Title: Evolution of conserved noncoding sequences in *Arabidopsis thaliana*

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Abstract:

Recent pangenome studies have revealed a large fraction of the gene content within a species exhibits presence-absence variation (PAV). However, coding regions alone provide an incomplete assessment of functional genomic sequence variation at the species level. Little to no attention has been paid to noncoding regulatory regions in pangenome studies, though these sequences directly modulate gene expression and phenotype. To uncover regulatory genetic variation, we generated chromosome-scale genome assemblies for thirty *Arabidopsis thaliana* accessions from multiple distinct habitats and characterized species level variation in Conserved Noncoding Sequences (CNS). Our analyses uncovered not only evidence for PAV and positional variation (PosV) but that diversity in CNS is non-random, with variants shared across different accessions. Using evolutionary analyses and chromatin accessibility data, we provide further evidence supporting conserved and variable CNS roles in gene regulation. Characterizing species-level diversity in all functional genomic sequences may later uncover previously unknown mechanistic links between genotype and phenotype.

Introduction:

Conserved noncoding DNA remain a highly understudied class of functional genomic features compared to protein-coding genes. Previous comparative genomic analyses have identified stretches, generally 15-150 base pairs (bp) long (Fig S1), of noncoding regions that are positionally-conserved with identical (or near identical) sequence across distantly related species. These sequences, commonly referred to as Conserved Noncoding Sequences (CNS), are regions in the genome displaying much higher similarity across different taxa than expected by chance. Background mutation and genetic drift purges non-functional sequences over long evolutionary distances. Therefore, sequence conservation above expectation implies purifying selection actively conserves these CNS. Indeed, Williamson et al. (1) discovered elevated signatures of purifying selection in CNS regions compared to other classes of noncoding DNA in *Capsella grandiflora*. Previous studies demonstrated CNS contain transcription factor binding sites (TFBS) (2–4).

TFBS are typically 6-12 base-pair (bp) long (5). CNS exceed this length, as they are thought to consist of arrays of TFBS capable of recruiting independent or cooperative transcriptional protein complexes. The length of CNS enables high confidence identification of orthologous cis-regulatory elements in comparator genomes. Querying genomes for TFBS alone results in a high false positive rate, as there are >30,000 expected occurrences of a given 6 bp sequence expected by chance even in the relatively small (~135 Mb) *Arabidopsis thaliana* genome. In contrast, there is < 1 expected random

occurrence of our shortest CNS (15bp). TFBS colocalize with accessible chromatin in mammals, as do CNS as demonstrated previously in plants (6–9).

Alexandre and coworkers previously investigated variation in signatures of accessible chromatin and sequence diversity of differentially accessible regions across five diverse *A. thaliana* accessions (10). They discovered ~15% of accessible chromatin regions differed across the five accessions, with a minority of those sites displaying sequence divergence. Mapping data from non-reference genotypes to a reference genome may result in incorrectly assigning reads to the reference (11). By assembling separate genome assemblies for each accession, we mitigate this reference mapping bias. We add to the findings of Alexandre and coworkers by characterizing sequence diversity directly on a larger panel of thirty accessions, focused on a CNS set consisting of more than 3Mb of sequence, and discover significant relationships between variable sequence and regions of accessible chromatin.

Genes fall under a wide spectrum of selective pressures, with some genes on one end being under strong purifying selection to be retained (to resist deletion) (12) whereas on the other end negative selection actively purges genes from the genome (13). Certain gene families are known to exhibit high birth-death dynamics because ancestral genes are lost from the lineage, whereas other gene families are relatively stable in size (14, 15). Thus, some genes are present in all eukaryotes, whereas others may be lineage specific (16). Equivalently, a subset of CNS identified across Brassicaceae (17) are identifiable across all surveyed angiosperms including *Amborella* (3) whereas others are uniquely shared by only a subset of Brassicaceae.

Previous pangenome studies aimed to capture presence-absence variation in transcribed regions to characterize the core and dispensable gene content, however, these studies often focus on *de novo* assembly of only the non-reference gene space (18–21). These studies consistently find core genes (those present across most individuals within a species) are enriched in essential cellular processes, whereas dispensable genes often display higher mutation rates and are biased towards adaptive processes. We hypothesize dispensable CNS follow patterns observed for dispensable coding regions such as representing a pool of sequences contributing to adaptive processes and potentially important agronomic traits.

Though tens of thousands of CNS have already been identified in plant genomes, these comparisons are often performed between single representatives of select distantly related species. To our knowledge, the variation in CNS content across the genome of multiple individuals within a single species has never been addressed in plants. Here, we assembled chromosome-scale genomes for thirty *A. thaliana* accessions and leveraged one of the largest annotated CNS datasets (17), to investigate the

levels and patterns of intraspecific variation of CNS and the impact of this variation on gene expression in *A. thaliana*.

Results:

What proportion of CNS vary within a species?

CNS are typically identified through whole genome comparisons of single representative genomes of different species spanning various phylogenetic distances. Therefore, the variation of these sequences at the species level remains poorly understood, especially in plants. To investigate the variation in CNS content and position, we assembled the genomes of thirty *A. thaliana* accessions using a hybrid reference and *de novo* method (Supplementary Methods). Two main types of variation were monitored: presence-absence variation (PAV) and positional variation (PosV). We define PAV CNS as those present in the reference accession (Col-0), but absent in at least one other accession. PosV CNS are those which exist in a different locus in an accession relative to its position in Col-0.

Importantly, we only investigate CNS present in the *A. thaliana* reference accession Col-0. We generated an independent assembly of Col-0 to serve as a control for false positive PAV CNS. For newly positioned CNS, PosV, we arbitrarily defined Col-0 positions to be our reference. When a non-reference accession has a CNS at a position not in Col-0, we label that CNS as PosV. Our independent Col-0 assembly (Col-0') was analyzed for variation using the same methods as the other accessions. As Col-0' and the reference genome should have identical CNS structure, few differences are expected due methodological differences between CNS reference generation and accession annotation. Of the 62,916 CNS analyzed, there were only 26 found absent in Col-0' (PAV), compared to an average of 163 displaying PAV per wild accession. More strikingly, only 31 exhibited PosV in Col-0', compared to an average of 910 (~1.45% total CNS) exhibiting PosV per accession. Therefore, our assembly method identified novel PosV and PAV events unlikely to be caused simply by false positive identification attributable to poor or biased assembly quality. Throughout the manuscript, CNS exhibiting PAV in at least one accession will be referred to as PAV CNS. A similar syntax will follow for CNS showing PosV in at least one accession. CNS in either of the aforementioned classes will be referred to as variable CNS, whilst those showing no variation are referred to as collinear CNS.

As the set of query CNS were characterized for their presence in multiple different species across Brassicaceae spanning ~32 million years of evolution (22), low proportions of variation were expected. Indeed, only 0.25% (n = 163) and 1.45% (n = 910) CNS on average per accession exhibit PAV and PosV respectively. However, given the large number of variable CNS in the query set (62,916), this

represents a definable class of sequence (>1,000 sequences per accession) with observable variation patterns we aim to examine further.

Is CNS variation shared between accessions?

CNS variation is highly shared among accessions. If PAV and PosV CNS occurred independently in each accession, we expect 4,529 and 21,724 different CNS to be lost and positionally variable respectively in at least a single accession (Supplementary Methods).We calculated these values empirically by repeatedly assigning random CNS to the PAV and PosV category in sample sizes matching that observed in the data. In contrast to random expectation, we only observe 1,524 and 4,801 different CNS lost and positionally variable respectively (Fig S2,a Fig S3). Therefore, PAV and PosV CNS events are unlikely independent among individuals. This indicates variable CNS are often variable in more than a single accession. There is little overlap of PAV and PosV CNS. There are 118 CNS absent in at least one accession and positionally variable in at least one other accession (<10% of either set). This is not significantly different than expected by chance (hypergeometric test p-value = 0.4227782).

Random subsampling of CNS analyzed in the thirty accessions assembled indicate the majority of the natural CNS variation is likely captured and is sufficient to investigate the functional consequences of this variation (Fig S2 Fig S3). Furthermore, there is strong observed overlap in variable CNS across accessions (Fig S4 Fig S5), indicating there may be subclasses of CNS which are more likely to exhibit variation than others. This phenomenon is similar to certain classes of gene families that often display copy-number variation (14, 23, 24).

How does CNS variation compare to gene content variation?

Several previous pan-genome studies assessed species level diversity in gene content and structural variants (18–21). Most of these studies often do not fully assemble genomes for each individual of the species, rather, only assembling the sequence not present in the reference. These approaches fail to identify positional conservation and rearrangements in non-reference individuals. However, some previous pangenome studies (e.g. Brachypodium; (18)) have assembled full genomes but focused on only coding gene content variation. Our approach uses a hybrid reference guided and *de novo* assembly approach to obtain chromosome-scale sequences for each individual accession. This permits the analysis of PAV and positional variation of both CNS and transcriptional unit content.

Our analyses revealed that CNS variation occurs at a much lower rate than genic variation (Fig S6). This implies stronger purifying selection acts on noncoding regulatory regions than protein-coding genes. This may be the case, however, the set of noncoding regions investigated in this study are also

present throughout Brassicaceae, biasing our annotations to CNS likely experiencing greater levels of purifying selection. It is therefore unsurprising we observe a lower rate of variation in CNS compared to coding regions. The true rate of variation in functional noncoding regions may only be identified through complete annotation of functional *cis*-regulatory regions, a difficult feat relative to coding region annotation. Thus, it is imperative that future efforts identify species-specific CNS to assess the full scope of regulatory variation that exists at the species level.

What is the length distribution of variable CNS?

The distribution of the lengths of CNS was investigated (Fig S7). CNS retaining their syntenic position in every accession (collinear CNS) have a length distribution similar to that of all CNS in the reference accession. This is not surprising since >90% of all CNS (n = 56,803) are in this class. PAV CNS on average have a longer length than collinear CNS (collinear average = 39.84, PAV average = 44.41, *KS* test p-value < 2.2e-16). The PAV CNS length distribution appears bimodal (Fig S7). PosV CNS are much shorter on average than either collinear or PAV CNS (PosV average = 18.97).

What is the distribution of CNS transposition events?

PosV CNS are those found outside of their respective syntenic block in the reference genotype. In other words, their order among CNS is different in the accession compared to the Col-0 reference genome. We observe no apparent bias in transposition location besides towards gene-rich regions (KS test p-value < 2.2×10^{-16}; Fig S8).

In addition to genomic positional changes, CNS distance to their proximate gene was investigated. Figure 1 compares the distance of CNS to their proximate genes across a few different classes of CNS. The largest concentration of CNS is intergenic and close to genes in the genome (37.17% of CNS +/- 500 bp of and between transcriptional start or termination sites). There is a reduction in the concentration of CNS around the nearest gene for PosV CNS, relative to CNS in accessions that retain their syntenic position relative to Col-0. Position relative to the proximate gene does not seem to predispose a CNS from exhibiting PAV in the global population.

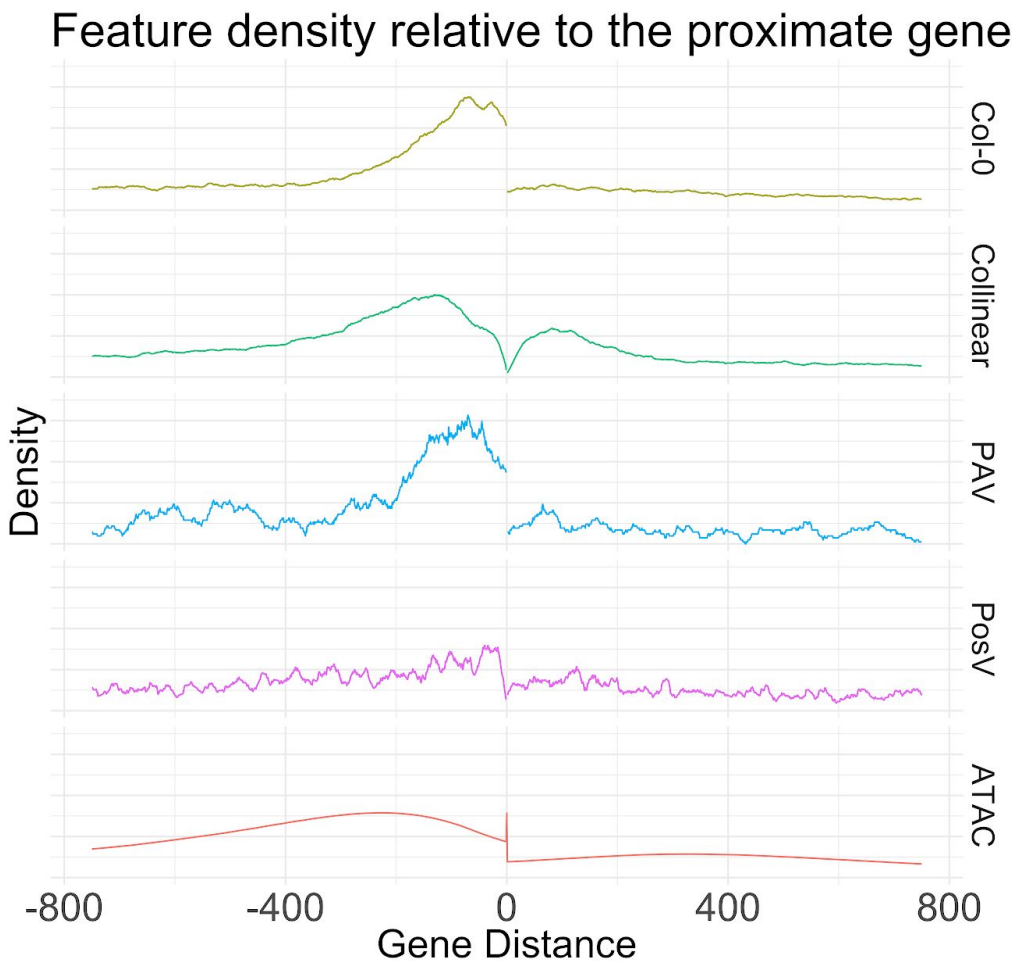

Figure 1: Distributions of different features relative to their proximate gene are shown, where the x-coordinate zero represents the location of the proximate gene. The top panel (Gold) shows all CNS in the reference accession Col-0. The second panel (green) shows across all accessions the distribution of CNS that remain in the same syntenic position as the reference accession (Collinear CNS). The middle panel (blue) shows the position in the reference accession where PAV CNS are located, ie the position in Col-0 where CNS display PAV in accessions. The fourth row (purple) shows the position of PosV CNS across all accessions, ie the location to which these CNS "moved". The final panel (red) shows the distribution of ATAC sequencing peaks across all accessions sampled.

Are variable CNS unique to certain genetic admixture groups of Arabidopsis?

Principal Components Analysis (PCA) was performed to examine similarities in CNS variation across accessions. PCA was performed separately using PAV CNS and PosV CNS as input. The first two principal components (PCs) for PAV CNS explained 10.8% and 8.29% of the total variance. There are two distinct clusters of accessions defined by the first two PCs of this analysis for PAV CNS. The first two PCs for PosV CNS explained 6.83% and 5.57% of the total variance. Two distinct clusters are apparent for

PosV CNS, similar to PAV CNS. The division is not as striking as that in PAV CNS, however the individuals in each PAV CNS cluster are still split by a line in the PosV CNS plot (Fig 2). We investigated whether clustering by CNS annotation aligns with the genetic admixture group assigned by the 1001 Genomes Consortium (25). The first two PCs for PAV CNS did not display distinct differences between admixture groups overall, however, admixture groups did cluster within the two overall clusters. PosV CNS admixture groups clustered closely when split by the first two PCs. PCA performed combining PAV and PosV CNS closely reflected the PosV CNS clustering, as is expected since 80% of the data comes from PosV information (Fig S9).

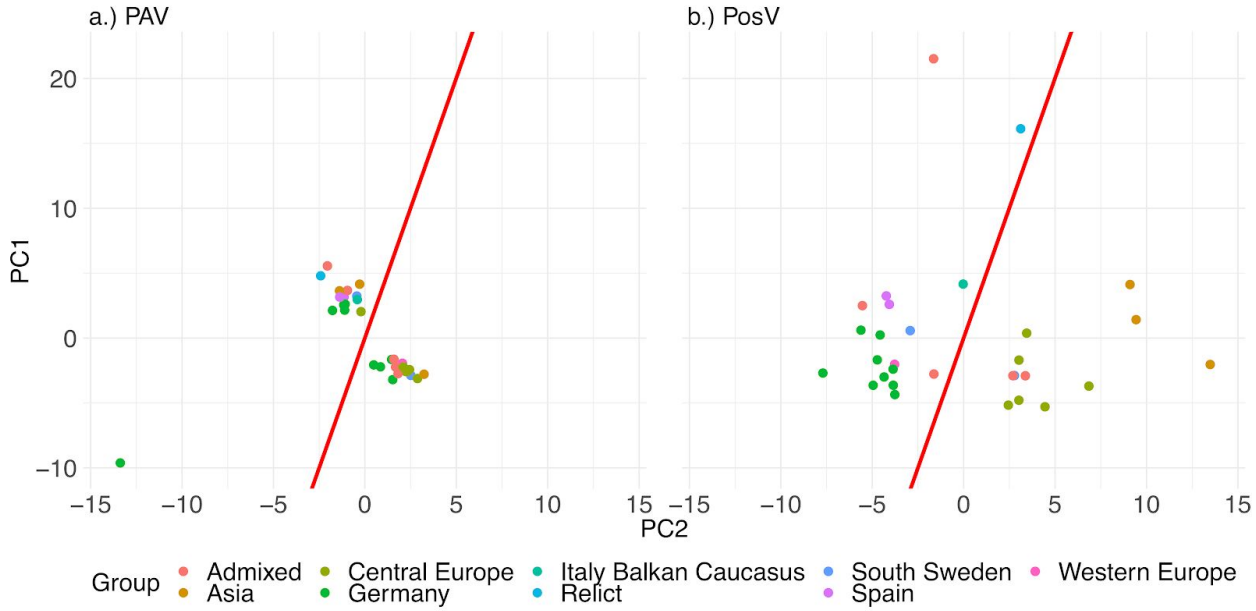

Figure 2: Principal Components Analysis (PCA) for each of the thirty accessions using either PAV CNS (a) or PosV CNS (b) as information. Accessions are colored by their admixture group as assigned by the 1001 Genomes Consortium (25). The red line shown is an arbitrarily drawn line matching the equation y = 4x.

Are variable CNS still associated with accessible chromatin?

We performed Assay for Transposase-Accessible Chromatin sequencing (ATAC-seq) in leaf tissue for eighteen accessions, including the reference accession Col-0. This sequencing technique identifies genomic regions accessible by a Tn5 transposase, a signature of accessible chromatin (26). We utilized a protocol which combines fluorescence-activated nuclei sorting and ATAC-seq (FANS-ATAC-seq; (27). As we hypothesize CNS to be regulatory sequences, we expect active regulators will overlap signatures of accessible chromatin. ATAC-seq reads were aligned to their respective genome, and peaks, regions of

statistically enriched clusters of sequencing reads, were identified. Collinear CNS demonstrated much stronger overlap with ATAC peaks than expected by chance (average fold-enrichment = 2.457, average p-value < 1x10^-10). Across all accessions, an average of 16.49% of CNS annotations overlapped an ATAC peak.

Furthermore, we tested whether CNS which deviate from their position in the Col-0 accession (PosV CNS) still overlapped ATAC peaks. Nearly every accession displayed a significant enrichment of overlap between PosV CNS and ATAC peaks than expected by chance (Table S1). The average fold enrichment for PosV CNS across all accessions was 1.41. The average percent overlap was 9.47%, lower than observed for collinear CNS.

Strong evidence of CNS overlapping signatures of accessible chromatin has been reported previously (2, 6, 7, 9). In each case, the set of CNS queried was different, with estimates ranging from 14% to 48% of CNS overlapping signatures of accessible chromatin. The percentage reported here, 16%, is in line with previous estimates. In Figure 3, we demonstrate an instance where CNS loss is associated with loss of accessible chromatin in a given accession. Additionally, we show a novel CNS insertion in an accession associated with an accession-specific chromatin accessible region.

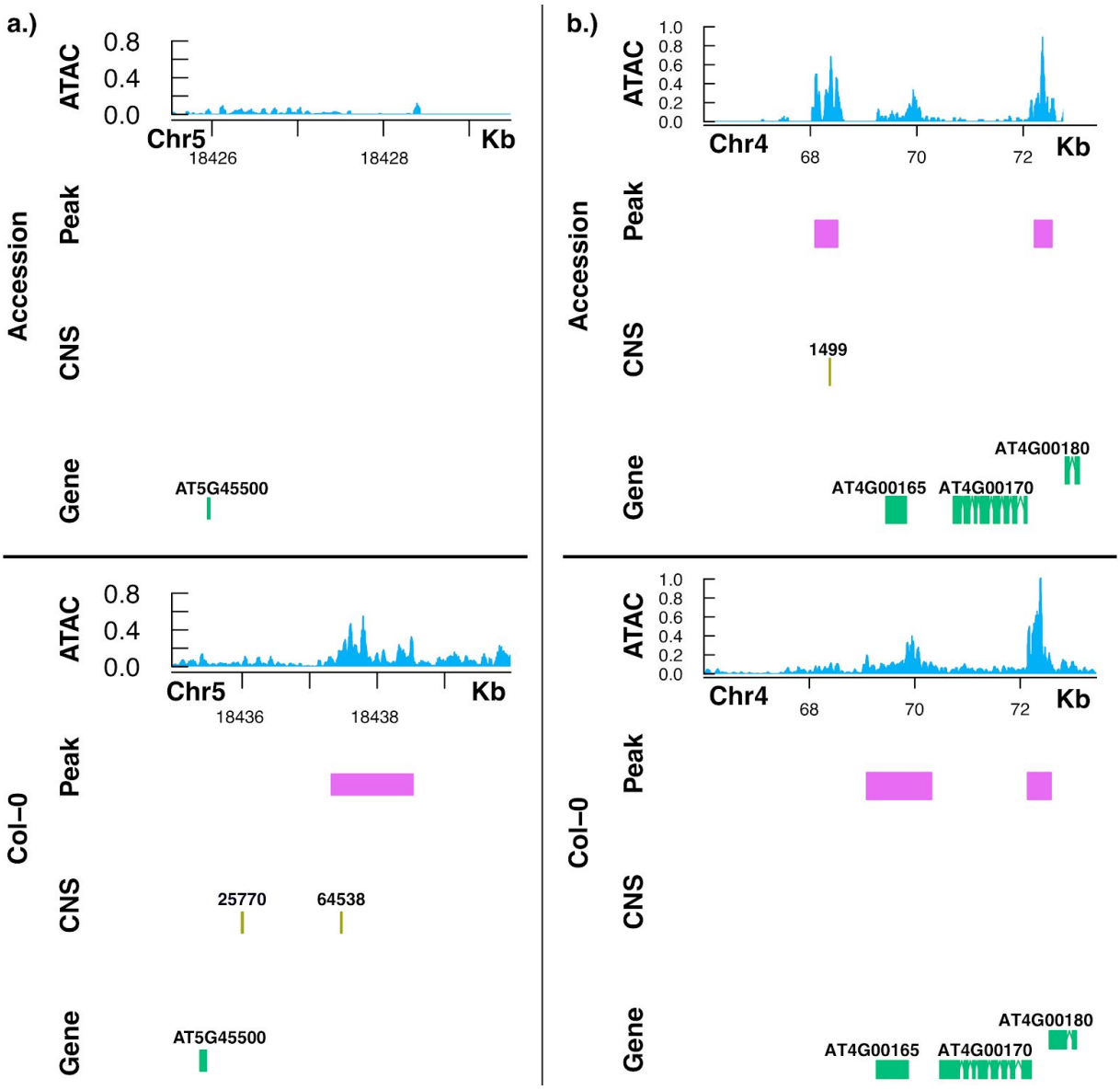

Figure 3: Genome browser tracks are shown for two different syntenic regions. (a) Shows loss of CNS 64538 and 25770 associated with loss of ATAC-seq peaks downstream the locus AT5G45500. Part (b) demonstrates a gain of CNS 1499 associated with the gain of a CNS peak upstream the locus AT4G00165.

Though there is significant overlap between PosV CNS and accessible chromatin, the majority of PosV CNS do not overlap ATAC peaks. The true proportion of putatively functional PosV CNS is likely greater than observed here, potentially because the ATAC sequencing was performed at a single time point under normal growing conditions. As CNS are hypothesized to perform regulatory functions, their binding partner may require distinct spatial-temporal context and/or environmental stimuli to activate. Given a single environmental stimulus was sampled for the ATAC sequencing data, it is unlikely every

PosV CNS which may exist in regions of accessible chromatin under different conditions will be identified. In addition to responding to distinct environmental stimuli, regulatory functions of some CNS may also be tissue or developmental stage specific, further lending to their absence in regions of open chromatin observed here. Lastly, PosV CNS and ATAC peak overlap was lower than that of collinear CNS. PosV CNS may act as adaptive sequences, changing over shorter evolutionary distances, similar to certain classes of genes that exhibit higher transposition and duplication rates (15, 23, 28). They may be involved in specific stress responses and therefore may not demonstrate overlap with open chromatin in healthy leaf tissue.

It should be noted previous studies posited accessible region differences between *A. thaliana* cell types were quantitative rather than qualitative (29). Perhaps PosV CNS not overlapping with accessible chromatin align with this trend and exhibit low signatures, rather than the absence, of accessible chromatin below our detection threshold. This is worth investigating in the future.

Is CNS loss and gain associated with gene expression differences?

RNA-sequencing (RNA-seq) data was analyzed for four of the accessions investigated in this study to identify differentially expressed genes in leaf tissue between each accession and Col-0 (30). Genes with a greater number of CNS associated with them in a given accession were more likely to upregulated in that accession (Table 1). Genes with a lower number of CNS associated with them in a given accession were more likely to be downregulated in that accession. Genes without CNS changes relative to Col-0 were significantly underrepresented for differentially expressed genes. This demonstrates a strong association between changes in *cis*-regulatory sequence and divergent expression, a phenomenon also demonstrated across populations of sticklebacks (31). If the true ratio of activator binding sites to repressor binding sites was equal, we would expect no enrichment for differentially expressed genes for those gaining or losing CNS. Our results suggest CNS variation tilts towards activator binding sites. Regardless, we observe a strong relationship between CNS and expression divergence.

Gene Type	Average number of upregulated genes per accession (%)	P-value (Hypergeometric test)	Average number of downregulated genes per accession(%)	P-value (Hypergeometric test)
CNS Gain	208.5 (7.927)	$< 1 \times 10^{-10}$	76.5 (2.908)	8.395×10^{-06}
CNS Loss	26.25 (2.449)	0.093*	121.75 (11.357)	$< 1 \times 10^{-10}$
No CNS Change	489.75 (2.212)	$< 1 \times 10^{-10}$	748.5 (3.380)	$< 1 \times 10^{-10}$

*Do not pass Bonferroni correction p-value 0.01 / 6 = 0.00167

Underrepresented

Overrepresented

Table 1: Tests for over and under representation of differentially expressed genes in CNS with greater than (CNS Gain), less than (CNS Loss), or no change (No CNS Change) relative to Col-0. Numbers in parenthesis refer to the percent of the gene types which are up or down regulated.

Are variable CNS biased towards certain GO terms?

Each CNS identified in the Col-0 accession (17) was assigned to its proximate gene. This enabled gene-ontology (GO) enrichment analyses on the genes in the Col-0 accession which experience CNS change in other accessions. GO-term enrichment analysis was performed for the set of PAV and PosV CNS. A strict significance threshold was issued (p-value $< 10^{-5}$, bonferroni correction). GO:0006355, regulation of DNA transcription, was the only overrepresented GO term. Interestingly, this same GO term was enriched in both the PAV and PosV sets. Therefore, CNS variation highly biases towards the regulatory regions of genes which influence DNA transcription.

Are variable CNS enriched with certain binding motifs?

PAV and PosV CNS were searched for enriched motifs with the program HOMER (34). The set of all PAV and PosV CNS were tested separately. Motifs for the binding targets of several stress responsive transcription factor families were enriched. Specifically, in the set of PosV CNS sequences, the binding motifs of MYB113, C2H2, ABF3, HSF21, WRKY8, and CBF4 were enriched. For PAV CNS, WRKY50, RAV1, and Dof2 motifs were enriched. The global pattern for enriched motifs were for stress responsive

elements. Given there are environmental differences experienced by different accessions, differences in regulatory patterns governing an accession's stress response are expected.

One enriched motif in the set of PosV CNS is the target of HSFA4A. HSFA4A has been shown to regulate abiotic stress response pathways (35, 36) and has also shown accession-specific (Cvi-0) induction in response to biotic stresses (37). In the accession Cvi-0, the gene (AT4G18890) has lost 3 of 7 CNS that had been associated with it in the reference accession Col-0. A change in CNS structure may have resulted in rewiring of this transcription factor resulting in gene expression changes in certain environmental contexts.

Are CNS changes associated with altered selective constraints?

As mentioned earlier, each CNS is associated with a gene in the Col-0 reference genome. Therefore, we can track the orthologous genes in each accession and determine if the genes in accessions which lose CNS exhibit signatures of positive or negative selection compared to those which have retained the CNS, including the Col-0 reference.

We assigned PosV CNS to their proximate gene to investigate changes in the CNS structure of orthologous genes across accessions. For example, we investigated any correlation between CNS gain or loss relative to Col-0 and Ka/Ks ratio (ratio of non-synonymous to synonymous substitution rate) for each gene in every accession. This revealed no clear correlation between Ka/Ks ratio and CNS count (Fig S10).

We were interested if a coding sequences' association with a CNS in Col-0 altered the Ka/Ks pattern compared to those without an associated CNS. There was a statistically significant (KS test p-value $< 1 \times 10^{-10}$) difference between these two distributions indicating genes associated with a CNS in Col-0 generally display lower Ka/Ks values compared to genes with no associated CNS (all genes median Ka/Ks = 0.3853; CNS associated genes median Ka/Ks = 0.3549).

We were also interested if changes in CNS structure affect the Ka/Ks distribution, as calculated by comparing CDS from each accession to its orthologous CDS in the reference Col-0 accession. The Ka/Ks distribution for all gene pairs across all accessions is bimodal (Fig S11). The first peak is centered on 0, representing groups of identical shared alleles. The second peak occurs at a Ka/Ks ~ 0.45. The density of identical gene pairs is lower in orthologous pairs experiencing CNS change. There is, however, an increase in the density of orthologous gene pairs with a low Ka/Ks ratio (0.1 - 0.3). Given this observed CNS variation occurs at the species level, therefore a short evolutionary time frame, perhaps the change in CNS structure has already begun to exert positive selective pressure (evidenced by a higher Ka/Ks ratio).

The Ks distribution was investigated (Fig S12). The median Ks divergence of all orthologous gene pairs was 0.0040. The Ks distribution for all these gene pair groups showed a significant peak at 0, with a secondary peak at Ks ~ 0.003 followed by an exponential decay. The Ks distribution of orthologous gene pairs with less CNS in the accession relative to Col-0 (median Ks = 0.0169) and more CNS (median Ks = 0.0055) were observably different. Both distributions (CNS gain and loss) were shifted right. The CNS loss associated gene pair Ks distribution was the most shifted right.

Are there relationships between CNS class and transposable elements or gene duplicates?

We investigated the proximity and density of transposable elements (TEs) for different classes of CNS. We identified putative TEs in each accession by searching for a set of previously annotated *A. thaliana* TEs within each genome using BLAST. Only matches at an e-value of lower than $1x10^{-10}$ were retained. Figure S15 demonstrates a clear bias in colocalization between PosV CNS and TEs relative to collinear CNS. Not only were PosV CNS closer to the nearest TE, but the density of TE matches both overlapping and within a 1,000 bp window was observably elevated in PosV CNS relative to collinear CNS. However, we observe elevated TE density for <25% of PosV CNS, indicating the majority of PosV CNS do not demonstrate elevated TE density relative to collinear CNS.

Lastly, we compared CNS content for different classes of duplicates (Fig S13). Considering only genes with a CNS associated with them, tandem duplicates had the fewest CNS associated with them (mean CNS count = 0.2442). This may be an artifact of CNS identification algorithms which struggle with tandem repeats. Genes without any duplicate in the genome (mean CNS count = 0.7064) had less CNS associated with them than genes with a duplicate pair dating back to the most recent whole genome duplication (At-alpha) shared by *A. thaliana* (mean CNS count = 0.9824) (22). This observation is consistent with previous studies; genes associated with CNS were more likely to be retained as duplicate pairs through diploidization potentially due to gene dosage constraints (38) or simply that these genes have long subfunctionalizable regulatory regions, or both explanations might be correct.

Discussion:

This study is, to our knowledge, the first genome-wide survey of CNS PAV and PosV at the species level in plants. The rate of variable CNS, while small compared to variable genes, is quite high in *A. thaliana*. However, the numbers reported here are likely underestimates of variable functional noncoding sequences given that our CNS set are heavily skewed towards those likely under stronger purifying selection. These positionally-conserved CNS were identified by aligning multiple Brassicaceae

genomes spanning millions of years of evolution (17). Thus, new methods are needed to identify the full complement of functional regulatory sequences that are lineage and even species specific.

How is it that nearly 1,000 PosV CNS are at different loci in distinct accessions? We present two non-mutually exclusive hypotheses. First, we propose a *de novo* origin hypothesis. We find the distribution of PosV CNS to be noticeably shorter than the length distribution of all CNS (Fig S7). PosV CNS are often less than 20 bp in length. Therefore, perhaps the majority of the CNS sequence already exists in alternate loci, and only a few base-pair changes are needed to convert an existing background sequence to a CNS (Figure 4). A DNA sequence which is very similar to a binding motif may experience partial binding of a given transcription factor. This may be the selective pressure required to convert, or rather select for beneficial mutations on the existing sequence to further strengthen that TF's binding. Elevated mutation rates in recombination hotspots may contribute to the evolution of PosV CNS. Future studies are needed to test whether PosV CNS sites are associated with regions of higher recombination. Second, the movement of regulatory elements may involve transposable elements (TEs) as shown previously (39–41). Indeed, we observe strong bias with respect to the colocalization of PosV CNS and TEs relative to collinear CNS (Figure S15, Figure S16). These hypotheses are not mutually exclusive and both likely contribute to PosV CNS being at new, unexpected locations.

Evolution of enhancer elements (histone modification H3K27ac) has been well studied in mammals (42, 43). These studies revealed thousands of lineage-specific enhancer elements have evolved across mammals and often occur in "ancient" DNA that is significantly under enriched for flanking repetitive elements. This suggests lineage-specific enhancer elements may arise through *de novo* origins via random mutations, in line with one of our hypotheses. Additionally, a few studies in *Drosophila* demonstrated *de novo* origins of TFBS (6bp-8bp) can occur on the order of 10^3-10^6 years under a model of neutral evolution (44, 45) which is within the divergence time (10^4-10^5 years) between *A. thaliana* accessions (25). Mustonen and Lassig (46) model binding site evolution in a manner we predict CNS *de novo* origins occur in plants. According to their model, selective strength on random mutations depends upon the mutation's effect on the binding strength of its associated transcription factor. Therefore, selection for partial transcription factor binding may drive sequence conversion from partial to full CNS sequence as shown in Figure 4.

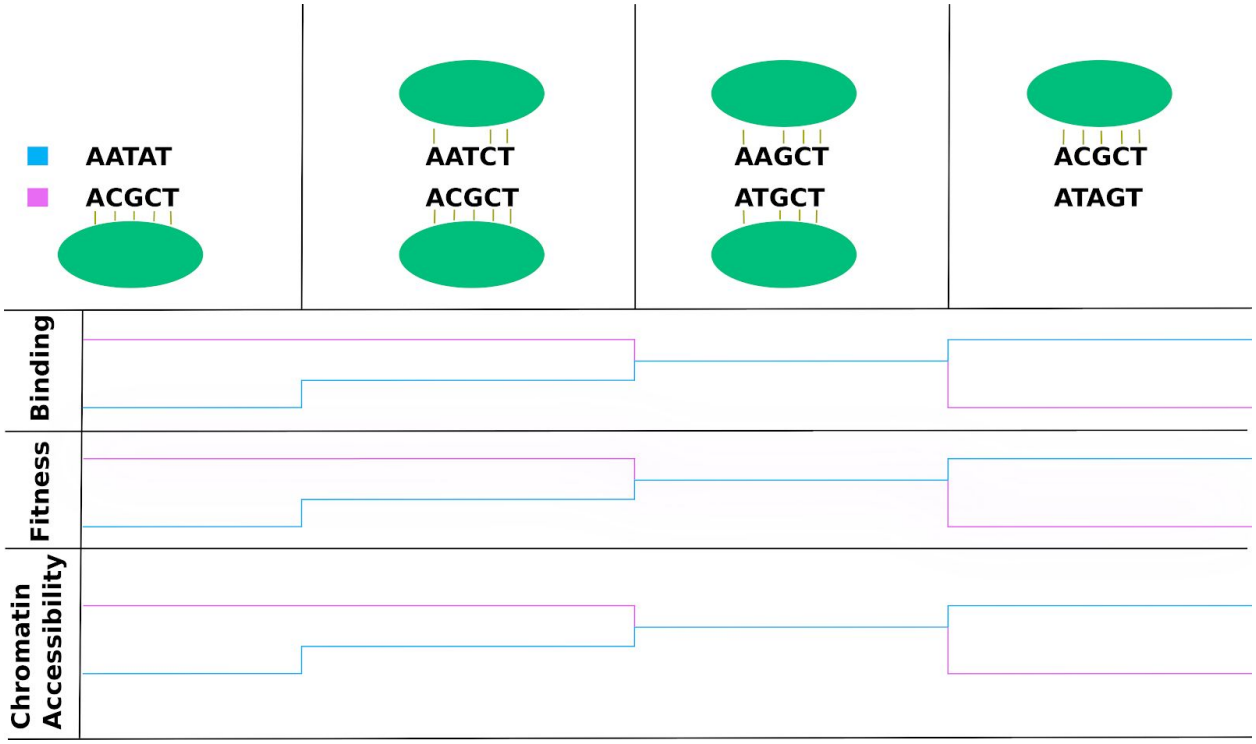

Figure 4: Hypothesized changes to transcription factor binding, fitness, and chromatin accessibility around two regions of DNA: the new PosV CNS location (top, pink), and the ancestral position as observed in Col-0 (bottom, blue). Each column in the first row depicts a snapshot of the state of the two CNS locations as time progresses along the x-axis . The hypothesized changes to TF binding, organism fitness, and chromatin accessibility align with the different time points.

Lastly, we provide evidence positionally variable CNS retain strong associations with regions of accessible chromatin. Being open for business does not prove that business is actually being conducted, but functional genes must be open. Additional evidence for the function of PosV CNS, such as the effect of CNS change on gene expression, should be the focus of future studies in *A. thaliana*. This may need to involve genome editing of target CNS to assess its direct impact on gene expression and phenotype. We hypothesize PAV and shuffling of existing CNS at the population level serves as a mechanism to navigate the evolutionary landscape, providing more rapid alterations to the expression of genes that improve fitness.

Author Contributions:

All authors performed research and/or analyzed data; A.E.Y and P.P.E. drafted the manuscript. All authors reviewed and edited the manuscript.

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Methods:

More details on all methods can be found in the Supplementary Methods file. Genome assemblies, gene annotations, and cns annotations will be made available on Dryad repository (https://datadryad.org/).

Genome assembly:

A separate genome assembly for each accession was generated using a hybrid reference-guided and *de novo* assembly method described in Supplementary Methods.

Gene prediction:

Genes were predicted for each accession independently using the MAKER pipeline.

CNS annotation:

CNS were annotated in each genome with the BLAST (47) program combined with stringent filtering. To increase the confidence in CNS annotations, all CNS below 15 base-pairs in length were dropped. After querying each ecotype's genome with the final set of 62,916 CNS, the resulting hits were filtered to remove any match with a bit score lower than 28.2. Specifically, this corresponds to an exact 15 base-pair match. Hits were also dropped if they covered < 60% of the length of the CNS considered in that hit. Hits on separate chromosomes were also removed.

These steps were also followed for the reference genome to allow for accurate annotation of the CNS position in the reference. This annotation was used in comparison with that of each accession to determine CNS which exist outside of syntenic CNS blocks with a block size of 5. Synteny was determined using the MCScanX program (48).

Identification of regions of accessible chromatin:

Regions of accessible chromatin were identified using MACS2 (49).

Ka/Ks calculation:

Ka/Ks ratios were calculated using a series of custom script found on Github: https://github.com/Aeyocca/ka_ks_pipe. Briefly, syntenic orthologs were identified using JCVI Utilites Library (50) between each ecotype and the reference ecotype Col-0. The protein sequence of each pair was aligned using MUSCLE v3.8.31 (51). The protein alignment was converted to a coding sequence alignment using a modified version of PAL2NAL v14 (52) available on Github. Alignments were fed into

PAML Version 4.9h (53) codeml function to calculate Ka/Ks values.

PCA:

Principal Components Analysis was performed with the prcomp() function in R version 3.5.0 (54). We decided not to scale variance, as CNS variability is not normally distributed.

RNA-Sequencing:

RNA sequencing data was taken for five accessions (Kn-0, Tsu-0, Ler-0, No-0, Col-0), from GSE30814 (30). Reads were mapped to their respective assembly using HISAT2/2.1.0 on default parameters (55). The resulting SAM file was converted to a BAM file using Picard Tools v2.18.1 (56). The BAM file was converted to a count matrix using StringTie/1.3.5 along with the accompanying script prepDE.py with minor modifications to handle variable gene names (57). The expression matrices were used to identify differentially expressed genes for each ecotype to the reference Col-0 using the R package DESeq2 (58).

Motif Enrichment:

Enriched motifs were identified using HOMER (34). Enrichment was performed for each ecotype separately as well as all ecotypes combined. For each set of ecotypes, enrichment was performed on PAV CNS and PosV CNS separately. The background set of sequences was set to a set of random sequences given the same composition of the query sequence using the scrambleFasta.pl script provided with HOMER.

Transposable Element analysis:

Transposable elements were putatively identified by searching the TAIR10 TE annotation against each genome separately using BLAST. Matches with an e-value < $1x10^{-10}$ were filtered out.