Hypermethylation and small RNA expression are associated with increased age in almond (*Prunus dulcis* [Mill.] D.A. Webb) accessions

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Summary

- The focus of this study is to profile changes in DNA methylation and small RNA expression occurring with increased age in almond breeding germplasm to identify possible biomarkers of age that can be used to assess the potential of individuals to develop aging-related disorders.
- To profile DNA methylation in almond germplasm, 70 methylomes were generated from almond individuals representing three age cohorts (11, 7, and 2 years old) using an enzymatic methyl-seq approach followed by analysis to call differentially methylated regions (DMRs) within these cohorts. Small RNA (sRNA) expression was profiled in three breeding selections, each from two age cohorts (1 and 6 years old) using sRNA-Seq followed by differential expression analysis.
- Weighted chromosome-level methylation analysis reveals hypermethylation in 11-year-old almond breeding selections when compared to 2-year-old selections in the CG and CHH contexts. Seventeen consensus DMRs were identified in all age contrasts. sRNA expression differed significantly between the two age cohorts tested, with significantly decreased expression in sRNAs in the 6-year-old selections compared to the 1-year-old.
- Almond shows a pattern of hypermethylation and decreased sRNA expression with increased age. Identified DMRs and differentially expressed sRNAs could function as putative biomarkers of age following validation in additional age groups.

Keywords: DNA methylation, enzymatic methyl-seq, juvenility, miRNA, RNASeq, small RNA

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Introduction

The study of aging has centered primarily around mammalian systems with a focus on humans (Kirkwood, 2005; Ferrucci *et al.*, 2020); however, the aging process has also been shown to impact plants with emphasis placed on long-lived perennials (Munné-Bosch, 2007; Brutovská *et al.*, 2013; Thomas, 2013; Woo *et al.*, 2018). These impacts can include diminished growth and reduced flower and fruit production, as well as the development of aging-related disorders (Kester & Jones, 1970; Van Dijk, 2009). In perennial plants and other organisms such as humans, causal mechanisms underlying the development of age-related phenotypes include genetic alterations such as somatic mutations or differential chromatin marks as well as changes in expression of small non-coding RNAs (sRNAs) (Jaligot *et al.*, 2000; Kato *et al.*, 2011; Dubrovina & Kiselev, 2016; Ogneva *et al.*, 2016; Xiao *et al.*, 2019; Wang *et al.*, 2020). In fact, DNA methylation has been proposed as a biomarker of aging in many systems, serving as a biological "clock" that can be used to track aging and predict aging outcomes (Runov *et al.*, 2015; Jylhävä *et al.*, 2017; Xiao *et al.*, 2019).

Profiling genome-wide DNA methylation is one approach to quantify differential epigenetic marks and model alterations associated with advanced age. Identification of specific regions of the genome showing changes in methylation associated with aging provides the opportunity to develop biomarkers to track aging and information on those genes or genic regions that might contribute to the development of age-related phenotypes (Xiao *et al.*, 2019). Alterations in DNA methylation patterns associated with aging have been recently reported in *Pinus*, suggesting DNA methylation could serve as a biomarker for tracking age in plants (Gardner *et al.*, 2023).

In addition to DNA methylation, sRNAs are known to modulate plant development and have been previously shown to be associated with aging (Chen, 2009; D'Ario *et al.*, 2017; You *et al.*, 2022). The function of sRNAs, specifically microRNAs, in these processes occurs primarily through regulating target gene expression and via post-transcriptional control (Chen, 2009; D'Ario *et al.*, 2017; You *et al.*, 2022). Due to their direct association and involvement in regulating plant developmental processes, including the juvenile-to-adult transition, microRNAs represent putative targets for developing biomarkers of age in a clonally propagated species such as almond (Raihan *et al.*, 2021; You *et al.*, 2022).

Studying alterations like differential DNA methylation and sRNA expression associated with advanced age in perennial plant systems can: (1) provide a means to track aging in these systems and (2) lead to an increased understanding of the development of age-related disorders or degeneration of important physiological processes in plants. This information is valuable to agricultural industries that rely on sustained production of perennial crops, including fruit and nut trees. Almond (*Prunus dulcis* [Mill.] D.A. Webb) is an example of a perennial nut crop that is negatively affected by the aging process through the exhibition of non-infectious bud failure, an aging-associated disorder (Kester & Jones, 1970; Micke, 1996; Kester *et al.*, 2004). Additionally, almond trees are primarily produced by clonal propagation for orchard establishment, meaning age and thus susceptibility to age-related impacts is difficult to determine (Ally *et al.*, 2010; de Witte & Stöcklin, 2010; Salguero-Gomez, 2018). A method to track aging, particularly in crops like almond produced by clonal propagation or shown to exhibit age-related disorders, would benefit growers, producers, and consumers by helping to protect the supply chain of these valuable commodities.

In this study, we utilize almond breeding germplasm produced in pedigreed crosses as part of the almond breeding program at the University of California, Davis. The individuals used in this study are grown from seed and thus are of known age, making them particularly useful to generate models to track aging in this species where clonal propagation is standard. The goal of this study was to examine DNA methylation patterns in the genome of a productive perennial crop by performing an exhaustive methylome profiling of ~70 almond individuals from three distinct age cohorts. The hypothesis is that the almond breeding selection cohorts will exhibit, on average, divergent DNA methylation profiles associated with age. Further, we performed small RNA sequencing almond selections from two age cohorts to identify differentially expressed sRNAs associated with aging. Our overall aim is to identify variability in the almond methylome and transcriptome that could enable model development to track aging in this clonally propagated crop and provide targets (i.e., differentially methylated regions, differentially expressed sRNAs) for further investigation into mechanisms influencing age-related phenotypes such as non-infectious bud failure or the juvenile-to-adult transition. This work also serves as a model to explore aging and its impacts on other important perennial crops.

Materials and Methods

102 *Plant Material*

103 Almond leaf samples were collected in May 2019 from the canopy of 30 distinct breeding
104 selections planted in 2008, 2012, and 2017, totaling 90 individuals sampled. These selections
105 represent three almond age cohorts aged 11, 7, and 2 years at the time of sampling. Almond
106 breeding germplasm sampled for this study is maintained at the Wolfskill Experimental Orchards
107 (Almond Breeding Program, University of California – Davis, Winters, CA). Leaf samples were
108 collected in the field and immediately stored on ice and then at -20 °C until shipping. Samples
109 were shipped on ice to the Ohio Agricultural Research and Development Center (OARDC; The
110 Ohio State University, Wooster, OH, USA) and immediately stored at -20 °C until sample
111 processing. Almond leaf tissue from the canopy of three breeding selections planted in 2015 and
112 2020 was collected in May 2021 from the Wolfskill Experimental Orchards. Samples were
113 collected, stored on dry ice, and immediately sent to Novogene for processing and small RNA
114 sequencing.

115 *DNA Extraction*

116 High-quality DNA was extracted from leaves following a modified version of the protocol
117 outlined in Vilanova et al., 2020. Briefly, samples were ground to a fine powder with a mortar
118 and pestle in liquid nitrogen, and 50 mg of the ground material was added to 1 mL of extraction
119 buffer (2% w/v CTAB; 2% w/v PVP-40; 20 mM EDTA; 100 mM Tris-HCl [pH 8.0]; 1.4 M
120 NaCl), 14 µL beta-mercaptoethanol, and 2 µL RNase (10 mg/mL). The solution was incubated at
121 65°C for 30 mins and on ice for 5 mins, followed by a phase separation with 700 µL
122 chloroform:isoamyl alcohol (24:1). The aqueous phase (~800 µL) was recovered, and 480 µL
123 binding buffer (2.5 M NaCl; 20% w/v PEG 8000) was added followed by 720 µL 100% ice-cold
124 ethanol.

125 A silica matrix buffer was prepared by adding 10 g silicon dioxide to 50 mL ultra-pure
126 water prior to incubation and centrifugation steps. Silica matrix buffer (20 µL) was added to each
127 sample, and samples were gently mixed for 5 mins. Samples were spun for 10 secs, and the
128 supernatant was removed. To resuspend the remaining mucilaginous material (but not the pellet),
129 500 µL of cold 70% ethanol was used, and the supernatant was removed. Another 500 µL cold
130 70% ethanol was added to resuspend the silica pellet, the tubes were spun for 5 secs, and the
131 supernatant was removed. The pellet was allowed to dry at room temperature for 5 mins and was
132 resuspended in 100 µL elution buffer (10 mM Trish HCl [pH 8.0]; 1 mM EDTA [pH 8.0])

133 followed by a 5 min incubation at 65°C. Samples were centrifuged at 14,000 rpm for 10 mins at
134 room temperature, and 90 µL of supernatant was transferred to a new tube. DNA concentration
135 was assessed by fluorometry using a Qubit™ 4 and Qubit™ 1X dsDNA HS Assay Kit
136 (ThermoFisher Scientific, Waltham, MA, USA).
137 *RNA Extraction*
138 For small RNA sequencing, RNA was isolated from almond leaves using the Quick-RNA Plant
139 Miniprep Kit (Zymo cat# R2024) with minor modifications. Leaf tissue was transferred into 800
140 µl of DNA/RNA Shield in the BashingBead tubes (instead of 800 µl of RNA Lysis Buffer as
141 written in the protocol) and homogenized using an MP FastPrep-24 with the following settings:
142 6m/s for 60s, repeat for a total of 2 cycles. After centrifuging to pellet debris, 400 µl of cleared
143 lysate was taken out and mixed thoroughly with 1200 µl (3 volumes) of RNA Lysis Buffer. This
144 mixture was then added to the ZymoSpin IIICG column as described in Step 4 of the protocol,
145 and then the rest of the protocol was followed as written. DNase treatment was performed in the
146 column according to the appendix on page 6.
147 *Enzymatic Methyl-Seq Library Preparation and Illumina Sequencing*
148 Whole-genome enzymatic methylation sequencing is equivalent to the "gold standard" bisulfite
149 sequencing approach to profile the methylome at the nucleotide level (Feng *et al.*, 2020).
150 Utilizing this approach provides information on both genome-wide methylation in each context
151 (CG, CHG, and CHH [H = A, T, or C]) and allows for the identification of differentially
152 methylated regions (DMRs), pinpointing regions of the genome showing dynamic patterns of
153 methylation associated with increased age (Feng *et al.*, 2020; Vaisvila *et al.*, 2020). Whole-
154 genome enzymatic methyl-seq libraries were prepared using the NEBNext® Enzymatic Methyl-
155 seq kit (New England BioLabs® Inc., Ipswich, MA, USA) according to the manufacturer's
156 instructions. Each sample was prepared using 100 ng input DNA in 48 µL TE buffer (1 mM
157 Tris-HCl; 0.1 mM EDTA; pH 8.0) with 1 µL spikes of both the CpG unmethylated Lambda and
158 CpG methylated pUC19 control DNA provided in the kit. The samples were sonicated using a
159 Covaris® S220 focused-ultrasonicator in microTUBE AFA Fiber Pre-Slit Snap-Cap 6×16 mm
160 tubes (Covaris®, Woburn, MA, USA) with the following program parameters: peak incident
161 power (W) = 140; duty factor = 10%; cycles per burst = 200; treatment time (s) = 80.
162 Following library preparation, library concentration and quality were assessed by fluorometry
163 using a Qubit™ 4 and Qubit™ 1X dsDNA HS Assay Kit (ThermoFisher Scientific) and by

164 electrophoresis using a TapeStation (Agilent, Santa Clara, CA, USA). Library concentration was
165 further quantified by qPCR using the NEBNext® Library Quant Kit for Illumina® (New
166 England BioLabs® Inc.). Libraries were equimolarly pooled in batches of ~15 (five libraries per
167 age cohort) and cleaned using an equal volume of NEBNext® Sample Purification Beads (New
168 England BioLabs® Inc.). The library pools were eluted in 25 μL TE buffer (1 mM Tris-HCl; 0.1
169 mM EDTA; pH 8.0), and concentration and quality were assessed by fluorometry and
170 electrophoresis as above. Library pools were sequenced on two lanes of the Illumina®
171 HiSeq4000 platform to generate 150-bp paired-end reads.
172 *small RNA-Seq Library Preparation and Illumina Sequencing*
173 The NEBNext Small RNA Library Prep Set for Illumina was used according to the
174 manufacturer's instructions. Briefly, 3' and 5' adaptors were ligated to the 3' and 5' ends of the
175 small RNA, respectively. Then the first-strand cDNA was synthesized after hybridization with a
176 reverse transcription primer. The double-stranded cDNA library was generated through PCR
177 enrichment. After purification and size selection, libraries with insertions between 18~40 bp
178 were ready for single-end sequencing 50-nt read length with Illumina NovaSeq, 10 million raw
179 reads per sample.
180 Detailed analysis methods for enzymatic methyl-seq libraries, including identification of
181 differentially methylated regions (DMRs) and annotation of genetic features and transposable
182 elements, and analysis of small RNA libraries, including examining differential expression, are
183 presented in Methods S1. The general methodology, including software packages and references
184 used for this study, is illustrated in Figure 1.
185
186 **Results**
187 *Genome-wide methylation analysis in almond accessions representing three age cohorts*
188 Following DNA isolation, library preparation, and Illumina sequencing, a total of 21 almond
189 breeding selections were used for subsequent analysis in the 2-year-old age cohort, 25 in the 7-
190 year-old age cohort, and 24 in the 11-year-old age cohort. Sequencing results show aligned
191 coverage for almond accessions ranged from 3.85 – 50.41X (**average:** 12.7 X; **median:** 11.3X)
192 with an average of 49.8 % reads uniquely aligned reads (Data S1). Conversion efficiency was
193 greater than 98% based on alignment to the Lambda reference sequence file (Data S1).

194 Analysis of weighted genome-wide percent methylation within all methylation contexts
195 (CG, CHG, and CHH) revealed a significant increase in weighted methylation in the 11-year-old
196 age cohort compared to the 2-year-old in the CG (p-value = 0.0105) and CHH (p-value = 0.0399)
197 contexts, respectively (Fig. 2a, c). There was also a significant increase in CG methylation in the
198 11-year-old age cohort compared to the 7-year-old age cohort (p-value = 0.0115; Fig. 2a). There
199 was not a significant difference in weighted genome-wide methylation in the CHG context when
200 comparing age cohorts (Fig. 2b).
201 To further analyze weighted methylation in these samples, methylation data for each
202 individual was processed per chromosome, and weighted methylation was analyzed at the
203 chromosome level for each methylation context. (Fig. S1a-c). Pairwise comparisons of DNA
204 methylation within each chromosome revealed significant differences in cytosine methylation on
205 distinct chromosomes for each methylation context (Table S1). In the CG context, both the 2 –
206 11 year and the 7 – 11 year age contrasts were significant on chromosomes 1, 3, 5, 7, and 8
207 (Table S1). In the CHG context, both the 2 – 11 year and the 7 – 11 year age contrasts were
208 significant on chromosome 5, the 7 – 11 year age contrast was significant on chromosome 7, and
209 the 2 – 11 year age contrast was significant on chromosome 8 (Table S1). Finally, in the CHH
210 context, the 2 – 11 year age contrast was significant on chromosomes 5, 7, and 8 (Table S1).
211 Overall, significant differences in chromosome-level DNA methylation between age cohorts tend
212 to occur on chromosomes 5, 7, and 8.
213 *Identification and classification of differentially methylated regions (DMRs) between age cohorts*
214 DMRs were identified based on comparisons between the age cohorts in each
215 methylation context. Most DMRs identified are in the CG context, followed by CHH and CHG,
216 respectively (Table 1). These DMRs were further classified as hyper- and hypomethylated where
217 hypermethylated indicates the older cohort is more methylated than the younger cohort and
218 hypomethylated indicates the older cohort is less methylated than the younger cohort for each
219 DMR. In the CG context, 96%, 94%, and 64% of the identified DMRs were hypermethylated in
220 the older trees for the 11 – 2 year, 11 – 7 year, and 7 – 2 year age contrasts, respectively (Table
221 1). In the CHG context, 68%, 52%, and 64% of DMRs were hypermethylated in the older trees
222 for the 11 – 2 year, 11 – 7 year, and 7 – 2 year age contrasts, respectively (Table 1). Finally, in
223 the CHH context, 82%, 38%, and 82% of DMRs were hypermethylated in the older trees for the
224 11 – 2 year, 11 – 7 year, and 7 – 2 year age contrasts, respectively (Table 1). The cumulative

225 binomial probability of the occurrence of hypermethylated DMRs was less than 1×10^{-6} for all
226 age contrasts except 11 – 7 in the CHG and CHH contexts, suggesting there are more
227 hypermethylated DMRs than would be expected given an equal probability of hyper- and
228 hypomethylated DMRs in the genome. Identified DMRs ranged in length from 51- 4,824 base
229 pairs, with an average length of 200 base pairs and a median of 139 base pairs (Fig. S2a-l) The
230 average length of CG, CHG, and CHH DMRs is 212, 201, and 177 base pairs, respectively. The
231 average length of a gene in the 'Nonpareil' genome is 2,912 bp, so most of the identified DMRs
232 are much shorter than the average gene.
233 The distribution of CG-context DMRs showed a similar pattern across all chromosomes,
234 where the 11 – 2 year age contrast has the highest number of DMRs per chromosome, followed
235 by the 11 – 7 year and 7 – 2 year age contrasts (Fig. S3a). In the CHG and CHH contexts, the
236 distribution of DMRs showed greater variability, with the 11 – 7 year age contrast typically
237 showing the lowest number of DMRs across all chromosomes, while the 11 – 2 and 11 – 7 year
238 age contrasts oscillate in number of DMRs occurring on each chromosome across the genome
239 (Fig. S3b,c).
240 *Classification of DMRs as hyper- or hypomethylated in the age cohort comparisons*
241 Using the classifications of hyper- and hypomethylated, DMRs were plotted across the
242 eight chromosomes of the 'Nonpareil' genome revealing unique distributions based on both
243 methylation context and age contrast, as well as indicating DMR enrichment in specific
244 chromosomes (Fig. 2). In the CG context, DMR enrichment occurs in the 11 – 2 year age
245 contrast, with predominantly hypermethylated DMRs, though enrichment of hypomethylated
246 DMRs appears on chromosome 5 (Fig. 2a). The CHG context represents the lowest overall
247 enrichment of DMRs compared to the other methylation contexts with regions throughout the
248 genome showing a concentrated enrichment of DMRs across the genome (Fig. 2b). Finally,
249 DMRs in the CHH context show similar patterns in enrichment for both the 7 – 2 year and 11 – 2
250 year age contrasts, with evident DMR enrichment occurring on chromosomes 3 and 8 (Fig. 2c).
251 The 11 – 7 year age contrast in the CHH methylation context is the only contrast to have a higher
252 number of hypomethylated DMRs compared to hypermethylated (Table 1; Fig. 2c).
253 Following the classification of DMRs as either hyper- or hypomethylated in each age
254 contrast, DMRs were compared among age contrasts to identify overlapping genomic regions.
255 This analysis revealed several overlapping DMRs from distinct age contrasts. The highest

256 number of overlaps occurred in CG context hypermethylated DMRs, particularly when
257 comparing the 11 – 2 by 11 – 7 and 11 – 2 by 7 – 2 age contrasts (Table 2). Interestingly, the 11
258 – 7 by 7 – 2 age contrast revealed very few overlaps in hypermethylated DMRs, and no
259 overlapping hypomethylated DMRs (Table 2). Finally, a comparison was performed to identify
260 DMRs with overlapping genomic regions among all three age contrasts, showing the 11 – 2 age
261 contrast contains DMRs that share a genomic region with the overlapping DMRs in the 11 – 7 by
262 7 – 2 comparison (Table 2). This final analysis revealed 17 overlapping DMRs among the three
263 age contrasts, meaning these DMRs share overlapping genomic coordinates (Table S2). These 17
264 DMRs are the longest (ranging from 106 – 1,504 base pairs) in the 11 – 2 age contrast, followed
265 by the 11 – 7 (56 – 713 base pairs) and 7 – 2 (52 – 1,037 base pairs) age contrasts (Table S2).
266 Analysis of the average percent methylation of cytosines within the genomic regions identified in
267 the 11 – 7 age contrasts show that in most of these regions, cytosines become more methylated
268 with increased age across the three age cohorts (Figs. S4a-c, S5a-m, S6a-c).
269 *Annotation of hyper- and hypomethylated differentially methylated regions (DMRs)*
270 Annotation was performed by classifying all hyper- and hypomethylated DMRs in each
271 methylation context into four categories (gene, exon, 5' untranslated region [UTR], and 3' UTR)
272 based on their association with features in the 'Nonpareil' genome annotation. CG context
273 DMRs generally tended to have higher associations with genes and exons compared to the other
274 methylation contexts, while CHG DMRs tended to have higher associations with 5' UTRs and
275 CHH DMRs with 3' UTRs compared to the other contexts (Table S3).
276 Identified DMRs were then annotated using the 'Nonpareil' genome annotation file to
277 determine the closest gene associated with each DMR. Enrichment analysis was performed for
278 both hyper- and hypomethylated DMR-associated genes in all methylation contexts for each age
279 contrast, revealing a suite of biological process, molecular function, and cellular component gene
280 ontology (GO) terms associated with each contrast (Tables S4-S9). Comparing annotations
281 between age contrasts identified GO terms unique to each age contrast in each methylation
282 context and degree of methylation (i.e., hyper or hypo). For example, a subset of genes
283 associated with hypermethylated DMRs in the CG context from all three age contrasts was
284 assigned the molecular function GO terms transmembrane transporter activity, protein
285 serine/threonine kinase activity, and DNA-binding transcription factor activity (Table S4b).

286 *Annotation of genes associated with 17 hypermethylated DMRs identified in all three age cohort*
287 *age contrasts*
288 Of the DMRs identified in each age contrast, 17 hypermethylated DMRs were found to share
289 genomic regions in all three age contrasts, meaning these regions showed consistent significant
290 increases in methylation in the older age cohort relative to the younger in each age contrast. The
291 17 DMRs were annotated using the 'Nonpareil' genome annotation to identify the closest
292 associated gene. In total, eight previously annotated genes, including *FAR1-RELATED*
293 *SEQUENCE 5* (*FRS5*), a receptor-interacting serine/threonine-protein kinase 4 (*Ripk4*), and
294 dCTP pyrophosphatase 1 (*Dctpp1*) were identified as associated with nine of the DMRs (Table
295 3). One CG DMR and one CHG DMR are associated with the same gene, Tryptophan
296 aminotransferase-related protein 3 (*TAR3*) (Table 3). The remaining eight DMRs are associated
297 with genes of unknown function (Table 3). These eight unknown protein sequences were used as
298 input into three programs to determine properties, including predicted motifs, localization, and
299 weight. Two of these unknown proteins contained transposase_24 motifs, and four are predicted
300 to be localized to the nucleus (Table S10).
301 In addition to identifying genes associated with these 17 shared DMRs, the DMR
302 genomic sequences (Data S2) were searched against the modified miRBase database using blastn
303 to identify any potential miRNAs within these regions. Results from this analysis showed that 12
304 of the DMRs contained at least one previously identified miRNA sequence (Table S11).
305 *Profiling of DMRs overlapping transposable elements in two age cohorts*
306 The 2- and 7-year-old age cohorts were used to determine overlap of DMRs with transposable
307 elements in the almond genome, as this contrast had the largest sample size and represents the
308 typical transition from juvenile to mature adult in almond (occurring ~ 5 years old). Of the
309 DMRs identified in the 2-7 age contrast, 493 overlapped with 495 predicted transposable
310 elements (Data S3). These overlaps occurred among transposable elements in 11 categories (Fig.
311 S7. Out of those transposable elements with a defined taxonomy, the majority of these overlaps
312 occurred within Mutator Terminal Inverted Repeat (TIR) transposons (132) and Long Terminal
313 Repeat (LTR) retrotransposons (87). The smallest proportion of DMRs occurred within Long
314 Interspersed Nuclear Elements (LINEs). The most common methylation context occurring within
315 transposable elements was CG (252), followed by CHG (156) and CHH (87). The length of the
316 DMRs varied from 50 to 978 base pairs, and the overlap with transposable elements varied

317 between 41 to 381 base pairs, with 90% of the overlaps occurring between 1 and 121 base pairs
318 and 95% of the transposable elements being between 71 and 1171 base pairs long. Interestingly,
319 most of the DMRs overlapping with transposable elements occurred along chromosome 4 (91),
320 followed by chromosome 2 (71), chromosome 1 (70) and chromosome 8 (67), chromosome 3
321 (56), chromosome 7 (48), chromosome 6 (46) and chromosome 5 (42); four additional DMRs
322 occurred in unassembled contigs. This pattern deviates from the expectation that longer
323 chromosomes tend to have more transposable elements and, therefore, higher chances of
324 overlapping with DMRs.

325 *Profiling small RNA expression and identifying differentially expressed small RNAs in two age*
326 *cohorts*

327 Small RNA expression was profiled in two almond breeding selection cohorts aged 1 and 6 years
328 at the time of sampling. Three individual almond breeding selections were sequenced from each
329 of the two cohorts. Analysis of the sRNA sequencing data by principal component analysis
330 revealed clustering based on age in 20, 21, 23, and 24 nucleotide sRNAs, with the age cohort
331 explaining 30%, 35%, 36%, and 37% of variance in the small RNA expression profiles,
332 respectively (Fig. 4). Differential expression analysis showed 1,768 significantly differentially
333 expressed sRNAs, and 1,450 of those have a negative log2fold change value, indicating overall
334 down regulation in the 6-year-old compared to the 1-year-olds. This trend is particularly apparent
335 in the 21 and 22 nucleotide sRNAs, where most of the significantly differentially expressed
336 sRNAs are downregulated in the 6-year-olds (Fig. 5). Interestingly, the 23 and 24 nucleotide
337 sRNAs show the opposite pattern, where most of the significantly differentially expressed
338 sRNAs are upregulated in the 6-year-olds compared to the 1-year-olds (Fig. 5). None of the 20
339 nucleotide sRNAs show significant differential expression between the two age cohorts (Fig. 5).

340 Subsequent BLAST analysis of the sRNAs against the miRbase database showed
341 significant alignment of 455 sRNAs to previously identified microRNA families. Among those,
342 18 are significantly differentially expressed and align to a total of 9 microRNA families within
343 the miRbase database (Fig. 6). The microRNA families include miR1511, mir159, miR171,
344 miR395, miR477, miR482, miR5742, miR6274, and miR7125 (Fig. 6).

345

346 **Discussion**

347 Perennial plant aging and the impacts of this process, particularly on productive fruit and nut
348 crops, is a neglected area of research with potential applications for agricultural production and
349 crop improvement. The ability to track age in clonally propagated crops could aid in the
350 mitigation of age-related disorders like non-infectious bud failure (Kester *et al.*, 2004) and, more
351 broadly, in overcoming the decrease in plant performance resulting from intense production
352 systems that affect orchard/vineyard longevity. Biomarkers of age in these species, however, are
353 lacking. The aim of this study was to test the hypothesis that, on average, almond breeding
354 selection cohorts will exhibit divergent DNA methylation profiles associated with age. The long-
355 term goals of this work are to develop biomarkers of age in almond, a clonally propagated crop,
356 and to further our understanding of the aging process in perennial species. To address this,
357 whole-genome DNA methylation profiles were generated for ~70 almond individuals from three
358 distinct age cohorts, and comparisons were made between cohorts to identify regions of interest
359 for further study into their involvement in the aging process and utility as biomarkers of age in
360 almond.
361 *DNA hypermethylation in the CG and CHH contexts is associated with increased age in almond*
362 The DNA methylation profiles generated for individuals in the three age cohorts (11, 7, and 2
363 years old) were compared at the whole-genome and chromosome level, which showed that
364 hypermethylation in the CG and CHH methylation contexts is associated with increased age in
365 almond. Further, the probability of identifying the number of hypermethylated DMRs observed
366 in this study was very low for most age contrasts, suggesting there was a disproportionately high
367 number of hypermethylated DMRs identified compared to hypomethylated DMRs. This result
368 supports previous work theorizing an increase in total genomic DNA methylation with increased
369 age in plants (Dubrovina & Kiselev, 2016). Previous studies have also shown that genome-wide
370 hypermethylation can result in a high number of identified hypermethylated DMRs in subsequent
371 analyses, as was reported in several species, including Monterey pine (*Pinus radiata* D.Don),
372 peach (*P. persica*), and coast redwood (*Sequoia sempervirens* [D.Don] Endl.) (Bitonti *et al.*,
373 2002; Fraga *et al.*, 2002b; Huang *et al.*, 2012).
374 DNA methylation has been proposed as a "biological clock" capable of predicting the
375 true, ontogenetic age of an individual due to observed patterns of increased methylation with
376 increased age in a variety of species (Runov *et al.*, 2015). Results in this study suggest that
377 almond fits this pattern of hypermethylation, and thus DNA methylation may serve as a

378 biomarker of age in this species. Whole-genome hypermethylation with increased age represents
379 an opportunity to develop high-throughput screening methods that do not require whole-genome
380 sequencing. These methods could include high-performance liquid chromatography or capillary
381 electrophoresis (Stach *et al.*, 2003; Armstrong *et al.*, 2011).
382 Regulation by DNA methylation, histone modifications, and chromatin remodeling has
383 also been shown to modulate the juvenile-to-adult phase transition in plants, including in
384 gymnosperms like Monterey pine and angiosperms such as peach (Bitonti *et al.*, 2002; Fraga *et*
385 *al.*, 2002a; Xu *et al.*, 2018). The juvenile period in almond is approximately 3-4 years; thus, the
386 differential patterns of methylation observed in this study between the 2- and 7-year cohorts and
387 the 2- and 11-year cohorts could be associated with the juvenile-to-adult transition as has been
388 documented in other plants (Dubrovina & Kiselev, 2016). Patterns of differential methylation
389 identified in this study and associated with specific regions of the genome further demonstrate
390 the potential involvement of DNA methylation in regulating this transition in almond. Further
391 investigation is needed focusing on the involvement of DNA-methylation in the juvenile-to-adult
392 transition in almond and other perennial species, including those with available transgenic
393 germplasm exhibiting reduced juvenility, such as apple (Flachowsky *et al.*, 2011; Kumar *et al.*,
394 2020).
395 *Differentially methylated regions (DMRs) in the CG and CHH contexts are enriched on specific*
396 *chromosomes in the almond genome*
397 Following the identification of DMRs in the three age contrasts, these regions were plotted
398 across the almond genome showing enrichment of DMRs on specific chromosomes, particularly
399 in the CG and CHH methylation contexts. These so-called "hotspots" of differential DNA
400 methylation could suggest loci in these regions are prone to chromatin alterations, including
401 methylation. Transposable elements (TEs) tend to be heavily methylated and have been reported
402 to be involved in developmental processes in almond, such as the juvenile-to-adult transition
403 (Han *et al.*, 2018; Corso-Díaz *et al.*, 2020; Wyler *et al.*, 2020). In our study, we found that in the
404 2-7 age contrast, there is a high proportion of TEs overlapping with DMRs in chromosomes 3, 4,
405 7, and 8, which corresponds with DMR enrichment hotspots observed in the age cohort
406 comparisons. This type of pattern has been documented in other species, such as rice, where a
407 study on salt tolerance identified DMRs that tended to cluster on specific chromosomes and were
408 typically associated with TEs on these chromosomes (Ferreira *et al.*, 2019).

409 In this study, hypermethylated CG DMRs were enriched on chromosome 8, and
410 hypermethylated CHH DMRs on chromosomes 3 and 8. As we have shown, increased levels of
411 methylation tend to occur in regions rich in TEs, which seem to become increasingly methylated
412 with age. A study in almond characterized the TE landscape in the 'Texas' cultivar and
413 compared the distribution of TEs in the genome to that of peach (Alioto *et al.*, 2020). This study
414 revealed not only an increased involvement of TEs in trait diversity in almond compared to
415 peach but also showed enrichment of TEs on almond chromosomes 3 and 8 (Alioto *et al.*, 2020),
416 corresponding to the chromosomes identified in this study to show enrichment of
417 hypermethylated CG and CHH DMRs. Chromosomes 3 and 8 are targets for further exploration
418 of biomarkers of age and to understand their association with the juvenile-to-adult transition in
419 almond.
420 Interestingly, a study in *Brachypodium distachyon* (L.) P.Beauv. found that DMRs were
421 highly correlated with genetic diversity as classified by the presence of single nucleotide
422 polymorphisms (SNPs) throughout the genome (Eichten *et al.*, 2016). This genetic diversity was
423 found to be related to the presence of TEs at these sites, potentially contributing to the formation
424 of SNPs as well as leading to differential levels of methylation between the lines tested (Eichten
425 *et al.*, 2016). Given the heterozygosity and diversity in almond germplasm, it may be relevant to
426 compare regions enriched in DMRs from the age contrasts to SNP data in almond to test for a
427 correlation between increased methylation and genetic diversity, particularly for traits associated
428 with growth and development and length of juvenility.
429 *DMRs as potential biomarkers of age in almond*
430 The DMRs identified in this study represent those regions in the genome that showed either an
431 increase or a decrease in cytosine methylation with increased age in almond. The results herein
432 suggest that DMRs tend to be hypermethylated in older trees. This pattern fits with the weighted
433 genome-wide methylation patterns showing significant increases in methylation in the CG and
434 CHH contexts between the 2- and 11-year-old age cohorts. Unique, hypermethylated DMRs
435 were identified in each age contrast, providing information on DNA methylation dynamics
436 associated with age. Interestingly, no hypomethylated DMRs were identified in each age
437 contrast, suggesting that hypermethylation is more prominent in aging in almond. Regions that
438 show increased methylation in each age contrast are of particular interest due to their potential
439 suitability as biomarkers of age since these regions show incremental increases in methylation

440 from 2-to-7 years and again from 7-to-11 years old. There were 17 hypermethylated DMRs
441 common to all three contrasts that may be particularly useful as biomarkers. Once these regions
442 are validated via DNA methylation profiling in additional almond cohorts of known age, a
443 predictive model based on these regions could be developed and applied to clonal germplasm to
444 predict ontogenetic age, providing a basis to screen germplasm for susceptibility to undesirable,
445 age-related phenotypes. These tools may have implications for germplasm management in
446 breeding, production (orchard), propagation (nursery), and conservation (repository) settings.
447 The genetic features associated with these specific DMRs could also be involved in
448 developmental processes, including the juvenile-to-age transition. Of the 17 DMRs, nine were
449 found to be associated with eight annotated genes. These genes include *FRS5*, a *FAR1-related*
450 protein in the *FAR1* gene family which is involved in light perception and was demonstrated to
451 be involved in plant development and regulation of aging processes in Arabidopsis (Lin &
452 Wang, 2004; Ma & Li, 2018; Xie *et al.*, 2020). Further, *FAR1-related* genes have been
453 previously found to be domesticated TEs (Lin *et al.*, 2007). In the 'Nonpareil' genome
454 annotation, 528 genes are found to have the annotation of *FAR1-related*. Given the occurrence of
455 this annotation in the genome, this suggests that these genes may also be domesticated TEs. The
456 gene *TAR3* was associated with two DMRs, one in the CG context and one in the CHG context.
457 This gene is part of the *TRYPTOPHAN AMINOTRANSFERASE (TAR)* gene family, whose
458 members are a component of one of the major auxin biosynthetic pathways (Hofmann, 2011).
459 Auxin is a well-known regulator of plant development and senescence processes (Ljung, 2013;
460 Khan *et al.*, 2014; Mueller-Roeber & Balazadeh, 2014), and disruption of *TAR3* expression could
461 impede auxin production (Hofmann, 2011). Two receptor-like kinase (RLK) genes were also
462 found to be associated with DMRs in the CG and CHG context. RLKs have been extensively
463 studied in plants and are known to be involved in cell signaling and related to plant defense and
464 plant developmental processes (Afzal *et al.*, 2008). Additionally, eight proteins of unknown
465 function were associated with the overlapping DMRs. These genes and the others identified
466 represent interesting targets for future study on their potential involvement in aging processes in
467 almond, including in the vegetative transition.
468 *Putative role of miRNAs in almond aging*
469 In addition to identifying nearby genes associated with these DMRs, microRNAs
470 (miRNAs) were also surveyed in these regions. CGDMR5 contained two putative miRNA

471 sequences with best hits to *Glycine max* miR172e and miR172d, members of the miR172 family
472 of microRNAs. The miR172 family are major regulators of development and phase transition in
473 plants (Wu *et al.*, 2009; Tang *et al.*, 2018; Zhang & Chen, 2021). MiR172 increases in
474 abundance with age, acting antagonistically with miR156 to regulate phase transition from
475 vegetative to reproductive in plants (Auckerman & Sakai, 2003; Bastías *et al.*, 2016). If miR172
476 activity is involved in the juvenile-to-adult transition in almond, as suggested in other plants,
477 significant upregulation of this miRNA would be expected in the 6-year-old cohort compared to
478 the 2-year-old cohort in this study. The sRNA expression analysis in this study revealed several
479 significantly differentially expressed miRNAs; however, miR172 was not found to be
480 significantly differentially expressed. It is possible that expression was not detected during the
481 time points sampled because the miRNA is not active or because the correct time points were not
482 chosen. Further work is needed in almond to examine miR172 activity, including expression,
483 during the vegetative transition to understand its involvement in aging. Among the differentially
484 expressed small RNAs, miR171 was found to be significant. This microRNA has been
485 previously shown to be involved in regulating the GRAS transcription factor family which is
486 involved in regulating flowering and meristem development (Wang *et al.*, 2010). Work in barley
487 has shown that miR171 activity is also involved in phase transitions regulated by the
488 miR156/miR172 pathway (Curaba *et al.*, 2013).
489 In addition to specific microRNA expression patterns, overall small RNA expression
490 profiles in the two age cohorts revealed an association between small RNA expression and aging.
491 An association between sRNAs and aging has been identified in other organisms, and small
492 RNA expression has been suggested as a biomarker of aging and aging-associated disorders
493 (Chen *et al.*, 2010; Gao *et al.*, 2012; Proshkina *et al.*, 2020). The correlation between small RNA
494 expression and age in almond suggests that sRNA expression profiles are potential biomarkers of
495 age and could be used along with DMRs to generate models of aging in almond and other
496 *Prunus* species.
497 Biomarkers of age are valuable for clonally propagated crops, whose ontogenetic age can
498 be difficult to determine, to screen and select germplasm with low potential for developing age-
499 related disorders. Further, the DMRs and small RNAs identified in this study can be used to
500 guide future studies aimed at increasing our understanding of plant aging and vegetative phase
501 transition in perennials. Perennial plants, including almond, are known for having long juvenile

502 periods, which can inhibit breeding and improvement efforts. Alteration of DNA methylation or
503 sRNA expression provides another approach for manipulating phase transition and developing
504 perennial crops with shorter juvenile periods, dramatically shortening breeding cycles for these
505 species.

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516 **Competing interests**

517 The authors declare no competing interests.

518 **Author contributions**

519 KMDW and JFR conceptualized and designed the study. KMDW and TMG performed the tissue
520 sampling. KMDW and ESA performed all the laboratory portions of the project. KMDW
521 performed all analyses with the assistance of JFR and CEN. KMDW prepared the manuscript
522 with the assistance of JFR and CEN. All authors contributed to editing the manuscript prior to
523 submission. All the authors approved the submission and revised version of this manuscript.

524 **Data availability**

525 The 'Nonpareil' almond reference genome can be found at
526 https://www.rosaceae.org/Analysis/13738196. All sequencing data for this project has been
527 deposited to the NCBI Sequence Read Archive under Bioproject PRJNA933198 including
528 biosamples: SAMN33228162 to SAMN33228237. All code used to perform analyses reported in
529 the manuscript can be found at (https://github.com/kmdamico/AgeCohortAnalysis).

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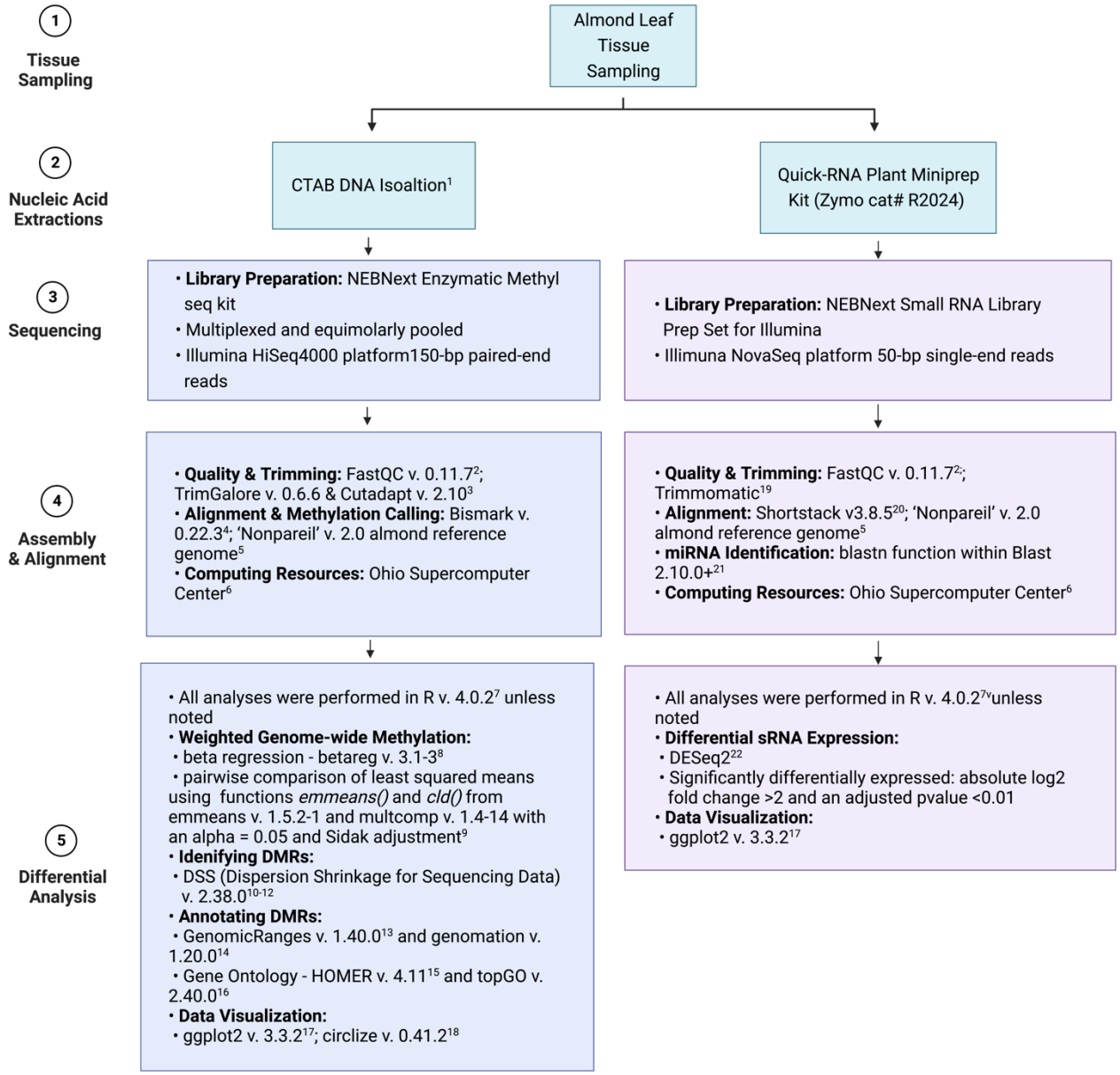
1 **Figures**



2 **Fig 1.** Pipeline of methodology following almond leaf tissue sampling, including DNA and RNA
3 isolations, sequencing library preparation, Illumina sequencing platform, and data analysis
4 approaches and tools. ([1]Vilanova *et al.*, 2020; [2]Andrews, 2010; [3]Krueger, 2016; [4]Krueger &
5 Andrews, 2011; [5]D'Amico-Willman *et al.*, 2022; [6]Ohio Supercomputer Center, 1987; [7]R Core
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9 [21]Camacho, 2009; [22]Love *et al.*, 2014) (Image created with BioRender.com)

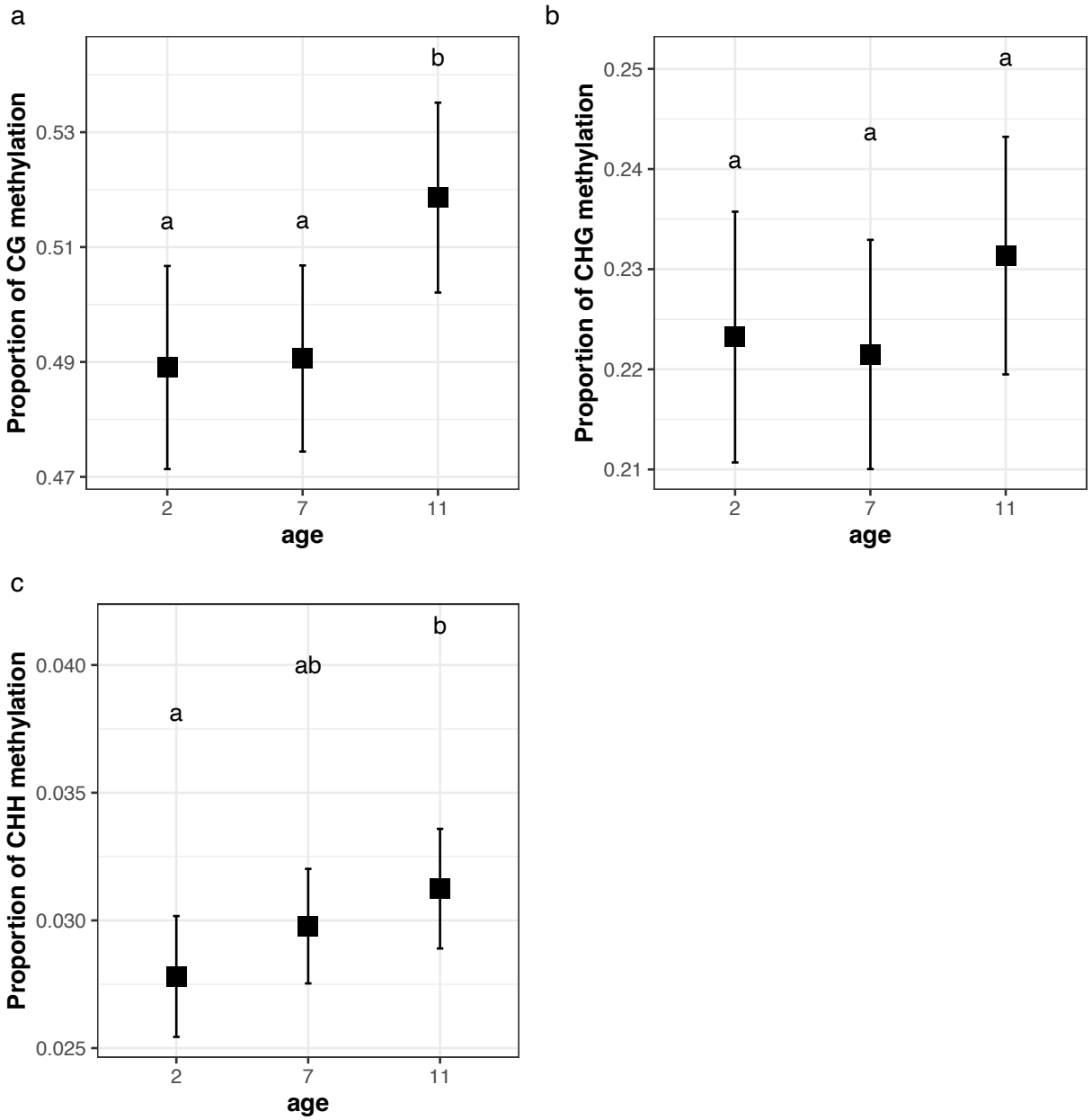


Fig 2. Proportion of weighted genome-wide methylation in the CG **(a)**, CHG **(b)**, and CHH **(c)** methylation-contexts for each age cohort (2, 7, and 11 years old). Letter groups represent significant differences based on pairwise comparisons using least squared means (alpha = 0.05).

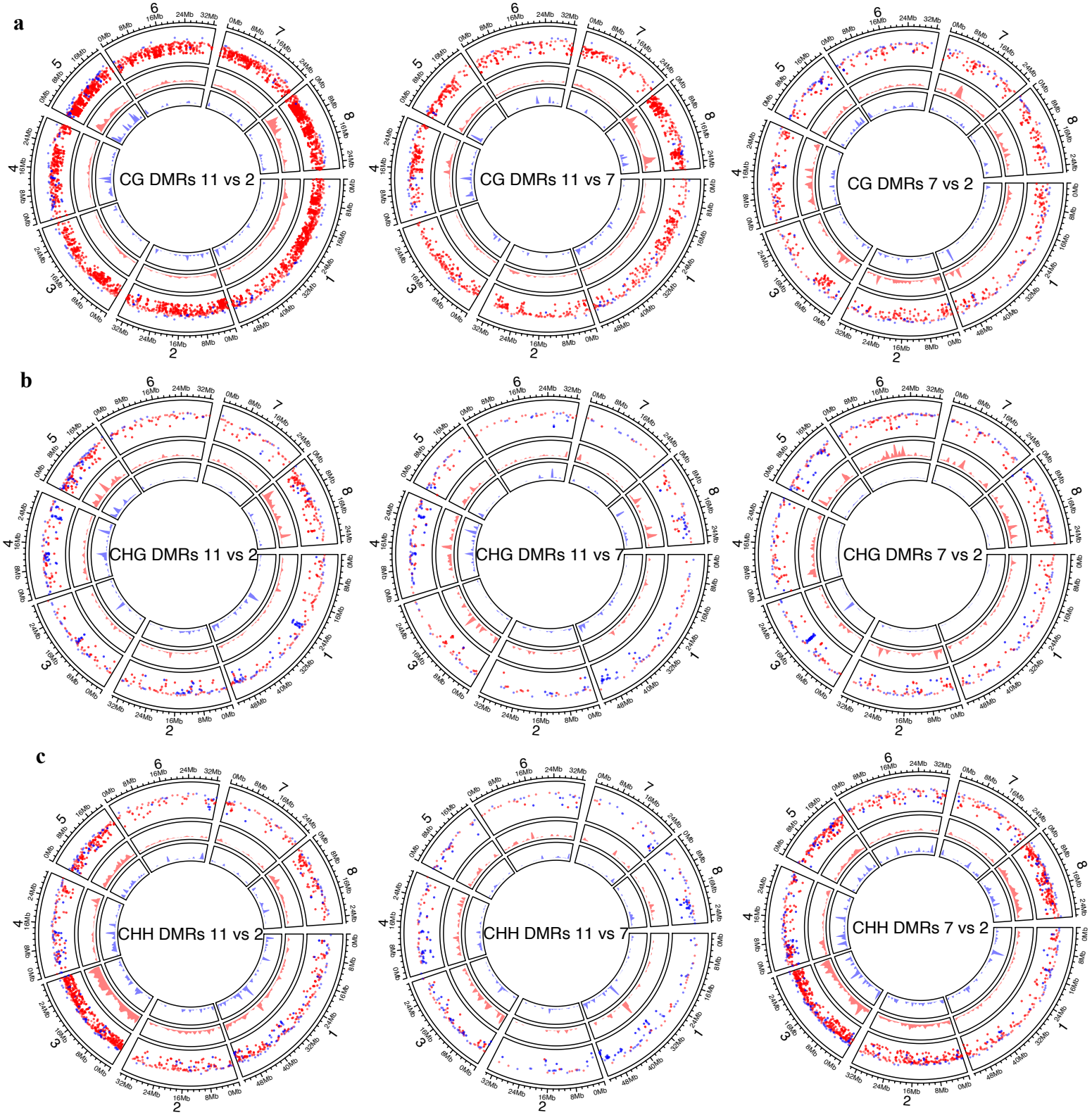


Fig 3a-c. Circos plots depicting individual hyper- (red) and hypo- (blue) methylated differentially methylated regions (DMRs) identified in each contrast and methylation-context. The outer ring of each plot gives approximate location of the individual DMRs on each of the eight 'Nonpareil' chromosomes represented by red and blue dots. The middle ring of each plot represents enrichment of hypermethylated DMRs across each chromosome, and the innermost

22 ring of each plot represents enrichment of hypomethylated DMRs across each chromosome.
23 Panel **a** shows the distribution of DMRs in the CG context, panel **b** shows distribution of DMRs
24 in the CHG context, and panel **c** shows distribution of DMRs in the CHH context.

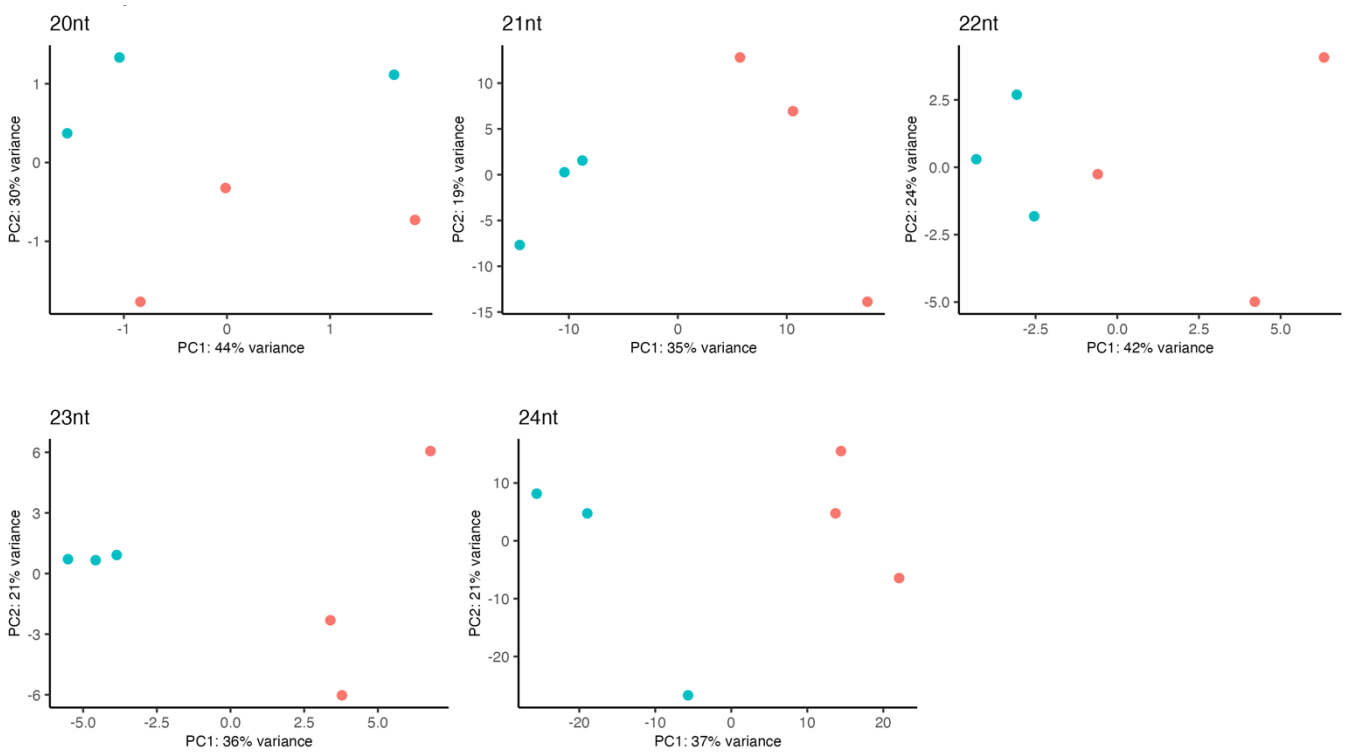
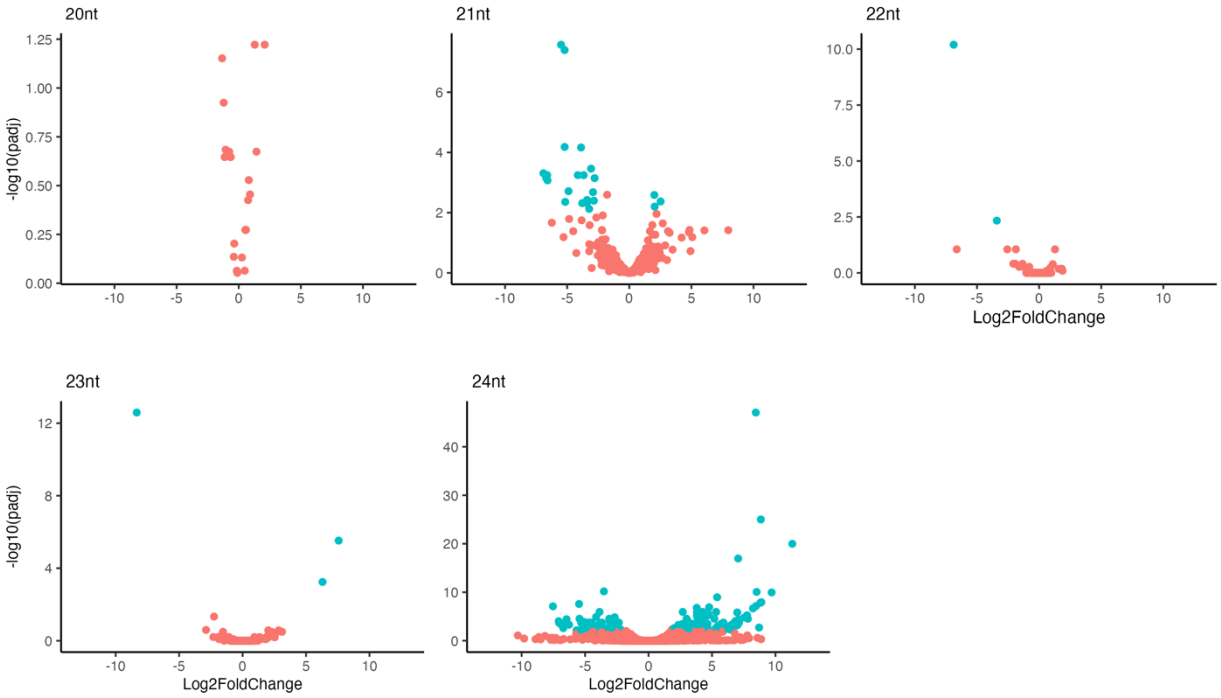


Fig 4. Analysis of small RNA expression profiles using principal component analysis following rlog transformation subset by the small RNA size (20, 21, 22, 23, and 24 nucleotides [nt]). All small RNA sizes with the exception of 22 nt show a cluster of 1-year-old individuals (pink) and 6-year-old (teal) individuals.

33



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36 **Fig 5.** A volcano plot shows differential expression patterns of individual small RNAs based on
37 size (20, 21, 22, 23, and 24 nucleotides [nt]), where a positive fold change indicates upregulation
38 of small RNAs in the 6-year-old cohort compared to the 1-year-old cohort. Pink dots represent
39 small RNAs that are not significantly differentially expressed, and teal dots represent small
40 RNAs that are significantly differentially expressed ($p < 0.01$).

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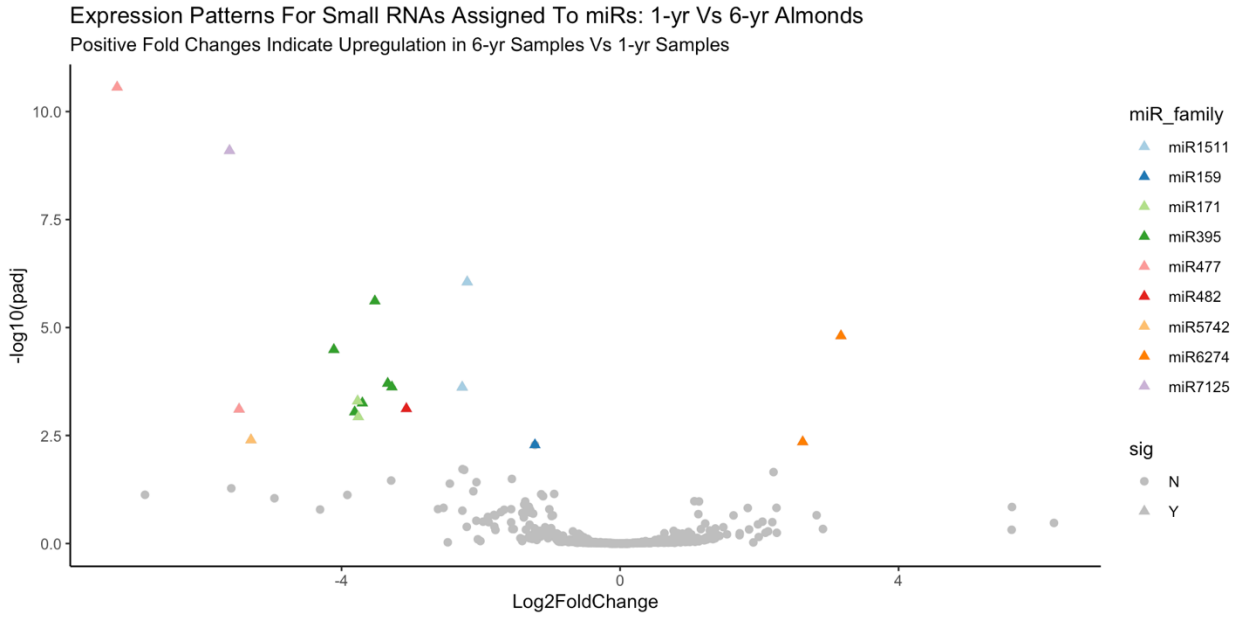

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47 **Fig 6.** Volcano plot depicting the 455 differentially expressed small RNAs that significantly
48 align to known microRNA families in the miRbase database based on BLAST analysis.
49 Significantly differentially expressed small RNAs are identified as triangles, and the associated
50 microRNA family based on significant BLAST alignment is indicated by color of the triangle.

Table 1. Number of identified differentially methylated regions (DMRs) in each methylation-context when comparing the three age cohorts. DMRs were identified with a threshold of $p \leq 0.0001$. DMRs are classified as hypermethylated if the percent methylation in that region is greater in the older age cohort compared to the younger age cohort within each contrast. DMRs are classified as hypomethylated if the percent methylation in that region is lesser in the older age cohort compared to the younger age cohort within each contrast. Hypermethylated DMR values in bold represent those with a cumulative binomial probability $< 1\times10^{-6}$.

Methylation Context	Contrast	Number of DMRs	Hypermethylated DMRs	Hypomethylated DMRs
CG	11-2	6479	**6232**	247
	11-7	2105	**1983**	122
	7-2	1211	**985**	226
CHG	11-2	1129	**763**	366
	11-7	485	252	233
	7-2	813	**524**	289
CHH	11-2	2059	**1690**	369
	11-7	567	216	351
	7-2	2259	**1849**	410

Table 2. Number of occurrences of overlap when comparing differentially methylated regions (DMRs) identified in each contrast to those identified in the other contrasts. The number of overlaps means the number of times a DMR in a particular age-contrast (e.g., 11-2) overlaps the genomic region of a DMR in one of the other age-contrasts (e.g., 11-7). The overall comparison indicates the number of DMRs occurring in overlapping genomic regions in all three contrasts. DMRs are classified as either hyper- or hypomethylated in each methylation context.

Methylation Context	Hyper/Hypo	11-2 ∗ 11-7	11-2 ∗ 7-2	11-7 ∗ 7-2	11-2 ∗ 11-7 ∗ 7-2
CG	Hyper	677	646	13	13
	Hypo	37	58	0	0
CHG	Hyper	75	161	3	3
	Hypo	74	62	0	0
CHH	Hyper	95	607	1	1
	Hypo	78	146	0	0

Table 3. Annotation of genes associated with 17 hypermethylated differentially methylated regions (DMRs) occurring in all three age cohort contrasts. The chromosome (chr) and genomic coordinates (start and end) of each gene are listed along with the gene identification from the 'Nonpareil' genome annotation. Protein identifiers from InterPro and Pfam databases are also included, as well as gene ontology (GO) terms associated with the gene.

Methylation Context	Chr	Start	End	GeneID	InterPro	Pfam	GO
CG	chr6	11481648	11484599	*BGLU12*: Beta-glucosidase	IPR001360	PF00232	GO:0004553 GO:0005975
	chr6	5122822	5124703	At3g47570: Probable LRR receptor-like serine/threonine-protein kinase	IPR001245 IPR001611 IPR013210	PF00560 PF07714 PF08263	GO:0004672 GO:0005515 GO:0006468
	chr8	14686870	14697541	Protein of unknown function1			
	chr1	36988003	36989001	*ESD4*: Ubiquitin-like-specific protease	IPR003653	PF02902	GO:0006508 GO:0008234
	chr1	17181984	17183843	Protein of unknown function2	IPR004252	PF03004	
	chr7	7732940	7736793	Protein of unknown function3			
	chr2	12422670	12423066	Protein of unknown function4			
	chr6	3439053	3439763	Protein of unknown function5	IPR009769	PF07059	
	chr8	7299785	7304401	*PS1*: FHA domain-containing protein	IPR000253 IPR002716	PF00498 PF13638	GO:0005515
	chr8	21331964	21333852	*Dctpp1*: dCTP pyrophosphatase 1	IPR025984	PF12643	GO:0009143 GO:0047429
	chr8	7041990	7043388	Protein of unknown function6			
	chr8	5019298	5021435	*TAR3*: Tryptophan aminotransferase-related protein 3	IPR006948	PF04864	GO:0016846
	chr1	1101269	1101943	Protein of unknown function7			

CHG	chr8	7202236	7205963	*FRS5*: Protein FAR1-RELATED SEQUENCE 5	IPR004330 IPR007527 IPR018289	PF03101 PF04434 PF10551 PF13561	GO:0008270
	chr3	20612169	20614252	*Ripk4*: Receptor-interacting serine/threonine-protein kinase 4	IPR020683 IPR026961	PF12796 PF13962	
	chr8	5019298	5021435	*TAR3*: Tryptophan aminotransferase-related protein 3	IPR006948	PF04864	GO:0016846
CHH	chr1	34468253	34469756	Protein of unknown function8			

Processing and Alignment of Enzymatic Methyl-Seq Libraries

Methyl-Seq read quality was initially assessed using FastQC v. 0.11.7 (Andrews, 2010), and reads were trimmed using TrimGalore v. 0.6.6 and Cutadapt v. 2.10 with default parameters (Krueger, 2016). Forward read fastq and reverse read fastq files from the two HiSeq4000 lanes were merged for each library to produce single fastq files for both read one and read two. Reads were aligned to the 'Nonpareil' v. 2.0 almond reference genome (D'Amico-Willman *et al.*, 2022), deduplicated, and methylation calls were generated using Bismark v. 0.22.3 (Krueger & Andrews, 2011) with default parameters in paired-end mode. To test conversion efficiency, reads were also aligned to both the Lambda and pUC19 nucleotide sequence fasta files provided by NEB (https://www.neb.com/tools-and-resources/interactive-tools/dna-sequences-and-maps-tool). All analyses were performed using the Ohio Supercomputer Center computing resources (Ohio Supercomputer Center, 1987).

Weighted Genome-wide Methylation Analysis of Age Cohorts

Weighted genome-wide percent methylation values were calculated for each individual within each cohort by taking the total number of methylated reads at each cytosine and dividing this by the total number of reads (methylated + unmethylated) at each cytosine. Weighted values were calculated for each methylation context. These values were used as input to R v. 4.0.2 (R Core Team, 2020) to perform beta regression using the package betareg v. 3.1-3 (Cribari-Neto & Zeileis, 2010). Pairwise comparison of least squared means was completed by the functions *emmeans()* and *cld()* from the R packages emmeans v. 1.5.2-1 and multcomp v. 1.4-14 with an alpha = 0.05 and Sidak adjustment (Hothorn *et al.*, 2008). The R package ggplot2 v. 3.3.2 was used to create plots for weighted percent methylation within each methylation context (Wickham, 2016). Files were then subset by chromosome (chr1 – chr8), and weighted percent

methylation values were calculated for all individuals by chromosome using the same formula as above for each methylation context. These values were used as input in R v. 4.0.2 (R Core Team, 2020) to perform beta regression and subsequent pairwise comparison of least squared means as performed above for the genome-wide weighted percent methylation values.

Differential Methylation Analysis of Age Cohorts

Coverage files for each methylation context produced by Bismark were prepared for input into the R package DSS (Dispersion Shrinkage for Sequencing Data) v. 2.38.0 (Wu *et al.*, 2013; Feng *et al.*, 2014; Park & Wu, 2016). The functions *DMLtest()* and *callDMR()* were used with a significance p.threshold set to 0.0001 to identify differentially methylated regions (DMRs) through pairwise comparisons between the three age cohorts. Comparisons were made relative to the oldest cohort in each DMR test (i.e., 11-year-old cohort relative to 2-year-old cohort).

Following identification of DMRs in each age contrast (11 – 2 years; 11 – 7 years; 7 – 2 years) and methylation context, DMRs were further characterized based on the directionality of differential methylation. Hypermethylated DMRs are those that show increased methylation in the oldest cohort in each contrast, and hypomethylated DMRs are those that show decreased methylation in the oldest cohort in each contrast. The cumulative binomial probability of identifying an equal or greater number of hypermethylated DMRs in each age contrast by methylation context was calculated using the R base package stats command *pbinom()* where x = the number of hypermethylated DMRs in each age contrast by methylation context, size = the total number of DMRs identified in each age contrast/methylation context, p = 0.5, and lower.tail = FALSE.

To visualize enrichment of DMRs across the eight chromosomes in the 'Nonpareil' genome, circos plots were generated with one track depicting each DMR classified as either

hyper- or hypomethylated and two additional tracks depicting DMR enrichment across the genome. To create the circos plots, the R package circlize v. 0.41.2 (Gu *et al.*, 2014) was used along with the bed files for all hyper- and hypomethylated DMRs in each methylation context for all age contrasts. The command *circos.genomicRainfall()* was used to create the first track with dots representing each individual DMR (red – hypermethylated, blue – hypomethylated) and positioned based on the number of DMRs occurring in that location. The command *circos.genomicDensity()* was used to create the two additional tracks representing enrichment of hyper- and hypomethylated DMRs on each chromosome where the taller the peak, the higher the number of DMRs occurring in the specific region (Gu *et al.*, 2014).

Following classification into hyper- and hypomethylated regions, bed files were generated for these DMRs using genomic coordinates. These bed files were used as input along with the 'Nonpareil' genome annotation file into the R v. 4.0.2 (R Core Team, 2020) packages GenomicRanges v. 1.40.0 (Lawrence *et al.*, 2013) and genomation v. 1.20.0 (Akalin *et al.*, 2015) to prepare a GRanges object and annotate DMRs using the command *annotateWithFeatures()*. Initial annotation of DMRs by features includes the percentage of DMRs overlapping one of four features: gene, exon, 5' untranslated region (UTR), and 3' UTR. The DMRs were further annotated, and gene ontology (GO) enrichment was performed using the software HOMER v. 4.11 (Heinz *et al.*, 2010) and the R package topGO v. 2.40.0 (Alexa A, 2020). Initially, all DMRs were annotated by assigning the gene with the closest transcriptional start site to each DMR using *annotatePeaks.pl -noann* with the 'Nonpareil' genome and genome annotation files. This produced a list of gene identifiers from the genome annotation file that are associated with each DMR. The GO terms assigned to each DMR-associated gene were used as input along with the 'Nonpareil' genomic annotation file to determine enrichment of GO terms in each age contrast

DMR-associated gene set. The DMR-associated genes in each methylation context were classified based on biological process, molecular function, and cellular component GO term to produce tables depicting the number of DMR-associated genes assigned to each descriptor.

The DMRs were then further classified based on the occurrence of overlapping genomic regions among DMRs when comparing age contrasts. The bed files generated above were used as input in the bedtools v. 2.29.2 (Quinlan & Hall, 2010) command *intersect -wao* to identify overlaps in DMRs from each of the age contrasts (i.e., 11-7 contrast compared to 11-2 contrast). Finally, genomic regions were identified that contain significant DMRs in all three age contrasts using bedtools *intersect*. A similar process was used to determine DMRs overlapping transposable elements between two age cohorts (2-year-old *vs.* 7-year-old) using the annotation file to determine the most likely transposable element using EDTA ver. 2.0.0 (Ou et al., 2019) The DMRs overlapping genes were annotated using the *annotatePeaks.pl* script as above to find DMR-associated genes as well as GO terms, Pfam identifiers, and Interpro identifiers associated with each gene. The genomic DMR sequence was extracted from the 'Nonpareil' genome fasta file, and individual DMR fasta files were searched against the miRbase database v. 22.1 (Kozomara *et al.*, 2019) using blastn (Camacho *et al.*, 2009) to identify any putative microRNAs (miRNAs) within those regions. Searches were performed using an e-value cutoff of 1 after filtering the blast database to include only the following genera: *Arabidopsis*, *Prunus*, *Malus*, *Glycine*, *Medicago*, *Populus*, and *Solanum*.

Hits were subsequently filtered based on length of the putative microRNA within each DMR sequence with a cutoff of n – 2 base pairs based on the length of the identified putative microRNA within the database. A further filtering step was performed based on the e-value of the hits returning only those microRNAs with the lowest e-value for each potential match to the

DMR sequences. This process resulted in at least one microRNA representing the best hit for each putative microRNA sequence within each DMR. In some cases, more than one best hit is returned if the e-values are equal for more than one hit.

Annotation of unknown protein sequences associated with DMRs

A total of eight unknown proteins were identified as associated with the DMRs shared between the three age contrasts. Several programs were used to annotate these protein sequences and determine additional information about their putative functions. The program ProtParam was used to characterize protein properties, including molecular weight (Gasteiger *et al.*, 2005). To predict subcellular localization, the program YLoc was used (Briesemeister *et al.*, 2010a,b). Finally, the Motif tool on the GenomeNet website (https://www.genome.jp/tools/motif/) was used to search a protein query against several databases to identify putative alignments (Marchler-Bauer *et al.*, 2013; Sigrist *et al.*, 2013; Finn *et al.*, 2014).

Small RNA-Seq Differential Expression Analysis

Following sequencing, Trimmomatic (Bolger, 2014) was run in single end mode to remove adaptor sequences and trim low-quality bases from the ends of raw reads. The expected adaptor sequence was '*AGATCGGAAGAGCACACGTCTGAACTCCAGTCAC.*' Values for the seed mismatch, palindrome clip threshold, and simple clip threshold parameters within the ILLUMINACLIP argument were set to 2, 30, and 6, respectively. Other options passed to Trimmomatic included LEADING:3, TRAILING:3, SLIDINGWINDOW:6:20, and MINLEN:12. Trimmed reads were aligned to the '*Prunus dulcis* Nonpareil' reference genome (D'Amico-Willman *et al.*, 2022) with Shortstack v3.8.5 (Johnson *et al.*, 2016) using default parameters. All aligned small RNA sequences were obtained and used as input for a Blast analysis.

A custom Blast database was generated by downloading the mature miRNA database from miRbase and filtering it for entries associated with the genera *Prunus*, *Arabidopsis*, *Malus*, *Glycine*, *Medicago*, *Populus*, or *Solanum*. The aligned small RNA sequences were searched against this custom database using the blastn function within Blast 2.10.0+ (Camacho, 2009) with the following settings: -evalue: 1, -task: blasn-short, -word_size: 4, -gapopen: 25, -gapextend: 10, -reward: 5, -penalty: 4, -dust: no, and -soft_masking: false. The initial set of Blast hits was filtered to retain only those that had an aligned length no less than (mature miR length – 2). For each unique query sequence, the hit with the best (lowest) e-value was retained, and results were categorized into miRNA families.

The counts table obtained from ShortStack was used as input to DESeq2 (Love *et al.*, 2014) to test each aligned small RNA for evidence of differential expression between the two age groups. Significant differentially expressed genes were defined as those with an absolute log2 fold change >2 and an adjusted p-value <0.01.

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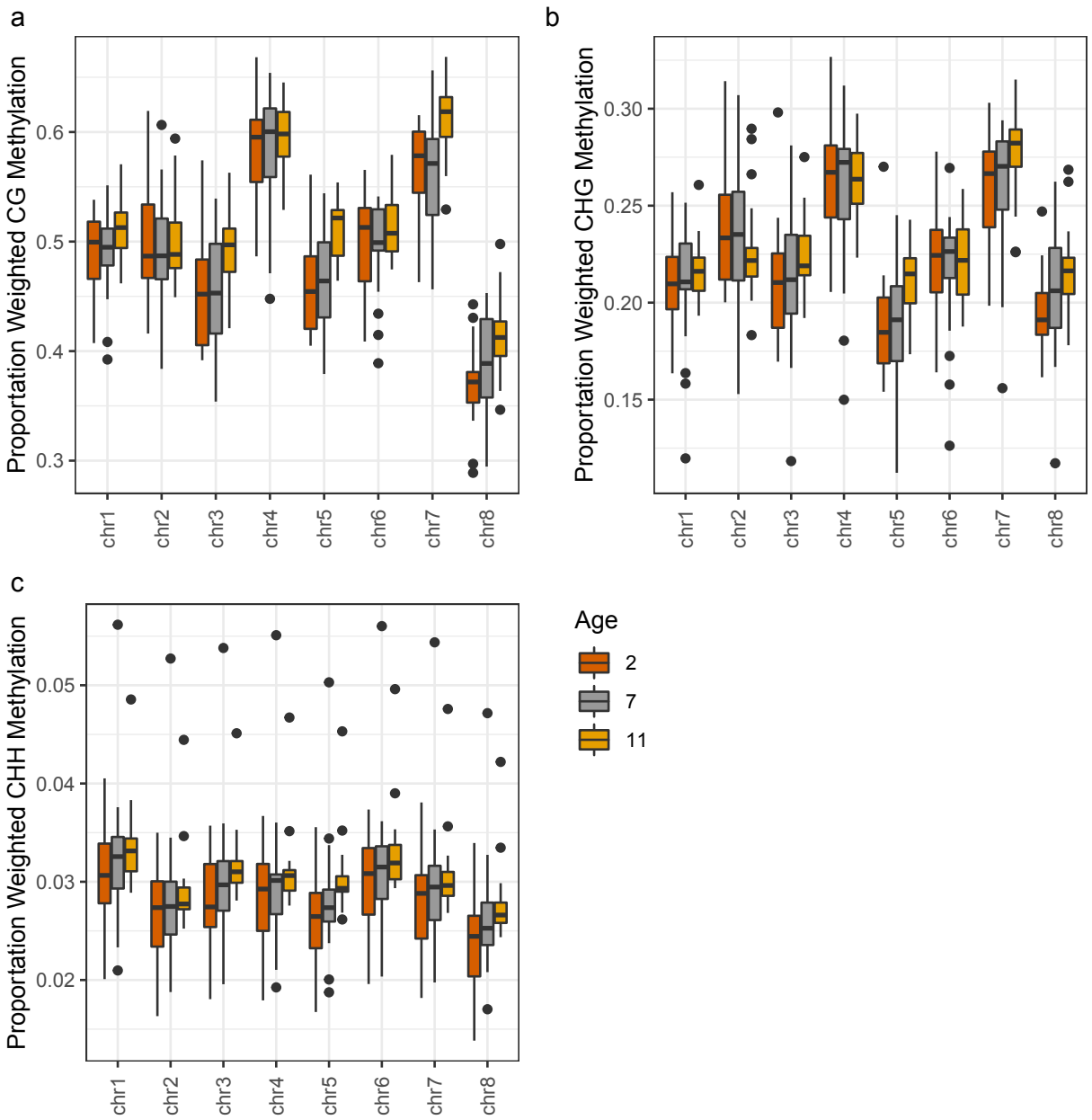


Figure S1. Boxplots depicting the proportion of weighted methylation in each age cohort (2 years old – red; 7 years old – grey; 11 years old – yellow) across the three methylation contexts: **(a)** CG, **(b)** CHG, and **(c)** CHH. The black dots represent outliers.

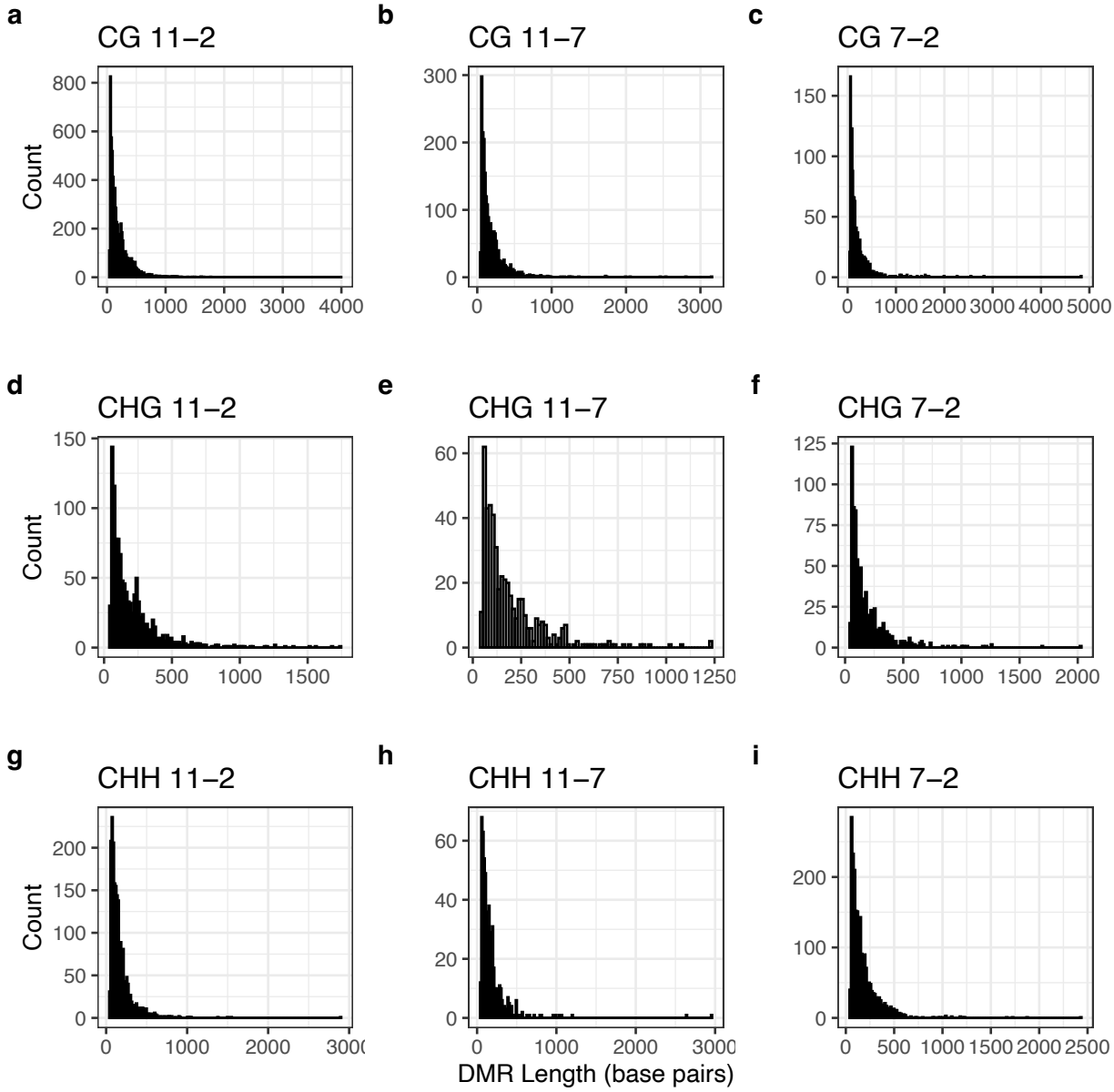


Figure S2a-l. Distribution of lengths in base pairs of differentially methylated regions (DMRs) identified in each age contrast and methylation context. Panels **a-c** show distribution of DMRs identified in the CG context, panels **d-f** show distribution in the CHG context, and panels **g-l** show distribution in the CHH context. The values listed next to the methylation context indicate the age-contrast (11 – 2 year, 11 – 7 year, and 7 – 2 year).

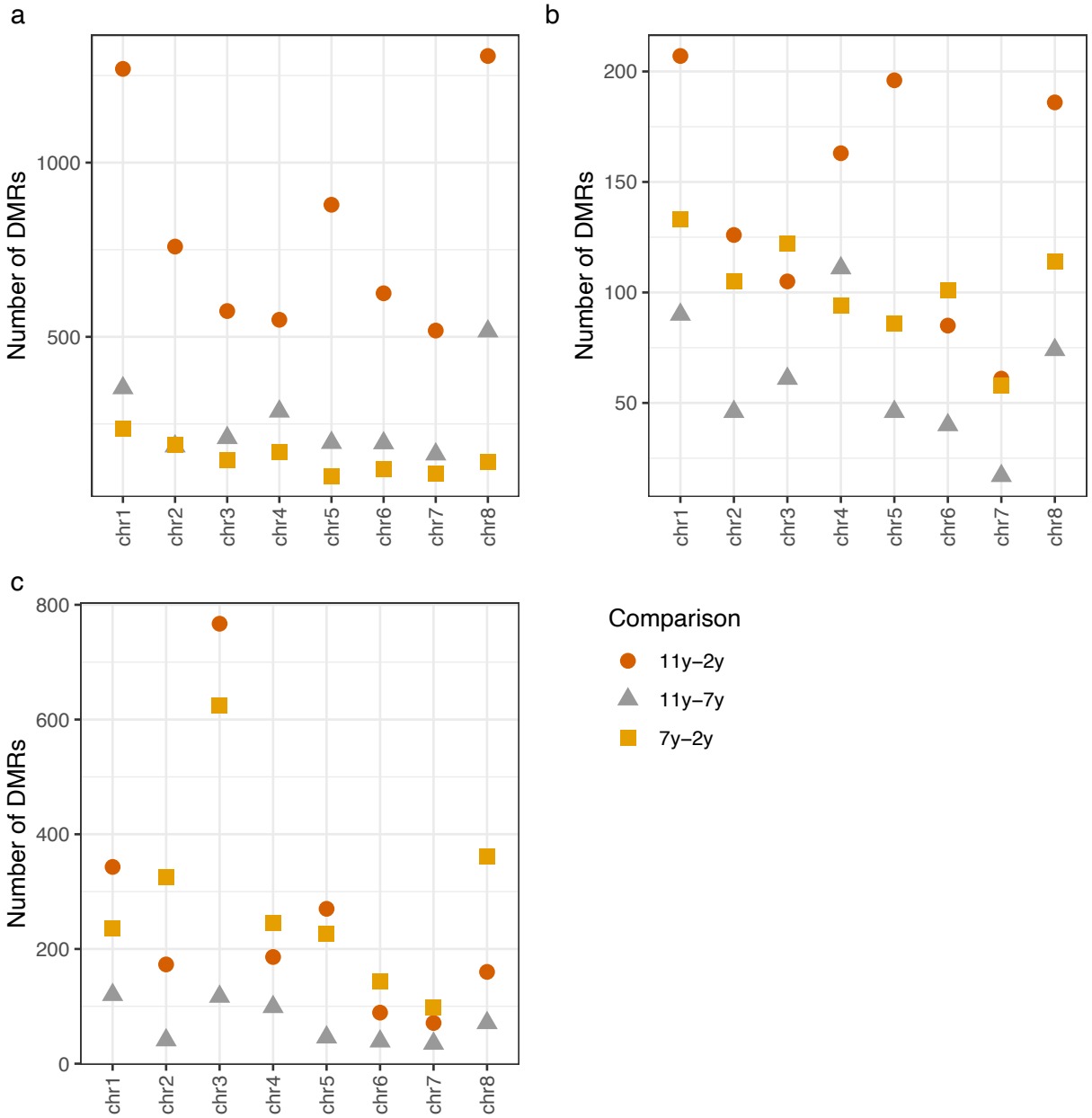
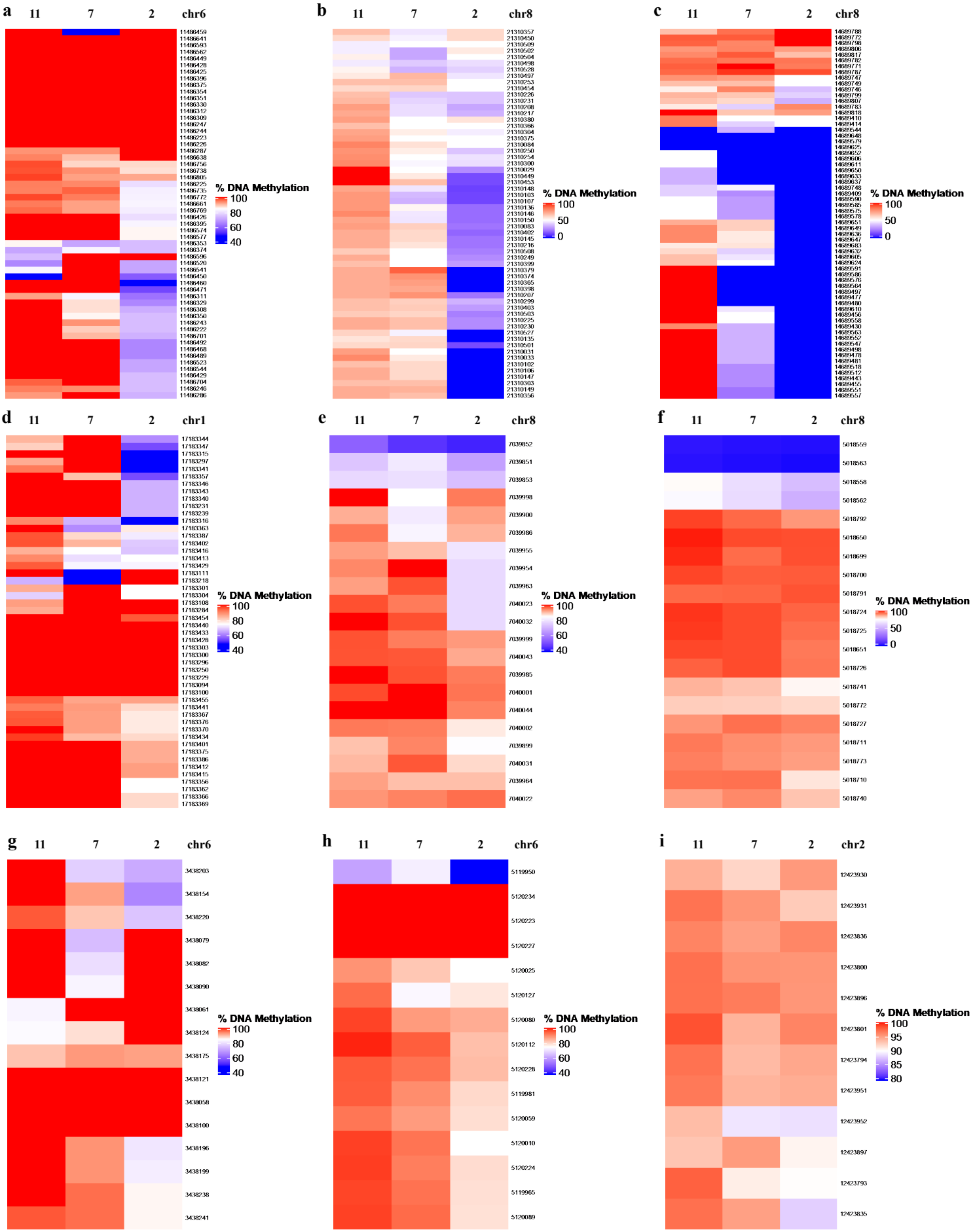


Figure S3a-c. The dot plots represent the number of significant ($p < 0.0001$) differentially methylated regions (DMRs) identified in each of the contrasts (11 – 2 years: red; 11 – 7 years: grey; 7 – 2 years: yellow) in each methylation-context: **(a)** CG, **(b)** CHG, and **(c)** CHH.


a
11
7
2
chr6
% DNA Methylation
100
80
60
40
b
11
7
2
chr8
% DNA Methylation
100
50
0
c
11
7
2
chr8
% DNA Methylation
100
50
0
d
11
7
2
chr1
% DNA Methylation
100
80
60
40
e
11
7
2
chr8
% DNA Methylation
100
80
60
40
f
11
7
2
chr8
% DNA Methylation
100
50
0
g
11
7
2
chr6
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80
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7
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11
7
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chr2
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100
95
90
85
80

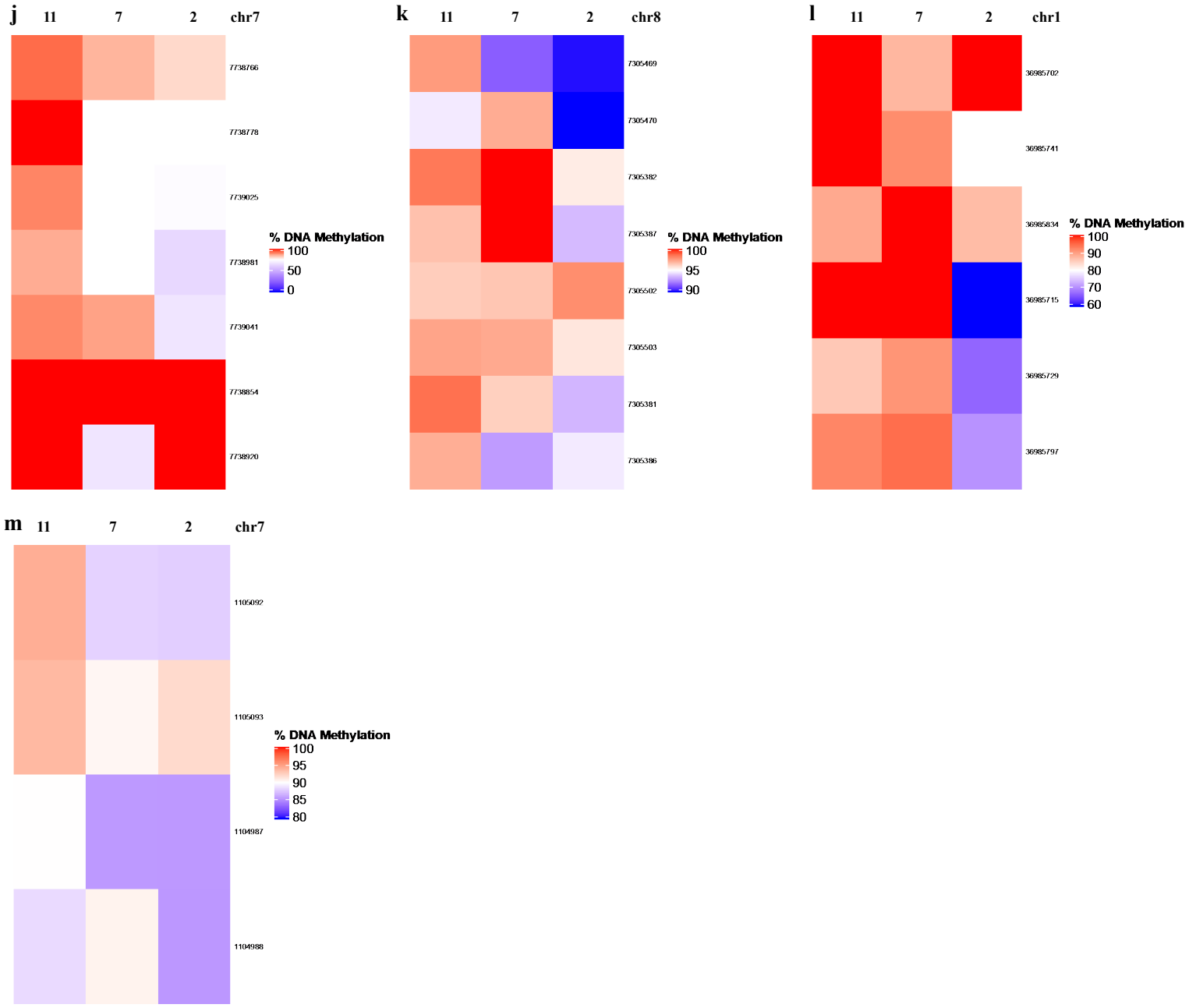

Figure S4a-m. Heatmaps displaying average percent DNA methylation across cytosines in the 11-year, 7-year, and 2-year age cohorts within the genomic range of 13 overlapping differentially methylated regions (DMRs) in the CG context identified in the three age-contrasts. The regions correspond to CGDMR1-13 **(a-m; see Table S2),** and the values to the right of each heatmap represent the genomic position of each cytosine on the respective chromosome.

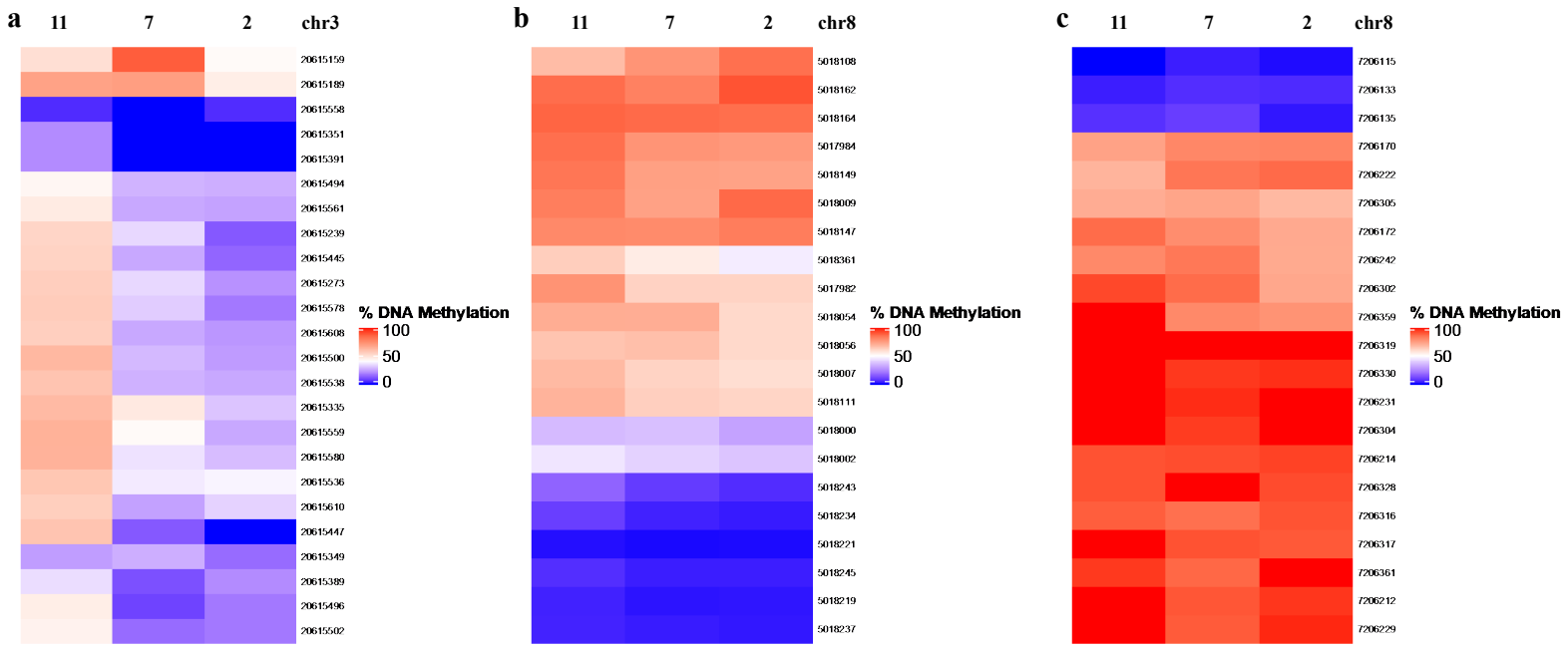

Figure S5a-c. Heatmaps displaying average percent DNA methylation across cytosines in the 11-year, 7-year, and 2-year age cohorts within the genomic range of 3 overlapping differentially methylated regions (DMRs) in the CHG context identified in the three age-contrasts. The regions correspond to CHGDMR1-3 **(a-c; see Table S2),** and the values to the right of each heatmap represent the genomic position of each cytosine on the respective chromosome.

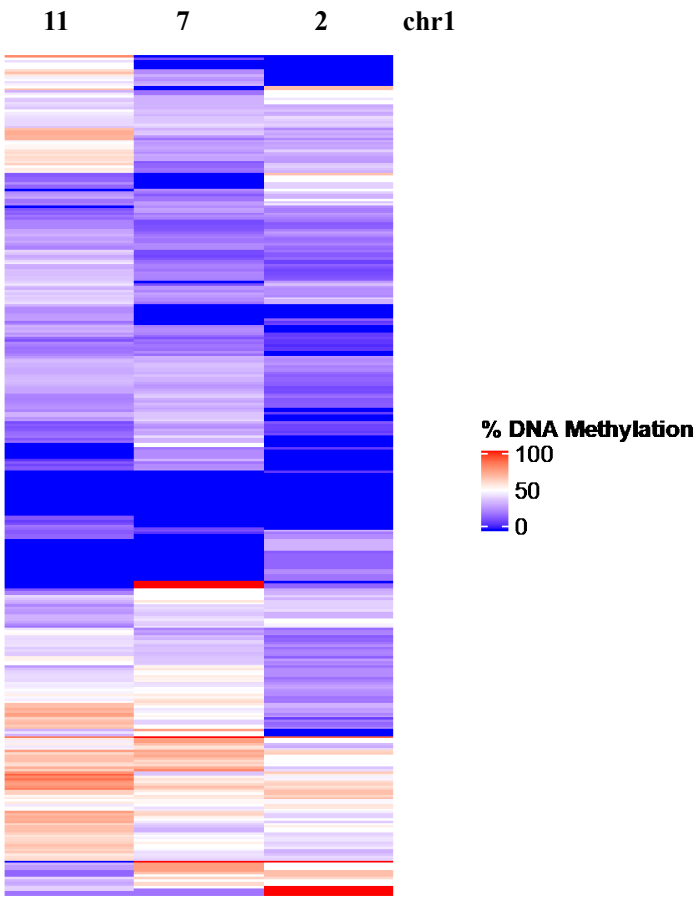

Figure S6. Heatmap displaying average percent DNA methylation across cytosines in the 11-year, 7-year, and 2-year age cohorts within the genomic range of the overlapping differentially methylated region (DMR) in the CHH context identified in the three age-contrasts. The regions correspond to CHHDMR1 **(see Table S2)**.

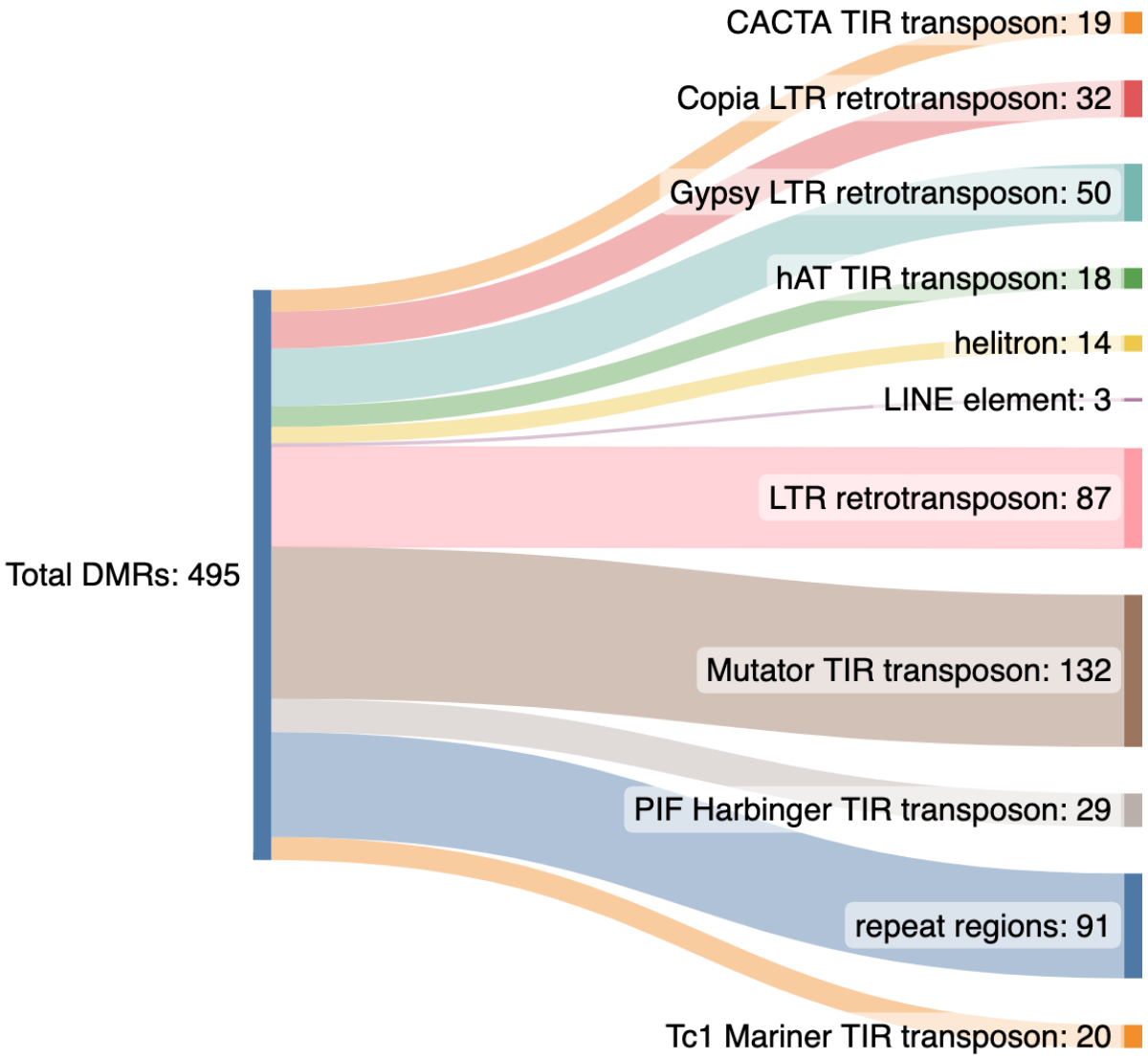

Figure S7. Distribution by type of transposable elements overlapping with 493 differentially methylated regions (DMRs) identified in the 2 – 7-year-old age contrast.

Table S1. Pairwise comparison of least squared means of weighted percent methylation in the CG, CHG, and CHH contexts for each chromosome in the 'Nonpareil' almond genome. Age cohort contrasts include the 2 – 11, the 7 – 11, and the 2 – 7-year contrasts. Significant contrasts are represented in bold with an alpha = 0.05.

Chromosome	Age-Contrast	CG context p-value	CHG context p-value	CHH context p-value
Chr1	11-2	**0.0235**	0.5329	0.0595
	11-7	**0.0422**	0.4425	0.7068
	7-2	0.9436	0.9949	0.2780
Chr2	11-2	0.9973	0.3587	0.1320
	11-7	0.7356	0.9063	0.6008
	7-2	0.7924	0.5948	0.5698
Chr3	11-2	**0.0020**	0.2137	**0.0138**
	11-7	**0.0046**	0.1647	0.3543
	7-2	0.9267	0.9980	0.2883
Chr4	11-2	0.6659	0.9917	0.0972
	11-7	0.5390	0.8626	0.6030
	7-2	0.9867	0.8071	0.4789
Chr5	11-2	**<.0001**	**0.0056**	**0.0020**
	11-7	**<.0001**	**0.0049**	0.1935
	7-2	0.8706	0.9954	0.1873
Chr6	11-2	0.3472	0.9922	0.0675
	11-7	0.1645	0.7924	0.5824
	7-2	0.9342	0.8679	0.4042
Chr7	11-2	**0.0003**	0.0658	0.0956
	11-7	**0.0002**	**0.0263**	0.7183
	7-2	0.9963	0.9676	0.3716
Chr8	11-2	**0.0004**	**0.0163**	**0.0055**
	11-7	**0.0295**	0.1837	0.4246
	7-2	0.3440	0.5279	0.1329

Table S2. Genomic coordinates and length in base pairs for the 17 overlapping DMRs occurring in each of the three age-contrasts.

		11-2			11-7			7-2		
DMR_ID	**Chr**	**Start**	**End**	**Length (bp)**	**Start**	**End**	**Length (bp)**	**Start**	**End**	**Length (bp)**
CGDMR1	6	11486222	11486807	585	11486637	11486807	170	11486637	11486807	170
CGDMR2	8	21310028	21310528	500	21310028	21310149	121	21310028	21310403	375
CGDMR3	8	14689409	14689818	409	14689430	14689807	377	14689477	14689547	70
CGDMR4	1	17183093	17183455	362	17183249	17183343	94	17183249	17183315	66
CGDMR5	8	7039851	7040044	193	7039954	7040044	90	7039899	7040044	145
CGDMR6	8	5018558	5018792	234	5018650	5018792	142	5018740	5018792	52
CGDMR7	6	3438057	3438262	205	3438026	3438089	63	3438057	3438174	117
CGDMR8	6	5119949	5120234	285	5119949	5120126	177	5119949	5120126	177
CGDMR9	2	12423793	12423952	159	12423835	12423931	96	12423896	12423952	56
CGDMR10	7	7738726	7739046	320	7738980	7739046	66	7738980	7739046	66
CGDMR11	8	7305381	7305503	122	7305386	7305503	117	7305381	7305503	122
CGDMR12	1	36985701	36985875	174	36985796	36985875	79	36985796	36985875	79
CGDMR13	1	1104987	1105093	106	1104987	1105093	106	1104987	1105093	106
CHGDMR1	3	20615159	20615610	451	20615337	20615502	165	20615337	20615391	54
CHGDMR2	8	5017982	5018361	379	5018000	5018056	56	5018000	5018056	56
CHGDMR3	8	7206115	7206361	246	7206170	7206242	72	7206170	7206231	61
CHHDMR1	1	34468252	34469756	1504	34469043	34469756	713	34468083	34469120	1037

Table S3. Annotation of hyper- and hypomethylated differentially methylated regions (DMRs) in each methylation context and for each age-contrast. The 'Nonpareil' genome annotation was used to classify the DMRs into four categories: gene, exon, five prime untranslated region (5' UTR), and three prime untranslated region (3' UTR). The percentages under each classification represent the percentage of DMRs from each methylation-context and contrast in each of the four categories.

Methylation Context	Hyper/Hypo	Contrast	%Gene	%Exon	%5' UTR	%3' UTR
CG	Hyper	11 – 2	28.0	20.6	0.91	0.96
		11 – 7	34.2	25.1	1.51	1.46
		7 – 2	27.8	21.4	0.81	1.32
	Hypo	11 – 2	39.7	31.2	7.29	1.21
		11 – 7	22.1	14.8	0.82	3.28
		7 – 2	29.2	22.1	2.65	0.88
CHG	Hyper	11 – 2	27.7	20.1	2.49	1.70
		11 – 7	24.6	18.3	3.17	1.98
		7 – 2	24.8	17.2	1.91	0.76
	Hypo	11 – 2	23.5	17.8	3.28	1.37
		11 – 7	27.9	18.5	3.00	2.58
		7 – 2	19.4	13.8	2.77	0
CHH	Hyper	11 – 2	18.0	9.41	1.60	2.13
		11 – 7	19.0	12.0	0.46	1.39
		7 – 2	17.9	9.20	1.35	2.16
	Hypo	11 – 2	27.4	14.6	3.25	1.63
		11 – 7	24.5	14.0	3.99	1.99
		7 – 2	24.4	14.2	1.22	1.22

Table S4a-c. Number of CG hypermethylated DMR-associated genes associated with each biological process (**A**), molecular function **(B)**, and cellular component **(C)** gene ontology (GO) terms for each of the three age-contrasts (i.e., 11 – 2 year, 11 – 7 year, and 7 – 2 year). Values in each column represent the number of DMR-associated genes that are associated with each GO term. Black squares indicate no genes associated with that contrast were assigned the particular GO term.

A. Biological Process GO Term	**11-2**	**11-7**	**7-2**
proteolysis	37	36	8
protein phosphorylation	29	28	7
obsolete oxidation-reduction process	28	22	4
transmembrane transport	18	16	4
regulation of transcription, DNA-templated	9	13	2
carbohydrate metabolic process	10	11	4
steroid biosynthetic process	5		
tRNA aminoacylation for protein translation	3		
signal transduction	1	8	
translation	2	8	
biosynthetic process	1	7	
transcription, DNA-templated	1	7	1
DNA topological change		6	
cation transport	2	4	
endoplasmic reticulum to Golgi vesicle-mediated transport		3	
nitrogen compound metabolic process		3	1
proteolysis involved in cellular protein catabolic process		3	
tRNA processing	3	3	
ATP synthesis coupled proton transport		2	
attachment of GPI anchor to protein		2	
cell redox homeostasis		2	
cell wall modification		2	
defense response		2	
fatty acid biosynthetic process		2	
histone lysine methylation	2		
lipid metabolic process	1	2	
metal ion transport		2	
nucleotide-excision repair	2		
proteasome-mediated ubiquitin-dependent protein catabolic process	2		
recognition of pollen		2	
translational initiation		2	
cell wall macromolecule catabolic process		1	
cellular glucan metabolic process		1	
cellular modified amino acid biosynthetic process	1	1	

cellulose biosynthetic process	1		1
chitin catabolic process		1	
dephosphorylation		1	
DNA replication		1	
DNA-templated transcription, termination	1		
drug transmembrane transport		1	
endoplasmic reticulum organization		1	
fatty acid beta-oxidation	2	1	
glutamine biosynthetic process		1	
intermembrane lipid transfer		1	
intracellular protein transport		1	
intracellular transport		1	
ion transport		1	
malate transport	1		
mitochondrial pyruvate transmembrane transport		1	
mRNA processing		1	
nucleobase-containing compound metabolic process		1	
nucleotide transmembrane transport		1	
nucleotide transport			1
nucleosome assembly		1	
phosphatidylserine biosynthetic process		1	
photosynthesis	1		
photosynthesis, light reaction		1	
photosynthetic electron transport in photosystem II		1	
phytochromobilin biosynthetic process		1	
potassium ion transport		1	
protein folding	2	1	
protein kinase C-activating G protein-coupled receptor signaling pathway	1		
protein neddylation		1	
protein ubiquitination	1	1	
proton transmembrane transport	1		
pseudouridine synthesis			1
pyrimidine nucleotide-sugar transmembrane transport		1	
regulation of translational fidelity	1		
response to auxin			1
response to hormone		1	
RNA modification			1
RNA processing		1	
rRNA processing		1	
sucrose metabolic process		1	1
translation termination			1
terpenoid biosynthetic process	1		
trehalose biosynthetic process	1		
tRNA wobble uridine modification		1	

B. Molecular Function GO Term	11-2	11-7	7-2
ATP binding	41	33	11
cysteine-type peptidase activity	36	32	8
hydrolase activity, acting on ester bonds	26	28	4
protein binding	35	27	10
protein kinase activity	18	26	5
DNA binding	13	20	5
zinc ion binding	20	20	7
ADP binding	3	18	
nucleic acid binding	18	16	3
oxidoreductase activity	3	13	1
transferase activity, transferring hexosyl groups		11	3
catalytic activity	4	9	
DNA-binding transcription factor activity	7	8	1
structural constituent of ribosome	2	8	
DNA topoisomerase activity		6	
transmembrane transporter activity	3	6	1
hydrolase activity, hydrolyzing O-glycosyl compounds	6	5	2
polygalacturonase activity	4	5	2
RNA binding	1	5	1
sequence-specific DNA binding	1	5	
transferase activity, transferring acyl groups other than amino-acyl groups	3	5	1
acetylglucosaminyltransferase activity	1	4	
aminoacyl-tRNA ligase activity	3		
DNA-directed 5'-3' RNA polymerase activity	1	4	1
heme binding	10	4	
iron ion binding	10	4	
lyase activity	4	4	
magnesium ion binding	4	4	
nucleotide binding	3		
oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	9	4	
phosphatidylinositol binding			4
protein dimerization activity	4	4	1
RNA-DNA hybrid ribonuclease activity	10	4	2
solute:proton antiporter activity	1	4	
terpene synthase activity	4	4	
GTP binding	4	3	1
GTPase activity		3	1
hydrolase activity	1	3	
oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	5	3	
threonine-type endopeptidase activity		3	
3-beta-hydroxy-delta5-steroid dehydrogenase activity	5		

ATPase activity	7	2	1
calcium ion binding	1	2	
copper ion binding	1	2	
damaged DNA binding	2		
electron transfer activity		2	
enzyme inhibitor activity	2	2	
histone-lysine N-methyltransferase activity	2		
metal ion binding		2	
methyltransferase activity	2	2	
nickel cation binding		2	
nutrient reservoir activity	2		1
O-methyltransferase activity	1	2	
obsolete coenzyme binding	2	2	
oxidoreductase activity, acting on NAD(P)H, oxygen as acceptor	1	2	
pectinesterase activity		2	
peroxidase activity	2	2	
protein disulfide oxidoreductase activity		2	
protein serine/threonine kinase activity	11	2	2
proton transmembrane transporter activity		2	
serine-type carboxypeptidase activity		2	
serine-type endopeptidase activity	2	2	
transcription factor binding	2		
transferase activity, transferring acyl groups	2		1
translation initiation factor activity		2	
2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase activity	1		
3'-5' exonuclease activity		1	
acetyl-CoA carboxylase activity		1	
acyl-CoA oxidase activity	2	1	
antioxidant activity		1	
antiporter activity	1	1	
ATPase-coupled transmembrane transporter activity	5	1	1
ATP:ADP antiporter activity			1
cation transmembrane transporter activity	1		
cellulose synthase (UDP-forming) activity	1		1
channel activity	1	1	
chitin binding		1	
chitinase activity		1	
cobalt ion binding		1	
diacylglycerol kinase activity	1		
DNA-directed DNA polymerase activity		1	
electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity		1	
endonuclease activity		1	
endopeptidase inhibitor activity	1	1	
FAD binding	1		

glutamate-ammonia ligase activity		1	
glutamate-cysteine ligase activity	1	1	
glycerol-3-phosphate O-acyltransferase activity	1		
GTPase activator activity	1	1	
helicase activity		1	
inorganic diphosphatase activity	1		
intramolecular lyase activity		1	
intramolecular transferase activity, phosphotransferases		1	
ion channel activity		1	
lipid binding		1	
lipid transfer activity		1	
iron-sulfur cluster binding	1		
malate dehydrogenase (decarboxylating) (NAD+) activity		1	
metal ion transmembrane transporter activity		1	
metallopeptidase activity		1	
NAD binding		1	
NEDD8 activating enzyme activity		1	
nucleoside transmembrane transporter activity		1	
oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen		1	
oxidoreductase activity, acting on the CH-CH group of donors	2	1	
oxidoreductase activity, acting on the CH-CH group of donors, iron-sulfur protein as acceptor		1	
peptide-methionine (S)-S-oxide reductase activity	4	1	
peptidyl-prolyl cis-trans isomerase activity		1	
phospho-N-acetylmuramoyl-pentapeptide-transferase activity		1	
polysaccharide binding		1	
protein tyrosine/serine/threonine phosphatase activity		1	
pseudouridine synthase activity			1
pyridoxal phosphate binding	1	1	
pyrimidine nucleotide-sugar transmembrane transporter activity		1	
pyrophosphate hydrolysis-driven proton transmembrane transporter activity	1		
racemase activity, acting on amino acids and derivatives			1
strictosidine synthase activity		1	
sucrose synthase activity		1	1
translation release factor activity			1
ubiquitin-like modifier activating enzyme activity		1	
ubiquitin-protein transferase activity	1	1	
unfolded protein binding	2	1	
uridylyltransferase activity		1	
xyloglucan:xyloglucosyl transferase activity		1	

C. Cellular Component GO Term	11-2	11-7	7-2
integral component of membrane	16	18	4
membrane	10	16	4
nucleus	5	9	2
ribosome	2	8	
endoplasmic reticulum	2		
endoplasmic reticulum membrane		4	
proteasome core complex		3	
cytoplasm		2	
GPI-anchor transamidase complex		2	
mitochondrial proton-transporting ATP synthase complex, coupling factor F(o)		2	
nucleolus	2		
nucleosome		2	
acetyl-CoA carboxylase complex		1	
apoplast		1	
cell wall		1	
chromosome		1	
elongator holoenzyme complex		1	
Golgi membrane		1	
Las1 complex		1	
mitochondrial inner membrane		1	
nuclear pore		1	
peroxisome	2	1	
photosystem I	1		
photosystem I reaction center	1		

Table S5a-c. Number of CG hypomethylated DMR-associated genes associated with each biological process (**A**), molecular function **(B)**, and cellular component **(C)** gene ontology (GO) terms for each of the three age-contrasts (i.e., 11 – 2 year, 11 – 7 year, and 7 – 2 year). Values in each column represent the number of DMR-associated genes that are associated with each GO term. Black squares indicate no genes associated with that contrast were assigned the particular GO term.

A. Biological Process GO Term	**11-2**	**11-7**	7-2
protein phosphorylation	5	1	8
proteolysis	4		7
cell redox homeostasis	3	1	
regulation of transcription, DNA-templated	3	2	7
cellulose biosynthetic process	2		1
obsolete oxidation-reduction process	2	2	12
signal transduction	2		
translational elongation	2		
transmembrane transport	2	1	
tRNA aminoacylation for protein translation	2	1	
ubiquitin-dependent protein catabolic process			2
ATP synthesis coupled proton transport	1		
biosynthetic process	1		1
carbohydrate metabolic process	1	1	4
carboxylic acid metabolic process			1
cell wall modification			1
defense response			1
detection of visible light	1		
dolichol-linked oligosaccharide biosynthetic process	1		1
glutaminyl-tRNA aminoacylation	1		
Golgi vesicle transport	1	1	
histone lysine methylation	1		
intracellular protein transport	1		
photosynthesis			1
protein-chromophore linkage	1		
protein ubiquitination			1
proteolysis involved in cellular protein catabolic process			1
response to oxidative stress			1
transcription, DNA-templated			1
translation	1	2	3
trehalose biosynthetic process	1		1
tRNA aminoacylation	1		
tRNA aminoacylation for protein translation			1

B. Molecular Function GO Term	11-2	11-7	7-2
protein binding	13	3	14
ATP binding	8	4	9
protein kinase activity	5	1	8
cysteine-type peptidase activity	4		7
heme binding	1	2	7
DNA binding	1	2	6
iron ion binding	1	2	6
oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	1	2	6
transferase activity, transferring hexosyl groups	1	1	5
zinc ion binding	5	1	5
catalytic activity	4	3	4
DNA-binding transcription factor activity	1	1	4
hydrolase activity, hydrolyzing O-glycosyl compounds			4
electron transfer activity	3	1	
nucleic acid binding	4	1	3
oxidoreductase activity	1		3
protein disulfide oxidoreductase activity	3		
sequence-specific DNA binding	1		3
structural constituent of ribosome	1	2	3
acetylglucosaminyltransferase activity			2
ADP binding	1	1	2
carbohydrate binding	2	1	
GTP binding		1	2
pyridoxal phosphate binding	1		2
RNA-DNA hybrid ribonuclease activity			2
translation elongation factor activity	2		
transmembrane transporter activity	1		2
actin binding			1
aminoacyl-tRNA ligase activity	2	1	1
ATPase activity	1	1	
ATPase-coupled transmembrane transporter activity	1	1	
calcium ion binding			1
carbon-sulfur lyase activity			1
carbonate dehydratase activity	1		1
carboxy-lyase activity			1
cellulose synthase (UDP-forming) activity	2		1
channel activity			1
copper ion binding			1
DNA-directed 5'-3' RNA polymerase activity			1
double-stranded DNA binding			1
endopeptidase activity			1
enzyme inhibitor activity			1
flavin adenine dinucleotide binding			1

galactose binding	1		
glutamine-tRNA ligase activity	1		
GTPase activity		1	
histone-lysine N-methyltransferase activity	1		
hydrolase activity			1
hydrolase activity, acting on ester bonds			1
kinase activity			1
Lys48-specific deubiquitinase activity		1	
lyase activity	1	2	
magnesium ion binding	1	2	
manganese ion binding			1
metal ion binding			1
metallopeptidase activity			1
methyltransferase activity	1	1	
nucleotide binding	2	1	1
obsolete coenzyme binding			1
oxidoreductase activity, acting on CH-OH group of donors			1
oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	1		1
pectinesterase activity			1
peroxidase activity			1
phospho-N-acetylmuramoyl-pentapeptide-transferase activity			1
phospholipid bidning		1	
phosphorelay sensor kinase activity	1		
polygalacturonase activity	1	1	1
protein dimerization activity		1	1
protein-containing complex binding			1
proton-transporting ATP synthase activity, rotational mechanism	1		
RNA binding	1	1	
serine-type endopeptidase activity	1		
terpene synthase activity	1	2	
thiol-dependent ubiquitin-specific protease activity		1	
threonine-type endopeptidase activity			1
transferase activity, transferring acyl groups other than amino-acyl groups	1	2	
translation initiation factor activity	1		
ubiquitin-ubiquitin ligase activity			1
uridylyltransferase activity	1		1

C. Cellular Component GO Term	11-2	11-7	7-2
membrane	6	2	6
integral component of membrane	5	1	3
ribosome	1	2	3
cytoplasm	2		
nucleus	2	1	2
eukaryotic translation initiation factor 3 complex	1		
mitochondrial proton-transporting ATP synthase complex, catalytic sector F(1)	1		
mitochondrion	1		1
photosystem II			1
proteasome core complex			1
proteasome core complex, alpha-subunit complex			1
ubiquitin ligase complex			1

Table S6a-c. Number of CHG hypermethylated DMR-associated genes associated with each biological process (**A**), molecular function **(B)**, and cellular component **(C)** gene ontology (GO) terms for each of the three age-contrasts (i.e., 11 – 2 year, 11 – 7 year, and 7 – 2 year). Values in each column represent the number of DMR-associated genes that are associated with each GO term. Black squares indicate no genes associated with that contrast were assigned the particular GO term.

A. Biological Process GO Term	**11-2**	**11-7**	**7-2**
proteolysis	16	16	4
obsolete oxidation-reduction process	7	13	2
protein phosphorylation	5	11	5
carbohydrate metabolic process	4	4	
regulation of transcription, DNA-templated	4	4	2
transmembrane transport	5	4	2
positive regulation of stomatal complex development		3	
biosynthetic process	1	2	1
fatty acid biosynthetic process		2	
nitrogen compound metabolic process	2		1
protein ubiquitination		2	
response to auxin	2		
signal transduction	5	2	1
translational termination	2		1
cation transport		1	
cell population proliferation		1	
cell redox homeostasis	1	1	
cell wall modification		1	1
DNA topological change	1		
drug transmembrane transport			1
glycerolipid biosynthetic process	1		
intracellular protein transport		1	
intracellular signal transduction	1	1	
ion transport	1		
lipid metabolic process	1	1	
mistmatch repair	1		
nucleoside metabolic process	1		1
nucleosome assembly		1	
potassium ion transport		1	
recognition of pollen			1
response to oxidative stress		1	2
terpenoid biosynthetic process	1		
transcription, DNA-templated		1	1
translation	2	1	1

vesicle-mediated transport	[redacted]	1	[redacted]

B. Molecular Function GO Term	11-2	11-7	7-2
cysteine-type peptidase activity	14	15	2
protein binding	14	9	7
ATP binding	10	7	8
zinc ion binding	8	3	6
nucleic acid binding	7	4	1
ADP binding	5	5	1
protein kinase activity	5	11	5
hydrolase activity, hydrolyzing O-glycosyl compounds		4	
catalytic activity	3	2	
copper ion binding		3	
DNA binding	3	2	6
RNA-DNA hybrid ribonuclease activity	3	1	
transmembrane transporter activity	3	3	1
actin binding	2		1
endopeptidase inhibitor activity	2	2	
GTP binding	2		
heme binding	2	5	2
hydrolase activity, acting on ester bonds	2	8	2
hydrolase activity, acting on glycosyl bonds		2	
iron ion binding	2	4	
nickel cation binding	2		
oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	2	4	
polygalacturonase activity	2		
protein dimerization activity	2	3	
RNA binding		2	
sequence-specific DNA binding	2	2	
serine-type endopeptidase activity	2	1	
structural constituent of ribosome	2	1	1
translation release factor activity	2		1
ubiquitin-protein transferase activity		2	
2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase activity	1		
acid phosphatase activity			1
alpha-amylase activity	1		
antioxidant activity		1	
ATP-dependent peptidase activity	1		
ATPase activity			1
calcium ion binding	1	1	
diacylglycerol O-acyltransferase activity	1		
DNA topoisomerase activity	1		
DNA-binding transcription factor activity	1	1	1
DNA-directed 5'-3' RNA polymerase activity			1
double-stranded DNA binding	1		
electron transfer activity	1	1	

endonuclease activity		1	
enzyme inhibitor activity		1	1
flavin adenine dinucleotide binding	1		
growth factor activity		1	
GTPase activator activity	1	1	
hydrolase activity		1	2
ion channel activity	1		
ionotropic glutamate receptor activity	1		
lyase activity		1	
magnesium ion binding		1	
malonyl-CoA decarboxylase activity		1	
metal ion binding		1	2
mismatched DNA binding	1		
NAD binding		1	
nutrient reservoir activity	1		
oxidoreductase activity	1	6	
oxidoreductase activity, acting on CH-OH group of donors	1		
oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	1		
oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor		1	
pectinesterase activity		1	1
peptide-methionine (S)-S-oxide reductase activity	1	1	
peroxidase activity		1	2
phosphotransferase activity, alcohol group as acceptor	1		
polysaccharide binding	1		
protein disulfide oxidoreductase activity	1	1	
protein phosphatase regulator activity	1	1	
racemase activity, acting on amino acids and derivatives			1
ribonuclease activity		1	
serine-type carboxypeptidase activity	1		2
solute:proton antiporter activity		1	
strictosidine synthase activity			1
terpene synthase activity		1	
transferase activity, transferring acyl groups		1	1
transferase activity, transferring acyl groups other than amino-acyl groups	1	2	2
transferase activity, transferring hexosyl groups	1		1
ubiquitin-like modifier activating enzyme activity	1		1

C. Cellular Component GO Term	11-2	11-7	7-2
membrane	5	4	1
integral component of membrane	1	3	1
AP-5 adaptor complex		1	
COPI vesicle coat		1	
extracellular region		1	
membrane coat		1	
nucleus	2	1	4
protein phosphatase type 2A complex	1	1	
proton-transporting two-sector ATPase complex, catalytic domain		1	
ribosome	2	1	1
membrane		4	

Table S7a-c. Number of CHG hypomethylated DMR-associated genes associated with each biological process (**A**), molecular function **(B)**, and cellular component **(C)** gene ontology (GO) terms for each of the three age-contrasts (i.e. 11 – 2 year, 11 – 7 year, and 7 – 2 year). Values in each column represent the number of DMR-associated genes that are associated with each GO term. Black squares indicate no genes associated with that contrast were assigned the particular GO term.

A. Biological Process GO Term	**11-2**	**11-7**	**7-2**
obsolete oxidation-reduction process	5	3	9
protein phosphorylation	5	5	6
proteolysis	5	8	8
regulation of transcription, DNA-templated	4	5	2
carbohydrate metabolic process	2		2
cysteinyl-tRNA aminoacylation	2		
phospholipid biosynthetic process			2
response to auxin	2		1
transmembrane transport	2	1	5
amine metabolic process	1		1
ATP metabolic process	1		
autophagy	1		
base-excision repair		1	
cell redox homeostasis	1		
defense response			1
drug transmembrane transport	1	1	
G protein-coupled receptor signaling pathway	1		
intracellular protein transport		1	
lipid biosynthetic process	1		1
magnesium ion transport	1		
metal ion transport	1	1	
mistmatch repair			1
nucleobase-containing compound metabolic process		1	
nucleosome assembly			1
organic substance metabolic process			1
proton transmembrane transport	1		
purine nucleobase biosynthetic process	1	1	
regulation of cyclin-dependent protein serine/threonine kinase activity			1
response to oxidative stress			1
rRNA processing			1
steroid biosynthetic process		1	
transcription, DNA-templated		1	
translation	1	2	2

translational elongation	1	1	
trehalose biosynthetic process			1
tRNA processing			1
ubiquitin-dependent protein catabolic process			1

B. Molecular Function GO Term	11-2	11-7	7-2
ATP binding	10	5	10
protein binding	9	3	9
zinc ion binding	8	5	8
cysteine-type peptidase activity	5	7	7
DNA binding	5	5	1
protein kinase activity	5	5	6
iron ion binding	4	2	5
heme binding	3	2	5
nucleic acid binding	3	2	5
oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	3	2	4
transferase activity, transferring acyl groups other than amino-acyl groups	3		
3'-5' exonuclease activity		1	
catalytic activity	2	3	2
cysteine-tRNA ligase activity	2		
DNA-binding transcription factor activity	2	2	1
hydrolase activity	2	2	1
hydrolase activity, hydrolyzing O-glycosyl compounds	2		1
Lys48-specific deubiquitinase activity	2		
metal ion binding	2	4	
methyltransferase activity		2	
nucleotide binding	2		
phosphatidylserine decarboxylase activity			2
sequence-specific DNA binding	2	1	1
serine-type endopeptidase activity	2		
thiol-dependent ubiquitin-specific protease activity	2		
acid phosphatase activity	1	2	
ADP binding	1	1	2
aminopeptidase activity			1
ATPase activity			1
calcium ion binding	1	1	
calcium-dependent phospholipid binding	1	1	
carbohydrate binding	1	1	
carbon-sulfur lyase activity			1
chromatin binding			1
copper ion binding	1		1
DNA-3-methyladenine glycosylase activity		1	
DNA-directed 5'-3' RNA polymerase activity		1	
electron transfer activity	1		
endopeptidase inhibitor activity			1
enzyme inhibitor activity			1
flavin adenine dinucleotide binding			1
glycopeptide alpha-N-acetylgalactosaminidase activity	1		

GTPase activity			1
hydrolase activity, acting on ester bonds	1	1	
intramolecular transferase activity, phosphotransferases			1
ionotropic glutamate receptor activity	1	1	
lyase activity	1	2	
magnesium ion binding	1	2	
magnesium ion transmembrane transporter activity	1		
mismatched DNA binding			1
oxidoreductase activity	1	1	2
peroxidase activity			1
phospholipid binding	1	1	
phosphoribosylamine-glycine ligase activity	1	1	
polysaccharide binding		1	
primary amine oxidase activity	1		1
protein dimerization activity	1		2
protein disulfide oxidoreductase activity	1		
protein kinase binding			1
protein serine/threonine kinase activity		1	1
quinone binding	1		1
RNA-DNA hybrid ribonuclease activity	1	1	2
RNA binding		1	
serine-type carboxypeptidase activity		1	
structural constituent of ribosome	1	2	2
terpene synthase activity	1	2	
transferase activity, transferring glycosyl groups			1
transferase activity, transferring hexosyl groups	1	1	
translation elongation factor activity	1	1	
transmembrane transporter activity	1		3
tRNA dihydrouridine synthase activity			1
ubiquitin protein ligase binding			1

C. Cellular Component GO Term	11-2	11-7	7-2
integral component of membrane	4	1	3
cytoplasm	3		
membrane	1	2	3
nucleus	1	1	3
ribosome	1	2	2
anchored component of plasma membrane			1

Table S8a-c. Number of CHH hypermethylated DMR-associated genes associated with each biological process (**A**), molecular function **(B)**, and cellular component **(C)** gene ontology (GO) terms for each of the three age-contrasts (i.e., 11 – 2 year, 11 – 7 year, and 7 – 2 year). Values in each column represent the number of DMR-associated genes that are associated with each GO term. Black squares indicate no genes associated with that contrast were assigned the particular GO term.

A. Biological Process GO Term	**11-2**	**11-7**	**7-2**
protein phosphorylation	14	7	28
proteolysis	13	6	21
obsolete oxidation-reduction process	8	4	20
regulation of transcription, DNA-templated	7	2	15
translation	1	2	8
transmembrane transport	5	4	8
signal transduction	3	1	6
carbohydrate metabolic process	2	2	4
defense response		1	3
tRNA aminoacylation for protein translation	1		3
cation transport		2	
cell redox homeostasis	1		2
cell wall modification		1	2
DNA topological change			2
exocytosis			2
fatty acid beta-oxidation			2
histone lysine methylation			2
lipid metabolic process		2	2
nitrate assimilation	3		2
positive regulation of Notch signaling pathway	2		
protein ubiquitination			2
pyrimidine nucleotide biosynthetic process	2		
transcription, DNA-templated			2
ATP metabolic process			1
biosynthetic process	1		1
carboxylic acid metabolic process		1	
cell wall biogenesis	1		
cell wall macromolecule catabolic process			1
cellular amino acid metabolic process		1	
cellular glucan metabolic process		1	
cellulose biosynthetic process			1
cellulose microfibril organization	1		1
chitin catabolic process			1
DNA-templated transcription, initiation		1	

drug transmembrane transport			1
endocytosis			1
fatty acid biosynthetic process		1	1
glutathione biosynthetic process		1	
glycolytic process	1		1
glycyl-tRNA aminoacylation			1
guanosine tetraphosphate metabolic process	1		
intermembrane lipid transfer			1
intracellular protein transport	1		1
intracellular signal transduction			1
ion transport	1		1
lipid catabolic process		2	1
malate transport		1	
mannose metabolic process	2		1
mRNA export from nucleus	2		1
nucleobase-containing compound metabolic process			1
nucleosome assembly			1
phosphatidylinositol metabolic process	1		1
phospholipid biosynthetic process		1	
photosynthesis			1
proteasome assembly	2		1
protein kinase C-activating G protein-coupled receptor signaling pathway	1		
protein neddylation			1
protein peptidyl-prolyl isomerization		1	
proteolysis involved in cellular protein catabolic process		1	
proton transmembrane transport			1
regulation of systemic acquired resistance	1		
RNA processing	1		
response to oxidative stress	1		
retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum			1
ribosome biogenesis		1	1
rRNA processing			1
sulfate transport		1	
terpenoid biosynthetic process	1		
transcription by RNA polymerase II			1
transcription initiation from RNA polymerase II promoter	1	1	1
translational elongation			1
tryptophan catabolic process to kynurenine			1
tryptophan metabolic process		1	
ubiquitin-dependent protein catabolic process		1	1
valyl-tRNA aminoacylation			1
vesicle docking involved in exocytosis			1
vesicle-mediated transport	1		1

B. Molecular Function GO Term	11-2	11-7	7-2
protein binding	20	6	42
ATP binding	21	10	37
protein kinase activity	14	7	28
cysteine-type peptidase activity	12	4	20
DNA binding	8	1	19
ADP binding	5	3	16
nucleic acid binding	11	5	15
zinc ion binding	8	2	14
hydrolase activity, acting on ester bonds	5	4	13
protein dimerization activity	5	1	13
structural constituent of ribosome	1	2	8
oxidoreductase activity	7	1	7
DNA-binding transcription factor activity	2	1	6
RNA binding	1		6
acetylglucosaminyltransferase activity	2	1	5
RNA-DNA hybrid ribonuclease activity	4		5
3-hydroxyisobutyryl-CoA hydrolase activity			4
heme binding	2	1	4
iron ion binding	1	1	4
nucleotide binding	1		4
oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	1	1	4
polysaccharide binding	1	2	4
sequence-specific DNA binding	2	1	4
transferase activity, transferring acyl groups	2		4
aminoacyl-tRNA ligase activity	1		3
ATPase activity	5	1	3
calcium ion binding	1		3
catalytic activity	4	3	3
electron transfer activity	1		3
GTPase activity	3		
hydrolase activity			3
oxidoreductase activity, acting on the CH-CH group of donors			3
serine-type endopeptidase activity	1	1	3
transferase activity, transferring hexosyl groups	4	1	3
ubiquitin-like modifier activating enzyme activity	1		3
acyl-CoA oxidase activity			2
DNA topoisomerase activity			2
flavin adenine dinucleotide binding			2
GTP binding	5	1	2
helicase activity			2
histone-lysine N-methyltransferase activity			2
hydrolase activity, hydrolyzing O-glycosyl compounds		1	2
metal ion binding		2	2

methyltransferase activity			2
molybdenum ion binding	3		2
nutrient reservoir activity	2		
oxidoreductase activity, acting on CH-OH group of donors			2
pectinesterase activity		1	2
protein disulfide oxidoreductase activity	1		2
solute:proton antiporter activity		2	
transferase activity, transferring glycosyl groups			2
ubiquitin-protein transferase activity			2
1-deoxy-D-xylulose-5-phosphate synthase activity	1		
3'-5' exonuclease activity			1
alpha-amylase activity	1		
alpha-mannosidase activity	2		1
antioxidant activity			1
arylformamidase activity			1
ATPase-coupled transmembrane transporter activity			1
calcium-dependent phospholipid binding			1
carboxy-lyase activity		1	
cellulose synthase (UDP-forming) activity			1
channel activity		1	1
chitin binding			1
chitinase activity			1
chromatin binding		2	1
copper ion binding	1		1
cysteine-type endopeptidase inhibitor activity			1
diacylglycerol kinase activity	1		
DNA topoisomerase type II (double strand cut, ATP-hydrolyzing) activity			1
DNA-directed 5'-3' RNA polymerase activity			1
endopeptidase activity		1	
enzyme inhibitor activity		2	1
galactoside 2-alpha-L-fucosyltransferase activity	1		
glutathione synthase activity		1	
glycine-tRNA ligase activity			1
glycopeptide alpha-N-acetylgalactosaminidase activity	1		
heat shock protein binding			1
ion channel activity	1		1
lipid transfer activity			1
magnesium ion binding	2		1
mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase activity			1
microtubule minus-end binding			1
NEDD8 activating enzyme activity			1
O-methyltransferase activity			1
obsolete coenzyme binding		1	1
peptidyl-prolyl cis-trans isomerase activity		1	

peroxidase activity	1		
phosphatidylinositol binding			1
phosphatidylinositol phosphate kinase activity	1		1
phosphatidylserine decarboxylase activity		1	
polygalacturonase activity			1
potassium ion binding	1		1
protein serine/threonine kinase activity		1	
proton-transporting ATPase activity, rotational mechanism		1	
pyridoxal phosphate binding		1	1
pyruvate kinase activity	1		1
ribonuclease T2 activity			1
serine-type carboxypeptidase activity	1	1	
serine-type exopeptidase activity		1	
serine-type peptidase activity		1	
sulfate transmembrane transporter activity		1	
TBP-class protein binding		1	
threonine-type endopeptidase activity		1	
thiamine pyrophosphate binding	1		
thiolester hydrolase activity			1
transaminase activity			1
transferase activity, transferring acyl groups other than amino-acyl groups	1	2	1
translation elongation factor activity			1
transmembrane transporter activity	2	1	1
tRNA binding			1
tryptophan synthase activity		1	
unfolded protein binding			1
valine-tRNA ligase activity			1
xyloglucan:xyloglucosyl transferase activity		1	

C. Cellular Component GO Term	11-2	11-7	7-2
integral component of membrane	3	5	15
membrane	10	4	14
ribosome	1	2	8
nucleus		1	7
cytoplasm			4
chloroplast			2
chromosome			2
exocyst			2
peroxisome			2
anchored component of membrane	1		1
apoplast		1	
cell wall		1	
endoplasmic reticulum membrane	1		
extrinsic component of membrane			1
Golgi transport complex			1
nucleolus		1	
nucleosome			1
photosystem II			1
photosystem II oxygen evolving complex			1
proteasome core complex		1	
proteasome core complex, alpha-subunit complex		1	
proteasome regulatory particle, lid subcomplex	2		1
proton-transporting two-sector ATPase complex, catalytic domain		1	
transcription factor TFIIA complex	1		1

Table S9a-c. Number of CHH hypomethylated DMR-associated genes associated with each biological process (**A**), molecular function **(B)**, and cellular component **(C)** gene ontology (GO) terms for each of the three age-contrasts (i.e., 11 – 2 year, 11 – 7 year, and 7 – 2 year). Values in each column represent the number of DMR-associated genes that are associated with each GO term. Black squares indicate no genes associated with that contrast were assigned the particular GO term.

A. Biological Process GO Term	**11-2**	**11-7**	**7-2**
protein phosphorylation	2	9	1
regulation of transcription, DNA-templated	6	9	
proteolysis	2	5	4
transmembrane transport	2	5	
carbohydrate metabolic process		3	1
obsolete oxidation-reduction process	5	3	6
translation	1	3	
ATP metabolic process		2	
base-excision repair	1	2	
nucleobase-containing compound metabolic process		2	
proton transmembrane transport		2	
response to hormone		2	
response to oxidative stress	2		2
cell redox homeostasis			1
cell wall macromolecule catabolic process		1	
chitin catabolic process		1	
defense response		1	
DNA repair		1	
DNA topological change			1
exocytosis		1	
intermembrane lipid transfer			1
intracellular protein transport	1	1	
lipid metabolic process	1		1
metal ion transport	1	1	1
nitrogen compound metabolic process			1
phytochromobilin biosynthetic process		1	
protein folding	1		
rRNA processing			1
signal transduction		1	
steroid biosynthetic process			1
sucrose metabolic process			1
superoxide metabolic process	1		
translational initiation		1	

B. Molecular Function GO Term	11-2	11-7	7-2
ATP binding	3	14	3
DNA binding	5	13	2
protein binding	4	9	3
protein kinase activity	2	9	1
zinc ion binding		6	2
cysteine-type peptidase activity	2	5	4
RNA binding		5	
sequence-specific DNA binding	4	5	
DNA-binding transcription factor activity	5	4	
metal ion binding	1	4	
ATPase activity		3	
ATPase-coupled transmembrane transporter activity		3	
protein dimerization activity	1	3	1
structural constituent of ribosome	1	3	
3'-5' exonuclease activity		2	
ADP binding	1	2	
DNA-3-methyladenine glycosylase activity	1	2	
glutathione peroxidase activity	2		2
heme binding			2
hydrolase activity	1	2	2
hydrolase activity, acting on ester bonds		2	3
iron ion binding			2
nucleic acid binding		2	4
oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen			2
polygalacturonase activity		2	
pyridoxal phosphate binding		2	
transaminase activity		2	
3-beta-hydroxy-delta5-steroid dehydrogenase activity			1
acetylglucosaminyltransferase activity	1	1	2
acid phosphatase activity		1	
carbohydrate binding		1	
catalytic activity	1	1	2
chitin binding		1	
chitinase activity		1	
cobalt ion binding		1	
DNA topoisomerase activity			1
flavin adenine dinucleotide binding	1		
hydrolase activity, hydrolyzing O-glycosyl compounds		1	1
intramolecular lyase activity		1	
lipid transfer activity			1
Lys48-specific deubiquitinase activity		1	
metal ion transmembrane transporter activity	1		1
methyltransferase activity		1	1

microtubule minus-end binding		1	
O-methyltransferase activity		1	
obsolete coenzyme binding			1
oxidoreductase activity	2		1
oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor			1
oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen		1	
oxidoreductase activity, acting on the CH-CH group of donors, iron-sulfur protein as acceptor		1	
polysaccharide binding	1		1
racemase activity, acting on amino acids and derivatives			1
sucrose synthase activity			1
superoxide dismutase activity	1		
thiol-dependent ubiquitin-specific protease activity		1	
transferase activity, transferring acyl groups other than amino-acyl groups		1	
transferase activity, transferring hexosyl groups	1	1	
translation initiation factor activity		1	

C. Cellular Component GO Term	11-2	11-7	7-2
integral component of membrane		5	
ribosome	1	3	
membrane	2	2	4
nucleus		2	1
cytoplasm			1
exocyst		1	

Table S10. Characterization of eight unknown proteins associated with the 17 shared DMR sequences identified among the three age-contrasts. The unknown protein ID corresponds to the unknown proteins associated with the shared DMR sequences. The putative motifs identified within each protein sequence include the position of the motif within the sequence and the e-value. The number of amino acids and estimated molecular weight (kDa) are also included for each protein sequence. Finally, the predicted localization of each protein is provided, as well as the calculated probability of this prediction.

Protein ID	Putative Motifs (position and e-value)	Number of Amino Acids	Estimated Molecular Weight (kDa)	Predicted Location (probability)
unknown protein1	none found	1,122	122,388.22	chloroplast (98.98%)
unknown protein2	○ transposase_24 (213-319; $8e^{-7}$)	438	48,372.76	nucleus (50.2%)
unknown protein3	○ transposase_24 (186-312; $5e^{-11}$) ○ AbiJ N-terminal domain 4 (114-226; 0.014)	610	69,422.01	nucleus (90.87%)
unknown protein4	none found	100	11,346.45	mitochondrion (89.43%)
unknown protein5	○ DUF1336 (15-106; $5e^{-9}$) ○ DUF924 (22-89; 0.0093)	124	14,296.34	cytoplasm (93.95%)
unknown protein6	none found	339	38,963.80	nucleus (97.83%)
unknown protein7	none found	86	9,893.82	secreted pathway (85.92%)
unknown protein8	○ GIT coiled-coil Rho guanine nucleotide exchange factor (77-109; 0.0019) ○ bZIP transcription factor (76-106; 0.0033) ○ Fungal N-terminal domain of STAND proteins (54-111; 0.0084) ○ Uncharacterised protein family (UPF0242) N-terminus (54-121; 0.014) ○ Leucine-rich repeats of kinetochore protein Cenp-F/LEK1 (62-119; 0.028) ○ DUF4514 (72-146; 0.019)	158	17,972.46	nucleus (99.25%)

- Axonemal dynein light chain (47-115; 0.038)
- RNA polymerase II transcription mediator complex subunit 9 (59-117; 0.067)
- EvpB/VC_A0108, tail sheath N-terminal domain (86-141; 0.17)
- Centrosome localisation domain of PPC89 (76-111; 0.3)
- Septum formation initiator (71-105; 0.47)

Table S11. Identification of microRNAs found within the 17 identified DMR sequences based on BLAST analysis using a modified miRbase database containing plant-only entries. The BLAST results were filtered to include only those regions within the DMR that are n – 2 bp in length in relation to the closest associated microRNA and are the best hit based on the associated e-value to each microRNA within the database.

DMR ID	e-value	Best Hit	DMR Sequence (5' – 3')	microRNA Sequence in miRbase database (5' – 3')
CGDMR1	0.63	mtr-miR2672; ath-miR163	TTAATAAACCACGTCGGTTCTA; TGTAGACGACGTTGAACTTCTA	TTAATCGACCAAGTGGGTACTA; TGAAGAGGACTTGGAACTTCGA
CGDMR10	0.41	ppe-miR8130-3p; mdm-miR7124b; mdm-miR7124a	CCTTCCTGTGAGGCATGCCC; AAATAAAGATGGGATTGCTG; AAATAAAGATGGGATTGCTG	CCTTCCAGTAAGGCACCCCC; AAATAAAGTTGATATTGGTG; AAATAAAGTTGATATTGGTG
CGDMR11	0.46	gma-miR10409	AGGGTTTTAATGTCCTCAAA	AGGCTTTTAATATCTTCAGA
CGDMR13	0.39	ath-miR5014a-3p	TGTAAAGATATAAATGTACG	TGTACAAATTTAAGTGTACG
CGDMR2	0.79	ath-miR5021; gma-miR10420	AAAAGAAAAAGAAAAAAA; AAAAAAAATCTGGTTCAG	AGAAGAAGAAGAAGAAAA; AAAAAAATGATGGTTCAG
CGDMR4	1	mtr-miR7699-3p; mtr-miR7699-5p	TGCAATCAATTAATTAGATAC; TCTGCAATCAATTAATTAGAT	TGTAATCAATGCATTAAATGC; TGTGTAATCAATGCATTAAAT
CGDMR5	0.53	gma-miR172e; gma-miR172d	CTGCCGCAGCTTCTTCTATTTTCC; CTGCCGCAGCTTCTTCTATTTTCC	CTGCTGCAGCATCATCAAGATTCC; CTGCTGCAGCATCATCAAGATTCC
CGDMR6	0.08	mtr-miR5234	TCTGCCATCCACACCAGAA	TCTGCCATCCACAACAAAA

CGDMR8	0.56	gma-miR4348a-3p	TCACAATACCCTCATCTTG	TCACAATGTCATCATCTTG
CGDMR9	0.63	stu-miR8035	AGAAAGGGAGTTTGAAGGTG	AGAAAGTGATATTGAAGATG
CHGDMR1	0.022	ath-miR5021	AGAAGAAGAAAAAGAAAA	AGAAGAAGAAGAAGAAAA
CHGDMR2	0.072	gma-miR10425	AAAACCCTCTTTGAATTTGCCT	ACAACCGTCTTTGAAATCGCCT
CHHDMR1	0.43	gma-miR1534	TGACAGTTTACCCAAAAT	TGACTATTTACCCAAAAT

Data S1

Hypermethylation is associated with increased age in almond (Prunus dulcis [Mill.] D.A. Webb) accessions

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DataS1. File containing sequnecing statistics, conversion efficiencies, total percent methylation, and percent methylation within each context (CG, CHG, CHH) for almond accessions presented in this study.

Contents:

AgeCohort_MethylSeq:

samp_ID - the unique sample identifier assigned to each almond accession; age - in years; num_reads - the number of reads generated in total for each individual; cov_seq - the coverage across the reference 'Nonpareil' almond genome based on the number of reads generated by HiSeq4000 sequencing; num_reads_align - the number of reads that aligned to the reference 'Nonpareil' almond genome; cov_align - the coverage across the reference 'Nonpareil' almond genome based on the number of reads that aligned following Bismark alignment; per_align - mapping efficiency; per_CG - percent methylation in the CG context; per_CHG - percent methylation in the CHG context; per_CHH - percent methylation in the CHH context; per_lambda - percent methylated cytosines in the CG context following alignment to the Lambda reference; per_puc19 - percent methylated cytosines in the CG context following alignment to the pUC19 reference; per_meth - total percent methyaltion following alignment to the 'Nonpareil' almond reference genome; Female_parent: female progenitor of the accession; Male_parent: male progenitor of the accession.

samp_ID	age	num_reads	cov_seq	num_reads_align	cov_align	per_align	per_CG	per_CHG	per_CHH	per_lambda	per_puc19	per_meth	Female_parent	Male_parent
51	2	31297380	18.8	13749685	8.2	0.439	0.512	0.211	0.037	0.002	0.976	0.116	05,5-367	05,9-396
55	2	26341622	15.8	12252616	7.4	0.465	0.487	0.228	0.02	0.003	0.942	0.103	Nonpareil	2005,5-17
56	2	28016948	16.8	12329600	7.4	0.44	0.515	0.224	0.025	0.003	0.981	0.112	Nonpareil	2004,8-160
46	2	32861503	19.72	17661490	10.597	0.537	0.475	0.229	0.024	0.003	0.967	0.108	Nonpareil	2004,8-201
45	2	44230441	26.54	23808875	14.29	0.538	0.479	0.227	0.029	0.001	0.975	0.111	Nonpareil	2005,4-60
49	2	48170341	28.9	25501433	15.3	0.529	0.409	0.182	0.029	0.001	0.909	0.098	Nonpareil	2005,4-60
52	2	41430789	24.86	20859398	12.52	0.503	0.508	0.225	0.032	0.002	0.976	0.115	MidHors	OP
54	2	48531019	29.12	23620182	14.17	0.487	0.441	0.202	0.021	0.002	0.921	0.095	MidHors	OP
57	2	37613337	22.57	20384490	12.23	0.542	0.417	0.176	0.025	0.002	0.802	0.092	Nonpareil	2005,5-396
35	2	50541320	30.32	24043007	14.43	0.476	0.435	0.201	0.023	0.004	0.904	0.096	05,5-367	05,9-396
39	2	52674838	31.6	25747370	15.45	0.489	0.49	0.235	0.025	0.002	0.978	0.11	Nonpareil	2005,4-170
41	2	41279612	24.8	20377533	12.23	0.494	0.514	0.226	0.026	0.002	1	0.113	A05,6-340	2004,8-160
42	2	16534210	9.9	6438416	3.86	0.389	0.556	0.278	0.034	0.002	0.967	0.139	A05,6-340	2004,8-160
44	2	49540541	29.7	26723876	16.03	0.539	0.456	0.193	0.028	0.001	0.968	0.104	Nonpareil	2005,5-17
40	2	20246774	12.1	9225312	5.54	0.456	0.431	0.192	0.028	0.002	0.975	0.1	Nonpareil	2005,7-100
38	2	23618228	14.2	12251103	7.35	0.519	0.501	0.227	0.031	0.002	0.956	0.116	Nonpareil	2005,5–80
36	2	34890738	20.9	17723383	10.63	0.508	0.527	0.244	0.032	0.002	0.981	0.121	A05,6-340	2004,8-160
37	2	28345188	17	12636660	7.58	0.446	0.437	0.2	0.018	0.003	0.985	0.095	MidHors	OP
47	2	98319896	59	50290060	30.17	0.511	0.503	0.236	0.03	0.002	0.972	0.116	Nonpareil	2005,4-170
48	2	55093356	33.1	27736869	16.64	0.503	0.524	0.248	0.032	0.002	0.984	0.121	Nonpareil	2006,3-105
50	2	33033951	19.8	16544985	9.93	0.501	0.506	0.227	0.031	0.003	0.977	0.115	05,5-367	05,9-396
124	7	35055353	21	15277723	9.2	0.436	0.528	0.231	0.028	0.001	0.987	0.116	Nonpareil	99,9-86+03,1-54+03,3-144+03,2-191+04,14-158+04,14-49+02,7-159+04,8-160
126	7	28593912	17.2	11983479	7.2	0.419	0.377	0.126	0.019	0.002	0.906	0.077	Ferragnes	2000,3-385
132	7	29585255	17.8	15054356	9	0.509	0.433	0.167	0.021	0.002	0.973	0.092	Nonpareil	2000,1-180+2000,1-385
133	7	30210415	18.1	15329804	9.2	0.507	0.469	0.194	0.026	0.001	0.972	0.1	Nonpareil	2000,1-180+2000,1-385
135	7	44613939	26.8	21668740	13	0.486	0.472	0.218	0.031	0.003	0.97	0.112	Tardy- Nonpareil	95,1-26
136	7	17422158	10.5	7932753	4.8	0.455	0.503	0.238	0.032	0.002	0.973	0.117	Tardy- Nonpareil	95,1-26
144	7	36246652	21.7	17346965	10.4	0.479	0.491	0.216	0.028	0.001	0.978	0.11	Nonpareil	2000,1-180+2000,1-385
145	7	21126080	12.7	9442150	5.7	0.447	0.532	0.24	0.035	0.002	0.983	0.12	Nonpareil	2000,1-180+2000,1-385
146	7	29914559	17.9	14792824	8.9	0.495	0.491	0.228	0.026	0.002	0.966	0.109	Nonpareil	2000,1-180+2000,1-385
150	7	35719010	21.43	18468179	11.081	0.517	0.515	0.236	0.031	0.002	0.973	0.116	Nonpareil	99,9-86+03,1-54+03,3-144+03,2-191+04,14-158+04,14-49+02,7-159+04,8-160
147	7	47988999	28.79	26576252	15.946	0.554	0.514	0.235	0.031	0.001	0.936	0.118	Nonpareil	99,9-86+03,1-54+03,3-144+03,2-191+04,14-158+04,14-49+02,7-159+04,8-160
130	7	45786720	27.47	21973306	13.18	0.48	0.502	0.224	0.026	0.0008	0.967	0.11	Tardy- Nonpareil	95,1-26
140	7	40648845	24.39	17395055	10.44	0.428	0.429	0.204	0.032	0.001	0.973	0.106	Ferragnes	2000,3-385
143	7	47930901	28.76	24235561	14.54	0.506	0.527	0.243	0.031	0.001	0.975	0.12	Nonpareil	2000,1-180+2000,1-385
148	7	48362108	29.02	23725211	14.24	0.491	0.478	0.201	0.029	0.001	0.973	0.107	Nonpareil	99,9-86+03,1-54+03,3-144+03,2-191+04,14-158+04,14-49+02,7-159+04,8-160
134	7	23974597	14.4	13022640	7.81	0.543	0.502	0.232	0.03	0.002	0.978	0.115	Nonpareil	2000,1-180+2000,1-385
137	7	50634207	30.4	27310455	16.39	0.539	0.492	0.225	0.031	0.002	0.978	0.113	Tardy- Nonpareil	95,1-26
139	7	79328288	47.6	39787558	23.87	0.502	0.425	0.206	0.027	0.002	0.976	0.102	Ferragnes	2000,3-385
131	7	63570292	38.1	33958542	20.38	0.534	0.407	0.175	0.026	0.003	0.923	0.092	Nonpareil	2000,1-180+2000,1-385
127	7	13002485	7.8	6411422	3.85	0.493	0.432	0.205	0.026	0.002	0.982	0.108	Nonpareil	2000,1-180+2000,1-385
122	7	40529732	24.3	19104709	11.46	0.471	0.537	0.266	0.034	0.002	0.98	0.13	Nonpareil	2000,1-180+2000,1-385
123	7	71971846	43.2	38491179	23.09	0.535	0.51	0.24	0.032	0.002	0.975	0.119	Nonpareil	99,9-86+03,1-54+03,3-144+03,2-191+04,14-158+04,14-49+02,7-159+04,8-160
125	7	49197657	29.5	24866398	14.92	0.505	0.511	0.227	0.029	0.002	0.979	0.115	Nonpareil	2000,1-180+2000,1-385
128	7	32918109	19.8	16682419	10.01	0.507	0.52	0.243	0.03	0.003	0.979	0.118	Nonpareil	2000,1-180+2000,1-385
129	7	29512271	17.7	14920804	8.95	0.506	0.503	0.256	0.054	0.016	0.971	0.135	Nonpareil	2000,1-180+2000,1-385
61	11	43894112	26.3	20244951	12.1	0.461	0.51	0.227	0.032	0.002	0.978	0.116	Nonpareil	2000,16-81+2000,13-162
76	11	40616818	24.4	18502909	11.1	0.456	0.513	0.213	0.029	0.001	0.984	0.112	Nonpareil	2000,2-3
77	11	42005872	25.2	20771654	12.5	0.494	0.49	0.213	0.031	0.001	0.987	0.11	Ferragnes	2000,2-3+2000,8-27+2000,13-162
82	11	33498595	20.1	16231217	9.7	0.485	0.479	0.195	0.028	0.001	0.971	0.11	Winters	2000,8-27
83	11	37716302	22.6	17936056	10.8	0.476	0.496	0.21	0.031	0.003	0.976	0.111	Nonpareil	2000,16-81+2000,13-162
84	11	29776754	17.9	14797650	8.9	0.497	0.558	0.244	0.032	0.002	0.988	0.121	Nonpareil	2000,16-81+2000,13-162
63	11	33537550	20.12	17079402	10.248	0.509	0.484	0.239	0.047	0.0011	0.983	0.127	Nonpareil	99,9-86+03,1-54+03,3-144+03,2-191+04,14-158+04,14-49+02,7-159+04,8-160
62	11	32601035	19.56	18217095	10.93	0.559	0.547	0.235	0.036	0.0005	0.981	0.124	Nonpareil	2000,16-81+2000,13-162
67	11	42773275	25.66	20980483	12.59	0.491	0.517	0.224	0.029	0.001	0.973	0.113	Winters	2000,8-27
68	11	43876467	26.33	22474208	13.48	0.512	0.508	0.23	0.029	0.001	0.979	0.114	Winters	2000,8-27
87	11	46860369	28.12	24753547	14.85	0.528	0.549	0.263	0.028	0.002	0.979	0.123	Nonpareil	2000,2-3
89	11	33877345	20.33	16613073	9.97	0.49	0.515	0.218	0.029	0.0009	0.992	0.113	Winters	2000,8-27
90	11	37995583	22.8	19222328	11.53	0.506	0.522	0.229	0.031	0.001	0.973	0.117	Winters	2000,8-27
75	11	62939431	37.8	34541436	20.72	0.549	0.509	0.224	0.032	0.004	0.965	0.115	Winters	2000,9-157+2000,8-27
78	11	45447750	27.3	24392741	14.64	0.537	0.515	0.228	0.029	0.001	0.981	0.115	Nonpareil	2000,8-27
69	11	41923186	25.2	21990000	13.19	0.525	0.458	0.207	0.029	0.002	0.977	0.105	Ferragnes	2000,2-3+2000,8-27+2000,13-162
74	11	29962426	18	16477632	9.89	0.55	0.529	0.217	0.031	0.002	0.979	0.116	Winters	2000,9-157+2000,8-27
85	11	152581225	91.5	84021777	50.41	0.551	0.487	0.224	0.031	0.002	0.975	0.112	Nonpareil	2000,16-81+2000,13-162
64	11	32586742	19.6	17646055	10.59	0.542	0.567	0.266	0.032	0.001	0.975	0.128	Nonpareil	2000,2-3
72	11	77215051	46.3	38735265	23.24	0.502	0.529	0.242	0.03	0.001	0.982	0.12	Winters	2000,8-27
73	11	46167391	27.7	21701280	13.02	0.47	0.53	0.244	0.031	0.003	0.979	0.123	Winters	2000,8-27
79	11	14657373	8.8	7194411	4.32	0.491	0.498	0.23	0.029	0.002	0.986	0.113	Winters	2000,9-157+2000,8-27
80	11	56648577	34	28375628	17.03	0.501	0.504	0.225	0.028	0.002	0.972	0.112	Winters	2000,9-157+2000,8-27
81	11	35066675	21	17503781	10.5	0.499	0.521	0.23	0.03	0.003	0.978	0.117	Ferragnes	2000,2-3+2000,8-27+2000,13-162

Data S2

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Data S3

Hypermethylation is associated with increased age in almond (Prunus dulcis [Mill.] D.A. Webb) accessions

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DataS3. File containing general infromation on DMRs overlapping transposable elements.

Contents:

AgeCohortRep_DMRs_classified:

Chromosome - chromosome where DMR is located; Start - starting position of the DMR; End - ending position of the DMR; DMR_length- lenght of the DMR; ID - identificator f the DMR; ChrAligned - Chromosome where the transposable element is located; Source - software used for the prediction of TEs (EDTA); TEType - type of transposable element; TeStart - begining of the TE; TEEnd - end of the TE; TE_length - actual length of the TE; TE_ID - identifyier of the specific transposable lement in the Nonpareil almond genome; Parent - main repetitive region for TE; Name - Name of homologous TE in database; Calssifciation - class in which the TE falls, Seq_Ontology - ontology for the TE, Method - whether the TE was predicted based on homology or structural features; Motif - sequence motifi for TE, TSD - Target Site Duplication, TIR - Terminal Inverted Repeat; Overlpa - overlap in bp between the DMR and the TE

Chromosome	Start	End	DMR_lenght	ID	Score	ChrAligned	Source	TEType	TEStart	TEEnd	TE_lenght	Strand	ID_TE	Parent	Name	Classification	Seq_Ontology	Identity	Method	Motif	TSD	TIR	Overlap
Chr5	10489608	10489881	273	CG_Chr5_10489608_10489881	-156.0763596	Chr5	EDTA	LTR_retrotransposon	10489300	10492396	3096	-	TE_homo_138776		TE_00000877_LTR	LTR/unknown	SO:0000186	0.827	homology				273
Chr7	15441839	15442239	400	CG_Chr7_15441839_15442239	-119.3748303	Chr7	EDTA	repeat_region	15441485	15442497	1012	-	TE_homo_188243		RLX_76433|LTR_Mt_chr_02_100|LTR|02.01.01.99|3880|Medicago	Unspecified	SO:0000657	0.72	homology				400
Chr3	27300763	27301067	304	CG_Chr3_27300763_27301067	-116.8497717	Chr3	EDTA	Mutator_TIR_transposon	27300965	27301198	233	+	TE_homo_100867		TE_00001943	DNA/DTM	SO:0000280	0.802	homology				103
Chr2	29875858	29875989	131	CG_Chr2_29875858_29875989	-106.2533983	Chr2	EDTA	repeat_region	29875886	29876010	124	-	TE_homo_73153		TE_00000010	Unknown	SO:0000657	0.876	homology				104
Chr1	49531825	49531956	131	CG_Chr1_49531825_49531956	-91.03358906	Chr1	EDTA	repeat_region	49531852	49531974	122	-	TE_homo_43179		TE_00000010	Unknown	SO:0000657	0.849	homology				105
Chr5	20223728	20224022	294	CG_Chr5_20223728_20224022	-86.95932889	Chr5	EDTA	Mutator_TIR_transposon	20223925	20224134	209	+	TE_homo_144374		TE_00001630	DNA/DTM	SO:0000280	0.852	homology				98
Chr3	2506089	2506183	94	CG_Chr3_2506089_2506183	-84.14051566	Chr3	EDTA	Gypsy_LTR_retrotransposon	2506161	2506291	130	+	TE_homo_78406		TE_00001643_LTR	LTR/Gypsy	SO:0000265	0.792	homology				23
Chr4	3096521	3096718	197	CG_Chr4_3096521_3096718	-78.89252508	Chr4	EDTA	Mutator_TIR_transposon	3096465	3096693	228	+	TE_homo_104034		TE_00001943	DNA/DTM	SO:0000280	0.764	homology				172
Chr4	808748	808966	218	CG_Chr4_808748_808966	-77.13755145	Chr4	EDTA	Mutator_TIR_transposon	808902	809027	125	-	TE_homo_102750		TE_00001943	DNA/DTM	SO:0000280	0.858	homology				65
Chr4	5001657	5001732	75	CG_Chr4_5001657_5001732	-73.82986463	Chr4	EDTA	repeat_region	5001638	5001796	158	+	TE_homo_104993		TE_00000010	Unknown	SO:0000657	0.861	homology				75
Chr2	29880215	29880306	91	CG_Chr2_29880215_29880306	-69.15006938	Chr2	EDTA	repeat_region	29880265	29880330	125	-	TE_homo_73190		TE_00000010	Unknown	SO:0000657	0.869	homology				91
Chr4	2171411	2171621	210	CG_Chr4_2171411_2171621	-65.96384984	Chr4	EDTA	Mutator_TIR_transposon	2171549	2171877	328	-	TE_homo_103614		TE_00001943	DNA/DTM	SO:0000280	0.826	homology				73
Chr8	13551400	13551574	174	CG_Chr8_13551400_13551574	-65.21442832	Chr8	EDTA	Gypsy_LTR_retrotransposon	13551311	13551490	179	-	TE_homo_209210		TE_00001492_LTR	LTR/Gypsy	SO:0000265	0.917	homology				90
Chr1	49521911	49522023	112	CG_Chr1_49521911_49522023	-65.1827759	Chr1	EDTA	repeat_region	49521880	49522075	195	-	TE_homo_43107		TE_00000010	Unknown	SO:0000657	0.793	homology				112
Chr7	18130050	18130149	99	CG_Chr7_18130050_18130149	-61.52712576	Chr7	EDTA	Mutator_TIR_transposon	18130023	18130324	301	+	TE_homo_190405		TE_00001630	DNA/DTM	SO:0000280	0.806	homology				99
Chr4	30642943	30643153	210	CG_Chr4_30642943_30643153	-61.14175077	Chr4	EDTA	repeat_region	30641478	30643765	2287	-	TE_homo_128821		RLG_56030|LTR_Al_scaffold_0003_560|LTR/Gypsy|02.01.01.10.99|59689|Arabidopsis	Unspecified	SO:0000657	0.963	homology				210
Chr6	25516205	25516347	142	CG_Chr6_25516205_25516347	57.09078035	Chr6	EDTA	LTR_retrotransposon	25516064	25516362	298	-	TE_homo_168184		TE_00000854_INT	LTR/unknown	SO:0000186	0.834	homology				142
Chr5	20294807	20294942	135	CG_Chr5_20294807_20294942	-56.57389137	Chr5	EDTA	Mutator_TIR_transposon	20294739	20295129	390	+	TE_homo_144398		TE_00001943	DNA/DTM	SO:0000280	0.814	homology				135
Chr6	25521396	25521538	142	CG_Chr6_25521396_25521538	56.5667467	Chr6	EDTA	LTR_retrotransposon	25521200	25521502	302	-	TE_homo_168208		TE_00000854_INT	LTR/unknown	SO:0000186	0.828	homology				106
Chr8	22810116	22810224	108	CG_Chr8_22810116_22810224	-56.09482472	Chr8	EDTA	repeat_region	22810075	22810268	193	+	TE_homo_215690		TE_00000010	Unknown	SO:0000657	0.788	homology				108
Chr4	4998847	4998933	86	CG_Chr4_4998847_4998933	-55.23768428	Chr4	EDTA	repeat_region	4998861	4998977	116	-	TE_homo_104969		TE_00000010	Unknown	SO:0000657	0.904	homology				73
Chr5	20121611	20121817	206	CG_Chr5_20121611_20121817	-54.82663656	Chr5	EDTA	repeat_region	20121413	20121728	315	+	TE_homo_144344		TE_00000378	Unknown	SO:0000657	0.941	homology				117
Chr5	10489939	10490019	80	CG_Chr5_10489939_10490019	-54.76687063	Chr5	EDTA	LTR_retrotransposon	10489300	10492396	3096	-	TE_homo_138776		TE_00000877_LTR	LTR/unknown	SO:0000186	0.827	homology				80
Chr4	30642774	30642891	117	CG_Chr4_30642774_30642891	-52.08506729	Chr4	EDTA	repeat_region	30641478	30643765	2287	-	TE_homo_128821		RLG_56030|LTR_Al_scaffold_0003_560|LTR/Gypsy|02.01.01.10.99|59689|Arabidopsis	Unspecified	SO:0000657	0.963	homology				117
Chr1	16239049	16239120	71	CG_Chr1_16239049_16239120	-51.66783133	Chr1	EDTA	LTR_retrotransposon	16238785	16239552	767	+	TE_homo_16332		TE_00001283_LTR	LTR/unknown	SO:0000186	0.859	homology				71
Chr2	22289722	22289829	107	CG_Chr2_22289722_22289829	-50.22925891	Chr2	EDTA	Mutator_TIR_transposon	22289672	22289759	87	+	TE_homo_68133		TE_00001630	DNA/DTM	SO:0000280	0.807	homology				37
Chr1	48859193	48859300	107	CG_Chr1_48859193_48859300	-49.91934691	Chr1	EDTA	Mutator_TIR_transposon	48859159	48859370	211	+	TE_homo_42318		TE_00001180	MITE/DTM	SO:0000280	0.821	homology				107
Chr5	1181623	1181704	81	CG_Chr5_1181623_1181704	-48.66645341	Chr5	EDTA	helitron	1181530	1181715	185	-	TE_homo_129859		TE_00000707	DNA/Helitron	SO:0000544	0.828	homology				81
Chr4	5006037	5006128	91	CG_Chr4_5006037_5006128	-48.0817507	Chr4	EDTA	repeat_region	5006015	5006138	123	+	TE_homo_105035		TE_00000010	Unknown	SO:0000657	0.883	homology				91
Chr8	7522206	7522331	125	CG_Chr8_7522206_7522331	-47.93015609	Chr8	EDTA	repeat_region	7522248	7522362	114	-	TE_homo_202634		TE_00000117	Unknown	SO:0000657	0.86	homology				84
Chr5	19801517	19801651	134	CG_Chr5_19801517_19801651	-47.79353916	Chr5	EDTA	Mutator_TIR_transposon	19801530	19801622	92	-	TE_homo_144252		TE_00001630	DNA/DTM	SO:0000280	0.846	homology				93
Chr4	5731333	5731395	62	CG_Chr4_5731333_5731395	-46.72663954	Chr4	EDTA	Mutator_TIR_transposon	5731192	5731513	321	-	TE_homo_105519		TE_00001943	DNA/DTM	SO:0000280	0.787	homology				62
Chr8	3281758	3281830	72	CG_Chr8_3281758_3281830	-45.32342205	Chr8	EDTA	LTR_retrotransposon	3281098	3281847	749	+	TE_homo_198270		TE_00000854_INT	LTR/unknown	SO:0000186	0.829	homology				72
Chr5	15549780	15549865	85	CG_Chr5_15549780_15549865	-44.30408033	Chr5	EDTA	Mutator_TIR_transposon	15549767	15550106	339	-	TE_homo_142165		TE_00001943	DNA/DTM	SO:0000280	0.771	homology				85
Chr8	7522882	7523060	178	CG_Chr8_7522882_7523060	-41.74771496	Chr8	EDTA	repeat_region	7522926	7523067	141	+	TE_homo_202637		TE_00000043	Unknown	SO:0000657	0.887	homology				135
Chr4	30638289	30638351	62	CG_Chr4_30638289_30638351	-41.21932452	Chr4	EDTA	Mutator_TIR_transposon	30637971	30639533	1562	.	TE_struc_793		CM037991.1:30637971..30639533	DNA/DTM	SO:0000280	0.9	structural		AGGCAAC_AGGCAAC_100.0	CGATTTGTTG_CAACATATCG	62
Chr8	3353884	3353963	79	CG_Chr8_3353884_3353963	-40.93229082	Chr8	EDTA	LTR_retrotransposon	3351280	3354337	3057	+	TE_homo_198370		TE_00000877_LTR	LTR/unknown	SO:0000186	0.897	homology				79
Chr4	1388366	1388429	63	CG_Chr4_1388366_1388429	-40.59939913	Chr4	EDTA	LTR_retrotransposon	1388264	1388615	351	+	TE_homo_103032		TE_00001622_INT	LTR/unknown	SO:0000186	0.842	homology				63
Chr8	18409015	18409084	69	CG_Chr8_18409015_18409084	-40.52143798	Chr8	EDTA	Tc1_Mariner_TIR_transposon	18408382	18409070	688	-	TE_homo_213133		TE_00001239	DNA/DTT	SO:0000278	0.875	homology				55
Chr5	15552203	15552299	96	CG_Chr5_15552203_15552299	-40.37981098	Chr5	EDTA	LTR_retrotransposon	15551682	15552272	590	+	TE_homo_142176		TE_00000854_INT	LTR/unknown	SO:0000186	0.83	homology				69
Chr8	5559737	5559901	164	CG_Chr8_5559737_5559901	-40.25396803	Chr8	EDTA	repeat_region	5558468	5560106	1638	-	TE_homo_200556		TE_00000161	Unknown	SO:0000657	0.998	homology				164
Chr4	5000263	5000322	59	CG_Chr4_5000263_5000322	-39.71210695	Chr4	EDTA	repeat_region	5000226	5000375	149	-	TE_homo_104981		TE_00000010	Unknown	SO:0000657	0.904	homology				59
Chr2	20567931	20568094	163	CG_Chr2_20567931_20568094	-38.10748561	Chr2	EDTA	Mutator_TIR_transposon	20568051	20568165	114	+	TE_homo_66696		TE_00002081	DNA/DTM	SO:0000280	0.93	homology				44
Chr5	20295337	20295551	214	CG_Chr5_20295337_20295551	-37.93489835	Chr5	EDTA	repeat_region	20295370	20296048	678	-	TE_homo_144400		TE_00000378	Unknown	SO:0000657	0.963	homology				182
Chr4	1386347	1386574	227	CG_Chr4_1386347_1386574	-37.82209082	Chr4	EDTA	LTR_retrotransposon	1386430	1387160	730	-	TE_homo_103027		TE_00000807_INT	LTR/unknown	SO:0000186	0.862	homology				145
Chr8	19411804	19411888	84	CG_Chr8_19411804_19411888	-37.75727308	Chr8	EDTA	Mutator_TIR_transposon	19411721	19411821	100	+	TE_homo_213876		TE_00001943	DNA/DTM	SO:0000280	0.77	homology				17
Chr5	13861386	13861598	212	CG_Chr5_13861386_13861598	-36.35235891	Chr5	EDTA	repeat_region	13861255	13861620	365	+	TE_homo_141247		TE_00000151	Unknown	SO:0000657	0.961	homology				212
Chr5	19742612	19742733	121	CG_Chr5_19742612_19742733	-36.26888402	Chr5	EDTA	Mutator_TIR_transposon	19742613	19742770	157	-	TE_homo_144224		TE_00001943	DNA/DTM	SO:0000280	0.807	homology				121
Chr3	1874294	1874367	73	CG_Chr3_1874294_1874367	-36.15838738	Chr3	EDTA	LTR_retrotransposon	1874354	1874494	140	+	TE_homo_77742		TE_00000854_INT	LTR/unknown	SO:0000186	0.829	homology				14
Chr6	15830832	15830933	101	CG_Chr6_15830832_15830933	-35.96766064	Chr6	EDTA	repeat_region	15830840	15831001	161	+	TE_homo_158847		XXX_8114|ARSiRGRR00500014|rRNA|10.01.01.02|3702|Arabidopsis	Unspecified	SO:0000657	0.91	homology				94
Chr5	15784860	15784949	89	CG_Chr5_15784860_15784949	-35.86637335	Chr5	EDTA	Mutator_TIR_transposon	15784720	15784872	152	-	TE_homo_142269		TE_00001630	DNA/DTM	SO:0000280	0.846	homology				12
Chr4	6969150	6969205	55	CG_Chr4_6969150_6969205	-35.64652029	Chr4	EDTA	repeat_region	6969069	6969228	159	+	TE_homo_106399		TE_00000010	Unknown	SO:0000657	0.862	homology				55
Chr7	16101571	16101656	85	CG_Chr7_16101571_16101656	-34.87671705	Chr7	EDTA	repeat_region	16101521	16101737	216	+	TE_homo_188864		TE_00000010	Unknown	SO:0000657	0.963	homology				85
Chr4	4000739	4000808	69	CG_Chr4_4000739_4000808	-34.40566606	Chr4	EDTA	Mutator_TIR_transposon	4000568	4000830	262	+	TE_homo_104492		TE_00001943	DNA/DTM	SO:0000280	0.777	homology				69
Chr3	1352238	1352340	102	CG_Chr3_1352238_1352340	-33.44815159	Chr3	EDTA	Mutator_TIR_transposon	1352151	1352427	276	+	TE_homo_77199		TE_00001943	DNA/DTM	SO:0000280	0.77	homology				102
Chr6	2159140	2159365	225	CG_Chr6_2159140_2159365	-32.80998994	Chr6	EDTA	PIF_Harbinger_TIR_transposon	2158858	2159187	329	+	TE_homo_146572		TE_00001066	DNA/DTH	SO:0000284	0.867	homology				47
Chr2	22136375	22136689	314	CG_Chr2_22136375_22136689	-32.77043783	Chr2	EDTA	repeat_region	22136356	22136659	303	+	TE_homo_68035		TE_00000102	Unknown	SO:0000657	0.908	homology				284
Chr4	15376345	15377349	1004	CG_Chr4_15376345_15377349	-32.23714136	Chr4	EDTA	Gypsy_LTR_retrotransposon	15376692	15377112	420	-	TE_homo_113085		TE_00000651_INT	LTR/Gypsy	SO:0000265	0.859	homology				421
Chr4	9433794	9433846	52	CG_Chr4_9433794_9433846	-31.74543231	Chr4	EDTA	Mutator_TIR_transposon	9433520	9433838	318	-	TE_homo_108070		TE_00000698	DNA/DTM	SO:0000280	0.795	homology				44
Chr6	3043318	3043420	102	CG_Chr6_3043318_3043420	-31.1471301	Chr6	EDTA	Gypsy_LTR_retrotransposon	3043288	3043647	359	-	TE_homo_147025		TE_00000971_INT	LTR/Gypsy	SO:0000265	0.882	homology				102
Chr6	28384068	28384140	72	CG_Chr6_28384068_28384140	-31.12163731	Chr6	EDTA	Mutator_TIR_transposon	28383514	28384150	636	-	TE_homo_170093		TE_00000488	DNA/DTM	SO:0000280	0.931	homology				72
Chr1	27637081	27637192	111	CG_Chr1_27637081_27637192	-31.12008529	Chr1	EDTA	LTR_retrotransposon	27635258	27637750	2492	+	TE_homo_27921		TE_00000877_LTR	LTR/unknown	SO:0000186	0.817	homology				111
Chr8	11412363	11412434	71	CG_Chr8_11412363_11412434	-30.87267257	Chr8	EDTA	LTR_retrotransposon	11410747	11415450	4703	?	LTRRT_1902	repeat_region_1902	Name=TE_00001023	Classification=LTR/unknown	SO:0000186	0.996	structural	TGCA	ATGGA		71
Chr6	2878556	2878669	113	CG_Chr6_2878556_2878669	-30.82302069	Chr6	EDTA	LTR_retrotransposon	2877886	2879683	1797	?	LTRRT_1390	repeat_region_1390	Name=CM037993.1:2877886..2879683	Classification=LTR/unknown	SO:0000186	0.9915	structural	TGCA	AATCC		113
Chr1	49154528	49154679	151	CG_Chr1_49154528_49154679	-30.81233976	Chr1	EDTA	repeat_region	49153763	49155349	1586	-	TE_homo_42582		TE_00000031	Unknown	SO:0000657	0.91	homology				151
Chr8	11412950	11413081	131	CG_Chr8_11412950_11413081	-30.7745516	Chr8	EDTA	LTR_retrotransposon	11410747	11415450	4703	?	LTRRT_1902	repeat_region_1902	Name=TE_00001023	Classification=LTR/unknown	SO:0000186	0.996	structural	TGCA	ATGGA		131
Chr4	2172251	2172316	65	CG_Chr4_2172251_2172316	-30.24300801	Chr4	EDTA	Mutator_TIR_transposon	2172152	2172341	189	-	TE_homo_103615		TE_00001943	DNA/DTM	SO:0000280	0.827	homology				65
Chr3	2293429	2293511	82	CG_Chr3_2293429_2293511	-29.9764014	Chr3	EDTA	Mutator_TIR_transposon	2293260	2293517	257	+	TE_homo_78127		TE_00001943	DNA/DTM	SO:0000280	0.833	homology				82
Chr4	5084067	5084119	52	CG_Chr4_5084067_5084119	-29.8420094	Chr4	EDTA	Mutator_TIR_transposon	5083853	5084589	736	+	TE_homo_105099		TE_00001943	DNA/DTM	SO:0000280	0.783	homology				52
Chr4	4966637	4966795	158	CG_Chr4_4966637_4966795	-29.8067176	Chr4	EDTA	Mutator_TIR_transposon	4966605	4966710	105	-	TE_homo_104944		TE_00001407	DNA/DTM	SO:0000280	0.857	homology				73
Chr2	32187547	32187655	108	CG_Chr2_32187547_32187655	-29.2530622	Chr2	EDTA	Mutator_TIR_transposon	32187603	32187693	90	+	TE_homo_74282		TE_00001943	DNA/DTM	SO:0000280	0.8	homology				53
Chr5	13598987	13599074	87	CG_Chr5_13598987_13599074	-29.01899672	Chr5	EDTA	Gypsy_LTR_retrotransposon	13598596	13599026	430	-	TE_homo_141029		TE_00000618_INT	LTR/Gypsy	SO:0000265	0.831	homology				39
Chr2	23609066	23609347	281	CG_Chr2_23609066_23609347	-28.94797846	Chr2	EDTA	Gypsy_LTR_retrotransposon	23608980	23609161	181	-	TE_homo_69249		TE_00000651_INT	LTR/Gypsy	SO:0000265	0.929	homology				95
Chr6	12844580	12844755	175	CG_Chr6_12844580_12844755	-28.86673848	Chr6	EDTA	repeat_region	12844711	12844864	153	-	TE_homo_155607		TE_00000087	Unknown	SO:0000657	0.921	homology				45
Chr8	18408496	18408602	106	CG_Chr8_18408496_18408602	-28.68163445	Chr8	EDTA	Tc1_Mariner_TIR_transposon	18408382	18409070	688	-	TE_homo_213133		TE_00001239	DNA/DTT	SO:0000278	0.875	homology				106
Chr7	16484372	16484447	75	CG_Chr7_16484372_16484447	-28.50727476	Chr7	EDTA	LTR_retrotransposon	16482457	16484536	2079	+	TE_homo_189308		TE_00000877_LTR	LTR/unknown	SO:0000186	0.827	homology				75
Chr8	4333973	4334033	60	CG_Chr8_4333973_4334033	-28.26543046	Chr8	EDTA	LTR_retrotransposon	4332798	4334341	1543	+	TE_homo_199356		TE_00000877_LTR	LTR/unknown	SO:0000186	0.84	homology				60
Chr8	11016625	11016685	60	CG_Chr8_11016625_11016685	-28.06767564	Chr8	EDTA	CACTA_TIR_transposon	11016510	11016716	206	+	TE_homo_206441		TE_00000009	DNA/DTC	SO:0000285	0.981	homology				60
Chr2	1350251	1350335	84	CG_Chr2_1350251_1350335	-27.84011536	Chr2	EDTA	CACTA_TIR_transposon	1350073	1351085	1012	+	TE_homo_46929		TE_00000475	DNA/DTC	SO:0000285	0.949	homology				84
Chr1	15260536	15260724	188	CG_Chr1_15260536_15260724	-27.77111061	Chr1	EDTA	Mutator_TIR_transposon	15260528	15260671	143	-	TE_homo_15174		TE_00001935	MITE/DTM	SO:0000280	0.713	homology				135
Chr2	13649329	13649430	101	CG_Chr2_13649329_13649430	-27.73653916	Chr2	EDTA	repeat_region	13649179	13649427	248	+	TE_homo_59110		TE_00000419	Unknown	SO:0000657	0.838	homology				98
Chr4	3991297	3991354	57	CG_Chr4_3991297_3991354	-27.69356882	Chr4	EDTA	Tc1_Mariner_TIR_transposon	3991155	3991561	406	+	TE_homo_104465		TE_00001239	DNA/DTT	SO:0000278	0.817	homology				57
Chr4	5742241	5742302	61	CG_Chr4_5742241_5742302	-27.52911826	Chr4	EDTA	Mutator_TIR_transposon	5742200	5742350	150	-	TE_homo_105531		TE_00001943	DNA/DTM	SO:0000280	0.78	homology				61
Chr3	17747442	17747532	90	CG_Chr3_17747442_17747532	27.51884767	Chr3	EDTA	CACTA_TIR_transposon	17747410	17747566	156	+	TE_homo_92472		TE_00000993	DNA/DTC	SO:0000285	0.807	homology				90
Chr5	14730276	14730385	109	CG_Chr5_14730276_14730385	-27.26078059	Chr5	EDTA	LTR_retrotransposon	14730225	14730630	405	+	TE_homo_141836		TE_00000569_INT	LTR/unknown	SO:0000186	0.739	homology				109
Chr4	1833006	1833058	52	CG_Chr4_1833006_1833058	-27.16254145	Chr4	EDTA	PIF_Harbinger_TIR_transposon	1832825	1833010	185	+	TE_homo_103507		TE_00001588	MITE/DTH	SO:0000284	0.824	homology				4
Chr1	50800167	50800264	97	CG_Chr1_50800167_50800264	-27.11585835	Chr1	EDTA	Mutator_TIR_transposon	50800193	50800420	227	+	TE_homo_44037		TE_00001943	DNA/DTM	SO:0000280	0.794	homology				72
Chr4	15303555	15303741	186	CG_Chr4_15303555_15303741	-26.74208071	Chr4	EDTA	hAT_TIR_transposon	15303372	15303669	297	-	TE_homo_112988		TE_00001598	MITE/DTA	SO:0000279	0.96	homology				114
Chr2	17857247	17857331	84	CG_Chr2_17857247_17857331	26.67914938	Chr2	EDTA	repeat_region	17857246	17857347	101	+	TE_homo_64108		RLX_72394|LTR_Gm_14_4511|LTR|02.01.01.99|3847|Glycine	Unspecified	SO:0000657	0.814	homology				84
Chr1	5537818	5537906	88	CG_Chr1_5537818_5537906	-26.23426632	Chr1	EDTA	Mutator_TIR_transposon	5537114	5539152	2038	.	TE_struc_58		TE_00001668	DNA/DTM	SO:0000280	0.9	structural		AAAATTTTA_AAAATTTTA_100.0	GGGCTAATGA_TTATTAGCCC	88
Chr4	30643208	30643274	66	CG_Chr4_30643208_30643274	-25.54199414	Chr4	EDTA	repeat_region	30641478	30643765	2287	-	TE_homo_128821		RLG_56030|LTR_Al_scaffold_0003_560|LTR/Gypsy|02.01.01.10.99|59689|Arabidopsis	Unspecified	SO:0000657	0.963	homology				66
Chr2	23604783	23604948	165	CG_Chr2_23604783_23604948	-25.47729619	Chr2	EDTA	repeat_region	23604785	23605107	322	-	TE_homo_69242		TE_00000419	Unknown	SO:0000657	0.9	homology				164
Chr7	23025524	23025595	71	CG_Chr7_23025524_23025595	-25.24510833	Chr7	EDTA	Mutator_TIR_transposon	23025277	23025732	455	-	TE_homo_193003		TE_00001943	DNA/DTM	SO:0000280	0.782	homology				71
Chr5	12481905	12481989	84	CG_Chr5_12481905_12481989	-24.97882218	Chr5	EDTA	Mutator_TIR_transposon	12481840	12482084	244	+	TE_homo_140376		TE_00001943	DNA/DTM	SO:0000280	0.798	homology				84
Chr5	19662104	19662159	55	CG_Chr5_19662104_19662159	-24.75274441	Chr5	EDTA	Mutator_TIR_transposon	19662134	19662567	433	+	TE_homo_144213		TE_00001943	DNA/DTM	SO:0000280	0.786	homology				26
Chr1	47194722	47194800	78	CG_Chr1_47194722_47194800	-24.69046442	Chr1	EDTA	Mutator_TIR_transposon	47194739	47194868	129	-	TE_homo_41194		TE_00001943	DNA/DTM	SO:0000280	0.782	homology				62
Chr7	24180164	24180281	117	CG_Chr7_24180164_24180281	-24.63869743	Chr7	EDTA	Mutator_TIR_transposon	24180148	24180240	92	-	TE_homo_193443		TE_00001943	DNA/DTM	SO:0000280	0.779	homology				76
Chr4	3992134	3992221	87	CG_Chr4_3992134_3992221	-24.50362415	Chr4	EDTA	Tc1_Mariner_TIR_transposon	3991714	3992192	478	+	TE_homo_104467		TE_00001239	DNA/DTT	SO:0000278	0.803	homology				58
Chr6	8593561	8593645	84	CG_Chr6_8593561_8593645	-24.40143847	Chr6	EDTA	LTR_retrotransposon	8593189	8593668	479	+	TE_homo_159884		TE_00001959_INT	LTR/unknown	SO:0000186	0.908	homology				84
Chr1	15616760	15616905	145	CG_Chr1_15616760_15616905	-24.27271316	Chr1	EDTA	repeat_region	15616382	15616996	614	-	TE_homo_15660		TE_00000007	Unknown	SO:0000657	0.909	homology				145
Chr8	5874207	5874263	56	CG_Chr8_5874207_5874263	-24.19294258	Chr8	EDTA	LTR_retrotransposon	5873603	5875211	1608	-	TE_homo_200893		TE_00000877_LTR	LTR/unknown	SO:0000186	0.815	homology				56
Chr3	26889040	26889150	110	CG_Chr3_26889040_26889150	-24.01667887	Chr3	EDTA	LTR_retrotransposon	26888870	26889062	192	+	TE_homo_100567		TE_00001707_LTR	LTR/unknown	SO:0000186	0.815	homology				22
Chr6	17069780	17069838	58	CG_Chr6_17069780_17069838	-23.99630274	Chr6	EDTA	Gypsy_LTR_retrotransposon	17069498	17069862	364	+	TE_homo_160288		TE_00001951_INT	LTR/Gypsy	SO:0000265	0.807	homology				58
Chr2	18081001	18081173	172	CG_Chr2_18081001_18081173	-23.82437372	Chr2	EDTA	Gypsy_LTR_retrotransposon	18080915	18081331	416	+	TE_homo_64347		TE_00001643_LTR	LTR/Gypsy	SO:0000265	0.753	homology				172
Chr1	16476685	16476745	60	CG_Chr1_16476685_16476745	-23.52835826	Chr1	EDTA	Mutator_TIR_transposon	16476147	16476731	584	+	TE_homo_16514		TE_00000772	DNA/DTM	SO:0000280	0.726	homology				46
Chr7	18200433	18200489	56	CG_Chr7_18200433_18200489	-23.4352379	Chr7	EDTA	Mutator_TIR_transposon	18200355	18200490	135	+	TE_homo_190452		TE_00001943	DNA/DTM	SO:0000280	0.831	homology				56
Chr4	16345968	16346054	86	CG_Chr4_16345968_16346054	-23.22866082	Chr4	EDTA	Mutator_TIR_transposon	16345950	16346127	177	-	TE_homo_113913		TE_00001943	DNA/DTM	SO:0000280	0.798	homology				86
Chr8	7522706	7522810	104	CG_Chr8_7522706_7522810	-23.06661126	Chr8	EDTA	repeat_region	7522395	7522717	322	-	TE_homo_202636		TE_00000117	Unknown	SO:0000657	0.894	homology				11
Chr3	27527610	27527663	53	CG_Chr3_27527610_27527663	-22.81272149	Chr3	EDTA	Copia_LTR_retrotransposon	27527397	27527751	354	-	TE_homo_101142		TE_00000705_INT	LTR/Copia	SO:0000264	0.754	homology				53
Chr5	15936626	15936696	70	CG_Chr5_15936626_15936696	-22.68747354	Chr5	EDTA	Tc1_Mariner_TIR_transposon	15936550	15936725

Chr5	15552355	15552406	51	CG_Chr5_15552355_15552406	-22.03061075	Chr5	EDTA	LTR_retrotransposon	15552339	15553112	773	+	TE_homo_142178		TE_00000854_INT	LTR/unknown	SO:0000186	0.807	homology						51
Chr4	15429601	15430079	478	CG_Chr4_15429601_15430079	-21.95248299	Chr4	EDTA	Gypsy_LTR_retrotransposon	15429761	15431065	1304	-	TE_homo_113160		TE_00001809_LTR	LTR/Gypsy	SO:0002265	0.912	homology						319
Chr8	21294142	21294237	95	CG_Chr8_21294142_21294237	-21.93199994	Chr8	EDTA	LTR_retrotransposon	21293801	21294477	676	-	TE_homo_214761		TE_00000854_INT	LTR/unknown	SO:0000186	0.822	homology						95
Chr4	30637709	30637768	59	CG_Chr4_30637709_30637768	-21.8825431	Chr4	EDTA	repeat_region	30636599	30637822	1223	+	TE_homo_128814		XXX_152605|PRSgRGRR00000024|rRNA|10.01.01.01|4070|Solanaceae	Unspecified	SO:0000657	0.868	homology						59
ctg15	4716	4827	111	CG_ctg015_4716_4827	-21.76153681	ctg15	EDTA	Tc1_Mariner_TIR_transposon	4608	4876	268	-	TE_homo_423		TE_00000598	DNA/DTT	SO:0002278	0.996	homology						111
Chr4	1246683	1246762	79	CG_Chr4_1246683_1246762	-21.6777342	Chr4	EDTA	Tc1_Mariner_TIR_transposon	1246661	1247139	478	+	TE_homo_102902		TE_00001239	DNA/DTT	SO:0002278	0.798	homology						79
Chr6	25520197	25520251	54	CG_Chr6_25520197_25520251	21.31213051	Chr6	EDTA	LTR_retrotransposon	25519916	25520216	300	-	TE_homo_168202		TE_00000854_INT	LTR/unknown	SO:0000186	0.833	homology						19
Chr4	3990056	3990111	55	CG_Chr4_3990056_3990111	-21.08255387	Chr4	EDTA	Tc1_Mariner_TIR_transposon	3989886	3990149	263	+	TE_homo_104456		TE_00001239	DNA/DTT	SO:0002278	0.867	homology						55
Chr4	1801625	1801680	55	CG_Chr4_1801625_1801680	-20.87039935	Chr4	EDTA	Tc1_Mariner_TIR_transposon	1801475	1801807	332	+	TE_homo_103469		TE_00001239	DNA/DTT	SO:0002278	0.801	homology						55
Chr4	15432624	15432736	112	CG_Chr4_15432624_15432736	-20.2848498	Chr4	EDTA	hAT_TIR_transposon	15432693	15434027	1334	.	TE_struc_713		CM037991.1:15432693..15434027	DNA/DTA	SO:0000279	0 structural		GTCATCTG_gTCATCTG_87.5	CAATGGCGGA_tccgccactg				44
Chr1	6948932	6949012	80	CG_Chr1_6948932_6949012	-20.26042475	Chr1	EDTA	LTR_retrotransposon	6948789	6949386	597	+	TE_homo_7661		TE_00000877_LTR	LTR/unknown	SO:0000186	0.884	homology						80
Chr8	21903228	21903328	50	CG_Chr8_21903228_21903328	-20.18755676	Chr8	EDTA	Mutator_TIR_transposon	21903318	21903443	125	+	TE_homo_215161		TE_00001943	DNA/DTM	SO:0002280	0.813	homology						11
Chr6	26904051	26904180	129	CG_Chr6_26904051_26904180	-20.0148447	Chr6	EDTA	repeat_region	26903852	26904155	303	+	TE_homo_169291		TE_00000102	Unknown	SO:0000657	0.93	homology						104
Chr3	5625862	5625984	122	CG_Chr3_5625862_5625984	-19.92787254	Chr3	EDTA	Mutator_TIR_transposon	5625388	5625932	544	+	TE_homo_80409		TE_00001242	DNA/DTM	SO:0002280	0.918	homology						70
Chr3	8740248	8740305	57	CG_Chr3_8740248_8740305	-19.73837325	Chr3	EDTA	Copia_LTR_retrotransposon	8739146	8744048	4902	+	LTRRT_753	repeat_region_753	CM037990.1:8739146..8744048	LTR/Copia	SO:0002264	0.9969 structural	TGCA	TCCAA					57
Chr5	1811909	1811959	50	CG_Chr5_1811909_1811959	-19.52987533	Chr5	EDTA	LTR_retrotransposon	1811868	1812480	612	-	TE_homo_130493		TE_00000854_INT	LTR/unknown	SO:0000186	0.841	homology						50
Chr8	19050933	19050987	54	CG_Chr8_19050933_19050987	-19.31131007	Chr8	EDTA	repeat_region	19050842	19051045	203	-	TE_homo_213603		RLG_72372|LTR_Gm_01_33|LTR/Gypsy|02.01.01.10.99|3847|Glycine	Unspecified	SO:0000657	0.701	homology						54
Chr4	13925091	13925162	71	CG_Chr4_13925091_13925162	-19.30076914	Chr4	EDTA	repeat_region	13925014	13925220	206	-	TE_homo_111451		TE_00000169	Unknown	SO:0000657	0.757	homology						71
Chr3	6484081	6484158	77	CG_Chr3_6484081_6484158	-19.28762845	Chr3	EDTA	Gypsy_LTR_retrotransposon	6483511	6486403	2892	+	TE_homo_81264		TE_00001882_LTR	LTR/Gypsy	SO:0002265	0.823	homology						77
Chr8	17484387	17484443	56	CG_Chr8_17484387_17484443	-19.22110396	Chr8	EDTA	LTR_retrotransposon	17481168	17487311	6143	?	LTRRT_1953	repeat_region_1953	TE_00002131	LTR/unknown	SO:0000186	0.9979 structural	TGCA	AAATC					56
Chr7	20668415	20668497	82	CG_Chr7_20668415_20668497	-19.08831213	Chr7	EDTA	Mutator_TIR_transposon	20668402	20668540	138	+	TE_homo_191649		TE_00001943	DNA/DTM	SO:0002280	0.797	homology						82
Chr4	30637090	30637146	56	CG_Chr4_30637090_30637146	-19.04761776	Chr4	EDTA	repeat_region	30635543	30637389	1846	-	TE_homo_128813		XXX_8638|ARSiSTOTOT00000014|rRNA|10.01.01.99|3702|Arabidopsis	Unspecified	SO:0000657	0.972	homology						56
Chr1	52328873	52328954	81	CG_Chr1_52328873_52328954	-18.85009763	Chr1	EDTA	Mutator_TIR_transposon	52328913	52329017	104	-	TE_homo_45064		TE_00001630	DNA/DTM	SO:0002280	0.814	homology						42
Chr2	8861933	8861985	52	CG_Chr2_8861933_8861985	-18.62572684	Chr2	EDTA	LTR_retrotransposon	8861947	8862096	149	-	TE_homo_54336		TE_00001006_LTR	LTR/unknown	SO:0000186	0.926	homology						39
Chr6	2878830	2878949	119	CG_Chr6_2878830_2878949	-18.55444178	Chr6	EDTA	LTR_retrotransposon	2877886	2879683	1797	?	LTRRT_1390	repeat_region_1390	CM037993.1:2877886..2879683	LTR/unknown	SO:0000186	0.9915 structural	TGCA	AATCC					119
Chr2	1925351	1925423	72	CG_Chr2_1925351_1925423	-18.51259113	Chr2	EDTA	helitron	1925295	1925432	137	-	TE_homo_47500		TE_00000570	DNA/Helitron	SO:0000544	0.775	homology						72
Chr1	7132496	7132549	53	CG_Chr1_7132496_7132549	-18.43738757	Chr1	EDTA	PIF_Harbinger_TIR_transposon	7132338	7132948	610	.	TE_struc_72		TE_00001354	DNA/DTH	SO:0002284	0.3 structural		tta_tta_100.0	gagCCACTCC_ggagttgctc				53
Chr1	14602781	14602847	66	CG_Chr1_14602781_14602847	-18.37643863	Chr1	EDTA	repeat_region	14602750	14602910	160	-	TE_homo_14533		TE_00000265	Unknown	SO:0000657	0.823	homology						66
Chr4	21448874	21448947	73	CG_Chr4_21448874_21448947	-18.26566511	Chr4	EDTA	CACTA_TIR_transposon	21448733	21448893	160	+	TE_homo_119245		TE_00001454	DNA/DTC	SO:0002285	0.76	homology						19
Chr2	23649718	23650130	412	CG_Chr2_23649718_23650130	-18.21652369	Chr2	EDTA	repeat_region	23650108	23650295	187	-	TE_homo_69315		TE_00000657	Unknown	SO:0000657	0.925	homology						23
Chr6	27261191	27261257	66	CG_Chr6_27261191_27261257	18.1219926	Chr6	EDTA	hAT_TIR_transposon	27261139	27261308	169	+	TE_homo_169472		TE_00001751	MITE/DTA	SO:0002279	0.757	homology						66
Chr8	4733022	4733088	66	CG_Chr8_4733022_4733088	-18.03945765	Chr8	EDTA	Mutator_TIR_transposon	4732970	4733080	110	-	TE_homo_199773		TE_00001760	DNA/DTM	SO:0002280	0.881	homology						58
Chr2	57805	57910	105	CG_Chr2_57805_57910	-17.75456172	Chr2	EDTA	Gypsy_LTR_retrotransposon	57361	58326	965	-	TE_homo_45733		TE_00001809_LTR	LTR/Gypsy	SO:0002265	0.834	homology						105
Chr1	47351310	47351372	62	CG_Chr1_47351310_47351372	-17.44056145	Chr1	EDTA	Mutator_TIR_transposon	47351283	47351434	151	+	TE_homo_41296		TE_00001943	DNA/DTM	SO:0002280	0.815	homology						62
Chr8	24307853	24307953	72	CG_Chr8_24307881_24307953	-17.40093235	Chr8	EDTA	Mutator_TIR_transposon	24306148	24307932	1784	.	TE_struc_1373		CM037995.1:24306148..24307932	DNA/DTM	SO:0002280	0.9 structural		TAATTATAA_TAATTATAA_100.0	GGATTTGGAT_ATCCGAATCC				51
Chr3	11189463	11189536	73	CG_Chr3_11189463_11189536	-17.31110377	Chr3	EDTA	LTR_retrotransposon	11189219	11189484	265	+	TE_homo_85638		TE_00001715_INT	LTR/unknown	SO:0000186	0.95 homology							21
Chr2	26663544	26663620	76	CG_Chr2_26663544_26663620	-17.23009725	Chr2	EDTA	CACTA_TIR_transposon	26660968	26665828	4860	-	TE_struc_434		TE_00000505	DNA/DTC	SO:0002285	0.9 structural		CT_CT_100.0	CACTGTGACA_TGTCACTGTG				76
Chr3	9780647	9780720	73	CG_Chr3_9780647_9780720	-17.16097355	Chr3	EDTA	LINE_element	9779931	9780883	952	-	TE_homo_84119		TE_00000199	LINE/unknown	SO:0000194	0.708	homology						73
Chr8	11030934	11031035	101	CG_Chr8_11030934_11031035	-17.07645243	Chr8	EDTA	repeat_region	11030846	11030936	90	+	TE_homo_206457		RLC_8448|ARSiTERT00100008|LTR/Copia|02.01.01.05.99|3702|Arabidopsis	Unspecified	SO:0000657	0.927	homology						2
Chr1	29617322	29617415	93	CG_Chr1_29617322_29617415	-17.0308731	Chr1	EDTA	LTR_retrotransposon	29616355	29617669	1314	+	TE_homo_29554		TE_00002156_LTR	LTR/unknown	SO:0000186	0.949	homology						93
Chr2	20612259	20612311	52	CG_Chr2_20612259_20612311	-16.98707178	Chr2	EDTA	PIF_Harbinger_TIR_transposon	20612216	20612517	301	+	TE_homo_66761		TE_00001066_INT	DNA/DTH	SO:0002284	0.817	homology						52
Chr3	20753296	20753376	80	CG_Chr3_20753296_20753376	-16.74165779	Chr3	EDTA	LTR_retrotransposon	20751664	20757900	6236	?	LTRRT_900	repeat_region_900	TE_00001638	LTR/unknown	SO:0000186	1 structural	TGCA	TAAGG					80
Chr2	21545935	21546229	294	CG_Chr2_21545935_21546229	-16.70042292	Chr2	EDTA	PIF_Harbinger_TIR_transposon	21546078	21546207	129	+	TE_homo_67488		TE_00000590	DNA/DTH	SO:0002284	0.814	homology						130
Chr1	46495675	46495731	56	CG_Chr1_46495675_46495731	-16.60686702	Chr1	EDTA	CACTA_TIR_transposon	46495670	46495768	98	-	TE_homo_40771		TE_00000518	DNA/DTC	SO:0002285	0.923	homology						56
Chr1	7999612	7999665	53	CG_Chr1_7999612_7999665	-16.56105395	Chr1	EDTA	CACTA_TIR_transposon	7999369	8000229	860	-	TE_homo_8811		TE_00000883	DNA/DTC	SO:0002285	0.825	homology						53
Chr8	18082361	18082413	52	CG_Chr8_18082361_18082413	-16.14321472	Chr8	EDTA	Mutator_TIR_transposon	18082307	18082491	184	-	TE_homo_212981		TE_00000488	DNA/DTM	SO:0002280	0.73 homology							52
Chr6	3038983	3039035	52	CG_Chr6_3038983_3039035	-15.95759561	Chr6	EDTA	hAT_TIR_transposon	3038909	3039243	234	+	TE_homo_147018		TE_00001109	DNA/DTA	SO:0002279	0.788	homology						27
Chr7	21282363	21282428	65	CG_Chr7_21282363_21282428	-15.86012648	Chr7	EDTA	repeat_region	21282371	21282569	198	+	TE_homo_191979		RLX_76096|LTR_Mt_chr_03_243|LTR|02.01.01.99|3880|Medicago	Unspecified	SO:0000657	0.752	homology						58
Chr2	402223	402274	51	CG_Chr2_402223_402274	-15.65054389	Chr2	EDTA	Gypsy_LTR_retrotransposon	398637	408515	9878	+	LTRRT_389	repeat_region_389	CM037989.1:398637..408515	LTR/Gypsy	SO:0002265	0.9978 structural	TGCA	AGTAG					51
Chr1	48916128	48916194	66	CG_Chr1_48916128_48916194	-15.6058013	Chr1	EDTA	Gypsy_LTR_retrotransposon	48906686	48918383	11697	-	LTRRT_362	repeat_region_362	CM037988.1:48906686..48918383	LTR/Gypsy	SO:0002265	0.9884 structural	TGCA	TCCTT					66
Chr2	8893443	8893606	163	CG_Chr2_8893443_8893606	-15.44696938	Chr2	EDTA	LTR_retrotransposon	8893310	8894530	1220	-	TE_homo_54377		TE_00001452_INT	LTR/unknown	SO:0000186	0.794	homology						163
Chr7	114591	114666	75	CG_Chr7_114591_114666	-15.20566228	Chr7	EDTA	LTR_retrotransposon	114234	114626	392	+	TE_homo_172611		TE_00002159_LTR	LTR/unknown	SO:0000186	0.98 homology							35
Chr3	8564715	8564886	171	CG_Chr3_8564715_8564886	-15.07828354	Chr3	EDTA	Gypsy_LTR_retrotransposon	8564581	8565885	1304	-	TE_homo_83043		TE_00001809_LTR	LTR/Gypsy	SO:0002265	0.841	homology						171
Chr8	22961793	22961956	163	CG_Chr8_22961793_22961956	-15.07017567	Chr8	EDTA	Gypsy_LTR_retrotransposon	22961936	22962249	313	+	TE_homo_215822		TE_00001612_INT	LTR/Gypsy	SO:0002265	0.914	homology						21
Chr1	4118935	4118996	61	CG_Chr1_4118935_4118996	-14.93029158	Chr1	EDTA	Tc1_Mariner_TIR_transposon	4118996	4119158	162	+	TE_homo_5051		TE_00000519	DNA/DTT	SO:0002278	0.767	homology						1
Chr7	7157433	7157575	142	CG_Chr7_7157433_7157575	-14.75297681	Chr7	EDTA	CACTA_TIR_transposon	7157460	7157655	195	-	TE_homo_180004		TE_00001907	DNA/DTC	SO:0002285	0.755	homology						116
Chr2	7388434	7388499	65	CG_Chr2_7388434_7388499	-14.74709941	Chr2	EDTA	repeat_region	7388410	7388601	191	-	TE_homo_52814		TE_00000070	Unknown	SO:0000657	0.905	homology						65
Chr8	8582840	8582931	91	CG_Chr8_8582840_8582931	-14.72870959	Chr8	EDTA	Gypsy_LTR_retrotransposon	8582735	8582996	261	-	TE_homo_203926		TE_00000971_INT	LTR/Gypsy	SO:0002265	0.943	homology						91
Chr8	8582840	8582931	91	CG_Chr8_8582840_8582931	-14.72870959	Chr8	EDTA	helitron	8578023	8592239	15216	-	TE_struc_1251		TE_00001086	DNA/Helitron	SO:0000544	NA structural							91
Chr2	1067896	1067949	53	CG_Chr2_1067896_1067949	-14.52653926	Chr2	EDTA	CACTA_TIR_transposon	1067648	1068016	368	+	TE_homo_46606		TE_00000318	DNA/DTC	SO:0002285	0.818	homology						53
Chr2	30338120	30338273	153	CG_Chr2_30338120_30338273	-14.49002507	Chr2	EDTA	LINE_element	30338112	30338285	173	-	TE_homo_73409		TE_00000049	LINE/unknown	SO:0000194	0.82 homology							153
Chr1	45118929	45119002	73	CG_Chr1_45118929_45119002	-14.42950355	Chr1	EDTA	hAT_TIR_transposon	45118990	45119336	346	+	TE_homo_39831		TE_00001223	DNA/DTA	SO:0002279	0.89 homology							13
Chr4	2738754	2738887	133	CG_Chr4_2738754_2738887	-14.42226963	Chr4	EDTA	Mutator_TIR_transposon	2738713	2738825	112	+	TE_homo_103851		TE_00001068	DNA/DTM	SO:0002280	0.796	homology						71
Chr7	11457670	11458017	347	CG_Chr7_11457670_11458017	-14.39497192	Chr7	EDTA	Gypsy_LTR_retrotransposon	11457661	11457743	82	+	TE_homo_184849		TE_00000651_INT	LTR/Gypsy	SO:0002265	0.94 homology							73
Chr2	8593251	8593306	55	CG_Chr2_8593251_8593306	-14.25224173	Chr2	EDTA	repeat_region	8593083	8593816	733	-	TE_homo_64020		TE_00000657	Unknown	SO:0000657	0.942	homology						55
Chr2	8831581	8831644	63	CG_Chr2_8831581_8831644	-14.24607164	Chr2	EDTA	repeat_region	8830806	8831725	919	+	TE_homo_54300		TE_00000038	Unknown	SO:0000657	0.966	homology						63
Chr2	10312459	10312525	66	CG_Chr2_10312459_10312525	-14.17414238	Chr2	EDTA	CACTA_TIR_transposon	10311740	10312512	772	-	TE_homo_56138		TE_00000318	DNA/DTC	SO:0002285	0.92 homology							53
Chr1	4353754	4353866	112	CG_Chr1_4353754_4353866	-14.0715296	Chr1	EDTA	Gypsy_LTR_retrotransposon	4353342	4353903	561	-	TE_homo_5246		TE_00001809_LTR	LTR/Gypsy	SO:0002265	0.916	homology						112
Chr2	16162803	16162869	66	CG_Chr2_16162803_16162869	-13.99597624	Chr2	EDTA	repeat_region	16162652	16163162	510	+	TE_homo_62279		TE_00000416	Unknown	SO:0000657	0.886	homology						66
Chr3	22787447	22787498	51	CG_Chr3_22787447_22787498	-13.98565698	Chr3	EDTA	Mutator_TIR_transposon	22787390	22787511	121	-	TE_homo_97361		TE_00001943	DNA/DTM	SO:0002280	0.803	homology						51
Chr8	14688496	14688558	62	CG_Chr8_14688496_14688558	-13.86540111	Chr8	EDTA	LTR_retrotransposon	14688056	14690928	2872	+	TE_homo_210120		TE_00000877_LTR	LTR/unknown	SO:0000186	0.89 homology							62
Chr2	15636459	15636522	63	CG_Chr2_15636459_15636522	-13.819023	Chr2	EDTA	repeat_region	15635668	15636620	952	+	TE_homo_61629		RLX_72352|LTR_Gm_17_5606|LTR|02.01.01.99|3847|Glycine	Unspecified	SO:0000657	0.731	homology						63
Chr7	24147272	24147323	51	CG_Chr7_24147272_24147323	-13.7281971	Chr7	EDTA	Tc1_Mariner_TIR_transposon	24147210	24147344	134	+	TE_homo_193430		TE_00001239	DNA/DTT	SO:0002278	0.766	homology						51
Chr3	21362525	21362579	54	CG_Chr3_21362525_21362579	-13.50636111	Chr3	EDTA	repeat_region	21362056	21362538	482	+	TE_homo_96057		TE_00000215	Unknown	SO:0000657	0.804	homology						13
Chr2	22571973	22572071	98	CG_Chr2_22571973_22572071	-13.45984289	Chr2	EDTA	Tc1_Mariner_TIR_transposon	22571951	22572711	760	-	TE_homo_68355		TE_00001239	DNA/DTT	SO:0002278	0.769	homology						98
Chr3	22136782	22136841	59	CG_Chr3_22136782_22136841	-13.41582875	Chr3	EDTA	Copia_LTR_retrotransposon	22136785	22136908	123	-	TE_homo_96642		TE_00001837_LTR	LTR/Copia	SO:0002264	0.81 homology							57
Chr4	21448696	21448749	53	CG_Chr4_21448696_21448749	-13.41327245	Chr4	EDTA	CACTA_TIR_transposon	21448733	21448893	160	+	TE_homo_119245		TE_00001454	DNA/DTC	SO:0002285	0.76 homology							17
Chr4	20420350	20420412	62	CG_Chr4_20420350_20420412	-13.37974064	Chr4	EDTA	CACTA_TIR_transposon	20420386	20420619	233	+	TE_homo_117951		TE_00000475	DNA/DTC	SO:0002285	0.788	homology						27
Chr2	20433835	20433907	72	CG_Chr2_20433835_20433907	-13.32508004	Chr2	EDTA	repeat_region	20433549	20434075	526	-	TE_homo_66531		TE_00000281	Unknown	SO:0000657	0.892	homology						72
Chr7	22429615	22429689	74	CG_Chr7_22429615_22429689	-13.30262653	Chr7	EDTA	PIF_Harbinger_TIR_transposon	22429561	22429666	105	+	TE_homo_192578		TE_00000796	DNA/DTH	SO:0002284	0.887	homology						51
Chr1	31235940	31235993	53	CG_Chr1_31235940_31235993	-13.16219555	Chr1	EDTA	Gypsy_LTR_retrotransposon	31235258	31236303	1045	-	TE_homo_30790		TE_00001882_LTR	LTR/Gypsy	SO:0002265	0.769	homology						53
Chr7	15684285	15684362	77	CG_Chr7_15684285_15684362	-13.10912622	Chr7	EDTA	repeat_region	15684094	15685049	955	+	TE_homo_188547		RLX_76433|LTR_Mt_chr_02_100|LTR|02.01.01.99|3880|Medicago	Unspecified	SO:0000657	0.719	homology						77
Chr1	36007418	36007470	52	CG_Chr1_36007418_36007470	-12.93721285	Chr1	EDTA	Mutator_TIR_transposon	36007401	36007579	178	-	TE_homo_34083		TE_00001328	DNA/DTM	SO:0002280	0.853	homology						52
Chr2	6772900	6773071	171	CG_Chr2_6772900_6773071	-12.84622603	Chr2	EDTA	repeat_region	6772969	6773435	466	+	TE_homo_52143		RLX_70769|LTR_Gm_20_6544|LTR|02.01.01.99|3847|Glycine	Unspecified	SO:0000657	0.714	homology						103
Chr6	28759860	28759917	57	CG_Chr6_28759860_28759917	-12.84576104	Chr6	EDTA	Copia_LTR_retrotransposon	28759682	28760064	382	+	TE_homo_170263		TE_00000929_INT	LTR/Copia	SO:0002264	0.856	homology						57
Chr2	7933	7984	51	CG_Chr2_7933_7984	-12.78507888	Chr2	EDTA	LTR_retrotransposon	6977	8190	1213	?	LTRRT_385	repeat_region_385	TE_00001403	LTR/unknown	SO:0000186	0.9524 structural	TGCA	ACAAA					51
Chr1	18950671	18950727	56	CG_Chr1_18950671_18950727	-12.75678816	Chr1	EDTA	repeat_region	18950705	18950794	89	-	TE_homo_19533		TE_00000101	Unknown	SO:0000657	0.862	homology						23
Chr4	30638186	30638237	51	CG_Chr4_30638186_30638237	-12.74425769	Chr4	EDTA	LTR_retrotransposon	30638125	30638855	730	-	TE_homo_128816		TE_00001403_INT	LTR/unknown	SO:0000186	0.994	homology						51
Chr4	30638186	30638237	51	CG_Chr4_30638186_30638237	-12.74425769	Chr4	EDTA	Mutator_TIR_transposon	30637971	30639533	1562	.	TE_struc_793		CM037991.1:30637971..30639533	DNA/DTM	SO:0002280	0.9 structural		AGGCAAC_AGGCAAC_100.0	CGATTTGTTG_CAACATATCG				51
Chr3	28349927	28349992	65	CG_Chr3_28349927_28349992	-12.69263161	Chr3	EDTA	PIF_Harbinger_TIR_transposon	28349938	28350080	142	+	TE_homo_101600		TE_00001066	DNA/DTH	SO:0002284	0.838	homology						55
Chr5	1811789	1811845	56	CG_Chr5_1811789_1811845	-12.69138415	Chr5	EDTA	Tc1_Mariner_TIR_transposon	1811585	1811979	394	+	TE_homo_130492		TE_00001239	DNA/DTT	SO:0002278	0.764	homology						56
Chr2	23604118	23604171	53	CG_Chr2_23604118_23604171	-12.62416578	Chr2	EDTA	repeat_region	23604100	23604196	96	+	TE_homo_69239		TE_00000270	Unknown	SO:0000657	0.844	homology						53
Chr7	11469355	11469672	317	CG_Chr7_11469355_11469672	-12.52003734	Chr7	EDTA	Gypsy_LTR_retrotransposon	11469631	11470378	747	+	TE_homo_184863		TE_00001809_LTR	LTR/Gypsy	SO:0002265	0.873	homology						42
Chr3	24180399	24180450	51	CG_Chr3_24180399_24180450	-12.45439075	Chr3	EDTA	LTR_retrotransposon	24179702	24180488	786	+	TE_homo_98671		TE_00001854_INT	LTR/unknown	SO:0000186	0.836	homology						51
Chr4	2882233	2882346	113	CG_Chr4_2882233_2882346	-12.42463181	Chr4	EDTA	LTR_retrotransposon	2882215	2882880	665	+	TE_homo_103934		TE_00001911_INT	LTR/unknown	SO:0000186	0.981	homology						113
Chr2	13697910	13698092	182	CG_Chr2_13697910_13698092	-12.41280252	Chr2	EDTA	repeat_region	13697777	13698014	237	+	TE_homo_59169		TE_00000419	Unknown	SO:0000657	0.824	homology						104
Chr2	4520283	4520358	75	CG_Chr2_4520283_4520358	-12.40824046	Chr2	EDTA	repeat_region	4520086	4520302	216	-	TE_homo_50055		TE_00000337	Unknown	SO:0000657	0.758	homology						19
Chr2	22138815	22138910	95	CG_Chr2_22138815_22138910	-12.21863802	Chr2	EDTA	PIF_Harbinger_TIR_transposon	22138593	22138916	323	-	TE_homo_68038		TE_00001588	MITE/DTH	SO:0002284	0.884	homology						95
Chr1	8219973	8220083	110	CG_Chr1_8219973_8220083	-12.19532187	Chr1	EDTA	repeat_region	8219197	8220719	1522	+	TE_homo_9050		RLX_70769|LTR_Gm_20_6544|LTR|02.01.01.99|3847|Glycine	Unspecified	SO:0000657	0.715	homology						110
Chr4	28530486	28530549	63	CG_Chr4_28530486_28530549	-12.14136165	Chr4	EDTA	Gypsy_LTR_retrotransposon	28522344	28533317	10973	-	LTRRT_1189	repeat_region_1189	CM037991.1:28522344..28533317	LTR/Gypsy	SO:0002265	1 structural	TGCA	GTTAC					63
Chr2	30797959	30798033	74	CG_Chr2_30797959_30798033	-12.13756739	Chr2	EDTA	Mutator_TIR_transposon	30797561	30798237	676	-	TE_homo_73680		TE_00001943	DNA/DTM	SO:0002280	0.815	homology						74
Chr1	406957	407013	56	CG_Chr1_406957_407013	-12.02188986	Chr1	EDTA	LTR_retrotransposon	404924	407457	2533	?	LTRRT_9	repeat_region_9	TE_00000940	LTR/unknown	SO:0000186	0.9965 structural	TGCA	TAATA					56
Chr7	9709612	9709667	55	CG_Chr7_9709612_9709667	-12.02141766	Chr7	EDTA	Mutator_TIR_transposon	9709124	9709747	623	-	TE_homo_182875		TE_00000074	DNA/DTM	SO:0002280	0.712	homology						55
Chr2	2551470	2551550	80	CG_Chr2_2551470_2551550	-11.95451808	Chr2	EDTA	LTR_retrotransposon	2550128	2551853	1725	+	TE_homo_48077		TE_00000569_INT	LTR/unknown	SO:0000186	0.909	homology						80
Chr4	13029912	13030001	89	CG_Chr4_13029912_13030001	-11.88871265	Chr4	EDTA	Gypsy_LTR_retrotransposon	13029081	13030150	1069	-	TE_homo_110748		TE_00001492_LTR	LTR/Gypsy	SO:0002265	0.901	homology						89
Chr1	34078	34142	64	CG_Chr1_34078_34142	-11.73962953	Chr1	EDTA	Mutator_TIR_transposon	33876	35837	1961	-	TE_homo_1817		TE_00001081	DNA/DTM	SO:0002280	0.826	homology

Chr1	13501811	13501861	50	CG_Chr1_13501811_13501861	-10.63826677	Chr1	EDTA	repeat_region	13501758	13501990	232	-	TE_homo_13451			TE_00000166	Unknown	SO:0000657	0.961	homology					50
Chr7	11057309	11057383	74	CG_Chr7_11057309_11057383	-10.58402159	Chr7	EDTA	LTR_retrotransposon	11051563	11058032	6469	?	LTRRT_1707	repeat_region_1707		TE_00001156	LTR/unknown	SO:0000186	1	structural	TGCA	TCTCC			74
Chr6	16174918	16174984	66	CG_Chr6_16174918_16174984	-10.4781204	Chr6	EDTA	Copia_LTR_retrotransposon	16174000	16178267	4267	+	LTRRT_1491	repeat_region_1491		CM037993.1:16174000..16178267	LTR/Copia	SO:0000264	0.9402	structural	TGCA	AAATT			66
Chr2	13095504	13095574	70	CG_Chr2_13095504_13095574	-10.42915888	Chr2	EDTA	Mutator_TIR_transposon	13095446	13096626	1180	-	TE_homo_58529			TE_00001712	DNA/DTM	SO:0000280	0.747	homology					70
Chr6	13104031	13104081	50	CG_Chr6_13104031_13104081	-10.39094446	Chr6	EDTA	Mutator_TIR_transposon	13103880	13104059	179	+	TE_homo_155898			TE_00001063	MITE/DTM	SO:0000280	0.863	homology					28
Chr1	4361383	4361493	110	CG_Chr1_4361383_4361493	-10.38002514	Chr1	EDTA	Mutator_TIR_transposon	4360686	4361502	816	-	TE_homo_5252			TE_00001302	DNA/DTM	SO:0000280	0.892	homology					110
Chr3	11778777	11778836	59	CG_Chr3_11778777_11778836	-10.34584618	Chr3	EDTA	repeat_region	11778641	11778896	255	-	TE_homo_86383			TE_00000416	Unknown	SO:0000657	0.718	homology					59
Chr3	5633730	5633960	230	CG_Chr3_5633730_5633960	-10.32085645	Chr3	EDTA	Mutator_TIR_transposon	5633871	5633992	121	+	TE_homo_80421			TE_00001426	DNA/DTM	SO:0000280	0.771	homology					90
Chr1	33898200	33898296	96	CG_Chr1_33898200_33898296	-10.25539195	Chr1	EDTA	Mutator_TIR_transposon	33898275	33898450	175	+	TE_homo_32688			TE_00001394	DNA/DTM	SO:0000280	0.771	homology					22
Chr8	7389110	7389171	61	CG_Chr8_7389110_7389171	-10.23493732	Chr8	EDTA	Copia_LTR_retrotransposon	7386555	7391031	4476	-	LTRRT_1862	repeat_region_1862		CM037995.1:7386555..7391031	LTR/Copia	SO:0000264	0.9615	structural	TGCA	AGATG			61
Chr8	16865903	16866043	140	CG_Chr8_16865903_16866043	-10.00473825	Chr8	EDTA	Mutator_TIR_transposon	16865879	16866048	169	+	TE_homo_211897			TE_00001394	DNA/DTM	SO:0000280	0.752	homology					140
Chr6	16386739	16386793	54	CG_Chr6_16386739_16386793	-9.960409301	Chr6	EDTA	hAT_TIR_transposon	16386747	16387383	636	+	TE_homo_159515			TE_00000722	DNA/DTA	SO:0000279	0.872	homology					47
Chr6	28965274	28965370	96	CG_Chr6_28965274_28965370	-9.897528463	Chr6	EDTA	repeat_region	28965232	28965371	139	-	TE_homo_170336			TE_00000070	Unknown	SO:0000657	0.928	homology					96
Chr2	19082332	19082387	55	CG_Chr2_19082332_19082387	-9.630721926	Chr2	EDTA	LTR_retrotransposon	19082012	19082358	346	-	TE_homo_65333			TE_00000619_INT	LTR/unknown	SO:0000186	0.959	homology					26
Chr2	624529	624729	200	CG_Chr2_624529_624729	-9.173019978	Chr2	EDTA	Mutator_TIR_transposon	624533	624673	140	-	TE_homo_46209			TE_00000501	DNA/DTM	SO:0000280	0.737	homology					141
Chr7	25964223	25964274	51	CG_Chr7_25964223_25964274	-7.940285651	Chr7	EDTA	Mutator_TIR_transposon	25963502	25965168	1666	-	TE_homo_194759			TE_00001081	DNA/DTM	SO:0000280	0.798	homology					51
Chr7	19514967	19515044	77	CG_Chr7_19514967_19515044	-7.834303618	Chr7	EDTA	Mutator_TIR_transposon	19514912	19515019	107	+	TE_homo_191035			TE_00002102	DNA/DTM	SO:0000280	0.766	homology					52
Chr1	7391768	7391825	57	CG_Chr1_7391768_7391825	-7.739721099	Chr1	EDTA	CACTA_TIR_transposon	7391085	7391806	721	-	TE_homo_8095			TE_00000475	DNA/DTC	SO:0000285	0.964	homology					38
Chr1	34349857	34349978	121	CG_Chr1_34349857_34349978	-7.577062122	Chr1	EDTA	Copia_LTR_retrotransposon	34349702	34350963	1261	+	TE_homo_32951			TE_00000705_INT	LTR/Copia	SO:0000264	0.842	homology					121
Chr8	12248636	12248710	74	CG_Chr8_12248636_12248710	6.513597169	Chr8	EDTA	Mutator_TIR_transposon	12248706	12248791	85	+	TE_homo_207743			TE_00000603	DNA/DTM	SO:0000280	0.824	homology					5
Chr1	23255506	23255564	58	CG_Chr1_23255506_23255564	-4.81983369	Chr1	EDTA	LTR_retrotransposon	23252857	23261459	8602	-	TE_homo_24190			TE_00000849_LTR	LTR/unknown	SO:0000186	0.844	homology					58
Chr7	13145039	13145091	52	CG_Chr7_13145039_13145091	-4.578586952	Chr7	EDTA	LTR_retrotransposon	13144225	13145740	1515	+	TE_homo_186388			TE_00000912_LTR	LTR/unknown	SO:0000186	0.88	homology					52
Chr1	32289590	32289642	52	CG_Chr1_32289590_32289642	-1.48078934	Chr1	EDTA	PIF_Harbinger_TIR_transposon	32289515	32290119	604	+	TE_homo_31534			TE_00000771	DNA/DTH	SO:0000284	0.88	homology					52
Chr5	20295241	20295517	276	CG_Chr5_20295241_20295517	-61.85665518	Chr5	EDTA	repeat_region	20295370	20296048	678	-	TE_homo_144400			TE_00000378	Unknown	SO:0000657	0.963	homology					148
Chr4	3096614	3096856	242	CG_Chr4_3096614_3096856	-59.89458865	Chr4	EDTA	Mutator_TIR_transposon	3096465	3096693	228	+	TE_homo_104034			TE_00001943	DNA/DTM	SO:0000280	0.764	homology					79
Chr5	15549782	15549957	175	CG_Chr5_15549782_15549957	-55.69738751	Chr5	EDTA	Mutator_TIR_transposon	15549767	15550106	339	-	TE_homo_142165			TE_00001943	DNA/DTM	SO:0000280	0.771	homology					175
Chr4	30642996	30643180	184	CG_Chr4_30642996_30643180	-50.31373374	Chr4	EDTA	repeat_region	30641478	30643765	2287	-	TE_homo_128821			RLG_56030|LTR_AI_scaffold_0003_560|LTR/Gypsy|02.01.01.10.99|59689|Arabidopsis	Unspecified	SO:0000657	0.963	homology					184
Chr8	21903277	21903446	169	CG_Chr8_21903277_21903446	-48.5533794	Chr8	EDTA	Mutator_TIR_transposon	21903318	21903443	125	+	TE_homo_215161			TE_00001943	DNA/DTM	SO:0000280	0.813	homology					126
Chr3	27300762	27301069	307	CG_Chr3_27300762_27301069	-47.25244363	Chr3	EDTA	Mutator_TIR_transposon	27300965	27301198	233	+	TE_homo_100867			TE_00001943	DNA/DTM	SO:0000280	0.802	homology					105
Chr3	1352222	1352415	193	CG_Chr3_1352222_1352415	-45.4666929	Chr3	EDTA	Mutator_TIR_transposon	1352151	1352427	276	+	TE_homo_77199			TE_00001943	DNA/DTM	SO:0000280	0.77	homology					193
Chr7	23025297	23025559	262	CG_Chr7_23025297_23025559	-44.19520504	Chr7	EDTA	Mutator_TIR_transposon	23025277	23025732	455	-	TE_homo_193003			TE_00001943	DNA/DTM	SO:0000280	0.782	homology					262
Chr1	29765238	29765364	126	CG_Chr1_29765238_29765364	42.21087443	Chr1	EDTA	repeat_region	29764813	29765270	457	+	TE_homo_29689			RIX_8691|BRSiTERT00300017|LINE|02.01.02.05|3708|Brassica	Unspecified	SO:0000657	0.736	homology					32
Chr3	6020035	6020119	84	CG_Chr3_6020035_6020119	-40.85963866	Chr3	EDTA	Mutator_TIR_transposon	6019912	6020108	196	-	TE_homo_80741			TE_00001943	DNA/DTM	SO:0000280	0.778	homology					73
Chr3	5130264	5130466	202	CG_Chr3_5130264_5130466	-36.73692019	Chr3	EDTA	Copia_LTR_retrotransposon	5130209	5130619	410	-	TE_homo_80074			TE_00000633_LTR	LTR/Copia	SO:0000264	0.953	homology					202
Chr8	5559942	5560019	77	CG_Chr8_5559942_5560019	-36.56239254	Chr8	EDTA	repeat_region	5558468	5560106	1638	-	TE_homo_200556			TE_00000161	Unknown	SO:0000657	0.998	homology					77
Chr7	10933767	10933856	89	CG_Chr7_10933767_10933856	34.9096557	Chr7	EDTA	PIF_Harbinger_TIR_transposon	10933615	10933789	174	+	TE_homo_184343			TE_00001268	DNA/DTH	SO:0000284	0.84	homology					22
Chr4	30642675	30642820	145	CG_Chr4_30642675_30642820	-33.31172315	Chr4	EDTA	repeat_region	30641478	30643765	2287	-	TE_homo_128821			RLG_56030|LTR_AI_scaffold_0003_560|LTR/Gypsy|02.01.01.10.99|59689|Arabidopsis	Unspecified	SO:0000657	0.963	homology					145
Chr4	4966710	4966846	136	CG_Chr4_4966710_4966846	-31.63261502	Chr4	EDTA	PIF_Harbinger_TIR_transposon	4966619	4966730	111	-	TE_homo_104945			TE_00001842	DNA/DTH	SO:0000284	0.836	homology					20
Chr3	8582193	8582281	88	CG_Chr3_8582193_8582281	-30.71975223	Chr3	EDTA	Mutator_TIR_transposon	8582006	8582329	323	-	TE_homo_83054			TE_00001440	DNA/DTM	SO:0000280	0.969	homology					88
Chr3	20857411	20857634	223	CG_Chr3_20857411_20857634	-29.54555558	Chr3	EDTA	LTR_retrotransposon	20857066	20858569	1503	?	LTRRT_903	repeat_region_903		CM037990.1:20857066..20858569	LTR/unknown	SO:0000186	0.9571	structural	TGCA	CTTCA			223
Chr5	20072521	20072619	98	CG_Chr5_20072521_20072619	-29.47514704	Chr5	EDTA	LINE_element	20072271	20072691	420	-	TE_homo_144334			TE_00000186	LINE/unknown	SO:0000194	0.86	homology					98
Chr6	117210	117326	116	CG_Chr6_117210_117326	28.96028027	Chr6	EDTA	Copia_LTR_retrotransposon	117053	117591	538	+	TE_homo_144826			TE_00001999_INT	LTR/Copia	SO:0000264	0.77	homology					116
Chr2	8251331	8251455	124	CG_Chr2_8251331_8251455	-28.48103761	Chr2	EDTA	Mutator_TIR_transposon	8250686	8251499	813	-	TE_homo_53674			TE_00001319	DNA/DTM	SO:0000280	0.737	homology					124
Chr3	10081585	10081649	64	CG_Chr3_10081585_10081649	-28.45965158	Chr3	EDTA	Copia_LTR_retrotransposon	10081366	10081674	308	-	TE_homo_84473			TE_00000463_INT	LTR/Copia	SO:0000264	0.993	homology					64
Chr2	19467453	19467513	60	CG_Chr2_19467453_19467513	-27.11458342	Chr2	EDTA	Copia_LTR_retrotransposon	19463380	19468468	5088	-	LTRRT_607	repeat_region_607		CM037989.1:19463380..19468468	LTR/Copia	SO:0000264	1	structural	TGTA	GTGTT			60
Chr8	17645465	17645538	73	CG_Chr8_17645465_17645538	-27.0950445	Chr8	EDTA	Gypsy_LTR_retrotransposon	17644823	17645795	972	-	TE_homo_212616			TE_00001809_LTR	LTR/Gypsy	SO:0000265	0.842	homology					73
Chr7	22369963	22370067	104	CG_Chr7_22369963_22370067	-26.95483882	Chr7	EDTA	Mutator_TIR_transposon	22369879	22370215	336	+	TE_homo_192347			TE_00001618	DNA/DTM	SO:0000280	0.778	homology					104
Chr2	2745014	2745074	60	CG_Chr2_2745014_2745074	-26.44692462	Chr2	EDTA	CACTA_TIR_transposon	2744915	2745099	184	-	TE_homo_48267			TE_00000890	DNA/DTC	SO:0000285	0.81	homology					60
Chr4	15429906	15429993	87	CG_Chr4_15429906_15429993	-26.18850108	Chr4	EDTA	Gypsy_LTR_retrotransposon	15429761	15431065	1304	-	TE_homo_113160			TE_00001809_LTR	LTR/Gypsy	SO:0000265	0.912	homology					87
Chr5	15552286	15552356	70	CG_Chr5_15552286_15552356	-25.43672317	Chr5	EDTA	LTR_retrotransposon	15552339	15553112	773	+	TE_homo_142178			TE_00000854_INT	LTR/unknown	SO:0000186	0.807	homology					18
Chr7	15684334	15684394	60	CG_Chr7_15684334_15684394	-25.42386584	Chr7	EDTA	repeat_region	15684094	15685049	955	+	TE_homo_188547			RLX_76433|LTR_Mt_chr_02_100|LTR|02.01.01.99|3880|Medicago	Unspecified	SO:0000657	0.719	homology					60
Chr4	30642465	30642539	74	CG_Chr4_30642465_30642539	-24.64653605	Chr4	EDTA	repeat_region	30641478	30643765	2287	-	TE_homo_128821			RLG_56030|LTR_AI_scaffold_0003_560|LTR/Gypsy|02.01.01.10.99|59689|Arabidopsis	Unspecified	SO:0000657	0.963	homology					74
Chr5	19367406	19367458	52	CG_Chr5_19367406_19367458	-24.27144138	Chr5	EDTA	repeat_region	19367396	19367633	237	+	TE_homo_144088			TE_00000079	Unknown	SO:0000657	0.922	homology					52
Chr1	31698717	31698844	127	CG_Chr1_31698717_31698844	-23.99880146	Chr1	EDTA	Gypsy_LTR_retrotransposon	31698179	31698728	549	-	TE_homo_31122			TE_00000745_INT	LTR/Gypsy	SO:0000265	0.734	homology					11
Chr2	21545268	21545327	59	CG_Chr2_21545268_21545327	-23.95507292	Chr2	EDTA	PIF_Harbinger_TIR_transposon	21545246	21545664	418	+	TE_homo_67487			TE_00001807	MITE/DTH	SO:0000284	0.816	homology					59
Chr4	30642873	30642925	52	CG_Chr4_30642873_30642925	-23.84711826	Chr4	EDTA	repeat_region	30641478	30643765	2287	-	TE_homo_128821			RLG_56030|LTR_AI_scaffold_0003_560|LTR/Gypsy|02.01.01.10.99|59689|Arabidopsis	Unspecified	SO:0000657	0.963	homology					52
Chr4	13609032	13609087	55	CG_Chr4_13609032_13609087	-23.54573093	Chr4	EDTA	LTR_retrotransposon	13607258	13613739	6481	?	LTRRT_1055	repeat_region_1055		TE_00002131	LTR/unknown	SO:0000186	1	structural	TGCA	GAGAA			55
Chr1	50800202	50800259	57	CG_Chr1_50800202_50800259	-23.41248202	Chr1	EDTA	Mutator_TIR_transposon	50800193	50800420	227	+	TE_homo_44037			TE_00001943	DNA/DTM	SO:0000280	0.794	homology					57
Chr7	15684066	15684136	70	CG_Chr7_15684066_15684136	-23.29980472	Chr7	EDTA	repeat_region	15684094	15685049	955	+	TE_homo_188547			RLX_76433|LTR_Mt_chr_02_100|LTR|02.01.01.99|3880|Medicago	Unspecified	SO:0000657	0.719	homology					43
Chr8	18408438	18408522	84	CG_Chr8_18408438_18408522	-23.17426919	Chr8	EDTA	Tc1_Mariner_TIR_transposon	18408382	18408453	71	+	TE_homo_213132			TE_00001239	DNA/DTT	SO:0000278	0.911	homology					15
Chr8	11412303	11412417	114	CG_Chr8_11412303_11412417	-22.49047507	Chr8	EDTA	LTR_retrotransposon	11410747	11415450	4703	?	LTRRT_1902	repeat_region_1902		TE_00001023	LTR/unknown	SO:0000186	0.996	structural	TGCA	ATGGA			114
Chr4	12534679	12534739	60	CG_Chr4_12534679_12534739	-22.1100329	Chr4	EDTA	Mutator_TIR_transposon	12534690	12534842	152	-	TE_homo_110411			TE_00001939	DNA/DTM	SO:0000280	0.928	homology					50
Chr3	7005503	7005564	61	CG_Chr3_7005503_7005564	-21.74579591	Chr3	EDTA	repeat_region	7005147	7005658	511	+	TE_homo_81629			TE_00000254	Unknown	SO:0000657	0.889	homology					61
Chr4	2234375	2234453	78	CG_Chr4_2234375_2234453	-21.59679015	Chr4	EDTA	Mutator_TIR_transposon	2234240	2234627	387	-	TE_homo_103654			TE_00001943	DNA/DTM	SO:0000280	0.8	homology					78
Chr1	12901298	12901291	93	CG_Chr1_12901298_12901291	-21.40811134	Chr1	EDTA	Mutator_TIR_transposon	12901098	12901437	339	-	TE_homo_13004			TE_00000755	DNA/DTM	SO:0000280	0.838	homology					93
Chr2	8874030	8874082	52	CG_Chr2_8874030_8874082	-21.05291736	Chr2	EDTA	Gypsy_LTR_retrotransposon	8873754	8875168	1414	-	TE_homo_54350			TE_00001320_INT	LTR/Gypsy	SO:0000265	0.913	homology					52
Chr7	17095286	17095405	119	CG_Chr7_17095286_17095405	20.85890838	Chr7	EDTA	repeat_region	17094430	17098556	4126	+	TE_homo_189663			RLC_13537|MtChr4L476|LTR/Copia|02.01.01.05.99|3880|Medicago	Unspecified	SO:0000657	0.703	homology					119
Chr7	16641117	16641241	124	CG_Chr7_16641117_16641241	-20.18339601	Chr7	EDTA	Mutator_TIR_transposon	16641087	16641215	128	-	TE_homo_189425			TE_00001943	DNA/DTM	SO:0000280	0.812	homology					98
Chr3	24681511	24681562	51	CG_Chr3_24681511_24681562	-20.12363545	Chr3	EDTA	PIF_Harbinger_TIR_transposon	24681266	24681533	267	-	TE_homo_99006			TE_00001380	DNA/DTM	SO:0000284	0.794	homology					22
Chr1	43091629	43091700	71	CG_Chr1_43091629_43091700	-19.77512286	Chr1	EDTA	repeat_region	43091540	43093155	1615	+	TE_homo_37955			TE_00000161	Unknown	SO:0000657	0.989	homology					71
Chr4	28643652	28643724	72	CG_Chr4_28643652_28643724	-18.78636891	Chr4	EDTA	hAT_TIR_transposon	28643644	28644141	497	+	TE_strux_788			CM037991.1:28643644..28644141	MITE/DTA	SO:0000279	0.7	structural		GGTGACGT_GGTGACGT_100.0	CAGAGGCGGA_tcCGCCACTG		72
Chr6	27194310	27194400	90	CG_Chr6_27194310_27194400	-18.67434688	Chr6	EDTA	Tc1_Mariner_TIR_transposon	27194325	27194461	136	+	TE_homo_169439			TE_00001239	DNA/DTT	SO:0000278	0.836	homology					76
ctg6	14464	14547	83	CG_ctg006_14464_14547	-18.61106578	ctg6	EDTA	repeat_region	13775	15340	1565	-	TE_homo_221			RLX_123308|LTR_SI_chr_10_2001|LTR|02.01.01.99|4081|Lycopersicon	Unspecified	SO:0000657	0.709	homology					83
Chr1	39620842	39620892	50	CG_Chr1_39620842_39620892	-18.51789217	Chr1	EDTA	CACTA_TIR_transposon	39620817	39620991	174	+	TE_homo_36007			TE_00000890	DNA/DTC	SO:0000285	0.782	homology					50
Chr8	11412279	11412878	99	CG_Chr8_11412279_11412878	-18.31246288	Chr8	EDTA	LTR_retrotransposon	11410747	11415450	4703	?	LTRRT_1902	repeat_region_1902		TE_00001023	LTR/unknown	SO:0000186	0.996	structural	TGCA	ATGGA			99
Chr5	16199039	16199117	78	CG_Chr5_16199039_16199117	-18.12114138	Chr5	EDTA	Mutator_TIR_transposon	16199012	16199128	116	+	TE_00001630			TE_00001630	DNA/DTM	SO:0000280	0.798	homology					78
Chr8	5179776	5179870	94	CG_Chr8_5179776_5179870	-17.903796	Chr8	EDTA	Copia_LTR_retrotransposon	5179652	5179867	215	+	TE_homo_200207			TE_00002115_LTR	LTR/Copia	SO:0000264	0.981	homology					91
Chr2	1800717	1800803	86	CG_Chr2_1800717_1800803	-17.66624453	Chr2	EDTA	Gypsy_LTR_retrotransposon	1800137	1802158	2021	+	TE_homo_47325			TE_00000675_LTR	LTR/Gypsy	SO:0000265	0.841	homology					86
Chr2	2619630	2619681	51	CG_Chr2_2619630_2619681	-17.49027864	Chr2	EDTA	repeat_region	2619626	2619958	332	+	TE_homo_48149			RLC_76533|LTR_Mt_chr_07_831|LTR/Copia|02.01.01.05.99|3880|Medicago	Unspecified	SO:0000657	0.769	homology					51
Chr8	13280185	13280241	56	CG_Chr8_13280185_13280241	17.47726449	Chr8	EDTA	Copia_LTR_retrotransposon	13280035	13285594	5559	+	LTRRT_1915	repeat_region_1915		CM037995.1:13280035..13285594	LTR/Copia	SO:0000264	1	structural	TGCA	GAAAG			56
Chr4	6255251	6255302	51	CG_Chr4_6255251_6255302	-17.29446339	Chr4	EDTA	Mutator_TIR_transposon	6255132	6255383	251	-	TE_homo_105776			TE_00001943	DNA/DTM	SO:0000280	0.789	homology					51
Chr4	6248202	6248567	365	CG_Chr4_6248202_6248567	-17.09145408	Chr4	EDTA	LTR_retrotransposon	6248291	6248397	106	-	TE_homo_105758			TE_00000854_INT	LTR/unknown	SO:0000186	0.86	homology					107
Chr2	13649365	13649579	214	CG_Chr2_13649365_13649579	-17.04261748	Chr2	EDTA	repeat_region	13649179	13649427	248	+	TE_homo_59110			TE_00000419	Unknown	SO:0000657	0.838	homology					62
Chr8	23307725	23307819	94	CG_Chr8_23307725_23307819	-17.02486864	Chr8	EDTA	Mutator_TIR_transposon	23307671	23307938	267	-	TE_homo_216017			TE_00001943	DNA/DTM	SO:0000280	0.757	homology					94
Chr3	26490554	26490647	93	CG_Chr3_26490554_26490647	-16.93756567	Chr3	EDTA	LTR_retrotransposon	26490148	26490899	751	+	TE_homo_100286			TE_00002131_INT	LTR/unknown	SO:0000186	0.89	homology					93
Chr7	24347764	24347867	103	CG_Chr7_24347764_24347867	-16.51353606	Chr7	EDTA	Mutator_TIR_transposon	24347627	24347973	346	-	TE_homo_193515			TE_00001943	DNA/DTM	SO:0000280	0.778	homology					103
Chr3	5796799	5796886	87	CG_Chr3_5796799_5796886	-16.15041286	Chr3	EDTA	Mutator_TIR_transposon	5796641	5796901	260	+	TE_homo_80536			TE_00001943	DNA/DTM	SO:0000280	0.806	homology					87
Chr5	9438781	9438833	52	CG_Chr5_9438781_9438833	-16.04312372	Chr5	EDTA	hAT_TIR_transposon	9437861	9438836	975	+	TE_homo_137660			TE_00000641	DNA/DTA	SO:0000279	0.719	homology					52
Chr1	27705485	27705550	65	CG_Chr1_27705485_27705550	-15.7916887	Chr1	EDTA	helitron	27705475	27707177	1702	-	TE_homo_27967			TE_00000824	DNA/Helitron	SO:0000544	0.923	homology					65
Chr7	22932638	22932691	53	CG_Chr7_22932638_22932691	-15.52133904	Chr7	EDTA	Gypsy_LTR_retrotransposon	22932541	22932857	316	-	TE_homo_192978			TE_00001595_LTR	LTR/Gypsy	SO:0000265	0.956	homology					53
Chr8	1123227	1123279	52	CG_Chr8_1123227_1123279	15.47382573	Chr8	EDTA	Gypsy_LTR_retrotransposon	1123266	1123557	291	-	TE_homo_196396			TE_00001814_LTR	LTR/Gypsy	SO:0000265	0.738	homology					14
Chr4	25557073	25557127	54	CG_Chr4_25557073_25557127	-15.04284307	Chr4	EDTA	LTR_retrotransposon	25552335	25564337	12002	-	TE_homo_123339			TE_00000849_LTR	LTR/unknown	SO:0000186	0.846	homology					54
Chr2	23630504	23630616	112	CG_Chr2_23630504_23630616	14.91242501	Chr2	EDTA	LTR_retrotransposon	23630271	23630553	282	+	TE_homo_69288			TE_00001678_LTR	LTR/unknown	SO:0000186	0.749	homology					49
Chr2	23630504	23630616	112	CG_Chr2_23630504_23630616	14.91242501	Chr2	EDTA	Gypsy_LTR_retrotransposon	23630535	23630625	90	-	TE_homo_69289			TE_00001643_LTR	LTR/Gypsy	SO:0000265	0.846	homology					82
Chr6	11837416	11837524	108	CG_Chr6_11837416_11837524	14.9116447	Chr6	EDTA	repeat_region	11836709	11837593	884	-	TE_homo_154553			RLX_55597|LTR_AI_scaffold_0002_336|LTR|02.01.01.99|59689|Arabidopsis	Unspecified	SO:0000657	0.95	homology					108
Chr4	20804913	20804992	79	CG_Chr4_20804913_20804992	-14.8001032	Chr4	EDTA	LTR_retrotransposon	20802127	20819084	16957	?	LTRRT_1116	repeat_region_1116		TE_00001111	LTR/unknown	SO:0000186	0.9341	structural	TGCA	ACTTT			79
Chr4	808913	809007	94	CG_Chr4_808913_809007	-14.75097389	Chr4	EDTA	Mutator_TIR_transposon	808902	809027	125	-	TE_homo_102750			TE_00001943	DNA/DTM	SO:0000280	0.858	homology					94
Chr3	8983462	8983545	83	CG_Chr3_8983462_8983545	-14.73581473	Chr3	EDTA	Mutator_TIR_transposon	8983364	8983580	216	+	TE_homo_83373			TE_00001599	DNA/DTM	SO:0000280	0.772	homology					83
Chr6	5931797	5931864	67	CG_Chr6_5931797_5931864	-14.72860868	Chr6	EDTA	LTR_retrotransposon	5931783	5931867	84	-	TE_homo_148885			TE_00001117_LTR	LTR/unknown	SO:0000186	0.824	homology					67
Chr2	8004009	8004059	50	CG_Chr2_8004009_8004059	-14.61935304	Chr2	EDTA	Copia_LTR_retrotransposon	8003178	8004228	1050	-	TE_homo_53409			TE_00000762	DNA/DTC	SO:0000264	0.813	homology					50
Chr3	3264886	3265064	178	CG_Chr3_3264886_3265064	-14.47345472	Chr3	EDTA	helitron	3264761	3264955	194	+	TE_homo_78891			TE_00000568	DNA/Helitron	SO:0000544	0.856	homology					69
Chr3	23257494	23257549	55	CG_Chr3_23257494_23257549	-14.47067018	Chr3	EDTA	Copia_LTR_retrotransposon	23257398	23257543	145	+	TE_homo_97876			TE_00000704_INT	LTR/Copia	SO:0000264	0.929	homology					49
Chr8	17238675	17238765	90	CG_Chr8_17238675_17238765	-14.4642086	Chr8	EDTA	Gypsy_LTR_retrotransposon	17238676	17240483	1807	+	TE_homo_212198			TE_00000602_INT	LTR/Gypsy	SO:0000265	0.983	homology					90
Chr4	30638073	30638127	54	CG_Chr4_30638073_30638127	-14.40156888	Chr4	EDTA	Mutator_TIR_transposon	30637971	30639533	1562	-	TE_strux_793			CM037991.1:30637971..30639533	DNA/DTM	SO:0000280	0.9	structural		AGGCAAC_AGGCAAC_100.0	CGATTTGTTG_CAACATATCG		54
Chr6	1905284	1905376	92	CG_Chr6_1905284_1905376	-14.2954791	Chr6	EDTA	Gypsy_LTR_retrotransposon	1904223	1909699	5476	+	LTRRT_1382	repeat_region_1382		CM037993.1:1904223..1909699	LTR/Gypsy	SO:0000265	1	structural	TGCA	AGGAG			92
Chr6	10040719	10040772	53	CG_Ch

Chr8	4914703	4914781	78	CHG_Chr8_4914703_4914781	-12.97538499	Chr8	EDTA	Gypsy_LTR_retrotransposon	4914026	4916517	2491	-	TE_homo_199930		TE_00001179_INT	LTR/Gypsy	SO:0000265	0.765	homology							78
Chr4	11049546	11049716	170	CHG_Chr4_11049546_11049716	-12.82589548	Chr4	EDTA	PIF_Harbinger_TIR_transposon	11049656	11049837	181	-	TE_homo_109227		TE_00001372	MITE/DTH	SO:0000284	0.823	homology							61
Chr8	14845441	14845497	56	CHG_Chr8_14845441_14845497	-12.82436464	Chr8	EDTA	Mutator_TIR_transposon	14845390	14845511	121	-	TE_homo_210269		TE_00001630	DNA/DTM	SO:0000284	0.841	homology							56
Chr8	10885379	10885444	65	CHG_Chr8_10885379_10885444	12.79712355	Chr8	EDTA	Mutator_TIR_transposon	10885201	10885837	636	+	TE_homo_206257		TE_00000074	DNA/DTM	SO:0000284	0.83	homology							65
Chr8	5785576	5785638	62	CHG_Chr8_5785576_5785638	-12.64599538	Chr8	EDTA	LTR_retrotransposon	5784196	5785977	1781	-	TE_homo_200782		TE_00001670_LTR	LTR/unknown	SO:0000186	0.806	homology							62
Chr7	24549013	24549065	52	CHG_Chr7_24549013_24549065	-12.55999964	Chr7	EDTA	Mutator_TIR_transposon	24548590	24549581	991	-	TE_homo_193574		TE_00001943	DNA/DTM	SO:0000284	0.796	homology							52
Chr8	5571730	5571781	51	CHG_Chr8_5571730_5571781	12.34745637	Chr8	EDTA	LTR_retrotransposon	5571740	5571893	153	+	TE_homo_200567		TE_00001015_LTR	LTR/unknown	SO:0000186	0.841	homology							42
Chr7	19044390	19044443	53	CHG_Chr7_19044390_19044443	-12.28632822	Chr7	EDTA	Mutator_TIR_transposon	19044241	19044924	683	+	TE_homo_190809		TE_00001943	DNA/DTM	SO:0000284	0.802	homology							53
Chr6	15823290	15823358	68	CHG_Chr6_15823290_15823358	-12.24308294	Chr6	EDTA	Gypsy_LTR_retrotransposon	15819981	15823507	3526	+	TE_homo_158835		TE_00001179_INT	LTR/Gypsy	SO:0000265	0.797	homology							68
Chr6	11284659	11284727	68	CHG_Chr6_11284659_11284727	-12.18703308	Chr6	EDTA	Gypsy_LTR_retrotransposon	11278398	11288730	10332	+	LTRRT_1458	repeat_region_1458	CM037993.1:11278398..11288730	LTR/Gypsy	SO:0000265	0.9978	structural	TGCA	AATCT					68
Chr4	25519759	25519838	79	CHG_Chr4_25519759_25519838	-12.18583616	Chr4	EDTA	LTR_retrotransposon	25518133	25532138	14005	-	TE_homo_123320		TE_00000849_LTR	LTR/unknown	SO:0000186	0.844	homology							79
Chr4	25341606	25341724	118	CHG_Chr4_25341606_25341724	-12.10487785	Chr4	EDTA	LTR_retrotransposon	25338950	25344836	5886	+	TE_homo_123179		TE_00000849_LTR	LTR/unknown	SO:0000186	0.836	homology							118
Chr3	15052607	15052768	161	CHG_Chr3_15052607_15052768	12.02616797	Chr3	EDTA	Gypsy_LTR_retrotransposon	15048058	15056620	8562	+	LTRRT_849	repeat_region_849	TE_00001695	LTR/Gypsy	SO:0000265	0.9995	structural	TGCA	TTATG					161
Chr7	11905160	11905217	57	CHG_Chr7_11905160_11905217	-12.01967072	Chr7	EDTA	hAT_TIR_transposon	11902268	11905544	3276	.	TE_struc_1180		CM037994.1:11902268..11905544	DNA/DTA	SO:0000279	0.9	structural		ATCCTCAA_ATCCTCAA_100.0	CAGTGGCGGA_TCCGCCCCTG				57
Chr1	27807405	27807466	61	CHG_Chr1_27807405_27807466	-12.00950047	Chr1	EDTA	CACTA_TIR_transposon	27807339	27807779	440	-	TE_homo_28063		TE_00000446	DNA/DTC	SO:0000285	0.877	homology							61
Chr8	9685140	9685193	53	CHG_Chr8_9685140_9685193	-11.86647357	Chr8	EDTA	repeat_region	9684860	9686490	1630	+	TE_homo_204739		TE_00000016	Unknown	SO:0000657	0.96	homology							53
Chr7	19049025	19049083	58	CHG_Chr7_19049025_19049083	-11.81224642	Chr7	EDTA	Mutator_TIR_transposon	19048210	19049088	878	-	TE_homo_190823		TE_00001943	DNA/DTM	SO:0000284	0.802	homology							58
Chr5	13800070	13800123	53	CHG_Chr5_13800070_13800123	-11.72668155	Chr5	EDTA	Tc1_Mariner_TIR_transposon	13799562	13800202	640	-	TE_homo_141182		TE_00001239	DNA/DTT	SO:0000278	0.793	homology							53
Chr1	6498633	6498684	51	CHG_Chr1_6498633_6498684	-11.7255389	Chr1	EDTA	LTR_retrotransposon	6498663	6499337	674	+	TE_homo_7281		TE_00001670_LTR	LTR/unknown	SO:0000186	0.779	homology							22
Chr6	10722244	10722296	52	CHG_Chr6_10722244_10722296	11.61230887	Chr6	EDTA	Mutator_TIR_transposon	10721656	10722767	1111	+	TE_homo_153001		TE_00000711	DNA/DTM	SO:0000284	0.794	homology							52
Chr8	4188749	4188847	98	CHG_Chr8_4188749_4188847	-11.58169033	Chr8	EDTA	Copia_LTR_retrotransposon	4188809	4188968	159	-	TE_homo_199148		TE_00001046_LTR	LTR/Copia	SO:0000264	0.703	homology							39
Chr3	28100432	28100490	58	CHG_Chr3_28100432_28100490	-11.54991012	Chr3	EDTA	Gypsy_LTR_retrotransposon	28100338	28100800	462	+	TE_homo_101514		TE_00001052_LTR	LTR/Gypsy	SO:0000265	0.893	homology							58
Chr1	4164933	4165043	110	CHG_Chr1_4164933_4165043	-11.50810336	Chr1	EDTA	LTR_retrotransposon	4164763	4165011	248	+	TE_homo_5087		TE_00001707_LTR	LTR/unknown	SO:0000186	0.873	homology							78
Chr4	2236680	2236732	52	CHG_Chr4_2236680_2236732	-11.44310847	Chr4	EDTA	Mutator_TIR_transposon	2236259	2236746	487	-	TE_homo_103662		TE_00001943	DNA/DTM	SO:0000284	0.766	homology							52
Chr4	24664863	24664917	54	CHG_Chr4_24664863_24664917	11.43947124	Chr4	EDTA	LTR_retrotransposon	24659159	24665652	6493	+	TE_homo_122784		TE_00000849_LTR	LTR/unknown	SO:0000186	0.845	homology							54
Chr4	3589508	3589577	69	CHG_Chr4_3589508_3589577	-11.41023148	Chr4	EDTA	Copia_LTR_retrotransposon	3589102	3594035	4933	-	LTRRT_989	repeat_region_989	CM037991.1:3589102..3594035	LTR/Copia	SO:0000264	1	structural	TGCA	TCTTC					69
Chr3	14435218	14435342	124	CHG_Chr3_14435218_14435342	11.16403127	Chr3	EDTA	Gypsy_LTR_retrotransposon	14433910	14435298	1388	+	TE_homo_89128		TE_00001581_LTR	LTR/Gypsy	SO:0000265	0.979	homology							80
Chr2	121960	122013	53	CHG_Chr2_121960_122013	-11.0332252	Chr2	EDTA	Copia_LTR_retrotransposon	121694	122126	432	-	TE_homo_45805		TE_00000719_INT	LTR/Copia	SO:0000264	0.977	homology							53
ctg5	581	633	52	CHG_ctg005_581_633	-11.01726828	ctg5	EDTA	Gypsy_LTR_retrotransposon	1	1151	1150	+	TE_homo_152		TE_00000675_LTR	LTR/Gypsy	SO:0000265	0.892	homology							52
Chr8	11671699	11671793	94	CHG_Chr8_11671699_11671793	-10.89169342	Chr8	EDTA	Gypsy_LTR_retrotransposon	11671173	11672466	1293	-	TE_homo_207127		TE_00000675_LTR	LTR/Gypsy	SO:0000265	0.847	homology							94
Chr5	15787107	15787157	50	CHG_Chr5_15787107_15787157	-10.80231069	Chr5	EDTA	Mutator_TIR_transposon	15787103	15787278	175	-	TE_homo_142272		TE_00001630	DNA/DTM	SO:0000284	0.831	homology							50
Chr8	22059063	22059126	63	CHG_Chr8_22059063_22059126	-10.77980717	Chr8	EDTA	Copia_LTR_retrotransposon	22057397	22062325	4928	+	LTRRT_1984	repeat_region_1984	CM037995.1:22057397..22062325	LTR/Copia	SO:0000264	0.9853	structural	TGTA	CAGGT					63
Chr3	16803902	16803960	58	CHG_Chr3_16803902_16803960	-10.49102869	Chr3	EDTA	Gypsy_LTR_retrotransposon	16801095	16811497	10402	-	LTRRT_874	repeat_region_874	CM037990.1:16801095..16811497	LTR/Gypsy	SO:0000265	0.9957	structural	TGCA	GAAGC					58
Chr4	13176500	13176559	59	CHG_Chr4_13176500_13176559	-10.43576781	Chr4	EDTA	Mutator_TIR_transposon	13176481	13176858	377	-	TE_homo_110859		TE_00001874	DNA/DTM	SO:0000284	0.847	homology							59
Chr8	8367746	8367810	64	CHG_Chr8_8367746_8367810	-10.41013132	Chr8	EDTA	LTR_retrotransposon	8367772	8368073	301	-	TE_homo_203701		TE_00001111_INT	LTR/unknown	SO:0000186	0.83	homology							39
Chr8	22302169	22302220	51	CHG_Chr8_22302169_22302220	-10.38931179	Chr8	EDTA	Gypsy_LTR_retrotransposon	22301040	22307026	5986	+	LTRRT_1986	repeat_region_1986	CM037995.1:22301040..22307026	LTR/Gypsy	SO:0000265	1	structural	TGCA	GTTAT					51
Chr3	9646590	9646641	51	CHG_Chr3_9646590_9646641	-10.38331631	Chr3	EDTA	Copia_LTR_retrotransposon	9645396	9650414	5018	+	LTRRT_767	repeat_region_767	CM037990.1:9645396..9650414	LTR/Copia	SO:0000264	0.9424	structural	TGCA	CAAGG					51
Chr2	13347915	13347982	67	CHG_Chr2_13347915_13347982	-10.34756649	Chr2	EDTA	Copia_LTR_retrotransposon	13347064	13348100	1036	+	TE_homo_58757		TE_00002099_LTR	LTR/Copia	SO:0000264	0.893	homology							67
Chr3	7513135	7513208	73	CHG_Chr3_7513135_7513208	-10.34070159	Chr3	EDTA	Gypsy_LTR_retrotransposon	7513097	7513224	127	+	TE_homo_82123		TE_00000721_INT	LTR/Gypsy	SO:0000265	0.969	homology							73
Chr4	25186193	25186345	152	CHG_Chr4_25186193_25186345	10.27242883	Chr4	EDTA	LTR_retrotransposon	25181068	25187480	6412	-	TE_homo_123091		TE_00000849_LTR	LTR/unknown	SO:0000186	0.845	homology							152
Chr4	25473275	25473335	60	CHG_Chr4_25473275_25473335	-10.21795692	Chr4	EDTA	LTR_retrotransposon	25457486	25479056	21570	-	TE_homo_123284		TE_00000849_LTR	LTR/unknown	SO:0000186	0.845	homology							60
Chr6	29951248	29951334	86	CHG_Chr6_29951248_29951334	-10.03872312	Chr6	EDTA	LTR_retrotransposon	29951072	29951803	731	+	TE_homo_170858		TE_00001436_LTR	LTR/unknown	SO:0000186	0.889	homology							86
Chr7	7203039	7203090	51	CHG_Chr7_7203039_7203090	-9.956654285	Chr7	EDTA	CACTA_TIR_transposon	7203066	7203263	197	-	TE_homo_180077		TE_00001907	DNA/DTC	SO:0000285	0.784	homology							25
Chr1	42632983	42633055	72	CHG_Chr1_42632983_42633055	-9.901817116	Chr1	EDTA	Gypsy_LTR_retrotransposon	42627979	42638187	10208	-	LTRRT_334	repeat_region_334	CM037988.1:42627979..42638187	LTR/Gypsy	SO:0000265	0.9716	structural	TGCA	CTTGC					72
Chr2	5036737	5036810	73	CHG_Chr2_5036737_5036810	-9.856522731	Chr2	EDTA	repeat_region	5035760	5036875	1115	-	TE_homo_50553		TE_00000003	Unknown	SO:0000657	0.801	homology							73
Chr1	21365983	21366046	63	CHG_Chr1_21365983_21366046	-9.808092373	Chr1	EDTA	LTR_retrotransposon	21364822	21366209	1387	+	TE_homo_22026		TE_00000912_LTR	LTR/unknown	SO:0000186	0.884	homology							63
Chr7	25032560	25032611	51	CHG_Chr7_25032560_25032611	-9.76238208	Chr7	EDTA	LTR_retrotransposon	25032598	25033335	737	-	TE_homo_185781		TE_00000854_INT	LTR/unknown	SO:0000186	0.821	homology							14
Chr1	22284365	22284432	67	CHG_Chr1_22284365_22284432	-9.680578882	Chr1	EDTA	LTR_retrotransposon	22283743	22284415	672	-	TE_homo_23089		TE_00001670_LTR	LTR/unknown	SO:0000186	0.854	homology							50
Chr1	20876298	20876354	56	CHG_Chr1_20876298_20876354	-9.648802553	Chr1	EDTA	CACTA_TIR_transposon	20876354	20876887	533	+	TE_homo_21475		TE_00000247	DNA/DTC	SO:0000285	0.854	homology							1
Chr3	18478725	18478799	74	CHG_Chr3_18478725_18478799	-9.466145688	Chr3	EDTA	helitron	18478342	18478751	409	+	TE_homo_93357		TE_00000566	DNA/Helitron	SO:0000544	0.898	homology							26
Chr8	7321284	7321351	67	CHG_Chr8_7321284_7321351	-9.101847937	Chr8	EDTA	LTR_retrotransposon	7321307	7321541	234	-	TE_homo_202409		TE_00001312_INT	LTR/unknown	SO:0000186	0.796	homology							45
Chr4	6249040	6249131	91	CHG_Chr4_6249040_6249131	-8.743623183	Chr4	EDTA	Tc1_Mariner_TIR_transposon	6248615	6250067	1452	-	TE_homo_105760		TE_00001239	DNA/DTT	SO:0000278	0.775	homology							91
Chr8	15927002	15927071	69	CHG_Chr8_15927002_15927071	8.690354087	Chr8	EDTA	Gypsy_LTR_retrotransposon	15926141	15928882	2741	+	TE_00001882_LTR		TE_00001882_LTR	LTR/Gypsy	SO:0000265	0.768	homology							69
Chr2	9892948	9893015	67	CHG_Chr2_9892948_9893015	-8.583792321	Chr2	EDTA	repeat_region	9892362	9893319	957	-	TE_homo_55625		RLX_121827|LTR_St_chr_02_336|LTR|02.01.01.99|4113|Solanum	Unspecified	SO:0000657	0.702	homology							67
Chr3	14488453	14488507	54	CHG_Chr3_14488453_14488507	8.568727051	Chr3	EDTA	LTR_retrotransposon	14487442	14490288	2846	-	TE_homo_89172		TE_00000849_LTR	LTR/unknown	SO:0000186	0.847	homology							54
Chr4	28831428	28831480	52	CHG_Chr4_28831428_28831480	-8.492786619	Chr4	EDTA	Gypsy_LTR_retrotransposon	28829757	28832613	2856	+	TE_homo_126767		TE_00000675_LTR	LTR/Gypsy	SO:0000265	0.83	homology							52
Chr7	2589999	2590060	61	CHG_Chr7_2589999_2590060	-7.846400697	Chr7	EDTA	LTR_retrotransposon	2587669	2590710	3041	-	TE_homo_175278		TE_00000877_LTR	LTR/unknown	SO:0000186	0.837	homology							61
Chr7	7567394	7567449	55	CHG_Chr7_7567394_7567449	-7.826648451	Chr7	EDTA	Gypsy_LTR_retrotransposon	7567184	7567720	536	+	TE_homo_180421		TE_00001951_INT	LTR/Gypsy	SO:0000265	0.968	homology							55
Chr7	5586043	5586185	142	CHG_Chr7_5586043_5586185	5.183325773	Chr7	EDTA	LTR_retrotransposon	5582776	5592031	9255	+	TE_00000849_LTR		TE_00000849_LTR	LTR/unknown	SO:0000186	0.845	homology							142
Chr8	25349529	25349594	65	CHG_Chr8_25349529_25349594	-3.457576414	Chr8	EDTA	LTR_retrotransposon	25349255	25350097	842	+	TE_homo_217462		TE_00002156_LTR	LTR/unknown	SO:0000186	0.779	homology							65
Chr5	19560558	19560839	281	CHG_Chr5_19560558_19560839	2.255587144	Chr5	EDTA	Mutator_TIR_transposon	19560484	19560805	321	+	TE_homo_144176		TE_00000462	DNA/DTM	SO:0000284	0.913	homology							247
Chr1	4151959	4152038	79	CHG_Chr1_4151959_4152038	-2.089689909	Chr1	EDTA	Copia_LTR_retrotransposon	4148038	4152946	4908	+	LTRRT_45	repeat_region_45	CM037988.1:4148038..4152946	LTR/Copia	SO:0000264	0.9886	structural	TGCA	GTTTT					79
Chr5	17349070	17349186	116	CHG_Chr5_17349070_17349186	-2.052508533	Chr5	EDTA	Mutator_TIR_transposon	17349164	17349341	177	+	TE_homo_142977		TE_00001943	DNA/DTM	SO:0000284	0.8	homology							23
Chr4	10657447	10657498	51	CHG_Chr4_10657447_10657498	1.783515161	Chr4	EDTA	Copia_LTR_retrotransposon	10653951	10658861	4910	-	LTRRT_1028	repeat_region_1028	CM037991.1:10653951..10658861	LTR/Copia	SO:0000264	1	structural	TGCA	AGCAT					51
Chr4	808750	809001	251	CHG_Chr4_808750_809001	-123.2232500	Chr4	EDTA	Mutator_TIR_transposon	808902	809027	125	-	TE_homo_102750		TE_00001943	DNA/DTM	SO:0000284	0.858	homology							100
Chr3	24794986	24795108	122	CHG_Chr3_24794986_24795108	-110.3448469	Chr3	EDTA	repeat_region	24794945	24795114	169	+	TE_homo_99077		TE_00000144	Unknown	SO:0000657	0.912	homology							122
Chr6	23040424	23040538	114	CHG_Chr6_23040424_23040538	-93.68615278	Chr6	EDTA	helitron	23040402	23040558	156	-	TE_homo_166375		TE_00000509	DNA/Helitron	SO:0000544	0.768	homology							114
Chr5	18793277	18793424	147	CHG_Chr5_18793277_18793424	-92.33533344	Chr5	EDTA	PIF_Harbinger_TIR_transposon	18793037	18796314	3277	.	TE_struc_900		CM037992.1:18793037..18796314	DNA/DTH	SO:0000284	0.9	structural		TTA_TTA_100.0	GAGCATCTGC_GCGGATGCTC				147
Chr4	11050033	11050112	79	CHG_Chr4_11050033_11050112	-91.8770444	Chr4	EDTA	PIF_Harbinger_TIR_transposon	11050024	11050280	256	-	TE_homo_109228		TE_00001361	MITE/DTH	SO:0000284	0.82	homology							79
Chr4	22329369	22329521	152	CHG_Chr4_22329369_22329521	-91.7665524	Chr4	EDTA	Mutator_TIR_transposon	22329314	22329521	207	-	TE_homo_120187		TE_00000718	DNA/DTM	SO:0000284	0.842	homology							152
Chr3	24681494	24681598	104	CHG_Chr3_24681494_24681598	-89.77599071	Chr3	EDTA	PIF_Harbinger_TIR_transposon	24681266	24681533	267	-	TE_homo_99006		TE_00001380	DNA/DTH	SO:0000284	0.794	homology							39
Chr7	11954213	11954342	129	CHG_Chr7_11954213_11954342	-86.67900654	Chr7	EDTA	Gypsy_LTR_retrotransposon	11954191	11954568	377	-	TE_homo_185351		TE_00001847_INT	LTR/Gypsy	SO:0000265	0.974	homology							129
Chr1	39620825	39620921	96	CHG_Chr1_39620825_39620921	-86.34620755	Chr1	EDTA	CACTA_TIR_transposon	39620817	39620991	174	+	TE_homo_36007		TE_00000890	DNA/DTC	SO:0000285	0.782	homology							96
Chr4	17680012	17680100	88	CHG_Chr4_17680012_17680100	-84.33079047	Chr4	EDTA	LTR_retrotransposon	17679887	17680122	235	-	TE_homo_115053		TE_00002109_LTR	LTR/unknown	SO:0000186	0.975	homology							88
Chr4	1236790	1236893	103	CHG_Chr4_1236790_1236893	-83.73355201	Chr4	EDTA	helitron	1236798	1236892	94	-	TE_homo_102899		TE_00000548	DNA/Helitron	SO:0000544	0.789	homology							95
Chr1	38910824	38910896	72	CHG_Chr1_38910824_38910896	-78.42916384	Chr1	EDTA	Tc1_Mariner_TIR_transposon	38910800	38911004	204	+	TE_homo_35672		TE_00000519	DNA/DTT	SO:0000278	0.866	homology							72
Chr2	611285	611403	118	CHG_Chr2_611285_611403	-77.9429012	Chr2	EDTA	hAT_TIR_transposon	611042	611393	351	+	TE_homo_46202		TE_00001101	DNA/DTA	SO:0000279	0.986	homology							108
Chr4	26755931	26756038	107	CHG_Chr4_26755931_26756038	-77.42658072	Chr4	EDTA	Mutator_TIR_transposon	26755868	26756108	240	-	TE_homo_124558		TE_00000553	DNA/DTM	SO:0000284	0.917	homology							107
Chr1	27356942	27357065	123	CHG_Chr1_27356942_27357065	-74.41213065	Chr1	EDTA	repeat_region	27356609	27357039	430	-	TE_homo_27646		TE_00000164	Unknown	SO:0000657	0.924	homology							97
Chr6	26848801	26848906	105	CHG_Chr6_26848801_26848906	-72.1957153	Chr6	EDTA	Mutator_TIR_transposon	26848801	26848966	165	+	TE_homo_169251		TE_00001207	MITE/DTM	SO:0000284	0.8	homology							105
Chr5	15549783	15549906	123	CHG_Chr5_15549783_15549906	-70.7972407	Chr5	EDTA	Mutator_TIR_transposon	15549767	15550106	339	+	TE_homo_142165		TE_00001943	DNA/DTM	SO:0000284	0.771	homology							123
Chr1	3427230	3427312	82	CHG_Chr1_3427230_3427312	-68.03592556	Chr1	EDTA	Gypsy_LTR_retrotransposon	3427100	3429184	2084	+	TE_homo_4577		TE_00002140_LTR	LTR/Gypsy	SO:0000265	0.94	homology							82
Chr8	21569635	21569692	57	CHG_Chr8_21569635_21569692	-67.7517714	Chr8	EDTA	Mutator_TIR_transposon	21569555	21569702	147	+	TE_homo_214949		TE_00001159	DNA/DTM	SO:0000284	0.731	homology							57
Chr1	21664206	21664269	63	CHG_Chr1_21664206_21664269	-64.30317912	Chr1	EDTA	Mutator_TIR_transposon	21663776	21664280	504	+	TE_homo_22349		TE_00000576	DNA/DTM	SO:0000284	0.942	homology							63
Chr4	18052799	18052897	98	CHG_Chr4_18052799_18052897	-62.17387601	Chr4	EDTA	Mutator_TIR_transposon	18052767	18052903	136	-	TE_homo_115377		TE_00001405	DNA/DTM	SO:0000284	0.909	homology							98
Chr2	21545237	21545293	56	CHG_Chr2_21545237_21545293	-60.02156549	Chr2	EDTA	PIF_Harbinger_TIR_transposon	21545246	21545664	418	+	TE_homo_67487		TE_00001807	MITE/DTH	SO:0000284	0.816	homology							48
Chr1	42433280	42433332	52	CHG_Chr1_42433280_42433332	-58.94996885	Chr1	EDTA	Mutator_TIR_transposon	42433302	42433396	94	-	TE_homo_37453		TE_00001207	MITE/DTM	SO:0000284	0.821	homology							31
Chr7	20294339	20294397	58	CHG_Chr7_20294339_20294397	-58.84323209	Chr7	EDTA	PIF_Harbinger_TIR_transposon	20294108	20294516	408	+	TE_homo_191321		TE_00001745	DNA/DTM	SO:0000284	0.839	homology							58
ctg6	12217	12347	130	CHG_ctg006_12217_12347	-58.01584418	ctg6	EDTA	Mutator_TIR_transposon	12128	12267	139	-	TE_homo_219		TE_00001943	DNA/DTM	SO:0000284	0.829	homology							50
Chr1	30086195	30086273	78	CHG_Chr1_30086195_30086273	-57.64600812	Chr1	EDTA	PIF_Harbinger_TIR_transposon	30086156	30086434	278	-	TE_homo_29915		TE_00001066	DNA/DTH	SO:0000284	0.75	homology							78
Chr8	22068417	22068493	76	CHG_Chr8_22068417_22068493	-57.00373137	Chr8	EDTA	PIF_Harbinger_TIR_transposon	22068324	22068522	198	-	TE_homo_215269		TE_00001563	DNA/DTH	SO:0000284	0.847	homology							76
Chr4	2738751	2738833	82	CHG_Chr4_2738751_2738833	-56.56690107	Chr4	EDTA	Mutator_TIR_transposon	2738713	2738825	112	+	TE_homo_103851		TE_00001068	DNA/DTM	SO:0000284	0.796	homology							74
Chr5	20524131	20524207	76	CHG_Chr5_20524131_20524207	-56.08380585	Chr5	EDTA	Copia_LTR_retrotransposon	20523836	20524996	1160	-	TE_homo_144499		TE_00002099_LTR	LTR/Copia	SO:0000264	0.84	homology							76
Chr7	9930002	9930079	77	CHG_Chr7_9930002_9930079	-53.61328817	Chr7	EDTA	hAT_TIR_transposon	9929885	9930238	353	-	TE_homo_183135		TE_00001101	DNA/DTA	SO:0000279	0.992	homology							77
Chr5	1851781	1851848	67	CHG_Chr5_1851781_1851848	-53.51035864	Chr5	EDTA	helitron	1851729	1851870	141	-	TE_homo_130576		TE_00000509	DNA/Helitron	SO:0000544	0.852	homology							67
Chr8	19314927	19314993	66	CHG_Chr8_19314927_19314993	-53.36043513	Chr8	EDTA	PIF_Harbinger_TIR_transposon	19314924	19315230	306	+	TE_homo_213816		TE_00000796	DNA/DTH	SO:0000284	0.901	homology							66
Chr2	26979666	26979731	65	CHG_Chr2_26979666_26979731	-53.06868439	Chr2	EDTA	Mutator_TIR_transposon	26979545	26979789	244	+	TE_homo_71241		TE_00001965	DNA/DTM	SO:0000284	0.878	homology							65
Chr2	21297424	21297488	64	CHG_Chr2_21297424_21297488	-52.64536593	Chr2	EDTA	repeat_region	21297267	21297527	260	+	TE_homo_67282		RLC_76440|LTR_Mt_chr_01_64|LTR/Copia|02.01.01.05.99|3880|Medicago	Unspecified	SO:0000657	0.739	homology							64
Chr6	1786724	1786792	68	CHG_Chr6_1786724_1786792	-52.46108112	Chr6	EDTA	LTR_retrotransposon	1785907	1788636	2723	?	LTRRT_1381	repeat_region_1381	CM037993.1:1785907..1788630	LTR/unknown	SO:0000186	0.9591	structural	TGCA	ATTAA					68
Chr6	24120422	24120488	66	CHG_Chr6_24120422_24120488	-51.34206267	Chr6	EDTA	Mutator_TIR_transposon	24120234	24120487	253	+	TE_homo_167231		TE_00000576	DNA/DTM	SO:0000284	0.793	homology							65
Chr5	16480201	16480290	89	CHG_Chr5_16480201_16480290	-50.86359731	Chr5	EDTA	Tc1_Mariner_TIR_transposon	16480135	16480230	95	+	TE_homo_142600		TE_00000519	DNA/DTT	SO:0000278	0.726	homology							29
Chr1	28608149	28608303	154	CHG_Chr1_28608149_28608303	-50.75740684	Chr1	EDTA	repeat_region	28607845	28609037	1192	+	TE_homo_28803		RLX_76087|LTR_Mt_chr_04_454|LTR|02.01.01.99|3880|Medicago	Unspecified	SO:0000657	0.857	homology							154
Chr8	8048578	8048648	70	CHG_Chr8_8048578_8048648	-50.19875412	Chr8	EDTA	repeat_region	8048367	8048711	344	-	TE_homo_203331		TE_00000025	Unknown	SO:0000657	0.771	homology							70
Chr8	18146399	18146456	57	CHG_Chr8_18146399_18146456	-48.11455974	Chr8	EDTA	Mutator_TIR_transposon	18145411	18146460	1049	-	TE_homo_213004		TE_00001599	DNA/DTM	SO:0000284	0.99	homology							57
Chr2	15286038	15286091	53	CHG_Chr2_15286038_15286091	-48.01775384	Chr2	EDTA	PIF_Harbinger_TIR_transposon	15285989	15286323	334	+	TE_homo_61140		T

Chr6	9487412	9487462	50	CHH_Chr6_9487412_9487462	-37.73800988	Chr6	EDTA	hAT_TIR_transposon	9487165	9487492	327	+	TE_homo_151653		TE_00000774	DNA/DTA	SO:0000279	0.844	homology				50
Chr8	12637525	12637588	63	CHH_Chr8_12637525_12637588	-34.21731571	Chr8	EDTA	Mutator_TIR_transposon	12637335	12637590	255	-	TE_homo_208173		TE_00001819	DNA/DTM	SO:0000280	0.91	homology				63
Chr1	28607921	28607981	60	CHH_Chr1_28607921_28607981	-33.42180663	Chr1	EDTA	repeat_region	28607845	28609037	1192	+	TE_homo_28803		RLX_76087|LTR_Mt_chr_04_454|LTR|02.01.01.99|3880|Medicago	Unspecified	SO:0000657	0.857	homology				60
Chr6	7127943	7127996	53	CHH_Chr6_7127943_7127996	-32.41603208	Chr6	EDTA	helitron	7127758	7128027	269	+	TE_homo_149726		TE_00000570	DNA/Helitron	SO:0000544	0.81	homology				53
Chr1	32327224	32327288	64	CHH_Chr1_32327224_32327288	-30.50173993	Chr1	EDTA	Copia_LTR_retrotransposon	32327089	32327332	243	+	TE_homo_31544		TE_00001832_LTR	LTR/Copia	SO:0002264	0.767	homology				64
Chr2	18199732	18199799	67	CHH_Chr2_18199732_18199799	-30.26334138	Chr2	EDTA	helitron	18199498	18199749	251	-	TE_homo_64511		TE_00000605	DNA/Helitron	SO:0000544	0.958	homology				17
Chr8	24255430	24255480	50	CHH_Chr8_24255430_24255480	-29.92180874	Chr8	EDTA	Mutator_TIR_transposon	24255433	24255552	119	-	TE_homo_216610		TE_00000501	DNA/DTM	SO:0000280	0.812	homology				48
Chr6	31256513	31256579	66	CHH_Chr6_31256513_31256579	-29.35764921	Chr6	EDTA	hAT_TIR_transposon	31256511	31256860	349	-	TE_homo_171550		TE_00001101	DNA/DTA	SO:0000279	0.842	homology				66
Chr1	20308447	20308507	60	CHH_Chr1_20308447_20308507	-29.28681553	Chr1	EDTA	repeat_region	20307204	20313758	6554	?	repeat_region_187		TE_00002131	LTR/unknown	SO:0000657	0.9946	structural	TGCA AAAAC			60
Chr3	6270392	6270444	52	CHH_Chr3_6270392_6270444	-28.76118632	Chr3	EDTA	Mutator_TIR_transposon	6270323	6270564	241	+	TE_homo_80986		TE_00000718	DNA/DTM	SO:0000280	0.955	homology				52
Chr8	15834118	15834171	53	CHH_Chr8_15834118_15834171	-28.68307282	Chr8	EDTA	PIF_Harbinger_TIR_transposon	15833931	15834311	380	+	TE_homo_211095		TE_00001563	DNA/DTH	SO:0000284	0.871	homology				53
Chr4	802990	803040	50	CHH_Chr4_802990_803040	-28.29159509	Chr4	EDTA	hAT_TIR_transposon	802952	803324	372	-	TE_homo_102747		TE_00001101	DNA/DTA	SO:0002279	0.981	homology				50
Chr5	12481956	12482012	56	CHH_Chr5_12481956_12482012	-28.18296357	Chr5	EDTA	Mutator_TIR_transposon	12481840	12482084	244	+	TE_homo_140376		TE_00001943	DNA/DTM	SO:0002280	0.798	homology				56
Chr7	24549012	24549066	54	CHH_Chr7_24549012_24549066	-26.79073151	Chr7	EDTA	Mutator_TIR_transposon	24548590	24549581	991	-	TE_homo_193574		TE_00001943	DNA/DTM	SO:0002280	0.796	homology				54
Chr4	4824515	4824571	56	CHH_Chr4_4824515_4824571	-26.44766962	Chr4	EDTA	Mutator_TIR_transposon	4824412	4824573	161	+	TE_homo_104804		TE_00001063	MITE/DTM	SO:0002280	0.847	homology				56
Chr5	14502282	14502332	50	CHH_Chr5_14502282_14502332	-26.19427645	Chr5	EDTA	repeat_region	14502205	14502544	339	+	TE_homo_141683		TE_00000020	Unknown	SO:0000657	0.965	homology				50
Chr4	13422667	13422719	52	CHH_Chr4_13422667_13422719	-25.70376241	Chr4	EDTA	PIF_Harbinger_TIR_transposon	13422608	13422770	162	-	TE_homo_111001		TE_00001066	DNA/DTH	SO:0002284	0.759	homology				52
Chr3	5742954	5743011	57	CHH_Chr3_5742954_5743011	-25.29973524	Chr3	EDTA	PIF_Harbinger_TIR_transposon	5742665	5743017	352	-	TE_homo_80516		TE_00001343	DNA/DTH	SO:0002284	0.803	homology				57
Chr1	20182498	20182566	68	CHH_Chr1_20182498_20182566	-24.82543009	Chr1	EDTA	hAT_TIR_transposon	20182451	20182537	86	-	TE_homo_20702		TE_00000692	DNA/DTA	SO:0002279	0.857	homology				39
Chr8	9799041	9799093	52	CHH_Chr8_9799041_9799093	-23.74433659	Chr8	EDTA	LTR_retrotransposon	9798955	9799102	147	+	TE_homo_204877		TE_00002144_LTR	LTR/unknown	SO:0000186	0.865	homology				52
Chr1	44718212	44718262	50	CHH_Chr1_44718212_44718262	-22.84340865	Chr1	EDTA	PIF_Harbinger_TIR_transposon	44718048	44718348	300	+	TE_homo_39592		TE_00001578	MITE/DTH	SO:0002284	0.861	homology				50
Chr3	20798612	20798666	54	CHH_Chr3_20798612_20798666	-22.3425446	Chr3	EDTA	LTR_retrotransposon	20797064	20803803	6739	?	LTRRT_901	repeat_region_901	TE_00001156	LTR/unknown	SO:0000186	1	structural	TGCA ACTTT			54
Chr7	24548868	24548936	68	CHH_Chr7_24548868_24548936	-22.0820078	Chr7	EDTA	Mutator_TIR_transposon	24548590	24549581	991	-	TE_homo_193574		TE_00001943	DNA/DTM	SO:0002280	0.796	homology				68
Chr4	11857136	11857190	54	CHH_Chr4_11857136_11857190	-21.80776433	Chr4	EDTA	LTR_retrotransposon	11856995	11858037	1042	+	TE_homo_109855		TE_00000524_INT	LTR/unknown	SO:0000186	0.952	homology				54
Chr6	27617882	27617944	62	CHH_Chr6_27617882_27617944	-21.71693731	Chr6	EDTA	Mutator_TIR_transposon	27617809	27618046	237	-	TE_homo_169669		TE_00001819	DNA/DTM	SO:0002280	0.855	homology				62
Chr7	17263276	17263327	51	CHH_Chr7_17263276_17263327	-20.88165126	Chr7	EDTA	Mutator_TIR_transposon	17263175	17263345	170	-	TE_homo_189820		TE_00001405	DNA/DTM	SO:0002280	0.812	homology				51
Chr6	26927361	26927411	50	CHH_Chr6_26927361_26927411	-20.33463133	Chr6	EDTA	helitron	26927147	26927500	353	-	TE_homo_169312		TE_00002110	DNA/Helitron	SO:0000544	0.901	homology				50
Chr1	18830331	18830382	51	CHH_Chr1_18830331_18830382	-20.02172979	Chr1	EDTA	helitron	18830340	18830454	114	-	TE_homo_19374		TE_00000539	DNA/Helitron	SO:0000544	0.919	homology				43
Chr6	19041248	19041298	50	CHH_Chr6_19041248_19041298	-19.96269012	Chr6	EDTA	Copia_LTR_retrotransposon	19040390	19041316	926	-	TE_homo_162258		TE_00000705_INT	LTR/Copia	SO:0002264	0.879	homology				50
Chr4	17556054	17556113	59	CHH_Chr4_17556054_17556113	-18.49539752	Chr4	EDTA	Mutator_TIR_transposon	17556088	17556223	135	-	TE_homo_114987		TE_00000628	DNA/DTM	SO:0002280	0.807	homology				26
Chr1	7859425	7859480	55	CHH_Chr1_7859425_7859480	-18.098756	Chr1	EDTA	helitron	7859320	7859613	293	-	TE_homo_8621		TE_00000604	DNA/Helitron	SO:0000544	0.95	homology				55
Chr1	20196514	20196566	52	CHH_Chr1_20196514_20196566	-16.2390626	Chr1	EDTA	repeat_region	20195884	20197044	1160	-	TE_homo_20709		RLX_76087|LTR_Mt_chr_04_454|LTR|02.01.01.99|3880|Medicago	Unspecified	SO:0000657	0.836	homology				52
Chr1	51540790	51540840	50	CHH_Chr1_51540790_51540840	-15.84360776	Chr1	EDTA	Mutator_TIR_transposon	51539995	51541366	1371	-	TE_homo_44565		TE_00001943	DNA/DTM	SO:0002280	0.802	homology				50
Chr4	3096964	3097032	68	CHH_Chr4_3096964_3097032	-15.09657096	Chr4	EDTA	Mutator_TIR_transposon	3096907	3097126	219	+	TE_homo_104035		TE_00001943	DNA/DTM	SO:0002280	0.839	homology				68
Chr2	7663077	7663128	51	CHH_Chr2_7663077_7663128	-14.17159157	Chr2	EDTA	Mutator_TIR_transposon	7662947	7663262	315	+	TE_homo_53079		TE_00001819	DNA/DTM	SO:0002280	0.862	homology				51
Chr2	30835063	30835113	50	CHH_Chr2_30835063_30835113	-13.92431845	Chr2	EDTA	Mutator_TIR_transposon	30834666	30835286	620	-	TE_homo_73780		TE_00001943	DNA/DTM	SO:0002280	0.81	homology				50