291 | AT3G42850 | - |
| Chr3 | 14946187 | 14948167 | AT3G42860 | - |
| Chr3 | 16789979 | 16790582 | AT3G45730 | + |
| Chr3 | 16922752 | 16923247 | AT3G46080 | - |
| Chr3 | 18078473 | 18086817 | AT3G48770 | - |
| Chr3 | 18929525 | 18931839 | AT3G50930 | + |
| Chr3 | 19326332 | 19328323 | AT3G52115 | + |

| | | | | |
|------|----------|----------|-----------|---|
| Chr3 | 20050643 | 20052815 | AT3G54150 | - |
| Chr3 | 21070647 | 21072702 | AT3G56920 | + |
| Chr3 | 21575886 | 21577845 | AT3G58270 | - |
| Chr4 | 935085 | 940191 | AT4G02110 | + |
| Chr4 | 1049956 | 1054065 | AT4G02390 | + |
| Chr4 | 2555089 | 2557046 | AT4G04990 | + |
| Chr4 | 2736134 | 2736584 | AT4G05370 | + |
| Chr4 | 2737145 | 2737983 | AT4G05380 | + |
| Chr4 | 7777792 | 7780366 | AT4G13370 | - |
| Chr4 | 8392840 | 8393813 | AT4G14630 | + |
| Chr4 | 9752823 | 9753867 | AT4G17490 | - |
| Chr4 | 10069693 | 10071115 | AT4G18195 | + |
| Chr4 | 10466476 | 10469092 | AT4G19130 | - |
| Chr4 | 11248077 | 11252724 | AT4G21070 | + |
| Chr4 | 12030019 | 12033137 | AT4G22960 | + |
| Chr4 | 12141031 | 12143833 | AT4G23190 | - |
| Chr4 | 12957833 | 12958714 | AT4G25330 | + |
| Chr4 | 13056183 | 13058802 | AT4G25580 | + |
| Chr4 | 13369532 | 13370011 | AT4G26460 | + |
| Chr4 | 13921676 | 13923570 | AT4G27980 | + |
| Chr4 | 14026576 | 14028622 | AT4G28350 | + |
| Chr4 | 14277993 | 14279984 | AT4G28950 | + |
| Chr4 | 14382838 | 14385375 | AT4G29170 | + |
| Chr4 | 16422165 | 16423948 | AT4G34320 | + |
| Chr4 | 16491795 | 16493418 | AT4G34510 | + |
| Chr4 | 16936119 | 16940332 | AT4G35740 | + |
| Chr4 | 17451927 | 17454760 | AT4G37030 | + |
| Chr4 | 17549683 | 17550257 | AT4G37290 | - |
| Chr4 | 17569827 | 17571704 | AT4G37370 | - |
| Chr4 | 17593122 | 17594889 | AT4G37420 | + |
| Chr4 | 17621885 | 17624285 | AT4G37490 | - |
| Chr4 | 18029197 | 18031333 | AT4G38560 | + |
| Chr4 | 18366949 | 18368359 | AT4G39500 | - |
| Chr4 | 18410171 | 18411000 | AT4G39670 | + |
| Chr5 | 91919 | 92324 | AT5G01225 | + |
| Chr5 | 441706 | 442146 | AT5G02220 | - |
| Chr5 | 999101 | 1001029 | AT5G03780 | - |
| Chr5 | 2406067 | 2407330 | AT5G07610 | + |
| Chr5 | 2407400 | 2409066 | AT5G07620 | - |
| Chr5 | 3636613 | 3638059 | AT5G11400 | - |
| Chr5 | 3656810 | 3658931 | AT5G11460 | - |
| Chr5 | 4670778 | 4672072 | AT5G14490 | - |
| Chr5 | 4828640 | 4830955 | AT5G14930 | + |
| Chr5 | 4991346 | 4994826 | AT5G15380 | + |
| Chr5 | 6040918 | 6042938 | AT5G18270 | - |
| Chr5 | 7070585 | 7072951 | AT5G20850 | - |
| Chr5 | 7478929 | 7479527 | AT5G22520 | + |
| Chr5 | 7480526 | 7481194 | AT5G22530 | + |
| Chr5 | 7489421 | 7490503 | AT5G22555 | + |

| | | | | |
|------|----------|----------|-----------|---|
| Chr5 | 7536289 | 7537990 | AT5G22660 | - |
| Chr5 | 8068451 | 8072991 | AT5G23910 | + |
| Chr5 | 8153114 | 8154709 | AT5G24110 | - |
| Chr5 | 8251377 | 8262154 | AT5G24280 | - |
| Chr5 | 9147175 | 9148128 | AT5G26170 | - |
| Chr5 | 9508763 | 9515407 | AT5G27030 | - |
| Chr5 | 9684071 | 9685561 | AT5G27420 | + |
| Chr5 | 14604366 | 14605194 | AT5G36970 | - |
| Chr5 | 15883178 | 15884067 | AT5G39670 | + |
| Chr5 | 16020217 | 16021762 | AT5G40010 | - |
| Chr5 | 16041918 | 16043494 | AT5G40090 | - |
| Chr5 | 16359429 | 16363792 | AT5G40840 | - |
| Chr5 | 16693908 | 16698943 | AT5G41750 | + |
| Chr5 | 16866039 | 16870887 | AT5G42210 | + |
| Chr5 | 18207362 | 18209045 | AT5G45095 | + |
| Chr5 | 18398989 | 18401644 | AT5G45400 | + |
| Chr5 | 19462657 | 19464957 | AT5G48020 | - |
| Chr5 | 19758880 | 19761721 | AT5G48720 | + |
| Chr5 | 19900202 | 19905925 | AT5G49110 | + |
| Chr5 | 20189654 | 20191390 | AT5G49690 | - |
| Chr5 | 20800583 | 20801416 | AT5G51190 | - |
| Chr5 | 20952441 | 20953393 | AT5G51580 | - |
| Chr5 | 21384042 | 21384924 | AT5G52750 | + |
| Chr5 | 22419156 | 22420410 | AT5G55270 | + |
| Chr5 | 22478711 | 22481148 | AT5G55490 | - |
| Chr5 | 23187839 | 23189857 | AT5G57220 | + |
| Chr5 | 23289163 | 23289556 | AT5G57510 | - |
| Chr5 | 23686770 | 23691053 | AT5G58610 | - |
| Chr5 | 24252157 | 24254849 | AT5G60250 | + |
| Chr5 | 25633535 | 25635781 | AT5G64060 | - |
| Chr5 | 25908412 | 25909803 | AT5G64810 | + |
| Chr5 | 26095146 | 26095771 | AT5G65300 | - |
| Chr5 | 26216125 | 26218153 | AT5G65600 | - |
| Chr5 | 26434063 | 26437222 | AT5G66130 | + |
| Chr5 | 26599383 | 26601867 | AT5G66640 | + |
| Chr5 | 26921583 | 26923274 | AT5G67460 | - |

mpared to control seedlings. (> 4-fold increase ; FDR of 1e-2 using a Benjamini-Hochberg correction of F

isher's Exact Test)

Table S2. Genes and transposons upregulated upon irradiation (100Gy treatment) in wild type seedlings as c

| Chromosome | Start | Stop | Gene | Strand |
|------------|----------|----------|------------|--------|
| Chr1 | 9125777 | 9126902 | AT1TE29390 | - |
| Chr1 | 21833196 | 21838009 | AT1TE72060 | - |
| Chr3 | 490910 | 491312 | AT3TE02100 | - |
| Chr3 | 10687034 | 10687244 | AT3TE44395 | - |
| Chr3 | 10716963 | 10717265 | AT3TE44530 | - |
| Chr4 | 8393675 | 8394263 | AT4TE37230 | + |
| Chr5 | 2222046 | 2222111 | AT5TE08070 | + |
| Chr5 | 2222112 | 2222331 | AT5TE08075 | + |
| Chr5 | 7069517 | 7070690 | AT5TE25580 | - |
| Chr5 | 16356372 | 16359539 | AT5TE59075 | + |
| Chr5 | 16359540 | 16359601 | AT5TE59080 | - |
| Chr5 | 16698234 | 16698950 | AT5TE60280 | + |

mpared to control seedlings. (> 4-fold increase ; FDR of 1e-2 using a Benjamini-Hochberg correction of F

Table S3. DAVID (<http://david.abcc.ncifcrf.gov/home.jsp>) Gene Ontology Analysis of Top 200 Genes Co-express

| GO Term | Term | Count | % | PValue | Genes |
|------------|---|-------|------|-----------|-----------|
| GO:0006259 | DNA metabolic process | 40 | 20 | 1.08E-34 | AT5G2085C |
| GO:0007049 | cell cycle | 35 | 17.5 | 4.37E-34 | AT5G6241C |
| GO:0051301 | cell division | 27 | 13.5 | 1.37E-26 | AT5G6241C |
| GO:0022402 | cell cycle process | 23 | 11.5 | 2.45E-23 | AT3G5706C |
| GO:0007017 | microtubule-based process | 22 | 11 | 9.16E-23 | AT5G2755C |
| GO:0007018 | microtubule-based movement | 19 | 9.5 | 3.08E-22 | AT5G2755C |
| GO:0051726 | regulation of cell cycle | 21 | 10.5 | 6.83E-22 | AT1G0727C |
| GO:0000279 | M phase | 16 | 8 | 4.00E-17 | AT3G5706C |
| GO:0006260 | DNA replication | 18 | 9 | 7.82E-17 | AT1G0727C |
| GO:0022403 | cell cycle phase | 16 | 8 | 3.74E-16 | AT3G5706C |
| GO:0051276 | chromosome organization | 21 | 10.5 | 1.18E-14 | AT4G1847C |
| GO:0006310 | DNA recombination | 12 | 6 | 1.41E-12 | AT5G2085C |
| GO:0006974 | response to DNA damage stimulus | 17 | 8.5 | 1.71E-12 | AT5G2085C |
| GO:0007067 | mitosis | 10 | 5 | 9.22E-12 | AT3G5706C |
| GO:0000087 | M phase of mitotic cell cycle | 10 | 5 | 9.22E-12 | AT3G5706C |
| GO:0006281 | DNA repair | 16 | 8 | 1.22E-11 | AT5G2085C |
| GO:0000280 | nuclear division | 10 | 5 | 2.53E-11 | AT3G5706C |
| GO:0000278 | mitotic cell cycle | 10 | 5 | 2.06E-10 | AT3G5706C |
| GO:0051327 | M phase of meiotic cell cycle | 9 | 4.5 | 1.69E-09 | AT5G6241C |
| GO:0007126 | meiosis | 9 | 4.5 | 1.69E-09 | AT5G6241C |
| GO:0048285 | organelle fission | 10 | 5 | 2.60E-09 | AT3G5706C |
| GO:0006323 | DNA packaging | 10 | 5 | 9.19E-09 | AT3G5706C |
| GO:0006325 | chromatin organization | 14 | 7 | 1.83E-08 | AT4G1847C |
| GO:0051321 | meiotic cell cycle | 9 | 4.5 | 2.87E-08 | AT5G6241C |
| GO:0000910 | cytokinesis | 8 | 4 | 2.93E-08 | AT1G5314C |
| GO:0007059 | chromosome segregation | 7 | 3.5 | 4.39E-08 | AT3G2389C |
| GO:0030261 | chromosome condensation | 5 | 2.5 | 5.55E-08 | AT3G5706C |
| GO:0006261 | DNA-dependent DNA replication | 8 | 4 | 9.17E-08 | AT3G2510C |
| GO:0016568 | chromatin modification | 11 | 5.5 | 1.29E-07 | AT4G1847C |
| GO:0033554 | cellular response to stress | 17 | 8.5 | 2.36E-07 | AT5G2085C |
| GO:0006302 | double-strand break repair | 6 | 3 | 1.08E-06 | AT5G2085C |
| GO:0010564 | regulation of cell cycle process | 6 | 3 | 1.65E-06 | AT2G3356C |
| GO:0010212 | response to ionizing radiation | 5 | 2.5 | 6.33E-06 | AT5G2085C |
| GO:0033205 | cytokinesis during cell cycle | 5 | 2.5 | 2.02E-05 | AT4G1415C |
| GO:0006333 | chromatin assembly or disassembly | 7 | 3.5 | 9.45E-05 | AT1G5782C |
| GO:0000725 | recombinational repair | 4 | 2 | 1.01E-04 | AT4G0002C |
| GO:0000724 | double-strand break repair via homologo | 4 | 2 | 1.01E-04 | AT4G0002C |
| GO:0006270 | DNA replication initiation | 4 | 2 | 1.01E-04 | AT3G2510C |
| GO:0048229 | gametophyte development | 9 | 4.5 | 1.24E-04 | AT4G0002C |
| GO:0007010 | cytoskeleton organization | 7 | 3.5 | 2.27E-04 | AT4G2127C |
| GO:0070828 | heterochromatin organization | 3 | 1.5 | 3.70E-04 | AT1G5782C |
| GO:0031507 | heterochromatin formation | 3 | 1.5 | 3.70E-04 | AT1G5782C |
| GO:0016572 | histone phosphorylation | 3 | 1.5 | 3.70E-04 | AT2G4549C |
| GO:0051052 | regulation of DNA metabolic process | 4 | 2 | 7.66E-04 | AT3G18524 |
| GO:0032776 | DNA methylation on cytosine | 3 | 1.5 | 9.16E-04 | AT1G5782C |
| GO:0016570 | histone modification | 5 | 2.5 | 0.0010015 | AT4G1847C |
| GO:0016569 | covalent chromatin modification | 5 | 2.5 | 0.0012186 | AT4G1847C |

| | | | | | |
|------------|---|---|-----|-----------|-----------|
| GO:0051053 | negative regulation of DNA metabolic prc | 3 | 1.5 | 0.0021633 | AT3G18524 |
| GO:0031497 | chromatin assembly | 5 | 2.5 | 0.0024192 | AT1G5782C |
| GO:0065004 | protein-DNA complex assembly | 5 | 2.5 | 0.0025461 | AT1G5782C |
| GO:0010332 | response to gamma radiation | 3 | 1.5 | 0.0026902 | AT5G2085C |
| GO:0000226 | microtubule cytoskeleton organization | 4 | 2 | 0.0033454 | AT4G2127C |
| GO:0009555 | pollen development | 6 | 3 | 0.0036173 | AT4G1415C |
| GO:0006275 | regulation of DNA replication | 3 | 1.5 | 0.0053287 | AT1G0297C |
| GO:0006338 | chromatin remodeling | 3 | 1.5 | 0.0069546 | AT1G5782C |
| GO:0007346 | regulation of mitotic cell cycle | 3 | 1.5 | 0.008776 | AT2G3356C |
| GO:0000911 | cytokinesis by cell plate formation | 3 | 1.5 | 0.008776 | AT4G1415C |
| GO:0010070 | zygote asymmetric cell division | 2 | 1 | 0.0157971 | AT5G4916C |
| GO:0010069 | zygote asymmetric cytokinesis in the emk | 2 | 1 | 0.0157971 | AT5G4916C |
| GO:0045934 | negative regulation of nucleobase, nucleo | 4 | 2 | 0.0161002 | AT3G18524 |
| GO:0051172 | negative regulation of nitrogen compoun | 4 | 2 | 0.0161002 | AT3G18524 |
| GO:0006334 | nucleosome assembly | 4 | 2 | 0.0174102 | AT1G6547C |
| GO:0034728 | nucleosome organization | 4 | 2 | 0.0174102 | AT1G6547C |
| GO:0009553 | embryo sac development | 4 | 2 | 0.0224524 | AT4G0002C |
| GO:0051304 | chromosome separation | 2 | 1 | 0.0236026 | AT5G6392C |
| GO:0051307 | meiotic chromosome separation | 2 | 1 | 0.0236026 | AT5G6392C |
| GO:0033261 | regulation of S phase | 2 | 1 | 0.0236026 | AT4G0002C |
| GO:0051225 | spindle assembly | 2 | 1 | 0.0236026 | AT4G2127C |
| GO:0007090 | regulation of S phase of mitotic cell cycle | 2 | 1 | 0.0236026 | AT4G0002C |
| GO:0034622 | cellular macromolecular complex assemb | 6 | 3 | 0.0249275 | AT1G5782C |
| GO:0006306 | DNA methylation | 3 | 1.5 | 0.0249497 | AT1G5782C |
| GO:0006305 | DNA alkylation | 3 | 1.5 | 0.0249497 | AT1G5782C |
| GO:0006304 | DNA modification | 3 | 1.5 | 0.0280418 | AT1G5782C |
| GO:0007051 | spindle organization | 2 | 1 | 0.0313468 | AT4G2127C |
| GO:0034621 | cellular macromolecular complex subunit | 6 | 3 | 0.0339384 | AT1G5782C |
| GO:0045787 | positive regulation of cell cycle | 2 | 1 | 0.0390302 | AT1G0826C |
| GO:0007349 | cellularization | 2 | 1 | 0.0390302 | AT2G4419C |
| GO:0009561 | megagametogenesis | 3 | 1.5 | 0.0436784 | AT4G0002C |
| GO:0008156 | negative regulation of DNA replication | 2 | 1 | 0.0466531 | AT1G0297C |
| GO:0031032 | actomyosin structure organization | 2 | 1 | 0.0466531 | AT4G1415C |
| GO:0000912 | formation of actomyosin apparatus invol | 2 | 1 | 0.0466531 | AT4G1415C |
| GO:0000914 | phragmoplast formation | 2 | 1 | 0.0466531 | AT4G1415C |
| GO:0008356 | asymmetric cell division | 2 | 1 | 0.0466531 | AT5G4916C |
| GO:0000075 | cell cycle checkpoint | 2 | 1 | 0.0542161 | AT2G3356C |
| GO:0048366 | leaf development | 5 | 2.5 | 0.0586443 | AT4G3774C |
| GO:0065003 | macromolecular complex assembly | 6 | 3 | 0.0636477 | AT1G5782C |
| GO:0045132 | meiotic chromosome segregation | 2 | 1 | 0.0691642 | AT5G6392C |
| GO:0010948 | negative regulation of cell cycle process | 2 | 1 | 0.0691642 | AT2G3356C |
| GO:0048509 | regulation of meristem development | 3 | 1.5 | 0.0705404 | AT1G6547C |
| GO:0048827 | phyllome development | 5 | 2.5 | 0.0790675 | AT4G3774C |
| GO:0043933 | macromolecular complex subunit organiz | 6 | 3 | 0.0799126 | AT1G5782C |
| GO:0006268 | DNA unwinding during replication | 2 | 1 | 0.0911484 | AT5G6392C |
| GO:0009960 | endosperm development | 2 | 1 | 0.0983615 | AT4G2297C |

| Enriched GO terms associated with At-STUbL2 (GOTERM_BP_FAT category) | | | | | | | |
|--|-------|----------|-----------|-------------|------------|-----------|-----|
| List | Total | Pop Hits | Pop Total | Fold Enrich | Bonferroni | Benjamini | FDR |
| 112 | 350 | 13998 | 14.283673 | 3.35E-32 | 3.35E-32 | 1.45E-31 | |
| 112 | 234 | 13998 | 18.69391 | 1.35E-31 | 6.77E-32 | 5.86E-31 | |
| 112 | 170 | 13998 | 19.850105 | 4.24E-24 | 1.41E-24 | 1.84E-23 | |
| 112 | 133 | 13998 | 21.613453 | 7.58E-21 | 1.90E-21 | 3.28E-20 | |
| 112 | 121 | 13998 | 22.724026 | 2.84E-20 | 5.68E-21 | 1.23E-19 | |
| 112 | 76 | 13998 | 31.245536 | 9.54E-20 | 1.59E-20 | 4.13E-19 | |
| 112 | 113 | 13998 | 23.22677 | 2.12E-19 | 3.02E-20 | 9.17E-19 | |
| 112 | 79 | 13998 | 25.312839 | 1.24E-14 | 1.55E-15 | 5.37E-14 | |
| 112 | 123 | 13998 | 18.29007 | 3.44E-14 | 3.77E-15 | 1.44E-13 | |
| 112 | 91 | 13998 | 21.974882 | 1.03E-13 | 1.03E-14 | 4.44E-13 | |
| 112 | 258 | 13998 | 10.172965 | 3.65E-12 | 3.32E-13 | 1.58E-11 | |
| 112 | 61 | 13998 | 24.586651 | 4.38E-10 | 3.65E-11 | 1.90E-09 | |
| 112 | 189 | 13998 | 11.24178 | 5.32E-10 | 4.09E-11 | 2.30E-09 | |
| 112 | 37 | 13998 | 33.778958 | 2.86E-09 | 2.04E-10 | 1.24E-08 | |
| 112 | 37 | 13998 | 33.778958 | 2.86E-09 | 2.04E-10 | 1.24E-08 | |
| 112 | 181 | 13998 | 11.048145 | 3.77E-09 | 2.51E-10 | 1.63E-08 | |
| 112 | 41 | 13998 | 30.483449 | 7.84E-09 | 4.90E-10 | 3.40E-08 | |
| 112 | 51 | 13998 | 24.506303 | 6.37E-08 | 3.75E-09 | 2.76E-07 | |
| 112 | 44 | 13998 | 25.564529 | 5.25E-07 | 2.92E-08 | 2.27E-06 | |
| 112 | 44 | 13998 | 25.564529 | 5.25E-07 | 2.92E-08 | 2.27E-06 | |
| 112 | 67 | 13998 | 18.654051 | 8.06E-07 | 4.24E-08 | 3.49E-06 | |
| 112 | 77 | 13998 | 16.231447 | 2.85E-06 | 1.42E-07 | 1.23E-05 | |
| 112 | 219 | 13998 | 7.989726 | 5.68E-06 | 2.71E-07 | 2.46E-05 | |
| 112 | 62 | 13998 | 18.142569 | 8.90E-06 | 4.04E-07 | 3.86E-05 | |
| 112 | 41 | 13998 | 24.38676 | 9.09E-06 | 3.95E-07 | 3.94E-05 | |
| 112 | 26 | 13998 | 33.649038 | 1.36E-05 | 5.67E-07 | 5.90E-05 | |
| 112 | 6 | 13998 | 104.15179 | 1.72E-05 | 6.88E-07 | 7.45E-05 | |
| 112 | 48 | 13998 | 20.830357 | 2.84E-05 | 1.09E-06 | 1.23E-04 | |
| 112 | 137 | 13998 | 10.035063 | 4.00E-05 | 1.48E-06 | 1.73E-04 | |
| 112 | 426 | 13998 | 4.9875503 | 7.31E-05 | 2.61E-06 | 3.17E-04 | |
| 112 | 24 | 13998 | 31.245536 | 3.35E-04 | 1.15E-05 | 0.0014495 | |
| 112 | 26 | 13998 | 28.842033 | 5.11E-04 | 1.70E-05 | 0.0022152 | |
| 112 | 16 | 13998 | 39.05692 | 0.0019613 | 6.33E-05 | 0.0085049 | |
| 112 | 21 | 13998 | 29.757653 | 0.0062421 | 1.96E-04 | 0.0271232 | |
| 112 | 93 | 13998 | 9.4072581 | 0.0288709 | 8.87E-04 | 0.126835 | |
| 112 | 12 | 13998 | 41.660714 | 0.0309301 | 9.24E-04 | 0.1360188 | |
| 112 | 12 | 13998 | 41.660714 | 0.0309301 | 9.24E-04 | 0.1360188 | |
| 112 | 12 | 13998 | 41.660714 | 0.0309301 | 9.24E-04 | 0.1360188 | |
| 112 | 188 | 13998 | 5.9831877 | 0.0376662 | 0.0010964 | 0.1661919 | |
| 112 | 109 | 13998 | 8.0263761 | 0.0678442 | 0.0019496 | 0.3038974 | |
| 112 | 4 | 13998 | 93.736607 | 0.1083957 | 0.0030961 | 0.4958127 | |
| 112 | 4 | 13998 | 93.736607 | 0.1083957 | 0.0030961 | 0.4958127 | |
| 112 | 4 | 13998 | 93.736607 | 0.1083957 | 0.0030961 | 0.4958127 | |
| 112 | 23 | 13998 | 21.736025 | 0.211344 | 0.0062285 | 1.0233012 | |
| 112 | 6 | 13998 | 62.491071 | 0.2471908 | 0.0072542 | 1.2225652 | |
| 112 | 56 | 13998 | 11.15912 | 0.2670105 | 0.0077355 | 1.3366712 | |
| 112 | 59 | 13998 | 10.591707 | 0.3147737 | 0.0091773 | 1.6242626 | |

| | | | | | | | |
|-----|-----|-------|-----------|-----------|-----------|-----------|-----------|
| 112 | 9 | 13998 | 41.660714 | 0.4889847 | 0.0158576 | 2.8665594 | |
| 112 | 71 | 13998 | 8.8015594 | 0.5280416 | 0.0173104 | 3.2005575 | |
| 112 | 72 | 13998 | 8.6793155 | 0.5462862 | 0.0178008 | 3.3657439 | |
| 112 | 10 | 13998 | 37.494643 | 0.5661586 | 0.0183861 | 3.5530608 | |
| 112 | 38 | 13998 | 13.156015 | 0.6461272 | 0.0223299 | 4.4006031 | |
| 112 | 129 | 13998 | 5.8131229 | 0.6748258 | 0.0236186 | 4.7502404 | |
| 112 | 14 | 13998 | 26.781888 | 0.8091562 | 0.0339177 | 6.924038 | |
| 112 | 16 | 13998 | 23.434152 | 0.8850718 | 0.0431915 | 8.9466794 | |
| 112 | 18 | 13998 | 20.830357 | 0.9349488 | 0.0531851 | 11.164239 | |
| 112 | 18 | 13998 | 20.830357 | 0.9349488 | 0.0531851 | 11.164239 | |
| 112 | 2 | 13998 | 124.98214 | 0.9928181 | 0.0922516 | 19.252701 | |
| 112 | 2 | 13998 | 124.98214 | 0.9928181 | 0.0922516 | 19.252701 | |
| 112 | 67 | 13998 | 7.4616205 | 0.9934722 | 0.092229 | 19.586053 | |
| 112 | 67 | 13998 | 7.4616205 | 0.9934722 | 0.092229 | 19.586053 | |
| 112 | 69 | 13998 | 7.2453416 | 0.9956809 | 0.0976298 | 21.012124 | |
| 112 | 69 | 13998 | 7.2453416 | 0.9956809 | 0.0976298 | 21.012124 | |
| 112 | 76 | 13998 | 6.5780075 | 0.9991235 | 0.1222225 | 26.285282 | |
| 112 | 3 | 13998 | 83.321429 | 0.9993915 | 0.1259592 | 27.441715 | |
| 112 | 3 | 13998 | 83.321429 | 0.9993915 | 0.1259592 | 27.441715 | |
| 112 | 3 | 13998 | 83.321429 | 0.9993915 | 0.1259592 | 27.441715 | |
| 112 | 3 | 13998 | 83.321429 | 0.9993915 | 0.1259592 | 27.441715 | |
| 112 | 3 | 13998 | 83.321429 | 0.9993915 | 0.1259592 | 27.441715 | |
| 112 | 208 | 13998 | 3.6052541 | 0.9996006 | 0.1304162 | 28.752828 | |
| 112 | 31 | 13998 | 12.095046 | 0.9996034 | 0.1283895 | 28.774593 | |
| 112 | 31 | 13998 | 12.095046 | 0.9996034 | 0.1283895 | 28.774593 | |
| 112 | 33 | 13998 | 11.362013 | 0.9998518 | 0.1410291 | 31.748976 | |
| 112 | 4 | 13998 | 62.491071 | 0.9999485 | 0.1540885 | 34.800737 | |
| 112 | 226 | 13998 | 3.31811 | 0.9999775 | 0.1633863 | 37.104792 | |
| 112 | 5 | 13998 | 49.992857 | 0.9999956 | 0.1831703 | 41.413841 | |
| 112 | 5 | 13998 | 49.992857 | 0.9999956 | 0.1831703 | 41.413841 | |
| 112 | 42 | 13998 | 8.9272959 | 0.999999 | 0.2001292 | 45.107286 | |
| 112 | 6 | 13998 | 41.660714 | 0.9999996 | 0.2095006 | 47.356587 | |
| 112 | 6 | 13998 | 41.660714 | 0.9999996 | 0.2095006 | 47.356587 | |
| 112 | 6 | 13998 | 41.660714 | 0.9999996 | 0.2095006 | 47.356587 | |
| 112 | 6 | 13998 | 41.660714 | 0.9999996 | 0.2095006 | 47.356587 | |
| 112 | 7 | 13998 | 35.709184 | | 1 | 0.2366177 | 52.696888 |
| 112 | 184 | 13998 | 3.3962539 | | 1 | 0.2504068 | 55.586233 |
| 112 | 270 | 13998 | 2.777381 | | 1 | 0.2657377 | 58.653879 |
| 112 | 9 | 13998 | 27.77381 | | 1 | 0.2822388 | 61.808118 |
| 112 | 9 | 13998 | 27.77381 | | 1 | 0.2822388 | 61.808118 |
| 112 | 55 | 13998 | 6.8172078 | | 1 | 0.2835785 | 62.559492 |
| 112 | 204 | 13998 | 3.0632878 | | 1 | 0.3093081 | 66.918458 |
| 112 | 289 | 13998 | 2.594785 | | 1 | 0.3084646 | 67.323859 |
| 112 | 12 | 13998 | 20.830357 | | 1 | 0.3411718 | 72.294367 |
| 112 | 13 | 13998 | 19.228022 | | 1 | 0.3596909 | 75.106054 |

Table S4. Sample manifest detailing the genotype, replicate number and name as presented in the figures.

Tissue Specificity Experiment (Figure 1)

Irradiation Response - 90 min post-exposure (Figure 1)

Irradiation Response - 24 hour post-exposure (Figure 1)

atbrca1 enhancement of atxr56 replication defect (Figure 2)

atbrca1 enhancement of atxr56 aberrant transcription (Figure 2)

Mapping of AtSAC3B EMS alleles (Figure 3)

Mapping of AtTHP1 EMS allele (Figure 3)

Validation of AtSAC3b identification (Figure S3)

Validation of AtTHP1 identification (Figure S3)

Mapping of MBD9 EMS allele (Figure 4)

Validation of MBD9 identification (Figure 4)

Mapping of atsubtl2 mutation (Figure 5)

atsubtl2 non-complementation (Figure S4)

Methylation profiling (Figure 6)

| Content in GEO database submission for high-throughput sequencing experiments detailed in the paper. Note that a | | |
|--|---------------------------|---|
| Experiment | Sample Name in Study Text | Genotype |
| DNA resequencing | atxr5/6 | atxr5 ; atxr6 |
| DNA resequencing | Col | wildtype |
| DNA resequencing | atxr5/6 | atxr5 ; atxr6 |
| DNA resequencing | Col | wildtype |
| RNA-seq | atxr5/6 | atxr5 ; atxr6 |
| RNA-seq | atxr5/6 | atxr5 ; atxr6 |
| RNA-seq | Col | wildtype |
| RNA-seq | Col | wildtype |
| RNA-seq | atxr5/6 | atxr5 ; atxr6 |
| RNA-seq | atxr5/6 | atxr5 ; atxr6 |
| RNA-seq | Col | wildtype |
| RNA-seq | Col | wildtype |
| RNA-seq | atxr5/6 | atxr5 ; atxr6 |
| RNA-seq | atxr5/6 | atxr5 ; atxr6 |
| RNA-seq | Col | wildtype |
| RNA-seq | Col | wildtype |
| RNA-seq | atxr5/6 | atxr5 ; atxr6 |
| RNA-seq | atxr5/6 | atxr5 ; atxr6 |
| RNA-seq | atxr5/6 | atxr5 ; atxr6 |
| RNA-seq | atxr5/6 | atxr5 ; atxr6 |
| RNA-seq | Col | wildtype |
| RNA-seq | atxr5/6 | atxr5 ; atxr6 |
| RNA-seq | atxr5/6 | atxr5 ; atxr6 |
| RNA-seq | Col | wildtype |
| RNA-seq | Col | wildtype |
| DNA resequencing | atbrca1 ; atxr56 | atbrca1-1 ; atxr56 |
| DNA resequencing | atbrca1 ; atxr56 | atbrca1-1 ; atxr56 |
| DNA resequencing | atxr5/6 | atxr5 ; atxr6 |
| DNA resequencing | Col | wildtype |
| RNA-seq | atbrca1 | atbrca1-1 |
| RNA-seq | atbrca1 | atbrca1-1 |
| RNA-seq | atbrca1 ; atxr56 | atbrca1-1 ; atxr56 |
| RNA-seq | atbrca1 ; atxr56 | atbrca1-1 ; atxr56 |
| RNA-seq | atxr5/6 | atxr5 ; atxr6 |
| RNA-seq | atxr5/6 | atxr5 ; atxr6 |
| RNA-seq | Col | wildtype |
| RNA-seq | Col | wildtype |
| DNA resequencing | EMS_2_209 (GFP -) | atsac3b-5 ; atxr5 ; atxr6 ; RAD51pro::G |
| DNA resequencing | EMS_2_37 (GFP -) | atsac3b-4 ; atxr5 ; atxr6 ; RAD51pro::G |
| DNA resequencing | RAD51pro::GFP | atxr5 ; atxr6 ; RAD51pro::GFP transge |
| RNA-seq | Col | wildtype |
| RNA-seq | EMS_2_37 (GFP -) | atsac3b-4 ; atxr5 ; atxr6 ; RAD51pro::G |
| RNA-seq | EMS_2_37 (GFP +) | atsac3b-4/+ ; atxr5 ; atxr6 ; RAD51pro::G |
| RNA-seq | RAD51pro::GFP | atxr5 ; atxr6 ; RAD51pro::GFP transge |
| DNA resequencing | EMS_2_300 (GFP -) | atthp1-5 ; atxr5 ; atxr6 ; RAD51pro::G |
| RNA-seq | EMS_2_300 (GFP -) | atthp1-5 ; atxr5 ; atxr6 ; RAD51pro::G |
| RNA-seq | EMS_2_300 (GFP +) | atthp1-5/+ ; atxr5 ; atxr6 ; RAD51pro::G |
| RNA-seq | atsac3b-3 | atsac3b-3 |

| | | |
|-----------------------------------|-------------------------------------|---|
| RNA-seq | atsac3b-3 | atsac3b-3 |
| RNA-seq | atsac3b-3 ; atxr5/6 | atsac3b-3 ; atxr5 ; atxr6 |
| RNA-seq | atsac3b-3 ; atxr5/6 | atsac3b-3 ; atxr5 ; atxr6 |
| RNA-seq | atxr5/6 | atxr5 ; atxr6 |
| RNA-seq | atxr5/6 | atxr5 ; atxr6 |
| RNA-seq | Col | wildtype |
| RNA-seq | Col | wildtype |
| RNA-seq | atxr5/6 | atxr5 ; atxr6 |
| RNA-seq | atxr5/6 | atxr5 ; atxr6 |
| RNA-seq | Col | wildtype |
| RNA-seq | Col | wildtype |
| RNA-seq | thp1-1 | thp1-1 |
| RNA-seq | thp1-1 | thp1-1 |
| RNA-seq | thp1-1 atxr5/6 | thp1-1 ; atxr5 ; atxr6 |
| DNA resequencing | EMS_2_129 (GFP -) | mbd9-4 ; atxr5 ; atxr6 |
| RNA-seq | atxr5/6 | atxr5 ; atxr6 |
| RNA-seq | atxr5/6 | atxr5 ; atxr6 |
| RNA-seq | Col | wildtype |
| RNA-seq | Col | wildtype |
| RNA-seq | mbd9-3 | mbd9-3 |
| RNA-seq | mbd9-3 ; atxr5/6 | mbd9-3 ; atxr5 ; atxr6 |
| DNA resequencing | EMS_2_325 (GFP -) | at-stubl2-1 ; atxr5 ; atxr6 ; RAD51pro: |
| RNA-seq | Col | wildtype |
| RNA-seq | EMS_2_325 (GFP -) | at-stubl2-1 ; atxr5 ; atxr6 ; RAD51pro: |
| RNA-seq | EMS_2_325 (GFP +) | at-stubl2-1/+ ; atxr5 ; atxr6 ; RAD51pro: |
| RNA-seq | RAD51pro::GFP | atxr5 ; atxr6 ; RAD51pro::GFP transge |
| RNA-seq | F1: at-stubl2-2 atxr5/6 x EMS_2_325 | at-stubl2-2/at-stubl2-1 ; atxr5 ; atxr6 |
| RNA-seq | F1: at-stubl2-2 atxr5/6 x atxr5/6 | at-stubl2-2/+ ; atxr5 ; atxr6 |
| Whole-genome bisulfite sequencing | Col | wildtype |
| Whole-genome bisulfite sequencing | atxr5/6 | atxr5 ; atxr6 |
| Whole-genome bisulfite sequencing | mbd9-3 | mbd9-3 |
| Whole-genome bisulfite sequencing | atsac3b-4 | atsac3b-4 |
| Whole-genome bisulfite sequencing | atthp1-1 | atthp1-1 |
| Whole-genome bisulfite sequencing | atsubtl2-2 | at-stubl2-2 |
| Whole-genome bisulfite sequencing | met1-3 | met1-3 |

Sample Name as Present in GEO archive

a56.1.cotyledon.DNA.110817

Col.1.cotyledon.DNA.110817

a56.1.flower.DNA.110817

Col.1.flower.DNA.110817

a56.3.cotyledon.RNA.131202

a56.3.cotyledon.RNA.140415

Col.3.cotyledon.RNA.131202

Col.3.cotyledon.RNA.140415

a56.1.flower.RNA.110906

a56.2.flower.RNA.110906

Col.1.flower.RNA.110906

Col.2.flower.RNA.110906

a56.0Gy.1.seedling.110907

a56.100Gy.1.seedling.110907

a56.0Gy.2.seedling.110907

a56.100Gy.2.seedling.110907

Col.0Gy.1.seedling.110907

Col.100Gy.1.seedling.110907

Col.0Gy.2.seedling.110907

Col.100Gy.2.seedling.110907

a56.0Gy24h.1.seedling.111226

a56.100Gy24h.1.seedling.111226

Col.0Gy24h.1.seedling.111226

Col.100Gy24h.1.seedling.111226

brca1a56.1.16C.DNA.110202

brca1a56.2.16C.DNA.110202

a56.1.16C.DNA.110202

Col.1.16C.DNA.110202

brca1.1.cotyledon.RNA.131202

brca1.2.cotyledon.RNA.140415

brca1a56.1.cotyledon.RNA.131202

brca1a56.2.cotyledon.RNA.140415

a56.1.cotyledon.RNA.131202

a56.2.cotyledon.RNA.140415

Col.1.cotyledon.RNA.131202

Col.2.cotyledon.RNA.140415

EMS_2_209.1.cotyledon.DNA.130925

EMS_2_37.1.cotyledon.DNA.130105

RAD51GFP.1.cotyledon.DNA.130105

Col.1.cotyledon.RNA.121116

EMS_2_37.GFPneg.1.cotyledon.RNA.121116

EMS_2_37.GFPpos.1.cotyledon.RNA.121116

RAD51GFP.1.cotyledon.RNA.121116

EMS_2_300.1.cotyledon.DNA.130227

EMS_2_300.GFPneg.1.cotyledon.RNA.130102

EMS_2_300.GFPpos.1.cotyledon.RNA.130102

sac3b.1.cotyledon.RNA.131202

sac3b.2.cotyledon.RNA.140415
sac3batxr56.1.cotyledon.RNA.131202
sac3batxr56.2.cotyledon.RNA.140415

a56.1.cotyledon.RNA.131202
a56.2.cotyledon.RNA.140415
Col.1.cotyledon.RNA.131202
Col.2.cotyledon.RNA.140415

a56.1.cotyledon.RNA.131202
a56.2.cotyledon.RNA.140415
Col.1.cotyledon.RNA.131202
Col.2.cotyledon.RNA.140415
thp1.1.cotyledon.RNA.131202
thp1.2.cotyledon.RNA.140415

thp1a56.1.cotyledon.RNA.140415

EMS_2_129.1.cotyledon.DNA.130602

a56.1.cotyledon.RNA.131202
a56.2.cotyledon.RNA.140415
Col.1.cotyledon.RNA.131202
Col.2.cotyledon.RNA.140415
mbd9.1.cotyledon.RNA.140415

mbd9a56.1.cotyledon.RNA.140415

EMS_2_325.1.cotyledon.DNA.130227

Col.1.cotyledon.RNA.121116
EMS_2_325.GFPneg.1.cotyledon.RNA.130102
EMS_2_325.GFPpos.1.cotyledon.RNA.130102
RAD51GFP.1.cotyledon.RNA.121116

atsubtl2.het.1.cotyledon.RNA.140415
atsubtl2.hom.1.cotyledon.RNA.140415

Col.1.leaf.meth.140417
a56.1.leaf.meth.140417
mbd9.1.leaf.meth.140417
sac3b.1.leaf.meth.140417
thp1.1.leaf.meth.140417
atsubtl2.1.leaf.meth.140417

Previous study