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Two adjacent NLR genes conferring quantitative resistance to clubroot disease in *Arabidopsis* are regulated by a stably inherited epiallelic variation

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ABSTRACT

Clubroot caused by the protist *Plasmodiophora brassicae* is a major disease affecting cultivated Brassicaceae. Using a combination of quantitative trait locus (QTL) fine mapping, CRISPR-Cas9 validation, and extensive analyses of DNA sequence and methylation patterns, we revealed that the two adjacent neighboring *NLR* (nucleotide-binding and leucine-rich repeat) genes *AT5G47260* and *AT5G47280* cooperate in controlling broad-spectrum quantitative partial resistance to the root pathogen *P. brassicae* in *Arabidopsis* and that they are epigenetically regulated. The variation in DNA methylation is not associated with any nucleotide variation or any transposable element presence/absence variants and is stably inherited. Variations in DNA methylation at the *Pb-At5.2* QTL are widespread across *Arabidopsis* accessions and correlate negatively with variations in expression of the two genes. Our study demonstrates that natural, stable, and transgenerationally inherited epigenetic variations can play an important role in shaping resistance to plant pathogens by modulating the expression of immune receptors.

Key words: methylation, clubroot, *Plasmodiophora brassicae*, *AT5G47260*, *AT5G47280*, ADR1-L3, *ddm1*

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INTRODUCTION

Intraspecific diversity in plant immune interactions is associated with a high level of sequence variation at hundreds of NLRs (nucleotide-binding and leucine-rich repeats), one of the largest and most rapidly evolving plant gene families (Meyers et al., 2003; Yue et al., 2012; Shao et al., 2016). On the basis of their N-terminal domains, NLRs have been classified into four subclasses: Toll/interleukin-1 receptor type (TIR-NLR or TNL), coil-coiled type (CC-NLR or CNL), RPW8-type CC-NLR (CCRPW8 NLR or RNL), and G10-type CC-NLR (CCG10 NLR) (Contreras et al., 2023). Many NLR proteins are involved in recognition of a small range of effector proteins secreted by specific strains of plant pathogens, potentially triggering the induction of strong plant defense responses that can rapidly stop pathogen invasion (Maekawa et al., 2011; Jones et al., 2016). The catalog of NLR genes expressed in a given plant genotype thus globally shapes the range of isolate-specific total resistances (incompatible interactions). However, this general rule has a few exceptions, including the existence of non-NLR-driven resistances (Thomas, 1998; Xiao et al., 2001; Larkan et al., 2013) and broad-spectrum NLR-driven resistances (Ernst et al., 2002; Qu et al., 2006).

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Effectors may be recognized in different ways: (1) NLRs can monitor the effect of pathogen effectors on their cellular targets; (2) pathogen effectors can be recognized by their direct interaction with one canonical NLR domain; or, alternatively, (3) effectors can be recognized by one non-canonical NLR domain, called an integrated decoy (ID), which mimics a protein domain of the effector target (Kourelis and van der Hoorn, 2018). Effector-activated CNLs then assemble into pentameric oligomers called resistosomes, driving a rapid intracellular inward Ca^{2+} flux that triggers downstream cellular defense responses (Förderer et al., 2022). Activated TNLs drive similar Ca^{2+}-mediated defense responses by an indirect pathway: assembled into tetrameric oligomers, their TIR domain mediates the biosynthesis of small signaling molecules, leading to downstream assembly of pentameric CCRPW8 NLR-based resistosomes that mediate Ca^{2+}-mediated defenses (Essuman et al., 2022). CCRPW8 NLRs thus play a central role in the integration of hub-connected TNL-based non-self-recognition processes and have therefore been called "helper NLRs" (Wu et al., 2017).

In contrast to *R*-gene-driven resistance, quantitative resistance is polygenic, i.e., it involves allelic variation at several quantitative trait loci (QTLs), which collectively contribute to post-invasive partial resistance in compatible plant–pathogen interactions. The nature of the few resistance QTLs cloned to date supports the premise that quantitative resistance genes (QRGs) are functionally more diverse than *R* genes (Nelson et al., 2017; Pilet-Nayel et al., 2017; Delplace et al., 2022). Among these QRGs, however, there are still genes encoding NLRs (Hayashi et al., 2010; Fukuoka et al., 2014; Xu et al., 2014; Debieu et al., 2016) and other receptors (Diener and Ausubel, 2005; Hurni et al., 2015) or co-receptors (Huard-Chauveau et al., 2013). Thus, variation in NLR genes (or other non-self-recognition loci) also appears to contribute to variations in basal resistance levels during compatible interactions.

To trigger effective resistance, cellular levels of NLR proteins must reach minimum thresholds. However, high levels of NLRs can also lead to autoimmunity drawbacks, including spontaneous hypersensitive response and retarded plant growth (Li et al., 2015; Lai and Eulgem, 2018). NLR abundance is thus tightly controlled by multiple mechanisms at the transcriptional, post-transcriptional (i.e., alternative splicing), and post-translational levels (i.e., ubiquitin-dependent proteolytic regulation) (Zhang and Gassmann, 2007; Li et al., 2015; Lai and Eulgem, 2018). NLR regulation also involves a multitude of epigenetic-related cellular processes, including redundant networks of small RNAs (sRNAs) (Shivaprasad et al., 2012; Fei et al., 2013; Deng et al., 2018; Huang et al., 2019), histone modifications (Palma et al., 2010; Xia et al., 2013; Zou et al., 2014; Ramirez-Prado et al., 2018), histone-mark-dependent alternative splicing (Tsuchiya and Eulgem, 2013), and regulation of chromatin structure and DNA methylation (Li et al., 2010; Deleris et al., 2016). There is increasing evidence that epigenetic processes can play a role in the transitory imprinting of some plant biotic stress responses, at least for a few generations (Molinier et al., 2006; Slaughter et al., 2011; Luna et al., 2012; López Sánchez et al., 2016, 2021; Morán-Diez et al., 2021). It is, however, not yet clear to what extent stable transgenerational inheritance of epigenetically regulated gene expression contributes to the natural intraspecific diversity of plant–pathogen interactions.

The few available examples of transgenerational epigenetically controlled traits are found mainly in plant species, where the association between natural or induced differentially methylated regions (DMRs) and phenotypic traits was shown to be stably or (more often) metastably inherited across generations (Quadrana and Colot, 2016; Furci et al., 2019; Liégard et al., 2019). Such regions, designated epialleles, can have an effect on relevant agronomic traits: compatibility, accumulation of vitamin E, and fruit ripening in tomato; starch metabolism, disease resistance, and sex determination in melon; and fruit productivity in oil palm (Manning et al., 2006; Martin et al., 2009; Durand et al., 2012; Silveira et al., 2013; Quadrana et al., 2014; Ong-Abdullah et al., 2015; He et al., 2018; Bhat et al., 2020).

Plant DNA methylation can occur at cytosines in the three sequence contexts CG, CHG, and CHH (Henderson and Jacobsen, 2007) (where H can be A, C, or T), and its effect varies depending on the targeted genomic features (i.e., transposable elements [TEs], gene promoters, or gene bodies). DNA methylation patterns result from the dynamic combination of *de novo* methylation, maintenance methylation, and demethylation. *De novo* DNA methylation is catalyzed by the canonical and non-canonical RNA-directed DNA methylation (RdDM) pathways, which are both guided by small interfering RNAs (Cuerda-Gil and Slotkin, 2016; Zhang et al., 2018). Maintenance of DNA methylation relies mainly on RNA-independent pathways and requires the activity of DDM1, MET1, and VIM proteins at CG sites and of DDM1, KYP, CMT2/3, and the histone mark HK9me2 at CHG and CHH sites (Law and Jacobsen, 2010; Matzke and Mosher, 2014). Previous studies have noted that natural DMRs are over-represented on genes of the NLR disease-resistance gene family (Kawakatsu et al., 2016). However, it remains unclear whether natural epigenetic variation in NLR genes can influence the outcome of interactions between plants and pathogens.

Here, we report the identification of two adjacent NLR genes controlled by a naturally occurring stable epigenetic variation underlying a QTL involved in partial resistance to clubroot in *Arabidopsis*. Clubroot is a root gall disease caused by the telluric biotrophic pathogen *Plasmodiophora brassicae* (Rhizaria) and affects all Brassicaceae crops such as oilseed rape, kale, and turnip. The infection process involves a primary infection in root hairs that lasts only a few days. Secondary plasmodia then develop in root cortical cells, causing hyperplasia and hypertrophy that ultimately impair plant water and nutrient uptake. The reference accessions Columbia-0 (Col-0) and Burren-0 (Bur-0) are fully susceptible and partially resistant to *P. brassicae* isolate eH, respectively (Alix et al., 2007; Jubault et al., 2008b) (Supplemental Figure 1). Four main QTLs, which act additively, determine this difference. Here, we combined fine mapping of the QTL *Pb-At5.2*, which had the strongest effect on resistance, with CRISPR-Cas9 validation to identify two adjacent NLR genes, *AT5G47260* and *AT5G47280*, both involved in the control of clubroot partial resistance. Expression levels of the two genes vary between the susceptible and resistant parents and are linked to the DNA methylation status of a small region that includes these two genes and a neighboring TE sequence. The methylation status of the two resistance genes is stable over generations and is not associated with any structural variation in the intervening transposon. Epiallelic variation at this locus is frequent among natural *Arabidopsis* accessions,

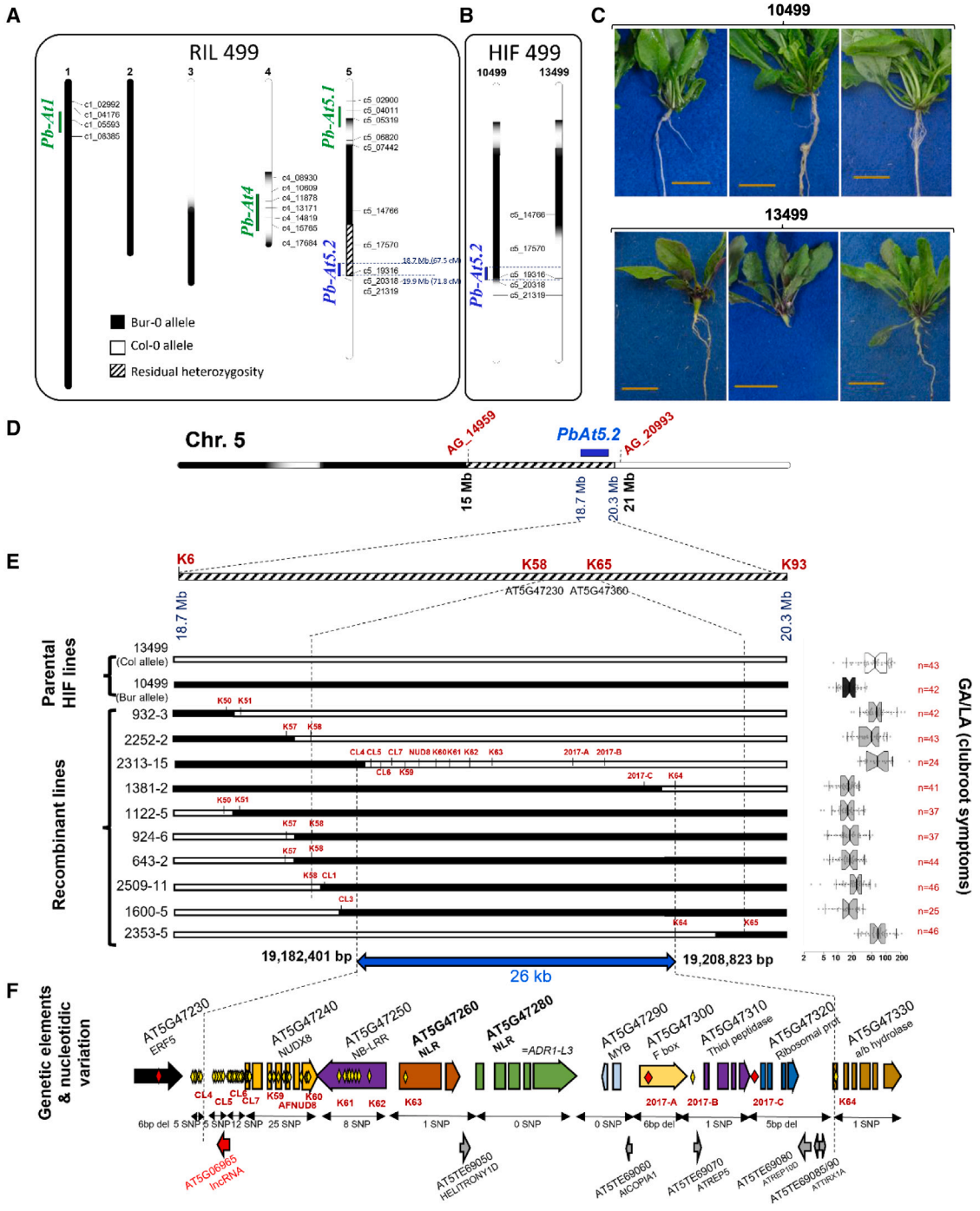

Figure 1. Fine mapping of *Pb-At5.2*.

(A) Genetic map and residual heterozygosity in the recombinant inbred line (RIL) 499 derived from Bur-0 and Col-0 (Alix et al., 2007), and genetic and physical positions of clubroot resistance QTLs (Jubault et al., 2008b). Black, Bur-0 allele; white, Col-0 allele; hatched, heterozygous (Col-0/Bur-0).

(B) Allele configuration at *Pb-At5.2* in the two derived HIF lines 10499 and 13499.

(C) Photos showing that *Pb-At5.2* conferred partial resistance to the eH isolate in the HIF 499 genetic background. HIF 10499 and 13499 harbored Bur-0 and Col-0 alleles, respectively, at *Pb-At5.2*. Observations were made 21 days post inoculation.

(D) First round of fine mapping: allelic structure in the F1 lines derived from reciprocal crosses between 10499 and 13499. A total of 554 F3 lines with recombination in the confidence interval were screened using 10 SNP markers between AG_14959 and AG_20993. High-density genotyping (94 SNPs

(legend continued on next page)

and the low methylated state was correlated with the expression levels of the two NLR genes and with increased quantitative resistance to *P. brassicae* among 126 accessions. We showed that the RNA-independent pathway involving DDM1, MET1, VIM, and CMT2/3 maintains the hypermethylated epiallele in the clubroot-susceptible Col-0 accession. Overall, our findings demonstrate that quantitative resistance to a major root disease of Brassicaceae is associated, in *Arabidopsis*, with stable inheritance of a natural epigenetic variation involved in controlling the constitutive expression of an NLR gene pair.

RESULTS

Fine mapping of the *Pb-At5.2* locus responsible for clubroot resistance

In previous work, we used a population of F7 recombinant inbred lines (RILs) between the partially resistant accession Bur-0 and the susceptible Col-0, to map a QTL (*Pb-At5.2*) on chromosome 5 between 67.5 and 71.8 cM that explained a significant proportion (R^2 = 20%) of the resistance (Figure 1A) (Alix et al., 2007; Jubault et al., 2008b). In TAIR10, this interval (between *AT5G46260* and *AT5G47690*) contains 158 annotated sequences, including protein-coding genes, TE genes, pre-tRNAs, and small nuclear RNAs. The effect and confidence interval of this QTL were also confirmed previously in the heterogeneous inbred family (HIF) lines 10499 and 13499 (Lemarié et al., 2015). Both lines were derived from the RIL 499, which harbors the homozygous Bur-0 (resistance) allele on the QTLs *Pb-At1* and *Pb-At5.1*, the homozygous Col-0 (susceptibility) allele on the QTL *Pb-At4*, and residual heterozygosity in the *Pb-At5.2* region. The lines 10499 and 13499 inherited the homozygous Bur-0 (resistance) allele and the Col-0 (susceptibility) allele, respectively, at the QTL *Pb-At5.2* (Figure 1B and 1C; Supplemental Text 1).

The initial aim of the present work was to fine map *Pb-At5.2*, starting with reciprocal crosses between HIF lines 10499 and 13499. Clubroot symptoms in individuals of the F1 progeny were as severe as those in the susceptible parental line HIF 13499, suggesting that the Bur-0 resistance allele was recessive (Supplemental Figure 2). The boundaries of the *Pb-At5.2* resistance locus were further refined through several rounds of genotyping and clubroot phenotyping (generations F3–F5 downstream of crosses 10499/13499) (details are given in Figure 1D–1F, Supplemental Figure 3, Supplemental Text 1, Supplemental Data 1, and Supplemental Text 3). This enabled us to narrow down the confidence interval to 26 kb between the markers CLG4 (19 182 401 bp, in the promoter region of *AT5G47240*) and K64 (19 208 823 bp, in *AT5G47330*), with the genetic markers being defined using the available *de novo* genome assembly of Bur-0 (Schneeberger et al., 2011). Comparison of the genetic sequences of Bur-0 and Col-0 in this 26-kb region revealed the absence of any structural variation and a low frequency of single-nucleotide polymorphisms (SNPs) (Figure 1F; details in Supplemental Text 3). This region contained eight annotated open reading frames (ORFs), including three NLR-encoding genes (*AT5G47250*, *AT5G47260*, and *AT5G47280*), six annotated TE sequences, and one long non-coding RNA gene (Figure 1F). The two F5 homozygous progeny lines 1381-2 and 2313-15, harboring the closest recombination events from both sides of the 26-kb interval (see Figure 1E), also showed partial resistance to a series of additional *P. brassicae* isolates (pathotypes 1, 4, and 7 following the classification of Some et al., 1996) and P1(+), which is representative of the new virulent strains that are emerging in Europe following breaking of clubroot resistance in oilseed rape varieties derived from the cultivar "Mendel" (Zamani-Noor et al., 2022). This result highlighted the broad spectrum of resistance conferred by the Bur-0 allele of *Pb-At5.2* (Supplemental Figure 4).

RNA-seq analysis revealed a constitutive expression polymorphism of two NLR genes in the 26-kb QTL confidence interval

RNA-sequencing (RNA-seq) analysis was performed on Bur-0 and Col-0 accessions and on recombinant HIF lines 10499 and 13499. Pathogen-induced gene expression patterns differed markedly between genotypes harboring alleles *Pb-At5.2*$_{BUR}$ and *Pb-At5.2*$_{COL}$ (Supplemental Figure 5 and Supplemental Data 2). This regulation was consistent with our previously published studies, i.e., suggesting a role of camalexin biosynthesis and salicylic acid–mediated responses in *Pb-At5.2*$_{BUR}$-mediated resistance and a role of jasmonic acid–driven induction of *ARGAH2* in *Pb-At5.2*$_{COL}$-mediated basal resistance (for details see Supplemental Text 2). We then focused on the eight ORFs in *Pb-At5.2*. Genes *AT5G47290* and *AT5G47300* showed no expression, and genes *AT5G47240*, *AT5G47250*, *AT5G47310*, and *AT5G47320* showed similar expression levels in all four accessions (Figure 2A). In the 26-kb interval, only two genes, *AT5G47260* and *AT5G47280*, both encoding proteins from the non-TIR-NLR gene family, were differentially expressed between resistant and susceptible accessions: these two genes were constitutively expressed in Bur-0 and 10499 roots (i.e., with the Bur-0 allele), but their expression was undetectable in Col-0 and 13499 (i.e., with the Col-0 allele) (Figure 2A). *AT5G47280* encodes ADR1-L3, an NBS-LRR protein related to the small family of ADR1-type RNLs (although the encoded protein lacks the N-ter RPW8 domain). *AT5G47260*, encodes a CC-NBS-LRR-X protein with an ID-like C-ter extension domain (Figure 2B) homologous to members of the IAN family

from K1 to K94) in 88 recombinant F3 lines and clubroot phenotyping of their bulked segregating F4 progenies led to the identification of a new interval between markers K58 (*AT5G47230*) and K65 (*AT5G47360*).

(E) Second round of fine mapping: recombination positions in homozygous individuals obtained from selected recombinant lines. For each line, the GA/LA index (disease symptoms, log scale) is indicated on the right panel. Center lines show the medians; box limits indicate the 25th and 75th percentiles as determined by R software; whiskers extend 1.5 times the interquartile range (IQR) from the 25th and 75th percentiles; outliers are represented by dots; data points are plotted as open circles. The number of individual plants analyzed for each genotype is indicated (*n*). The notches are defined as +/− 1.58 × IQR/sqrt(*n*) and represent the 95% confidence interval for each median. GA/LA values statistically different from those of 13499 are indicated by asterisks (*t*-test, ***$p < 0.001$). Genetic markers are indicated for each recombination position. Markers between CL5 and 2017-C were used in every line but are shown only for 2313-15.

(F) New 26-kb interval of *Pb-At5.2* between markers CL4 (excluded) and K64 (excluded), containing eight annotated ORFs, six transposons, and one long non-coding RNA. Yellow and red diamonds indicate SNPs and nucleotide deletions, respectively.

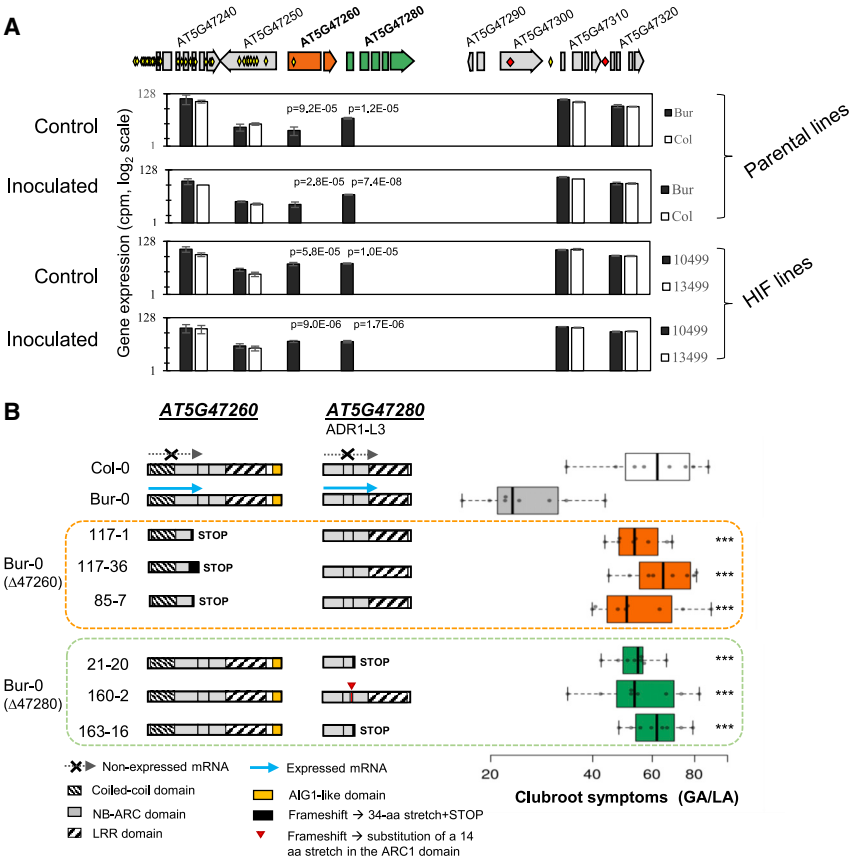

Figure 2. Identification and CRISPR-Cas9 validation of two NLR-encoding genes controlling clubroot resistance at QTL *Pb-At5.2*.

(A) Sequence variations and expression levels of genes in the *Pb-At5.2* region. Gene expression values are from RNA-seq analyses conducted under inoculated and control conditions at 14 days post inoculation (log_2 normalized CPM) with parental lines Col-0/Bur-0 and HIF lines 13499/10499 (the last two were derived from RIL 499 and are homozygous *Pb-At5.2*$_{Col/Col}$ and *Pb-At5.2*$_{Bur/Bur}$, respectively) (Supplemental Data 2). False discovery rate–adjusted *p* values are shown if less than 0.05. Yellow and red diamonds indicate SNP and INDEL variations, respectively.

(B) Effect of *AT5G47260* or *AT5G47280* knockout on GA/LA index (disease symptoms) in the Bur-0 background. Cas9-mediated mutations were obtained in the Bur-0 genetic background. For each targeted gene, three independent lines harboring independent homozygous mutations were used. Lines 117-1 and 21-20 no longer have the CRISPR-Cas9 cassette. For each line, the mean clubroot symptom score (GA/LA, log scale) was obtained by modeling raw data of eight biological replicates (with 10–12 individual plants per replicate). Center lines show the medians; box limits indicate the 25th and 75th percentiles as determined by R software; whiskers extend 1.5 times the IQR from the 25th and 75th percentiles; data points are plotted as open circles. GA/LA values of edited lines that are statistically different from the Bur-0 GA/LA value are indicated by asterisks (Dunnett's test) as follows: $*p < 0.05$; $**p < 0.01$; $***p < 0.001$.

of AIG1 (= *AvrRpt2-Induced Gene1*, *AT1G33960*)-related proteins (Martin et al., 2023). These two adjacent genes are separated by a helitron, *AT5TE69050* (Figures 1F and 3A). *AT5G47280* contained no SNPs, and *AT5G47260* contained only one non-synonymous SNP (Supplemental Figures 7 and 8, Supplemental Text 3). There was also no sequence variation in the helitron *AT5TE69050* located between the two genes.

CRIPSR-Cas9 validation of the role of NLR genes *AT5G47260* and *AT5G47280* in clubroot resistance

Given the contrasting expression levels of *AT5G47260 and AT5G47280* in Bur-0 and Col-0, we next addressed their functional significance in clubroot resistance by generating knockout lines via CRISPR (clustered regularly interspaced short palindromic repeats)-Cas9 (CRISPR-associated protein 9) technology. We targeted the regions encoding the NB-ARC domain of both genes with two single guide RNAs in both resistant Bur-0 and HIF 10499 (which contains the Bur-0 allele) accessions. The CRISPR-Cas9-generated mutations in *AT5G47260* and *AT5G47280* gave rise to premature stop codons in most mutant lines and to substitution of a stretch of 14 amino acids in the ARC1 domain in line 160-2 (Figure 2B, Supplemental Figures 6–8, and Supplemental Text 4). For the following experiments, we used three mutants from separate transformation events for each gene and each background (Bur-0 or HIF 10499). For each gene, one mutant without a T-DNA insertion was obtained in the Bur-0 background. The *AT5G47260* and *AT5G47280* CRISPR-knockout mutants were then evaluated for clubroot resistance in a complete randomized design. For both genes, clubroot symptoms were significantly higher in all lines edited in the Bur-0 genetic background than in the wild-type resistant Bur-0 accession and were as high as those of the susceptible accession Col-0 (Figure 2B), demonstrating the involvement of both *AT5G47260* and *AT5G47280* in clubroot resistance. Similar results were obtained for CRISPR-edited lines in the 10499 HIF genetic background (Supplemental Figure 9).

Expression polymorphism of both NLR genes is associated with stably inherited methylation variation

To understand why the two NLR genes *AT5G47260* and *AT5G47280* were differentially expressed in Bur-0 and Col-0, despite the absence of any sequence variation in their putative promoter regions, we analyzed the DNA methylation level of these regions in the two accessions using publicly available methylome data (Kawakatsu et al., 2016). The genomic interval between 19 188 411 and 19 196 559, which includes the two genes *AT5G47260* and *AT5G47280* and the intervening transposon *AT5TE69050*, was hypermethylated in Col-0 and hypomethylated in Bur-0 (Figure 3A). These contrasting methylation states were confirmed experimentally using DNA extracted from infected and non-infected roots of Col-0 and Bur-0 plants (Figure 3B) and CHOP–qPCR. The differences in DNA methylation were also found between the progeny HIF lines 10499 and 13499 and in the pair of HIF-derived homozygous near-isogenic lines 1381-2 and 2313-15 (Figure 3B), indicating that they are stably inherited independently of any DNA

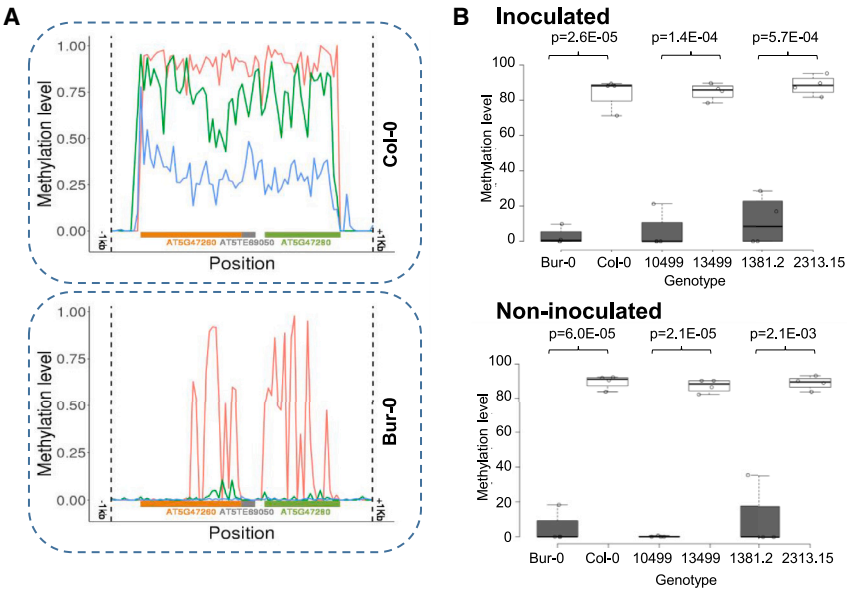

Figure 3. Methylation of the region surrounding the two NLR-encoding genes that control clubroot resistance at QTL *Pb-At5.2*.

(A) Methylation profiles in the *AT5G47260* and *AT5G47280* region of Col-0 and Bur-0 accessions inferred from bisulfite data previously reported in Kawakatsu et al. (2016). Average methylation level was calculated within non-overlapping 100-bp windows starting 1 kb before the transcription start site (TSS) of *AT5G47260* and stopping 1 kb after the trancription site end (TSE) site of *AT5G47280*. Red: methylation in the CG context. Green: methylation in the CHG context. Blue: methylation in the CHH context.

(B) Methylation profiles on *AT5G47260* obtained by CHOP–qPCR in inoculated and non-inoculated roots of Bur-0/Col-0, 10499/13499, and the homozygous recombinant lines 2313-15 ($Pb\text{-}At5.2_{Col/Col}$) and 1381-2 ($Pb\text{-}At5.2_{Bur/Bur}$). The last two genotypes harbor the narrowest recombination events from either side of *Pb-At5.2* (between markers CLG4 and K64, details in Figure 1). Center lines show the medians; box limits indicate the 25th and 75th percentiles as determined by R software; whiskers extend 1.5 times the IQR from the 25th and 75th percentiles; outliers are represented by dots; data points are plotted as open circles. $n = 4$ bulks of six plants, and p values are shown (two-sided t-test).

sequence polymorphism outside the locus. Moreover, the "Col-like" hypermethylation of *AT5G47260* and *AT5G47280* was systematically associated with low expression of the two NLR genes and a lower level of partial resistance to *P. brassicae* infection. To further investigate the inheritance of this epiallelic variation and its penetrance on gene expression and clubroot resistance, we investigated two groups of 100 individual plants, corresponding to the progenies derived from selfing the heterozygous 2509 and 1381 lines (harboring heterozygosity at the locus). Evaluation of plant disease for each individual plant in the two progenies revealed a 3:1 Mendelian segregation of the partial resistance phenotype. Clubroot symptoms in individuals with only one Bur-0 resistance allele were the same as in individuals with two susceptible Col-0 alleles (Figure 4A). In clubroot-inoculated roots of each individual plant from the 2509 progeny, the methylation state of the *Pb-At5.2* region was monitored by CHOP–qPCR on *AT5G47260*. The SNP allele status at *Pb-At5.2* was also investigated for each individual plant (for details of markers see Supplemental Data 1). Heterozygous Bur/Col individuals displayed intermediate parental methylation and expression values (Figure 4B–4D), providing a molecular explanation for the recessivity of the Bur-0 resistance allele. Together, these results suggested a link between partial resistance to *P. brassicae* and stably inherited epiallelic variation at *Pb-At5.2*, which controls the expression of two NLR genes.

The Bur-like hypomethylated epiallele is well represented among *Arabidopsis* accessions and contributes to reduction in clubroot symptoms

To assess the relative contribution of changes in DNA sequence and DNA methylation at *Pb-At5.2* to clubroot resistance, we investigated natural allelic and epiallelic diversity across *Arabidopsis* accessions. We took advantage of recently published Illumina short genome sequence reads obtained from 1135 *Arabidopsis* accessions (1001 Genomes Consortium, 2016) to document the species-wide molecular diversity of the *Pb-At5.2* genomic region. On the basis of quantitative horizontal and vertical coverage of short reads aligned to the Col-0 reference genome sequences, we identified two discrete groups of accessions. One group, containing 401 accessions, was characterized by high vertical and horizontal coverage (>0.75) and included the reference accession Col-0 as well as the partially clubroot-resistant Bur-0 (Figure 5A; for a detailed list of genotypes see Supplemental Data 3, sheet 1). The remaining 734 accessions contained diverse structural rearrangements, principally long deletions that translate into poor horizontal and vertical coverage compared with the reference Col-0 genome. Closer examination of coverage plots for the 401 Col-0/Bur-0-like accessions revealed a uniform haplotype structure that was present at high frequency at the species level (minor allele frequency [MAF] ~0.37). Nonetheless, the haplotype frequency varied among geographic groups, ranging from 52.7% in Spain to 17.7% in Asia (Supplemental Figure 10). We then analyzed DNA methylation levels in 287 accessions from among the 401 accessions that contained the Col-0/Bur-0-like *Pb-At5.2* and for which bisulfite data were publicly available (Kawakatsu et al., 2016). From these data, we could distinguish a group of 228 accessions, including Bur-0, that showed hypomethylation of *Pb-At5.2* and another group of 59 accessions, including Col-0, that displayed hypermethylation (Figure 5B). The prevalence of accessions with the Col-like (epi)haplotype varied considerably with geographic origin, ranging from 1.8% in Spain to 16.8% in central Europe (Supplemental Data 3 and Supplemental Figure 10). Consistent with a causal role for DNA methylation in the transcriptional regulation of *AT5G47260* and *AT5G47280*, reanalysis of publicly available RNA-seq data revealed a pronounced negative correlation between methylation level and *AT5G47260* and *AT5G47280* expression (Figure 5C). These results were further validated in infected roots from 20 natural accessions (Figure 5D).

Both Col-like and Bur-like epialleles were significantly represented among the natural accessions, offering interesting genetic

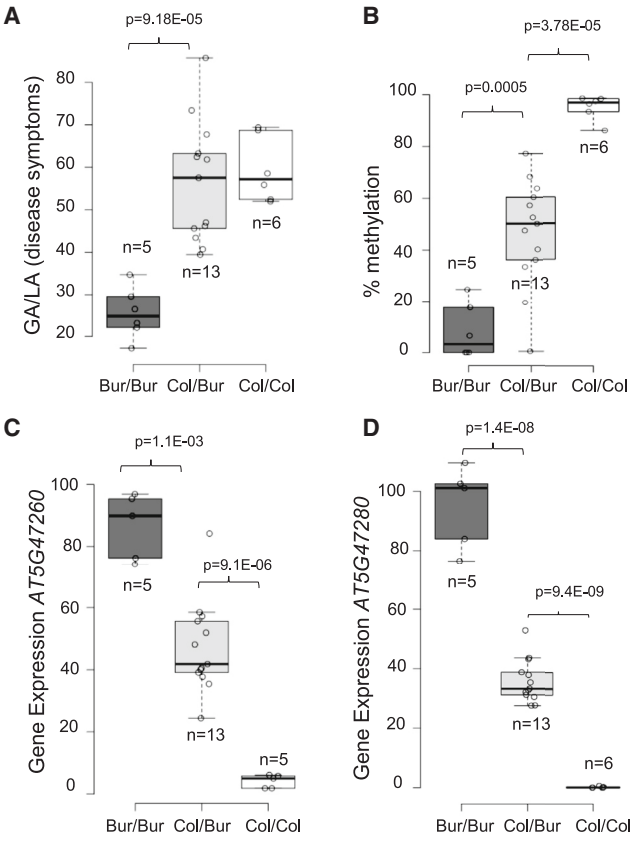

Figure 4. Intermediate methylation and transcript levels of candidate genes in heterozygous plants are associated with full clubroot susceptibility.

Eighty-three individual plants from the segregating progeny of recombinant line 2509 (heterozygous in Chr.5 region between genetic markers K58 and K93) were sampled at 21 days post inoculation. Leaves from each individual plant were used for genotyping (PCR marker CL_N8), which defined *n* pools of >3 plants of each zygosity profile: Bur/Bur (n = 5), Col/Bur (n = 13), and Col/Col (n = 6) (black, gray, and white boxes, respectively). Each plant pool was evaluated for **(A)** clubroot resistance (GA/LA), **(B)** percent methylation at the locus, and **(C and D)** candidate gene expression (*AT5G47260* and *AT5G47280*). Gene expression was quantified by RT–qPCR, and data were normalized over mean-Cp from the pools Bur/Bur following Pfaffl's method with two reference genes (Pfaffl, 2001). Center lines show the medians; box limits indicate the 25th and 75th percentiles as determined by R software; whiskers extend 1.5 times the IQR from the 25th and 75th percentiles; outliers are represented by dots; data points are plotted as open circles.

material with which to determine the actual contributions of DNA sequence and DNA methylation to the control of clubroot partial resistance. One hundred and twenty-six accessions were selected for their methylation levels at the *AT5G47260–AT5G47280* region in data from Kawakatsu et al. (2016), including 42 accessions with the Col-like epiallele and 85 accessions with the Bur-like epiallele, and then assessed for their resistance to *P. brassicae* isolate eH. Whereas no DNA sequence polymorphisms in *Pb-At5.2* showed an association with clubroot resistance (Supplemental Data 4), the low DNA methylation state of the *AT5G47260/AT5G47280* locus was significantly associated with enhanced resistance levels (Figure 6). Together, these results corroborate and extend the conclusions obtained by fine mapping of *Pb-At5.2* and provide strong evidence that natural epiallelic variations contribute to the quantitative differences in clubroot resistance observed among *Arabidopsis* accessions.

Pb-At5.2 epivariation is independent of *cis*-genetic variations

At the *Pb-At5.2* locus, the transposon *AT5TE69050* was present in both parental genotypes, with no sequence variation that might have been the primary cause of variation in DNA methylation on the two adjacent genes. Analysis of 34 out of the 287 accessions with the Col-0/Bur-0-like haplotype did not reveal the presence/absence of TE insertion variants within the 26-kb *Pb-At5.2* region (Quadrana et al., 2016; Stuart et al., 2016), with the exception of a helitron insertion in the accession NFA-10. Moreover, 18 and 16 of these accessions displayed hypermethylated and hypomethylated epialleles, respectively, indicating that variation in DNA methylation is not associated with TE presence/absence variants. In addition, the *cis*-nucleotide polymorphism located within the coding sequence of *AT5G47260* and detected in Bur-0 was absent in at least five other accessions sharing the hypomethylated epiallele (Supplemental Figure 11), indicating that the hypomethylated state of *Pb-At5.2* is not correlated with any specific DNA sequence polymorphism at the locus.

The hypermethylated epigenetic variant is maintained by the RNA-independent pathway

Analysis of sRNAs identified in Col-0 (Stroud et al., 2013) revealed that the *AT5G47260/AT5G47280* region is targeted mostly by 24-nt sRNAs, which prompted us to generate sRNA profiles from non-inoculated roots of Col-0 and Bur-0 and from roots inoculated with *P. brassicae* isolate eH 14 and 21 days after inoculation. Consistent with the previously observed pattern of DNA methylation, we found high levels of sRNAs only in Col-0 (Figure 7A). To further explore the mechanisms involved in the maintenance of methylation at this locus, we made use of publicly available methylomes of Col-0 mutant plants defective in one or several DNA methylation pathways (Stroud et al., 2013). Despite the high levels of sRNAs detected over the *AT5G47260/AT5G47280* region, mutations affecting the RdDM pathway did not influence its DNA methylation level (Supplemental Figure 12). Conversely, DNA methylation was largely lost in mutants defective in sRNA-independent maintenance of DNA methylation, i.e., *ddm1*, *cmt2/3*, *met1*, and *suvh456* (Figure 7B). These results raise questions about the role of sRNAs targeted to the Col-like hypermethylated region whereas methylation maintenance depends solely on the RNA-independent pathway.

DISCUSSION

To date, only a very small number of resistance QTLs have been characterized at the molecular level (Delplace et al., 2022). Detection and fine mapping of resistance QTLs is typically challenging not only because of the difficulties associated with measuring small variations in partial resistance in large numbers of individual progeny but also because resistance QTLs can be sensitive to environmental changes (Aoun et al., 2017; Laperche et al., 2017; Aigu et al., 2018). However, technical issues may have been only part of the problem.

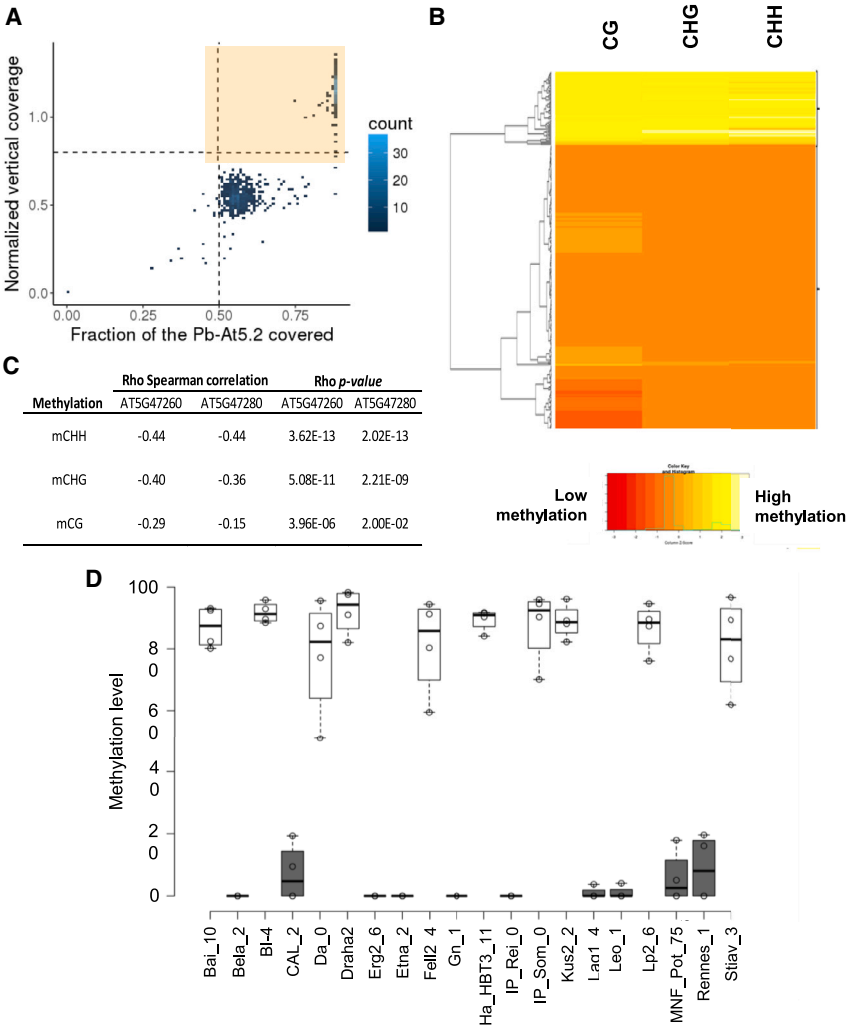

Figure 5. Natural epigenetic variation at *Pb-At5.2* affects expression of *AT5G47260*/*AT5G47280* in *Arabidopsis* accessions.

(A) Screening for 1001 Genomes *Arabidopsis* accessions that display a Col/Bur-like genomic structure at *Pb-At5.2* (chr5: 19 185 600–19 200 600). *x* axis: horizontal coverage region covered by at least one read. *y* axis: vertical coverage in read percentage. The 401 accessions framed in the northeast intercardinal region delimited by dotted lines have a vertical read coverage >0.8 and a horizontal DNA-seq >0.5 (DNA-seq data from Alonso-Blanco et al. (2016)).

(B) Clustering of a series of accessions harboring Col/Bur-like genomic structure at *Pb-At5.2* by their level of methylation on *AT5G47260* and *AT5G47280*. Bisulfite data were obtained from the 1001 Genomes project (Supplemental Data 3, sheet 2). Average methylation level was calculated beginning 1 kb before the TSS of *AT5G47260* and stopping 1 kb after the TSE site of *AT5G47280* for each context.

(C) Spearman correlation between methylation and gene expression of *AT5G47260* and *AT5G47280* in a subset of 253 *Arabidopsis* accessions for which expression data were available (RNA-seq data from Kawakatsu et al., 2016). The correlation between gene expression and methylation level is given for all three DNA methylation contexts in the interval from 1 kb before the TSS of *AT5G47260* to 1 kb after the TSE site of *AT5G47280*.

(D) Confirmation of methylation profiles at *AT5G47260* in inoculated roots from 20 ecotypes. Methylation level was determined using CHOP–qPCR. Black and white bars indicate genotypes with Bur-like and Col-like methylation patterns, respectively. Center lines show the medians; box limits indicate the 25th and 75th percentiles as determined by R software; whiskers extend 1.5 times the IQR from the 25th and 75th percentiles; outliers are represented by dots; data points are plotted as open circles. *n* = 4 bulks of six plants.

Recent developments in the field of epigenetics suggest that some inherited resistance factors may not be detected by classic genetic approaches that are based solely on DNA sequence variation. In the present work, a genome-wide association study (GWAS) failed to identify any nucleotide variation in the 26-kb interval of *Pb-At5.2* associated with clubroot response. By contrast, clubroot resistance was clearly related to epigenetic variation at two NLR genes in this interval. This work thus reveals for the first time an epigenetically driven expression polymorphism that makes a substantial contribution to the natural diversity of plant immune response.

Many examples of epialleles are metastable, i.e., they can be reversed by stochastic or unidentified factors (Weigel and Colot, 2012). Stability over multiple generations is a primary concern from both evolutionary and breeding perspectives. The epiallele described here seems to be extremely stable, as it was robustly detected in all our previous QTL investigations in *Arabidopsis*. This included two independent segregating progenies derived from Bur-0 and Col-0 (Jubault et al., 2008a) and additional studies with the HIF lines 10499/13499 (Lemarié et al., 2015; Gravot et al., 2016). The high level of methylation and absence of *AT5G47260* and *AT5G47280* expression observed in Col-0 were also found in a set of publicly available data obtained in different laboratories from diverse plant tissues and conditions (Winter et al., 2007; Stroud et al., 2013; Klepikova et al., 2016; 1001 Genomes Consortium, 2016; Kawakatsu et al., 2016). It was also confirmed by our own data generated from inoculated roots, non-inoculated roots, and leaf samples. Finally, this methylation pattern was also robustly found in multiple replicates of individual plants. Thus, *Pb-At5.2* can be classified as a stable epiallele without reservation.

There has only been one report of a plant disease resistance caused by an inherited methylation variant that affects expression of a resistance-related gene (Nishimura et al., 2017). In that study, a stable expression polymorphism (between Ler-0 and Ag-0 accessions) on the TIR-only encoding gene *RBA1* (*AT1G47370*) affected effector-triggered immunity responses to the *Pseudomonas syringae* effector *hopBA1*. This expression polymorphism was linked to the nearby presence/absence of a TE sequence in the promoter region of the gene and to *MET1*-dependent DNA methylation variation. However, because DNA methylation was reversed when the TE sequence was

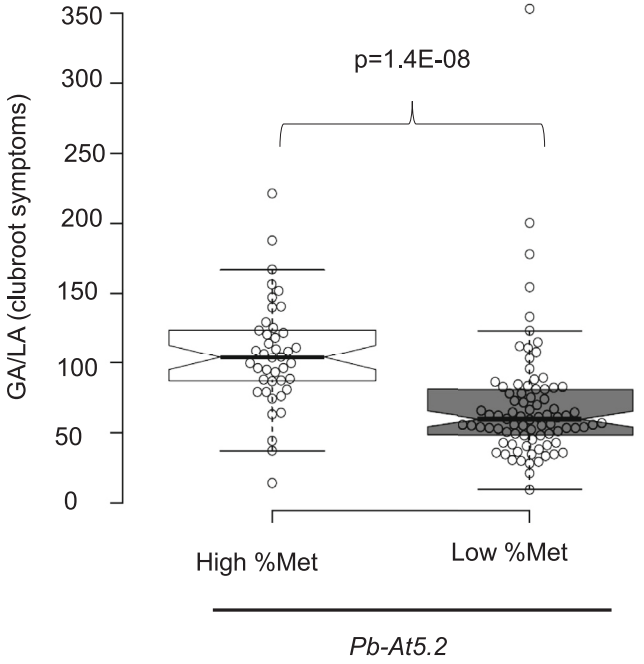

Figure 6. Variation in clubroot symptoms among *Arabidopsis* accessions is linked to epivariation at *Pb-At5.2*.

Effect of *Pb-At5.2* epiallele variation on clubroot susceptibility, evaluated in 126 *Arabidopsis* accessions with a similar Bur/Col-like genomic structure at the locus. Each open circle represents one accession. In total, 42 accessions had a Col-like epiallele (high percentage of methylation, High % Met), and 84 had a Bur-like epiallele (low percentage of methylation, Low % Met). For each accession, the mean GA/LA was obtained by modeling raw data of two biological replicates with two blocks (six individual plants in each block). Center lines show the medians; box limits indicate the 25th and 75th percentiles as determined by R software; whiskers extend 1.5 times the IQR from the 25th and 75th percentiles; outliers are represented by dots; data points are plotted as open circles. The notches are defined as +/− 1.58 × IQR/sqrt(*n*) and represent the 95% confidence interval for each median. The *p* value (Wilcoxon test) is indicated.

segregated away (Supplemental Figure 2 in Nishimura et al., 2017), this DNA methylation variation is not "epigenetic," as it is an obligate consequence of sequence variation (i.e., presence/absence of the TE sequence). In the present study, we showed that DNA methylation variation in the region between *AT5G47260* and *AT5G47280*, including the TE sequence *AT5TE69050*, is not linked to any nucleotide/structural variation at the locus or elsewhere in the genome. Thus, *Pb-At5.2*$_{COL}$ and *Pb-At5.2*$_{BUR}$ can be considered "pure epialleles" as defined by Richards (2006).

From available genomic and epigenomic data from the 1001 Genomes Project, it can be extrapolated that the Bur-like clubroot resistance epiallele is present in about half of the accessions from the "Relict," "Spain," and "Italy/Balkans/Caucasus" groups and 39% of the accessions from the "North Sweden" group (Supplemental Data 3). By contrast, the Bur-like epiallele is likely (taking into account missing methylation data) present at about 10% of the "Germany" group. On the other hand, the clubroot susceptibility of the Col-like epiallele was absent from the accessions in the "Relict" and "North Sweden" groups but reached at least 16.8% in the "Central Europe" group. This geographic structure suggests that both epialleles can confer fitness gains, depending on the environmental context. However, it does not appear to be obviously related to the incidence of clubroot in *Brassica* culture (usually low in the warm southern European regions). Keeping in mind that NLRs can detect unrelated effectors from distinct microbial species (Narusaka et al., 2009) and echoing previous work (Karasov et al., 2014), we hypothesize that maintenance of this epivariation in natural populations may reflect additional roles played by *Pb-At5.2* against other plant pathogens (besides the control of clubroot infection).

AT5G47280 has been annotated as *ADR1-Like 3* on the basis of its phylogenetic relationship with the small family of helper CC$_{RPW8}$-NLRs, including *ADR1*, *ADR1-L1*, and *ADR1-L2* (Saile et al., 2020, 2021). However, the absence of *RPW8* in *ADR1-L3* and the absence of *ADR1-L3* expression in Col-0 have raised questions about its actual role in plant immunity. *AT5G47260* and *AT5G47280* belong to a small heterogeneous cluster of three non-TIR-NLRs, which also includes *AT5G47250*. This small cluster is located on chromosome 5, not far from the largest NLR hotspot in the *Arabidopsis* genome (Meyers et al., 2003). None of these three genes has previously been shown to participate in plant–pathogen interactions. Here, we showed that expression of both *AT5G47260* and *AT5G47280* is necessary for partial resistance to *P. brassicae*. There are a few examples of tandem NLR genes encoding pairs of proteins that function as heterodimers (Cesari et al., 2014; Williams et al., 2014; Saucet et al., 2015). Similarly, the proteins encoded by these two jointly epigenetically regulated genes may function together in the control of cell defense responses during clubroot infection. Although the underlying molecular mechanisms are unknown, the canonical example of the TIR-NLR heterodimer *RRS1/RPS4* corresponds to a recessive resistance locus, similar to *Pb-At5.2*.

In *Arabidopsis*, DNA methylation is widely distributed in both the promoters and the bodies of most NB-LRR-encoding genes (Kong et al., 2018, 2020), predominantly in the CG sequence context. This suggests that plant genomes contain multiple functional resistance genes whose possible roles in biotic interactions are locked by epigenetic processes. This hypothesis is also supported by our previous study, in which we demonstrated that *ddm1*-triggered hypomethylation at different genomic loci resulted in the unlocking of genetic factors that ultimately exert significant control over clubroot symptom development (Liégard et al., 2019). It would now be interesting to carry out a careful genome-wide analysis of methylation profiles of all NLR genes among *Arabidopsis* accessions, which would take into account the structural diversity of all these individual genes (supported by additional targeted resequencing of NLR loci). The intraspecific diversity in methylation patterns of NLR and RLK/RLP genes in plants, their heritability, and their consequences for plant biotic interactions also deserve further attention in future studies.

METHODS

Plant materials and growth conditions

The HIF lines 10499 and 13499 and their parental accessions Col-0 (186AV) and Bur-0 (172AV) were provided by Versailles Arabidopsis Stock

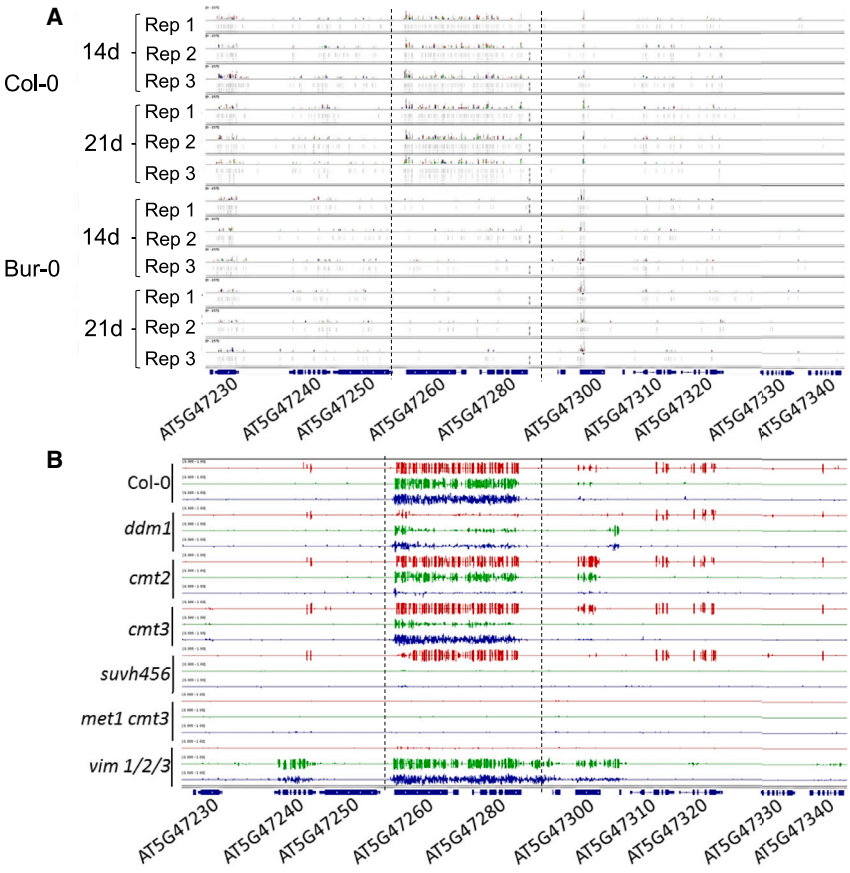

Figure 7. Epigenetic variation at *Pb-At5.2* correlates with the abundance of locus-targeted sRNA but is maintained by the RNA-independent methylation pathway.

(A) Mapping of sRNA-seq reads. Reads were obtained from roots of Col-0 and Bur-0 accessions at two time points 14 and 21 days after sowing. For each condition, three bulks (numbered from Rep 1 to Rep 3) of six plants were used.

(B) Methylation state at the *Pb-At5.2* locus in knockout lines (Col-0 genomic background) defective for the RdDM or non-RdDM pathway (Stroud et al., 2013).

Red: methylation in CG context. Green: methylation in CHG context. Blue: methylation in CHH context.

Center (http://publiclines.versailles.inrae.fr/). *Arabidopsis thaliana* accessions were all purchased from the Nottingham Stock Center. Individuals in the panel of 126 accessions were selected according to their methylation levels at the region of interest (Kawakatsu et al., 2016). All accessions and in-house-generated recombinant lines used in this study are listed in Supplemental Data 1 and Supplemental Data 3. Seed germination was synchronized by placing seeds on wet blotting paper in Petri dishes for 2 days at 4°C. Seeds were sown individually in pots (4-cm diameter) containing a sterilized mixture of two-thirds compost and one-third vermiculite. Growth chamber conditions of 16-h light (110 μmol m^{-2} s^{-1}) at 20°C and 8-h darkness at 18°C were used to grow plants. The 126 *Arabidopsis* accessions and HIF lines were challenged with *P. brassicae* in two biological replicates in a completely randomized block design (with two blocks per replicate, each block consisting of six plants per genotype). The *Arabidopsis* accessions Col-0 and Bur-0 and the HIFs 10499, 13499, 1381-2, and 2313-15 used in RNA-seq and sRNA-seq approaches were assessed when infected with *P. brassicae* or in the uninfected condition in three randomized blocks. The CRISPR-Cas9 edited lines and corresponding wild-type lines were challenged with *P. brassicae* in eight replicates in a completely randomized block design (each replicate consisting of 10–12 plants per genotype). Almost all clubroot tests were performed with the eH isolate of *P. brassicae* described by Fähling et al. (2003), which belongs to the most virulent pathotype, P1. The resistance spectrum of *Pb-At5.2* was also assessed using the additional isolates Pb137-522, Ms6, K92-16, and P1(+). For every isolate used in this study, the pathotype was validated in every experiment using the differential host set according to Some et al. (1996), also including two genotypes of *Brassica oleracea* ssp. *acephala* C10 and CB151. One milliliter of resting spore suspension (10^7 spores ml^{-1}) prepared according to Manzanares-Dauleux et al. (2000) was used for pathogen inoculation 10 days after germination (stage 1.04; Boyes et al., 2001). This inoculum was applied to the crown of each seedling.

Phenotyping

HIF lines and *Arabidopsis* accessions were phenotyped 3 weeks after inoculation (21 days post inoculation) for their susceptibility to *P. brassicae*. Plants were thoroughly rinsed with water and photographed. Infected roots were removed and frozen in liquid nitrogen. Clubroot symptoms were evaluated by image analysis using the gall area/leaf area (GA/LA) index calculated according to Gravot et al. (2011).

Fine mapping of the locus responsible for clubroot resistance

Fine mapping of *Pb-At5.2* was performed starting from crosses between HIF lines 10499 and 13499, followed by successive rounds of genotyping and clubroot phenotyping in subsequent plant generations (full details are given in Supplemental Text 1).

RNA isolation, mRNA sequencing, and differential gene expression analysis

Total RNA was extracted from frozen and lyophilized roots (collected 14 days after inoculation) using the mirVana miRNA Isolation Kit (Invitrogen) according to the manufacturer's instructions. After extraction, the RNA samples were quantified using NanoDrop ND-1000 technology, and their quality was assessed using the RNA 6000 assay kit (Agilent). Samples with an RNA integrity number (RIN) greater or equal to 7 were used for sequencing. cDNA-sequencing (cDNA-seq) library construction and sequencing were performed by the NGS platform at the Marie Curie Institute of Paris. Each library was sequenced in paired-end mode using the Illumina HiSeq 2500 platform. Reads were aligned to the TAIR10 genome annotation and assembly of Col-0 *A. thaliana* concatenated with the *P. brassicae* genome using STAR software version 2.5.3.a (Dobin et al., 2013). Alignment conditions were selected according to the *Arabidopsis* genome. A maximum of five multiple read alignments was accepted, and no more than three mismatches were allowed for each alignment. The resulting BAM files were used to determine read counts using the counts function in featureCounts software (version 1.4.6) and the TAIR10 gff file of *Arabidopsis* concatenated with the gff file of *P. brassicae*. Differentially expressed genes were determined using the edgeR package (Robinson et al., 2010) in R software version 3.3.0 (R Core Team, 2013). Raw counts obtained as described previously were used as input data for edgeR. After CPM (counts per million) values were determined, only genes with at least one CPM in three samples were retained. Expression signals were normalized using the TMM method (trimmed mean of M values) with the CalcNormFactors function in edgeR. Finally, differentially expressed genes were identified using

the decideTests function of edgeR with one minimum fold change between −1.5 and 1.5.

CRISPR-Cas9 constructs and plant transformation

Two guide sequences were designed for each targeted gene (i.e., *AT5G47260 and AT5G47280)* using CRISPOR software (Concordet and Haeussler, 2018), taking care to select sequences with very high specificity scores (Supplemental Data 5). Guide sequences were ordered as oligonucleotides (IDT) and cloned downstream of the *Arabidopsis* U6-26 promoter and upstream of an enhanced single guide RNA scaffold as reported previously (Chauvin et al., 2021) to produce individual guide modules. Assembly of guide modules for single genes was performed using PCR amplification with specific primers followed by classical restriction/ligation cloning (Supplemental Data 5, sheet 1). Guide assemblies were then cloned by a Gateway LR reaction (Thermo Fisher Scientific) into the pDe-Cas9 backbone (Fauser et al., 2014) harboring an *nptII* resistance cassette (Chauvin et al., 2021), resulting in two binary plasmids for CRISPR-mediated targeting of *AT5G47260* (pDe-Cas9_T79-80) and *AT5G47280* (pDe-Cas9_T81-82) (Supplemental Data 5, sheet 1). All constructs were checked by Sanger sequencing. The resulting plasmids were then transferred into *Agrobacterium tumefaciens* C58/GV3101pMP90 by heat shock and used to transform *Arabidopsis* plants via the floral dip method (Clough and Bent, 1998). Transgenic plants were screened on solid plates with half-strength Murashige–Skoog medium containing 50 mg l^{-1} kanamycin (Yeasen, cat. no. 60206ES10). A first screening was performed on the T1 generation using PCR and sequencing to identify plants with mutations in *AT5G47260* or *AT5G47280* (primer pairs are listed in Supplemental Data 5, sheet 2). A second round of screening enabled the identification of T2 plants homozygous for the mutations and free from CRISPR-Cas9 cassette T-DNA. T3 seedlings were used to evaluate *P. brassicae* resistance.

GWAS analyses

A conventional GWAS on GA/LA data from 126 accessions was performed with easyGWAS (Grimm et al., 2017) (https://easygwas.ethz.ch/). Association analysis was performed with EMMAX (Kang et al., 2010) using 1 806 554 SNPs with an MAF > 0.05, after correction for population structure by including the first three principal components in the additive model.

Small RNA isolation, sequencing, clustering, and differential presence determination

sRNA was extracted from frozen and lyophilized roots (collected 14 days after inoculation) using the mirVana miRNA Isolation Kit (Invitrogen) according to the manufacturer's instructions. After extraction, the sRNAs were quantified using a NanoDrop ND-1000 and quality controlled using the Small RNA assay kit (Agilent). Samples with an RIN greater than or equal to 7 were used for sequencing. Construction and sequencing of cDNA-seq libraries were performed on the NGS platform of the Marie Curie Institute of Paris. For each sample, single-ended (50 bp) sequencing was performed using the Illumina HiSeq 2500 platform. Reads were aligned to the TAIR10 genome annotation and assembly of Col-0 *A. thaliana* concatenated with the *P. brassicae* genome using STAR version 2.5.3.a (Dobin et al., 2013), then counted and clustered using ShortStack software (Axtell, 2013). The presence of differentially expressed sRNAs was determined using edgeR (Robinson et al., 2010) in R version 3.3.0 (R Core Team, 2013). Raw counts obtained as described previously were used as input data to edgeR. After CPMs were determined, only genes with at least one CPM in three samples were retained. Expression signals were normalized using the TMM method with the CalcNormFactors function in edgeR. Finally, differentially expressed sRNAs were identified using the decideTests function in edgeR with one minimum fold change between −1.5 and 1.5.

RNA isolation and RT–qPCR analysis

Total RNA was extracted from lyophilized roots of accessions and HIF lines 21 days after infection using the TRIzol extraction protocol. Samples with residual traces of DNA were treated with DNAse (Promega ref. M6 10A). Before reverse transcription of RNA to cDNA with SuperScript II (Invitrogen), RNA quality was verified by agarose gel electrophoresis. RT–qPCR was performed in a LightCycler 480 thermocycler (Roche) with cDNA obtained as described above. Gene expression was normalized using as references two *Arabidopsis* genes defined as stable during infection using RNA-seq data (*AT1G54610*, *AT5G38470*) following Pfaffl's method (Pfaffl, 2001). Primer sets were designed for each gene and are listed in Supplemental Table 1.

CHOP–PCR and qPCR assays

Gene methylation profiles were investigated using the enzyme McrBC (M0272L, BioLabs) (Zhang et al., 2014). Forty nanograms of DNA was incubated with 0.5 μl of BSA (20 mg/ml), 0.5 μl of guanosine triphosphate (20 mM), 5 μl of NE Buffer (10×), and 0.2 μl of McrBC (10 000 U/ml). For CHOP–PCR and qPCR, 2 ng of digested and undigested DNA was used. For CHOP–PCR, the temperature conditions were adjusted according to the primer design, and 35 amplification cycles were used. To determine the methylation state of the targeted region, each sample was digested or not (control) with McrBC before amplification. For CHOP–qPCR, the temperature conditions were adjusted according to the primer design, and 30 amplification cycles were used. Methylation levels of the target region were calculated as the percentage of molecules lost through McrBC digestion as described in Silveira et al. (2013) with the formula: (1 − (2 − (Ct digested sample − Ct undigested sample))) × 100. The percentages of DNA methylation for *AT5G13440* and *AT5G47400* were calculated in all CHOP qPCRs as controls. *AT5G13440* and *AT5G47400* were selected from 1001 Genomes data as hypomethylated and hypermethylated, respectively, in most *Arabidopsis* accessions, and their expression did not vary during clubroot infection. The primer sets designed for each gene are listed in Supplemental Table 1.

Published data

The DNA-seq data, RNA-seq data, variant sequences, and bisulfite data for the natural accessions studied here were obtained from previous studies (1001 Genomes Consortium, 2016; Kawakatsu et al., 2016) archived at the NCBI with SRA number SRP056687 and the NCBI Gene Expression Omnibus references GEO: GSE43857 and GSE80744. The bisulfite data and sRNA data for *Arabidopsis* mutants studied here were obtained from a previous report (Stroud et al., 2013) and are archived at the NCBI under accession GEO: GSE39901.

Statistical analysis

Data were statistically analyzed using the R program (R Core Team, 2013).

DATA AND CODE AVAILABILITY

The data supporting the findings of this study are available within the paper and its supplemental information files. All unique materials used are readily available from the authors.

SUPPLEMENTAL INFORMATION

Supplemental information is available at *Plant Communications Online*.

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AUTHOR CONTRIBUTIONS

B.L., A.G., M.J.M.-D., and M.J. designed and conducted the experiments. C.L. and A.G. carried out the fine mapping. C.L., J.L., J.B., T.B., B.L., A.G., and M.J. performed the phenotyping and sampling. B.L., A.G., J.B., J.L., and M.J. carried out epigenetic and gene expression studies. F.V. designed and performed the CRISPR-Cas9 constructs, and C.L. and T.B. carried out the transformation, selection, and handling of edited plants. B.L., Y.A., L.Q., and V.C. conducted bioinformatics analyses. A.G., B.L., L.Q., F.V., V.C., M.J.M.-D., and M.J. participated in drafting and revision of the manuscript.

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Plant Communications, Volume *5*

Supplemental information

Two adjacent NLR genes conferring quantitative resistance to clubroot disease in *Arabidopsis* are regulated by a stably inherited epiallelic variation

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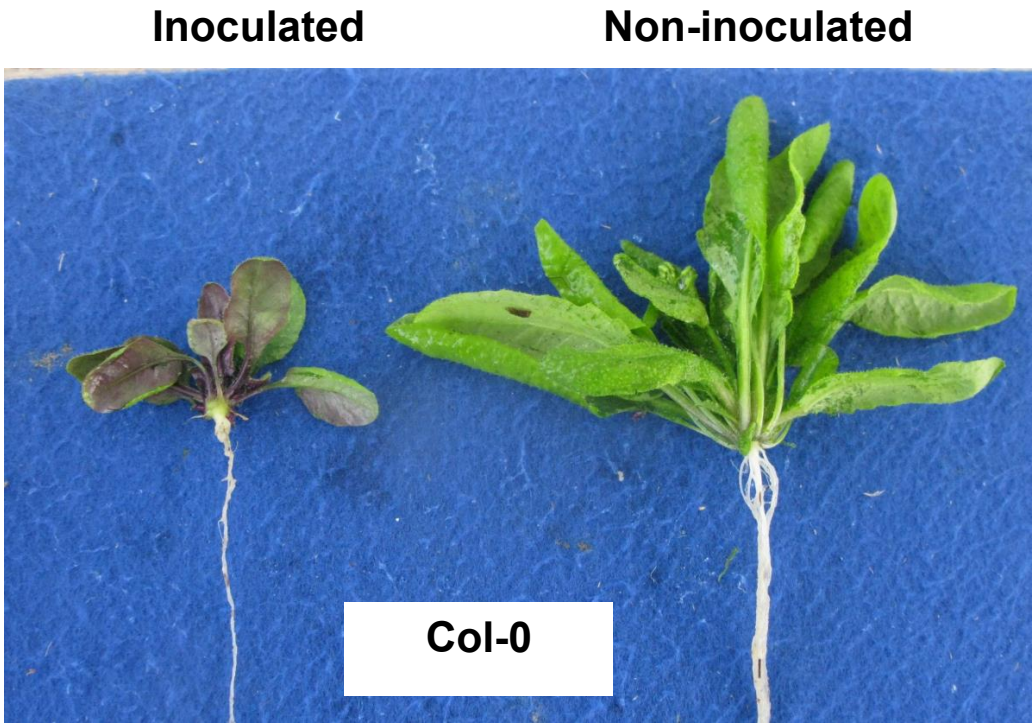
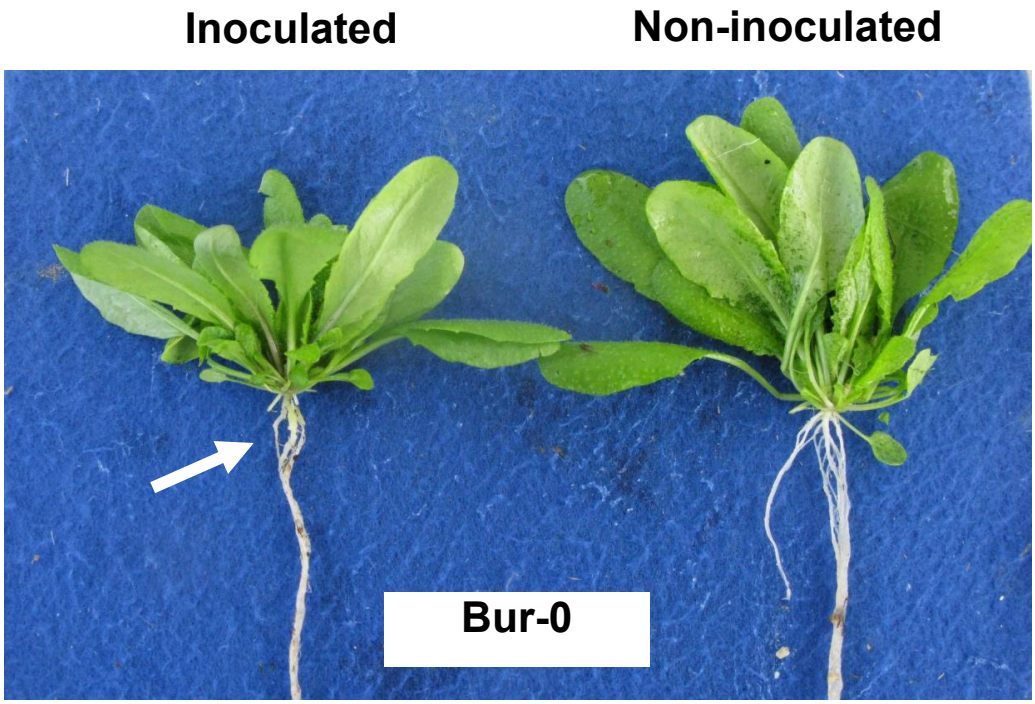
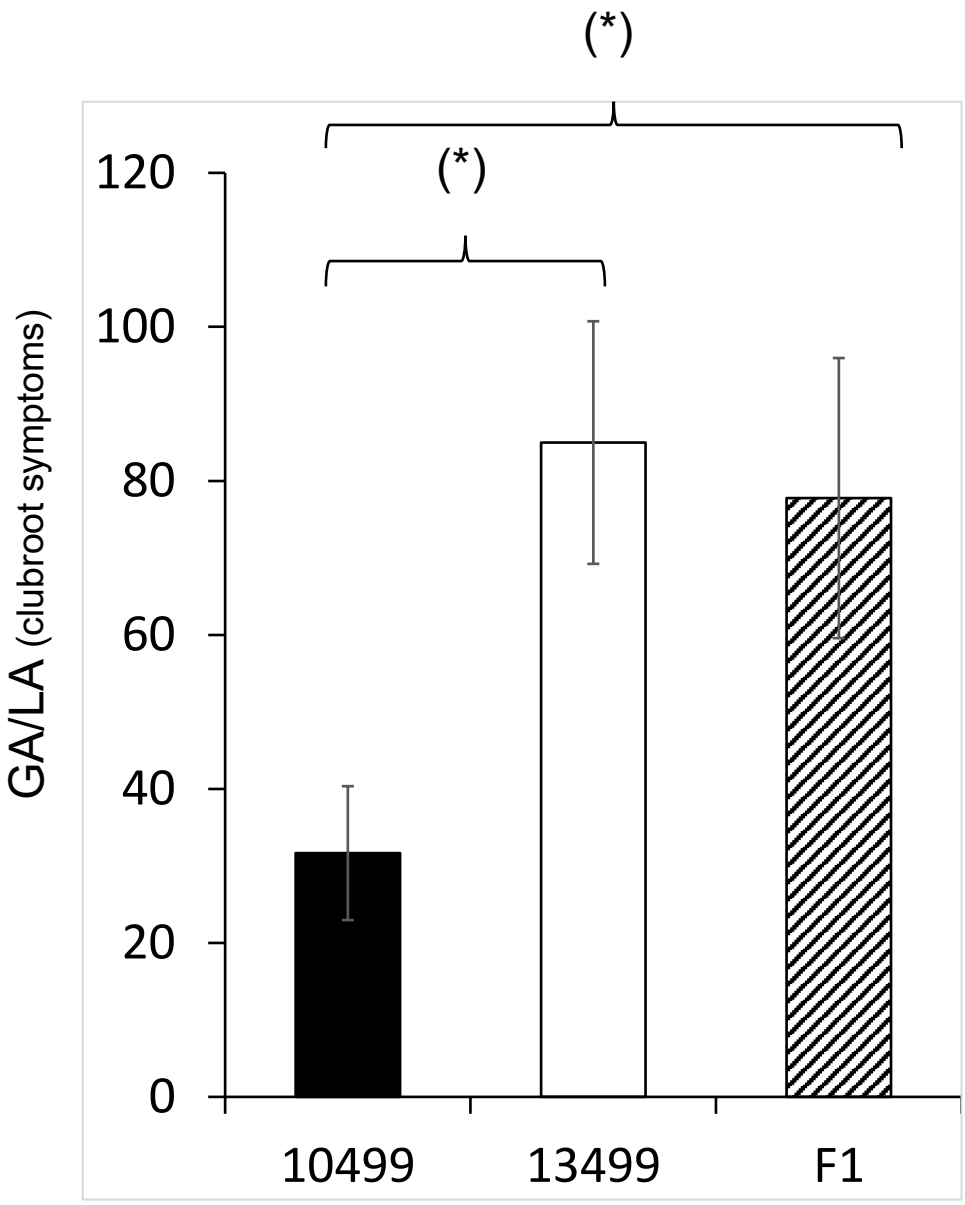
Supplementary Figures

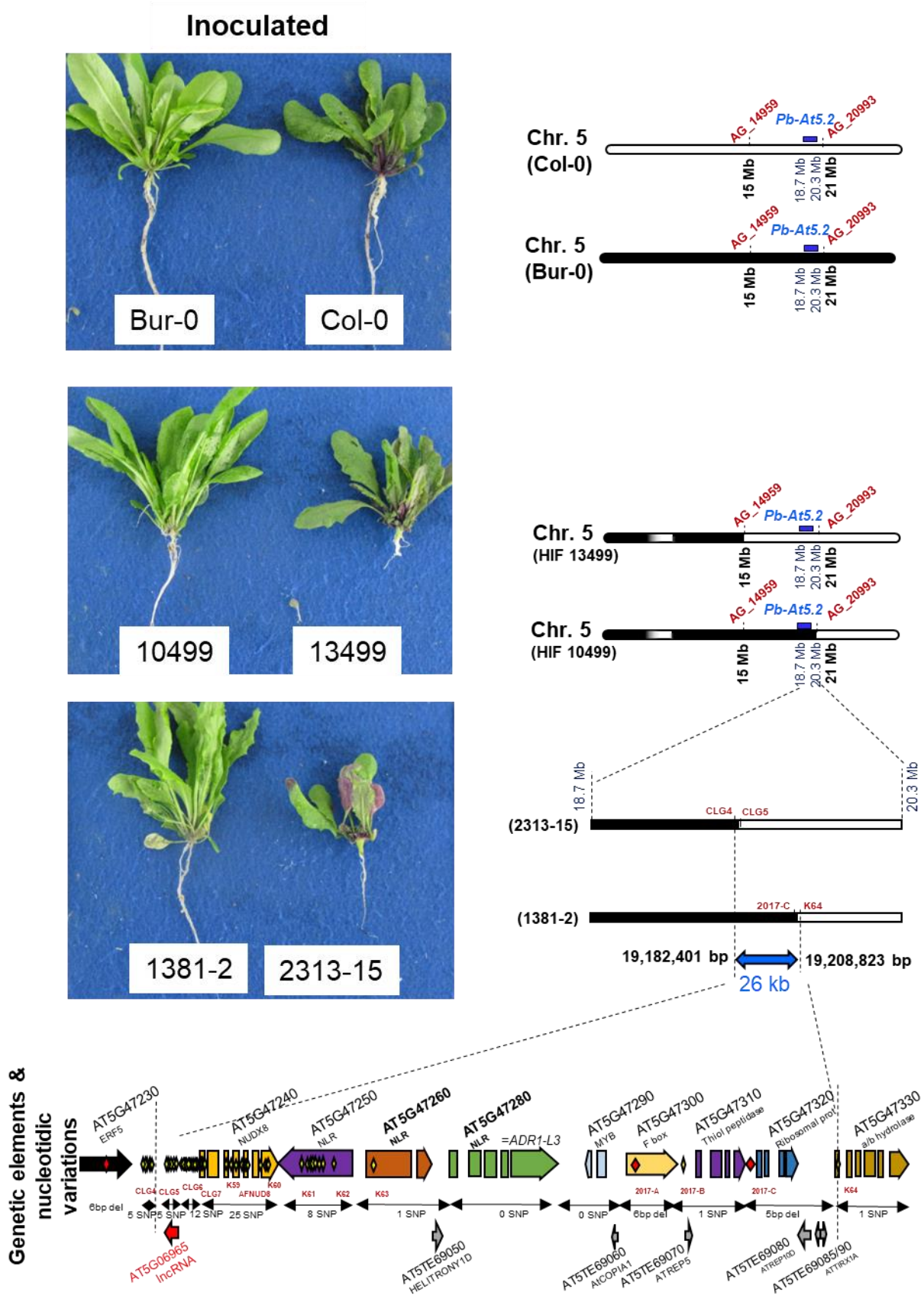




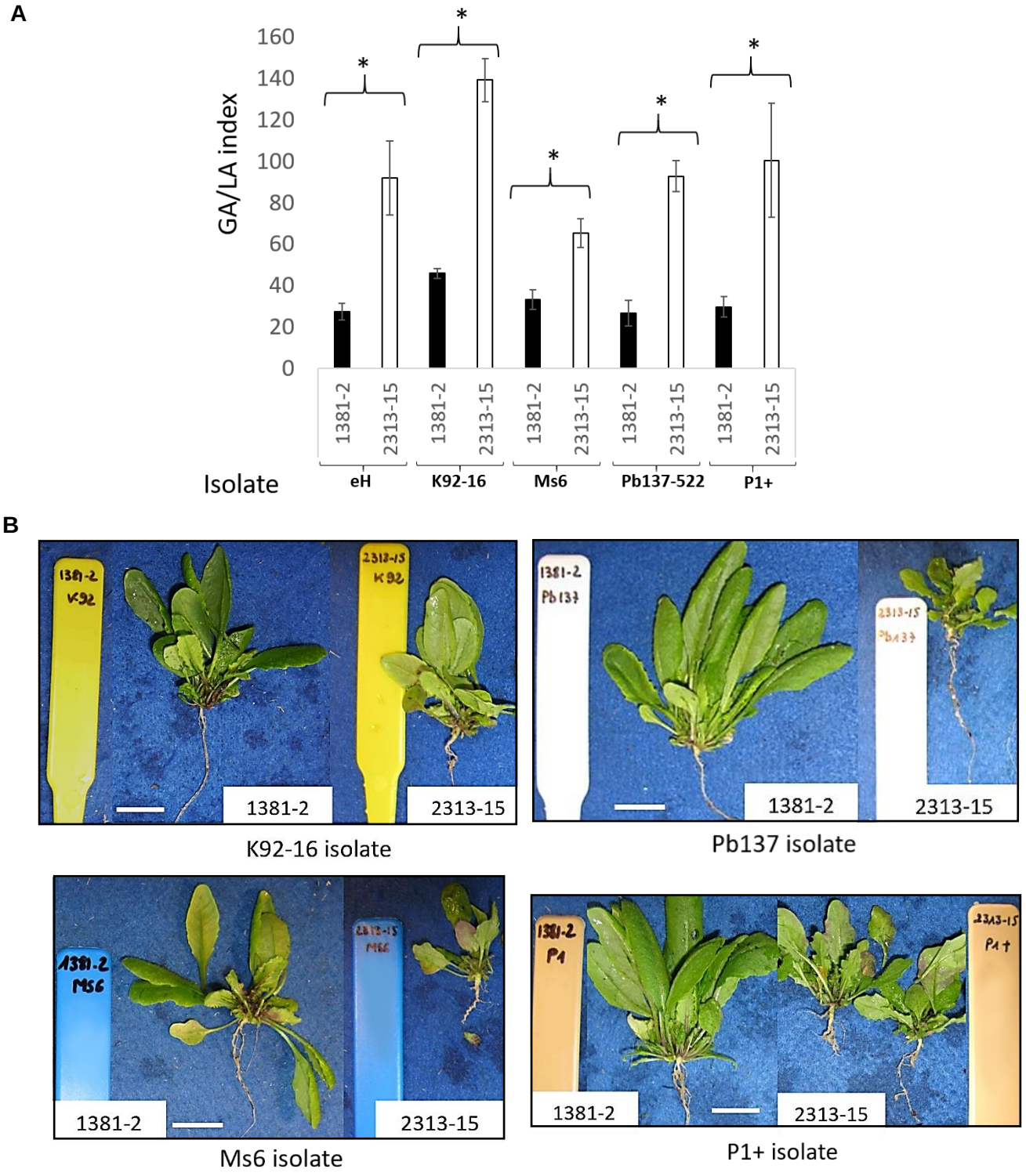
Supplementary Figure S1 | Illustration of partial resistance to eH isolate in Bur-0, compared to the full susceptibility in Col-0. Observations were done at 21 days post-inoculation. The white arrow indicates the presence of limited amount of galls in inoculated Bur-0. Plant individuals representative of standard observations made in our experimental conditions.



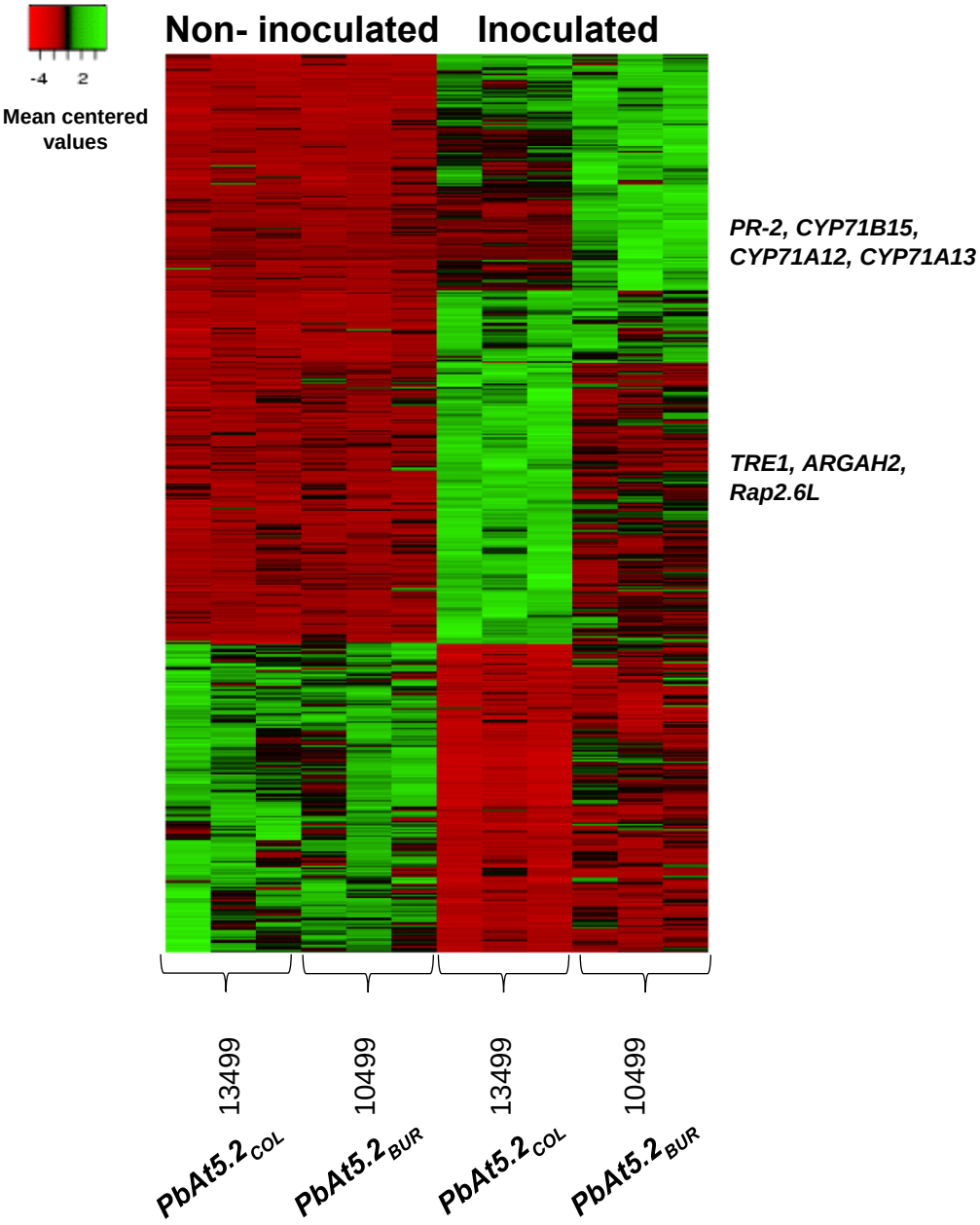
Supplementary Figure S2 | Comparison of GA/LA disease index in the F1 progeny and in the parental lines 10499 and 13499. GA/LA disease index is calculated through image analysis (details in the material and method part) from inoculated plants at 21 days post inoculation. Data are from 3 replicates (n=3). For each replicate, GA/LA disease index was calculated from 6 to 12 inoculated individual plants. Stars indicate statistical differences from the paired Student t-test (p=0.05).



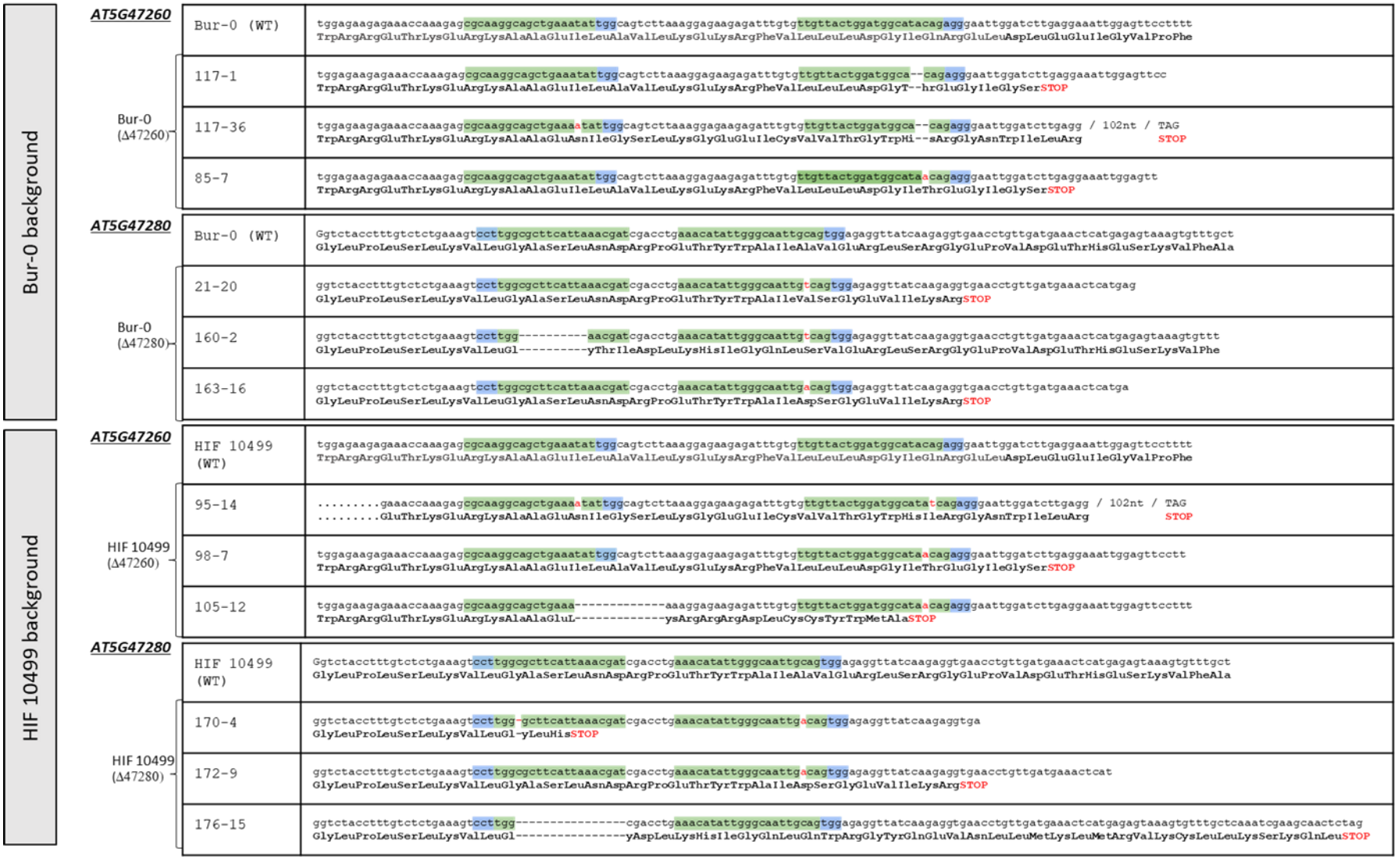
Supplementary Figure S3 | Illustration of clubroot symptoms in a selection of genotypes used for the fine mapping. Pictures of inoculated plants were taken at 21 days post inoculation. Genetic structure is indicated on the right side. Black=Bur-0 allele, white=Col-0 allele. Additional details in the legend of Figure 1.



Supplementary Figure S4 | Broad-spectrum resistance conferred by the Bur-0 allele of *Pb-At5.2* **A** GA/LA disease index and **B** photos of RIL499-derived near-isogenic lines 1381-2 and 2313-15 challenged with a series of four European monospore *P. brassicae* isolates (eH, K92-16, Ms6 and Pb137-522), and with the field isolate P1+. This last isolate is representative of emerging European strains that are virulent on the variety 'Mendel' (a clubroot-resistant oilseed rape variety which has been used as a source of resistance for the creation of several modern clubroot-resistant varieties). Data are means of 4 independent replicates (n=4). For each replicate, GA/LA values are means of 6 to 12 individual plants. Error bars indicate standard errors. Statistically different values (from Student T-test) are indicated by stars. Bars, 1.6 cm

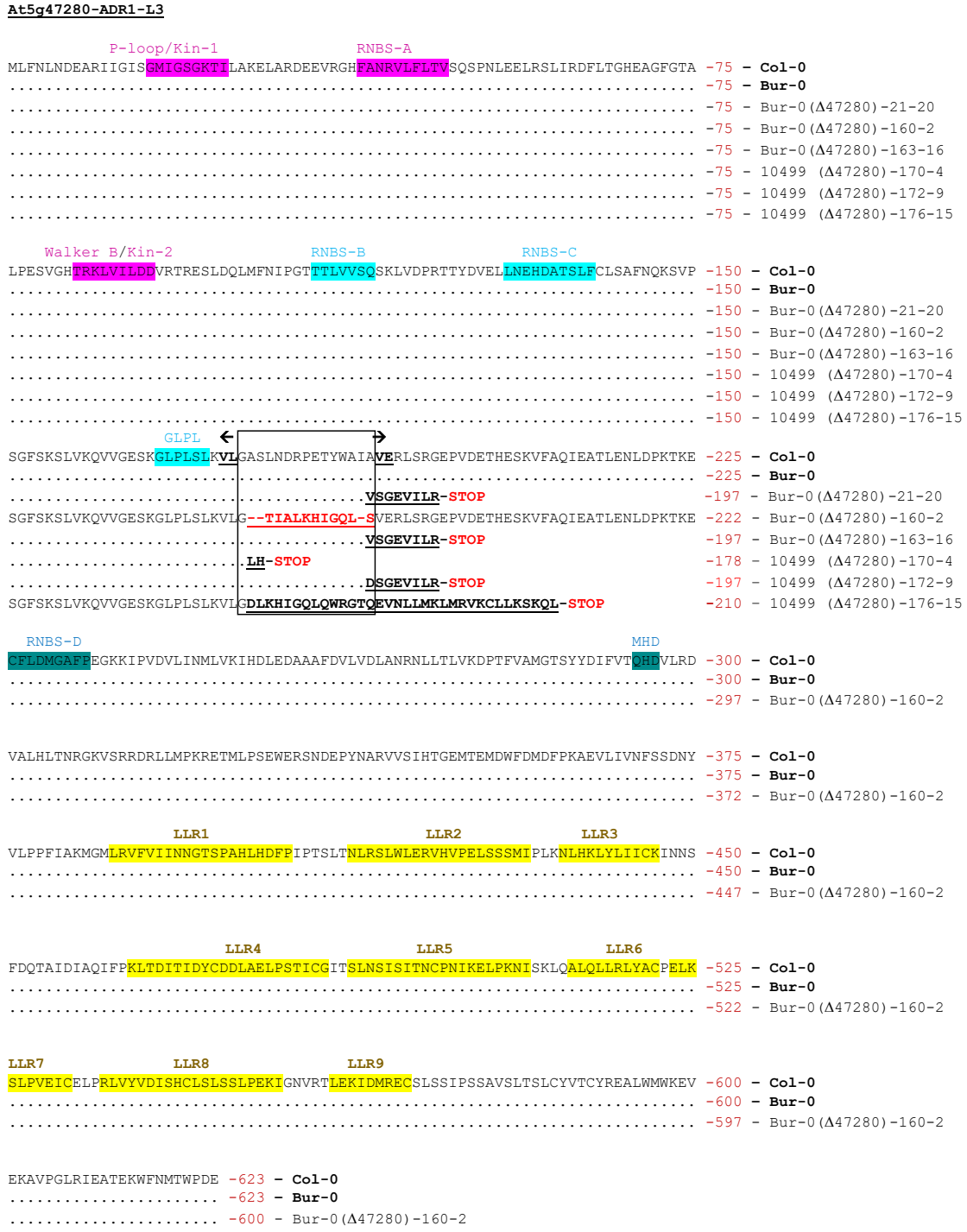


Supplementary Figure S5 | Transcriptional regulations induced by isolate eH at 14 dpi in the recombinant HIF lines 10499 and 13499 harboring Bur-0 or Col-0 allele at *PbAt5.2*. Data are mean-centered values of CPM (Counts Per Million). For each genotype, three columns are from three independent biological replicates. This set of 559 genes was selected as following: 1/Genes significantly induced (*p*-value<0.05 + log(FC)>2 or <-2) by eH isolate at 14 dpi in 10499 or 13499; 2/Mean gene expression>1. 61 genes, including *PR-2*, *CYP71B15*, *CYP71A12* and *CYP71A13*, were induced at higher levels in 10499 (*p*-value<0.05). 58 genes, including *TRE1*, *ARGAH2* and *Rap2.6L* were induced at higher levels in 13499 (*p*-value<0.05).

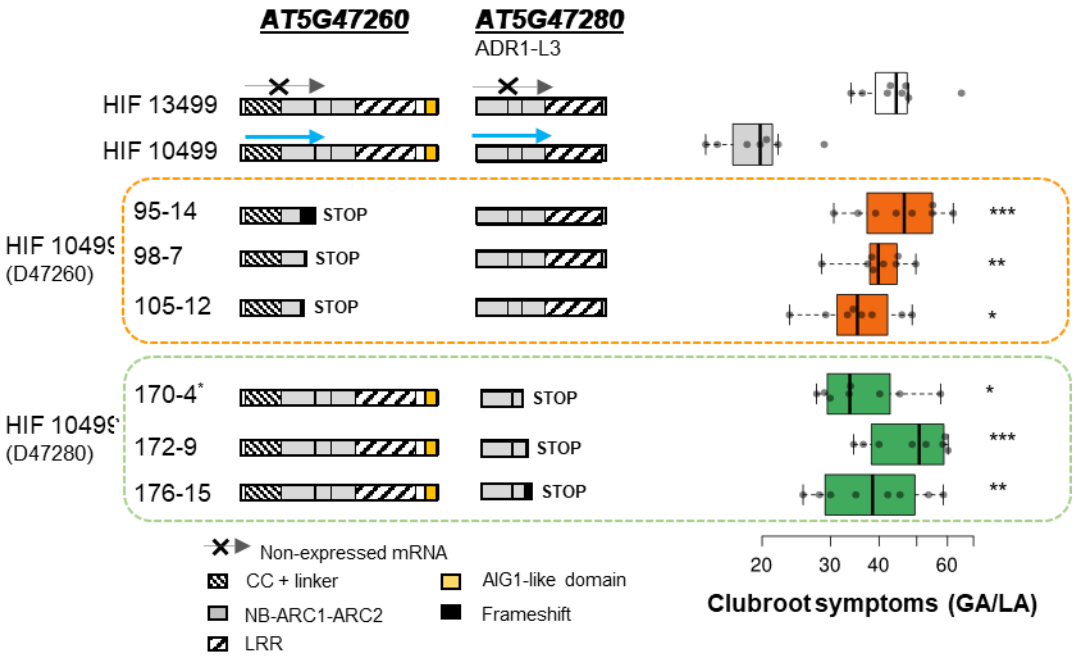


Supplementary Figure S6 | *AT5G47260* and *AT5G47280* mutated sequences in CRISPR-Cas9 edited lines in Bur-0 and HIF 10499 backgrounds. DNA and corresponding predicted protein sequences are detailed. Guide RNAs are highlighted on DNA sequence in green and protospacer-adjacent motif (PAM) in blue Mutations within AT5G47260 and AT5G47280 coding sequences are shown in red. aa, amino acids.

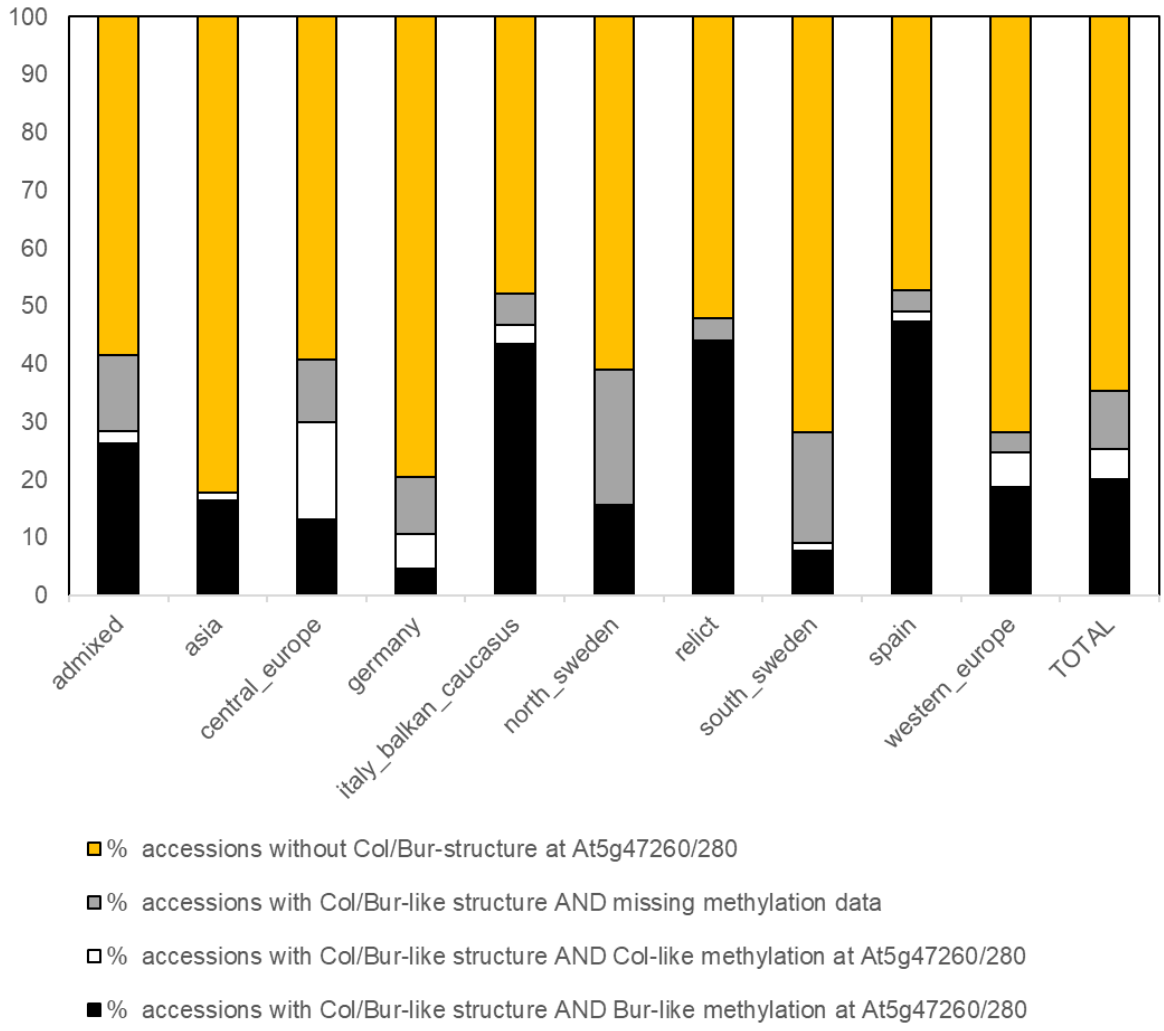
Supplementary Figure S7 | Full alignment of *AT5G47260* protein sequences in CRISPR-Cas9 edited lines in Bur-0 and HIF 10499 backgrounds.



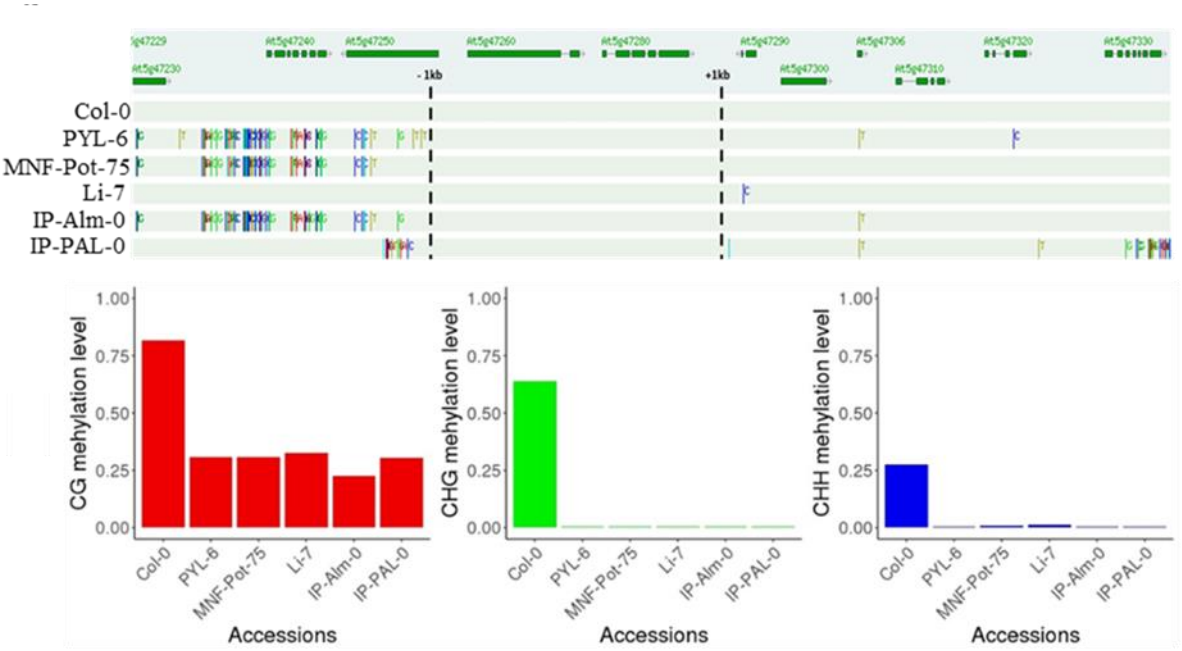
Supplementary Figure S8 | Full alignment of *AT5G47280* protein sequences in CRISPR-Cas9 edited lines in Bur-0 and HIF 10499 backgrounds.



Supplementary Figure S9 | Effect of *AT5G47260* or *AT5G47280* knock-out on GA/LA index (disease symptoms) in HIF 10499 background. Cas9-mediated mutations were obtained in the HIF 10499 genetic background. For each targeted gene, three independent lines harbouring independent homozygous mutations were used. Line 170-4 no longer has the CRISPR-Cas9 cassette. For each line, the mean clubroot symptoms score (GA/LA) was obtained by modelling raw data of eight biological replicates (with 10 to 12 individual plants per replicate). Center lines show the medians; box limits indicate the 25th and 75th percentiles as determined by R software; whiskers extend 1.5 times the interquartile range from the 25th and 75th percentiles, data points are plotted as open circles. Edited line GA/LA values statistically different from 10499 GA/LA value are indicated by stars (from Dunnett 's test) with the following code: * *p*-value <0.05; ** *p*-value <0.01; *** *p*-value <0.001.



Supplementary Figure S10 | Proportion of structural and epigenetic variations on the locus *Pb-At5.2* among Arabidopsis accessions in each admixture group (details in Supplementary Data 2).



Supplementary Figure S11 | The epigenetic variation on *AT5G47260* and *AT5G47280* is not related to SNP variations on *AT5G47260*. Sequence variant data were obtained from the signal SALK genome browser based on 1001 genome data. Average methylation level was calculated between 1 kb before the TSS site of *AT5G47260*, up to 1 kb after the TSE site of *AT5G47280*.

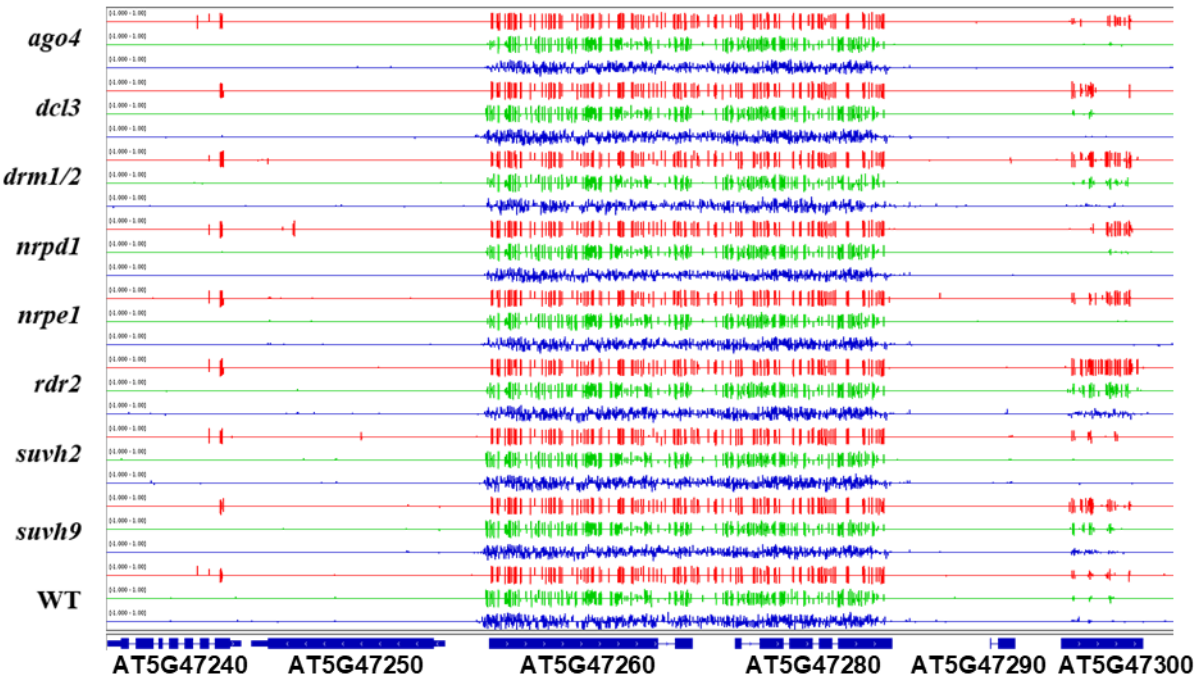


Figure S12 | Methylation of *PbAt-5.2* region in Col-0 and in mutants in genes involved in RdDM methylation maintenance (Stroud et al., 2013). In red the methylation in CG context. In blue the methylation in CHG context; in green the methylation in CHH context. WT indicates the methylation profile of Col-0.

Supplementary Text S1: Details of *PbAt5.2* fine mapping

Previous identification of *PbAt5.2*

A previous screen of *Arabidopsis thaliana* accessions found that Bur-0 is partially resistant to the *P. brassicae* eH isolate, whereas the canonical accession Col-0 is fully susceptible[1]. Two progenies were used to identify QTL controlling resistance to eH by linkage analysis: the first was derived from an initial Bur-0 (NASC accession N1028) x Col-0 (NASC accession N1092) cross followed by 6 generations of SSD (Recombinant Inbred Line set 20RV described in [2]). The second was derived from Col-0 x Bur-0 (described in [3]). These approaches led to the identification of a series of four additive QTL, including *PbAt5.2* (R^2=20%, Bur-0 allele at this locus confers partial resistance). The QTL peak of *PbAt5.2* was at the marker C5_19316 (around 19.3 Mb), with a confidence interval of 4.3 cM, between positions 18.7 Mb and 20.3 Mb (157 annotated genes between *At5g46260* and *At5g47690*).

HIF499 for *PbAt5.2* validation

Among the RIL set 20RV from Simon et al. (2008), one RIL line (RIL499) displayed a single residual heterozygous region including markers c5_17570, c5_19313 and c5_20318, framed by the homozygous loci c5_14766 and c5_21319. Heterogeneous Inbred Family (HIF) lines 10499 and 13499 were derived from RIL499 to obtain homozygosity at this locus (Institut Jean Pierre Bourgin, INRAE Versailles, France). These lines are near-isogenic, with identical combinations of Bur-0 and Col-0 homozygous genome sequences at every locus, except in the region between c5_14766 and c5_21319. The use of PCR-based markers (**Supplementary Data 1 Sheet 1**) allowed us to reduce this interval between markers CL5_15283 and CL5_20983 (excluded). HIF line 10499 displayed a higher level of partial resistance to eH isolate compared to 13499, thus confirming the position of *PbAt5.2* in this interval ([4], see also the Figure 1 in the present work).

Generation and phenotyping of F1 individuals derived from crosses between 10499 and 13499

Fine mapping of *PbAt5.2* started from the cross between HIF-13499 (allele Col-0) and HIF-10499 (allele Bur-0) lines. Crosses were made in both directions, *i.e.* using one or the other parent as female. Heterozygosity in the *PbAt5.2* region was checked in several F1 individuals using a series of PCR-based markers (**Supplementary Data 1 Sheet 1**). Clubroot index was evaluated in a series of F1 plants using the eH isolate, and was statistically identical to 13499, and higher than for 10499, thus suggesting that the Bur-0 resistant allele at *PbAt5.2* was recessive (**Supplementary Fig. 2**).

Screening of recombinant individuals in the segregating F2 progeny

One validated F1 plant was chosen from each of the two crosses. Those two plants were self-pollinized and approximately 3200 F2 plants were sown (about 1600 from each cross). Individual F2 from number 1 to 1581 were from a 10499 x 13499 cross. Individual F2 plants from 1582 to 3153 were from a 13499 x 10499 cross. DNA was extracted from young leaves sampled from these 3152 plants, and then subjected to a first round of genotyping using a series of 10 KASPAR SNP markers (list in **Supplementary Data 1 Sheet 2**). Analyses were performed on the GENTYANE platform using a LightCycler 480 device (UMR INRAE 1095, Clermont-Ferrand France). Due to low DNA concentrations in some samples, about 6% of the

genotyping points were 'negative'. Good or average-quality (i.e. genotyping ambiguity at maximum one marker) data were obtained for 2751 F2 individuals. Among those, 563 plants displayed at least one recombination in the region between *At5g37660* and *At5g51670*, which represented about 20.5 % of the F2 plants, and was consistent with the distance of about 22 cM between those two marker genes (**Supplementary Data 1 Sheet 3)**. This mean value of 20.5 however masked a clear disparity between genotypes derived from the 10499 x 13499 cross (32% of individuals with one recombination in the region) from the 13499 x 10499 cross (18% of individuals with one recombination in the chromosomal region). Nevertheless, most of this disequilibrium was focused in the region between the markers on *At5g42520* and *At5g44630* (i.e. outside the confidence interval of the clubroot resistance *PbAt5.2* QTL), and the male x female direction of the initial hybridization step did not affect the recombination rate in the region corresponding to the peak of the QTL (between *At5g46910, At5g47120* and *At5g47510*).

Phenotyping of recombinant F3 lines

One hundred and seven recombinant F2 lines were selected based on the presence of a recombination event near the closest markers to the QTL peak (19.3 Mb). Using the seeds derived from the selfing of those individual lines, the clubroot symptoms were estimated from 18 inoculated F3 plants (6 plants x 3 biological replicates). Those phenotyping data confirmed the presence of a segregating resistance locus in the region (**Supplementary Data 1 Sheet 4**). Lines with Bur or Col homozygous alleles at markers *At5g47120*/*At5g47510* displayed a mean GA/LA (clubroot symptoms) of 37.1 (SE=7.3) and 87.2 (SE=14.1), respectively. Lines with heterozygosity at those two markers displayed a mean GA/LA of 76.7 (SE=16), which was consistent with the above conclusion that the resistance Bur-0 allele was apparently recessive.

High-density genotyping of recombinant F2/F3 lines

A subset of 69 F2 recombinant lines was selected, based on the presence of a recombination event near the closest markers to the QTL peak (19.3 Mb). For each of these, 12 to 18 F3 progeny individuals were grown and their leaves were bulk-sampled, for subsequent analysis of 93 SNP (**Supplementary Table 1 Sheet 5**). All leaf samples were analyzed at the GENTYANE platform. SNP genotyping was performed with the KASPAR genotyping chemistry and Dynamic Array™ IFC 96*96 (UMR INRAE 1095, Clermont-Ferrand France). Genotyping data obtained from bulked leaves of F3 individuals represents the genotypes of the parental F2 individuals. This genotyping workflow was also applied to a series of non-recombinant F2 lines and parental HIF 10499 and 13499 lines, which were used as controls. The comparison of the 93 SNP genotyping data and clubroot GA/LA index for all those 69 lines (**Supplementary Table 1 Sheet 6**) finally led to the identification a small region between the markers K58=*At5g47230*prom (position 19,175,831 bp) and K65=*At5g47360* (position 19,214,446 bp). Due to the recessive status of the resistance allele, some recombinant lines with possibly interesting recombination events (especially in the line 1381) were not useful at this stage.

F4 lines with fixed alleles in the region of the resistance locus allowed further reduction of the *PbAt5.2* resistance locus interval

DNA was extracted from 12 to 18 individual F3 plants derived from selfing a series of F2 recombinant lines. Among them, F3 lines with homozygosity in the region of the resistance locus were screened using the following PCR-based markers: CL5_16921=*At5g42320*;

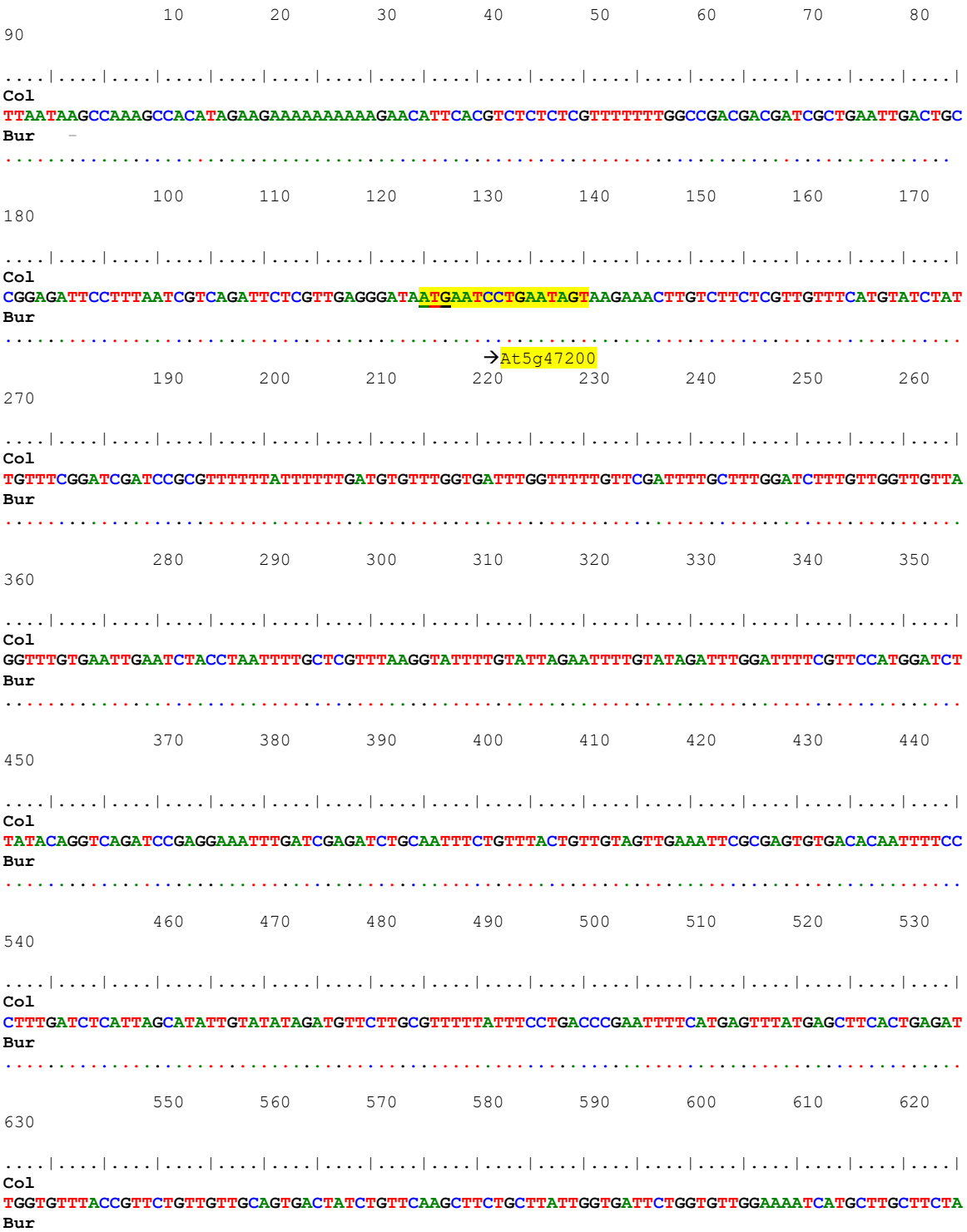
CL5_17802=*At5g44200*; CL5_18135=*At5g44900*; AF-NUD8; CL5_19601=*At5g48375* (details in **Supplementary Data 1 Sheet 7**). Homozygous F4 seed stocks were then obtained from the selfing of the selected homozygous F3 lines, and thereafter used for additional clubroot phenotyping assays. From the resulting data the interval could be reduced to a region between markers K58=*At5g47230*prom (position 19,175,831 bp) and K64 (position 19,208,823 bp), as shown in the **Figure 1e** (detailed phenotyping data also in **Supplementary Data 1 Sheet 8**). Finally, every other SNP and indel in the region was analyzed by sequencing the PCR-amplified fragments from 2313-15, 1381-2, 2509-11, and 1600-5 (details of primers are given in the **Supplementary Data 1 Sheet 1**). This allowed a final confidence interval of 26 kb between the marker CLG4 (19,182,401, in the promoter region of *At5g47240*), and the marker K64 (on SNP at position 19,208,823 bp, in *At5g47330*) to be identified.

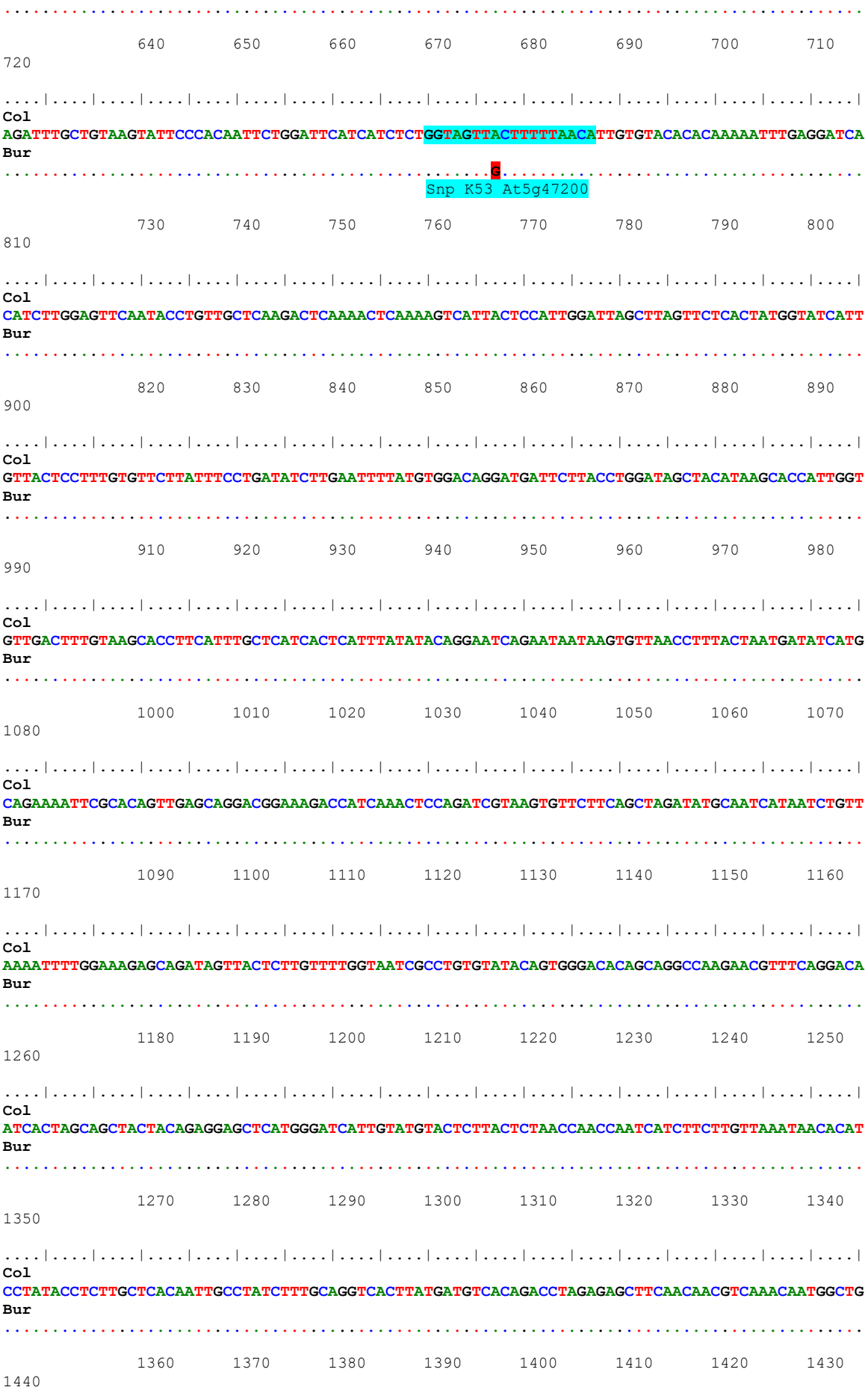
Supplementary Text S2: Influence of *PbAt5.2* on transcriptomic responses to clubroot infection

The analysis of transcriptome responses to isolate eH in 10499 and 13499 highlighted a series of 61 genes that were induced by infection only (or with higher range) in the presence of the resistance allele $PbAt5.2_{BUR}$ (**Supplementary Figure S5**). This series was enriched in genes associated with innate immunity, systemic acquired resistance, and notably included the SA-responsive gene *PR2*, and the set of genes *CYP71B15*, *CYP71A12*/*CYP71A13* involved in camalexin biosynthesis, confirming our previous studies on the cellular functions involved in clubroot resistance QTL *PbAt5.2*[5,6]. In contrast, a series of 58 genes was found to be induced by infection specifically (or with higher range) in the presence of the susceptibility allele $PbAt5.2_{COL}$. This set of genes included *ARGAH2*, a JA-regulated arginase encoding a protein involved in the biosynthesis of N-delta-acetylornithine, previously shown to play a role in basal resistance toward the eH isolate in genotypes harbouring the susceptible allele Col-0 on QTL *PbAt5.2* [6,7]. This list also included the trehalase encoding gene *TRE1*, involved in resistance to massive amounts of trehalose synthesized by *P. brassicae* during clubroot infection[8,9].

Supplementary Text S3: Aligned genomic sequences of Bur-0 and Col-at the *PbAt5.2* locus

Position of sequence polymorphisms, genetic markers and primers used in this study for the fine mapping in this region. The 26 kb region identified by fine mapping is between the marker CLG4 (sequenced using the two primers clonage_4for ATGTGTTTTGCGTCGACCTC and clonage_4rev AGCTCTCCGTGTCTACGACT) and the SNP marker K64. Additional details about primers and markers are given in Supplementary Data 1 SHEET1.

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Bur
Snp K53 At5g47200
730 740 750 760 770 780 790 800 810
Col
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Bur
820 830 840 850 860 870 880 890 900
Col
GTTACTCCTTTGTGTTCTTATTTCCTGATATCTTGAATTTTATGTGGACAGGATGATTCTTACCTGGATAGCTACATAAGCACCATTGGT
Bur
910 920 930 940 950 960 970 980 990
Col
GTTGACTTTGTAAGCACCTTCATTTGCTCATCACTCATTTATATACAGGAATCAGAATAATAAGTGTTAACCTTTACTAATGATATCATG
Bur
1000 1010 1020 1030 1040 1050 1060 1070 1080
Col
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Bur
1090 1100 1110 1120 1130 1140 1150 1160 1170
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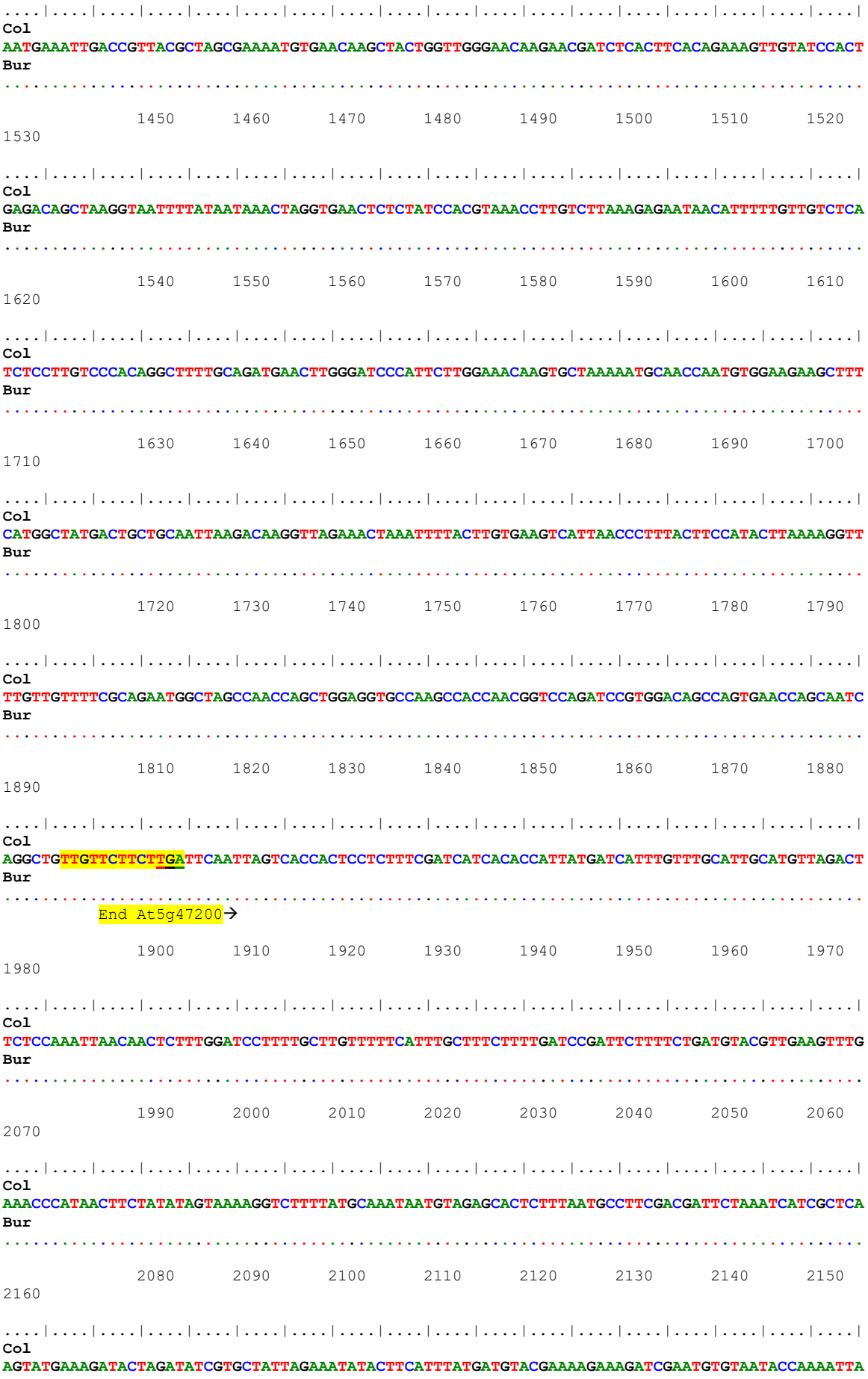
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1530
Col
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Bur
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Bur
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Col
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Bur
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1800
Col
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Bur
1810 1820 1830 1840 1850 1860 1870 1880
1890
Col
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End At5g47200
1900 1910 1920 1930 1940 1950 1960 1970
1980
Col
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1990 2000 2010 2020 2030 2040 2050 2060
2070
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Bur
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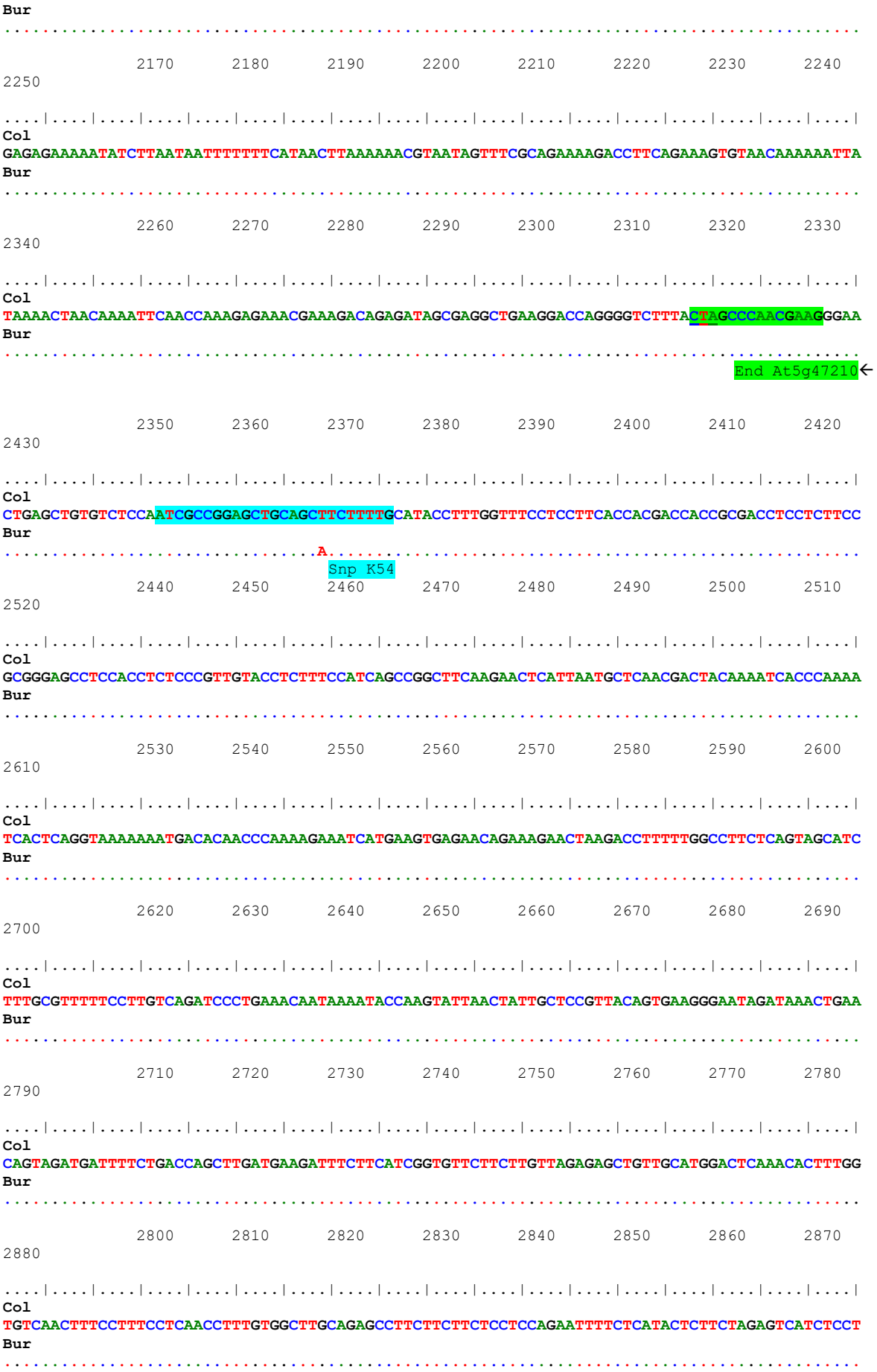
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2250
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Bur
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2340
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Bur
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2430
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Bur
A
Snp K54
2440 2450 2460 2470 2480 2490 2500 2510
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2620 2630 2640 2650 2660 2670 2680 2690
2700
Col
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2710 2720 2730 2740 2750 2760 2770 2780
2790
Col
CAGTAGATGATTTTCTGACCAGCTTGATGAAGATTTCTTCATCGGTGTTCTTCTTGTTAGAGAGCTGTTGCATGGACTCAAACACTTTGG
Bur
2800 2810 2820 2830 2840 2850 2860 2870
2880
Col
TGTCAACTTTCCTTTCCTCAACCTTTGTGGCTTGCAGAGCCTTCTTCTTCTCCTCCAGAATTTTCTCATACTCTTCTAGAGTCATCTCCT
Bur

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             2890       2900       2910       2920       2930       2940       2950       2960
2970

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
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Bur
.....................................................................................................

             2980       2990       3000       3010       3020       3030       3040       3050
3060

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
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Bur
.....................................................................................................

             3070       3080       3090       3100       3110       3120       3130       3140
3150

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CCTCCTTGCTTCTCAGCAACAGGGCTCTTCTCAACCTCTGTGGTAGGTTCCTCAGACGTTCTAATATAAGAACAACAAAAGTTTATAAAC
Bur
.....................................................................................................

             3160       3170       3180       3190       3200       3210       3220       3230
3240

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AACCTAAAGTTAAAGTCATATGGATAATTAAAGTGAAGACAAGGATGCTTACGGAGGGATATCATCTTCAGTAGTGCCCCAGTTTCCACG
Bur
.....................................................................................................

             3250       3260       3270       3280       3290       3300       3310       3320
3330

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
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Bur
.....................................................................................................

             3340       3350       3360       3370       3380       3390       3400       3410
3420

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TAAAGTAGTGGACAGAACAAAAAGAAAGCTTACCCATGACCTGTCCTGCTATGGCGGTCATAATTCCTCGGTGGGCGTTCAACATCACCA
Bur
.....................................................................................................

             3430       3440       3450       3460       3470       3480       3490       3500
3510

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GATTCCCCGTTGGCAACTCCACCACGGCGAGGTCCTTCACGACCACCGCCAACACGGTATCCACCAACAGACCCACCACGGCTTGCTCCA
Bur
.....................................................................................................

             3520       3530       3540       3550       3560       3570       3580       3590
3600

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TCAGCATCTTCAGAAGGTCTCCTGTATCCTCCAGAAAATCCATTCTCATTTCCAGGAGCATCATTGTTCCTGTTGTCCCGGTTGTATCCA
Bur
.....................................................................................................

             3610       3620       3630       3640       3650       3660       3670       3680
3690

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
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CCATTACCCCTGCCACGGGAAAATCCACCACGTCCACCAGTCCCACCACGACCTCCTTGAGGAGCATTCCTCGACTCCCTCACTACATTC
Bur
.....................................................................................................

              3700      3710      3720      3730      3740      3750      3760      3770
3780

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ATAACAAAAAGCTTTCAATATATATACTTATCCTAATCTAACAAAGTATTAAGCTTTACCCTAATCTAACAAAGCAGTAGAGAAACAAAA
Bur
.....................................................................................................

              3790      3800      3810      3820      3830      3840      3850      3860
3870

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TAAGATACGGAAGAAACTAACAAAGCAGCAAATGAAAAAAGCACACACATTTGACTATGGATCTTTCATGACAACCATAAACAAACTTCA
Bur
.....................................................................................................

              3880      3890      3900      3910      3920      3930      3940      3950
3960

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CTAGAACTAATCAATCAAACACTAGACAAAACACAGCTGAATCTAAATCTGTTAAGTATCAACATAAAGGAAAGAACTTTTACCTGCTTG
Bur
.....................................................................................................

              3970      3980      3990      4000      4010      4020      4030      4040
4050

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AGAAGGAGGAGCCGGCTTGGTTGGGAACTTAGCGGCCTTAGGAGGCTGAACAGCAGCAGCAGCTTTCTCGACTTTCTGAGACAAAGCCAC
Bur
.....................................................................................................



              4060      4070      4080      4090      4100      4110      4120      4130
4140

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AGCGAGCTGGCTTGGATCCTCAGCATCATCTCCTAGAAGATCGAAAGGGTTCAAAGACGCCATCACCAGTCTGGTAAGATCGAGTTAGGT
Bur
.....................................................................................................
                                                    Start At5g47210←
              4150      4160      4170      4180      4190      4200      4210      4220
4230

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ACAAGTCACAGGAGAAATTGGTTTACTTTGATGGGTTTATAGAGAGGGAAATCAGTAATTCATGGCGATATACAGAATCAGAAAAAAGAG
Bur
.....................................................................................................

              4240      4250      4260      4270      4280      4290      4300      4310
4320

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GTACTTGAAGAGAGATTATTCGGACAGAGCTGTTTGTGTTTAAGAGATAGCGAAACAAGAACCCTAAGAAAAGATGCGGCAGTGAGAGAG
Bur
.....................................................................................................

              4330      4340      4350      4360      4370      4380      4390      4400
4410

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AGAGGTGCGACTTAAAAACCTAATCTATAAACCCTTCCTGAGTTATTATTCTCTGCGGCGGGTGCTATTTAACTGTGTTCTGGTCCTCTC
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Bur
.....................................................................................................

             4420      4430      4440      4450      4460      4470      4480      4490
4500

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TTTATCTATCCGTGGGCTACAAACTGGTTAAGCCCATTAACAATAATAAATATCAGCTCTCGTTGGTTAAAGCCCATTAATGAAAAGAAT
Bur
.....................................................................................................

             4510      4520      4530      4540      4550      4560      4570      4580
4590

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ATTCGTTCTTAGTCCATTAAGAGAATAACTGGGTTTCAATACTGAATCCTCTAGGCGAGACACGGTTTTTCTCATTCTAAACCTTTATTG
Bur
.....................................................................................................

             4600      4610      4620      4630      4640      4650      4660      4670
4680

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GGTTCAAAGTTTTATGTGCTTCAAAAATCAAAGATATAAATTGATTGCTTAAATGAATTTTCTCTAGCAGAGCCTTTGCTTGTCGACCTT
Bur
.....................................................................................................

             4690      4700      4710      4720      4730      4740      4750      4760
4770

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AGACAGCTTCATCTTCTCAAGAGTATCAAACAGAAACATTTACAAGTGATTACACACTTAAGCTCACAACATTTACAACAAAAAAAAATC
Bur
.....................................................................................................

             4780      4790      4800      4810      4820      4830      4840      4850
4860

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TAAAATAGATAGGTTATTATTTATTGTCGCGCTACTGTTGATGGATTTTGGTTTTAGTAATTGTTACCTCTTCGATCAAGTTTTGGCTAC
Bur
.....................................................................................................

             4870      4880      4890      4900      4910      4920      4930      4940
4950

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TTAGCAATATAGAACTCAAATTGAGTTAAGAGATTGTATTAGGGGATATGGTGTAATACTTTAATAAAGCCGTGAATGTCATGTAAGAAA
Bur
.....................................................................................................

             4960      4970      4980      4990      5000      5010      5020      5030
5040

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TGAAACTAGATTGAAAAATTAACACTCACGGCTTTATTAAAGTGTCTATTTTGTTTATGGATTGAAGATATATGGCTCTGTTTAGTAACT
Bur
.....................................................................................................

             5050      5060      5070      5080      5090      5100      5110      5120
5130

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AATTTACATCACGGGAACACTTTTACTTGGTGCCTCAACATTTATAGCAAAACTATTCAACTACAAAACACACAAGATCAAACTTATGAA
Bur
.....................................................................................End At5g47220←

             5140      5150      5160      5170      5180      5190      5200      5210
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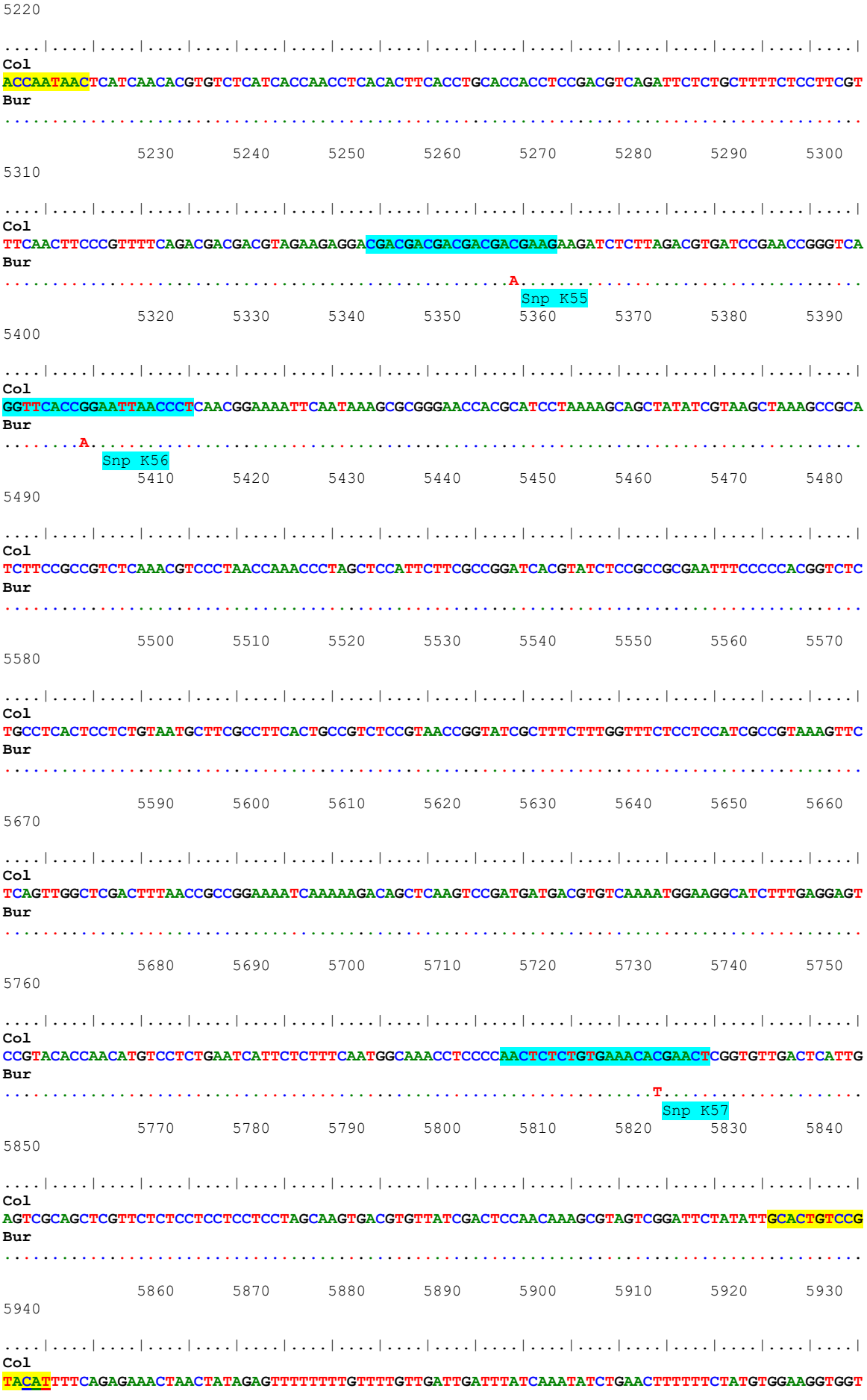
5220
Col
ACCAATAACTCATCAACACGTGTCTCATCACCAACCTCACACTTCACCTGCACCACCTCCGACGTCAGATTCTCTGCTTTTCTCCTTCGT
Bur
5230 5240 5250 5260 5270 5280 5290 5300
5310
Col
TTCAACTTCCCGTTTTCAGACGACGACGTAGAAGAGGACGACGACGACGACGACGAAGAAGATCTCTTAGACGTGATCCGAACCGGGTCA
Bur
A
Snp K55
5320 5330 5340 5350 5360 5370 5380 5390
5400
Col
GGTTCACCGGAATTAACCCTCAACGGAAAATTCAATAAAGCGCGGGAACCACGCATCCTAAAAGCAGCTATATCGTAAGCTAAAGCCGCA
Bur
A
Snp K56
5410 5420 5430 5440 5450 5460 5470 5480
5490
Col
TCTTCCGCCGTCTCAAACGTCCCTAACCAAACCCTAGCTCCATTCTTCGCCGGATCACGTATCTCCGCCGCGAATTTCCCCCACGGTCTC
Bur
5500 5510 5520 5530 5540 5550 5560 5570
5580
Col
TGCCTCACTCCTCTGTAATGCTTCGCCTTCACTGCCGTCTCCGTAACCGGTATCGCTTTCTTTGGTTTCTCCTCCATCGCCGTAAAGTTC
Bur
5590 5600 5610 5620 5630 5640 5650 5660
5670
Col
TCAGTTGGCTCGACTTTAACCGCCGGAAAATCAAAAAGACAGCTCAAGTCCGATGATGACGTGTCAAAATGGAAGGCATCTTTGAGGAGT
Bur
5680 5690 5700 5710 5720 5730 5740 5750
5760
Col
CCGTACACCAACATGTCCTCTGAATCATTCTCTTTCAATGGCAAACCTCCCCAACTCTCTGTGAAACACGAACTCGGTGTTGACTCATTG
Bur
T
Snp K57
5770 5780 5790 5800 5810 5820 5830 5840
5850
Col
AGTCGCAGCTCGTTCTCTCCTCCTCCTCCTAGCAAGTGACGTGTTATCGACTCCAACAAAGCGTAGTCGGATTCTATATTGCACTGTCCG
Bur
5860 5870 5880 5890 5900 5910 5920 5930
5940
Col
TACATTTTCAGAGAAACTAACTATAGAGTTTTTTTTGTTTTGTTGATTGATTTATCAAATATCTGAACTTTTTTCTATGTGGAAGGTGGT

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Bur
.....................................................................................A....
Start At5g47220←
               5950       5960       5970       5980       5990       6000       6010       6020
6030

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TAAGAGGTTTATATAGAGGGTACGAGGTTCACGAACCTGGAAAAAAAGAAAAAGTTTTTCATGTTTTTCCAAATTTGTTTTAGTTTAGTG
Bur
.........................G..T.....................................................

               6040       6050       6060       6070       6080       6090       6100       6110
6120

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GGTAATTAAAAAATATGAAAGTTGTGGATTTTTCGTTACTACGAAGGTTCGTGAATTAAACACGTGCGCTTTATCCACAGATATCACAAT
Bur
.....................................................................................

               6130       6140       6150       6160       6170       6180       6190       6200
6210

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GAAGAAGGGTCAAGATGACGTCATGTGGTCATGACATTTCTGGAAGAAAGATGCTGATTTGGTTTTGTCTCTCAACTTGTCCCTTGTTTT
Bur
.....................................................................................

               6220       6230       6240       6250       6260       6270       6280       6290
6300

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GTCGTTCGGTTTTGAATACGATTCCCGGTTTTATTAGGCAAAACTAGTGTTTAATTAGTTTGTTAATCGAAAACCAAGGTCTTAATTCAT
Bur
.....................................................................................

               6310       6320       6330       6340       6350       6360       6370       6380
6390

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TATACTTTGTTATATCGACATAAATTTTCAACTAAACTTATATTTCATCGCCTTACACTAGAGTAATAATTTTTGCTTAAGTATACTTTA
Bur
.................................................T.....................................

               6400       6410       6420       6430       6440       6450       6460       6470
6480

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col   TTAGATAGTATTGGCAAGTATATTATATGTTTAATTACATGAAATCTAAGCTTAGATCTTGTTATGGTGGTGAA-
TGAAAAATCTTAACG
Bur
..............A....T............G.....................................A..............

               6490       6500       6510       6520       6530       6540       6550       6560
6570

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AGGTGGGCCATAATTATATGAATGGGGACACTGAAAGTGTCTGCAAAAATCGGGATACATTTCTCCTGGTCACCAACCAATTCATATCAT
Bur
............................T.A.....................................................

               6580       6590       6600       6610       6620       6630       6640       6650
6660

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CATCTTTCCCTTTCACCTTTCATTTTTACTAATTTCTAATTTAGAATTTTCCTAATTGCCAATGTCATGTTTATTTTAGTACTTTTTGAT
Bur
.....................................C.....................................................C.

               6670       6680       6690       6700       6710       6720       6730       6740
6750
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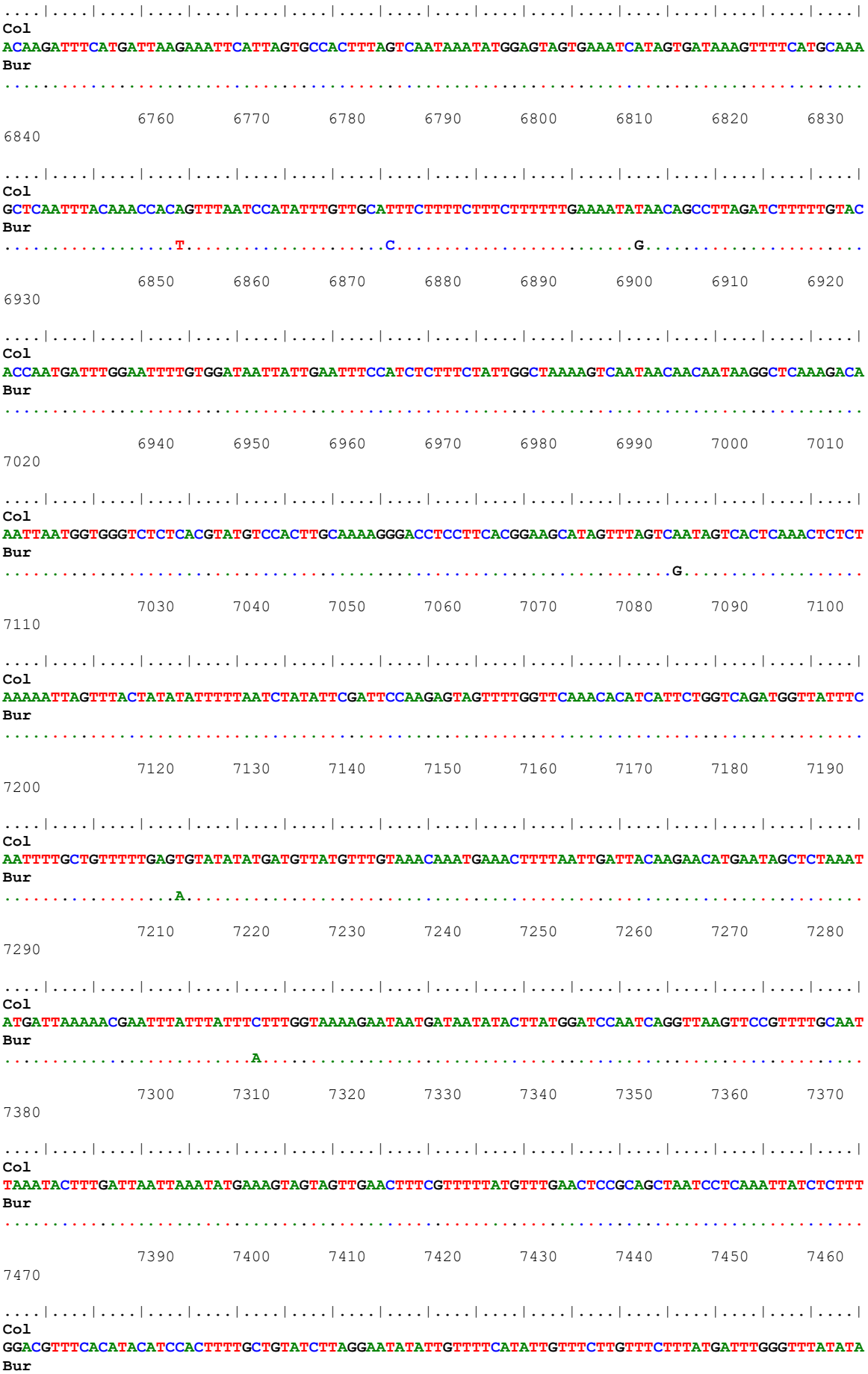
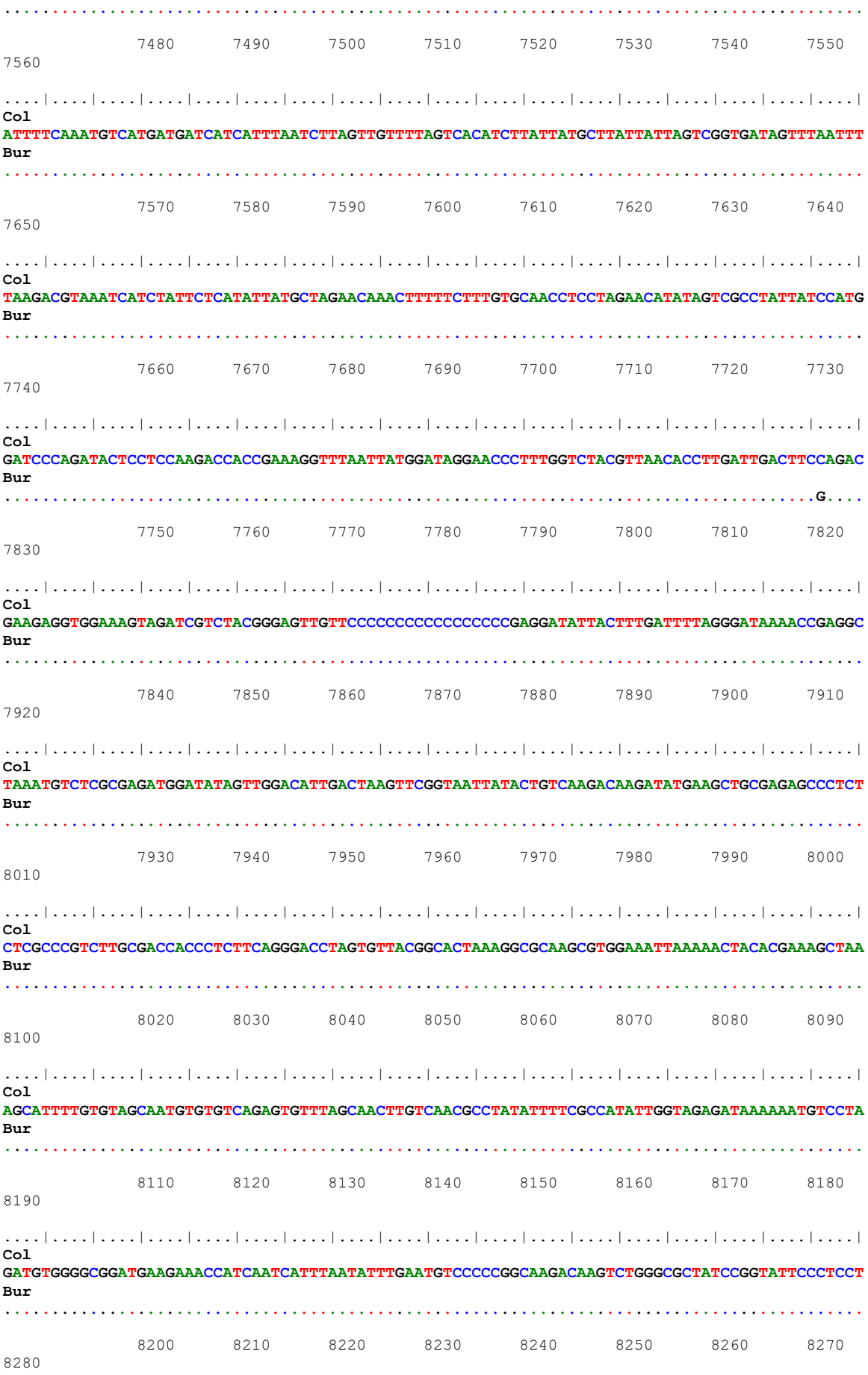
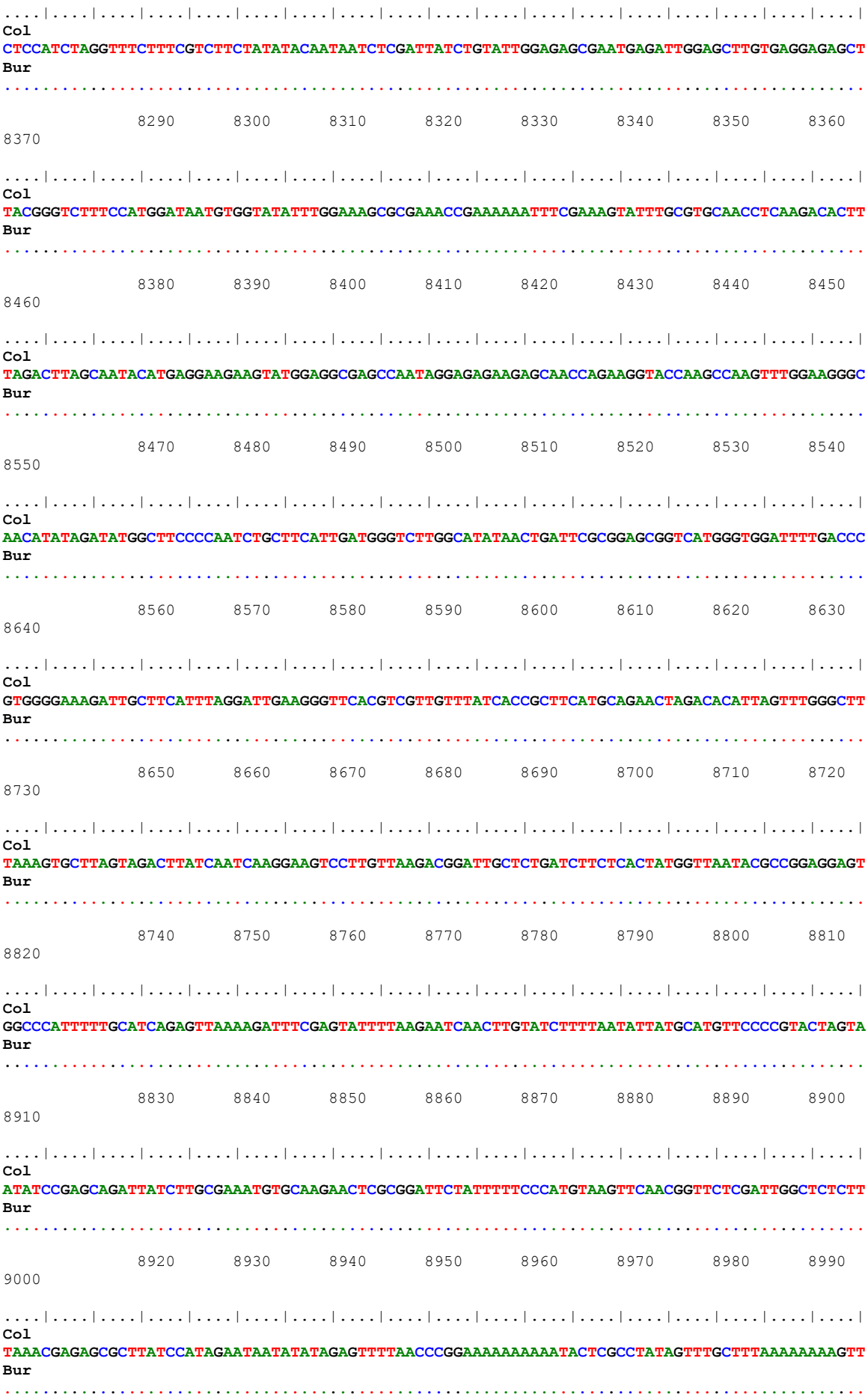

Col
ACAAGATTTCATGATTAAGAAATTCATTAGTGCCACTTTAGTCAATAAATATGGAGTAGTGAAATCATAGTGATAAAGTTTTCATGCAAA
Bur
6760 6770 6780 6790 6800 6810 6820 6830
6840
Col
GCTCAATTTACAAACCACAGTTTAATCCATATTTGTTGCATTTCTTTTCTTTCTTTTTTGAAAATATAACAGCCTTAGATCTTTTTGTAC
Bur
T C G
6850 6860 6870 6880 6890 6900 6910 6920
6930
Col
ACCAATGATTTGGAATTTTGTGGATAATTATTGAATTTCCATCTCTTTCTATTGGCTAAAAGTCAATAACAACAATAAGGCTCAAAGACA
Bur
6940 6950 6960 6970 6980 6990 7000 7010
7020
Col
AATTAATGGTGGGTCTCTCACGTATGTCCACTTGCAAAAGGGACCTCCTTCACGGAAGCATAGTTTAGTCAATAGTCACTCAAACTCTCT
Bur
G
7030 7040 7050 7060 7070 7080 7090 7100
7110
Col
AAAAATTAGTTTACTATATATTTTTAATCTATATTCGATTCCAAGAGTAGTTTTGGTTCAAACACATCATTCTGGTCAGATGGTTATTTC
Bur
7120 7130 7140 7150 7160 7170 7180 7190
7200
Col
AATTTTGCTGTTTTTGAGTGTATATATGATGTTATGTTTGTAAACAAATGAAACTTTTAATTGATTACAAGAACATGAATAGCTCTAAAT
Bur
A
7210 7220 7230 7240 7250 7260 7270 7280
7290
Col
ATGATTAAAAACGAATTTATTTATTTCTTTGGTAAAAGAATAATGATAATATACTTATGGATCCAATCAGGTTAAGTTCCGTTTTGCAAT
Bur
A
7300 7310 7320 7330 7340 7350 7360 7370
7380
Col
TAAATACTTTGATTAATTAAATATGAAAGTAGTAGTTGAACTTTCGTTTTTATGTTTGAACTCCGCAGCTAATCCTCAAATTATCTCTTT
Bur
7390 7400 7410 7420 7430 7440 7450 7460
7470
Col
GGACGTTTCACATACATCCACTTTTGCTGTATCTTAGGAATATATTGTTTTCATATTGTTTCTTGTTTCTTTATGATTTGGGTTTATATA
Bur


7480 7490 7500 7510 7520 7530 7540 7550 7560
Col
ATTTTCAAATGTCATGATGATCATCATTTAATCTTAGTTGTTTTAGTCACATCTTATTATGCTTATTATTAGTCGGTGATAGTTTAATTT
Bur
7570 7580 7590 7600 7610 7620 7630 7640 7650
Col
TAAGACGTAAATCATCTATTCTCATATTATGCTAGAACAAACTTTTTCTTTGTGCAACCTCCTAGAACATATAGTCGCCTATTATCCATG
Bur
7660 7670 7680 7690 7700 7710 7720 7730 7740
Col
GATCCCAGATACTCCTCCAAGACCACCGAAAGGTTTAATTATGGATAGGAACCCTTTGGTCTACGTTAACACCTTGATTGACTTCCAGAC
Bur
G
7750 7760 7770 7780 7790 7800 7810 7820 7830
Col
GAAGAGGTGGAAAGTAGATCGTCTACGGGAGTTGTTCCCCCCCCCCCCCCCCCGAGGATATTACTTTGATTTTAGGGATAAAACCGAGGC
Bur
7840 7850 7860 7870 7880 7890 7900 7910 7920
Col
TAAATGTCTCGCGAGATGGATATAGTTGGACATTGACTAAGTTCGGTAATTATACTGTCAAGACAAGATATGAAGCTGCGAGAGCCCTCT
Bur
7930 7940 7950 7960 7970 7980 7990 8000 8010
Col
CTCGCCCGTCTTGCGACCACCCTCTTCAGGGACCTAGTGTTACGGCACTAAAGGCGCAAGCGTGGAAATTAAAAACTACACGAAAGCTAA
Bur
8020 8030 8040 8050 8060 8070 8080 8090 8100
Col
AGCATTTTGTGTAGCAATGTGTGTCAGAGTGTTTAGCAACTTGTCAACGCCTATATTTTCGCCATATTGGTAGAGATAAAAAATGTCCTA
Bur
8110 8120 8130 8140 8150 8160 8170 8180 8190
Col
GATGTGGGGCGGATGAAGAAACCATCAATCATTTAATATTTGAATGTCCCCCGGCAAGACAAGTCTGGGCGCTATCCGGTATTCCCTCCT
Bur
8200 8210 8220 8230 8240 8250 8260 8270 8280


Col
CTCCATCTAGGTTTCTTTCGTCTTCTATATACAATAATCTCGATTATCTGTATTGGAGAGCGAATGAGATTGGAGCTTGTGAGGAGAGCT
Bur
8290 8300 8310 8320 8330 8340 8350 8360
8370
Col
TACGGGTCTTTCCATGGATAATGTGGTATATTTGGAAAGCGCGAAACCGAAAAAATTTCGAAAGTATTTGCGTGCAACCTCAAGACACTT
Bur
8380 8390 8400 8410 8420 8430 8440 8450
8460
Col
TAGACTTAGCAATACATGAGGAAGAAGTATGGAGGCGAGCCAATAGGAGAGAAGAGCAACCAGAAGGTACCAAGCCAAGTTTGGAAGGGC
Bur
8470 8480 8490 8500 8510 8520 8530 8540
8550
Col
AACATATAGATATGGCTTCCCCAATCTGCTTCATTGATGGGTCTTGGCATATAACTGATTCGCGGAGCGGTCATGGGTGGATTTTGACCC
Bur
8560 8570 8580 8590 8600 8610 8620 8630
8640
Col
GTGGGGAAAGATTGCTTCATTTAGGATTGAAGGGTTCACGTCGTTGTTTATCACCGCTTCATGCAGAACTAGACACATTAGTTTGGGCTT
Bur
8650 8660 8670 8680 8690 8700 8710 8720
8730
Col
TAAAGTGCTTAGTAGACTTATCAATCAAGGAAGTCCTTGTTAAGACGGATTGCTCTGATCTTCTCACTATGGTTAATACGCCGGAGGAGT
Bur
8740 8750 8760 8770 8780 8790 8800 8810
8820
Col
GGCCCATTTTTGCATCAGAGTTAAAAGATTTCGAGTATTTTAAGAATCAACTTGTATCTTTTAATATTATGCATGTTCCCCGTACTAGTA
Bur
8830 8840 8850 8860 8870 8880 8890 8900
8910
Col
ATATCCGAGCAGATTATCTTGCGAAATGTGCAAGAACTCGCGGATTCTATTTTTCCCATGTAAGTTCAACGGTTCTCGATTGGCTCTCTT
Bur
8920 8930 8940 8950 8960 8970 8980 8990
9000
Col
TAAACGAGAGCGCTTATCCATAGAATAATATATAGAGTTTTAACCCGGAAAAAAAAAATACTCGCCTATAGTTTGCTTTAAAAAAAGTT
Bur

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                9010       9020       9030       9040       9050       9060       9070       9080
9090

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TCTTCCAACCAACAAAAGCACTCACCTAATCTTACAACTGTGATTTTTGACCAATGTTTTTGTTCATATCTCTTCAAAAAAAAATTTATA
Bur
..........................................................T.....................................

                9100       9110       9120       9130       9140       9150       9160       9170
9180

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CTATAATGAGCATTATAATATATTTTCTATCACATATTATTGTGCAGAAATTAAGTATCAAGTTAAAGGCAAGTTTTAGCAAAAACACGA
Bur
..........................................................................................

                9190       9200       9210       9220       9230       9240       9250       9260
9270

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TTTACGGAATTAGCAACATTTACACGGACGATCGCATATTTCAGACAAGACAAATACAGAGGATAAAATATCATAAAAGGGAAAATGACG
Bur
..........................................................................................

                9280       9290       9300       9310       9320       9330       9340       9350
9360

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ACACAAATTATGTAGGCAGTGATTGGTACACATTGTTAGTTTTTTTTTAAAATATTACTATGTTTTTGCCAAAAAAAATTACGAATCAGAG
Bur
..........................................................................................

                9370       9380       9390       9400       9410       9420       9430       9440
9450

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CAATCATGCATAAAAATTAGAAGAATAGCGTAAATATTTTTCTCTTTTCTATTCACACCTTTACTCGCTTTTCTATTCATTTTCTTATTT
Bur
..........................................................................................

                9460       9470       9480       9490       9500       9510       9520       9530
9540

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TTCCTCTCAATTACTCCAAAAACATACCAATTAGAGTTTAGATTCATGATGTAATTGACGAAAAAAATCACCCATATGATTAGTTACACT
Bur
..........................................................................................

                9550       9560       9570       9580       9590       9600       9610       9620
9630

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ATATCCGAACACTAATATTCATAAATTTAGTGTCTCGGATTTATGCATACAAACTTTTCATGGAAGATGCTTCTCATTTACAAGCTGATG
Bur
..........................................................................................

                9640       9650       9660       9670       9680       9690       9700       9710
9720

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ATAAAATTGATCTTACATTTTTTAACAATGAAATGTCTTCTATTTTTTGTTATAGCCAAAATAACTCAGCTTTCAGTTATATATAATCTA
Bur
..........................................................................................

                9730       9740       9750       9760       9770       9780       9790       9800
9810

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
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Col
CAGTTTAGTGTATTTTGTTAACTTTAATCGATTCCTAATTCATTTTAATCAACACATCTATATGTAGGCAATTGGATGCAAAAGGTACAC
Bur
....................................................................................................

             9820      9830      9840      9850      9860      9870      9880      9890
9900

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AAAACAATGCAAAAGGAAGGATCAAAGGAAAGATGTTATATGACACGTCAGCAGTATTCAAAAGTTTGAAGTTGAACAAATCTAGTCATG
Bur
....................................................................................................

             9910      9920      9930      9940      9950      9960      9970      9980
9990

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TTTGACTTTGACCACTGACTTTTCAAACCTATCTTTTATTAGTAGCAAACTCAGTTCCATACGTGCAAACAACCTCACACGTGCGTTCCC
Bur
....................................................................................................

            10000     10010     10020     10030     10040     10050     10060     10070
10080

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ACCGCAATGTTTGAGGTTTTCTTCAACAGAAGACGATATTTCTTATTATTATAACGTTAGATTGAGAATTCAAAGATTCTCGACAAATGA
Bur
....................................................................................................

            10090     10100     10110     10120     10130     10140     10150     10160
10170

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ATGGTAACTTTTTTCTATAAGAATCACAATAATTAGTTTTAGTTATACAATTTTATAATGTTGGAGTAATTGTCACATAGATGATTGGTT
Bur
....................................................................................................

            10180     10190     10200     10210     10220     10230     10240     10250
10260

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GGTGATAATAGTTGTTTATGTATGATTGATCAATTAAACTTATAATTTTCCATTGGAATAATATTTTCTTGACCTTTAAATTTGGAATGT
Bur
....................................................................................................

            10270     10280     10290     10300     10310     10320     10330     10340
10350

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AGATTTATATGGAAAAAGTAGATAATCATTTTTGTGACGCTAATTAAATATGTTGTCCCATAACGACAGAAAAAAAAAAATGAAACAAAA
Bur    ....................................................................................-
..........

            10360     10370     10380     10390     10400     10410     10420     10430
10440

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ATAGAGACCAGATTGGTTCAAGAAAACGACACACAGTTTAGGATGCTAAAAAAGCTTTGTTAGTACCATATGATTGTTATATTGTTTATT
Bur
....................................................................................................

            10450     10460     10470     10480     10490     10500     10510     10520
10530

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GGTTCCTTAATAATGTATTTAGACGTCAAAAAATGTTTTTGTATTGATATGTGACCTCATAACTGGTTAGCTGCTTAGGGCCATTAGATT
Bur
....................................................................................................
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            10540     10550     10560     10570     10580     10590     10600     10610
10620

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AGAGTTTTGATTGTTTCAAATGTCAAATCTTACAGTCCGTCAAATTTTATTTGATGTGAAGTAAGTGAGTTGATAAATGGGACTACTTTC
Bur
....................................................................................

            10630     10640     10650     10660     10670     10680     10690     10700
10710

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TCCAGTTGGCTAGGGTCGACTGCTAATAACATTTCTCCAAGGAATTAATCTCAACGGGCTTGTTGCTCAGGCAACAATTTATAGGAATAG
Bur
....................................................................................

            10720     10730     10740     10750     10760     10770     10780     10790
10800

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AGATTGAACGAAATAATTAACAGATTACACAACAATGTTTCCTCTACTTTAAGCAAGCAATCTTCAAGGCTATATTGATCGACTGATTCG
Bur
....................................................................................

            10810     10820     10830     10840     10850     10860     10870     10880
10890

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AGACGCAATCGTCTTGTCAAGAAGAACCACAAAAACTATGATGATATGTAATGCAAACTTGACTCGTCTTTGAGTAACACTTCTTCATCT
Bur
....................................................................................

            10900     10910     10920     10930     10940     10950     10960     10970
10980

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AGTCCAATCGTCGCAGGGTTTCTTTTAATTTATTTATTTATTATCTTCTCTTTTGGTAAGAAAGAGCTTCTTTAATTTGGTTAAACTTTT
Bur
....................................................................................

            10990     11000     11010     11020     11030     11040     11050     11060
11070

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TTTTTTTGGTTAAGTACAAAACTTCTCATTCCTTAATAAAATTGATATCTATATTATAAAATATCAAATTTTGTAAAACAAAAATAATTA
Bur
....................................................................................

            11080     11090     11100     11110     11120     11130     11140     11150
11160

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AGAGTAGTGTTTCACAACAACAACAAATTAAAAAGACTACTATATAAATTAAAAAGACTACTTGGCTTTCTAGAAATTATTAAATATAAA
Bur
....................................................................................

            11170     11180     11190     11200     11210     11220     11230     11240
11250

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TTTTTATATTAAATCTCTGATTTGCTATATCATTTATTAAAAGTGTGAACTTTATTTTGTTTCATTGTAACAAGTAACAACATGACTTTC
Bur
....................................................................................

            11260     11270     11280     11290     11300     11310     11320     11330
11340

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
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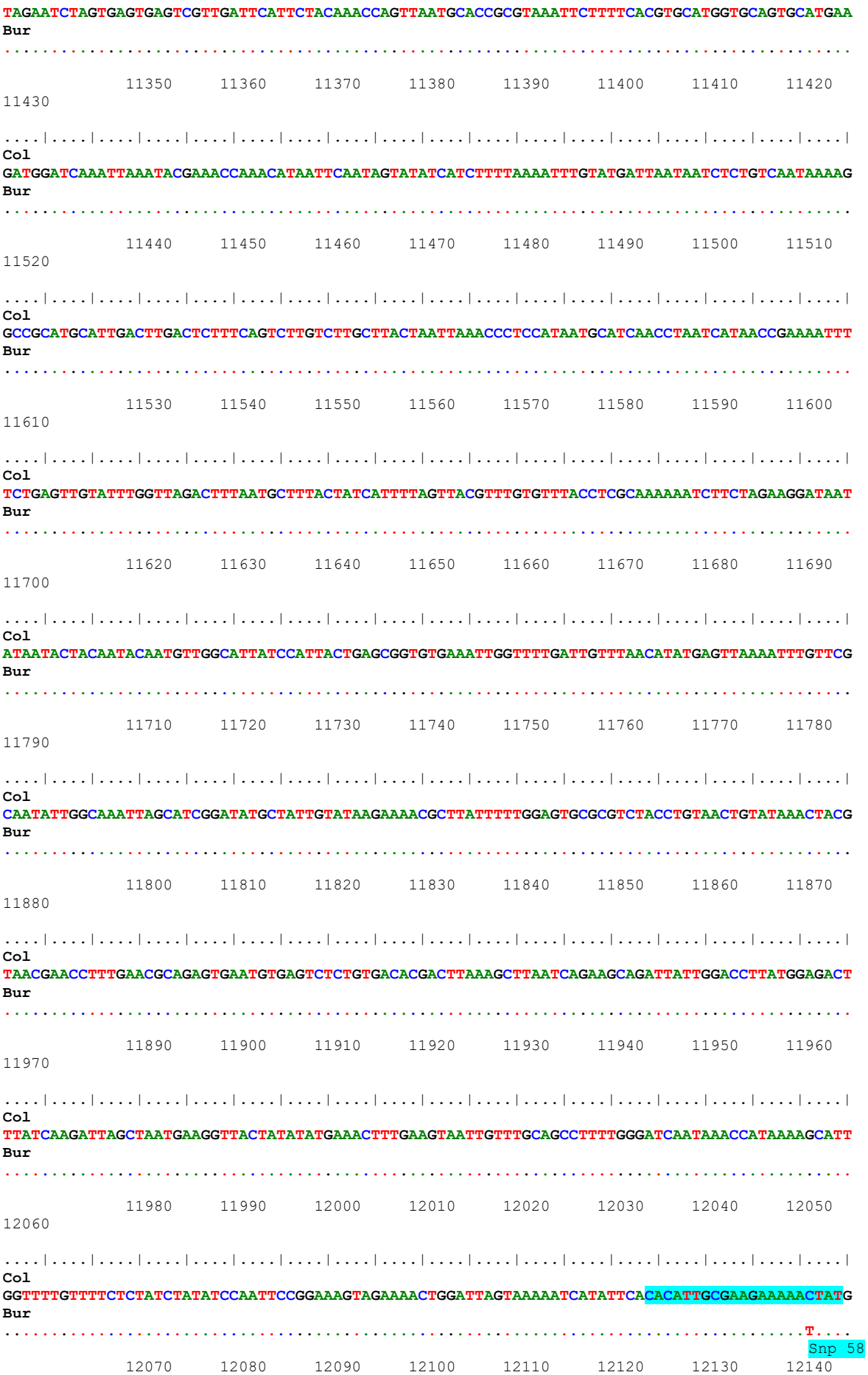
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Bur
11350 11360 11370 11380 11390 11400 11410 11420
11430
Col
GATGGATCAAATTAAATACGAAACCAAACATAATTCAATAGTATATCATCTTTTAAAATTTGTATGATTAATAATCTCTGTCAATAAAAG
Bur
11440 11450 11460 11470 11480 11490 11500 11510
11520
Col
GCCGCATGCATTGACTTGACTCTTTCAGTCTTGTCTTGCTTACTAATTAAACCCTCCATAATGCATCAACCTAATCATAACCGAAAATTT
Bur
11530 11540 11550 11560 11570 11580 11590 11600
11610
Col
TCTGAGTTGTATTTGGTTAGACTTTAATGCTTTACTATCATTTTAGTTACGTTTGTGTTTACCTCGCAAAAAATCTTCTAGAAGGATAAT
Bur
11620 11630 11640 11650 11660 11670 11680 11690
11700
Col
ATAATACTACAATACAATGTTGGCATTATCCATTACTGAGCGGTGTGAAATTGGTTTTGATTGTTTAACATATGAGTTAAAATTTGTTCG
Bur
11710 11720 11730 11740 11750 11760 11770 11780
11790
Col
CAATATTGGCAAATTAGCATCGGATATGCTATTGTATAAGAAAACGCTTATTTTTGGAGTGCGCGTCTACCTGTAACTGTATAAACTACG
Bur
11800 11810 11820 11830 11840 11850 11860 11870
11880
Col
TAACGAACCTTTGAACGCAGAGTGAATGTGAGTCTCTGTGACACGACTTAAAGCTTAATCAGAAGCAGATTATTGGACCTTATGGAGACT
Bur
11890 11900 11910 11920 11930 11940 11950 11960
11970
Col
TTATCAAGATTAGCTAATGAAGGTTACTATATATGAAACTTTGAAGTAATTGTTTGCAGCCTTTTGGGATCAATAAACCATAAAAGCATT
Bur
11980 11990 12000 12010 12020 12030 12040 12050
12060
Col
GGTTTTGTTTTCTCTATCTATATCCAATTCCGGAAAGTAGAAAACTGGATTAGTAAAAATCATATTCACACATTGCGAAGAAAAACTATG
Bur
T....
Snp 58
12070 12080 12090 12100 12110 12120 12130 12140

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12150

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TGCGCGCGGATACGTTGGGAAAATCTGCGCATGGTTTAAAGTTTTGCTTTCAGTCAATTATAATTCGTTTTTTATACTCCCTCTGTTCCA
Bur
....................................................................................................

            12160     12170     12180     12190     12200     12210     12220     12230
12240

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AGATACTTGATATTTTGGGTTTTTGCACAAGAATTAAGAAAAGTAACTTTTATATTTTTAATTATTCTTTTAGTTAGTTTAATAATATTA
Bur
..................A.................................................................................

            12250     12260     12270     12280     12290     12300     12310     12320
12330

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ATTTTACTTCTCTCATTTCATTATTGGTTACAAACAAAAATAATAATGATAGTTTTTCAAAACATCAATTTTGGTGGAACAAATAAAAAA
Bur
....................................................................................................

            12340     12350     12360     12370     12380     12390     12400     12410
12420

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ACTCAAAATATCAAATAACTTGAAACAGAGGGAGTAGTTAATTAAAAAAAGATATTTCACACTTTGACTTGGCGAAGCCTCATAACAATG
Bur
....................................................................................................

            12430     12440     12450     12460     12470     12480     12490     12500
12510

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AAGTTATGTATGAACTATATATGAAGTTAGAAACAATGGAAAACAGCTTGTAAATATTCATTGTTGTATATATGTTTTTTTGGGTCAATT
Bur
....................................................................................................

            12520     12530     12540     12550     12560     12570     12580     12590
12600

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TGGTGCATGAACAAAAATAAAAACGTAGATGAAAACCGGATATTTTGGTGTTAACATTTGCATTTGAACTTCGTGAAAGACGGATAAAAG
Bur
....................................................................................................

            12610     12620     12630     12640     12650     12660     12670     12680
12690

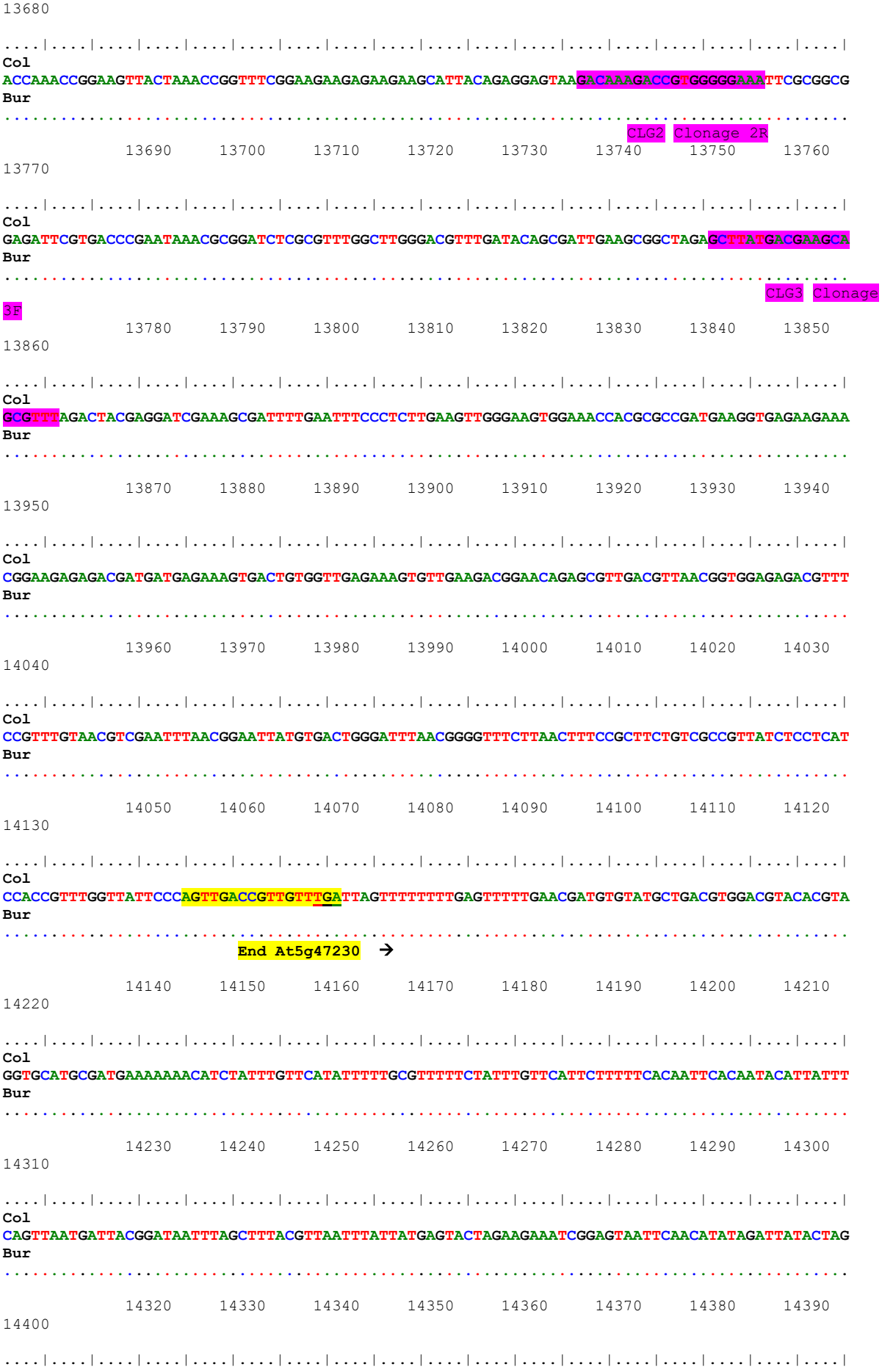
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CTCATTTTTGTTCTTTATTATATGGCTGCTATTAGTACACAGAGTTGAACTTTAGAATACTAAAAATCTCGACATCTTTTATTTTATTTT
Bur
....................................................................................................

            12700     12710     12720     12730     12740     12750     12760     12770
12780

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TGTCAAGCATCGACATCTTTTCTGTTCAAGAAAACGACCGCAATAGTCGAATAATATAACTCTTGGACTAGTTAATATATATTTGCGATA
Bur
....................................................................................................
                                  CLG1: Clonage 1F
            12790     12800     12810     12820     12830     12840     12850     12860
12870

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GATTTTCGATCTCACTTATATCTTATAACCAAGAGACAAAAACAATATTGCAGTCAAGTACAAAACGAAAACAATCACAATGTCGACTAT
```


Bur
12880 12890 12900 12910 12920 12930 12940 12950
12960
Col
AGATGAGTCGGTCATTCGATCCAACGGCTCTGAGTCCACGAAACACGCAACCAAGTGGTGCTCTCTTTTACACCAAATCATATTATAAAA
Bur
T..
CLG2: Clonage 2F
12970 12980 12990 13000 13010 13020 13030 13040
13050
Col
AACTTAAAAGAAAGAGAGGATGGTTCGTTGGCTCCTTCTTGTTCCTTAATTAATTCAAATTATATTCATCACCTCCATTGAATAAGTCCA
Bur
13060 13070 13080 13090 13100 13110 13120 13130
13140
Col
TTTCACGACAAAGTCACCAATGCTTCTTTTACATGTATATATACTTCTTTCCACTCCCTCTTCTCTACTCAAATCAAATCTTCTTCCTTC
Bur
13150 13160 13170 13180 13190 13200 13210 13220
13230
Col
TCTGTTTTCTTAAGCTTTTTGAAAATTTTATCAATGGCGACTCCTAACGAAGTATCTGCACTTTGGTTCATCGAGAAACATCTACTCGAC
Bur
Start At5g47230
13240 13250 13260 13270 13280 13290 13300 13310
13320
Col
GAGGCTTCTCCTGTGGCTACAGATCCATGGATGAAGCACGAATCATCATCAGCAACAGAATCTAGCTCTGACTCTTCTTCTATCATCTTC
Bur
C G
13330 13340 13350 13360 13370 13380 13390 13400
13410
Col
GGATCATCGTCCTCTTCTTTCGCCCCAATTGATTTCTCTGAATCCGTATGCAAACCTGAAATCATCGATCTCGATACTCCCAGATCTATG
Bur
CLG2: Clonage 1R
13420 13430 13440 13450 13460 13470 13480 13490
13500
Col
GAATTTCTATCGATTCCATTTGAATTTGACTCAGAAGTTTCTGTTTCTGATTTCGATTTTAAACCTTCTAATCAAAATCAAAATCAGTTT
Bur
13510 13520 13530 13540 13550 13560 13570 13580
13590
Col
GAACCGGAGCTTAAATCTCAAATTCGTAAACCGCCATTGAAGATTTCGCTTCCAGCTAAAACAGAGTGGATTCAATTCGCAGCTGAAAAC
Bur
13600 13610 13620 13630 13640 13650 13660 13670


13680
Col
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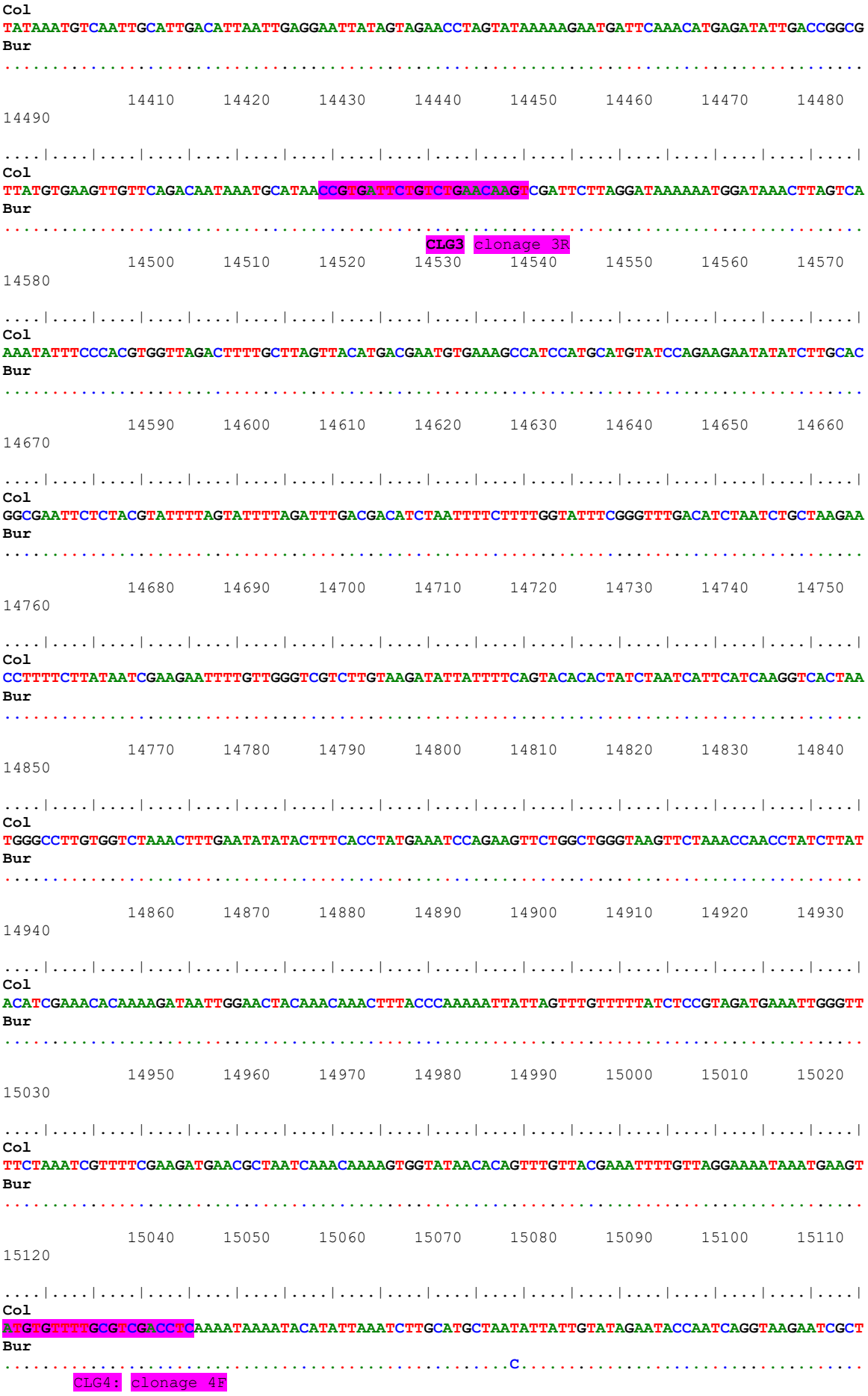
Bur
CLG2
Clonage 2R
13690
13700
13710
13720
13730
13740
13750
13760
13770
Col
GAGATTCGTGACCCGAATAAACGCGGATCTCGCGTTTGGCTTGGGACGTTTGATACAGCGATTGAAGCGGCTAGAGCTTATGACGAAGCA
Bur
CLG3
Clonage 3F
13780
13790
13800
13810
13820
13830
13840
13850
13860
Col
GCGTTTAGACTACGAGGATCGAAAGCGATTTTGAATTTCCCTCTTGAAGTTGGGAAGTGGAAACCACGCGCCGATGAAGGTGAGAAGAAA
Bur
13870
13880
13890
13900
13910
13920
13930
13940
13950
Col
CGGAAGAGAGACGATGATGAGAAAGTGACTGTGGTTGAGAAAGTGTTGAAGACGGAACAGAGCGTTGACGTTAACGGTGGAGAGACGTTT
Bur
13960
13970
13980
13990
14000
14010
14020
14030
14040
Col
CCGTTTGTAACGTCGAATTTAACGGAATTATGTGACTGGGATTTAACGGGGTTTCTTAACTTTCCGCTTCTGTCGCCGTTATCTCCTCAT
Bur
14050
14060
14070
14080
14090
14100
14110
14120
14130
Col
CCACCGTTTGGTTATTCCCAGTTGACCGTTGTTTGATTAGTTTTTTTTGAGTTTTTGAACGATGTGTATGCTGACGTGGACGTACACGTA
Bur
End At5g47230
14140
14150
14160
14170
14180
14190
14200
14210
14220
Col
GGTGCATGCGATGAAAAAAACATCTATTTGTTCATATTTTTGCGTTTTTCTATTTGTTCATTCTTTTTCACAATTCACAATACATTATTT
Bur
14230
14240
14250
14260
14270
14280
14290
14300
14310
Col
CAGTTAATGATTACGGATAATTTAGCTTTACGTTAATTTATTATGAGTACTAGAAGAAATCGGAGTAATTCAACATATAGATTATACTAG
Bur
14320
14330
14340
14350
14360
14370
14380
14390
14400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Bur
14410 14420 14430 14440 14450 14460 14470 14480
14490
Col
TTATGTGAAGTTGTTCAGACAATAAATGCATAACCGTGATTCTGTCTGAACAAGTCGATTCTTAGGATAAAAAATGGATAAACTTAGTCA
Bur
CLG3 clonage 3R
14500 14510 14520 14530 14540 14550 14560 14570
14580
Col
AAATATTTCCCACGTGGTTAGACTTTTGCTTAGTTACATGACGAATGTGAAAGCCATCCATGCATGTATCCAGAAGAATATATCTTGCAC
Bur
14590 14600 14610 14620 14630 14640 14650 14660
14670
Col
GGCGAATTCTCTACGTATTTTAGTATTTTAGATTTGACGACATCTAATTTTCTTTTGGTATTTCGGGTTTGACATCTAATCTGCTAAGAA
Bur
14680 14690 14700 14710 14720 14730 14740 14750
14760
Col
CCTTTTCTTATAATCGAAGAATTTTGTTGGGTCGTCTTGTAAGATATTATTTTCAGTACACACTATCTAATCATTCATCAAGGTCACTAA
Bur
14770 14780 14790 14800 14810 14820 14830 14840
14850
Col
TGGGCCTTGTGGTCTAAACTTTGAATATATACTTTCACCTATGAAATCCAGAAGTTCTGGCTGGGTAAGTTCTAAACCAACCTATCTTAT
Bur
14860 14870 14880 14890 14900 14910 14920 14930
14940
Col
ACATCGAAACACAAAAGATAATTGGAACTACAAACAAACTTTACCCAAAAATTATTAGTTTGTTTTTATCTCCGTAGATGAAATTGGGTT
Bur
14950 14960 14970 14980 14990 15000 15010 15020
15030
Col
TTCTAAATCGTTTTCGAAGATGAACGCTAATCAAACAAAAGTGGTATAACACAGTTTGTTACGAAATTTTGTTAGGAAAATAAATGAAGT
Bur
15040 15050 15060 15070 15080 15090 15100 15110
15120
Col
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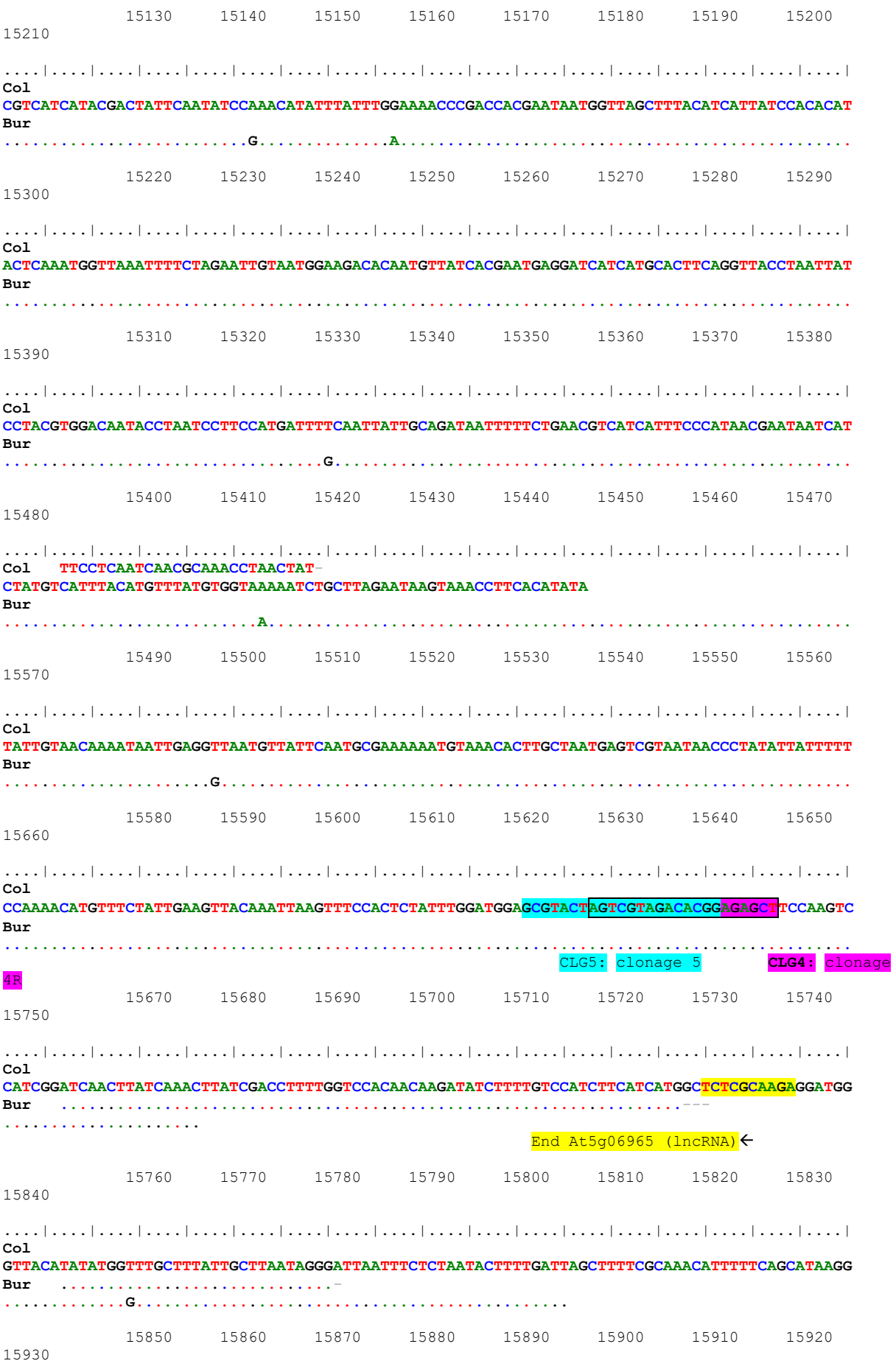
Bur
C
CLG4: clonage 4F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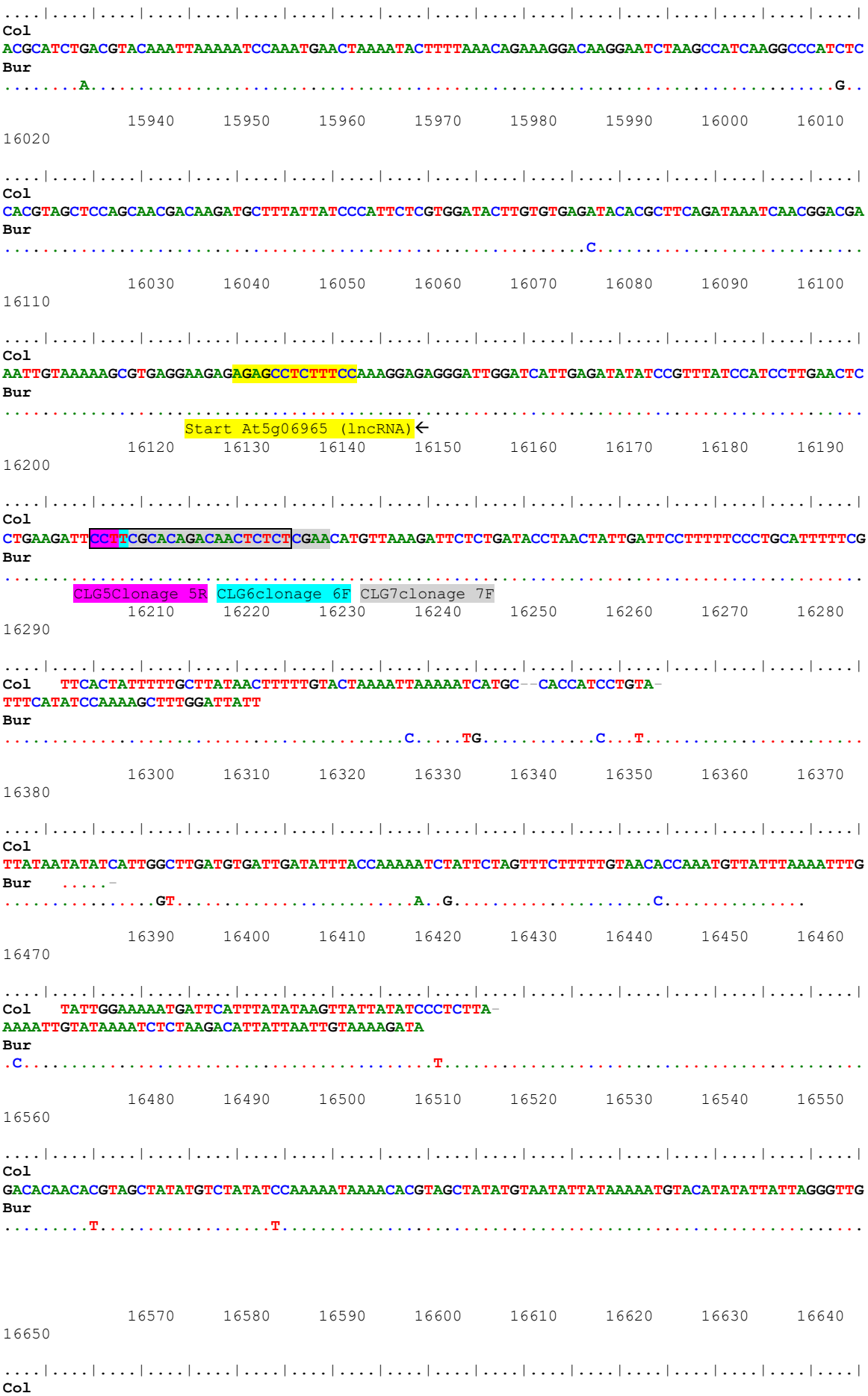
15210
Col
CGTCATCATACGACTATTCAATATCCAAACATATTTATTTGGAAAACCCGACCACGAATAATGGTTAGCTTTACATCATTATCCACACAT
Bur
15220 15230 15240 15250 15260 15270 15280 15290
15300
Col
ACTCAAATGGTTAAATTTTCTAGAATTGTAATGGAAGACACAATGTTATCACGAATGAGGATCATCATGCACTTCAGGTTACCTAATTAT
Bur
15310 15320 15330 15340 15350 15360 15370 15380
15390
Col
CCTACGTGGACAATACCTAATCCTTCCATGATTTTCAATTATTGCAGATAATTTTTCTGAACGTCATCATTTCCCATAACGAATAATCAT
Bur
15400 15410 15420 15430 15440 15450 15460 15470
15480
Col TTCCTCAATCAACGCAAACCTAACTAT
CTATGTCATTTACATGTTTATGTGGTAAAAATCTGCTTAGAATAAGTAAACCTTCACATATA
Bur
15490 15500 15510 15520 15530 15540 15550 15560
15570
Col
TATTGTAACAAAATAATTGAGGTTAATGTTATTCAATGCGAAAAAATGTAAACACTTGCTAATGAGTCGTAATAACCCTATATTATTTTT
Bur
15580 15590 15600 15610 15620 15630 15640 15650
15660
Col
CCAAAACATGTTTCTATTGAAGTTACAAATTAAGTTTCCACTCTATTTGGATGGAGCGTACTAGTCGTAGACACGGAGAGCTTCCAAGTC
Bur
CLG5: clonage 5 CLG4: clonage 4R
15670 15680 15690 15700 15710 15720 15730 15740
15750
Col
CATCGGATCAACTTATCAAACTTATCGACCTTTTGGTCCACAACAAGATATCTTTTGTCCATCTTCATCATGGCTCTCGCAAGAGGATGG
Bur
End At5g06965 (lncRNA)
15760 15770 15780 15790 15800 15810 15820 15830
15840
Col
GTTACATATATGGTTTGCTTTATTGCTTAATAGGGATTAATTTCTCTAATACTTTTGATTAGCTTTTCGCAAACATTTTTCAGCATAAGG
Bur
15850 15860 15870 15880 15890 15900 15910 15920
15930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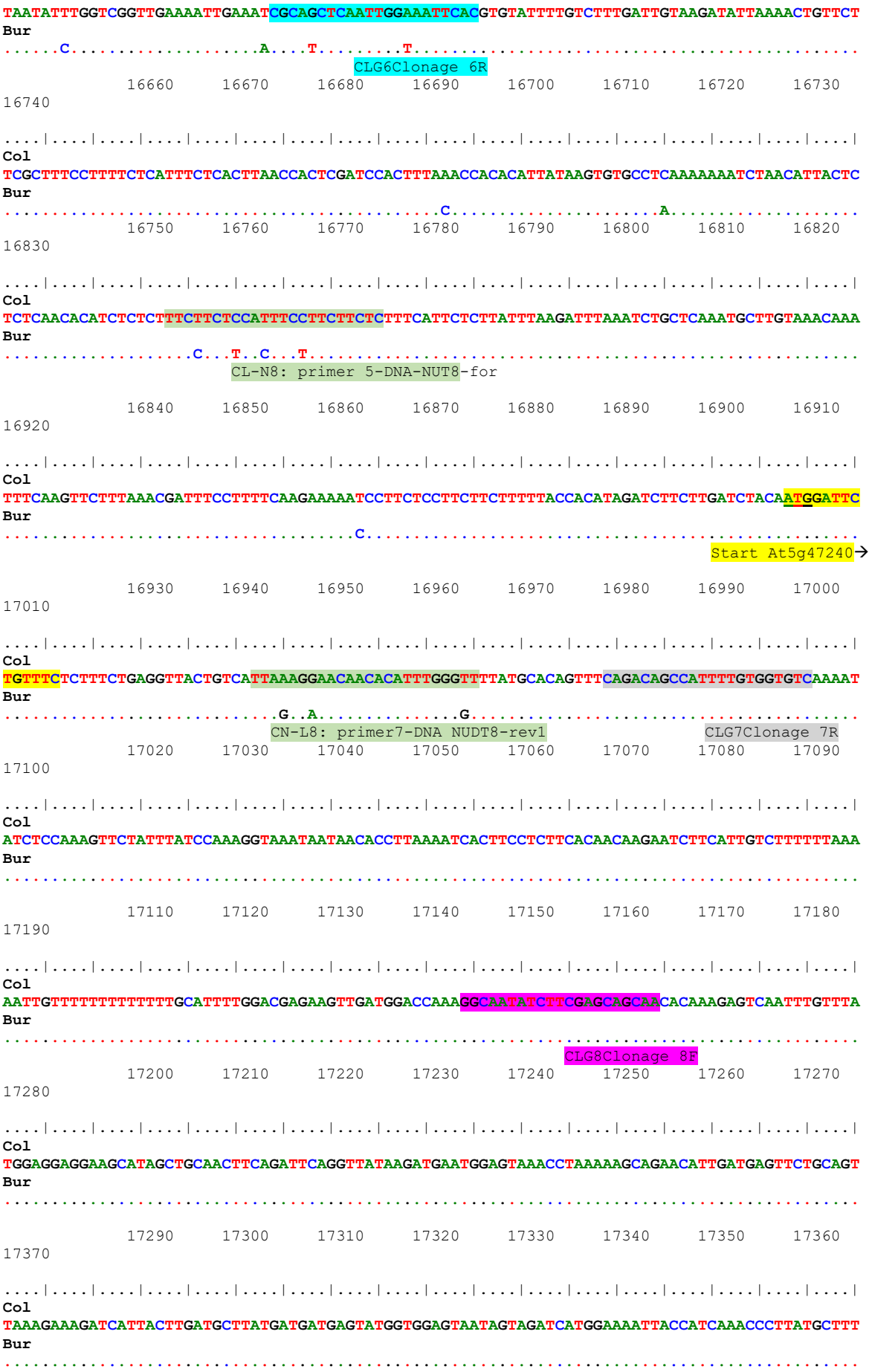
Bur
15940 15950 15960 15970 15980 15990 16000 16010
16020
Col
CACGTAGCTCCAGCAACGACAAGATGCTTTATTATCCCATTCTCGTGGATACTTGTGTGAGATACACGCTTCAGATAAATCAACGGACGA
Bur
16030 16040 16050 16060 16070 16080 16090 16100
16110
Col
AATTGTAAAAAGCGTGAGGAAGAGAGAGCCTCTTTCCAAAGGAGAGGGATTGGATCATTGAGATATATCCGTTTATCCATCCTTGAACTC
Bur
Start At5g06965 (lncRNA)
16120 16130 16140 16150 16160 16170 16180 16190
16200
Col
CTGAAGATTCCTTCGCACAGACAACTCTCTCGAACATGTTAAAGATTCTCTGATACCTAACTATTGATTCCTTTTTCCCTGCATTTTTCG
Bur
CLG5Clonage 5R
CLG6clonage 6F
CLG7clonage 7F
16210 16220 16230 16240 16250 16260 16270 16280
16290
Col TTCACTATTTTTGCTTATAACTTTTTGTACTAAAATTAAAAATCATGC--CACCATCCTGTA-
TTTCATATCCAAAAGCTTTGGATTATT
Bur
16300 16310 16320 16330 16340 16350 16360 16370
16380
Col
TTATAATATATCATTGGCTTGATGTGATTGATATTTACCAAAAATCTATTCTAGTTTCTTTTTGTAACACCAAATGTTATTTAAAATTTG
Bur -
16390 16400 16410 16420 16430 16440 16450 16460
16470
Col TATTGGAAAAATGATTCATTTATATAAGTTATTATATCCCTCTTA-
AAAATTGTATAAAATCTCTAAGACATTATTAATTGTAAAAGATA
Bur
16480 16490 16500 16510 16520 16530 16540 16550
16560
Col
GACACAACACGTAGCTATATGTCTATATCCAAAAATAAAACACGTAGCTATATGTAATATTATAAAAATGTACATATATTATTAGGGTTG
Bur
16570 16580 16590 16600 16610 16620 16630 16640
16650
Col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Bur
CLG6Clonage 6R
16660 16670 16680 16690 16700 16710 16720 16730
16740
Col
TCGCTTTCCTTTTCTCATTTCTCACTTAACCACTCGATCCACTTTAAACCACACATTATAAGTGTGCCTCAAAAAAATCTAACATTACTC
Bur
16750 16760 16770 16780 16790 16800 16810 16820
16830
Col
TCTCAACACATCTCTCTTTCTTCTCCATTTCCTTCTTCTCTTTCATTCTCTTATTTAAGATTTAAATCTGCTCAAATGCTTGTAAACAAA
Bur
CL-N8: primer 5-DNA-NUT8-for
16840 16850 16860 16870 16880 16890 16900 16910
16920
Col
TTTCAAGTTCTTTAAACGATTTCCTTTTCAAGAAAAATCCTTCTCCTTCTTCTTTTTACCACATAGATCTTCTTGATCTACAATGGATTC
Bur
Start At5g47240
16930 16940 16950 16960 16970 16980 16990 17000
17010
Col
TGTTTCTCTTTCTGAGGTTACTGTCATTAAAGGAACAACACATTTGGGTTTTATGCACAGTTTCAGACAGCCATTTTGTGGTGTCAAAAT
Bur
CN-L8: primer7-DNA NUDT8-rev1
CLG7Clonage 7R
17020 17030 17040 17050 17060 17070 17080 17090
17100
Col
ATCTCCAAAGTTCTATTTATCCAAAGGTAAATAATAACACCTTAAAATCACTTCCTCTTCACAACAAGAATCTTCATTGTCTTTTTTAAA
Bur
17110 17120 17130 17140 17150 17160 17170 17180
17190
Col
AATTGTTTTTTTTTTTTTGCATTTTGGACGAGAAGTTGATGGACCAAAGGCAATATCTTCGAGCAGCAACACAAAGAGTCAATTTGTTTA
Bur
CLG8Clonage 8F
17200 17210 17220 17230 17240 17250 17260 17270
17280
Col
TGGAGGAGGAAGCATAGCTGCAACTTCAGATTCAGGTTATAAGATGAATGGAGTAAACCTAAAAAGCAGAACATTGATGAGTTCTGCAGT
Bur
17290 17300 17310 17320 17330 17340 17350 17360
17370
Col
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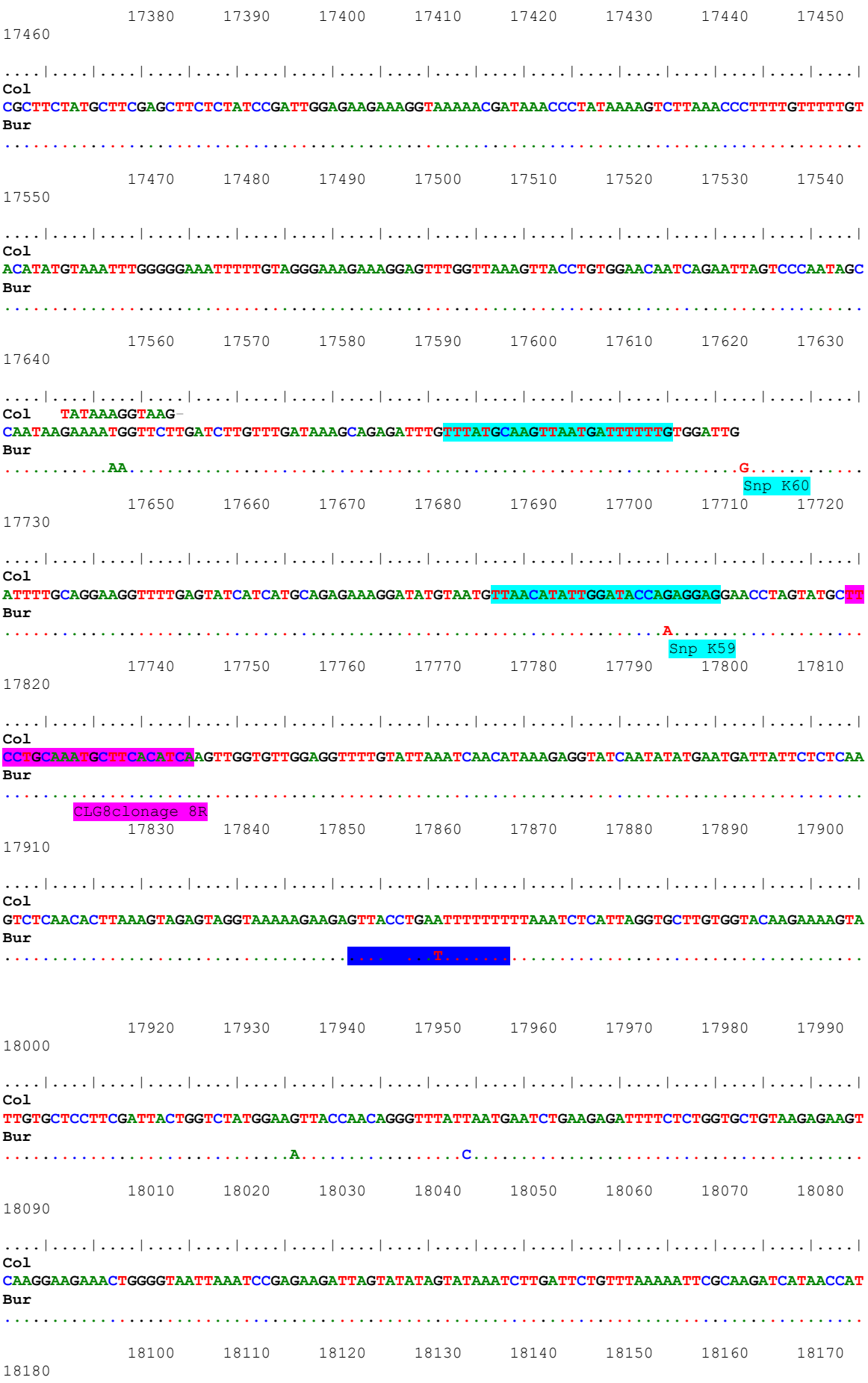
Bur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Bur
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Col
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Bur
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17640
Col TATAAAGGTAAG
CAATAAGAAAATGGTTCTTGATCTTGTTTGATAAAGCAGAGATTTGTTTATGCAAGTTAATGATTTTTTGTGGATTG
Bur
AA G
Snp K60
17650 17660 17670 17680 17690 17700 17710 17720
17730
Col
ATTTTGCAGGAAGGTTTTGAGTATCATCATGCAGAGAAAGGATATGTAATGTTAACATATTGGATACCAGAGGAGGAACCTAGTATGCTT
Bur
A
Snp K59
17740 17750 17760 17770 17780 17790 17800 17810
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Col
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Bur
CLG8clonage 8R
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17910
Col
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Bur
T
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18000
Col
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Bur
A C
18010 18020 18030 18040 18050 18060 18070 18080
18090
Col
CAAGGAAGAAACTGGGGTAATTAAATCCGAGAAGATTAGTATATAGTATAAATCTTGATTCTGTTTAAAAATTCGCAAGATCATAACCAT
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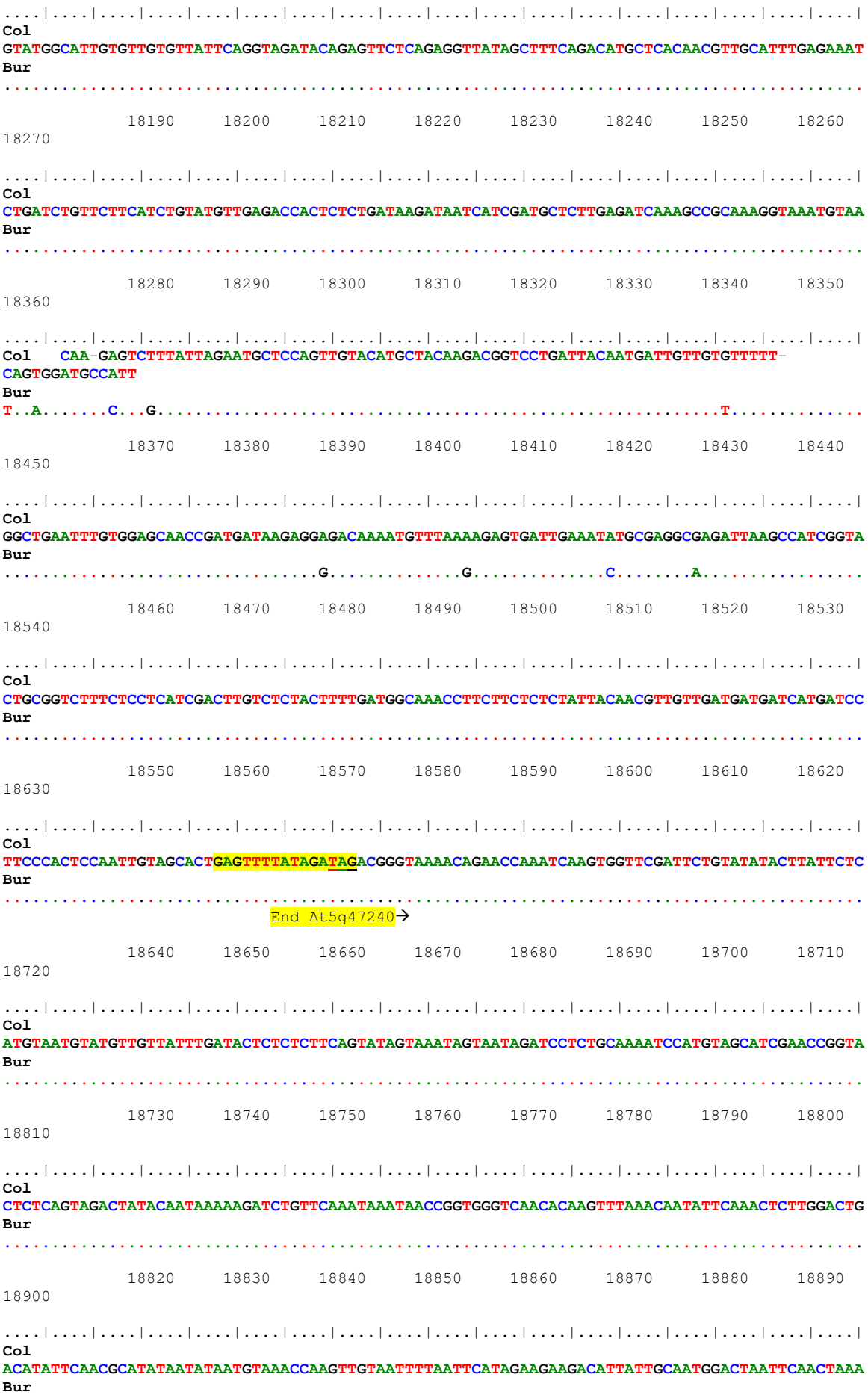
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Col
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Bur
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Col CAA-GAGTCTTTATTAGAATGCTCCAGTTGTACATGCTACAAGACGGTCCTGATTACAATGATTGTTGTGTTTTT-
CAGTGGATGCCATT
Bur
T..A.....C...G.....T.....
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18450
Col
GGCTGAATTTGTGGAGCAACCGATGATAAGAGGAGACAAAATGTTTAAAAGAGTGATTGAAATATGCGAGGCGAGATTAAGCCATCGGTA
Bur
.....G.....G.....C.....A.....
18460 18470 18480 18490 18500 18510 18520 18530
18540
Col
CTGCGGTCTTTCTCCTCATCGACTTGTCTCTACTTTTGATGGCAAACCTTCTTCTCTCTATTACAACGTTGTTGATGATGATCATGATCC
Bur
18550 18560 18570 18580 18590 18600 18610 18620
18630
Col
TTCCCACTCCAATTGTAGCACTGAGTTTTATAGATAGACGGGTAAAACAGAACCAAATCAAGTGGTTCGATTCTGTATATACTTATTCTC
Bur
End At5g47240→
18640 18650 18660 18670 18680 18690 18700 18710
18720
Col
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Bur
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18810
Col
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Bur
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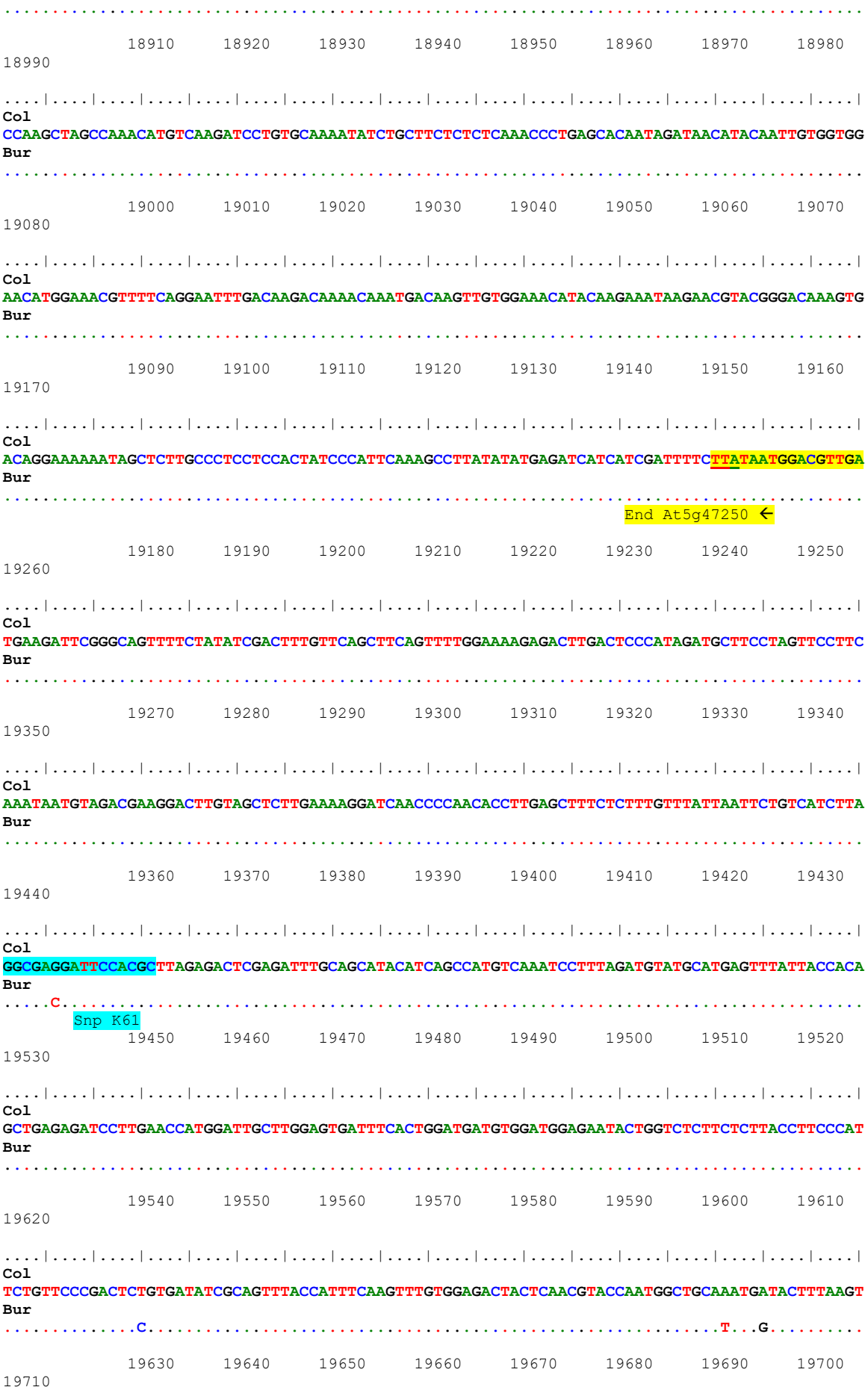
Bur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Col
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Bur
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Bur
End At5g47250
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Col
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Bur
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Col
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Bur
19360 19370 19380 19390 19400 19410 19420 19430 19440
Col
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Bur
Snp K61
19450 19460 19470 19480 19490 19500 19510 19520 19530
Col
GCTGAGAGATCCTTGAACCATGGATTGCTTGGAGTGATTTCACTGGATGATGTGGATGGAGAATACTGGTCTCTTCTCTTACCTTCCCAT
Bur
19540 19550 19560 19570 19580 19590 19600 19610 19620
Col
TCTGTTCCCGACTCTGTGATATCGCAGTTTACCATTTCAAGTTTGTGGAGACTACTCAACGTACCAATGGCTGCAAATGATACTTTAAGT
Bur
19630 19640 19650 19660 19670 19680 19690 19700 19710

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....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CCTTCTAGATATATACCCTGCGTCATCCCTGCCAATCTTGTGCTTCCTAGAAACTCTTCCAAAACAGAATCGTTATTCACAGTAACGGTC
Bur
.....A.......G.....................................................................................

             19720     19730     19740     19750     19760     19770     19780     19790     19800

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Col
AAAAGTTGTAAACCCTTCAACTGCTCCAAGATCTTGAGCAAGCAGCAATCTAATGCAGCAGCAGAACCATAAAATCTGAGAACCTGCAAC
Bur
.....................................................................T.....................

             19810     19820     19830     19840     19850     19860     19870     19880     19890

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Col
TTTTGTAATTCTGAAATCAGACCGACGCTTCGAAGATTGGAAGTGGACTCCAAATTCAAGTGAATCAATTTACTCAAGACTCCTAAACCT
Bur
.....................................................................................

             19900     19910     19920     19930     19940     19950     19960     19970     19980

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TCCGGCAGATGCTTTATACTCGTCCCTGATAAGTTGAGAAGCCGCAAAGAAACCAACGCCGAGATTCCTTTTGGCAACTCGGTGATTTGG
Bur
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             19990     20000     20010     20020     20030     20040     20050     20060     20070

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Col
AAGTTCCAAGATAGATCCAAAACCACCAGAGTCGACATGACCAGAAAGAATTTACCAACAATATCTACCAACCTGTTATTTTGAAGGAAC
Bur
.....................................................................................

             20080     20090     20100     20110     20120     20130     20140     20150     20160

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AAGGTTACAAGATTTGTCTGGTCAGGAAATTCAGGATCGTCTGGTATGTTCTTAATCTCATTGTTGAACAGAGACATCTTTGTCACAGTT
Bur
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             20170     20180     20190     20200     20210     20220     20230     20240     20250

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Col
GTCCAATCGGTGACATCAGGCAGTTGGCTTAAACCAGCATCTGTTTTCACAACATATCTTTCTCCATCCCTAAATTCAGATACTATCCAC
Bur
.....................................................................................

             20260     20270     20280     20290     20300     20310     20320     20330     20340

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Col
AATGCCATATCACGGATCATATCATGCATATACACTTTCTTATTAGACTCTAATAACAAACCTGCCCCAACAAGATTATCGATGATCTCA
Bur
.....................................................................................

             20350     20360     20370     20380     20390     20400     20410     20420     20430

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
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Bur
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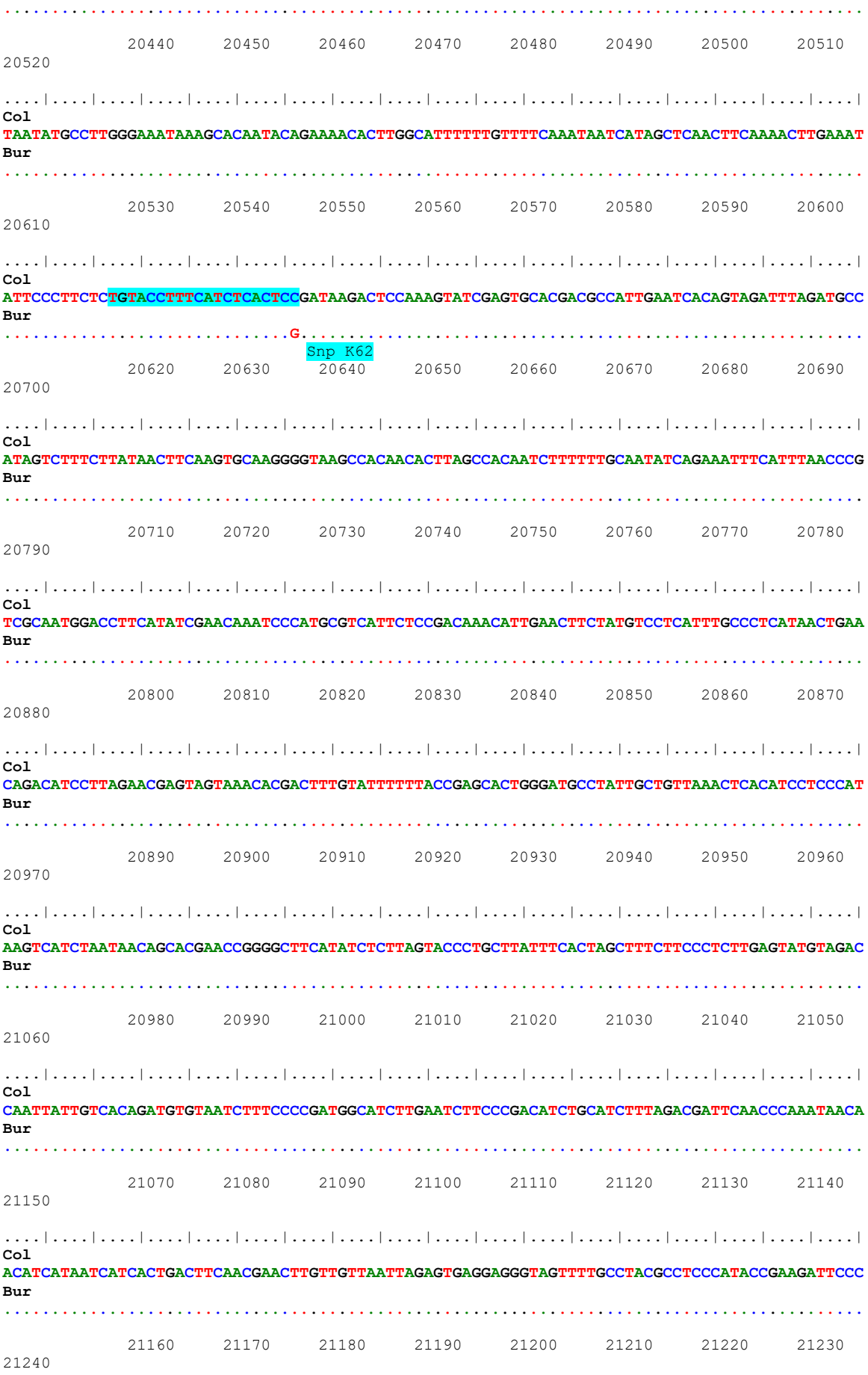
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Bur
20530 20540 20550 20560 20570 20580 20590 20600
20610
Col
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Bur
G
Snp K62
20620 20630 20640 20650 20660 20670 20680 20690
20700
Col
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Bur
20710 20720 20730 20740 20750 20760 20770 20780
20790
Col
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Bur
20800 20810 20820 20830 20840 20850 20860 20870
20880
Col
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Bur
20890 20900 20910 20920 20930 20940 20950 20960
20970
Col
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Bur
20980 20990 21000 21010 21020 21030 21040 21050
21060
Col
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Bur
21070 21080 21090 21100 21110 21120 21130 21140
21150
Col
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Bur
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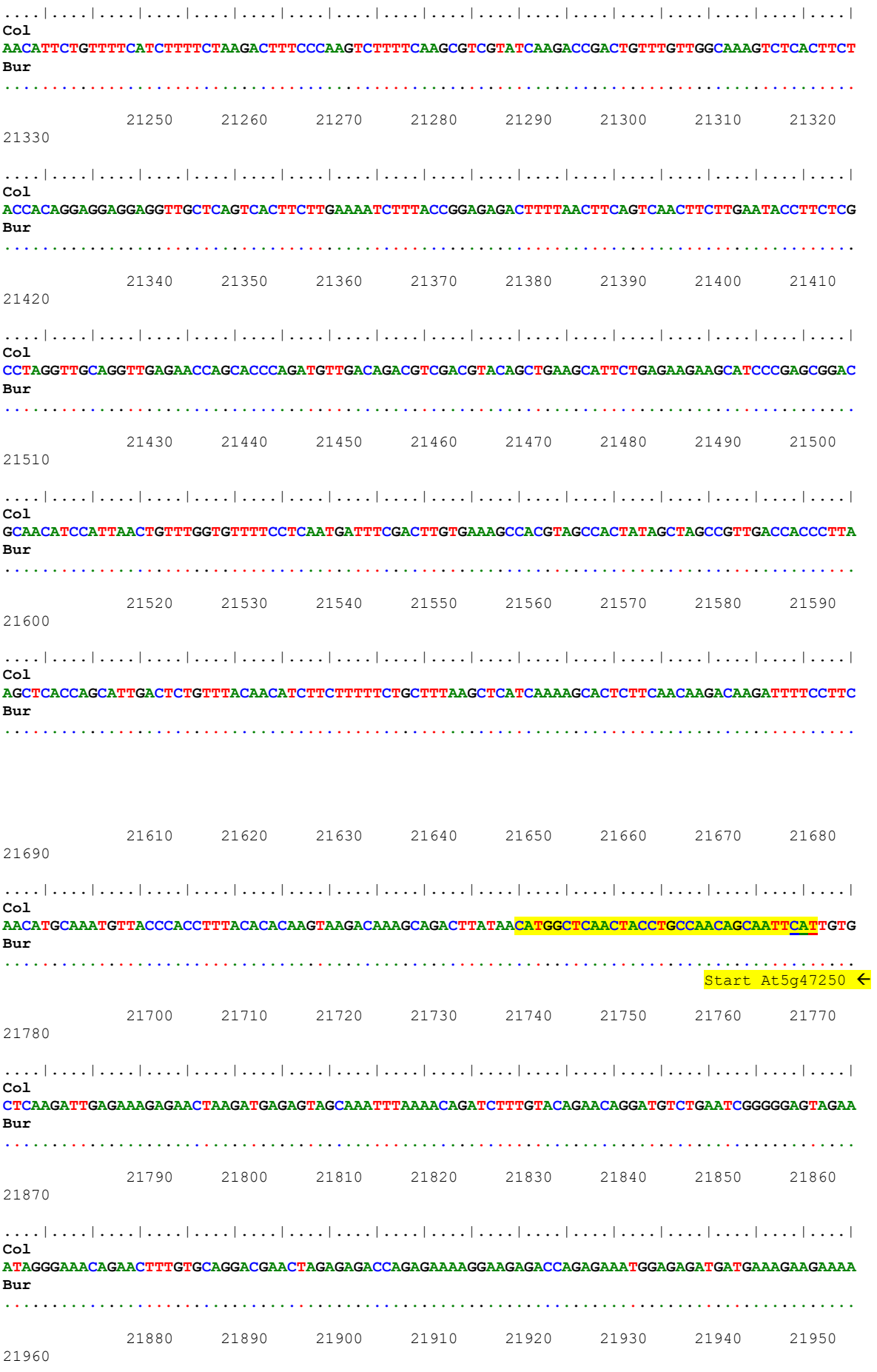
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Col
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Bur
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Col
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Bur
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Col
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Bur
21520 21530 21540 21550 21560 21570 21580 21590 21600
Col
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Bur
21610 21620 21630 21640 21650 21660 21670 21680 21690
Col
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Bur
Start At5g47250
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Col
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Bur
21790 21800 21810 21820 21830 21840 21850 21860 21870
Col
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Bur
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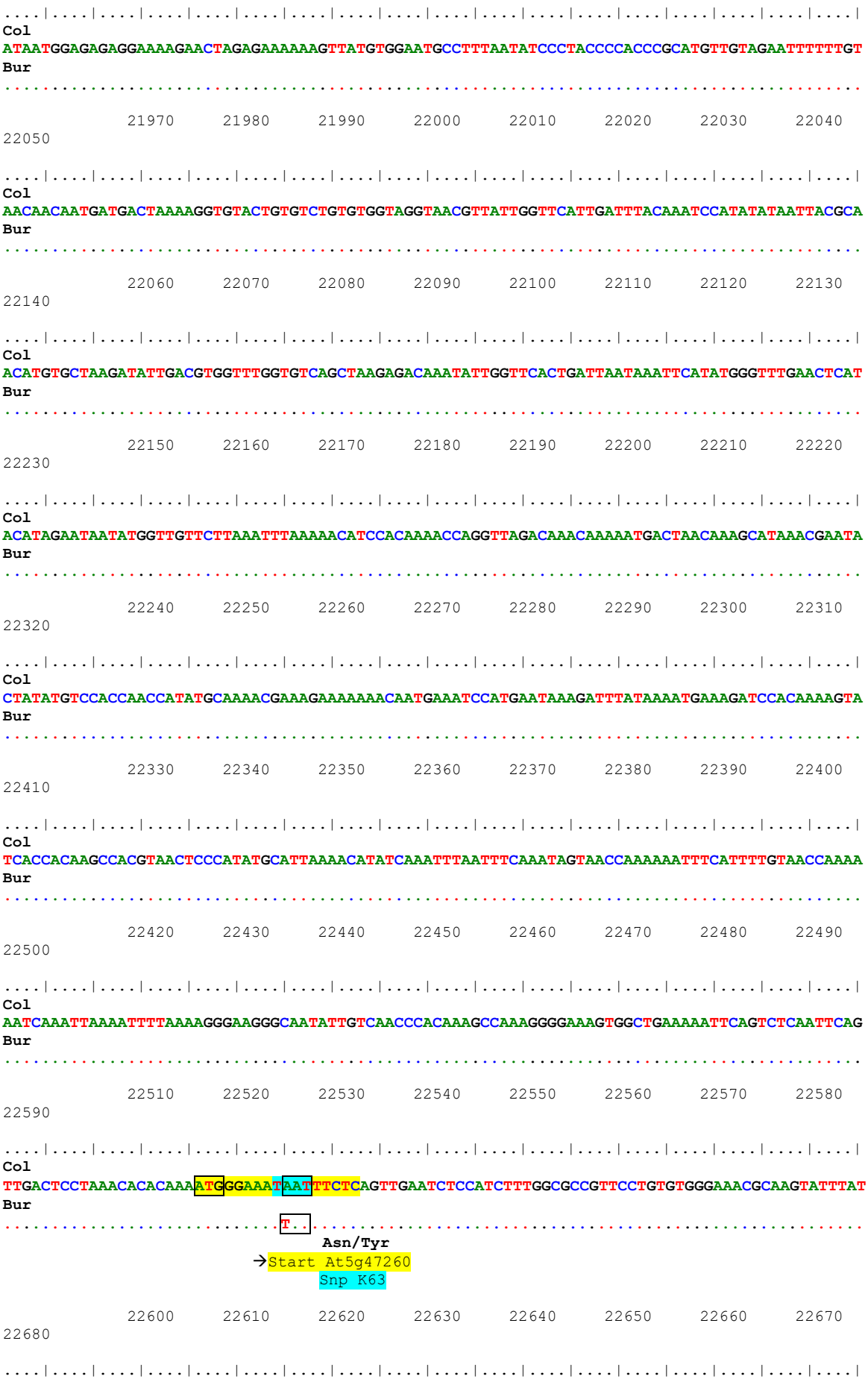
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22050
Col
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Bur
22060 22070 22080 22090 22100 22110 22120 22130
22140
Col
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Bur
22150 22160 22170 22180 22190 22200 22210 22220
22230
Col
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Bur
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22320
Col
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Bur
22330 22340 22350 22360 22370 22380 22390 22400
22410
Col
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Bur
22420 22430 22440 22450 22460 22470 22480 22490
22500
Col
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Bur
22510 22520 22530 22540 22550 22560 22570 22580
22590
Col
TTGACTCCTAAACACACAAAATGGGAAATAATTTCTCAGTTGAATCTCCATCTTTGGCGCCGTTCCTGTGTGGGAAACGCAAGTATTTAT
Bur
T..
Asn/Tyr
Start At5g47260
Snp K63
22600 22610 22620 22630 22640 22650 22660 22670
22680

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Col
ACAACCTGGAGAGAAATCTAGAGGCTTTGCATAAAGTAATGCAAGACCTCAACGCAATGAGAAACGATCTGTTGAAGAGGCTGTCGAAAG
Bur
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            22690     22700     22710     22720     22730     22740     22750     22760
22770

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Col
AGGAGGAGATAGGTCTACAAGGGCTACAAGAAGTCAAAGAGTGGATTTCAATGGTGGAAGAGATTGAACCTAAAGCCAATCGGCTGCTTG
Bur
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            22780     22790     22800     22810     22820     22830     22840     22850
22860

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Col
ATGAAAGTGTCTCTGAAATTCAGAGACTATCAAGGTACGGCTATTGTTCTCTGATCCCTGCGTCGACCTATCGTTACAGTGAAAAGGTAC
Bur
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            22870     22880     22890     22900     22910     22920     22930     22940
22950

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TTACGACTATGGAAGGAGTTGAAACTCTGAGATCTAAGGGAGTCTTCGAAGCTGTCGTTCACAGAGCTCTTCCGCCTCTTGTGATAAAGA
Bur
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            22960     22970     22980     22990     23000     23010     23020     23030
23040

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TGCCTCCAATTCAACTTACTGTTTCTCAAGCAAAGTTGCTTGATACGGCATGGGCTCGTCTAATGGACATAAATGTTGGGACTTTGGGTA
Bur
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            23050     23060     23070     23080     23090     23100     23110     23120
23130

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Col
TTTATGGTAGGGGTGGAGTAGGCAAAACCACCCTTCTTACTAAACTCAGAAACAAGTTACTTGTAGATGCATTTGGTCTTGTGATCTTTG
Bur
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            23140     23150     23160     23170     23180     23190     23200     23210
23220

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Col
TTGTTGTGGGGTTTGAAGAGGTCGAGAGCATACAGGATGAAATTGGTAAAAGATTAGGCCTCCAATGGAGAAGAGAAACCAAAGAGCGCA
Bur
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            23230     23240     23250     23260     23270     23280     23290     23300
23310

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Col
AGGCAGCTGAAATATTGGCAGTCTTAAAGGAGAAGAGATTTGTGTTGTTACTGGATGGCATACAGAGGGAATTGGATCTTGAGGAAATTG
Bur
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            23320     23330     23340     23350     23360     23370     23380     23390
23400

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Col
GAGTTCCTTTTCCCAGCCGAGATAATGGATGCAAAATTGTATTCACCACTCAATCTCTGGAAGCATGTGACGAAAGCAAGTGGGTTGATG
Bur
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            23410     23420     23430     23440     23450     23460     23470     23480
23490

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Col
CTAAGGTAGAAATTACATGTTTGAGCCCGGAAGAAGCATGGGATTTGTTTCAAGAGACTGTCGGAGAGAACACGTTGAGAAGTCATCAAG
Bur
.....................................................................................

            23500     23510     23520     23530     23540     23550     23560     23570
23580

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ACATACCTAAGCTCGCAAGAGTAGTTGCTAGTACATGCCGTGGTTTGCCCCTTGCTCTTAATCTCATTGGTGAGGCCATGTCAGGAAAAA
Bur
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            23590     23600     23610     23620     23630     23640     23650     23660
23670

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Col
GGACTGTACGCGAATGGCGTTACACAATTCATGTCTTGGCTTCATCCACAGCCGAATTTCCAGATATGGAAGATGGGACTCTTCCCATTT
Bur
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            23680     23690     23700     23710     23720     23730     23740     23750
23760

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Col
TAAAGTCTATCTATGATAATATGAGTGATGAGATCATCAGGTTATGCTTCCTTTATTGTGCTCTGTTTCCAGAAAATTTGGATATAGGAA
Bur
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            23770     23780     23790     23800     23810     23820     23830     23840
23850

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Col
AAGAAGATCTGGTAAACTACTGGATATGCGAGGGAATCCTTGCAAAAGAAGATAGAGAGGAAGCTGAGATCCAGGGATATGAAATTATCT
Bur
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            23860     23870     23880     23890     23900     23910     23920     23930
23940

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Col
GTGATTTGGTTAGGATGCGATTGTTGATGGAGAGTGGAAATGGAAATTGTGTAAAGATGCATGGTATGGTTCGTGAAATGGCCTTGTGGA
Bur
.....................................................................................

            23950     23960     23970     23980     23990     24000     24010     24020
24030

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TAGCATCTGAACACTTTGTTGTGGTAGGCGGTGAGAGAATACATCAGATGCTAAATGTCAATGACTGGCGGATGATTAGAAGAATGTCAG
Bur
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            24040     24050     24060     24070     24080     24090     24100     24110
24120

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TGACGTCTACTCAAATTCAGAATATATCAGATTCTCCCCAGTGTTCCGAGCTTACAACCCTGGTCTTTCGAAGAAACCGACACTTAAAAT
Bur
.....................................................................................

            24130     24140     24150     24160     24170     24180     24190     24200
24210

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Col
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GGATCTCAGGTGCTTTCTTTCAGTGGATGACAGGACTTGTAGTCTTGGATCTATCATTTAATAGAGAACTTGCTGAGTTGCCGGAAGAAG
Bur
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            24220     24230     24240     24250     24260     24270     24280     24290
24300

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Col
TTTCAAGCCTGGTGTTGCTGCGGTTTCTCAACTTATCATGGACATGTATAAAAGGATTGCCCCTTGGTTTAAAAGAGCTTAAGAGTTTGA
Bur
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            24310     24320     24330     24340     24350     24360     24370     24380
24390

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Col
TACACTTGGATTTGGATTACACATCTAATCTTCAAGAAGTTGACGTGATAGCAAGTTTATTGAATTTGCAAGTACTGAGATTATTTCATT
Bur
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            24400     24410     24420     24430     24440     24450     24460     24470
24480

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Col
CTGTTTCTATGGATCTCAAGTTAATGGAGGATATCCAACTTTTGAAGAGCCTGAAAGAGTTGAGTCTAACAGTGAGAGGATCTTCTGTTT
Bur
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            24490     24500     24510     24520     24530     24540     24550     24560
24570

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TGCAGCGGTTACTAAGTATCCAGCGATTAGCAAGTTCTATCCGACGTTTACATCTAACTGAAACTACAATAGTCGATGGAGGAATATTAT
Bur
.....................................................................................................

            24580     24590     24600     24610     24620     24630     24640     24650
24660

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CGTTGAATGCTATATTCAGTCTTTGTGAGCTTGATATTTTGGGATGTAATATCCTGGAGATAACCATTGATTGGAGATGCACCATCCAAA
Bur
.....................................................................................................

            24670     24680     24690     24700     24710     24720     24730     24740
24750

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GGGAAATAATTCCTCAATTCCAGAACATACGCACAATGACTATTCATCGGTGCGAATATCTTAGAGACTTGACATGGTTGCTATTAGCCC
Bur
.....................................................................................................

            24760     24770     24780     24790     24800     24810     24820     24830
24840

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CGTGTCTTGGTGAGCTAAGTGTATCTGAATGTCCGCAAATGGAAGAAGTAATAAGCAAAGATAAAGCTATGGCCAAGCTGGGTAATACGA
Bur
.....................................................................................................

            24850     24860     24870     24880     24890     24900     24910     24920
24930

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GTGAGCAGCCCTTTCAAAATCTAACTAAGCTCGTCTTAGATGGTTTACCTAAACTGGAGAGCATCTACTGGACTCCTCTACCCTTCCCAG
Bur
.....................................................................................................

            24940     24950     24960     24970     24980     24990     25000     25010
```

25020

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

Col

TTCTGGAATATTTAGTGATAAGGCGTTGTCCAGAGCTGAGAAGACTTCCATTCAACTCTGAGAGCACTATAGGAAATCAAGTTGAAACGA

Bur

.....

25030 25040 25050 25060 25070 25080 25090 25100 25110

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

Col

TAATTGAGGAGCAAGTGATAAAAATAGTTGAATGGGAGGATGAAGCTACAAAACAACGTTTCTCCCATTTCAATAACAGGTATCTTCTTC

Bur

.....

25120 25130 25140 25150 25160 25170 25180 25190 25200

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

Col

CTTATCCTACATTTTCTTCTCTATTTTTTTCGATAAGGTTTCTTAAATCTATAAAAGCTTGGCCATGAATAACTAGCATCTTCCCACGGG

Bur

.....

25210 25220 25230 25240 25250 25260 25270 25280 25290

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

Col

AATGTCACTTACCATCTTCTTAATTTTTTATATATTTCAATGTCACTCTTATTATTCATAGAATCTGGAAAGCTGATTTGATAAGATTTT

Bur

.....

25300 25310 25320 25330 25340 25350 25360 25370 25380

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

Col

GCAATGGTGATCCTTATTTTGATTGATCATTGTTTGTTCGAATTATGTAACAAACGAACGGAGTGCAGAGACTTTGTACAGATGGCTGAA

Bur

.....

25390 25400 25410 25420 25430 25440 25450 25460 25470

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

Col

GATCCGAAGATGGATGGTTTGACATCGGAGTCACATCCAATTCAAACCATAGACCTGGTCGGGACTACAGGAAGTGGAGAAACTGCCACT

Bur

.....

25480 25490 25500 25510 25520 25530 25540 25550 25560

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

Col

GCAAACAACATCCAAGGAAAGAAGGTGGTCCAATCGGGAACACACGCAACTGTTGTTACCATGGAATGCCAGACATATAAAGTTTTCACA

Bur

.....

25570 25580 25590 25600 25610 25620 25630 25640 25650

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

Col

CCAGATTGCCCCATCAACAATATGATTGACACTCCTGGTACGAATTTCCTTTTATGTTATACCTAACTAAATTATCATGCGTGGGAAGAA

Bur

.....

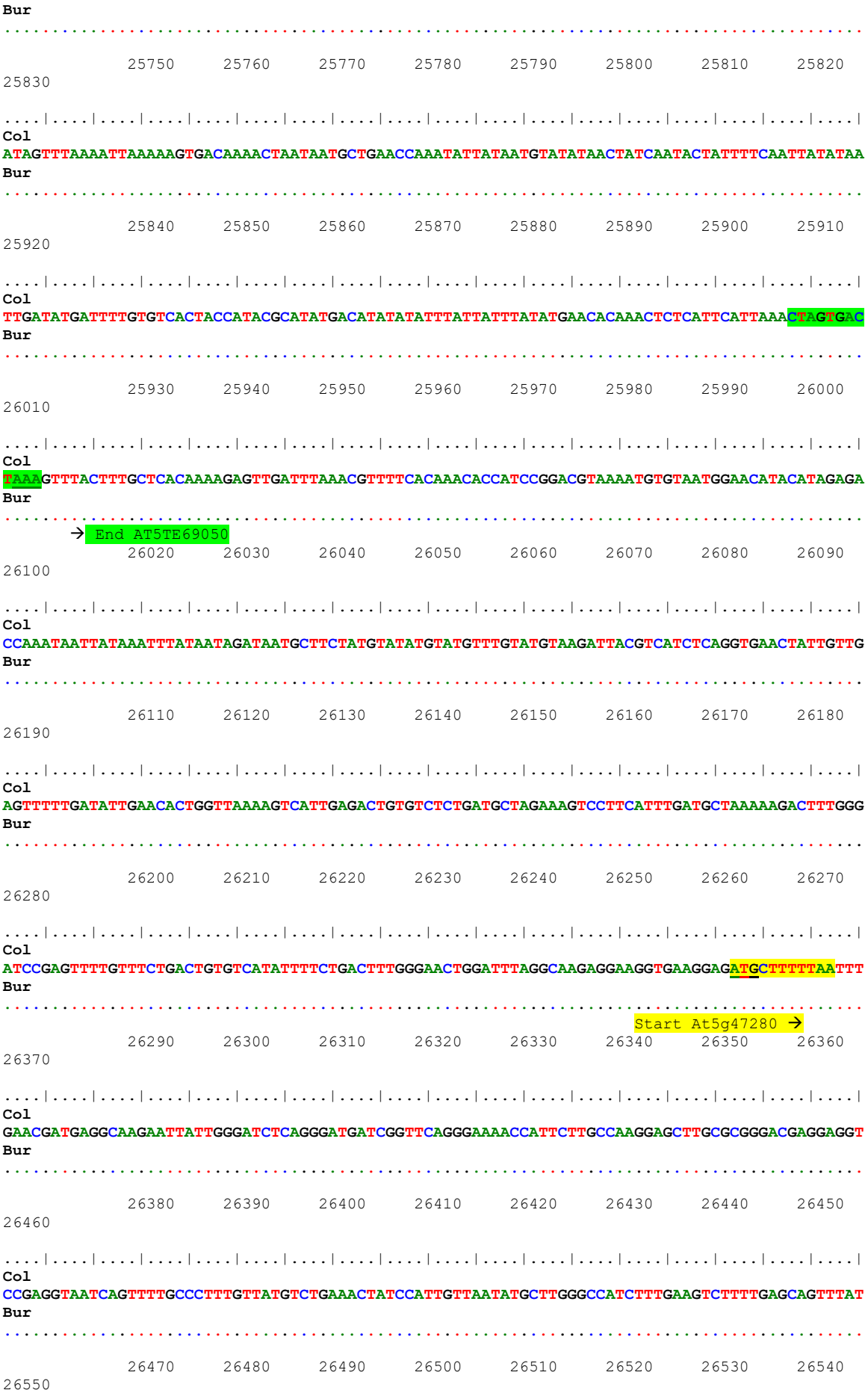
Start AT5TE69050→ End At5g47260→

25660 25670 25680 25690 25700 25710 25720 25730 25740

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

Col

AAAATACAAATTTTCTAATAAGTAAGGTTTGTACTTTACGTATACAATTAGAATAGGATCCACGTAAAATGTGTATTTCTAATTTTCTAT


Bur
25750 25760 25770 25780 25790 25800 25810 25820
25830
Col
ATAGTTTAAAATTAAAAAGTGACAAAACTAATAATGCTGAACCAAATATTATAATGTATATAACTATCAATACTATTTTCAATTATATAA
Bur
25840 25850 25860 25870 25880 25890 25900 25910
25920
Col
TTGATATGATTTTGTGTCACTACCATACGCATATGACATATATATTTATTATTTATATGAACACAAACTCTCATTCATTAAACTAGTGAC
Bur
25930 25940 25950 25960 25970 25980 25990 26000
26010
Col
TAAAGTTTACTTTGCTCACAAAAGAGTTGATTTAAACGTTTTCACAAACACCATCCGGACGTAAAATGTGTAATGGAACATACATAGAGA
Bur
End AT5TE69050
26020 26030 26040 26050 26060 26070 26080 26090
26100
Col
CCAAATAATTATAAATTTATAATAGATAATGCTTCTATGTATATGTATGTTTGTATGTAAGATTACGTCATCTCAGGTGAACTATTGTTG
Bur
26110 26120 26130 26140 26150 26160 26170 26180
26190
Col
AGTTTTTGATATTGAACACTGGTTAAAAGTCATTGAGACTGTGTCTCTGATGCTAGAAAGTCCTTCATTTGATGCTAAAAAGACTTTGGG
Bur
26200 26210 26220 26230 26240 26250 26260 26270
26280
Col
ATCCGAGTTTTGTTTCTGACTGTGTCATATTTTCTGACTTTGGGAACTGGATTTAGGCAAGAGGAAGGTGAAGGAGATGCTTTTTAATTT
Bur
Start At5g47280
26290 26300 26310 26320 26330 26340 26350 26360
26370
Col
GAACGATGAGGCAAGAATTATTGGGATCTCAGGGATGATCGGTTCAGGGAAAACCATTCTTGCCAAGGAGCTTGCGCGGGACGAGGAGGT
Bur
26380 26390 26400 26410 26420 26430 26440 26450
26460
Col
CCGAGGTAATCAGTTTTGCCCTTTGTTATGTCTGAAACTATCCATTGTTAATATGCTTGGGCCATCTTTGAAGTCTTTTGAGCAGTTTAT
Bur
26470 26480 26490 26500 26510 26520 26530 26540
26550

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....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GTTGTTGCTCAGTGGCATGTTTACTGGTTTATTTGGATGATCATGCATTTATCTCTGTATGTTCCATTGTGTCATGTTCATCTCCGGTGA
Bur
....................................................................................

            26560     26570     26580     26590     26600     26610     26620     26630
26640

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ACTGTTGATGAGTCGTATAGTTGAGTTCTTGATATTAGAATCTGTTAAGAGTCGGAGAGACTGTTCCTTTGATGCTAAAAAAGCTTTAAT
Bur
....................................................................................

            26650     26660     26670     26680     26690     26700     26710     26720
26730

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ACAGGCCATTTTGCGAACCGAGTTTTGTTTCTGACTGTGTCACAATCTCCCAATCTTGAGGAGCTGAGATCCCTTATACGGGATTTTCTT
Bur
....................................................................................

            26740     26750     26760     26770     26780     26790     26800     26810
26820

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ACTGGTCATGAGGCTGGCTTTGGTACCGCTCTTCCGGAATCCGTTGGTCATACACGGAAGCTAGTGATCCTTGATGATGTTAGGACAAGG
Bur
....................................................................................

            26830     26840     26850     26860     26870     26880     26890     26900
26910

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GAATCTCTAGACCAGCTGATGTTCAATATTCCTGGAACCACAACGCTTGTGGTCTCACAGTCTAAACTCGTAGATCCTAGAACCACCTAT
Bur
....................................................................................

            26920     26930     26940     26950     26960     26970     26980     26990
27000

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GATGTAGAGTTATTAAATGAACATGACGCAACATCTCTGTTCTGTCTCTCTGCTTTCAACCAGAAATCAGTTCCTTCAGGGTTCAGCAAA
Bur
....................................................................................

            27010     27020     27030     27040     27050     27060     27070     27080
27090

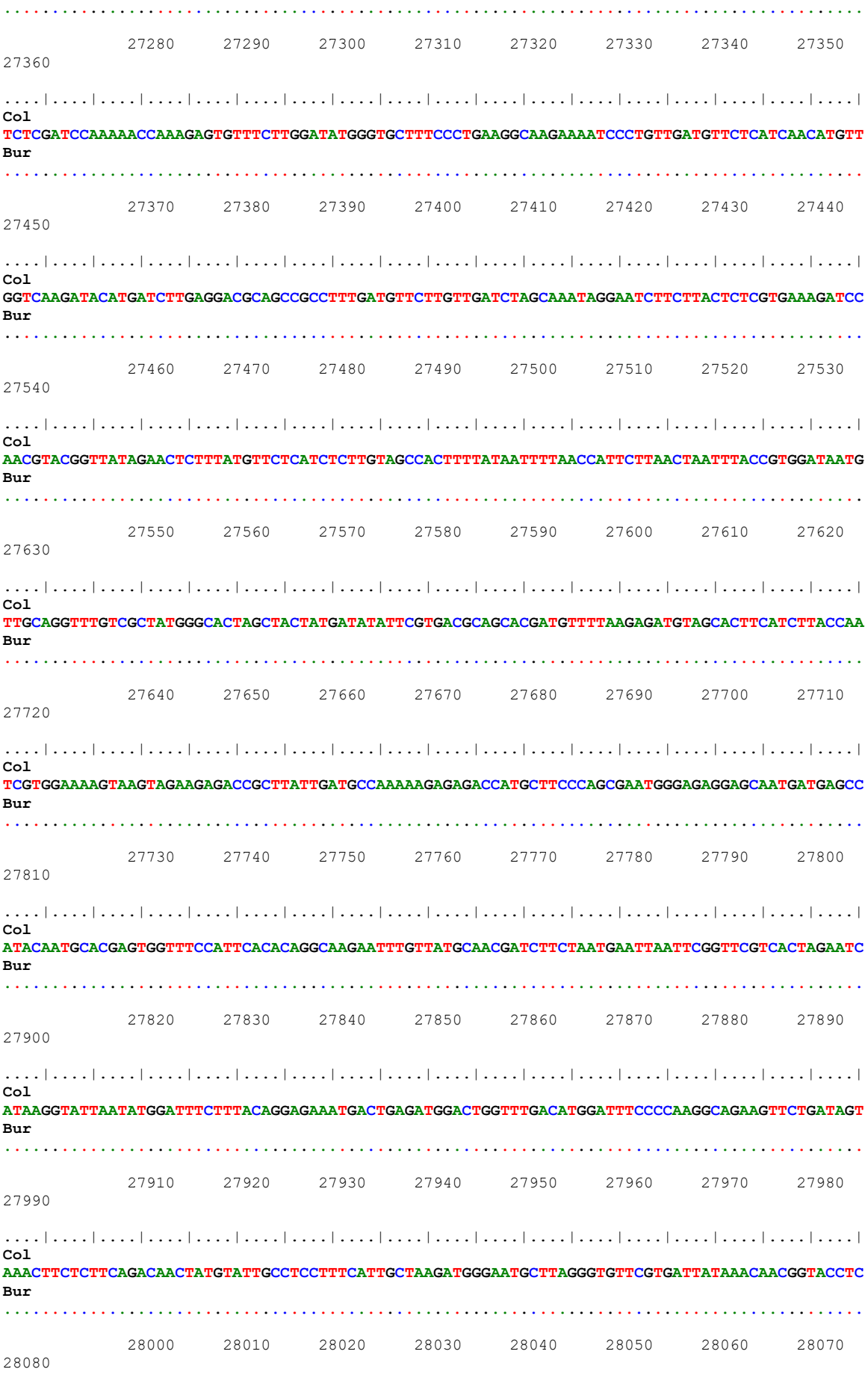
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AGTTTGGTCAAGCAGGTAATGGGTCTGCTACAAGTGTTACATGCATAGTAGTAATATTCTTTGTACTTTCAGTACTCATCTTGACTCTAT
Bur
....................................................................................

            27100     27110     27120     27130     27140     27150     27160     27170
27180

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TTGTTAGGTTGTTGGGGAGTCTAAAGGTCTACCTTTGTCTCTGAAAGTCCTTGGCGCTTCATTAAACGATCGACCTGAAACATATTGGGC
Bur
....................................................................................

            27190     27200     27210     27220     27230     27240     27250     27260
27270

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AATTGCAGTGGAGAGGTTATCAAGAGGTGAACCTGTTGATGAAACTCATGAGAGTAAAGTGTTTGCTCAAATCGAAGCAACTCTAGAAAA
Bur
```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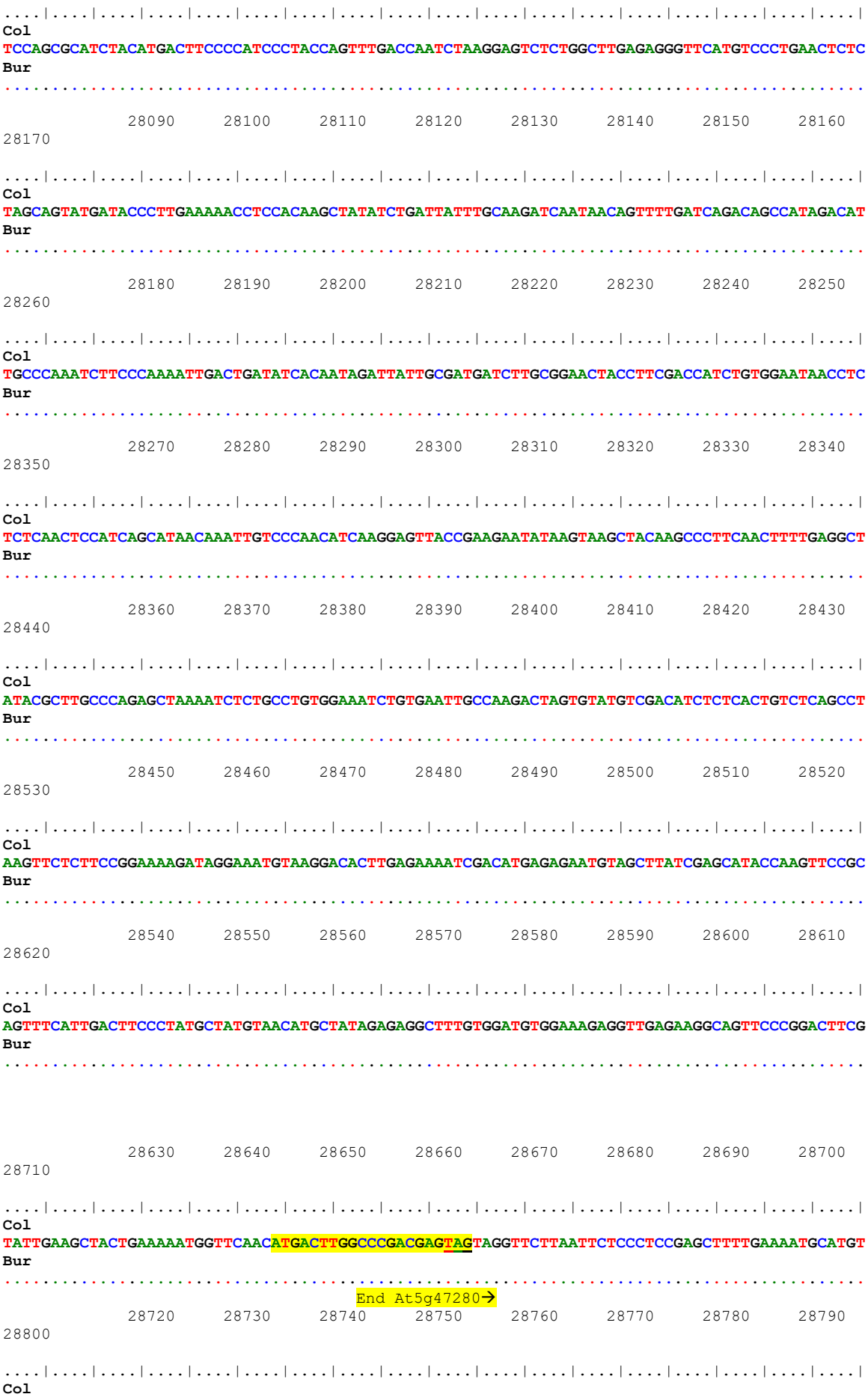
Col
TCTCGATCCAAAAACCAAAGAGTGTTTCTTGGATATGGGTGCTTTCCCTGAAGGCAAGAAAATCCCTGTTGATGTTCTCATCAACATGTT
Bur
27370 27380 27390 27400 27410 27420 27430 27440 27450
Col
GGTCAAGATACATGATCTTGAGGACGCAGCCGCCTTTGATGTTCTTGTTGATCTAGCAAATAGGAATCTTCTTACTCTCGTGAAAGATCC
Bur
27460 27470 27480 27490 27500 27510 27520 27530 27540
Col
AACGTACGGTTATAGAACTCTTTATGTTCTCATCTCTTGTAGCCACTTTTATAATTTTAACCATTCTTAACTAATTTACCGTGGATAATG
Bur
27550 27560 27570 27580 27590 27600 27610 27620 27630
Col
TTGCAGGTTTGTCGCTATGGGCACTAGCTACTATGATATATTCGTGACGCAGCACGATGTTTTAAGAGATGTAGCACTTCATCTTACCAA
Bur
27640 27650 27660 27670 27680 27690 27700 27710 27720
Col
TCGTGGAAAAGTAAGTAGAAGAGACCGCTTATTGATGCCAAAAAGAGAGACCATGCTTCCCAGCGAATGGGAGAGGAGCAATGATGAGCC
Bur
27730 27740 27750 27760 27770 27780 27790 27800 27810
Col
ATACAATGCACGAGTGGTTTCCATTCACACAGGCAAGAATTTGTTATGCAACGATCTTCTAATGAATTAATTCGGTTCGTCACTAGAATC
Bur
27820 27830 27840 27850 27860 27870 27880 27890 27900
Col
ATAAGGTATTAATATGGATTTCTTTACAGGAGAAATGACTGAGATGGACTGGTTTGACATGGATTTCCCCAAGGCAGAAGTTCTGATAGT
Bur
27910 27920 27930 27940 27950 27960 27970 27980 27990
Col
AAACTTCTCTTCAGACAACTATGTATTGCCTCCTTTCATTGCTAAGATGGGAATGCTTAGGGTGTTCGTGATTATAAACAACGGTACCTC
Bur
28000 28010 28020 28030 28040 28050 28060 28070 28080


Col
TCCAGCGCATCTACATGACTTCCCCATCCCTACCAGTTTGACCAATCTAAGGAGTCTCTGGCTTGAGAGGGTTCATGTCCCTGAACTCTC
Bur
28090 28100 28110 28120 28130 28140 28150 28160
28170
Col
TAGCAGTATGATACCCTTGAAAAACCTCCACAAGCTATATCTGATTATTTGCAAGATCAATAACAGTTTTGATCAGACAGCCATAGACAT
Bur
28180 28190 28200 28210 28220 28230 28240 28250
28260
Col
TGCCCAAATCTTCCCAAAATTGACTGATATCACAATAGATTATTGCGATGATCTTGCGGAACTACCTTCGACCATCTGTGGAATAACCTC
Bur
28270 28280 28290 28300 28310 28320 28330 28340
28350
Col
TCTCAACTCCATCAGCATAACAAATTGTCCCAACATCAAGGAGTTACCGAAGAATATAAGTAAGCTACAAGCCCTTCAACTTTTGAGGCT
Bur
28360 28370 28380 28390 28400 28410 28420 28430
28440
Col
ATACGCTTGCCCAGAGCTAAAATCTCTGCCTGTGGAAATCTGTGAATTGCCAAGACTAGTGTATGTCGACATCTCTCACTGTCTCAGCCT
Bur
28450 28460 28470 28480 28490 28500 28510 28520
28530
Col
AAGTTCTCTTCCGGAAAAGATAGGAAATGTAAGGACACTTGAGAAAATCGACATGAGAGAATGTAGCTTATCGAGCATACCAAGTTCCGC
Bur
28540 28550 28560 28570 28580 28590 28600 28610
28620
Col
AGTTTCATTGACTTCCCTATGCTATGTAACATGCTATAGAGAGGCTTTGTGGATGTGGAAAGAGGTTGAGAAGGCAGTTCCCGGACTTCG
Bur
28630 28640 28650 28660 28670 28680 28690 28700
28710
Col
TATTGAAGCTACTGAAAAATGGTTCAACATGACTTGGCCCGACGAGTAGTAGGTTCTTAATTCTCCCTCCGAGCTTTTGAAAATGCATGT
Bur
End At5g47280→
28720 28730 28740 28750 28760 28770 28780 28790
28800
Col

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TGTATTATTATTTATTAACTCGATTAGGACCCCTGTATGATATACGATTTTATTAATACATGTTTTGCTCTTATAACGTCAATATATAAA
Bur
.....................................................................................................

             28810     28820     28830     28840     28850     28860     28870     28880
28890

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TTATATGTTGATTTTAAGTATTAAAAGTTTCTATTTGGAATCTCAAAGATATGTTTTTAAAGATTCACTTATAAGTAATAACAAACAAAC
Bur
.....................................................................................................

             28900     28910     28920     28930     28940     28950     28960     28970
28980

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AAAAACTATTTAGCTTAATGGTAAAAAGCATGAGTCTATATAGAGAAGGGTTCATAATTTAAAATTAGTTTGAATGTTGTTTGTTATTAA
Bur
.....................................................................................................

             28990     29000     29010     29020     29030     29040     29050     29060
29070

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GTGAGATACATTTTAAAATAATTTAGTGAGATAAATATATCGTTAATATTATGCATGTGCTGATTATTATATGACCAATTATATGACCCA
Bur
.....................................................................................................

             29080     29090     29100     29110     29120     29130     29140     29150
29160

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TCAATAGTTGTCAACATTTTCTTGGTGGATCGACGAGGACGAACCCAATGATTTAGAAACAGGGATGATATATAACAAGTAAGTATAGTC
Bur
.....................................................................................................

             29170     29180     29190     29200     29210     29220     29230     29240
29250

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GCAAGTGTCCCTGATCTATAGTCATACAAGGTAAGGCCCACTGCTGAAAAGAGAAGTGGCGGTCGGATTTAAAACAATACAAGTGAAGTA
Bur
.....................................................................................................

             29260     29270     29280     29290     29300     29310     29320     29330
29340

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GTGTATCGAGCCCTTTGTAACATGAGATTGTATAGATCCCAGTAAGAGATGGTAGATTTTTAATCTGAGATAAGAAACTATCTCTATTTG
Bur
.....................................................................................................

             29350     29360     29370     29380     29390     29400     29410     29420
29430

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GAAATCAGAGAATACTTTAGCAGGGGAGAGGGATGGGAGCTACCTCGAGGGCATCAAGTTCTTCAAAACTGGAGAATCATCTTTGATTTG
Bur
.....................................................................................................

             29440     29450     29460     29470     29480     29490     29500     29510
29520

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GATATCAGAAAGAGAAGATATATCTATGGTTATAGTGGCTGAGACAAACGATTCTCTCTCCCAAGGATCATTGGGACTGCCTTGGCCATC
Bur
.....................................................................................................

             29530     29540     29550     29560     29570     29580     29590     29600
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```
29610

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TGGACTGCAAGGTATAAACAGGAAGAAATAAAAACAACAAAAATATCAAGGATATAGCACTACCAATATGATAAATGCATTGACAAAATC
Bur
....................................................................................................

            29620     29630     29640     29650     29660     29670     29680     29690     29700

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AGTCTTTTAAGTACAAAAATACTTTTGGTGAAGGGAAAACTAATAAAGGAAACTTGTGCTATTGAAGCGGACAAACAGCTACCCACACAC
Bur
....................................................................................................

            29710     29720     29730     29740     29750     29760     29770     29780     29790

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CATTGTGGGGGAATTTTGAGAAACAGATTTGAGACTTTTTATTGTTGATAGTAACATATACATAATGCTCTAGCTTCTTCTTTCTATGCG
Bur
....................................................................................................

            29800     29810     29820     29830     29840     29850     29860     29870     29880

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ACGAATCAACAATATTGTCCATGCTATCAACAATACAAATAATAGCTAAAACCCCAAAAATCATAAAACTAAGCAACAAGCTAATCTTCT
Bur
....................................................................................................

            29890     29900     29910     29920     29930     29940     29950     29960     29970

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TCAGTTTCAGAGCAAGAATCAAAATGTACAGTATTTAAAAGAGCTAGACAGACTTTAACGTAGAAGAAAAGAATCAATCTCCAGAGCCTT
Bur
....................................................................................................

            29980     29990     30000     30010     30020     30030     30040     30050     30060

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CCTTAGTCATCTCTGCTTCCTTTTTTTGCATCTTCACGTAATGTTGGTTATGCGATTTAACTTGTTATGGATTCCTAGTCTTTACAAATT
Bur
....................................................................................................

            30070     30080     30090     30100     30110     30120     30130     30140     30150

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CTCTAGATATGACCTCCCAAGCTCCTGGCCCTTTCGACTTTAGTCCTTCAAGAAAGAGTCTGAAAACGTACACCAAAGTAAATGGATAAT
Bur
....................................................................................................

            30160     30170     30180     30190     30200     30210     30220     30230     30240

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CAGATGAGAGATTCATCATATGATCTATATTTACCAAATTAGCAACTTTAAACAATTAATGCCTAAGCAAAGCCAAGACCTCCATCTAAC
Bur
....................................................................................................
      ← End At5g47290
            30250     30260     30270     30280     30290     30300     30310     30320     30330

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ATTCATCATCTTAAATTAGCAAGAAGACAACTTACTCGTGTTCTTGGGCTGACCAACGAGTTCCCTTCTTCGCCACTATCGGCGTCGCTG
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Bur
.....................................................................................................

            30340     30350     30360     30370     30380     30390     30400     30410
30420

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AACGTGGTGAGTACTCGGGCACAACATCTCTGCCGGATTCGATAACAGCAATATCTTGGAGCAGCTTATCGTAGTGGTATTTGATCTCAT
Bur
.....................................................................................................

            30430     30440     30450     30460     30470     30480     30490     30500
30510

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CCACCGACGTTCTCATTTGTGCAGCGATAATCTCCAGCTTTGCCGGCGAATCCGGGACTTGCACGAGTGCAACCTCGAAAGCTTTGTTCT
Bur
.....................................................................................................

            30520     30530     30540     30550     30560     30570     30580     30590
30600

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CCTCCCAAGTCCACTTCATCGTACCAGCCATTGTAGCCAAGAAAAGAAAGAAAAAGAATTGAGAGAGAGAGAGAGAAAGATCGAGCGAGT
Bur
.....................................................Start At5g47290←
            30610     30620     30630     30640     30650     30660     30670     30680
30690

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GTAACGACGTGGAGTTGAATCTGTTACGTAACAAGAATCTTTGCGATTTATATCTTTATACAGCAACAACACATTAAACCAAGAAATGAA
Bur
.....................................................................................................

            30700     30710     30720     30730     30740     30750     30760     30770
30780

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CCAAGATTACATCTTAATTAATTCATAAACCGGACATTCCAGAGCCCTTAACCGGAATTATATTAGTATATCACTATATACATGTTAATA
Bur
.....................................................................................................

            30790     30800     30810     30820     30830     30840     30850     30860
30870

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ATAGCCTTGATAAAATAATAGCAAAACAGATTAGCCTTTTAGTTTTTGACGTCATGCATGCACTTGTGGGTCTGTGAAAATCTCGCGTTT
Bur
.....................................................................................................

            30880     30890     30900     30910     30920     30930     30940     30950
30960

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TCTCGTGGAAAAGTGGATCGCTTACAAAACCTCAAGATATCTTTTTTTTTTTTTCAACTTGAACCTCAAGGTATCTAAGCCTTTAAACAA
Bur
.....................................................................................................

            30970     30980     30990     31000     31010     31020     31030     31040
31050

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ACTCTCTTCTACGTTTTATAATCAACAGAAAAATGTTAAAATATAAAACTTCAAATACAAATTAACAATTATCAAACTAGCCAAATGTTA
Bur
.....................................................................................................

            31060     31070     31080     31090     31100     31110     31120     31130
31140
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Col
TATTTCAAACATCATTGTTCATTGACTTTTTACATGTTTTCAAATATTTACTTTAATACAAAATAAACAAAATACTAGTGGCGTATAAAA
Bur
31150 31160 31170 31180 31190 31200 31210 31220
31230
Col
TATCATAAAACACGAGCAAATATCGGAGGATACTAGAAAACATATAAAGTTGAAAATAAACTAACTCCGTGTATAAAGAGGAAGAAGTTA
Bur
31240 31250 31260 31270 31280 31290 31300 31310
31320
Col
TCTTATGACTAGAAAATATATATATATATATATATAATATTAAAAGTGAGAGCACGGGTCGGAGCAAACAATAAAACCCTAATTAA
M T R K Y I Y I Y I L K V R A R
Bur
TATAT
AATATTAAAA
M T R K Y I Y I Y I L K V R A R
→Start At5g47300 polymorphism:2017-A:deletion 6bp Bur → 2 AA, no frameshift
31330 31340 31350 31360 31370 31380 31390 31400
31410
Col
CAATCAAAGCCACCTGATAGAGATGAGAAACACATTGATGTTGTCGGACCTTCCAGGAGATTTGTTAGAGGAGATACTTTGTCGCGTTCC
Bur
31420 31430 31440 31450 31460 31470 31480 31490
31500
Col
TGCCACATCTCTGAAGCAGTTACGATCTACTTGCAAACAATGGAACAATTTATTCAACAATGGGAGATTCACAAGAAAACACTTGGATAA
Bur
31510 31520 31530 31540 31550 31560 31570 31580
31590
Col
AGCCCCAAAGGATTTTCAGAATCTCATGTTGAGCGACTCTAGGGTATTTTCGATGAGTGTCAGTTTCCATGGAATTCCATCTGTAGAGGC
Bur
31600 31610 31620 31630 31640 31650 31660 31670
31680
Col
CACATGTGAACTTAGCCTAATCGACTCTTTTTCTAGTTTTGAAGATAAATTCGAGATTTCTCAAGTCTTTCACTGTGACGGCTTATTGTT
Bur
31690 31700 31710 31720 31730 31740 31750 31760
31770
Col
ATGCACCGACGCAGACAACACTAGAATCGTGGTTTGGAACCCGTGTACTGGTAAAACTAGGTGGATTGAACCCAATAATCGTTGCTACTA
Bur
31780 31790 31800 31810 31820 31830 31840 31850

31860

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

Col

CTATGCTTTTGGATCCTACTTGGACAAATCCTACGGTAATAGCTACAAAATATTGAGCTATAGTGGTTATGGCTACGAGAACCAAGAACT

Bur

.....

31870 31880 31890 31900 31910 31920 31930 31940 31950

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

Col

CGCAATCTATGAGATTAACTCTCAATCATGGAGGTTTCTTGATGTCACTCGTGACTGCATCCTCGAAAGATATACTGATTACGGTGTGTC

Bur

.....

31960 31970 31980 31990 32000 32010 32020 32030 32040

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

Col

TTTGAAGGGACATACTTACTGGTTTGCGTCAGATGAGAAAGAGAAAAATCTCAGCGTATTTCTAGTCAGTTTTGATTATACAACTGAAAG

Bur

.....

32050 32060 32070 32080 32090 32100 32110 32120 32130

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

Col

ATTTAGACGTCTACGTCTCCCGTATCAGTGCCCTGATTATAACACTGCGTCTTTATCCGTTGTTAGAGAAGAGAAACTTGCGGTGTTGTT

Bur

.....

32140 32150 32160 32170 32180 32190 32200 32210 32220

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

Col

ACAACGCGAAAATACATCAAGGACAGAGATATGGGTGACAAGTAGGATTGGTGAGACCAAAGTGGTGTCGTGGAGCATGGTCTTAGCAGT

Bur

.....

32230 32240 32250 32260 32270 32280 32290 32300 32310

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

Col

GGATTTCCCGTCCGAACTATTCATTTTGTCTGGCATAAGTTTCTTGGTCGATGCGGAGAAAAAATTCGTCGTATGTTGTGATAATTACTT

Bur

.....

32320 32330 32340 32350 32360 32370 32380 32390 32400

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

Col

CGGAGAGGATGAATACGATACCAAAAACTTGGTTCACATTGTTGGAGAGAACAACAAAGTGAGAGAAGTTAATTTCGGAGTATCCGAATC

Bur

.....

32410 32420 32430 32440 32450 32460 32470 32480 32490

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

Col

ATCTTGGCCATTTTTGTTTAATTATGTTCCAAGTTTGATTCAAATCTGGGAAGGTGTAGGAGGCAAAAGAAAGAGAGTCGAATAAGTAAG

Bur

.....

End At5g47300 →

32500 32510 32520 32530 32540 32550 32560 32570 32580

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

Col

CTTCACGCAAACCTGTTTTTTTTTTTTCCTTCTCACCGTTATCTTTGGTCATATCTAGTTATGTTTTGACTAACAAATGTTTCATACATA

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Bur
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             32590     32600     32610     32620     32630     32640     32650     32660
32670

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CTTGTTGCATTACTTTAAGACAGTTTTTTTTTTTTTTAATAGTTTCGTGATCAAAAAAGATCTGCATTAATGCCGCCTCCAGCAACATGGG
Bur
.....................................................................................................

             32680     32690     32700     32710     32720     32730     32740     32750
32760

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GGTTTCATTCTTCTTTTCTTAACACATACAAAGACAGAAAAAGCAATTAACCTAATGAAGAGACCAAACAAACATAATGAAGAGCTACGT
Bur
.....................................................................................................

             32770     32780     32790     32800     32810     32820     32830     32840
32850

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GTACGTTCCAAGTCTAGTTCCCCTTCCAGGATAAGATGGTTGTTTCGTGTTTCTAAGCTTAATTGGTATGTGATTGTTCATCTTCTGCCA
Bur
.....................................................................................................

             32860     32870     32880     32890     32900     32910     32920     32930
32940

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TCATATATGATAGTGCATATGTATTGAAATTGACTTTGGTTTTTGTGATACAACCTGGACACGTTTTAGGTCTTTGTCCACAGTTGTATC
Bur
.....................................................................................................

             32950     32960     32970     32980     32990     33000     33010     33020
33030

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AGTTTCGGTCATGTTTGTGGTATCAACAAAACTAAGATACACACATTCCAAGTATACATGACAAATTTCACTCTATGCTACAAATAACCA
Bur
.....................................................................................................

             33040     33050     33060     33070     33080     33090     33100     33110
33120

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AGGTTTGTACTAAAATCCAAATACAAAGAATTTGGATGAACCTTACAGAAGCTATATGGAACATTCTAACTTGATATACTTAATTTGAAT
Bur
.....................................................................................................

             33130     33140     33150     33160     33170     33180     33190     33200
33210

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AAACAAAAAAAGAAGTCATTATTTAGTTATTGAATACTTTTTTTCCCTTGACCTTACAGATTACTGATTACCATATACATACATATATGT
Bur
.....................................................................................................

             33220     33230     33240     33250     33260     33270     33280     33290
33300

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GAATTTTTGAAGAAGACAACATTGCATTTGTAACATACATTGCAAATGAGTAACAATGACCAACAACATTAACAGATTGTTTACCAAGAC
Bur
.....................................................................................................

             33310     33320     33330     33340     33350     33360     33370     33380
33390
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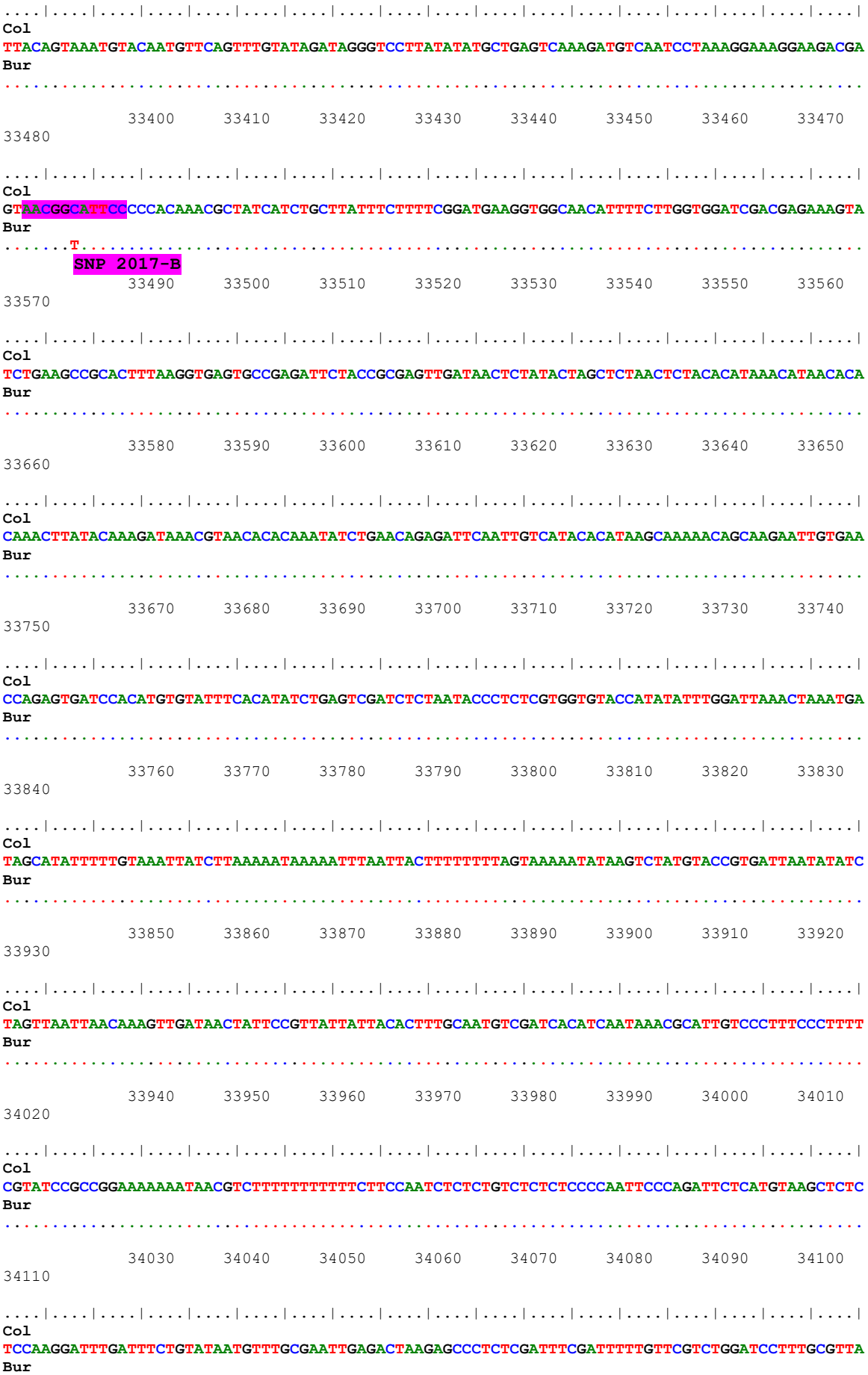
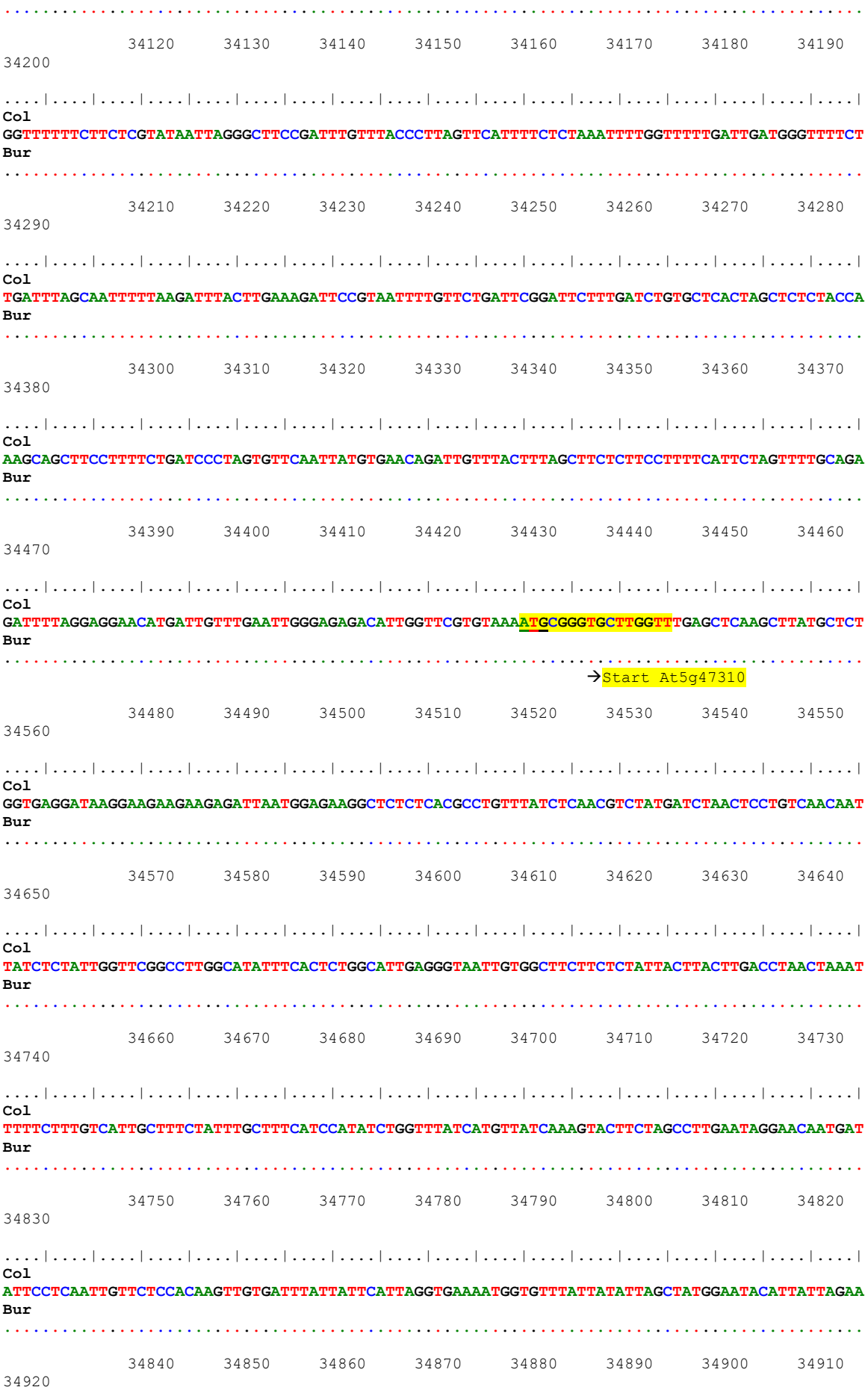

Col
TTACAGTAAATGTACAATGTTCAGTTTGTATAGATAGGGTCCTTATATATGCTGAGTCAAAGATGTCAATCCTAAAGGAAAGGAAGACGA
Bur
33400 33410 33420 33430 33440 33450 33460 33470
33480
Col
GTAACGGCATTCCCCCACAAACGCTATCATCTGCTTATTTCTTTTCGGATGAAGGTGGCAACATTTTCTTGGTGGATCGACGAGAAAGTA
Bur
T
SNP 2017-B
33490 33500 33510 33520 33530 33540 33550 33560
33570
Col
TCTGAAGCCGCACTTTAAGGTGAGTGCCGAGATTCTACCGCGAGTTGATAACTCTATACTAGCTCTAACTCTACACATAAACATAACACA
Bur
33580 33590 33600 33610 33620 33630 33640 33650
33660
Col
CAAACTTATACAAAGATAAACGTAACACACAAATATCTGAACAGAGATTCAATTGTCATACACATAAGCAAAAACAGCAAGAATTGTGAA
Bur
33670 33680 33690 33700 33710 33720 33730 33740
33750
Col
CCAGAGTGATCCACATGTGTATTTCACATATCTGAGTCGATCTCTAATACCCTCTCGTGGTGTACCATATATTTGGATTAAACTAAATGA
Bur
33760 33770 33780 33790 33800 33810 33820 33830
33840
Col
TAGCATATTTTTGTAAATTATCTTAAAAATAAAAATTTAATTACTTTTTTTTAGTAAAAATATAAGTCTATGTACCGTGATTAATATATC
Bur
33850 33860 33870 33880 33890 33900 33910 33920
33930
Col
TAGTTAATTAACAAAGTTGATAACTATTCCGTTATTATTACACTTTGCAATGTCGATCACATCAATAAACGCATTGTCCCTTTCCCTTTT
Bur
33940 33950 33960 33970 33980 33990 34000 34010
34020
Col
CGTATCCGCCGGAAAAAAATAACGTCTTTTTTTTTTTCTTCCAATCTCTCTGTCTCTCTCCCCAATTCCCAGATTCTCATGTAAGCTCTC
Bur
34030 34040 34050 34060 34070 34080 34090 34100
34110
Col
TCCAAGGATTTGATTTCTGTATAATGTTTGCGAATTGAGACTAAGAGCCCTCTCGATTTCGATTTTTGTTCGTCTGGATCCTTTGCGTTA
Bur


34120 34130 34140 34150 34160 34170 34180 34190 34200
Col
GGTTTTTTCTTCTCGTATAATTAGGGCTTCCGATTTGTTTACCCTTAGTTCATTTTCTCTAAATTTTGGTTTTTGATTGATGGGTTTTCT
Bur
34210 34220 34230 34240 34250 34260 34270 34280 34290
Col
TGATTTAGCAATTTTTAAGATTTACTTGAAAGATTCCGTAATTTTGTTCTGATTCGGATTCTTTGATCTGTGCTCACTAGCTCTCTACCA
Bur
34300 34310 34320 34330 34340 34350 34360 34370 34380
Col
AAGCAGCTTCCTTTTCTGATCCCTAGTGTTCAATTATGTGAACAGATTGTTTACTTTAGCTTCTCTTCCTTTTCATTCTAGTTTTGCAGA
Bur
34390 34400 34410 34420 34430 34440 34450 34460 34470
Col
GATTTTAGGAGGAACATGATTGTTTGAATTGGGAGAGACATTGGTTCGTGTAAAATGCGGGTGCTTGGTTTGAGCTCAAGCTTATGCTCT
Bur
Start At5g47310
34480 34490 34500 34510 34520 34530 34540 34550 34560
Col
GGTGAGGATAAGGAAGAAGAAGAGATTAATGGAGAAGGCTCTCTCACGCCTGTTTATCTCAACGTCTATGATCTAACTCCTGTCAACAAT
Bur
34570 34580 34590 34600 34610 34620 34630 34640 34650
Col
TATCTCTATTGGTTCGGCCTTGGCATATTTCACTCTGGCATTGAGGGTAATTGTGGCTTCTTCTCTATTACTTACTTGACCTAACTAAAT
Bur
34660 34670 34680 34690 34700 34710 34720 34730 34740
Col
TTTTCTTTGTCATTGCTTTCTATTTGCTTTCATCCATATCTGGTTTATCATGTTATCAAAGTACTTCTAGCCTTGAATAGGAACAATGAT
Bur
34750 34760 34770 34780 34790 34800 34810 34820 34830
Col
ATTCCTCAATTGTTCTCCACAAGTTGTGATTTATTATTCATTAGGTGAAAATGGTGTTTATTATATTAGCTATGGAATACATTATTAGAA
Bur
34840 34850 34860 34870 34880 34890 34900 34910 34920

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....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GGAAAAAGTGGAACAAGTTTTGAGGAATCTAGAATGGAATGCTTTTTCAAATCCTGCCTTATTGTCTGAAGCATTCTCTTTCAATAATTA
Bur
....................................................................................................

            34930     34940     34950     34960     34970     34980     34990     35000     35010

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GAACTTGCCTGATGAGTTATATAACTGTACTTCTGCTGAAACTGTTATTGTTGCTAAATGTTCATCTAATGTGGAGTTTTTTTTCACTTT
Bur
....................................................................................................

            35020     35030     35040     35050     35060     35070     35080     35090     35100

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GCCATGTGTACTACTAGCTCATGGTTTCGAATATGGATATGGAGCTCATGAGTATTCGAGCAGTGGGGTATTTGAGGTTGAACCTAGGAG
Bur
....................................................................................................

            35110     35120     35130     35140     35150     35160     35170     35180     35190

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CTGTCCAGGTTTCATCTTTAGGCGCTCAGTTTTGTTGGGAACCACCAGCATGTCTCGCTCTGATTTCCGCTCCTTCATGGAGAAGCTTTC
Bur
....................................................................................................

            35200     35210     35220     35230     35240     35250     35260     35270     35280

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GAGAAAGTATCATGGGGACACATACCATTTGATTGCCAAAAACTGTAACCATTTCACTGAAGAAGTATGCTTGCAGGTAACAGGAAAGCC
Bur
....................................................................................................

            35290     35300     35310     35320     35330     35340     35350     35360     35370

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TATTCCTGGATGGATTAATAGGATGGCTCGAGTTGGTAAGATAACTTTCTTATTCCAGCTTATTATTTCTTTACTGGTTCTTGTTGTTTG
Bur
....................................................................................................

            35380     35390     35400     35410     35420     35430     35440     35450     35460

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GCATATCTTTTTACATGGTTGCTTGTTCTTGAATTTTTTCAGGTTCGTTCTGTAACTGTATCCTTCCAGAAAGCATACAGCTCTCATCGG
Bur
....................................................................................................

            35470     35480     35490     35500     35510     35520     35530     35540     35550

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TTAATCATCCTGAAGCCCTCGAGTTCTCTGGTAAGTTAATCATGTTCGCTCTTCTTCACCTAAAAAAAACTGCAATAGGCATTTGGATTT
Bur
....................................................................................................

            35560     35570     35580     35590     35600     35610     35620     35630     35640

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CGGATAAACCAGTTGTGTTTCATCTCCATTGTAGATGATAACGATGGATCAGAAGAATCAGTTGCATCTTCTGTGTCATACGAAACAGAT
Bur
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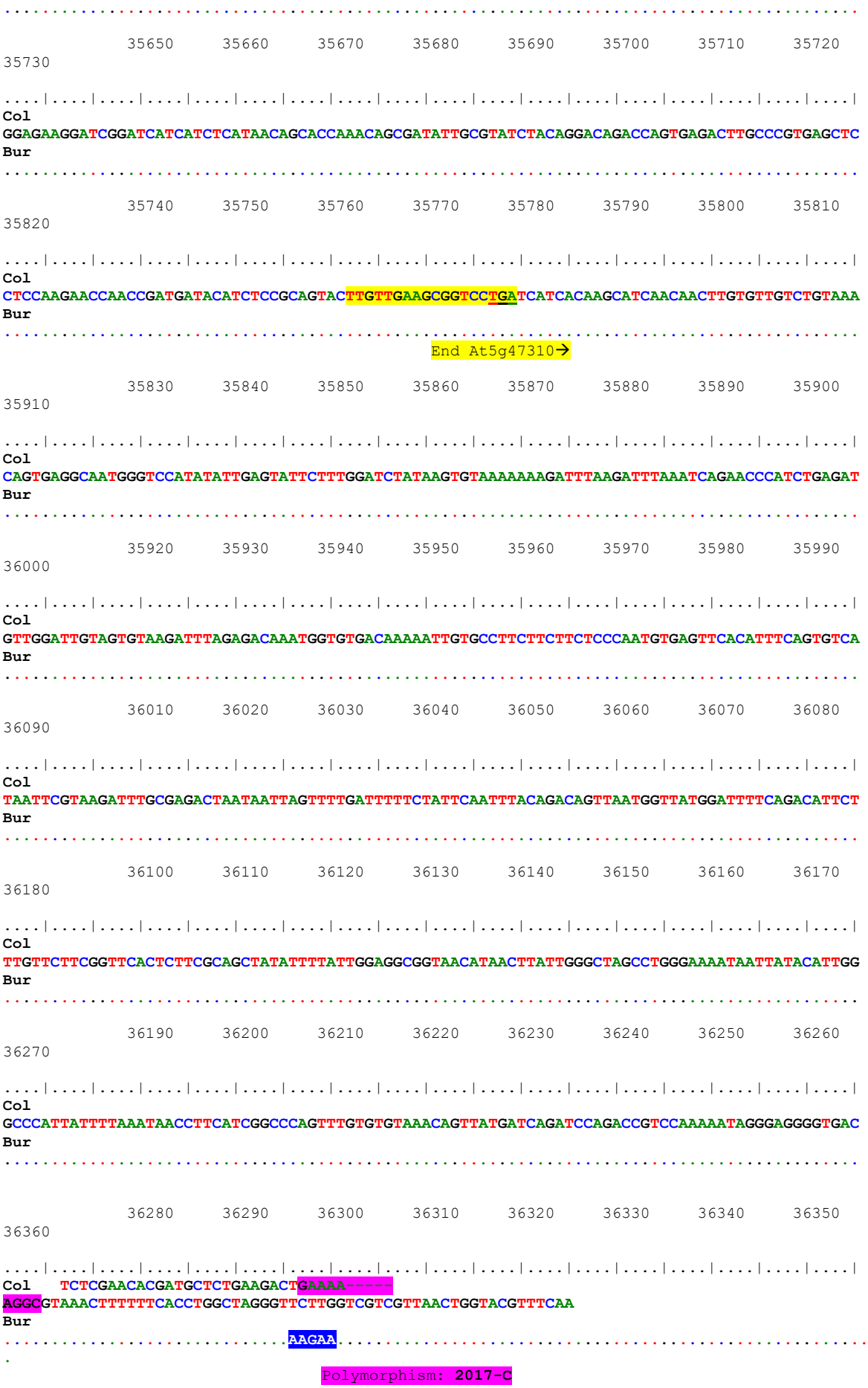
35650 35660 35670 35680 35690 35700 35710 35720 35730
Col
GGAGAAGGATCGGATCATCATCTCATAACAGCACCAAACAGCGATATTGCGTATCTACAGGACAGACCAGTGAGACTTGCCCGTGAGCTC
Bur
35740 35750 35760 35770 35780 35790 35800 35810 35820
Col
CTCCAAGAACCAACCGATGATACATCTCCGCAGTACTTGTTGAAGCGGTCCTGATCATCACAAGCATCAACAACTTGTGTTGTCTGTAAA
Bur
End At5g47310→
35830 35840 35850 35860 35870 35880 35890 35900 35910
Col
CAGTGAGGCAATGGGTCCATATATTGAGTATTCTTTGGATCTATAAGTGTAAAAAAAGATTTAAGATTTAAATCAGAACCCATCTGAGAT
Bur
35920 35930 35940 35950 35960 35970 35980 35990 36000
Col
GTTGGATTGTAGTGTAAGATTTAGAGACAAATGGTGTGACAAAAATTGTGCCTTCTTCTTCTCCCAATGTGAGTTCACATTTCAGTGTCA
Bur
36010 36020 36030 36040 36050 36060 36070 36080 36090
Col
TAATTCGTAAGATTTGCGAGACTAATAATTAGTTTTGATTTTTCTATTCAATTTACAGACAGTTAATGGTTATGGATTTTCAGACATTCT
Bur
36100 36110 36120 36130 36140 36150 36160 36170 36180
Col
TTGTTCTTCGGTTCACTCTTCGCAGCTATATTTTATTGGAGGCGGTAACATAACTTATTGGGCTAGCCTGGGAAAATAATTATACATTGG
Bur
36190 36200 36210 36220 36230 36240 36250 36260 36270
Col
GCCCATTATTTTAAATAACCTTCATCGGCCCAGTTTGTGTGTAAACAGTTATGATCAGATCCAGACCGTCCAAAAATAGGGAGGGGTGAC
Bur
36280 36290 36300 36310 36320 36330 36340 36350 36360
Col TCTCGAACACGATGCTCTGAAGACTGAAAA----
AGGCGTAAACTTTTTTCACCTGGCTAGGGTTCTTGGTCGTCGTTAACTGGTACGTTTCAA
Bur
AAGAA
Polymorphism: 2017-C

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            36370     36380     36390     36400     36410     36420     36430     36440
36450

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TGGTCTCTCTGTACTATCATTTCTGCGAAATGGGTCTTCTCTTTGGAGGCTAATCGACGTTGTGCTTAATCTAATTGCTCTTTTAGGTTG
Bur
.....................................................................................

            36460     36470     36480     36490     36500     36510     36520     36530
36540

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TTTAGAGGAATATATCACAGGTTTTCAATTAGATTGATCTGCTTAGTTTTGTAATCAGTGTAGGTTACCAGTGAATCATGAACTTCCGTT
Bur
.....................................................................................

            36550     36560     36570     36580     36590     36600     36610     36620
36630

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AGGGTTATAAGCTCTCTGTTTCTTTTCCTGACTTATCAATGTCACTAATTTAGATTTGATGCGTAGTTTAGCTTTTGAAGATCAGGGAAC
Bur
.....................................................................................

            36640     36650     36660     36670     36680     36690     36700     36710
36720

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TGAATATATCTGGTTTAAGGAAGCTTTGAATTTTCTGCTTGCCATGGACATTCGACTTATCAGTATTTTTGTACATTTTGGTTAATGTTT
Bur
.....................................................................................

            36730     36740     36750     36760     36770     36780     36790     36800
36810

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ATCGAATTGGTTTGATCAGTCTGTGGATTTTAACTTTACAAGTTAAGATGCTATTCTTTTAGGTCTAGTTGATAGGTCATGGATTTGTTG
Bur
.....................................................................................

            36820     36830     36840     36850     36860     36870     36880     36890
36900

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TTATATGGAGTCTAGACATTTTGCCACTGCTTTAGTGTTCTTAGCTTCTAAGGGTTTCGTTGATATATTGTACTGGGTTTATCGTTTCCA
Bur
.....................................................................................

            36910     36920     36930     36940     36950     36960     36970     36980
36990

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GGCATCTAGTATGGCTTTCTGCACTAAACTTGGCGGTCACTGGAAACAAGGGGTAAATGTTCCAGTGTCATCAATGCTCGGTTCTCTTCG
Bur
.....................................................................................
               →Start At5g47320

            37000     37010     37020     37030     37040     37050     37060     37070
37080

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CTACATGTCCACAAAACTTTATATTGGTGGTAAGTATAACTTCCTATCAGATTGTTTCATTTTCTTACTCTTCGCAGCTGTGGATGTTTT
Bur
.....................................................................................

            37090     37100     37110     37120     37130     37140     37150     37160
37170
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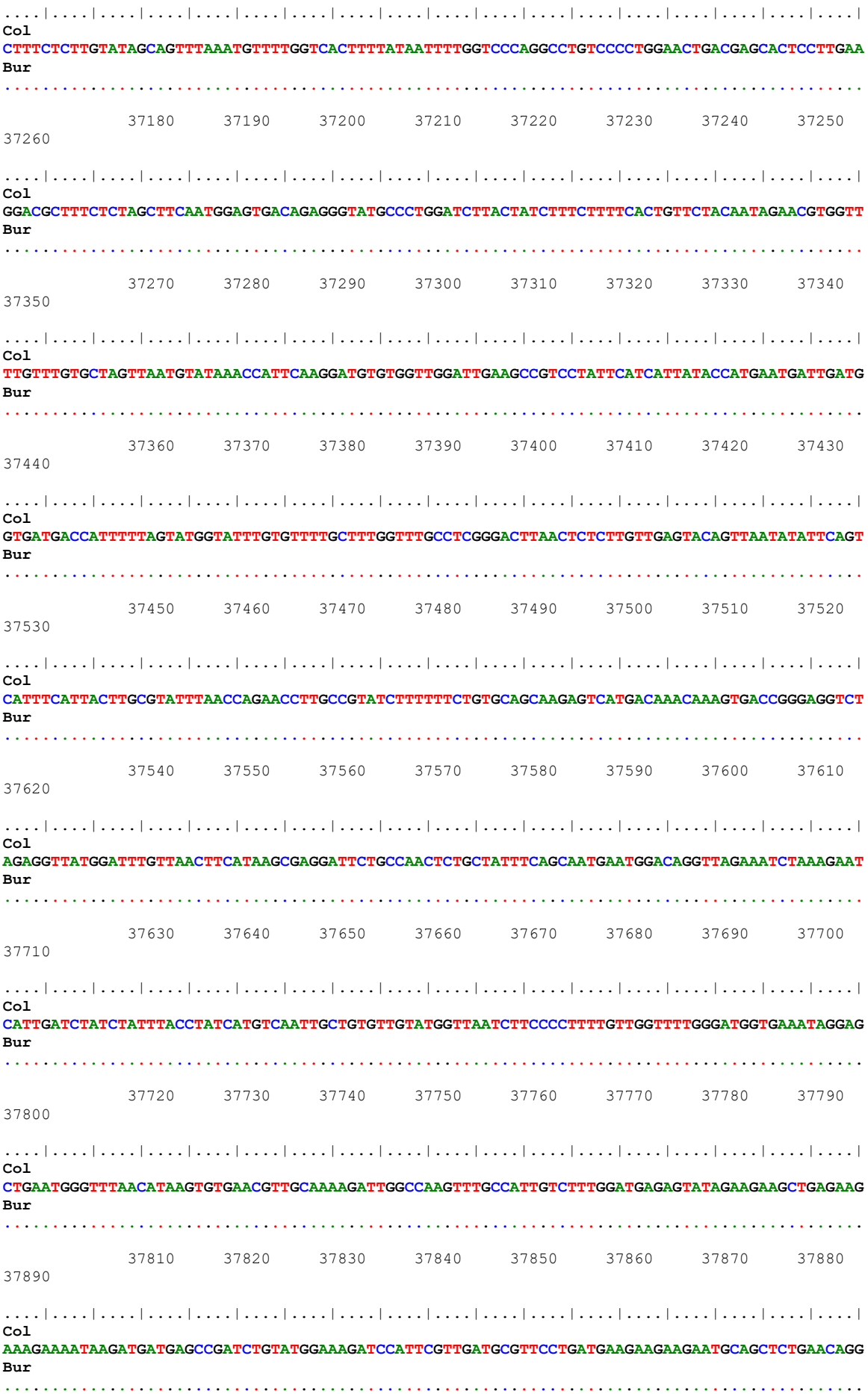
Col
CTTTCTCTTGTATAGCAGTTTAAATGTTTTGGTCACTTTTATAATTTTGGTCCCAGGCCTGTCCCCTGGAACTGACGAGCACTCCTTGAA
Bur
37180 37190 37200 37210 37220 37230 37240 37250
37260
Col
GGACGCTTTCTCTAGCTTCAATGGAGTGACAGAGGGTATGCCCTGGATCTTACTATCTTTCTTTTCACTGTTCTACAATAGAACGTGGTT
Bur
37270 37280 37290 37300 37310 37320 37330 37340
37350
Col
TTGTTTGTGCTAGTTAATGTATAAACCATTCAAGGATGTGTGGTTGGATTGAAGCCGTCCTATTCATCATTATACCATGAATGATTGATG
Bur
37360 37370 37380 37390 37400 37410 37420 37430
37440
Col
GTGATGACCATTTTTAGTATGGTATTTGTGTTTTGCTTTGGTTTGCCTCGGGACTTAACTCTCTTGTTGAGTACAGTTAATATATTCAGT
Bur
37450 37460 37470 37480 37490 37500 37510 37520
37530
Col
CATTTCATTACTTGCGTATTTAACCAGAACCTTGCCGTATCTTTTTTCTGTGCAGCAAGAGTCATGACAAACAAAGTGACCGGGAGGTCT
Bur
37540 37550 37560 37570 37580 37590 37600 37610
37620
Col
AGAGGTTATGGATTTGTTAACTTCATAAGCGAGGATTCTGCCAACTCTGCTATTTCAGCAATGAATGGACAGGTTAGAAATCTAAAGAAT
Bur
37630 37640 37650 37660 37670 37680 37690 37700
37710
Col
CATTGATCTATCTATTTACCTATCATGTCAATTGCTGTGTTGTATGGTTAATCTTCCCCTTTTGTTGGTTTTGGGATGGTGAAATAGGAG
Bur
37720 37730 37740 37750 37760 37770 37780 37790
37800
Col
CTGAATGGGTTTAACATAAGTGTGAACGTTGCAAAAGATTGGCCAAGTTTGCCATTGTCTTTGGATGAGAGTATAGAAGAAGCTGAGAAG
Bur
37810 37820 37830 37840 37850 37860 37870 37880
37890
Col
AAAGAAAATAAGATGATGAGCCGATCTGTATGGAAAGATCCATTCGTTGATGCGTTCCTGATGAAGAAGAAGAATGCAGCTCTGAACAGG
Bur

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            37900     37910     37920     37930     37940     37950     37960     37970
37980

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AAAATATGGTCAAGGAGATCGACGATTCTTCCCGAGTATGTTGATTCGGCGGTGAGAATCTACAACGGCAAAACTCATGTGCGTTGTAAG
Bur
.....................................................................................

            37990     38000     38010     38020     38030     38040     38050     38060
38070

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ATCACAGAGGGGAAAGTTGGGCATAAATTCGGAGAGTTTGCGTTTACAAGAAAAGTGAAGAAGCATGCTAAAGCAAAGTAGCATCTTTGA
Bur
.....................................................................................
                                                                  End At5g47220 →

            38080     38090     38100     38110     38120     38130     38140     38150
38160

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GAATGAATTGGTCAGCTGCTTGAAAGGATTGTGTTGAAAAGCCAAAAACGAATCAAATCAATAAATTCTCAATAGGTAAAACTCATTAGC
Bur
.....................................................................................

            38170     38180     38190     38200     38210     38220     38230     38240
38250

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TCACATGATCATGTAGACGAATATTGAGCTTTAGAAAGTCTTTAGTTTTCTTGTCGATTTCGTATTTTTGGACCACAAAAGTGCCAATGT
Bur
.....................................................................................

            38260     38270     38280     38290     38300     38310     38320     38330
38340

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TATTTTGGAATTCGATTAACAAATATCAATTGTGGAGCTTCAATAACCAAACGAACGATGCACCTCCATAGTGCTTGTTCAAGAACTTGT
Bur
.....................................................................................

            38350     38360     38370     38380     38390     38400     38410     38420
38430

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ATTGTTTATATACAGAAGCAAGCCAATGGGGCCATGTTGAGTATTCTATTCGATCTAAAGATGTAAAAGAAGATTGAAAATGAAATGAGA
Bur
.....................................................................................

            38440     38450     38460     38470     38480     38490     38500     38510
38520

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ATCCAGTTTAAGGTGTTGTTGGATGGTACTAGTGATATTAGAGGCAAATGGTGTGAACTTGTTGACAAAATTGTGTCTTCTTCTCTCTTT
Bur
.....................................................................................

            38530     38540     38550     38560     38570     38580     38590     38600
38610

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GAGTTCACATTTCAGTGTCATAATTCGTAAGATTTGCGAGACTAATAATTAGTACAAGAATTTATTAATCAATATTCGTCGTTACTGGTT
Bur
.....................................................................................

            38620     38630     38640     38650     38660     38670     38680     38690
38700
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....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ATGGATTTGATATGTTTACTCAGAAACTGTCGTCTAGGCTTGAAGGGATTTATTATTCAGTTCACATTTTCATGCAATGGAGCCCTCACA
Bur
....................................................................................

             38710     38720     38730     38740     38750     38760     38770     38780
38790

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AGACCTGTAATAAGACGAGTTCTATTTGTAAGTTTTTTATGATTTATAAAAAGCTCAGAAATTCATTTATAGTCTATAGCTTTTATGGTT
Bur
....................................................................................

             38800     38810     38820     38830     38840     38850     38860     38870
38880

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TACATCTTGAGCTGAAAAATTAAAACTTTTGCTTGTAGATATTATAACTTACATAAGCTATGAATTATATATATAAATTTGTATTTCGGA
Bur
....................................................................................

             38890     38900     38910     38920     38930     38940     38950     38960
38970

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GCTAAAAATGTTATAATTTTATTCATAGATTTCATACTTCTATGTTGCTTACCTAAAATGTTAATTCAACCATATATTTTGAGTGTTAAG
Bur
....................................................................................

             38980     38990     39000     39010     39020     39030     39040     39050
39060

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GGGGTGTAAAAGCATATGGAATTATTTGTGTTAAAATGACAAATCCTCTGTTATTCAATCATCAATATTAAAAAGTTTTATAAAAATCCA
Bur
....................................................................................

             39070     39080     39090     39100     39110     39120     39130     39140
39150

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TTGTTATTGAAATAATGATTCCAAAAAAGTACCATCAAATCCAGTATTATGGAAATATTATAACCACTGGATTTTTGAATGACTTTAAGG
Bur
....................................................................................

             39160     39170     39180     39190     39200     39210     39220     39230
39240

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TGGTTTATAAGATTTTAACATGTTTTGTTTTTTGGAATTTGGAAGAACTTTAGAACAAATCATAACATTTAATCTAAAATCACCCAAAAA
Bur
....................................................................................

             39250     39260     39270     39280     39290     39300     39310     39320
39330

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TTCATCTAAAAACTCATTAAAATTCGAATCATTCAAACTATATGGTTGGATAACATAGAATTTGTCATTTCAACACCAATCATTTCAATG
Bur
....................................................................................

             39340     39350     39360     39370     39380     39390     39400     39410
39420

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
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Bur
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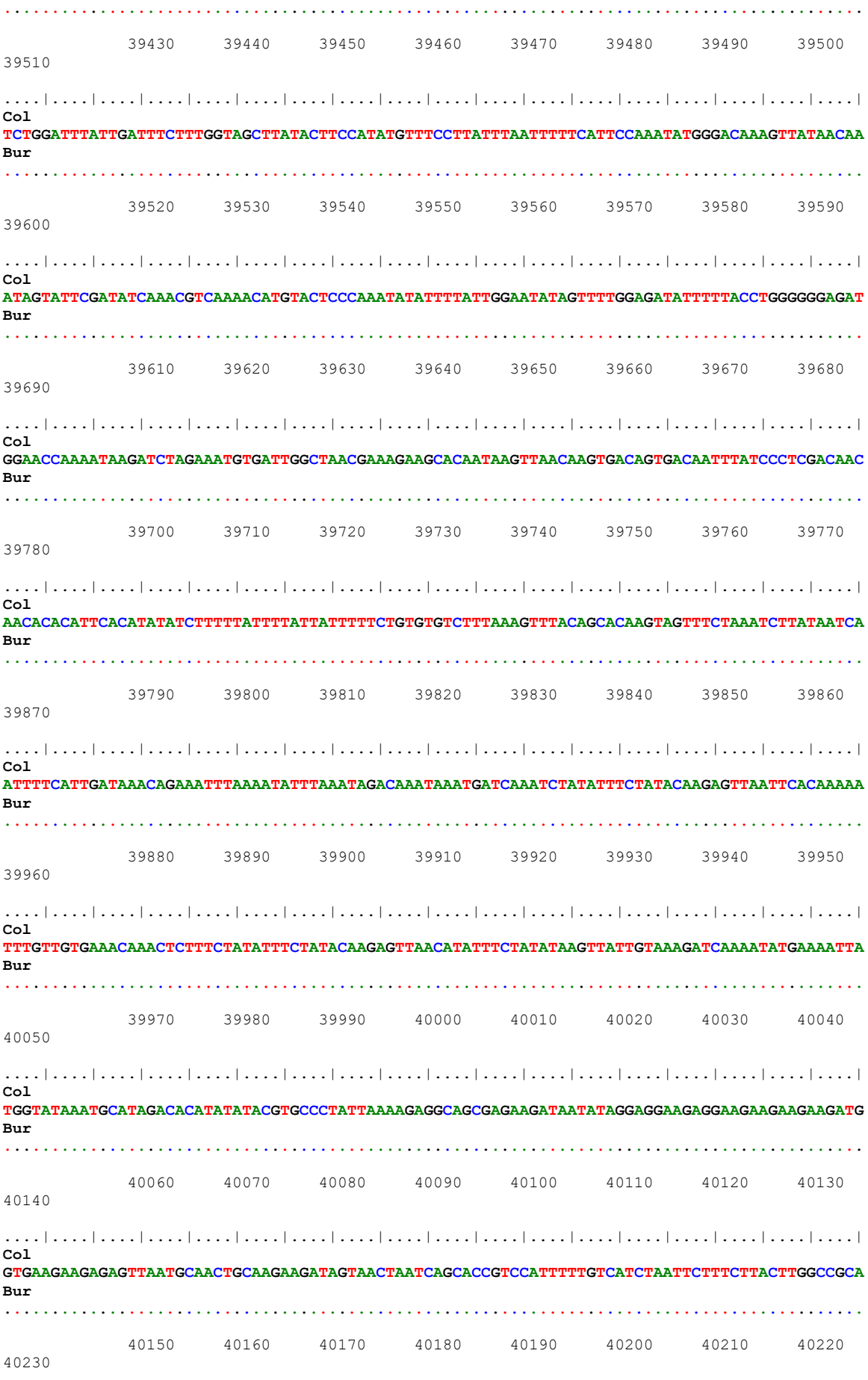
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39510
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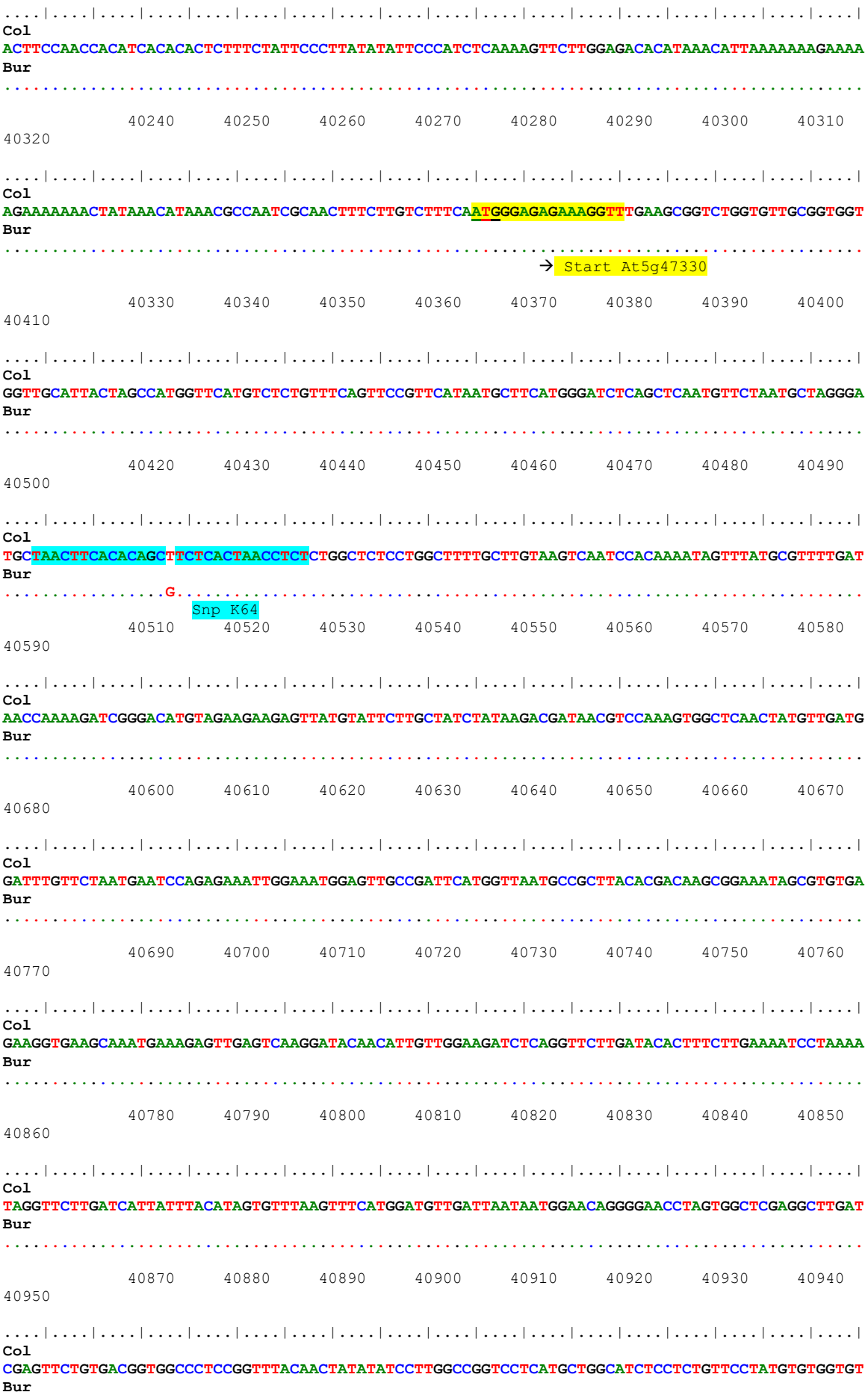
Bur
39520 39530 39540 39550 39560 39570 39580 39590
39600
Col
ATAGTATTCGATATCAAACGTCAAAACATGTACTCCCAAATATATTTTATTGGAATATAGTTTTGGAGATATTTTTACCTGGGGGGAGAT
Bur
39610 39620 39630 39640 39650 39660 39670 39680
39690
Col
GGAACCAAAATAAGATCTAGAAATGTGATTGGCTAACGAAAGAAGCACAATAAGTTAACAAGTGACAGTGACAATTTATCCCTCGACAAC
Bur
39700 39710 39720 39730 39740 39750 39760 39770
39780
Col
AACACACATTCACATATATCTTTTTATTTTATTATTTTTCTGTGTGTCTTTAAAGTTTACAGCACAAGTAGTTTCTAAATCTTATAATCA
Bur
39790 39800 39810 39820 39830 39840 39850 39860
39870
Col
ATTTTCATTGATAAACAGAAATTTAAAATATTTAAATAGACAAATAAATGATCAAATCTATATTTCTATACAAGAGTTAATTCACAAAAA
Bur
39880 39890 39900 39910 39920 39930 39940 39950
39960
Col
TTTGTTGTGAAACAAACTCTTTCTATATTTCTATACAAGAGTTAACATATTTCTATATAAGTTATTGTAAAGATCAAAATATGAAAATTA
Bur
39970 39980 39990 40000 40010 40020 40030 40040
40050
Col
TGGTATAAATGCATAGACACATATATACGTGCCCTATTAAAAGAGGCAGCGAGAAGATAATATAGGAGGAAGAGGAAGAAGAAGATG
Bur
40060 40070 40080 40090 40100 40110 40120 40130
40140
Col
GTGAAGAAGAGAGTTAATGCAACTGCAAGAAGATAGTAACTAATCAGCACCGTCCATTTTTGTCATCTAATTCTTTCTTACTTGGCCGCA
Bur
40150 40160 40170 40180 40190 40200 40210 40220
40230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Bur
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40320
Col
AGAAAAAAACTATAAACATAAACGCCAATCGCAACTTTCTTGTCTTTCAATGGGAGAGAAAGGTTTGAAGCGGTCTGGTGTTGCGGTGGT
Bur
Start At5g47330
40330 40340 40350 40360 40370 40380 40390 40400
40410
Col
GGTTGCATTACTAGCCATGGTTCATGTCTCTGTTTCAGTTCCGTTCATAATGCTTCATGGGATCTCAGCTCAATGTTCTAATGCTAGGGA
Bur
40420 40430 40440 40450 40460 40470 40480 40490
40500
Col
TGCTAACTTCACACAGCTTCTCACTAACCTCTCTGGCTCTCCTGGCTTTTGCTTGTAAGTCAATCCACAAAATAGTTTATGCGTTTTGAT
Bur
G
Snp K64
40510 40520 40530 40540 40550 40560 40570 40580
40590
Col
AACCAAAAGATCGGGACATGTAGAAGAAGAGTTATGTATTCTTGCTATCTATAAGACGATAACGTCCAAAGTGGCTCAACTATGTTGATG
Bur
40600 40610 40620 40630 40640 40650 40660 40670
40680
Col
GATTTGTTCTAATGAATCCAGAGAAATTGGAAATGGAGTTGCCGATTCATGGTTAATGCCGCTTACACGACAAGCGGAAATAGCGTGTGA
Bur
40690 40700 40710 40720 40730 40740 40750 40760
40770
Col
GAAGGTGAAGCAAATGAAAGAGTTGAGTCAAGGATACAACATTGTTGGAAGATCTCAGGTTCTTGATACACTTTCTTGAAAATCCTAAAA
Bur
40780 40790 40800 40810 40820 40830 40840 40850
40860
Col
TAGGTTCTTGATCATTATTTACATAGTGTTTAAGTTTCATGGATGTTGATTAATAATGGAACAGGGGAACCTAGTGGCTCGAGGCTTGAT
Bur
40870 40880 40890 40900 40910 40920 40930 40940
40950
Col
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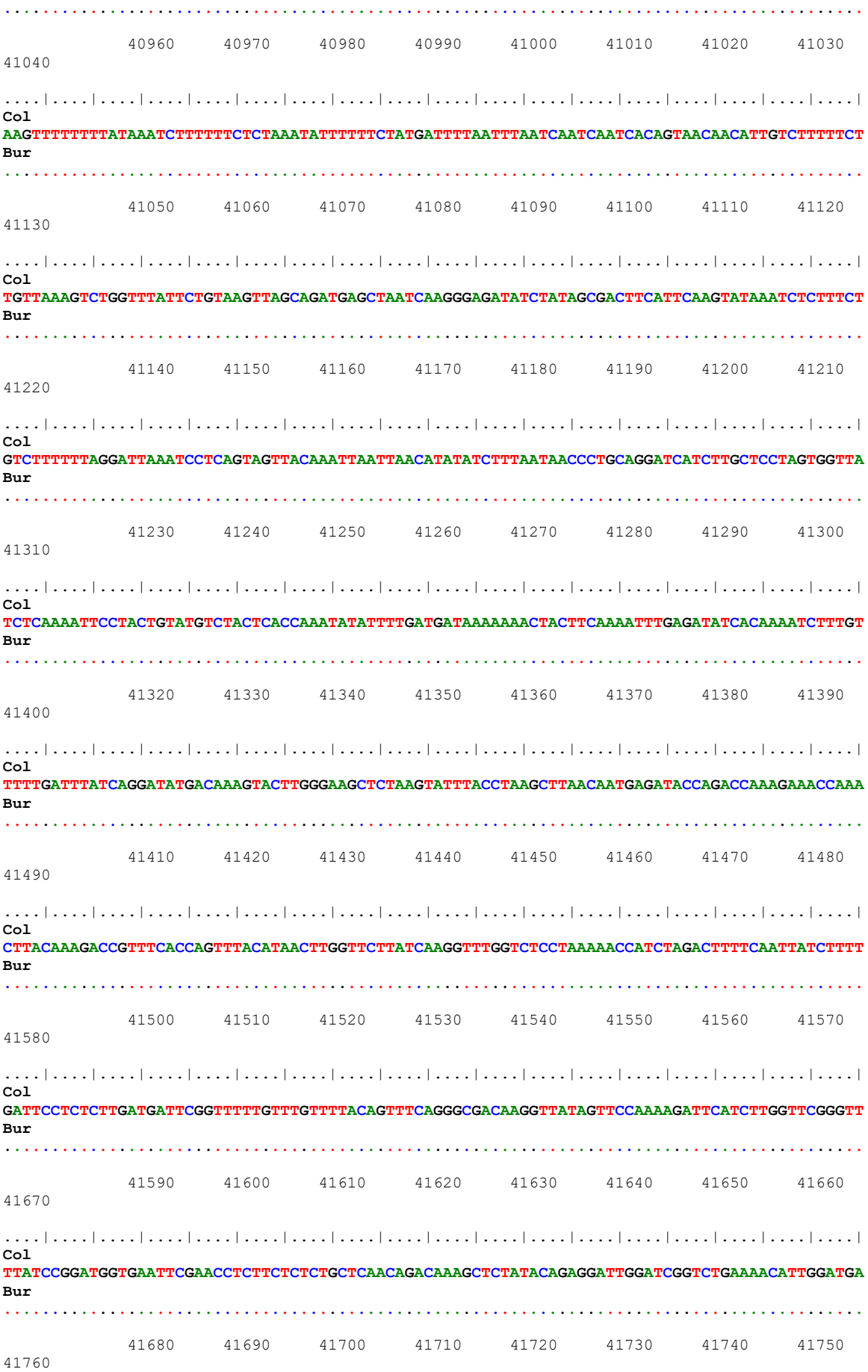
Bur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41040
Col
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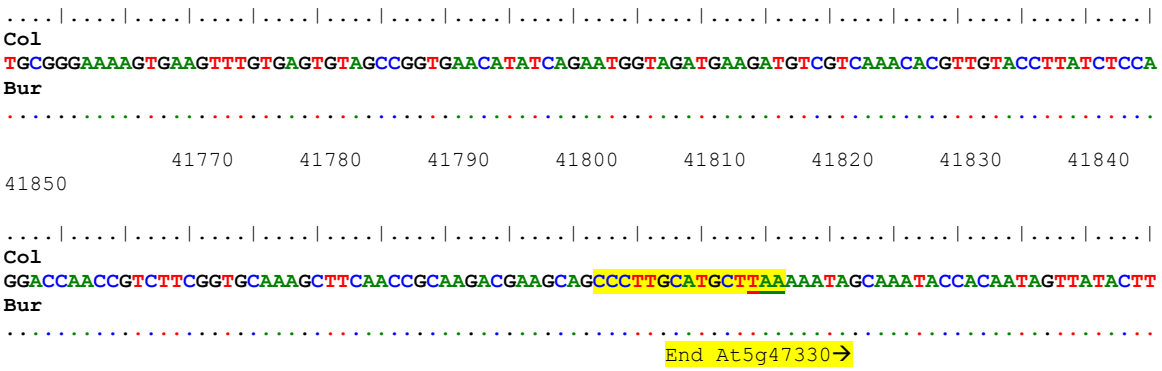
Bur
41050 41060 41070 41080 41090 41100 41110 41120
41130
Col
TGTTAAAGTCTGGTTTATTCTGTAAGTTAGCAGATGAGCTAATCAAGGGAGATATCTATAGCGACTTCATTCAAGTATAAATCTCTTTCT
Bur
41140 41150 41160 41170 41180 41190 41200 41210
41220
Col
GTCTTTTTTAGGATTAAATCCTCAGTAGTTACAAATTAATTAACATATATCTTTAATAACCCTGCAGGATCATCTTGCTCCTAGTGGTTA
Bur
41230 41240 41250 41260 41270 41280 41290 41300
41310
Col
TCTCAAAATTCCTACTGTATGTCTACTCACCAAATATATTTTGATGATAAAAAAACTACTTCAAAATTTGAGATATCACAAAATCTTTGT
Bur
41320 41330 41340 41350 41360 41370 41380 41390
41400
Col
TTTTGATTTATCAGGATATGACAAAGTACTTGGGAAGCTCTAAGTATTTACCTAAGCTTAACAATGAGATACCAGACCAAAGAAACCAAA
Bur
41410 41420 41430 41440 41450 41460 41470 41480
41490
Col
CTTACAAAGACCGTTTCACCAGTTTACATAACTTGGTTCTTATCAAGGTTTGGTCTCCTAAAAACCATCTAGACTTTTCAATTATCTTTT
Bur
41500 41510 41520 41530 41540 41550 41560 41570
41580
Col
GATTCCTCTCTTGATGATTCGGTTTTTGTTTGTTTTACAGTTTCAGGGCGACAAGGTTATAGTTCCAAAAGATTCATCTTGGTTCGGGTT
Bur
41590 41600 41610 41620 41630 41640 41650 41660
41670
Col
TTATCCGGATGGTGAATTCGAACCTCTTCTCTCTGCTCAACAGACAAAGCTCTATACAGAGGATTGGATCGGTCTGAAAACATTGGATGA
Bur
41680 41690 41700 41710 41720 41730 41740 41750
41760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Col
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Bur
41770 41780 41790 41800 41810 41820 41830 41840
41850
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GGACCAACCGTCTTCGGTGCAAAGCTTCAACCGCAAGACGAAGCAGCCCTTGCATGCTTAAAAATAGCAAATACCACAATAGTTATACTT
Bur
End At5g47330

Supplementary Text S4: *AT5G47260* and *AT5G47280* sequences in corresponding CRISPR-edited lines in Bur-0 and HIF10499 backgrounds.

Δ*AT5G47260* : CRISPR-edited lines for *AT5G47260*

WT

```
ggcctccaatggagaagagaaaccaaagagcgcaaggcagctgaaatattggcagtcttaaaggagaagagatttgtgttgttactggatggcatacagagggaattg
GlyLeuGlnTrpArgArgGluThrLysGluArgLysAlaAlaGluIleLeuAlaValLeuLysGluLysArgPheValLeuLeuLeuAspGlyIleGlnArgGluLeu
gatcttgaggaaattggagttccttttcccagccgagataatggatgcaaaattgtattcaccactcaatctctggaagcatgtgacgaaagcaagtgggttgat
AspLeuGluGluIleGlyValProPheProSerArgAspAsnGlyCysLysIleValPheThrThrGlnSerLeuGluAlaCysAspGluSerLysTrpValAsp
```

in Bur-0 background

117-1

```
tggagaagagaaaccaaagagcgcaaggcagctgaaatattggcagtcttaaaggagaagagatttgtgttgttactggatggca---cagagggaattggatcttgaggaaattggagttcc
TrpArgArgGluThrLysGluArgLysAlaAlaGluIleLeuAlaValLeuLysGluLysArgPheValLeuLeuLeuAspGlyT---hrGluGlyIleGlySer .
```

117-36

```
tggagaagagaaaccaaagagcgcaaggcagctgaaaatattggcagtcttaaaggagaagagatttgtgttgttactggatggca--cagagggaattggatcttgagg / 102nt / TAG
TrpArgArgGluThrLysGluArgLysAlaAlaGluAsnIleGlySerLeuLysGlyGluGluIleCysValValThrGlyTrpHi--sArgGlyAsnTrpIleLeuArg
```

85-7

```
tggagaagagaaaccaaagagcgcaaggcagctgaaatattggcagtcttaaaggagaagagatttgtgttgttactggatggcataacagagggaattggatcttgaggaaattggagtt
TrpArgArgGluThrLysGluArgLysAlaAlaGluIleLeuAlaValLeuLysGluLysArgPheValLeuLeuLeuAspGlyIleThrGluGlyIleGlySer .
```

in HIF 10499 background

95-14

```
gaaaccaaagagcgcaaggcagctgaaaatattggcagtcttaaaggagaagagatttgtgttgttactggatggcatatcagagggaattggatcttgagg / 102nt / TAG
GluThrLysGluArgLysAlaAlaGluAsnIleGlySerLeuLysGlyGluGluIleCysValValThrGlyTrpHisIleArgGlyAsnTrpIleLeuArg
```

98-7

```
tggagaagagaaaccaaagagcgcaaggcagctgaaatattggcagtcttaaaggagaagagatttgtgttgttactggatggcataacagagggaattggatcttgaggaaattggagttcctt
TrpArgArgGluThrLysGluArgLysAlaAlaGluIleLeuAlaValLeuLysGluLysArgPheValLeuLeuLeuAspGlyIleThrGluGlyIleGlySer .
```

105-12

```
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TrpArgArgGluThrLysGluArgLysAlaAlaGluL----------ysArgArgArgAspLeuCysCysTyrTrpMetAla .
```

ΔAt5g47280 : CRISPR-edited lines for AT5G47280

WT

```
Ggtctacctttgtctctgaaagtccttggcgcttcattaaacgatcgacctgaaacatattgggcaattgcagtggagaggttatcaagaggtgaacctgttgatgaaactcatgagagtaaagt
gtttgctcaaatcgaagca
GlyLeuProLeuSerLeuLysValLeuGlyAlaSerLeuAsnAspArgProGluThrTyrTrpAlaIleAlaValGluArgLeuSerArgGlyGluProValAspGluThrHisGluSerLysVa
lPheAlaGlnIleGluAla actctagaaaatctcgatccaaaaaccaaagagtgtttcttgatatgggtgctttccctgaaggcaagaaa
ThrLeuGluAsnLeuAspProLysThrLysGluCysPheLeuAspMetGlyAlaPheProGluGlyLysLys
```

in Bur-0 background

21-20

```
ggtctacctttgtctctgaaagtccttggcgcttcattaaacgatcgacctgaaacatattgggcaattgtcagtggagaggttatcaagaggtgaacctgttgatgaaactcatgag
GlyLeuProLeuSerLeuLysValLeuGlyAlaSerLeuAsnAspArgProGluThrTyrTrpAlaIleValSerGlyGluValIleLysArg .
```

160-2

Ggtctacctttgtctctgaaagtccttgg----------
aacgatcgacctgaaacatattgggcaattgtcagtggagaggttatcaagaggtgaacctgttgatgaaactcatgagagtaaagtgtttgctcaaatcgaagca
GlyLeuProLeuSerLeuLysValLeuGl----------
yThrIleAspLeuLysHisIleGlyGlnLeuSerValGluArgLeuSerArgGlyGluProValAspGluThrHisGluSerLysValPheAlaGlnIleGluAla

163-16

ggtctacctttgtctctgaaagtccttggcgcttcattaaacgatcgacctgaaacatattgggcaattgacagtggagaggttatcaagaggtgaacctgttgatgaaactcatga
GlyLeuProLeuSerLeuLysValLeuGlyAlaSerLeuAsnAspArgProGluThrTyrTrpAlaIleAspSerGlyGluValIleLysArg .

in HIF 10499 background

170-4

ggtctacctttgtctctgaaagtccttgg-gcttcattaaacgatcgacctgaaacatattgggcaattgacagtggagaggttatcaagaggtga
GlyLeuProLeuSerLeuLysValLeuGl-yLeuHis .

172-9

ggtctacctttgtctctgaaagtccttggcgcttcattaaacgatcgacctgaaacatattgggcaattgacagtggagaggttatcaagaggtgaacctgttgatgaaactcat
GlyLeuProLeuSerLeuLysValLeuGlyAlaSerLeuAsnAspArgProGluThrTyrTrpAlaIleAspSerGlyGluValIleLysArg .

176-15

ggtctacctttgtctctgaaagtccttgg----------------
cgacctgaaacatattgggcaattgcagtggagaggttatcaagaggtgaacctgttgatgaaactcatgagagtaaagtgtttgctcaaatcgaagcaactctag
GlyLeuProLeuSerLeuLysValLeuGl----------------
yAspLeuLysHisIleGlyGlnLeuGlnTrpArgGlyTyrGlnGluValAsnLeuLeuMetLysLeuMetArgValLysCysLeuLeuLysSerLysGlnLeu

Table S1: List of primers used for qPCR and CHOP qPCR

Gene	Experimentation	LP primer (5' > 3')	RP primer (5' > 3')
At1g47550	qPCR	CTCGCTCTTTCCGTCAAATC	CCCCAGTGTGAAAGTGCATC
At1g54610	qPCR	GGTCGGACAGAGGTAGAGCAG	GTATGGTTCACGGGGTTTGT
At5g38470	qPCR	TGTACTCGGGTATCCCTGCT	CTGGAGCTGCTGCTTGTTG
At5g47260	qPCR	AAGGTGGTCCAATCGGGAAC	GATGGGGCAATCTGGTGTGA
At5g47280	qPCR	AGTCTCTGGCTTGAGAGGGT	ATGGTCGAAGGTAGTTCCGC
At5g47260	CHOP qPCR	TGCGTCGACCTATCGTTACA	CCATGCCGTATCAAGCAAC
At5g13440	CHOP qPCR	ACAAGCCAATTTTTGCTGAGC	ACAACAGTCCGAGTGTCATGGT
At5g47400	CHOP qPCR	GAAGCCGAACTGCAAACTGT	ATGGTCCGGCTCTAGGAAAA

Supplementary references

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