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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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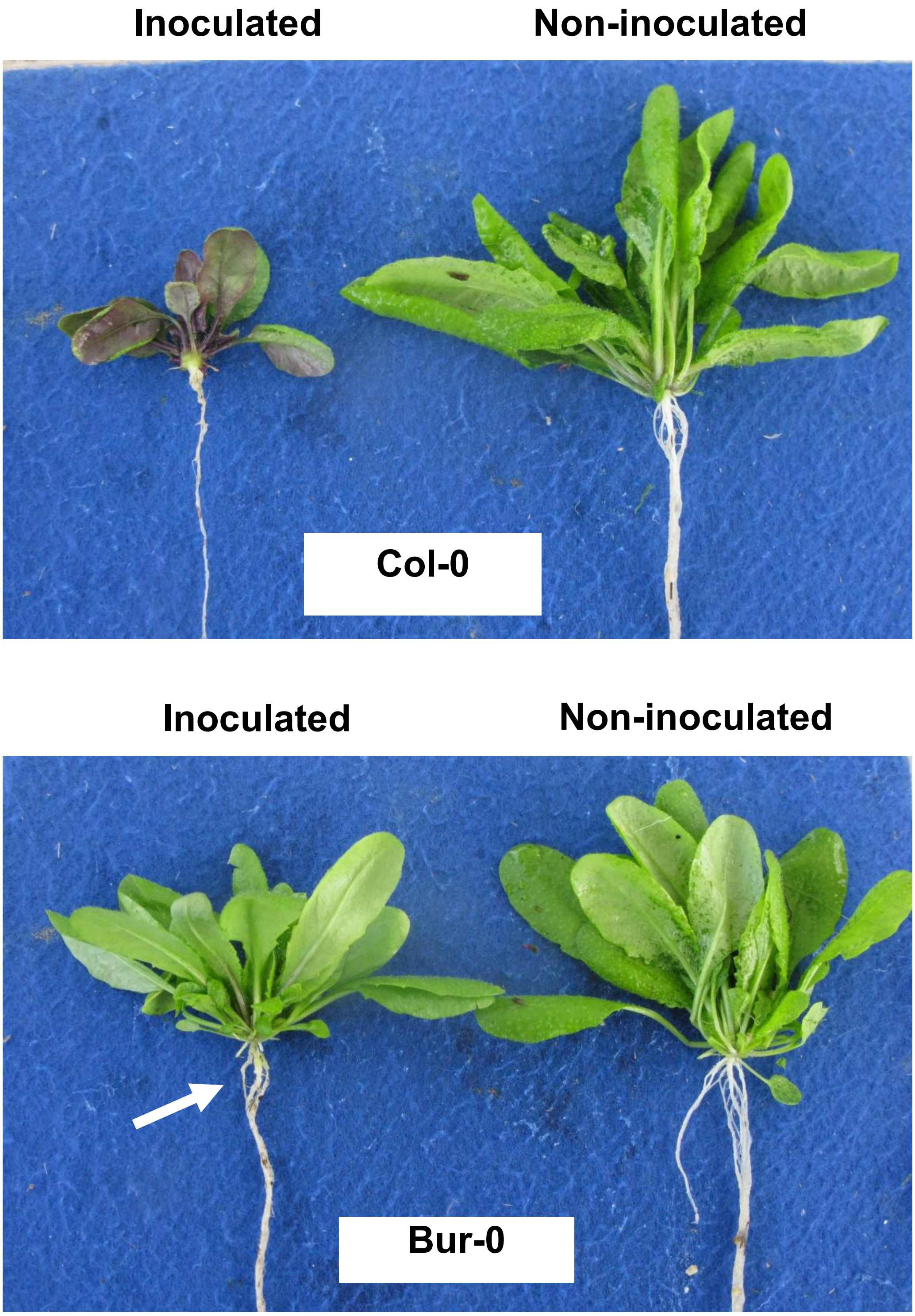
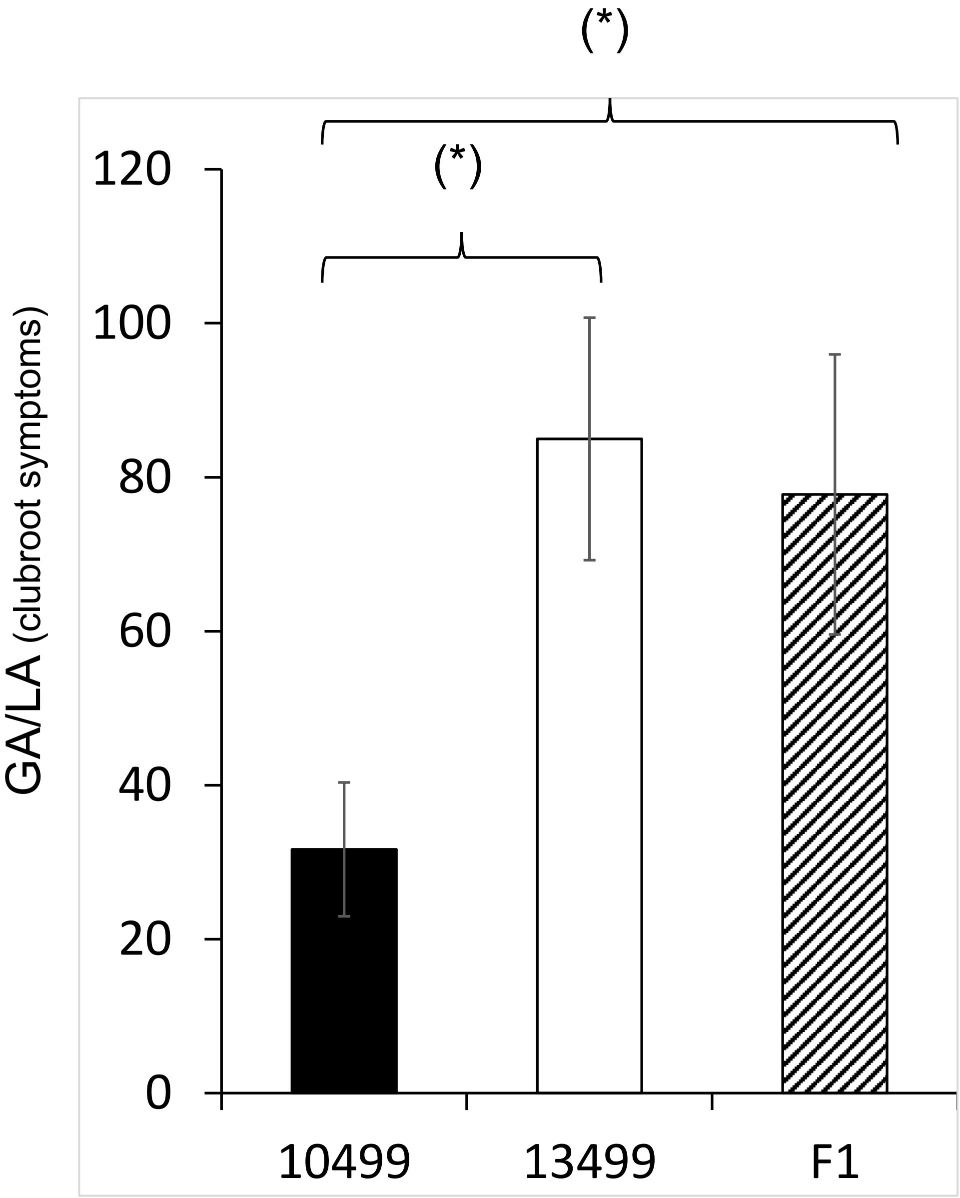
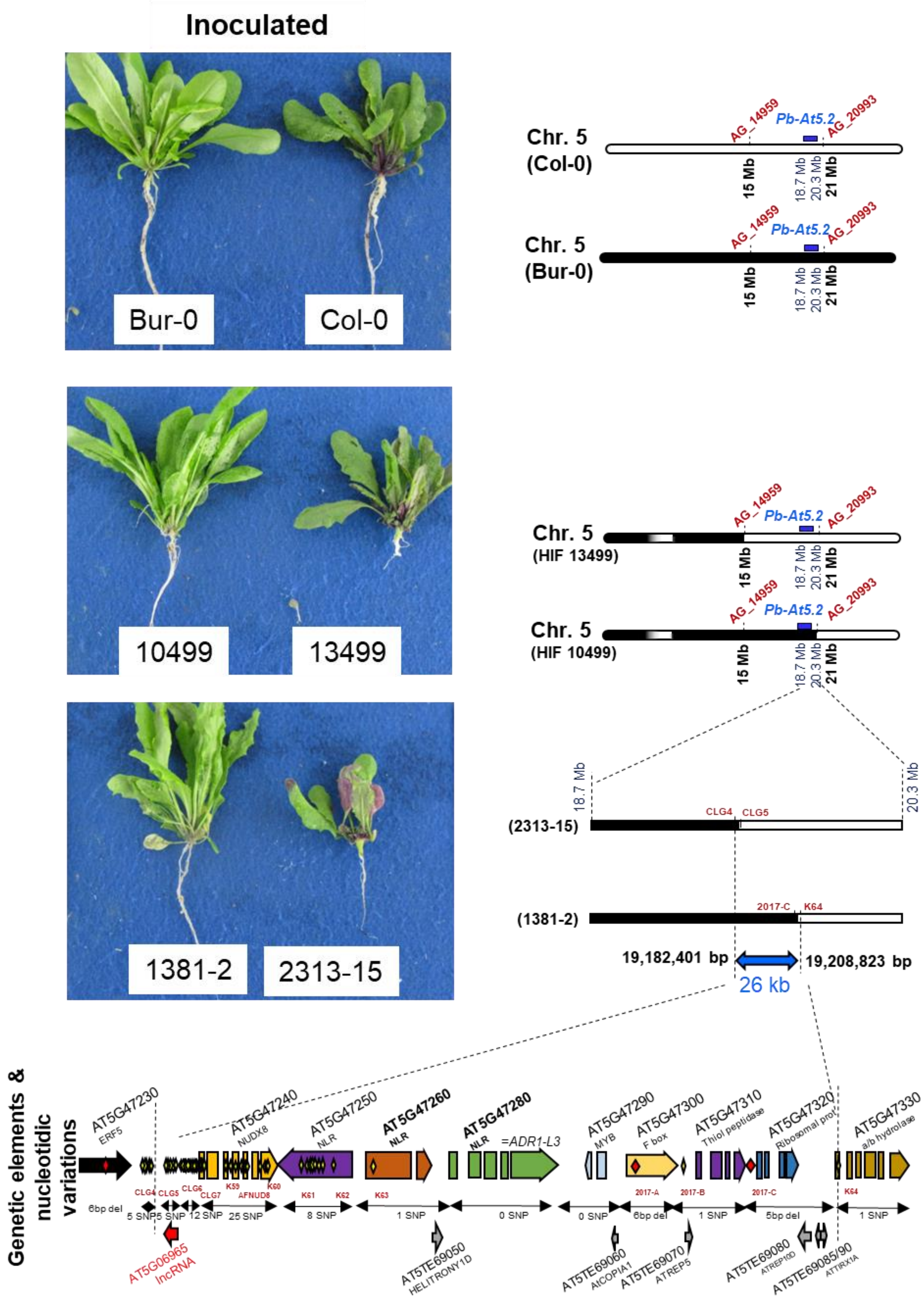
Supplementary Figures



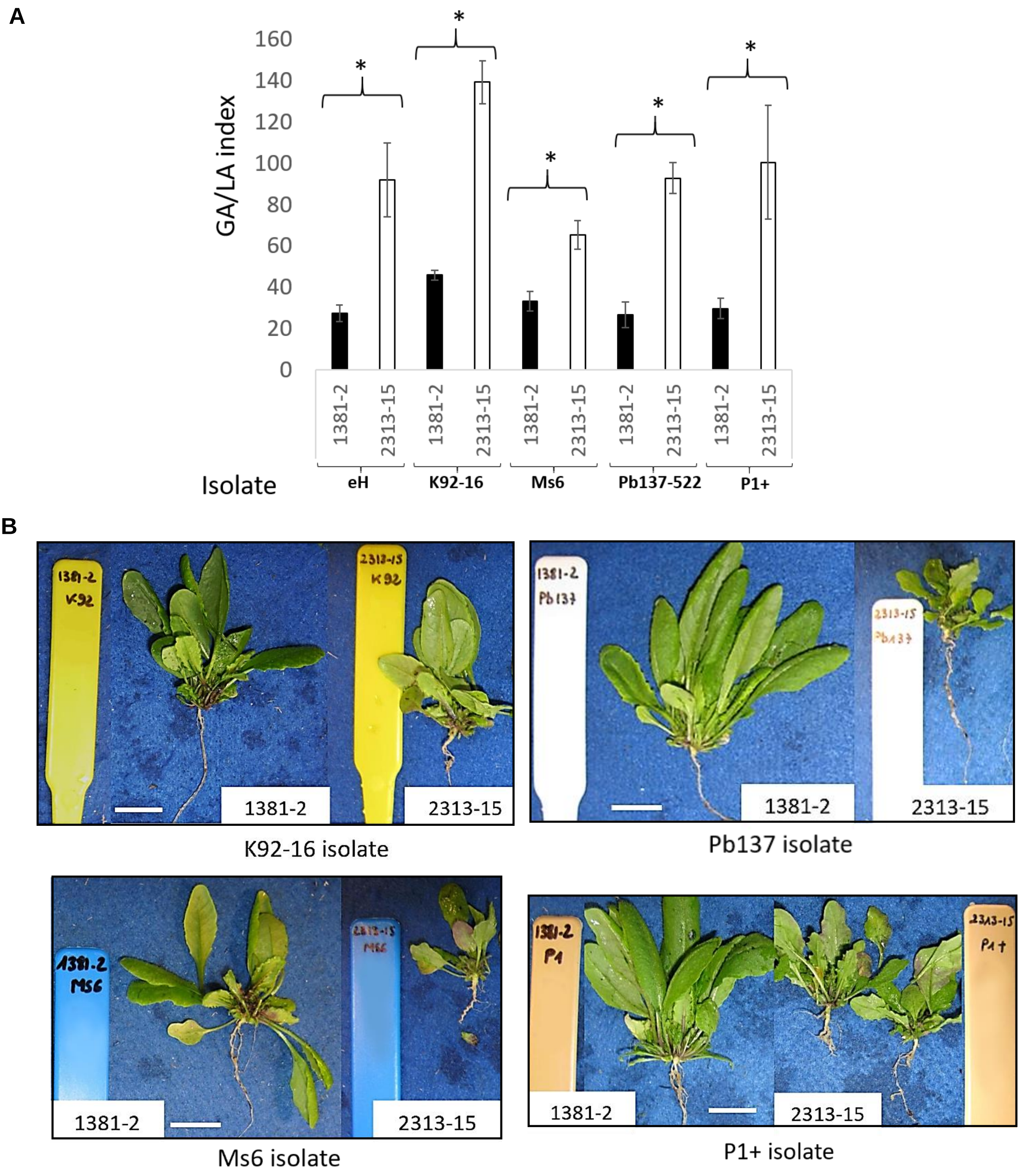
Supplementary Figure S1 | Illustration of partial resistance to eH isolate in Bur-0, compared to the full susceptibility in Col-0. Observations were done at 21 days post-inoculation. The white arrow indicates the presence of limited amount of galls in inoculated Bur-0. Plant individuals representative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



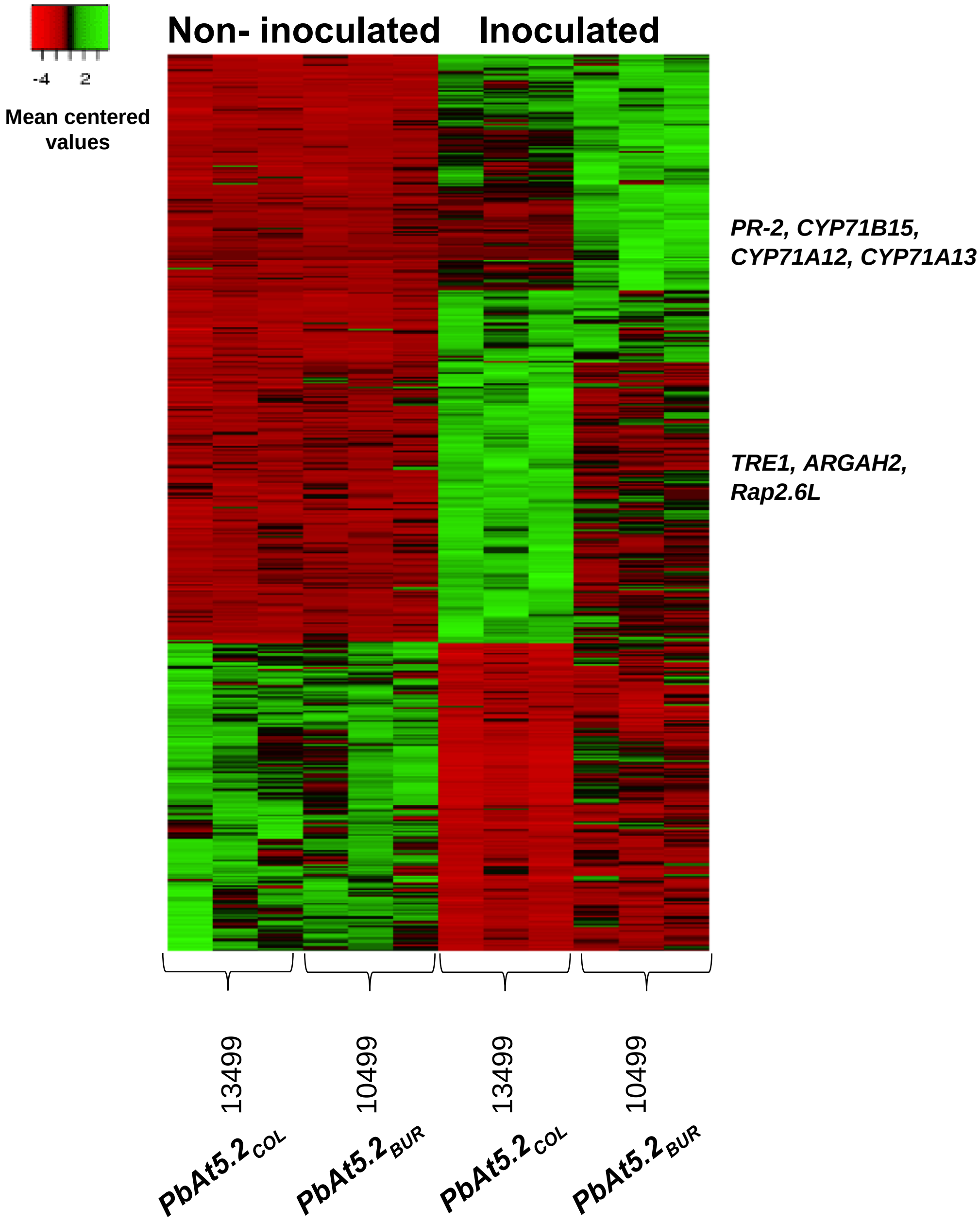
Supplementary Figure S2 | Comparison of GA/LA disease index in the F1 progeny and in the parental lines 10499 and 13499. GA/LA disease index is calculated through image analysis (details in the material and method part) from inoculated plants at 21 days post inoculation. Data are from 3 replicates (n=3). 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).

Bur-0 background	***AT5G47260***	Bur-0 (WT)	tggagaagagaaaccaaagagcgcaaggcagctgaaatattggcagtcttaaaggagaagagatttgtgttgttactggatggcatacagagggaattggatcttgaggaaattggagttcctttt TrpArgArgGluThrLysGluArgLysAlaAlaGluIleLeuAlaValLeuLysGluLysArgPheValLeuLeuLeuAspGlyIleGlnArgGluLeuAspLeuGluGluIleGlyValProPhe
	Bur-0 (Δ47260)	117-1	tggagaagagaaaccaaagagcgcaaggcagctgaaatattggcagtcttaaaggagaagagatttgtgttgttactggatggca--cagagggaattggatcttgaggaaattggagttcc TrpArgArgGluThrLysGluArgLysAlaAlaGluIleLeuAlaValLeuLysGluLysArgPheValLeuLeuLeuAspGlyT--hrGluGlyIleGlySerSTOP
		117-36	tggagaagagaaaccaaagagcgcaaggcagctgaaaatattggcagtcttaaaggagaagagatttgtgttgttactggatggca--cagagggaattggatcttgagg / 102nt / TAG TrpArgArgGluThrLysGluArgLysAlaAlaGluAsnIleGlySerLeuLysGlyGluGluIleCysValValThrGlyTrpHi--sArgGlyAsnTrpIleLeuArg STOP
		85-7	tggagaagagaaaccaaagagcgcaaggcagctgaaatattggcagtcttaaaggagaagagatttgtgttgttactggatggcataacagagggaattggatcttgaggaaattggagtt TrpArgArgGluThrLysGluArgLysAlaAlaGluIleLeuAlaValLeuLysGluLysArgPheValLeuLeuLeuAspGlyIleThrGluGlyIleGlySerSTOP
	AT5G47280	Bur-0 (WT)	Ggtctacctttgtctctgaaagtccttggcgcttcattaaacgatcgacctgaaacatattgggcaattgcagtggagaggttatcaagaggtgaacctgttgatgaaactcatgagagtaaagtgtttgct GlyLeuProLeuSerLeuLysValLeuGlyAlaSerLeuAsnAspArgProGluThrTyrTrpAlaIleAlaValGluArgLeuSerArgGlyGluProValAspGluThrHisGluSerLysValPheAla
	Bur-0 (Δ47280)	21-20	ggtctacctttgtctctgaaagtccttggcgcttcattaaacgatcgacctgaaacatattgggcaattgtcagtggagaggttatcaagaggtgaacctgttgatgaaactcatgag GlyLeuProLeuSerLeuLysValLeuGlyAlaSerLeuAsnAspArgProGluThrTyrTrpAlaIleValSerGlyGluValIleLysArgSTOP
		160-2	ggtctacctttgtctctgaaagtccttgg----------aacgatcgacctgaaacatattgggcaattgtcagtggagaggttatcaagaggtgaacctgttgatgaaactcatgagagtaaagtgttt GlyLeuProLeuSerLeuLysValLeuGl----------yThrIleAspLeuLysHisIleGlyGlnLeuSerValGluArgLeuSerArgGlyGluProValAspGluThrHisGluSerLysValPhe
		163-16	ggtctacctttgtctctgaaagtccttggcgcttcattaaacgatcgacctgaaacatattgggcaattgacagtggagaggttatcaagaggtgaacctgttgatgaaactcatga GlyLeuProLeuSerLeuLysValLeuGlyAlaSerLeuAsnAspArgProGluThrTyrTrpAlaIleAspSerGlyGluValIleLysArgSTOP
HIF 10499 background	***AT5G47260***	HIF 10499 (WT)	tggagaagagaaaccaaagagcgcaaggcagctgaaatattggcagtcttaaaggagaagagatttgtgttgttactggatggcatacagagggaattggatcttgaggaaattggagttcctttt TrpArgArgGluThrLysGluArgLysAlaAlaGluIleLeuAlaValLeuLysGluLysArgPheValLeuLeuLeuAspGlyIleGlnArgGluLeuAspLeuGluGluIleGlyValProPhe
	HIF 10499 (Δ47260)	95-14	.........gaaaccaaagagcgcaaggcagctgaaaatattggcagtcttaaaggagaagagatttgtgttgttactggatggcatatcagagggaattggatcttgagg / 102nt / TAG ....GluThrLysGluArgLysAlaAlaGluAsnIleGlySerLeuLysGlyGluGluIleCysValValThrGlyTrpHisIleArgGlyAsnTrpIleLeuArg STOP
		98-7	tggagaagagaaaccaaagagcgcaaggcagctgaaatattggcagtcttaaaggagaagagatttgtgttgttactggatggcataacagagggaattggatcttgaggaaattggagttcctt TrpArgArgGluThrLysGluArgLysAlaAlaGluIleLeuAlaValLeuLysGluLysArgPheValLeuLeuLeuAspGlyIleThrGluGlyIleGlySerSTOP
		105-12	tggagaagagaaaccaaagagcgcaaggcagctgaaa-------------aaaggagaagagatttgtgttgttactggatggcataacagagggaattggatcttgaggaaattggagttccttt TrpArgArgGluThrLysGluArgLysAlaAlaGluL-------------ysArgArgArgAspLeuCysCysTyrTrpMetAlaSTOP
	AT5G47280	HIF 10499 (WT)	Ggtctacctttgtctctgaaagtccttggcgcttcattaaacgatcgacctgaaacatattgggcaattgcagtggagaggttatcaagaggtgaacctgttgatgaaactcatgagagtaaagtgtttgct GlyLeuProLeuSerLeuLysValLeuGlyAlaSerLeuAsnAspArgProGluThrTyrTrpAlaIleAlaValGluArgLeuSerArgGlyGluProValAspGluThrHisGluSerLysValPheAla
	HIF 10499 (Δ47280)	170-4	ggtctacctttgtctctgaaagtccttgg-gcttcattaaacgatcgacctgaaacatattgggcaattgacagtggagaggttatcaagaggtga GlyLeuProLeuSerLeuLysValLeuGl-yLeuHisSTOP
		172-9	ggtctacctttgtctctgaaagtccttggcgcttcattaaacgatcgacctgaaacatattgggcaattgacagtggagaggttatcaagaggtgaacctgttgatgaaactcat GlyLeuProLeuSerLeuLysValLeuGlyAlaSerLeuAsnAspArgProGluThrTyrTrpAlaIleAspSerGlyGluValIleLysArgSTOP
		176-15	ggtctacctttgtctctgaaagtccttgg----------------cgacctgaaacatattgggcaattgcagtggagaggttatcaagaggtgaacctgttgatgaaactcatgagagtaaagtgtttgctcaaatcgaagcaactctag GlyLeuProLeuSerLeuLysValLeuGl----------------yAspLeuLysHisIleGlyGlnLeuGlnTrpArgGlyTyrGlnGluValAsnLeuLeuMetLysLeuMetArgValLysCysLeuLeuLysSerLysGlnLeuSTOP

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.

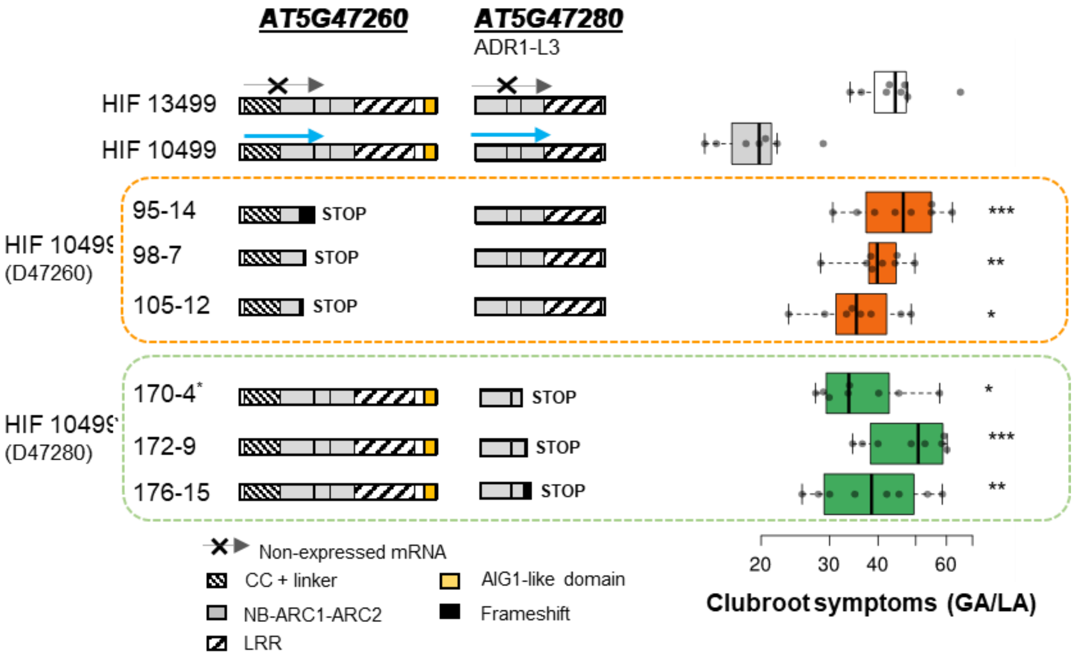
```
At5g47260

MGNNFSVESPSLAPFLCGKRKYLYNLERNLEALHKVMQDLNAMRNDLLKRLSKEEEIGLQGLQEVKEWISMVEEI -75 – Col-0
...T....................................................................... -75 – Bur-0
........................................................................... -75 – Bur-0(Δ47260)117-1
........................................................................... -75 – Bur-0(Δ47260)117-36
........................................................................... -75 – Bur-0(Δ47260)85-7
........................................................................... -75 – 10499(Δ47260)95-14
........................................................................... -75 – 10499(Δ47260)98-7
........................................................................... -75 – 10499(Δ47260)105-12

                             CC + linker
EPKANRLLDESVSEIQRLSRYGYCSLIPASTYRYSEKVLTTMEGVETLRSKGVFEAVVHRALPPLVIKMPPIQLT -150 – Col-0
........................................................................... -150 – Bur-0
........................................................................... -150 – Bur-0(Δ47260)117-1
........................................................................... -150 – Bur-0(Δ47260)117-36
........................................................................... -150 – Bur-0(Δ47260)85-7
........................................................................... -150 – 10499(Δ47260)95-14
........................................................................... -150 – 10499(Δ47260)98-7
........................................................................... -150 – 10499(Δ47260)105-12

VG-motif                 P-loop/Kin-1            RNBS-A
VSQAKLLDTAWARLMDINVGTLGIYGRGGVGKTTLLTKLRNKLLVDAFGLVIFVVVGFEEVESIQDEIGKRLGLQ -225 – Col-0
........................................................................... -225 – Bur-0
........................................................................... -225 – Bur-0(Δ47260)117-1
........................................................................... -225 – Bur-0(Δ47260)117-36
........................................................................... -225 – Bur-0(Δ47260)85-7
........................................................................... -225 – 10499(Δ47260)95-14
........................................................................... -225 – 10499(Δ47260)98-7
........................................................................... -225 – 10499(Δ47260)105-12

              → WalkerB/Kin-2 →                    RNBS-B
WRRETKERKAAEILAVLKEKRFVLLLDGIQRELDLEEIGVPFPSRDNGCKIVFTTQSLEACDESKWVDAKVEITC -300 – Col-0
........................................................................... -300 – Bur-0
............................-TEGIGS-STOP                                    -259 – Bur-0(Δ47260)117-1
............NIGSLKGEICVVTGWH-RGNWILR (+ 34aa) - STOP                        -294 – Bur-0(Δ47260)117-36
.............................TEGIGS-STOP                                    -260 – Bur-0(Δ47260)85-7
............NIGSLKGEICVVTGWHIRGNWILR (+34aa)-STOP                           -295 - 10499(Δ47260)95-14
.............................TEGIGS-STOP                                    -260 – 10499(Δ47260)98-7
............KRRRDLCCTWMA-STOP                                               -249 – 10499(Δ47260)105-12

 RNBS-C                               GLPL
LSPEEAWDLFQETVGENTLRSHQDIPKLARVVASTCRGLPLALNLIGEAMSGKRTVREWRYTIHVLASSTAEFPD -375 – Col-0
........................................................................... -375 – Bur-0

                         RNBS-D
MEDGTLPILKSIYDNMSDEIIRLCFLYCALFPENLDIGKEDLVNYWICEGILAKEDREEAEIQGYEIICDLVRMR -450 – Col-0
........................................................................... -375 – Bur-0

            MHD                                             LLR1
LLMESGNGNCVKMHGMVREMALWIASEHFVVVGGERIHQMLNVNDWRMIRRMSVTSTQIQNISDSPQCSELTTLV -525 – Col-0
........................................................................... -375 – Bur-0

   LRR2                    LLR3                    LLR4
FRRNRHLKWISGAFFQWMTGLVVLDLSFNRELAELPEEVSSLVLLRFLNLSWTCIKGLPLGLKELKSLIHLDLDY -600 – Col-0
........................................................................... -375 – Bur-0

  LRR5            LRR6                     LRR7
TSNLQEVDVIASLLNLQVLRLFHSVSMDLKLMEDIQLLKSLKELSLTVRGSSVLQRLLSIQRLASSIRRLHLTET -675 – Col-0
........................................................................... -375 – Bur-0

   LRR8              LLR9
TIVDGGILSLNAIFSLCELDILGCNILEITIDWRCTIQREIIPQFQNIRTMTIHRCEYLRDLTWLLLAPCLGELS -750 – Col-0
........................................................................... -375 – Bur-0

VSECPQMEEVISKDKAMAKLGNTSEQPFQNLTKLVLDGLPKLESIYWTPLPFPVLEYLVIRRCPELRRLPFNSES -825 – Col-0
........................................................................... -375 – Bur-0

TIGNQVETIIEEQVIKIVEWEDEATKQRFSHFNNRDFVQMAEDPKMDGLTSESHPIQTIDLVGTTGSGETATANN -900 – Col-0
........................................................................... -375 – Bur-0

 AIG1-type Nucleotide Binding Domain
IQGKKVVQSGTHATVVTMECQTYKVFTPDCPINNMIDTPGTNFLLCYT -948 – Col-0
```

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

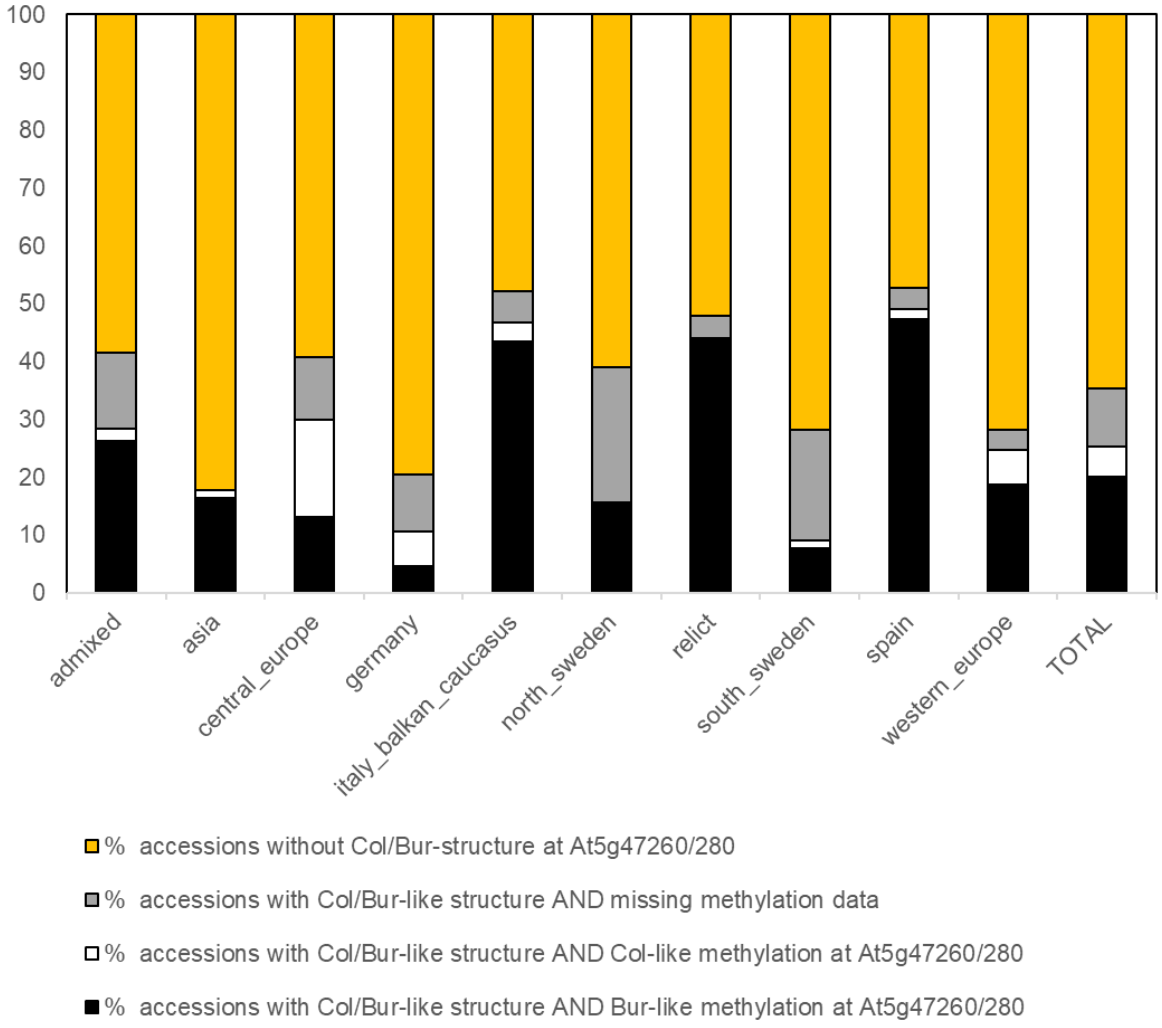
At5g47280-ADR1-L3

```
          P-loop/Kin-1             RNBS-A
MLFNLNDEARIIGISGMIGSGKTILAKELARDEEVRGHFANRVLFLTVSQSPNLEELRSLIRDFLTGHEAGFGTA -75 – Col-0
........................................................................... -75 – Bur-0
........................................................................... -75 – Bur-0(Δ47280)-21-20
........................................................................... -75 – Bur-0(Δ47280)-160-2
........................................................................... -75 – Bur-0(Δ47280)-163-16
........................................................................... -75 – 10499 (Δ47280)-170-4
........................................................................... -75 – 10499 (Δ47280)-172-9
........................................................................... -75 – 10499 (Δ47280)-176-15

   Walker B/Kin-2              RNBS-B                  RNBS-C
LPESVGHTRKLVILDDVRTRESLDQLMFNIPGTTTLVVSQSKLVDPRTTYDVELLNEHDATSLFCLSAFNQKSVP -150 – Col-0
........................................................................... -150 – Bur-0
........................................................................... -150 – Bur-0(Δ47280)-21-20
........................................................................... -150 – Bur-0(Δ47280)-160-2
........................................................................... -150 – Bur-0(Δ47280)-163-16
........................................................................... -150 – 10499 (Δ47280)-170-4
........................................................................... -150 – 10499 (Δ47280)-172-9
........................................................................... -150 – 10499 (Δ47280)-176-15

                 GLPL   ←               →
SGFSKSLVKQVVGESKGLPLSLKVLGASLNDRPETYWAIAVERLSRGEPVDETHESKVFAQIEATLENLDPKTKE -225 – Col-0
........................................................................... -225 – Bur-0
........................................VSGEVILR-STOP                       -197 – Bur-0(Δ47280)-21-20
SGFSKSLVKQVVGESKGLPLSLKVLG--TIALKHIGQL-SVERLSRGEPVDETHESKVFAQIEATLENLDPKTKE -222 – Bur-0(Δ47280)-160-2
........................................VSGEVILR-STOP                       -197 – Bur-0(Δ47280)-163-16
..........................LH-STOP                                           -178 – 10499 (Δ47280)-170-4
........................................DSGEVILR-STOP                       -197 – 10499 (Δ47280)-172-9
SGFSKSLVKQVVGESKGLPLSLKVLGDLKHIGQLQWRGTQEVNLLMKLMRVKCLLKSKQL-STOP           -210 – 10499 (Δ47280)-176-15

 RNBS-D                                                             MHD
CFLDMGAFPEGKKIPVDVLINMLVKIHDLEDAAAFDVLVDLANRNLLTLVKDPTFVAMGTSYYDIFVTQHDVLRD -300 – Col-0
........................................................................... -300 – Bur-0
........................................................................... -297 – Bur-0(Δ47280)-160-2

VALHLTNRGKVSRRDRLLMPKRETMLPSEWERSNDEPYNARVVSIHTGEMTEMDWFDMDFPKAEVLIVNFSSDNY -375 – Col-0
........................................................................... -375 – Bur-0
........................................................................... -372 – Bur-0(Δ47280)-160-2

                  LLR1                       LLR2             LLR3
VLPPFIAKMGMLRVFVIINNGTSPAHLHDFPIPTSLTNLRSLWLERVHVPELSSSMIPLKNLHKLYLIICKINNS -450 – Col-0
........................................................................... -450 – Bur-0
........................................................................... -447 – Bur-0(Δ47280)-160-2

                       LLR4                    LLR5                LLR6
FDQTAIDIAQIFPKLTDITIDYCDDLAELPSTICGITSLNSISITNCPNIKELPKNISKLQALQLLRLYACPELK -525 – Col-0
........................................................................... -525 – Bur-0
........................................................................... -522 – Bur-0(Δ47280)-160-2

LLR7              LLR8               LLR9
SLPVEICELPRLVYVDISHCLSLSSLPEKIGNVRTLEKIDMRECSLSSIPSSAVSLTSLCYVTCYREALWMWKEV -600 – Col-0
........................................................................... -600 – Bur-0
........................................................................... -597 – Bur-0(Δ47280)-160-2

EKAVPGLRIEATEKWFNMTWPDE -623 – Col-0
....................... -623 – Bur-0
....................... -600 – Bur-0(Δ47280)-160-2
```

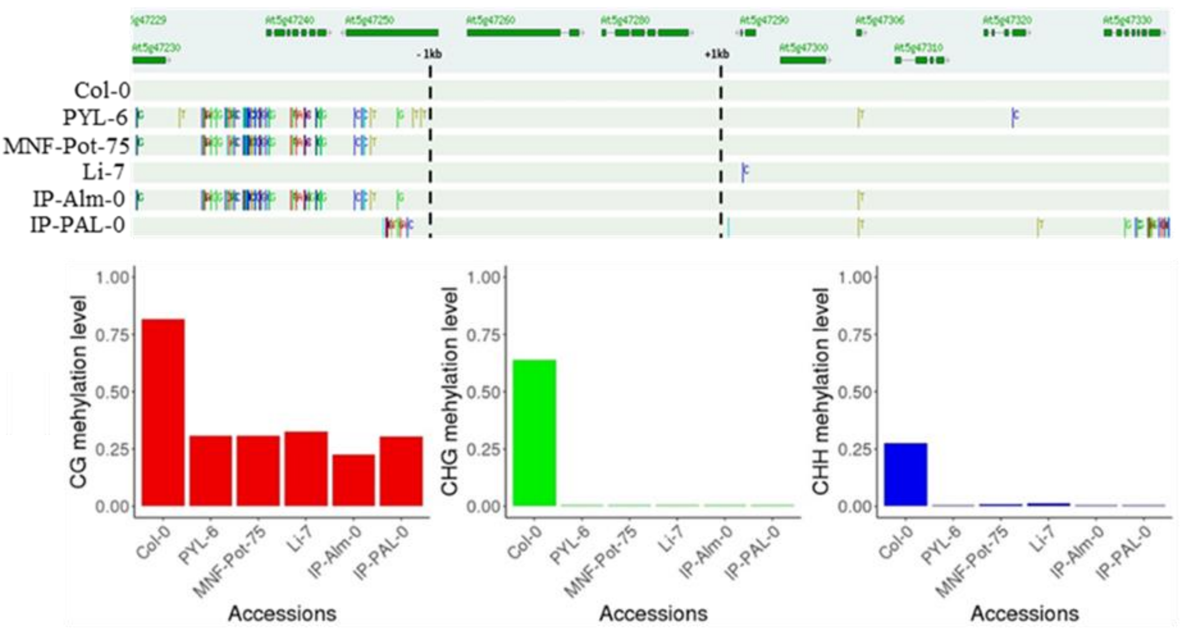
Supplementary Figure S8 | Full alignment of *AT5G47280* protein sequences in CRISPR-Cas9 edited lines in Bur-0 and HIF 10499 backgrounds.



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*.

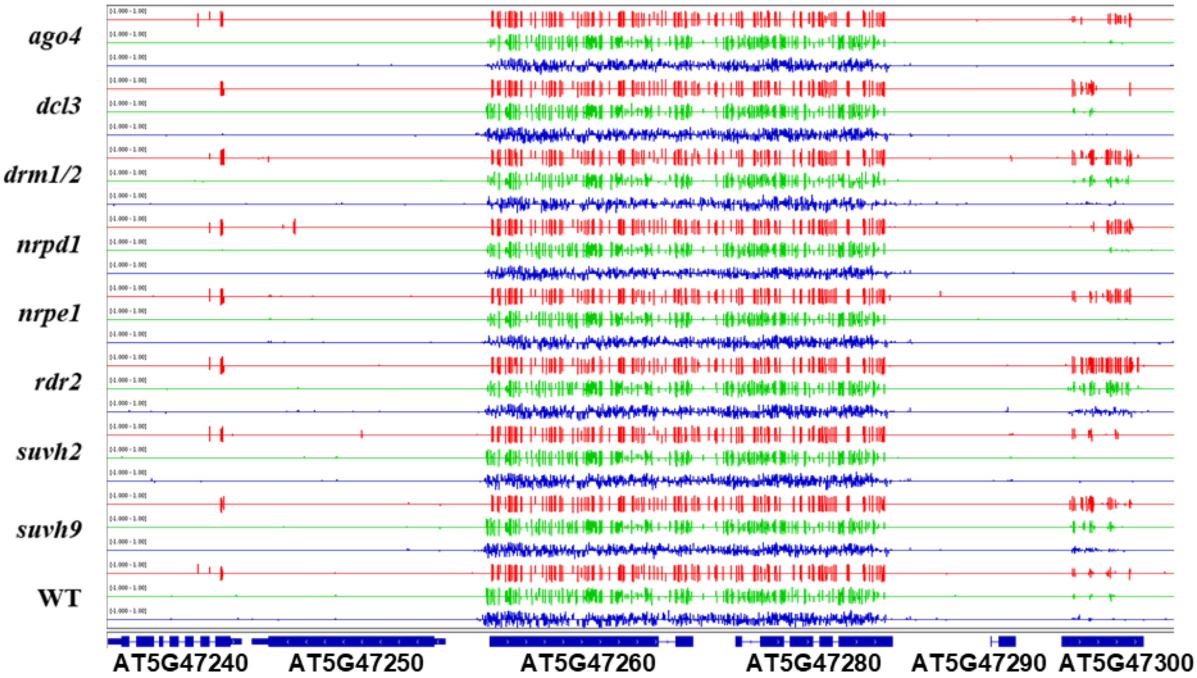


Figure S12 | Methylation of *PbAt-5.2* region in Col-0 and in mutants in genes involved in RdDM methylation maintenance (Stroud et al., 2013). In red the methylation in CG context. In blue the methylation in CHG context; in green the methylation in CHH context. WT indicates the methylation profile of 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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        10        20        30        40        50        60        70        80
90

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Col
TTAATAAGCCAAAGCCACATAGAAGAAAAAAAAAAGAACATTCACGTCTCTCTCGTTTTTTTGGCCGACGACGATCGCTGAATTGACTGC
Bur   -
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       100       110       120       130       140       150       160       170
180

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Col
CGGAGATTCCTTTAATCGTCAGATTCTCGTTGAGGGATAATGAATCCTGAATAGTAAGAAACTTGTCTTCTCGTTGTTTCATGTATCTAT
Bur
..........................................................................................
                                            →At5g47200
       190       200       210       220       230       240       250       260
270

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Col
TGTTTCGGATCGATCCGCGTTTTTTATTTTTTGATGTGTTTGGTGATTTGGTTTTTGTTCGATTTTGCTTTGGATCTTTGTTGGTTGTTA
Bur
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       280       290       300       310       320       330       340       350
360

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Col
GGTTTGTGAATTGAATCTACCTAATTTTGCTCGTTTAAGGTATTTTGTATTAGAATTTTGTATAGATTTGGATTTTCGTTCCATGGATCT
Bur
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       370       380       390       400       410       420       430       440
450

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Col
TATACAGGTCAGATCCGAGGAAATTTGATCGAGATCTGCAATTTCTGTTTACTGTTGTAGTTGAAATTCGCGAGTGTGACACAATTTTCC
Bur
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       460       470       480       490       500       510       520       530
540

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Col
CTTTGATCTCATTAGCATATTGTATATAGATGTTCTTGCGTTTTTATTTCCTGACCCGAATTTTCATGAGTTTATGAGCTTCACTGAGAT
Bur
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       550       560       570       580       590       600       610       620
630

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TGGTGTTTACCGTTCTGTTGTTGCAGTGACTATCTGTTCAAGCTTCTGCTTATTGGTGATTCTGGTGTTGGAAAATCATGCTTGCTTCTA
Bur
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                640       650       660       670       680       690       700       710
720

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Col
AGATTTGCTGTAAGTATTCCCACAATTCTGGATTCATCATCTCTGGTAGTTACTTTTTAACATTGTGTACACACAAAAATTTGAGGATCA
Bur
...................................................G......................................
                                            Snp K53 At5g47200

                730       740       750       760       770       780       790       800
810

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CATCTTGGAGTTCAATACCTGTTGCTCAAGACTCAAAACTCAAAAGTCATTACTCCATTGGATTAGCTTAGTTCTCACTATGGTATCATT
Bur
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                820       830       840       850       860       870       880       890
900

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Col
GTTACTCCTTTGTGTTCTTATTTCCTGATATCTTGAATTTTATGTGGACAGGATGATTCTTACCTGGATAGCTACATAAGCACCATTGGT
Bur
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                910       920       930       940       950       960       970       980
990

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Col
GTTGACTTTGTAAGCACCTTCATTTGCTCATCACTCATTTATATACAGGAATCAGAATAATAAGTGTTAACCTTTACTAATGATATCATG
Bur
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                1000      1010      1020      1030      1040      1050      1060      1070
1080

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CAGAAAATTCGCACAGTTGAGCAGGACGGAAAGACCATCAAACTCCAGATCGTAAGTGTTCTTCAGCTAGATATGCAATCATAATCTGTT
Bur
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                1090      1100      1110      1120      1130      1140      1150      1160
1170

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AAAATTTTGGAAAGAGCAGATAGTTACTCTTGTTTTGGTAATCGCCTGTGTATACAGTGGGACACAGCAGGCCAAGAACGTTTCAGGACA
Bur
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                1180      1190      1200      1210      1220      1230      1240      1250
1260

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ATCACTAGCAGCTACTACAGAGGAGCTCATGGGATCATTGTATGTACTCTTACTCTAACCAACCAATCATCTTCTTGTTAAATAACACAT
Bur
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                1270      1280      1290      1300      1310      1320      1330      1340
1350

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CCTATACCTCTTGCTCACAATTGCCTATCTTTGCAGGTCACTTATGATGTCACAGACCTAGAGAGCTTCAACAACGTCAAACAATGGCTG
Bur
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                1360      1370      1380      1390      1400      1410      1420      1430
1440
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Col
AATGAAATTGACCGTTACGCTAGCGAAAATGTGAACAAGCTACTGGTTGGGAACAAGAACGATCTCACTTCACAGAAAGTTGTATCCACT
Bur
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              1450      1460      1470      1480      1490      1500      1510      1520
1530

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GAGACAGCTAAGGTAATTTTATAATAAACTAGGTGAACTCTCTATCCACGTAAACCTTGTCTTAAAGAGAATAACATTTTTGTTGTCTCA
Bur
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              1540      1550      1560      1570      1580      1590      1600      1610
1620

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TCTCCTTGTCCCACAGGCTTTTGCAGATGAACTTGGGATCCCATTCTTGGAAACAAGTGCTAAAAATGCAACCAATGTGGAAGAAGCTTT
Bur
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              1630      1640      1650      1660      1670      1680      1690      1700
1710

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CATGGCTATGACTGCTGCAATTAAGACAAGGTTAGAAACTAAATTTTACTTGTGAAGTCATTAACCCTTTACTTCCATACTTAAAAGGTT
Bur
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              1720      1730      1740      1750      1760      1770      1780      1790
1800

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Col
TTGTTGTTTTCGCAGAATGGCTAGCCAACCAGCTGGAGGTGCCAAGCCACCAACGGTCCAGATCCGTGGACAGCCAGTGAACCAGCAATC
Bur
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              1810      1820      1830      1840      1850      1860      1870      1880
1890

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Col
AGGCTGTTGTTCTTCTTGATTCAATTAGTCACCACTCCTCTTTCGATCATCACACCATTATGATCATTTGTTTGCATTGCATGTTAGACT
Bur
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          End At5g47200→

              1900      1910      1920      1930      1940      1950      1960      1970
1980

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TCTCCAAATTAACAACTCTTTGGATCCTTTTGCTTGTTTTTCATTTGCTTTCTTTTGATCCGATTCTTTTCTGATGTACGTTGAAGTTTG
Bur
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              1990      2000      2010      2020      2030      2040      2050      2060
2070

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Col
AAACCCATAACTTCTATATAGTAAAAGGTCTTTTATGCAAATAATGTAGAGCACTCTTTAATGCCTTCGACGATTCTAAATCATCGCTCA
Bur
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              2080      2090      2100      2110      2120      2130      2140      2150
2160

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AGTATGAAAGATACTAGATATCGTGCTATTAGAAATATACTTCATTTATGATGTACGAAAAGAAAGATCGAATGTGTAATACCAAAATTA
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Bur
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              2170      2180      2190      2200      2210      2220      2230      2240
2250

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Col
GAGAGAAAAATATCTTAATAATTTTTTTCATAACTTAAAAAACGTAATAGTTTCGCAGAAAAGACCTTCAGAAAGTGTAACAAAAAATTA
Bur
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              2260      2270      2280      2290      2300      2310      2320      2330
2340

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Col
TAAAACTAACAAAATTCAACCAAAGAGAAACGAAAGACAGAGATAGCGAGGCTGAAGGACCAGGGGTCTTTACTAGCCCAACGAAGGGAA
Bur
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                                                                             End At5g47210←

              2350      2360      2370      2380      2390      2400      2410      2420
2430

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CTGAGCTGTGTCTCCAATCGCCGGAGCTGCAGCTTCTTTTGCATACCTTTGGTTTCCTCCTTCACCACGACCACCGCGACCTCCTCTTCC
Bur
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                                  Snp K54
              2440      2450      2460      2470      2480      2490      2500      2510
2520

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GCGGGAGCCTCCACCTCTCCCGTTGTACCTCTTTCCATCAGCCGGCTTCAAGAACTCATTAATGCTCAACGACTACAAAATCACCCAAAA
Bur
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              2530      2540      2550      2560      2570      2580      2590      2600
2610

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Col
TCACTCAGGTAAAAAAATGACACAACCCAAAAGAAATCATGAAGTGAGAACAGAAAGAACTAAGACCTTTTTGGCCTTCTCAGTAGCATC
Bur
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              2620      2630      2640      2650      2660      2670      2680      2690
2700

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TTTGCGTTTTTCCTTGTCAGATCCCTGAAACAATAAAATACCAAGTATTAACTATTGCTCCGTTACAGTGAAGGGAATAGATAAACTGAA
Bur
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              2710      2720      2730      2740      2750      2760      2770      2780
2790

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Col
CAGTAGATGATTTTCTGACCAGCTTGATGAAGATTTCTTCATCGGTGTTCTTCTTGTTAGAGAGCTGTTGCATGGACTCAAACACTTTGG
Bur
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              2800      2810      2820      2830      2840      2850      2860      2870
2880

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Col
TGTCAACTTTCCTTTCCTCAACCTTTGTGGCTTGCAGAGCCTTCTTCTTCTCCTCCAGAATTTTCTCATACTCTTCTAGAGTCATCTCCT
Bur
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              2890      2900      2910      2920      2930      2940      2950      2960
2970

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Col
ATATGACAAAACCATATCAGTTCAAAATGTTAGCAAACATTCTACTTCAAACTTAACTAAACCTCAAAAGATGTTTCAAGAGCTGTAAAT
Bur
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              2980      2990      3000      3010      3020      3030      3040      3050
3060

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Col
GATTGTACCCTGGCTTCAGCTTCTTCAGCTTCTTTCTGTGCTTTCTCTTCCGCAGTGAGTTCTTTCTTTGCTTCAGGGGTTTCATCCTCA
Bur
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              3070      3080      3090      3100      3110      3120      3130      3140
3150

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CCTCCTTGCTTCTCAGCAACAGGGCTCTTCTCAACCTCTGTGGTAGGTTCCTCAGACGTTCTAATATAAGAACAACAAAAGTTTATAAAC
Bur
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              3160      3170      3180      3190      3200      3210      3220      3230
3240

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Col
AACCTAAAGTTAAAGTCATATGGATAATTAAAGTGAAGACAAGGATGCTTACGGAGGGATATCATCTTCAGTAGTGCCCCAGTTTCCACG
Bur
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              3250      3260      3270      3280      3290      3300      3310      3320
3330

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Col
ACCTCCACCATTACGTTTCATGCCAGTACTATCAAACATCAAGTTAACATAAATGAATCACAAACAGAAGAAGTCAAACAAAGTAGTAAC
Bur
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              3340      3350      3360      3370      3380      3390      3400      3410
3420

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TAAAGTAGTGGACAGAACAAAAAGAAAGCTTACCCATGACCTGTCCTGCTATGGCGGTCATAATTCCTCGGTGGGCGTTCAACATCACCA
Bur
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              3430      3440      3450      3460      3470      3480      3490      3500
3510

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GATTCCCCGTTGGCAACTCCACCACGGCGAGGTCCTTCACGACCACCGCCAACACGGTATCCACCAACAGACCCACCACGGCTTGCTCCA
Bur
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              3520      3530      3540      3550      3560      3570      3580      3590
3600

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TCAGCATCTTCAGAAGGTCTCCTGTATCCTCCAGAAAATCCATTCTCATTTCCAGGAGCATCATTGTTCCTGTTGTCCCGGTTGTATCCA
Bur
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              3610      3620      3630      3640      3650      3660      3670      3680
3690

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
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CCATTACCCCTGCCACGGGAAAATCCACCACGTCCACCAGTCCCACCACGACCTCCTTGAGGAGCATTCCTCGACTCCCTCACTACATTC
Bur
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              3700      3710      3720      3730      3740      3750      3760      3770
3780

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Col
ATAACAAAAAGCTTTCAATATATATACTTATCCTAATCTAACAAAGTATTAAGCTTTACCCTAATCTAACAAAGCAGTAGAGAAACAAAA
Bur
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              3790      3800      3810      3820      3830      3840      3850      3860
3870

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TAAGATACGGAAGAAACTAACAAAGCAGCAAATGAAAAAAGCACACACATTTGACTATGGATCTTTCATGACAACCATAAACAAACTTCA
Bur
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              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
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              4240      4250      4260      4270      4280      4290      4300      4310
4320

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GTACTTGAAGAGAGATTATTCGGACAGAGCTGTTTGTGTTTAAGAGATAGCGAAACAAGAACCCTAAGAAAAGATGCGGCAGTGAGAGAG
Bur
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              4330      4340      4350      4360      4370      4380      4390      4400
4410

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

```
5220

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

              5230      5240      5250      5260      5270      5280      5290      5300
5310

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TTCAACTTCCCGTTTTCAGACGACGACGTAGAAGAGGACGACGACGACGACGAAGAAGATCTCTTAGACGTGATCCGAACCGGGTCA
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
```

```
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
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....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
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
TAAACGAGAGCGCTTATCCATAGAATAATATATAGAGTTTTAACCCGGAAAAAAAAAATACTCGCCTATAGTTTGCTTTAAAAAAAAGTT
Bur
..........................................................................................
```

```
              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
ACACAAATTATGTAGGCAGTGATTGGTACACATTGTTAGTTTTTTTTAAAATATTACTATGTTTTTGCCAAAAAAAATTACGAATCAGAG
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
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
```

```
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
```

```
TAGAATCTAGTGAGTGAGTCGTTGATTCATTCTACAAACCAGTTAATGCACCGCGTAAATTCTTTTCACGTGCATGGTGCAGTGCATGAA
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
```

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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      13220      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
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13680

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ACCAAACCGGAAGTTACTAAACCGGTTTCGGAAGAAGAGAAGAAGCATTACAGAGGAGTAAGACAAAGACCGTGGGGGAAATTCGCGGCG
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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```
Col
TATAAATGTCAATTGCATTGACATTAATTGAGGAATTATAGTAGAACCTAGTATAAAAAGAATGATTCAAACATGAGATATTGACCGGCG
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
ATGTGTTTTGCGTCGACCTCAAAATAAAATACATATTAAATCTTGCATGCTAATATTATTGTATAGAATACCAATCAGGTAAGAATCGCT
Bur
.....................................................C....................................
       CLG4: clonage 4F
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             15130     15140     15150     15160     15170     15180     15190     15200
15210

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CGTCATCATACGACTATTCAATATCCAAACATATTTATTTGGAAAACCCGACCACGAATAATGGTTAGCTTTACATCATTATCCACACAT
Bur
..........................G..............A................................................

             15220     15230     15240     15250     15260     15270     15280     15290
15300

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

             15310     15320     15330     15340     15350     15360     15370     15380
15390

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CCTACGTGGACAATACCTAATCCTTCCATGATTTTCAATTATTGCAGATAATTTTTCTGAACGTCATCATTTCCCATAACGAATAATCAT
Bur
..................................G.......................................................

             15400     15410     15420     15430     15440     15450     15460     15470
15480

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col   TTCCTCAATCAACGCAAACCTAACTAT-
CTATGTCATTTACATGTTTATGTGGTAAAAATCTGCTTAGAATAAGTAAACCTTCACATATA
Bur
...........................A..............................................................

             15490     15500     15510     15520     15530     15540     15550     15560
15570

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TATTGTAACAAAATAATTGAGGTTAATGTTATTCAATGCGAAAAAATGTAAACACTTGCTAATGAGTCGTAATAACCCTATATTATTTTT
Bur
......................G...................................................................

             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   .............................-
.............G..............................................

             15850     15860     15870     15880     15890     15900     15910     15920
15930
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....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ACGCATCTGACGTACAAATTAAAAATCCAAATGAACTAAAATACTTTTAAACAGAAAGGACAAGGAATCTAAGCCATCAAGGCCCATCTC
Bur
........A..............................................................................G..

             15940     15950     15960     15970     15980     15990     16000     16010
16020

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CACGTAGCTCCAGCAACGACAAGATGCTTTATTATCCCATTCTCGTGGATACTTGTGTGAGATACACGCTTCAGATAAATCAACGGACGA
Bur
.............................................................C............................

             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
..........................................C.....TG............C...T.......................

             16300     16310     16320     16330     16340     16350     16360     16370
16380

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TTATAATATATCATTGGCTTGATGTGATTGATATTTACCAAAAATCTATTCTAGTTTCTTTTTGTAACACCAAATGTTATTTAAAATTTG
Bur    .....-
................GT.........................A..G.....................C...............

             16390     16400     16410     16420     16430     16440     16450     16460
16470

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col    TATTGGAAAAATGATTCATTTATATAAGTTATTATATCCCTCTTA-
AAAATTGTATAAAATCTCTAAGACATTATTAATTGTAAAAGATA
Bur
.C...........................................T............................................

             16480     16490     16500     16510     16520     16530     16540     16550
16560

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GACACAACACGTAGCTATATGTCTATATCCAAAAATAAAACACGTAGCTATATGTAATATTATAAAAATGTACATATATTATTAGGGTTG
Bur
.........T..................T.............................................................



             16570     16580     16590     16600     16610     16620     16630     16640
16650

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
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TAATATTTGGTCGGTTGAAAATTGAAATCGCAGCTCAATTGGAAATTCACGTGTATTTTGTCTTTGATTGTAAGATATTAAAACTGTTCT
Bur
......C....................A....T.........T...............................................
                                     CLG6Clonage 6R
             16660     16670     16680     16690     16700     16710     16720     16730
16740

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TCGCTTTCCTTTTCTCATTTCTCACTTAACCACTCGATCCACTTTAAACCACACATTATAAGTGTGCCTCAAAAAAATCTAACATTACTC
Bur
..............................................C......................A....................
             16750     16760     16770     16780     16790     16800     16810     16820
16830

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TCTCAACACATCTCTCTTTCTTCTCCATTTCCTTCTTCTCTTTCATTCTCTTATTTAAGATTTAAATCTGCTCAAATGCTTGTAAACAAA
Bur
....................C...T..C...T..........................................................
                        CL-N8: primer 5-DNA-NUT8-for

             16840     16850     16860     16870     16880     16890     16900     16910
16920

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TTTCAAGTTCTTTAAACGATTTCCTTTTCAAGAAAAATCCTTCTCCTTCTTCTTTTTACCACATAGATCTTCTTGATCTACAATGGATTC
Bur
.....................................C....................................................
                                                                          Start At5g47240→

             16930     16940     16950     16960     16970     16980     16990     17000
17010

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TGTTTCTCTTTCTGAGGTTACTGTCATTAAAGGAACAACACATTTGGGTTTTATGCACAGTTTCAGACAGCCATTTTGTGGTGTCAAAAT
Bur
.............................G..A...............G.........................................
                            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
TAAAGAAAGATCATTACTTGATGCTTATGATGATGAGTATGGTGGAGTAATAGTAGATCATGGAAAATTACCATCAAACCCTTATGCTTT
Bur
..........................................................................................
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          17380     17390     17400     17410     17420     17430     17440     17450
17460

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

          17470     17480     17490     17500     17510     17520     17530     17540
17550

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

          17560     17570     17580     17590     17600     17610     17620     17630
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
17820

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CCTGCAAATGCTTCACATCAAGTTGGTGTTGGAGGTTTTGTATTAAATCAACATAAAGAGGTATCAATATATGAATGATTATTCTCTCAA
Bur
..........................................................................................
       CLG8clonage 8R
          17830     17840     17850     17860     17870     17880     17890     17900
17910

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GTCTCAACACTTAAAGTAGAGTAGGTAAAAAGAAGAGTTACCTGAATTTTTTTTTAAATCTCATTAGGTGCTTGTGGTACAAGAAAAGTA
Bur
........................................  ...T............................................


          17920     17930     17940     17950     17960     17970     17980     17990
18000

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TTGTGCTCCTTCGATTACTGGTCTATGGAAGTTACCAACAGGGTTTATTAATGAATCTGAAGAGATTTTCTCTGGTGCTGTAAGAGAAGT
Bur
..............................A.................C.........................................

          18010     18020     18030     18040     18050     18060     18070     18080
18090

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

          18100     18110     18120     18130     18140     18150     18160     18170
18180
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....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GTATGGCATTGTGTTGTGTTATTCAGGTAGATACAGAGTTCTCAGAGGTTATAGCTTTCAGACATGCTCACAACGTTGCATTTGAGAAAT
Bur
..........................................................................................

             18190     18200     18210     18220     18230     18240     18250     18260
18270

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

             18280     18290     18300     18310     18320     18330     18340     18350
18360

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col   CAA-GAGTCTTTATTAGAATGCTCCAGTTGTACATGCTACAAGACGGTCCTGATTACAATGATTGTTGTGTTTTT-
CAGTGGATGCCATT
Bur
T..A......C...G............................................................T..............

             18370     18380     18390     18400     18410     18420     18430     18440
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
ATGTAATGTATGTTGTTATTTGATACTCTCTCTTCAGTATAGTAAATAGTAATAGATCCTCTGCAAAATCCATGTAGCATCGAACCGGTA
Bur
..........................................................................................

             18730     18740     18750     18760     18770     18780     18790     18800
18810

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

             18820     18830     18840     18850     18860     18870     18880     18890
18900

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

                 18910     18920     18930     18940     18950     18960     18970     18980
18990

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

                 19000     19010     19020     19030     19040     19050     19060     19070
19080

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

                 19090     19100     19110     19120     19130     19140     19150     19160
19170

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ACAGGAAAAAATAGCTCTTGCCCTCCTCCACTATCCCATTCAAAGCCTTATATATGAGATCATCATCGATTTTCTTATAATGGACGTTGA
Bur
..........................................................................................
                                                                End At5g47250 ←

                 19180     19190     19200     19210     19220     19230     19240     19250
19260

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

                 19270     19280     19290     19300     19310     19320     19330     19340
19350

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

                 19360     19370     19380     19390     19400     19410     19420     19430
19440

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
GGCGAGGATTCCACGCTTAGAGACTCGAGATTTGCAGCATACATCAGCCATGTCAAATCCTTTAGATGTATGCATGAGTTTATTACCACA
Bur
.....C....................................................................................
      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
..............C............................................................T...G..........

                 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

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

             19810     19820     19830     19840     19850     19860     19870     19880
19890

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

             19900     19910     19920     19930     19940     19950     19960     19970
19980

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

             19990     20000     20010     20020     20030     20040     20050     20060
20070

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

             20080     20090     20100     20110     20120     20130     20140     20150
20160

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

             20170     20180     20190     20200     20210     20220     20230     20240
20250

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

             20260     20270     20280     20290     20300     20310     20320     20330
20340

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

             20350     20360     20370     20380     20390     20400     20410     20420
20430

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

             20440     20450     20460     20470     20480     20490     20500     20510
20520

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

             20530     20540     20550     20560     20570     20580     20590     20600
20610

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ATTCCCTTCTCTGTACCTTTCATCTCACTCCGATAAGACTCCAAAGTATCGAGTGCACGACGCCATTGAATCACAGTAGATTTAGATGCC
Bur
..............................G...........................................................
                                Snp K62
             20620     20630     20640     20650     20660     20670     20680     20690
20700

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

             20710     20720     20730     20740     20750     20760     20770     20780
20790

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

             20800     20810     20820     20830     20840     20850     20860     20870
20880

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

             20890     20900     20910     20920     20930     20940     20950     20960
20970

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

             20980     20990     21000     21010     21020     21030     21040     21050
21060

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

             21070     21080     21090     21100     21110     21120     21130     21140
21150

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

             21160     21170     21180     21190     21200     21210     21220     21230
21240
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....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AACATTCTGTTTTCATCTTTTCTAAGACTTTCCCAAGTCTTTTCAAGCGTCGTATCAAGACCGACTGTTTGTTGGCAAAGTCTCACTTCT
Bur
..........................................................................................

             21250     21260     21270     21280     21290     21300     21310     21320
21330

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

             21340     21350     21360     21370     21380     21390     21400     21410
21420

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

             21430     21440     21450     21460     21470     21480     21490     21500
21510

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

             21520     21530     21540     21550     21560     21570     21580     21590
21600

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



             21610     21620     21630     21640     21650     21660     21670     21680
21690

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AACATGCAAATGTTACCCACCTTTACACACAAGTAAGACAAAGCAGACTTATAACATGGCTCAACTACCTGCCAACAGCAATTCATTGTG
Bur
..........................................................................................
                                                                      Start At5g47250 ←

             21700     21710     21720     21730     21740     21750     21760     21770
21780

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

             21790     21800     21810     21820     21830     21840     21850     21860
21870

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

             21880     21890     21900     21910     21920     21930     21940     21950
21960
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....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ATAATGGAGAGAGGAAAAGAACTAGAGAAAAAAGTTATGTGGAATGCCTTTAATATCCCTACCCCACCCGCATGTTGTAGAATTTTTTGT
Bur
..........................................................................................

             21970     21980     21990     22000     22010     22020     22030     22040
22050

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

             22060     22070     22080     22090     22100     22110     22120     22130
22140

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

             22150     22160     22170     22180     22190     22200     22210     22220
22230

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

             22240     22250     22260     22270     22280     22290     22300     22310
22320

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

             22330     22340     22350     22360     22370     22380     22390     22400
22410

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

             22420     22430     22440     22450     22460     22470     22480     22490
22500

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AATCAAATTAAAATTTTAAAAGGGAAGGGCAATATTGTCAACCCACAAAGCCAAAGGGGAAAGTGGCTGAAAAATTCAGTCTCAATTCAG
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
..........................................................................................

             22690     22700     22710     22720     22730     22740     22750     22760
22770

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

             22780     22790     22800     22810     22820     22830     22840     22850
22860

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

             22870     22880     22890     22900     22910     22920     22930     22940
22950

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

             22960     22970     22980     22990     23000     23010     23020     23030
23040

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

             23050     23060     23070     23080     23090     23100     23110     23120
23130

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

             23140     23150     23160     23170     23180     23190     23200     23210
23220

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

             23230     23240     23250     23260     23270     23280     23290     23300
23310

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

             23320     23330     23340     23350     23360     23370     23380     23390
23400

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

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

                 23500     23510     23520     23530     23540     23550     23560     23570
23580

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

                 23590     23600     23610     23620     23630     23640     23650     23660
23670

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

                 23680     23690     23700     23710     23720     23730     23740     23750
23760

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

                 23770     23780     23790     23800     23810     23820     23830     23840
23850

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

                 23860     23870     23880     23890     23900     23910     23920     23930
23940

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

                 23950     23960     23970     23980     23990     24000     24010     24020
24030

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

                 24040     24050     24060     24070     24080     24090     24100     24110
24120

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

                 24130     24140     24150     24160     24170     24180     24190     24200
24210

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

             24220     24230     24240     24250     24260     24270     24280     24290
24300

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

             24310     24320     24330     24340     24350     24360     24370     24380
24390

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

             24400     24410     24420     24430     24440     24450     24460     24470
24480

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

             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
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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
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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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..........................................................................................

              27280     27290     27300     27310     27320     27330     27340     27350
27360

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
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
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....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
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
TCTTATGACTAGAAAATATATATATATATATATATATATAATATTAAAAGTGAGAGCACGGGTCGGAGCAAACAATAAAACCCTAATTAA
          M  T  R  K  Y  I  Y  I  Y  I  Y  I  I  L  K  V  R  A  R
Bur   ............................TATAT
AATATTAAAA.........................................
            M  T  R  K  Y  I  Y  I  Y  I        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
..........................................................................................

             32590      32600      32610      32620      32630      32640      32650      32660
32670

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
CTTGTTGCATTACTTTAAGACAGTTTTTTTTTTTTTAATAGTTTCGTGATCAAAAAAGATCTGCATTAATGCCGCCTCCAGCAACATGGG
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
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..........................................................................................

                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

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TGATTTATTGATTATATTTTTTATCATAGAGAGAGCAAAAATCTCTGTCAATGGCAAGTAGGTACCAAGTAGTGGCATGAGAGAGTGATG
Bur
```

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..........................................................................................

                 39430     39440     39450     39460     39470     39480     39490     39500
39510

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TCTGGATTTATTGATTTCTTTGGTAGCTTATACTTCCATATGTTTCCTTATTTAATTTTTCATTCCAAATATGGGACAAAGTTATAACAA
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
TGGTATAAATGCATAGACACATATATACGTGCCCTATTAAAAGAGGCAGCGAGAAGATAATATAGGAGGAAGAGGAAGAAGAAGAAGATG
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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....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
ACTTCCAACCACATCACACACTCTTTCTATTCCCTTATATATTCCCATCTCAAAAGTTCTTGGAGACACATAAACATTAAAAAAAGAAAA
Bur
..........................................................................................

             40240     40250     40260     40270     40280     40290     40300     40310
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
CGAGTTCTGTGACGGTGGCCCTCCGGTTTACAACTATATATCCTTGGCCGGTCCTCATGCTGGCATCTCCTCTGTTCCTATGTGTGGTGT
Bur
```

```
..........................................................................................

                40960     40970     40980     40990     41000     41010     41020     41030
41040

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
AAGTTTTTTTTATAAATCTTTTTTCTCTAAATATTTTTTCTATGATTTTAATTTAATCAATCAATCACAGTAACAACATTGTCTTTTTCT
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
```

```
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Col
TGCGGGAAAAGTGAAGTTTGTGAGTGTAGCCGGTGAACATATCAGAATGGTAGATGAAGATGTCGTCAAACACGTTGTACCTTATCTCCA
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
gatcttgaggaaattggagttcctttcccagccgagataatggatgcaaaattgtattcaccactcaatctctggaagcatgtgacgaaagcaagtgggttgat
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

```
tggagaagagaaaccaaagagcgcaaggcagctgaaa------------aaaggagaagagatttgtgttgttactggatggcataacagagggaattggatcttgaggaaattggagttccttt
TrpArgArgGluThrLysGluArgLysAlaAlaGluL------------ysArgArgArgAspLeuCysCysTyrTrpMetAla .
```

ΔAt5g47280 : CRISPR-edited lines for AT5G47280

WT

```
Ggtctacctttgtctctgaaagtccttggcgcttcattaaacgatcgacctgaaacatattgggcaattgcagtggagaggttatcaagaggtgaacctgttgatgaaactcatgagagtaaagt
gtttgctcaaatcgaagca
GlyLeuProLeuSerLeuLysValLeuGlyAlaSerLeuAsnAspArgProGluThrTyrTrpAlaIleAlaValGluArgLeuSerArgGlyGluProValAspGluThrHisGluSerLysVa
lPheAlaGlnIleGluAla actctagaaaatctcgatccaaaaaccaaagagtgtttcttggatatgggtgctttccctgaaggcaagaaa
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 .

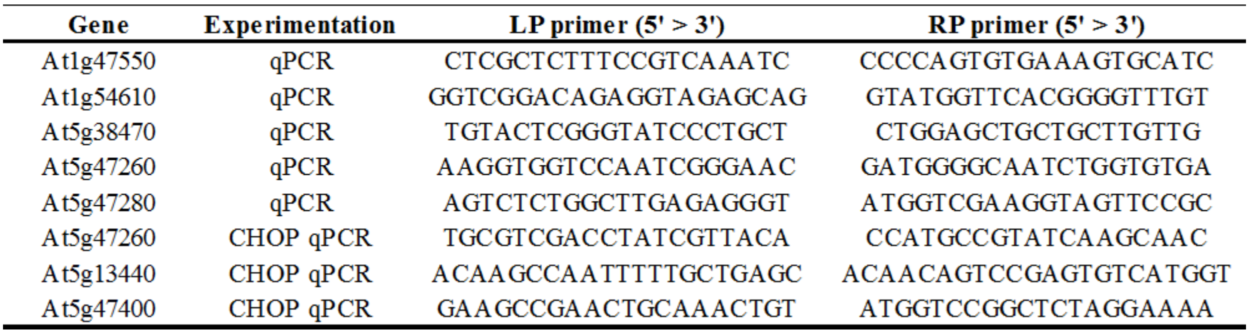
172-9

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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