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1 **Sequencing of *Tuta absoluta* genome to develop SNP**
2 **genotyping assays for species identification**

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4 Christine A. Tabuloc¹, Kyle M. Lewald¹, William R. Conner¹, Yoosook Lee²,
5 Ernest K. Lee¹, Alexander B. Cain³, Kristine E. Godfrey³, Judit Arnó⁴, Nuria
6 Agustí⁴, Clerison R. Perini⁵, Jerson C. Guedes⁵, Frank G. Zalom¹, Joanna C.
7 Chiu¹

8

9 ¹Department of Entomology and Nematology, University of California, Davis

10 ²Department of Pathology, Microbiology and Immunology, School of Veterinary
11 Medicine, University of California, Davis

12 ³Contained Research Facility, University of California, Davis

13 ⁴IRTA (Institute of Agrifood Research and Technology), Cabrils (Barcelona),
14 Spain

15 ⁵Department of Crop Protection, Universidade Federal de Santa Maria (UFSM), Santa
16 Maria, Rio Grande do Sul, Brazil

17 **Corresponding author:** Joanna C. Chiu, Email: jcchiu@ucdavis.edu.

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19 **Keywords:** South American tomato pinworm, tomato leaf miner, tomato borer,
20 Gelechiidae, invasive pest, single nucleotide polymorphism

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24 **Abstract**

25 *Tuta absoluta* is one of the most devastating pests of fresh market and
26 processing tomatoes. Native to South America, its detection was confined to that
27 continent until 2006 when it was identified in Spain. It has now spread to almost
28 every continent, threatening countries whose economies rely heavily on
29 tomatoes. This insect causes damage to all developmental stages of its host
30 plant, leading to crop losses as high as 80 to 100%. Although *T. absoluta* has yet
31 to be found in the U.S. and China, which makes up a large portion of the tomato
32 production in the world, computer models project a high likelihood of invasion. To
33 halt the continued spread of *T. absoluta* and limit economic loss associated with
34 tomato supply chain, it is necessary to develop accurate and efficient methods to
35 identify *T. absoluta* and strengthen surveillance programs. Current identification
36 of *T. absoluta* relies on examination of morphology and assessment of host plant
37 damage, which are difficult to differentiate from that of native tomato pests. To
38 address this need, we sequenced the genomes of *T. absoluta* and two closely
39 related Gelechiidae, *Keiferia lycopersicella*, and *Phthorimaea operculella*, and
40 developed a bioinformatic pipeline to design a panel of 21 SNP markers for
41 species identification. The accuracy of the SNP panel was validated in a
42 multiplex format using the iPLEX chemistry of Agena MassARRAY system.
43 Finally, the new *T. absoluta* genomic resources we generated can be leveraged
44 to study *T. absoluta* biology and develop species-specific management
45 strategies.

46 **Key Message**

- 47 • Surveillance and identification of *Tuta absoluta* are challenging because it is
48 morphologically similar to closely related species, e.g. *Keiferia lycopersicella*
49 and *Phthorimaea operculella*.
- 50 • We generated new genomic sequences for these three species and identified
51 single nucleotide polymorphisms (SNPs) to facilitate species identification.
- 52 • We validated a multiplex genotyping panel of 21 SNPs using the iPLEX
53 MassARRAY platform and confirmed its accuracy for species identification.
- 54 • We generated new molecular tools and genome resources to aid *Tuta*
55 *absoluta* management.

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57

58

59 **Introduction**

60 *Tuta absoluta* (Meyrick, 1917) (Lepidoptera: Gelechiidae), commonly
61 referred to as tomato leaf miner, tomato borer, or the South American tomato
62 pinworm, is a moth species that devastates fresh market and processing
63 tomatoes. *T. absoluta* was originally identified from samples collected in Peru by
64 Meyrick in 1917 (Povolny 1994; Đurić et al. 2014; Biondi et al. 2018). It was not
65 recognized as a serious pest until it was found damaging tomatoes in Argentina
66 in the 1960s (Bahamondes and Mallea, 1969), where it caused substantial crop
67 losses. *T. absoluta* causes crop losses as high as 80 to 100% because it will
68 damage all developmental stages of its host plant. Adult females oviposit on the
69 leaves, where the larvae will emerge from eggs and begin mining host tissues.
70 Larvae can also enter the stems through the buds, and feed within the tomato
71 fruit, leaving them unmarketable. Its distribution was largely confined to South
72 America until it was first detected in Spain in 2006 (Desneux et al. 2010;
73 Guillemaud et al. 2015). Since then *T. absoluta* has spread rapidly and is now
74 established in Europe, northern, southern, and eastern parts of Africa, southern
75 Central America, the Middle East, and in parts of South Asia (CABI 2016;
76 Campos et al. 2017; Mutamiswa et al. 2017; Biondi et al. 2018; Mansour et al.
77 2018; Han et al. 2018; 2019).

78 Although *T. absoluta* has not been reported in North America, Australia,
79 New Zealand, and some parts of Asia, CLIMEX computer modeling taking into
80 account pest life history, climate data, and host plant availability predicts that it
81 has a moderate to high likelihood of establishing in the commercial tomato-

82 growing regions around the globe including California and Arizona in the
83 southern United States (USDA 2011; Tonnang et al. 2015; Biondi et al. 2018).
84 Although the primary host of *T. absoluta* is tomato, *Solanum lycopersicum* L., it
85 can also colonize other solanaceous host plants such as potato, black
86 nightshade eggplant, sweet pepper, jimsonweed, and deadly nightshade
87 (Pereyra and Sanchez 2006; Desneux et. al 2010, 2011; Bawin et al 2015;
88 Mohamed et al. 2015; Negi et al. 2018). The ability of *T. absoluta* to inhabit a
89 wide variety of host plants is expected to greatly facilitate its range expansion.

90 Early detection of invasion and timely response are instrumental in halting
91 the continued spread of *T. absoluta* especially into the United States, Mexico,
92 and China, which together account for roughly 45% of tomato production in the
93 world (FAOSTAT 2017). Unfortunately, *T. absoluta* identification and monitoring
94 remain a challenge; *T. absoluta* larvae and adults are morphologically similar to
95 many other gelechiid species. The tomato pinworm, *Keiferia lycopersicella*
96 (Walshingham, 1897) and the potato tuber moth, *Phthorimaea operculella* (Zeller,
97 1873) are two primary gelechiids already occupying tomato-growing regions in
98 the U.S. in which *T. absoluta* will likely invade (Michalak 2011). Although less
99 commonly observed compared to *K. lycopersicella* and *P. operculella*, other
100 gelechiids such as *Sinoe capsana* (Lee and Brambila 2012) and *Tuta* sp. near
101 *chiquitella* (Gaskill 2013) have also been reported in the U.S. and have the
102 potential to be misidentified as *T. absoluta*. The Guatemalan potato tuber moth,
103 *Tecia solanivora* (Povolny, 1973), presents risks for future introductions into
104 many tomato-growing regions (EPPO Global Database 2019) and could be

105 misidentified as *T. absoluta*. This creates a serious problem for early detection.
106 Current identification requires the dissection and examination of male genitalia
107 (Povolny 1975; Michalak 2011; Đurić et. al 2014) by highly-practiced experts.
108 Furthermore, rearing to adulthood in order for male genitalia to fully develop is
109 not always practical if marketability of a shipment is to be maintained. While host
110 plant damage caused by *T. absoluta* at immature stages could potentially be
111 leveraged for identification and detection, damage is essentially indistinguishable
112 from the damage caused by other morphologically similar pests occupying the
113 same niche, e.g. *K. lycopersicella* and *P. operculella*.

114 Alternatively, DNA barcoding via PCR amplification of mitochondrial
115 cytochrome oxidase subunit I (COI) (Cifuentes et al. 2011) as well as RAPD-PCR
116 (RAPD, Random Amplified Polymorphic DNA) (Bettaibi et al. 2012) have been
117 utilized as molecular diagnostics to identify *T. absoluta* and to examine genetic
118 variations between different geographical populations. However, these molecular
119 diagnostics have not been tested for or utilized to differentiate between *T.*
120 *absoluta* and morphologically similar species such as *K. lycopersicella* and *P.*
121 *operculella*. Sint et al. (2016) developed species-specific primers from COI
122 sequences of *T. absoluta*, *P. operculella*, and *Symmetrischema tangolias* (Gyen,
123 1913) (Lepidoptera: Gelechiidae), and established multiplex PCR assays to
124 enable the identification of these three species and their parasitoids, but did not
125 include *K. lycopersicella* in their analysis.

126 In this study, we constructed a draft genome assembly for *T. absoluta*
127 using Linked-Read library preparation by 10X Genomics Chromium platform, and

128 performed genome sequencing for *K. lycopersicella* and the *P. operculella*. We
129 then designed and implemented a custom bioinformatic pipeline with the goal of
130 identifying single nucleotide polymorphisms (SNPs) to design a multiplex SNP
131 genotyping assay for robust molecular species diagnostics. SNP genotyping was
132 performed on the Agena MassARRAY system using iPLEX (Locus-specific
133 primer extension reaction) chemistry (Gabriel et al. 2009), allowing us to perform
134 multiplex reactions to detect over 20 SNPs simultaneously. We validated the
135 accuracy of this SNP panel to differentiate *T. absoluta* from *K. lycopersicella* and
136 *P. operculella* using specimens from multiple life stages and determined the
137 accuracy of species identification to be 100%.

138

139 **Materials and Methods**

140 ***Origins of the Gelechiidae specimens***

141 *T. absoluta* adults and larvae came from the laboratory colony maintained
142 at IRTA in Cabrils (Barcelona), Spain, Costa Rican field collections (by Y. G.
143 Bonilla), as well as collections from greenhouses and the field in eleven
144 geographical locations in Argentina, Brazil, Chile, Colombia, Ecuador, Paraguay,
145 Peru, and Uruguay (by J. C. Guedes and C. R. Perini) (Supplemental Table 1).
146 The colony in Spain was initiated from individuals collected from several
147 locations in the Barcelona province, as reported in Arnó et al. (2018). Live
148 samples were collected, preserved in 90-95% ethanol, and subsequently shipped
149 to UC Davis and stored at 4°C prior to genomic DNA (gDNA) extraction.

150 *K. lycopersicella* colonies were established from specimens collected in
151 Immokalee, Florida in the Fall of 2015 (by P. Stansly). Pupae were shipped to
152 UC Davis in January 2016. *K. lycopersicella* individuals were then reared on
153 tomato seedlings or small plants (cv Patio Princess, W. Atlee Burpee and
154 Company, Warminster, PA, USA) that were about 3 months old. Rearing was
155 performed in a Bugdorm cage (MegaView Science Education Services Co., Ltd.,
156 Taichung, Taiwan) and held at 23-24°C with overhead lights 24 hours a day.
157 Humidity was not controlled. Each cage consisted of 6-8 tomato plants in UC Mix
158 soil. The plants were watered as needed with a fertilizer solution (Miracle Gro
159 mixed according to the manufacturer's recipe for indoor plants). Adults were
160 introduced into a new cage and a generation lasts about 30 days on average.
161 Larvae, pupae, and adults were collected on dry ice, stored in -80°C, and
162 subjected to gDNA extraction.

163 *P. operculella* colonies were established from specimens collected from a
164 commercial potato field near Arvin, Kern County, California (CA) (by D. Haviland)
165 and shipped to UC Davis. At UC Davis, *P. operculella* individuals were reared on
166 yellow or russet potato tubers. Four to six small tubers were placed on a 1.25cm
167 bed of autoclaved sand in a tray covered with paper towels and placed into a
168 Bugdorm cage. Thirty to forty adult tuber moths were introduced into the cages.
169 The cages were held in the same environmental conditions as the *K.*
170 *lycopersicella* colonies. Over the course of their 45-day life cycle, larvae, pupae,
171 and adults were collected on dry ice, stored in -80°C, and subjected to genomic
172 gDNA extraction.

173

174 ***Genomic DNA extraction for *Tuta absoluta* reference genome sequencing***

175 A single adult *T. absoluta* collected from Spain and preserved in 95%
176 ethanol was first placed into nuclease-free water in a 1.5 ml tube for rehydration
177 at room temperature for 15 minutes. After removing water, the specimen was
178 subsequently homogenized in a 2% CTAB solution (100mM Tris-HCl (pH8.0),
179 10mM EDTA, 1.4M NaCl, and 2% CTAB). The sample was incubated at 65°C for
180 5 minutes and 200µl of chloroform was added to the tubes and then inverted
181 slowly 10 times to mix. To isolate nucleic acids, samples were centrifuged at
182 13,000 rpm for 10 minutes at 4°C. The aqueous layer was transferred to a new
183 tube and mixed with an equal volume of 100% isopropanol and left in -20°C
184 overnight for gDNA to precipitate. The DNA was then pelleted at 13,000 rpm for
185 15 minutes at 4°C. The DNA pellet was washed with 70% ethanol and spun
186 down at 13,000 rpm for 5 minutes at 4°C. After the pellet was air-dried, the gDNA
187 was re-suspended in nuclease-free water. DNA was quantified using the Qubit
188 dsDNA high sensitivity kit (Thermo Fisher Scientific, Pleasanton, CA, USA) in
189 combination with Qubit fluorometer (Thermo Fisher Scientific, Pleasanton, CA,
190 USA).

191

192 ***Library preparation, sequencing and assembly of *Tuta absoluta* reference***
193 ***genome***

194 Genomic DNA from a single *T. absoluta* adult was submitted to the UC
195 Davis DNA Technologies Core for Linked-Read library preparation using a

196 Chromium Controller and the Chromium Genome Reagent Kit (10x Genomics,
197 Pleasanton, CA, USA) according to manufacturer's protocols for v1 chemistry.
198 The barcoded library was sequenced on one lane of an Illumina HiSeq 4000
199 sequencer (Illumina, San Diego, CA, USA) to produce 2x150 paired-end reads.
200 A "pseudohap" assembly was generated from raw reads with Supernova 2.1.1
201 using 40 cpu cores. The only optional arguments used in *supernova run* were --
202 localcores and --localmem, which were set to the aforementioned values. This
203 assembly was used as the *T. absoluta* reference in subsequent analysis.
204 Genome size estimate was obtained from Supernova as well as GenomeScope
205 (Vurture et al. 2017) using k-mer length=21, read length=150, max k-mer
206 coverage=1000. For GenomeScope, the input histogram of k-mer frequencies
207 was generated using Jellyfish v2.2.5 (Marçais et al. 2011) with k-mer length=21.
208 The completeness of the *T. absoluta* assembly was assessed using BUSCO
209 (Benchmarking Universal Single-Copy Orthologs) v3.0.2 (Simao et al. 2015) in
210 genome mode with the insecta_odb9 lineage data, and by mapping RNA-seq
211 reads (NCBI SRA accession number SRX1134908) from a published *T. absoluta*
212 transcriptome (Carmago et al. 2015) to our assembly using STAR v2.6.1a (Dobin
213 et al. 2013) with default parameters. Ribosomal RNA sequences were removed
214 from the raw RNA-seq reads downloaded from NCBI using SortMeRNA v2.1
215 (Kopylova et al. 2012). The remaining reads were trimmed for quality and
216 adapter sequences using Trimmomatic v0.35 (Bolger et al. 2014) with
217 LEADING=10, TRAILING=10, ILLUMINACLIP=TrueSeq3-PE.fa:2:30:10, and
218 MINLEN=36 prior to mapping onto the *T. absoluta* genome assembly.

219

220 ***Library preparation and genome sequencing of Tuta absoluta, Keiferia***
221 ***lycopersicella and Phthorimaea operculella replicates for comparative***
222 ***sequence analysis and identification of species-specific SNPs***

223 Eight replicate libraries, each represents a single adult insect, were
224 prepared for each of the three species. Instead of separately sequencing an
225 individual at high depth similar to *T. absoluta*, we used one of the replicates as
226 reference for *K. lycopersicella* and *P. operculella* respectively. Genomic DNA was
227 extracted as described in Nieman et. al (2015) and Yamasaki et. al (2016) using
228 the Qiagen BioSprint 96 Automated Nucleic Acid Purification System and
229 reagents (Qiagen Sciences, Germantown, MD, USA). DNA libraries were then
230 prepared with 50ng input DNA per library using the Kapa HyperPlus Kit (Kapa
231 Biosystems, Wilmington, MA, USA). Libraries were quantified using the Qubit
232 dsDNA high sensitivity kit in combination with Qubit fluorometer (Thermo Fisher
233 Scientific, Pleasanton, CA, USA) and subjected to quality control using an Agilent
234 2100 Bioanalyzer with a High Sensitivity DNA chip (Agilent Technologies, Santa
235 Clara, CA, USA). Each library had an 8 bp-long barcode. The multiple barcoded
236 libraries were pooled and subjected to a two-tailed size selection, 0.35X and
237 0.7X, using AMPure XP beads (Beckman Coulter Life Sciences, Indianapolis, IN,
238 USA). The final pooled sample was eluted in 22ul of 10mM Tris-HCl, pH8.0 and
239 submitted to Novogene (Sacramento, CA, USA) for sequencing on a HiSeq 4000
240 platform (Illumina, San Diego, CA, USA). Raw reads from one replicate each of
241 *K. lycopersicella* and *P. operculella* were assembled using SOAPdenovo2 r240

242 (Luo et al. 2012) with kmer size of 63 to generate low coverage references for
243 subsequent analysis.

244

245 ***Bioinformatic pipeline for comparative genomic analysis and SNP***
246 ***identification for iPLEX primer design***

247 We developed a custom program *snp-id* (available in GitHub;
248 <https://github.com/ClockLabX/snp-id>) that can identify SNPs suitable for iPLEX or
249 other genotyping assays. The complete bioinformatics pipeline for our analysis is
250 illustrated in Figure 1. First, reads from each of the 8 replicates for each species
251 were mapped back to the respective reference using BWA (BWA-MEM) v0.7.9a
252 (Li and Durbin 2009). Reference genomes for all three species were aligned
253 using the multiple genome alignment tool, Mauve (progressiveMauve) (Darling et
254 al. 2010). The SNP identification script of *snp-id*, *search_iplex.py*, was then
255 invoked with the following input: (i) the reference genome sequence for each
256 species, (ii) alignment of each replicate to the corresponding reference genome
257 for each species, and (iii) the multiple genome alignment of the 3 species. High
258 quality SNPs that are more likely to be invariant within species are chosen by
259 requiring that SNPs be homozygous and uniform across all replicates within a
260 species with no less than 3 replicates with coverage at that position. To satisfy
261 the more stringent requirements for the iPLEX assay, only segments of 81-141
262 bases with non-polymorphic regions flanking the diagnostic SNP are chosen
263 (Figure 2). This selection criteria also satisfies the requirements of other SNP
264 identification assays. Finally, results were searched against the NCBI nucleotide

265 database using *blast_iplex.py*, which uses MegaBLAST (Zhang et al. 2000) with
266 an e-value cutoff of 1e-10, to identify common contaminants to be excluded for
267 iPLEX assay design.

268 The list of SNPs that were identified using *snp-id* (Supplemental File 1)
269 were then used as the input for the MassARRAY Typer 4.0 Assay Designer
270 Software (Agena Bioscience, San Diego, CA, USA) to design iPLEX PCR and
271 extension primers (Table 1). The markers were named by the SNP location on
272 the genome assembly, except in the case where the region clearly mapped to an
273 annotated gene when queried in BLAST (as in the case of Eif-4a).

274

275 ***MassARRAY system combined with iPLEX chemistry for species***

276 ***identification***

277 Genomic DNA from *K. lycopersicella*, *P. operculella*, and *T. absoluta* was
278 extracted using the method as described in Nieman et al. (2015) and Yamasaki
279 et al. (2016) using the Qiagen BioSprint 96 Automated Nucleic Acid Purification
280 System and reagents (Qiagen Sciences, Germantown, MD, USA). Samples at
281 different life stages were analyzed (Supplemental Table 1). Primer cocktails for
282 multiplex PCR of 21 loci were prepared as described in Gabriel et al (2009). DNA
283 samples, primer cocktails for multiplex PCR, and primers for iPLEX extension
284 reactions were then sent to the Veterinary Genetics Laboratory at UC Davis for
285 MassARRAY iPLEX genotyping assay (Agena Bioscience, San Diego, CA, USA).
286 MassARRAY 4.0 Typer Analyzer Software was used for genotype calling and
287 species identification.

288 The iPLEX workflow starts with a multiplex PCR reaction to amplify
289 specific gene regions containing the polymorphic SNPs between species. The
290 PCR products are then treated with shrimp alkaline phosphatase (SAP) to
291 neutralize any free nucleotides. This is followed by a second round of SNP
292 extension reaction that utilize end-terminating nucleotides. The extension primers
293 for the SNP extension step can be found in Table 1. Because the amplicons from
294 this reaction are identical in sequence for all samples except at the last
295 nucleotide, i.e. location of the SNP, the mass of the extension primer plus one
296 base of species-specific allele will produce variable spectra readings when
297 analyzed by a mass spectrophotometer (Gabriel et al 2009).

298

299 ***Phylogenetic analysis of gelechiid species COI sequences***

300 COI sequences were identified from the genomes for *K. lycopersicella*, *P.*
301 *operculella*, and *T. absoluta*, and from NCBI for *Sinoe robiniella* (Fitch, 1859)
302 (accession no. MG365151.1) and *T. solanivora* (accession no. NC_029386.1).
303 Alignment was performed with MAFFT v7.3.10 (Kato et al. 2013) using the L-
304 INS-I algorithm. Maximum likelihood analysis was performed with RAxML v8.2.12
305 (Stamatakis 2014) using the GTRGAMMA model with 1,000 rapid bootstrap
306 searches.

307

308 **Results**

309 ***Tuta absoluta reference genome***

310 A reference genome assembly of *T. absoluta* was generated from 638.8
311 million paired-end reads representing roughly 72X raw coverage. Counting only
312 scaffolds greater than 10kb, the assembly has a total size of 677.2Mb. The contig
313 N50 is 26.36Kb and the scaffold N50 is 112.89Kb as reported by Supernova. GC
314 content of the assembly is 38.11%. The genome size estimated by Supernova
315 varies widely from 674Mb when 252 million reads were used for a raw coverage
316 of 56X to 1.34Gb when all reads were used, whereas GenomeScope (Vurture et
317 al. 2017) produced an estimate of only 492Mb. Two metrics reported by
318 Supernova may explain the lower than expected scaffold sizes: (i) weighted
319 mean molecule size was reported to be 24.55Kb, which may reflect challenges in
320 extracting long DNA from *T. absoluta*, and (ii) the repeat content index, which is
321 the percent of read kmers with twice the expected depth, is 37.91%. However,
322 our SNP identification method is not sensitive to scaffold size.

323 To assess the completeness of our *T. absoluta* assembly, we compared it
324 to the Insecta set of universal single-copy orthologs with BUSCO v3.0.2 (Simao
325 et al. 2015). Of the 1,658 total BUSCO groups searched, 1,532 (92.4%) were
326 identified as complete in the assembly. Summarized benchmarking in BUSCO
327 notation is as follows: C:92.4% [S:66.0%, D:26.4%], F:4.4%, M:3.2%, n:1658
328 (C=Complete BUSCOs, S=Complete and single-copy, D=Complete and
329 duplicated, F=Fragmented, M=Missing, n=Total BUSCO groups searched).

330 We also examined the coverage of coding regions by mapping a
331 published *T. absoluta* transcriptome (Carmago et al. 2015) to our assembly.
332 After removing ribosomal RNA sequences and performing adapter and quality

333 trimming, 17,345,874 read pairs were mapped to our *T. absoluta* assembly using
334 STAR (Dobin et al. 2013). There are 75.89% of uniquely mapped reads, 11.84%
335 of multi-mapped reads, and 12.1% of reads that are too short to map. Only
336 0.17% of reads are unmapped for other reasons.

337 We observed the presence of *Wolbachia* sequences in the *T. absoluta*
338 genome assembly. A total of 1.198Mb in 148 scaffolds have significant BLAST
339 matches to *Wolbachia* strains in GenBank. We also identified *Wolbachia*
340 sequences in other *T. absoluta*, *K. lycopersicella*, and *P. operculella* genome
341 replicates analyzed in this study, suggesting *Wolbachia* infection is prevalent in
342 these species.

343

344 ***Bioinformatic analysis enables SNP identification and genotyping primer*** 345 ***design***

346 The bioinformatic workflow for genome assembly and comparative
347 genomic analysis of *T. absoluta*, *K. lycopersicella*, and *P. operculella* is outlined
348 in Figure 1, and a flow diagram charting the steps of the *snp-id* program to select
349 gene regions suitable for SNP genotyping using Agena MassARRAY platform in
350 combination with iPLEX chemistry (Gabriel et al. 2009) is presented in Figure 2.
351 Due to the stringent requirements used in identifying SNPs, the output of *snp-id*
352 (Supplemental File 1) can be readily adopted to be used for other SNP
353 genotyping assays. The stringency can also be tuned in the script by adjusting
354 (1) the minimum number of genome replicates required with the same SNP to
355 allow for genetic variability, (2) the maximum number of other polymorphisms

356 within the amplicon, and (3) the length of nucleotides flanking the target SNP in
357 each amplicon. Since all replicates, including the ones used to construct draft
358 genome references for *K. lycopersicella* and *P. operculella*, have relatively low
359 (~10x) sequencing depth, we showed that low coverage genomes are sufficient
360 in identifying SNPs for species identification with our workflow.

361

362 ***Multiplex SNP genotyping assay is successful in differentiating Tuta***
363 ***absoluta, Keiferia lycopersicella, and Phthorimaea operculella***

364 We extracted gDNA from at least 24 individuals at different life stages
365 (adults or larvae) of each species (Supplemental Table 1) to validate our panel of
366 21 species-specific markers. The markers were designed such that each SNP
367 specifically identifies *T. absoluta*, *K. lycopersicella*, or *P. operculella* from the
368 other two species (Table 2). All markers performed as expected, and all 137
369 specimens, 85 *T. absoluta*, 24 *K. lycopersicella*, and 28 *P. operculella*, were
370 correctly classified (Table 2). These include 5 adult specimens from Costa Rica
371 (CRA1-5) that were previously suspected to be *T. absoluta* based on
372 morphological characters but were not identified with certainty due to poor
373 conditions of the specimens (personal comm. Y. G. Bonilla). The positive
374 identification of the Costa Rican *T. absoluta* specimens speaks to the utility of the
375 SNP markers to enable identification of less than perfect specimens as well as
376 immature stages.

377

378 ***Phylogenetic analysis suggests that the likelihood of misidentifying U.S.***
379 ***gelechiids as Tuta absoluta using the SNP panel is low***

380 Although our SNP panel was designed to differentiate *T. absoluta* from *K.*
381 *lycopersicella* and *P. operculella*, two gelechiids that are morphologically similar
382 to *T. absoluta* and are the primary gelechiids that are found in commercial tomato
383 fields in the U.S., inclusion of other gelechiids in SNP design in future studies will
384 further improve the resolution and utility of our diagnostic markers for species
385 identification. Other gelechiids that are occasionally encountered in traps for
386 monitoring *T. absoluta* in the U.S. include *S. capsana* and *Tuta sp. near*
387 *chiquitella*. Another gelechiid species that is morphologically similar to *T.*
388 *absoluta* and presents a risk for invasion into North America, Africa, and Asia is
389 *T. solanivora* (Guatemalan potato tuber moth) (EPPO Global Database 2019).
390 There are no sequences available for *S. capsana* and *Tuta sp. near chiquitella* in
391 NCBI. However, COI sequences are available for *S. robiniella* and *T. solanivora*.
392 Together with COI sequences from our genome data for *T. absoluta*, *K.*
393 *lycopersicella*, and *P. operculella*, we used maximum likelihood tree estimation to
394 generate a phylogram to determine the genetic distances between these
395 gelechiids (Figure 3). We reasoned that if *K. lycopersicella* and *P. operculella* are
396 more closely related to *T. absoluta* as compared to *Sinoe* species and *T.*
397 *solanivora*, then it is less likely that our 21-SNP panel will misidentify *S. capsana*
398 and *T. solanivora* as *T. absoluta*. Indeed, this is what we observed (Figure 3).

399

400 **Discussion**

401 In this study, we generated a draft genome assembly for the devastating
402 tomato pest *T. absoluta* and genomic sequences for two other Gelechiidae, *K.*
403 *lycopersicella* and *P. operculella*, that show high levels of similarity in
404 morphology. Through the development and use of a custom bioinformatic
405 pipeline, we identified a large number of species-specific SNP markers
406 (Supplemental File 1) and designed a multiplex panel of 21 SNPs that can be
407 used to differentiate these three species at all life stages efficiently and
408 accurately with minimal DNA input. In addition to species identification, these
409 SNP markers will facilitate detection of hybridization among morphologically
410 similar species that colocalize and may impact the spread of undesirable traits
411 such as insecticide resistance (Teeter et al. 2010; Lee et al. 2013; Lee et al
412 2014).

413 Each SNP is selected based on the criteria that it is homozygous and is
414 invariant among the replicate species genomes we used for SNP identification.
415 These criteria were imposed to increase the chance that the SNP alleles are
416 conserved within each of the three species of interest, even for populations from
417 diverse geographical regions. Our SNP validation experiments using *T. absoluta*
418 specimens collected from 13 geographical locations in South America, Central
419 America, and Europe confirmed the utility of the high-quality SNPs designed
420 using our selection criteria to process samples from diverse geographical
421 populations. Although we were not able to collect different geographical
422 populations of *K. lycopersicella* and *P. operculella* for SNP validation, the fact
423 that the SNP alleles for identifying those two species were isolated using the

424 same criteria suggests that it is likely our SNP panel will be able to handle *K.*
425 *lycopersicella* and *P. operculella* specimens from diverse populations. This can
426 be confirmed in future studies when specimens from diverse locations become
427 available.

428 There are a number of assays one can employ for SNP genotyping to
429 facilitate species identification, e.g. TaqMan real-time PCR (Dhami et al. 2016;
430 Zhang et al. 2016; Linck et al. 2017), High-Resolution Melt (HRM) real-time PCR
431 (Dhami et al. 2014; Ajamma et al. 2016), species-specific PCR (Sint et al. 2016),
432 KASP genotyping (Middlesex, UK), and SNP microarrays. We chose to adopt the
433 Agena MassARRAY platform in combination with iPLEX chemistry (Gabriel et al.
434 2009) to maximize the number of SNP markers we can multiplex in a single
435 assay to reduce false positive rate and increase rigor of species identification.
436 The iPLEX method allows the multiplex detection of up to 40 SNPs in a single
437 reaction and can be completed within 5 hours after gDNA extraction. The
438 economical high multiplexing capacity of iPLEX assays provides increased
439 diagnostic accuracy when compared with other PCR-based techniques (Lee et
440 al. 2015).

441 We should point out that it is not necessary to use all 21 markers
442 simultaneously in order to determine the species identity of a specimen.
443 However, using a combination of the SNP markers will provide higher confidence
444 for species identification by reducing false positives (Lee et al. 2015), given the
445 presence of genetic variations in field populations. Other genotyping technologies
446 mentioned above can be used in combination with the SNP markers generated in

447 this study for *T. absoluta* species diagnostics, but the multiplexing capacity of
448 some of these technologies, e.g. HRM and TaqMan, will not be as high as
449 iPLEX.

450 We anticipate that increasing taxon sampling will continue to improve the
451 utility and accuracy of the SNP diagnostics presented here. Nevertheless we
452 believe that the SNP panel in its current format is valuable for quick screening of
453 adult and immature stages and complementary to morphological identifications to
454 monitor early introduction of *T. absoluta* into the U.S., given that the two primary
455 gelechiids commonly found in tomato hosts in the U.S., *K. lycopersicella* and *P.*
456 *operculella*, can be distinguished from *T. absoluta* using our SNP panel.

457 Finally, the new genomic resources for *T. absoluta*, *K. lycopersicella*, and
458 *P. operculella* can be leveraged for design of genetic pest control, e.g. RNA
459 interference (Carmago et al. 2015; 2016) and for understanding various aspects
460 of *T. absoluta* biology, e.g. *Wolbachia* infection, chemoreception, and insecticide
461 resistance, to improve management.

462

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467 and David Haviland (Entomology and IPM Farm Advisor, University of California
468 Cooperative Extension, Bakersfield, CA, USA) for the *P. operculella* samples.

469

470 **Author Contribution Statement**

471 JCC, FGZ, KEG, and CAT designed the research. CAT and KML conducted
472 experiments. ABC, JA, NA, KEG, CRP, and JCG contributed to specimen
473 collection and rearing. CAT, KML, WRC, YL, EKL, and JCC analyzed data and
474 performed bioinformatic analysis. JCC and CAT wrote the manuscript. All authors
475 read and approved the manuscript.

476

477 **Data Availability**

478 All genome sequencing data generated from this study have been
479 deposited to BioProject accession number PRJNA512383 in the NCBI BioProject
480 database (<https://www.ncbi.nlm.nih.gov/bioproject/>). The Whole Genome
481 Shotgun project of *T. absoluta* has been deposited at DDBJ/ENA/GenBank under
482 the accession SNMR00000000. The version described in this paper is version
483 SNMR01000000.

484

485 **Compliance with Ethical Standards**

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492

493 **Ethical approval.** This article does not contain any studies with human
494 participants or animals performed by any of the authors.

495

496 **Conflict of interest.** All authors declare that they have no conflict of interest.

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700 **Figure Legends**

701 **Figure 1: Schematic illustrating the bioinformatic workflow for genome**
702 **assembly and comparative genomic analysis.** Raw reads from one sample
703 each of *T. absoluta*, *K. lycopersicella*, and *P. operculella* were separately
704 assembled to create reference genomes. Eight replicates for each species were
705 then aligned back to their respective references. The 3 reference genomes were
706 also aligned to each other to create a multi-genome alignment. All the reference
707 genomes and alignments were passed to *snp-id*, which identified and generated
708 iPLEX-compatible SNPs and sequences for assay design.

709

710 **Figure 2: Flowchart describing the algorithm of the *snp-id* program.** The
711 `search_iplex.py` script of the *snp-id* program requires an input file (json) that
712 specifies all the reference genomes (Fasta), replicate alignments (BAM), and
713 multi-genome alignment (XMFA). It scans the multi-genome alignment for
714 candidate SNPs and tests for (i) polymorphisms in flanking regions, (ii)
715 homozygosity, and (iii) evidence in other replicates. SNPs that satisfy all
716 selection criteria are printed out in a format suitable for MassARRAY Typer 4.0
717 Assay Designer Software.

718

719 **Figure 3: Phylogram describing the genetic distances between *T. absoluta***
720 **and morphologically similar gelechiids.** Maximum likelihood tree of COI
721 nucleotide sequences showing the phylogenetic relationship between *T.*
722 *absoluta*, *K. lycopersicella*, *P. operculella*, *S. robinella*, and *T. solanivora*. The

723 GTRGAMMA model was used in the tree search. Branch lengths are number of
724 substitutions per site. Numbers in blue are bootstrap values from 1,000 rapid
725 bootstrap searches.

726 Table 1: Amplification and Extension primers for iPLEX MassARRAY SNP genotyping assay

SNP Loci	PCR Amplification Forward Primer ¹	PCR Amplification Reverse Primer	Extension Primer
LOC110375043	ACGTTGGATGGGTAAAATGTGCTCAGCTGG	ACGTTGGATGAACTCGTTCCCGAACCAGC	CCGAACCAGCTGATCTCG
LOC106138973	ACGTTGGATGGGAACAAATGCTTGGTCGC	ACGTTGGATGAGCAACTGGCACAAGTAGTC	GGGTGCACAAGTAGTCATGTCAG
LOC110369709	ACGTTGGATGCACTAGTGTGTATTATATTAC	ACGTTGGATGGTCGATTACAGTTAGACGG	CGGTCAACGTCGAAAT
LOC110369696_T ²	ACGTTGGATGGCAAGTTCCGTGTACTTGAG	ACGTTGGATGTCCCCTCAGGACCCGAGAA	CCCCTCGCAGTCGTT
LOC101743970	ACGTTGGATGCTTATTACAACATGTCATC	ACGTTGGATGCAGTAAACATTTTGCTGTTAG	TCAGTTTGCTGTTAGCTTTTATTTT
LOC105392331	ACGTTGGATGTGCATCAAGCACGTCGACTG	ACGTTGGATGTTCAACGAAAGTAAACAGC	CAAGTAAACAGCTGCTATTG
LOC106110340	ACGTTGGATGTCCCCTTTTCGTATCATCCTG	ACGTTGGATGTAAGTTATGCATGCTGTTT	CCTGTTCTAAATTATTTTCCAAATTAT
Eif-4a	ACGTTGGATGTGTGGCCAACCTCATCTAAG	ACGTTGGATGATCGCAATAGAACGCAGGAC	GGGGCACGCAGGACACAAAGTATAAA
LOC101746640	ACGTTGGATGTCATCAGCAGCATGGCTGTC	ACGTTGGATGTTTCGTCAAAATTCACAAAC	CTCCAAATTCACAAACAAAAAACC
LOC106131324	ACGTTGGATGGAAAATTATTTTCACTTACC	ACGTTGGATGATCAAAATTCGGCCCTTAC	TCACTTCTTCTTCGTCC
LOC110375524	ACGTTGGATGTAGAGACTTGTTGAAACAG	ACGTTGGATGCAATCCAGACTACAAGATCA	CTAAAAAATTCACAACACTTATTTTA
LOC105701312	ACGTTGGATGTTCCACTGCAGTGAACAAG	ACGTTGGATGATTATTGATGGCTCTGGCTC	TCCTTTTCTCATAGTCCACAT
LOC110384087	ACGTTGGATGTCACCGAGTCTACTAGTTAC	ACGTTGGATGTCAGCCTTTTTCGAATAGGAG	GAGCATTTTTCGAATAGGAGAATCATAAT
LOC106136952	ACGTTGGATGTAGTAGGAATCAAAATGCC	ACGTTGGATGGGAAGACTACATTTTGCCTC	CCATTTTGCCTCTAAATTTAACTTA
LOC110378105	ACGTTGGATGTCGACGCCGAAAAAATCAC	ACGTTGGATGTTGCCACACTTTTTTCCCCG	GACGGTGAATGAAAAGTTCCGG
LOC105393522	ACGTTGGATGCTGCAGTTAATTTGAATGGC	ACGTTGGATGCATACATAAAGATTAAGCATC	TGAGCATCTCTGCACCTTA
LOC110369696_K ³	ACGTTGGATGGGAATTACAACGTAGTGTGG	ACGTTGGATGGTTGATTGGTTGTTGTGCGG	AAACTGTTGTGCGGTGAGCG
LOC110999038	ACGTTGGATGTCGGCATTATAATGTCCATC	ACGTTGGATGAAAGAGTTTAGTAGGTCGAG	TCTAGAAACAAATTACTTGATTGC
LOC106137173	ACGTTGGATGGTGCCATAAATATCGATCCG	ACGTTGGATGCCAACAGTTTCTTTACCCC	CATATCACTGTACACGTTTTTCAG
LOC110371221	ACGTTGGATGTCTCCTTCGAGAAACAGACG	ACGTTGGATGTTTGTGTGGCCGTATTACCG	CGATGTAATGCAGAAACC
LOC106110944	ACGTTGGATGAGTTCAACCCTTTTGAGGGC	ACGTTGGATGCGTATTTATTCAACAATCAA	GTTATTCAACAATCAAATAAATATTACG

¹ All sequences are written 5' to 3'² This SNP genotyping assay identifies *T. absoluta*³ This SNP genotyping assay identifies *K. lycopersicella*

727 **Table 2: iPLEX MassARRAY SNP genotyping assays to differentiate *Tuta***
 728 ***absoluta* (*Ta*), *Keiferia lycopersicella* (*Kl*), and *Phthorimaea operculella***
 729 **(*Po*).**

	Species Comparison (species 1 vs. 2/3)	SNP Loci *	SNP species 1	SNP species 2/3
731	<i>Ta</i> vs. <i>Kl/Po</i>	Loc110375043	C	T
		Loc106138973	T	C
732		Loc110369709	A	G
733		Loc110369696_T	T	C
734		Loc101743970	A	G
735		Loc105392331	A	T
736		Loc106110340	A	C
737		Eif-4a	A	G
738		Loc101746640	G	A
739		Loc106131324	A	T
740	Loc110375524	C	T	
741	Loc105701312	C	T	
741	<i>Kl</i> vs. <i>Ta/Po</i>	Loc110384087	T	A
742		Loc106136952	C	A
743		Loc110378105	A	G
744		Loc105393522	A	G
745		Loc110369696_K	A	G
746	<i>Po</i> vs. <i>Ta/Kl</i>	Loc110999038	G	A
747		Loc106137173	G	A
748		Loc110371221	A	G
749		Loc106110944	T	C

750
 751
 752

*Number of specimens tested for this 21-SNP panel: 85 *T. absoluta*, 24 *K. lycopersicella*, and 28 *P. operculella*

Figure 1

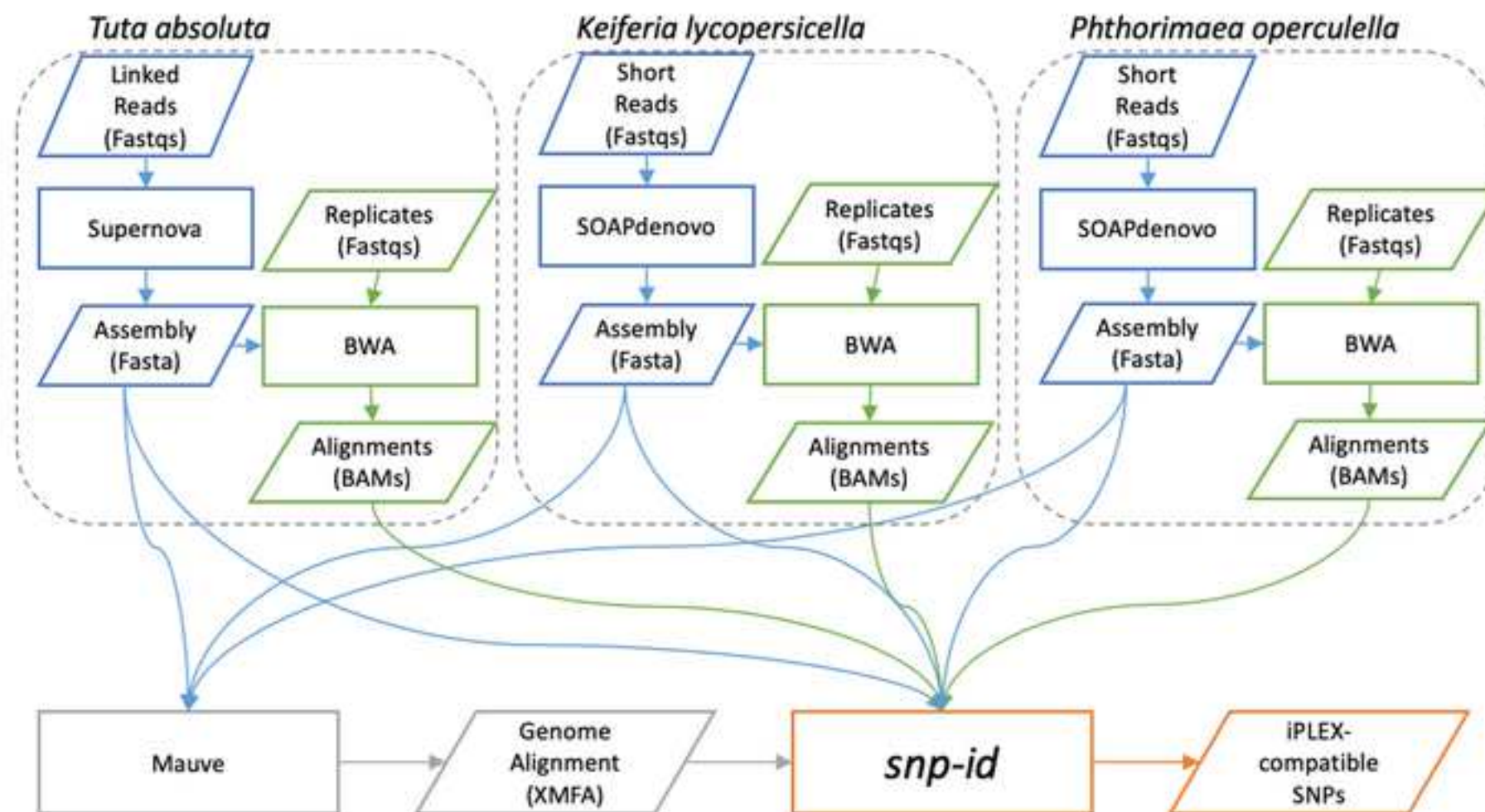
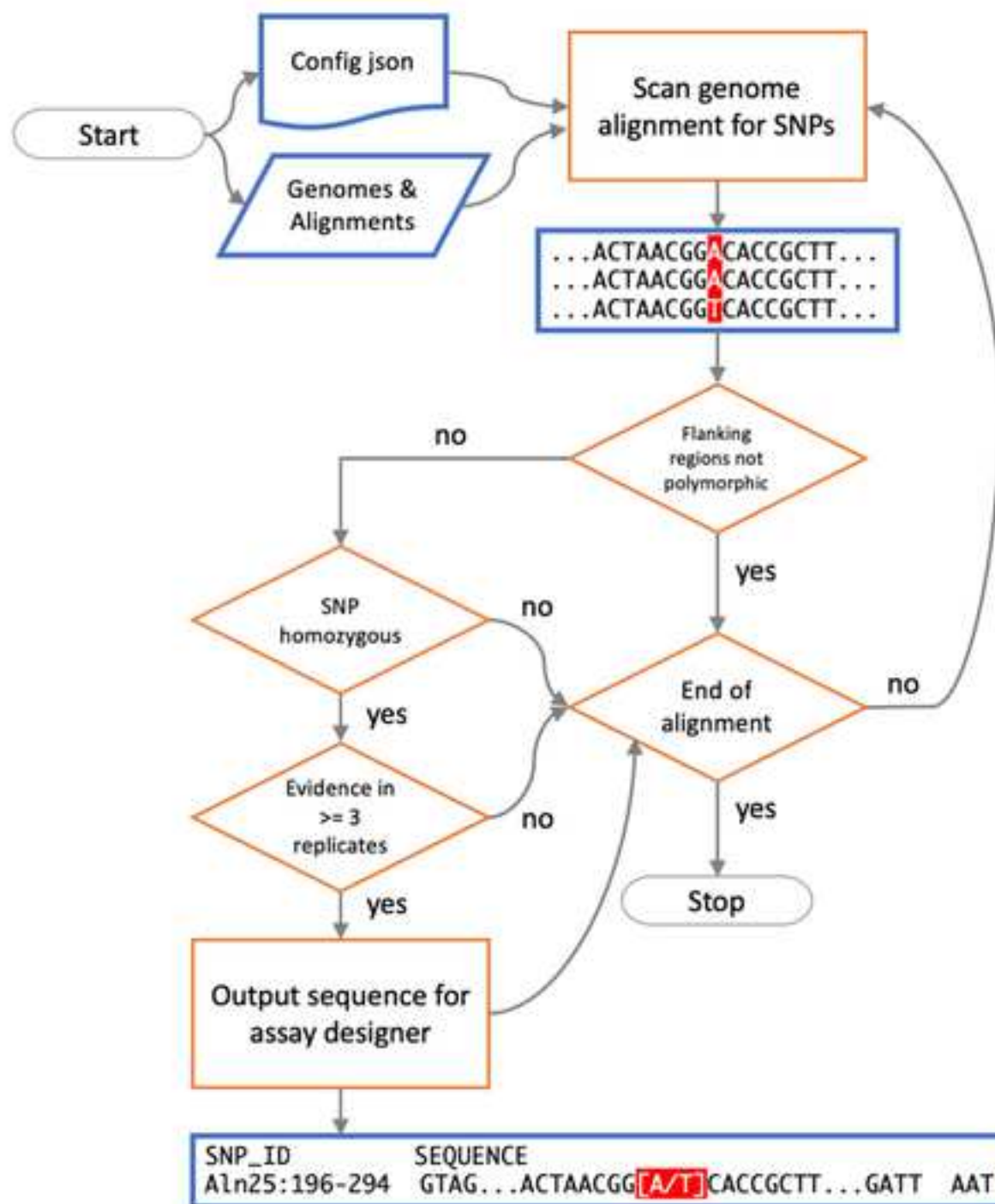
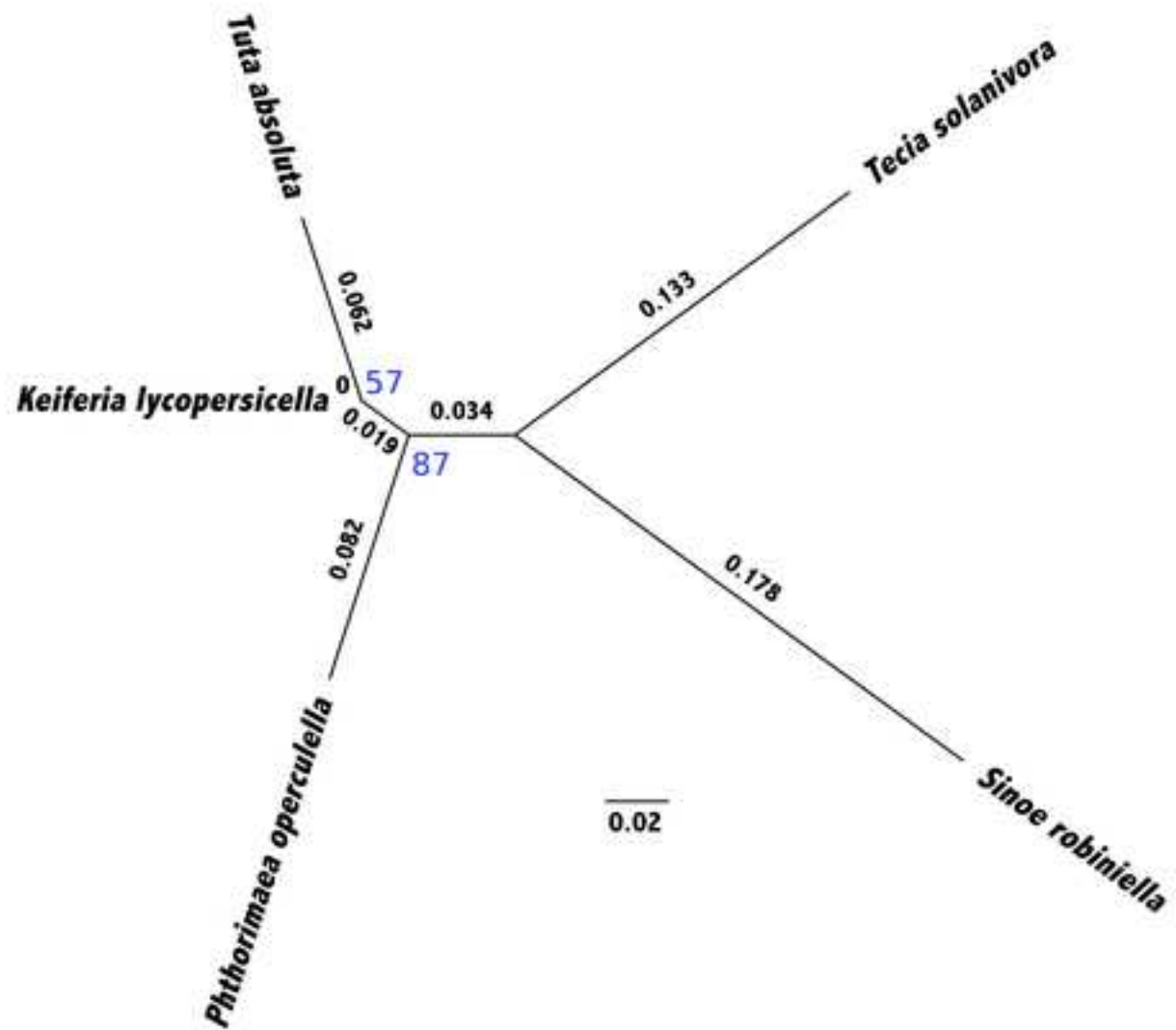


Figure 2





[Click here to view linked References](#)

I would like to thank Dr. Biondi and Dr. Traugott for handling our manuscript and providing us with comments and suggestions to further improve our manuscript.

Our responses to the subject editors' comments are in black regular font, and the reviews are shown in *red italics font*. We have made all the changes recommended by the subject editor.

COMMENTS TO THE AUTHOR:

I do appreciate the great efforts in revising the manuscript according to the referee comments. The paper is almost ready to be accepted for publication in J Pest Sci. However, as per the Journal Instruction for Authors (specific remarks), two separate sections for results and discussion should be provided.

Done. We have separated the "Results" and "Discussion" sections and edited these 2 sections accordingly (Lines 308-461).

Below, some further minor points.

I am looking forward receiving the new manuscript version for inclusion in the Tuta absoluta special issue.

L17: Please provide 4 to 6 keywords. Please avoid words already in the title. My suggestion is to provide the most common name for the main pest, i.e., South American tomato pinworm

Done. We have included common names of *T. absoluta* in the list of keywords (Lines 19-20).

L100: sp. Not italicized

Done (Line 100)

L104: EPPO Global Database 2019

Done (Line 104)

L139, L298, L463; L470, L477, L485, L496, L703: be consistent in not using the colon for headings

Done (Lines 139, 308, 400, 463, 470, 477, 485, 497, and 700)

L443: delete the heading and keep this text as last paragraph of the new discussion section

Done (Line 401)

L522, L542, L564, L577, L590, L597, L601, L604, L612, L629, L632, L638, L647, L666, L673, L691, L702: delete the issue number

Done (Lines 523, 542, 564, 577, 590, 597, 600, 603, 611, 628, 631, 637, 645, 664, 671, 689, and 699)

L536: delete 2017

Done (Line 537)

L588, 592: delete the full stop after the pub year

Done (Lines 588 and 592)

Electronic supplementary material: please provide one file with the author title and journal name and ensure that (i) each table has its own caption, (ii) all tables are cited at least once in the main text.

Done. We have now included one "supplementary material" document (with journal name, manuscript title, and authors) that includes Supplemental Table 1 and Supplemental File 1.

[Click here to view linked References](#)

Journal of Pest Science

Sequencing of *Tuta absoluta* genome to develop SNP genotyping assays for species identification

Christine A. Tabuloc, Kyle M. Lewald, William R. Conner, Yoosook Lee, Ernest K. Lee, Alexander B. Cain, Kristine E. Godfrey, Judit Arnó, Nuria Agustí, Clerison R. Perini, Jerson C. Guedes, Frank G. Zalom, Joanna C. Chiu

Supplemental Materials

Supplemental Table 1: Specimens used to validate iPLEX SNP genotyping assay

Supplemental File 1: Output of *snp-id* to identify gene regions for iPLEX primer design

Supplementary Table 1: Specimens used to validate iPLEX SNP genotyping assay

Sample name	Species and Life Stage	Sample Origin
SL1	<i>Tuta</i> larva	Barcelona, Catalonia, Spain
SL2	<i>Tuta</i> larva	Barcelona, Catalonia, Spain
SL3	<i>Tuta</i> larva	Barcelona, Catalonia, Spain
SL4	<i>Tuta</i> larva	Barcelona, Catalonia, Spain
SL5	<i>Tuta</i> larva	Barcelona, Catalonia, Spain
SL6	<i>Tuta</i> larva	Barcelona, Catalonia, Spain
SL7	<i>Tuta</i> larva	Barcelona, Catalonia, Spain
SL8	<i>Tuta</i> larva	Barcelona, Catalonia, Spain
SL9	<i>Tuta</i> larva	Barcelona, Catalonia, Spain
SL10	<i>Tuta</i> larva	Barcelona, Catalonia, Spain
SL11	<i>Tuta</i> larva	Barcelona, Catalonia, Spain
SL12	<i>Tuta</i> larva	Barcelona, Catalonia, Spain
SL13	<i>Tuta</i> larva	Barcelona, Catalonia, Spain
SL14	<i>Tuta</i> larva	Barcelona, Catalonia, Spain
SL15	<i>Tuta</i> larva	Barcelona, Catalonia, Spain
STA1	<i>Tuta</i> adult	Barcelona, Catalonia, Spain
STA2	<i>Tuta</i> adult	Barcelona, Catalonia, Spain
STA3	<i>Tuta</i> adult	Barcelona, Catalonia, Spain
STA4	<i>Tuta</i> adult	Barcelona, Catalonia, Spain
STA5	<i>Tuta</i> adult	Barcelona, Catalonia, Spain
STA6	<i>Tuta</i> adult	Barcelona, Catalonia, Spain
STA7	<i>Tuta</i> adult	Barcelona, Catalonia, Spain
STA8	<i>Tuta</i> adult	Barcelona, Catalonia, Spain
STA9	<i>Tuta</i> adult	Barcelona, Catalonia, Spain
STA10	<i>Tuta</i> adult	Barcelona, Catalonia, Spain
STA11	<i>Tuta</i> adult	Barcelona, Catalonia, Spain
STA12	<i>Tuta</i> adult	Barcelona, Catalonia, Spain
STA13	<i>Tuta</i> adult	Barcelona, Catalonia, Spain
STA14	<i>Tuta</i> adult	Barcelona, Catalonia, Spain
STA15	<i>Tuta</i> adult	Barcelona, Catalonia, Spain
TL1	Tomato pinworm larva	Immokalee, Florida, USA
TL2	Tomato pinworm larva	Immokalee, Florida, USA
TL3	Tomato pinworm larva	Immokalee, Florida, USA
TL4	Tomato pinworm larva	Immokalee, Florida, USA
TL5	Tomato pinworm larva	Immokalee, Florida, USA
TL6	Tomato pinworm larva	Immokalee, Florida, USA
TL7	Tomato pinworm larva	Immokalee, Florida, USA
TL8	Tomato pinworm larva	Immokalee, Florida, USA
TL9	Tomato pinworm larva	Immokalee, Florida, USA
TL10	Tomato pinworm larva	Immokalee, Florida, USA
TL11	Tomato pinworm larva	Immokalee, Florida, USA
TL12	Tomato pinworm larva	Immokalee, Florida, USA
TL13	Tomato pinworm larva	Immokalee, Florida, USA
TL14	Tomato pinworm larva	Immokalee, Florida, USA
TL15	Tomato pinworm larva	Immokalee, Florida, USA
TPA1	Tomato pinworm adult	Immokalee, Florida, USA
TPA2	Tomato pinworm adult	Immokalee, Florida, USA
TPA3	Tomato pinworm adult	Immokalee, Florida, USA
TPA4	Tomato pinworm adult	Immokalee, Florida, USA
TPA5	Tomato pinworm adult	Immokalee, Florida, USA
TPA6	Tomato pinworm adult	Immokalee, Florida, USA
TPA7	Tomato pinworm adult	Immokalee, Florida, USA
TPA8	Tomato pinworm adult	Immokalee, Florida, USA
TPA9	Tomato pinworm adult	Immokalee, Florida, USA
TPA10	Tomato pinworm adult	Immokalee, Florida, USA
TPA11	Tomato pinworm adult	Immokalee, Florida, USA
TPA12	Tomato pinworm adult	Immokalee, Florida, USA
TPA13	Tomato pinworm adult	Immokalee, Florida, USA
TPA14	Tomato pinworm adult	Immokalee, Florida, USA

TPA15	Tomato pinworm adult	Immokalee, Florida, USA
PL1	Potato tuber moth larva	Arvin, California, USA
PL2	Potato tuber moth larva	Arvin, California, USA
PL3	Potato tuber moth larva	Arvin, California, USA
PL4	Potato tuber moth larva	Arvin, California, USA
PL5	Potato tuber moth larva	Arvin, California, USA
PL6	Potato tuber moth larva	Arvin, California, USA
PL7	Potato tuber moth larva	Arvin, California, USA
PL8	Potato tuber moth larva	Arvin, California, USA
PL9	Potato tuber moth larva	Arvin, California, USA
PL10	Potato tuber moth larva	Arvin, California, USA
PL11	Potato tuber moth larva	Arvin, California, USA
PL12	Potato tuber moth larva	Arvin, California, USA
PL13	Potato tuber moth larva	Arvin, California, USA
PL14	Potato tuber moth larva	Arvin, California, USA
PL15	Potato tuber moth larva	Arvin, California, USA
PTA1	Potato tuber moth adult	Arvin, California, USA
PTA2	Potato tuber moth adult	Arvin, California, USA
PTA3	Potato tuber moth adult	Arvin, California, USA
PTA4	Potato tuber moth adult	Arvin, California, USA
PTA5	Potato tuber moth adult	Arvin, California, USA
PTA6	Potato tuber moth adult	Arvin, California, USA
PTA7	Potato tuber moth adult	Arvin, California, USA
PTA8	Potato tuber moth adult	Arvin, California, USA
PTA9	Potato tuber moth adult	Arvin, California, USA
PTA10	Potato tuber moth adult	Arvin, California, USA
PTA11	Potato tuber moth adult	Arvin, California, USA
PTA12	Potato tuber moth adult	Arvin, California, USA
PTA13	Potato tuber moth adult	Arvin, California, USA
PTA14	Potato tuber moth adult	Arvin, California, USA
PTA15	Potato tuber moth adult	Arvin, California, USA
CRA1	<i>Tuta</i> adult	Costa Rica
CRA2	<i>Tuta</i> adult	Costa Rica
CRA3	<i>Tuta</i> adult	Costa Rica
CRA4	<i>Tuta</i> adult	Costa Rica
CRA5	<i>Tuta</i> adult	Costa Rica
C01	<i>Tuta</i> larva	Ouro Verde, Goiás State, Brazil
C02	<i>Tuta</i> larva	Ouro Verde, Goiás State, Brazil
C03	<i>Tuta</i> larva	Ouro Verde, Goiás State, Brazil
C04	<i>Tuta</i> larva	Ouro Verde, Goiás State, Brazil
C05	<i>Tuta</i> larva	Ouro Verde, Goiás State, Brazil
C06	<i>Tuta</i> larva	Riobamba, Chimborazo State, Ecuador
C07	<i>Tuta</i> larva	Riobamba, Chimborazo State, Ecuador
C08	<i>Tuta</i> larva	Riobamba, Chimborazo State, Ecuador
C09	<i>Tuta</i> larva	Riobamba, Chimborazo State, Ecuador
C10	<i>Tuta</i> larva	Riobamba, Chimborazo State, Ecuador
C11	<i>Tuta</i> larva	Campo Nove, Caaguazu Department, Paraguay
C12	<i>Tuta</i> larva	Campo Nove, Caaguazu Department, Paraguay
C13	<i>Tuta</i> larva	Campo Nove, Caaguazu Department, Paraguay
C14	<i>Tuta</i> larva	Campo Nove, Caaguazu Department, Paraguay
C15	<i>Tuta</i> larva	Campo Nove, Caaguazu Department, Paraguay
C16	<i>Tuta</i> adult	Santiago del Estero, Santiago del Estero State, Argentina
C17	<i>Tuta</i> adult	Santiago del Estero, Santiago del Estero State, Argentina
C18	<i>Tuta</i> adult	Santiago del Estero, Santiago del Estero State, Argentina
C19	<i>Tuta</i> adult	Santiago del Estero, Santiago del Estero State, Argentina
C20	<i>Tuta</i> adult	Santiago del Estero, Santiago del Estero State, Argentina
C22	<i>Tuta</i> adult	Mar del Plata, Buenos Aires State, Argentina
C23	<i>Tuta</i> adult	Mar del Plata, Buenos Aires State, Argentina
C25	<i>Tuta</i> adult	Mar del Plata, Buenos Aires State, Argentina
C26	<i>Tuta</i> larva	Villa Alegre, Maule State, Chile
C27	<i>Tuta</i> larva	Villa Alegre, Maule State, Chile
C28	<i>Tuta</i> larva	Villa Alegre, Maule State, Chile

C29	<i>Tuta larva</i>	Villa Alegre, Maule State, Chile
C31	<i>Tuta larva</i>	Arica, Arica State, Chile (Greenhouse)
C32	<i>Tuta larva</i>	Arica, Arica State, Chile (Greenhouse)
C33	<i>Tuta larva</i>	Arica, Arica State, Chile (Greenhouse)
C34	<i>Tuta larva</i>	Arica, Arica State, Chile (Greenhouse)
C35	<i>Tuta larva</i>	Arica, Arica State, Chile (Greenhouse)
C36	<i>Tuta larva</i>	La Joia, Arequipa Department, Peru
C37	<i>Tuta larva</i>	La Joia, Arequipa Department, Peru
C38	<i>Tuta larva</i>	La Joia, Arequipa Department, Peru
C39	<i>Tuta larva</i>	La Joia, Arequipa Department, Peru
C40	<i>Tuta larva</i>	La Joia, Arequipa Department, Peru
C41	<i>Tuta larva</i>	La Curva, Arequipa Department, Peru
C42	<i>Tuta larva</i>	La Curva, Arequipa Department, Peru
C43	<i>Tuta larva</i>	La Curva, Arequipa Department, Peru
C44	<i>Tuta larva</i>	La Curva, Arequipa Department, Peru
C45	<i>Tuta larva</i>	La Curva, Arequipa Department, Peru
C46	<i>Tuta larva</i>	Rocha, Rocha Department, Uruguay
C47	<i>Tuta larva</i>	Rocha, Rocha Department, Uruguay
C48	<i>Tuta larva</i>	Rocha, Rocha Department, Uruguay
C49	<i>Tuta larva</i>	Rocha, Rocha Department, Uruguay
C50	<i>Tuta larva</i>	Rocha, Rocha Department, Uruguay
C51	<i>Tuta larva</i>	Chía, Cundinamarca State, Colombia
C52	<i>Tuta larva</i>	Chía, Cundinamarca State, Colombia
C53	<i>Tuta larva</i>	Chía, Cundinamarca State, Colombia
C54	<i>Tuta larva</i>	Chía, Cundinamarca State, Colombia
C55	<i>Tuta larva</i>	Chía, Cundinamarca State, Colombia

Supplemental File 1: Output of *snp-id* to identify gene regions for iPLEX primer design

Format of file output:

Alignment:Interval Sequence SNP ['Kl', 'Po', 'Ta']

Alignment24273:300-411

CCGCCATTGTTTTTAACTAGATATTTGAATTAAGTACTTA[C/T]TGCCTCTAAAATCTTATCATTAAATCT
TAATTGCAGAATAACAATAAAATATTGCCCTGAGGTTGGGGTCA CTC

Alignment24328:1001-1087

GATTACGAAATGACTTTCCAATTTTCCAAGA[C/T]GTATTGTTGCCACAGCACCGTGGTTTTAGCGTTTT
ATTTCTAGCCTCTGCAGTC TCC

Alignment24415:665-800

TAATTACAGTTACTTCATTATTTTAATAAAAAGTCTTCAATTTCTAACACTAAGGCTTCGAGTTT[C/T]AA
AACAAAATAAGCGGTCTATCATAAACTACGGTACGATACGTTCTATAATAATTCTCAATATAATTATA CTC

Alignment24727:40-149

TTTCCGGTTTCTTTTACCAGATGCTGTTGTCCACTTCGACGCTTCAAGTCCCGTCGTCCGAAGT[C/
G]GTTTCAGTCCGTGCCCTGGTGACCCCGTGCATGCCGACTT GGC

Alignment25352:923-1027

CTACTACGTTAATGTTTATTCACCGAGTCTACTAGTTACTATTTTATACTCCAAATTCOAAGT[A/T]ATT
ATGATTCTCCTATTCGAAAAGGCTGAAATAAATTTTA TAA

Alignment25476:45-137

GGGTTATAGGAGGAATGCGAGATGGAATGCTGGCGCTGGCTGGGAGGGCGG[C/T]CCAGTGTGCAGGTG
ACCTGCGACCCCGCGCTGTGTGGCGG CTT

Alignment25613:248-355

GGTTTCGGCGGCCTCTTAGGGGTCGCATCCAGTATGGGTGGAGAGAAGGGCCATTGGAATTTGGCGACA
AGCTG[C/T]TGGGGGAGTGCCTCCGTTCCCATTCTCGCC CTT

Alignment25843:196-294

GTAGCTCAATATGGAGCGCACGAACCTAACGG[A/T]CACCGCTTCTAAGAATGATGCAGGTAAAGCTTAC
ACTCTGACCTTAGACAGATTTGGCGCGAGATT AAT

Alignment26032:76-173

ATGGGCTATTTGTTATCATCTTTTGGCACTAATATAGCGCCATCGTTCGTCAGCTTGTTTTTGTCC[C/T]
CGTTGTGTCTGAAACAGGATCTTTTTATGG TCC

Alignment26127:70-168

GGAAAAATTCCTTCCAAATTCGGCAGTCATTTGTATTAAGTTGGTTTCTTGTTTTTCTGG[A/T]TCGCG
CGTTTTAGATAGCTTTGTCCCTATTGCATG TAT

Alignment26529:489-581

CGACCTCAACGTCTCCACATCATCCGATCGGACAACTCG[C/T]GGGATTCGTGTGCTCTCTCACCTGTT
GCTCGGATTGTGTTCAAGTTGATCA TCT

Alignment26866:217-309

ACAACCCCTTGTATTTTGGCTCAACAAACGATTTGTTTGGCTGTCAACAAACAAAGAA[A/G]AGGTGACGACC
GTCCAGACTCCGACCTTTATAAACC AAG

Alignment26951:3361-3462

GAGTTTAACGGCAATTTTATGCCCGTGAAAATAAGGCGTAATAAAATTTTAATATTTTACCAA[A/C]C
AATATTGATTGGACGCCTGCCCTTGGTCGACAGAT AAC

Alignment27035:5-141

CGATTGGCATTATTGCCTTGTGACCTGCGTTTCGGACGACAAGGTGAACGGAGTTCGTTGACCC[A/G]G
CTTACGTAAACGAATGCAATTATAATATTGTTTAGTTTTATTTTTCTGTTGGCACAACCTGGCGCGAAGG GAG

Alignment28235:590-696

GGTCATTGTTAAAATATCGATATCGTTACATACAAATCG[C/T]GGTTGTGGCGACAAAAGCTTGCGACA
ATGCCTATTGCGCAAATCTCGCTCGGGCTGGGCTAAGCGC CCT

Alignment28284:36-139

ATGTTTGGCTCGGAGTTTTTCGCAGCTTTTGGT[C/T]AATTGTAAGTTACATTGTTTCGAAATTTTGAGGTC
CATTGCTTTTCGCATGGTCATTTCTGAGTGAAAATT TCT

Alignment28324:247-335

GTGAACCTGGTCTGCCGACGCAGCGCCGCTATGGAGTCGGGCCGGTACCG[C/T]GGCAGCTGCTCACCCA
ACTCCTCGAGTTCCGAATCTG TCC

Alignment28539:1731-1821

TGTACGACAGTATTATTGATTTATTTACCTTTGCTAGTTATACATTGGTAAAAA[C/T]ATTAATGCTAT
GAAACAATTTGACTTAGCATTGG TCT

Alignment29254:681-784

AGTGCAAATCAGATCTCGCTAATACTTAGACCGTCGCCGTTTCATCGGTCAGTGTGGCAATATCCTAG[T/
G]AATATATTGAAAATTATTCTAAAAAATACGTTATC GGT

Alignment29314:124-221

GGCACTAGGTGGTTATTTTCGTTGTACATGCGACTCT[A/G]GCATGATAGGCTGCTAATGGTCAAGTGAC
ACAGATATCTTTGGCACACTTTACCTTGT AAG

Alignment29634:160-277

GGTTGATGTGAAATAATGGGGCATAACTGCATGTA[T/G]TCGAGATTGTTTATGATTTCTTAATATT
TTCCATCCCACACGTAGAGATCAATGATTAGCAGAGGTCGGTGGGGCGGG GGT

Alignment29743:532-621

CTTTTGAACCTCGTACGTTAATTTTAGACACAACCTTTGGCACAATCATAAATTAC[A/T]TTTTTATTGAGA
TACCGAAGGGGAAGACTTGGGG TAT

Alignment30518:426-510

ACGTTTTTAATTGCAACAGTTCAATTTTGGAGTCAGAACAACGTGATAATTT[C/G]AAAAAATGTGAC
TTTTATGGTTTATAATGA GGC

Alignment30554:6-147

GTTATTCACGTTCCATTACCTCAATTTTTTAGAGCCGAGGTGCCTGAAAAGGAACCCTTCACTCATTGT

GTCTCATCTTTGAATGGGCGGAGGGCCGCC[A/G]TGAAATTAATTTCTTTACATTATTCATTATTTTCTTTTT
GAG

Alignment30765:162-262

AGGGCGGGTGTGCCAGGCCGCCGGGGTTCGCTCCGC[A/C]GCCGCAGCGCCGCAGCCCTTGCGACAACAA
CGAAACTAATATTTTGTTCCTCACCCCGCTCCC CCA

Alignment30967:1658-1769

TATAGCGTGTGTGTTAGCTACAACCTTCTATATTATAAATCTACCTATAGCTCCTTACCTATCTTCTATC
TT[C/G]AATCTAAGTAGTCTGTGTCCCTTCGTTGTTAATCTC GCC

Alignment31269:143-261

CATCAATAACAATCATCAATTTGAGTGAAGAAGTCTAATTAAGAAGCCGTTACAAGTTACCTCCATAA
ATCTGAGC[A/T]GGAAACAATAGTGGCTATCCATTACTTAGGCCAATGTTTC ATA

Alignment31557:348-469

CCTGACAAAGACAAAAAGCTTTTTACGAGGAACCTCAAATCGAGGACACTTTACGTTTCAGTGTACTTCAG
GGACTCTCGGAACCGTTGC[C/G]GACTTGAAACATGGTTTTATATTGTTTTGAT GCC

Alignment32188:138-240

GCATGGAAATGATCTTACATTGCTAGCCTCGTG[A/G]GCGAGTGACGCTTGCTTGCCACTGCCATTGCGA
GCAACGGACCACGATGTCTCCGCCGATCCACGCT GGA

Alignment32219:809-907

TTTATAAAAATTCACATAATCCCTTGCATATGTGCATGCCTATAGTAACATACGTCA[A/T]CTAGCATAC
GTCTCTTTCAGACTTTCGCTTACCTCACAAG TAA

Alignment32292:6-94

TAACTTTTGGGCGCAATCAGTGGCAAGTCA[A/G]CGTAACTCTAACTTAACATTCAAATAGCTTCTAGC
TAGTAAACCAAGCAAAGCGTT GAA

Alignment32485:309-404

TTTCTAACGAGACGAAACCTCCAAATCATGCTGTTTAGTGCGAAATTATAGCGTTTT[A/G]AACGAGGC
GTTTAGGTGATTTGTACGTCTCTAATGGG GGA

Alignment32501:532-635

AGGCATCGATAACCCTCCATTCCGAACATAATGTTTCGCATAATTGGCGTAACATTTCCACTG[A/C]GAAC
CCTTCAAGACACCAGTGATGTTACGGCCTACATGT CCA

Alignment32513:2664-2800

AGAGGTCATTGAGAATCAACTGCGTGTAATAATCAAATAAACGATTCCACGCTAATGCCATTCTGAATT
TAAATAATTGGAATTTGGAAGCTGAC[A/G]TCGCGGTTTTGACGTCTTCATTCAAATTTGGAATAACGAG
GGA

Alignment32771:104-237

GCGGAGTTAGCTCAACTTTAAAGCAGTCGACAACATAAAAACAGAGAATTCTAAATTCCTCG[A/G]CGG
AGCGGATGCAGGCGCCGCAAGTTTGCCGACGACGGAAAATGGAAAAACCGGAGGGTGGAAAGGATAG AAG

Alignment32925:160-274

ACTAATGCTGTGTCGTATGTTTGTGTTTTAGCGCGCATGCGTAATAACTTTCCCTTCTGGCATACTAATATT
TGGCACCCGTTG[A/C]GGCAGAGGTACTGAGGTTGGGACTCAGCACC CCA

Alignment33365:31-148

ATCAGACGAACCGTCTCGTTGTGCGAGCCACTCGGGACGGATCTCGCCGCTCCAGCGTTAAGATCTGGTTA
GACTCGAC[A/G]GTCACCTCCTCTCGAAGTTGTCTTCGTTGCCCGATAA AGG

Alignment34120:885-974

GAGAACTTATTGTGTTGTAATACATGCCCAT[T/G]GTTTCACTATCAATTCCATTCCCTTGGTTAATTA
CTGTAACCATTTTCGCTACGCGC TGT

Alignment34376:210-310

GTTACAGGGATAGTTAGTTTCTAAGTATTAGTAGACCCATGTTAAAAAATACACCAGT[A/G]TCGATT
TTATGGAAAAGTTTATTTTGATATATAAAAAGG GAA

Alignment34517:261-392

CCCAACTCGTTCCCGAACCAGCTGATCTCG[C/T]TGCATCAGATCAGGAACTACGCTCACCAGCCGTCTGC
GCTGTTGCCAGCTGAGCACATTTTACCTCACGCTTATCGCACAAGGACAAACAGTAGACAAA TTC

Alignment35061:1159-1250

TCACGCTTACTTGCTAGTTTTATATTTTTCTTCATATAAAAATCTATTTA[A/G]AAGCTTACTTATTATC
TAAGTTATATTCCTCGAGGTAGT AGG

Alignment35778:236-344

TGGGCTTTGAGGACGTCTTTGCGAAGTTTAGCGGTACCCCAAATTCAGTTGGCCTCGCCCGATTA[C/G
]GAGTTGGCAATATCTTGGAATTTTCTGCTACCCTGGTGG CGC

Alignment36001:317-404

TCCTACAAATGGAAAGGCAACTCAGATCTTAAATAGCTAAGGAAGGGACGTCCT[A/C]CGTCGTTTGA
CGTTGGAAGAACATTGCCAG CCA

Alignment36412:61-154

TCGAAATGCTAAGAAAATATTGGATAGAGATTAGGCCATATACTTTTATTGG[A/G]TTTTCCACTATAT
TTATTTAACGTTCTTTTCTTCGTTGAT AGG

Alignment37318:132-221

CTGCCTGTGTGGCGCTGCCGTCAATTTTTT[C/T]TACACGGAAATTGTTTCACTGTCAATTTTGCAAGA
AATAATTGATTTATCTGTTTGT TCC

Alignment37590:1867-2003

TAAACAGAATCGAAATACGCCATTATCGAGGACAATAATC[A/G]TAATGATCGTATGAAATAGGGAGAA
CTAATTCTATGAATGTTTTAGTCGATAGCTTACGACATGTTTATTGTCATTGCGCTATAAAAGTGCGTC GGA

Alignment37806:844-944

AACTGTACTTTACTTACAATACGCCTTATATGGAGGCTG[T/G]GGGGCTATTCGCACGCAGATCGGGAC
AATTTATCAACGCTGTCAAATGTTGTGATTTAC TTG

Alignment38193:250-343

TTGAATTTATGTATTCCTAAAGAATTTGTACTTTAACTAG[A/C]TCTAAATTGCATTGTGAAACTGTAC
AATAGCCATACATTTAGGAATGGAGCG AAC

Alignment38280:66-206

CATTTTACAGCGTCATAAAGAACTTTTCGAGTCTCGGGG[C/T]GAGCATGCAGGTATGCGTACAACTTA

ATGGGCGTGCGACAGACAAAGTCCCTGTCCCGAACTAATGACCACTCGAAACGAGAAAATTACGCCACGCGGC
CTC

Alignment38827:6864-6959

CGATTACCTACTCGCTGATTAAGTAACTAAGATAACA[C/T]TGCCAATATAGAACGTCAAAGTCAAC
AAGGGTGAATGAAACGTTAAGTTGATTC CCT

Alignment39036:491-615

GAACGGCGACAGTGTTCTCCAATTAACGAGATAAGGCGGATTGAGTCCGCCCGATACAAACACCAGCTAA
GTAAACTATTGCA[C/G]TGGGTACAGATAAAATCGTAAGGGATTAGAAAAGCGAAAAA CGC

Alignment39049:135-245

TATCGCGAAATAAAATGAAATGAAAACACGAAGTGCATTT[A/C]ATATCGGTCTCAGATTTTTTCAGGAT
CCATTGGAGCTATATCGGAACTTTATCGCAGAAGCAATAAAGAC CAA

Alignment39469:305-404

AAACAAACCATGTTCTCACAGCAGTAAAAATAAAGACAAAAGACGACAACCATAAATT[T/G]CCGCTGA
AAAGTAACCAAAGCATTATACAGTTGCATAACA TGG

Alignment40043:362-456

GAAGAAAACTTTGTAGAATCTTCAAAGGCCGTAAACGAGATCAAGTAATTTAA[T/G]CCAAAATAAGCA
AAATTACTCGAGCATTGTCGGCTTCCCA GGT

Alignment40375:350-441

GCTTGTTTATAATTCTGCTTACCCTTGATCGGAGATTTG[C/T]CTTGGTTTTGTAATTCACCTGACTCT
TGCTTGAATGGCTAATCCGTGAAA TCC

Alignment40479:145-250

ATGAAATATGACCACAGAGTAGAATGATCAGTAGGTACACTAATTGACTGTCAAAGAAACGTG[C/T]G
GACATGACGTATGTGGATTTTAATATGGATACAGCTTGT CTT

Alignment40642:118-211

GCTCCGCTCGCGCCACACACACAGACACACGCACACTGAGCTTGTTGCATGC[C/T]TCCCGACGATCTATG
TACACTCCTCACCGCATGACTCCAG TCC

Alignment40971:1566-1649

ACTTAAAATCTAGTAAAATTTAAGTCATGTGG[C/T]TGATTAAATAAACCTTATATAAAATTTAGTACA
CAATGGTGTTTTTGTTT TTC

Alignment40982:204-338

TCAAATCAGTGAATTTATTAAGGGCCAGTAATTCGGATTGTGATTTTAAAGTAAGTAGGACAATGAAAC
ATTCCGGAAAGTTGTTTTGTCAATTGTTAT[C/T]GATTGAATTTAAAGAGTCTATCCAAATACGTATC TCC

Alignment41117:1742-1836

CCTGTAAATTCGTGCTAGGATTTTTAGTGAAATTATTACCTAAAATAAATAGT[A/G]AAGAGTAGCGCA
ATTCATTAATTACCTACCTAGTTGAGTA AAG

Alignment41730:92-182

AGGATCCCGAACAAAGAGCCGAAACGGCTCGCATTAAGG[A/T]GAATAAAAGATTCTCGCGACAGTTTCA
CTTGGCAACGGACACGGCGAATAT AAT

Alignment41922:1782-1923

GCGCAGCTCCTCCAGCAACTGGCACAAAGTAGTCATGTCAG[C/T]GCTGTTTTAACTTGTAAAGGTTTGC
CCAAGCATTTAGTTCCTTGAAAGAATTGAGTAATCATATGGTTAAGAATTCTCATTATAAAGAGCACATTATGC
CCT

Alignment42164:2213-2354

AAAACCTGGCAGTCGGTAGCGGGCGCGTGAAACACTATCTCCTAATCGACATAAAATGGTAGTCATTGA
GGCGGCGAGAGCGGAAACAACAAATCTTTAG[C/T]TGTAAGTTGAGCCGCGGCTTTTCTAGCGGCCTCTCACTTT
TTC

Alignment42456:181-289

ATGTACCATTATTTTTGAAGTAAATATACAAAATATTTACACTAGTGTGTATTATATTACATTGAATTT
TAATT[A/G]ATTTTCGACGTTGACCGTCTAACTGTGAATCGAC GGA

Alignment42459:1-136

CAGATGAATGCTTAGTTTATTTTTGAACCAACTAT[A/C]GAATGATTTACGAAGTTTACTTTGTGTTTTCG
AAGTATGACCAACAATCCTGTATACTATCTATTTCTTTAACATGTAATAATATATCTATTGTATTAATAC CCA

Alignment42657:181-276

CAACAGTTAGCCCGGTGGGCGAGTGAAGACGCGGT[C/T]CCGGCGGCGGTGGGGGCGCTGGGGGCGGCAG
GCGGTCGCGACTACTTCCCGTCGCCCC TCT

Alignment43101:11-128

ATAAGATATTTATAAAGAAATTTCCGATTCAGCAGC[A/G]AAGTTCAAATTTGACTCCATCTCCGCAA
AGAGTTTGGTGGCGTTTTCAATTTAACTTGAACAAGTTAAATAATGTGC AAG

Alignment44142:100-232

G TTCACGTGTGTAAAGTAGGTTACAGCGCACGAG[C/T]GAGATAAAAAAATAGGTCAAGTTATCTTTG
GTCGTCTCGCAACGATGAATTTATCGGCGTGATTGCGCGTGAAAAAATGGTTTACGTAACAGTA CTC

Alignment44164:71-158

AGGTAGTTGAGGTATTAACCTCTGCACAACCTTTGCT[A/G]AAGGCTTCAAATATGGAGTGGTCATAGAT
GGAAGTCAGATGGAATGATAA AAG

Alignment44384:18-114

GCGCCACTCGTGCGCAACACCGCGCGGCGCTACCGTTACACTGCACCCTTTGC[C/T]GGACAGTTAGCT
GCACGAGCTCGTGCTGATCATATGATGA CTC

Alignment44457:40-129

CAAACGTCATGCGAGTCATGGTCCGCCATGTTGAA[A/T]TTCGTGTAACGCAAAGGGAAATGTCAGCTGG
CGGCTGCCGTGTTATTTCTTTG AAT

Alignment44827:35-167

AAAGTTGACTTGGGATTCGTATTTCCATCCACAATCACAATATTTTTACGCGGAAATGATTCTCGGCGT
TATTTTCGACGACATCAATTT[A/T]GAAGCACTTGGTTGTAAAGTTTAAATGCACAAAATCGTT TAT

Alignment45092:276-408

TTTATATGGAAGACTACATTTTGCCTCTAAATTTAACTTA[A/C]TAATTTATAAGTACCATTCTTTATTT
TATATTTAAGGCATTTTGATTCTACTAAAATAGAAATTTACAAATCATCTCATGATTCCAGTAT CAA

Alignment45239:633-746

AACTTTGAGCTTGCTTCGTCCTCCGCTTGTAGAGTCTAGTCCGTTTTAGTTCCACGCTTGAAGCGGGCT
TGTGTAGA[A/C]TAAGCGCTTATTAATAACGAGATGTAAACATCCA CCA

Alignment45280:165-296

GCATCAAACCGGACACTTGCCATTCCGTTTCGCTTCTGACCTTTTCCCGTTTTGTTATGCAAAT[C/T]CCA
GTTCCCGGGGAATTACACAACGGGAATAAAAAGTATTGGAGTGTTTACACGCTGAGTCCGCG CCT

Alignment45285:194-328

GCCTACCTGCGCGGATGGAATGCCCGATACGC[A/T]CCTATAATGATGTTAAAACAAACTGTTAGCCTG
TCATTAACGCGACTCACAAACCAAATGGGGGAGACCCATTATAAAAATTTGTCCCATCCGTTTCGGC TTA

Alignment45364:201-320

CTGAATTACGCCATAAAGTTTCATAGAGGTACGGAGCTAGAGTTGAAGTCTTTTAGAATGCAAATGTGT
CTGCATTCC[A/G]GCTCTTTCAAACATTTCTAAGGGGCGACTAACTGAGGA AGA

Alignment45395:11180-11321

CTCGATGCAAATCATCCTAATACGTTCCGATTATAAAAAGCTATAATTTCCGGCATTATAATGTCCATCAA
AGTGTTTTACATATATAAAAATAAAAAGACC[A/G]GCAATCAAGTAATTTGTTTCTCGACCTACTAACTCTTTT
GAG

Alignment46177:1121-1235

TCACGAAAAAGGAAACAATTTAAAACCGTTAACC[A/G]AATCCCAGATATAGTGTCTCAACCGTATCCG
GGGCGGGTGAGAAGCGAAATGGGTTCAATCACTCCCAGACGTTGTCC GGA

Alignment46194:321-447

TCACAAAACGCGAAGCATGTTAATATTTAGA[A/T]CTGAATGTCCGTTTGAGCGCCAATGAATAGTTGG
CTCGATCGACTTCGTGCCTTGCCACGCTTGCTCGATTGTGATGTACAGCTTGCGGCAACA AAT

Alignment46370:460-585

AATATAGGAGAGGTGACGAAACGTTTCAGTCTCATTAT[C/T]CGAGAATTTATTAACGAATCGTCCGGAC
CGGAAAACCAAATGTGAAAGAAATAAAAATTCAACCTCGACCGCGGTCATCTAAGGTT CCT

Alignment47661:510-626

CTTCAATCAGCCGATAAGAAGTTCGGAATTTTCAGGCTATC[A/C/T]TTCGTCGTCATCCTGACGACCTCC
TCAGGTCTTTTTATATCACAAAACGGCGGCGATTTTAGGTCCGCCATGGTT CAT

Alignment47761:473-604

ACTCGAGTGCTGGTGGAACTCGTGTCGGATTGAAATATGCCTGCTTATATTCTTGAAAAG[A/G]ATATG
CCACAATGCTTTGTCTTATTCTTCCACAATAAATCTGCAGTCTTCTCTTAATCCTACGCATAT GAA

Alignment47958:131-231

GCCGCCGGGAAAGCTCCGCGCGGATTTAAGCTTTTATACGTGGATAAAAACGCTTTTAT[A/G]GGAAAA
TAAAGCTTCTCGCAGCGGGATATCGCACTTTAT GAA

Alignment48269:11861-11949

CAACTTTAGTGGCGTTTACCCTACGGCGAACAACCTACTTTTGAGAAATT[C/T]CGCTGCCTGGTTAAGC
GAATTTTCTAGTCTGCGTTC CCT

Alignment48702:116-201

ATTTAGTTGTCAAGATTCATCCCGTTGTTTTATTCCAAATAGTGGATGCTTA[C/T]GAGCGCCGAAATGC
TGATTCCCACCGAGTTAT CTC

Alignment48977:953-1070

AAGAAACAATAAGCAGTTTGTAAAATTTCCACATACGGCA[T/G]ACGGAAGAACACAATTTTCATTATGC
AGAATATTAACGAGTGGTGGGTGCTGGGTGTGCAAACAAAAACAGAGTT TGG

Alignment49096:69-157

TTATAGTAAACATAGTTTTCTAACAATTTAGGTAGC[A/T]GAGTCGGTGTTACATCGGGTGGTCGGCGA
AGATGCCAACAAGGTGGTTATA TAA

Alignment49990:2649-2790

TTATTTTTTATCAATTTACCCGGGTGGAGCCTTAAAAGC[C/G]TCGCCCGTTTTATTATAGGGACGTG
AATTAGCAAAAAGAGAATGGATTTTGGTTGTGATTATGTCAAAAATAATTAATTACTATCGATTCTGTGGGGAG
GGC

Alignment50404:775-863

GGTGGGTCGTGTAATACGATTTACATATTGTATGTT[T/G]GTGCTGCCGTCAAATAAAAAACAACCATTG
CCGCATGAATGGACCCACTGTT TGT

Alignment50770:1332-1457

TACAAAACCATGCCACCACATAAGGTGCGAACTTGGCTGACGCTTTAACTCCTATGTAAACCCATAAACT
CCTTTGTGTTAAGTTGTGCTC[C/G]AGGAATTTCCGACCCTAATGAACTTTATGGGC CGG

Alignment51147:556-694

TATCGTGTTATTGTCTTAGTTCTTGTTAAAATATATTGTAATATATCTTAGTTTAAAGTGAATAATG[C/
T]CTCCGTTTACGTGAATGTGAAAGAAGACTGCCCGTCGAGTGCTACGCGGCCATTTTACTTGCAATGCGGC
TCC

Alignment51154:221-352

ACATAATTCTAATTCAATGTCAAAGAACAATAAAATTACAAAATGGCTCTACACAGCGG[C/G]CACCG
GAGGCAGCTAACCGCGAAACGTCCATTTTCATTTCCATAATTTACAAAATGGCAGATTTAAAATCC CGG

Alignment51191:334-431

TATTGAGAAATAGTGGTGCATTGCAAATTTTCCGCTTCG[A/G]GCGCGTCAAAGGGATAATTTATTG
CAATTGAGATATAGCAGGCGCTTCGGGATCG AGA

Alignment51257:1508-1604

AATTAATCGCCAATCGGAATTGGGTTTGTGTGT[A/G]TCCGATCGCGTGATAAATTTGTGCGGTATTCTC
TGCTCCATTTAAAGTTTTAATCGCACCAC AGA

Alignment51508:1224-1329

CTGCCGGAATACAAAATGCAGTTTTAAAATCTTCTCAGCGTATTCTTAAAAGTTTAAATCGAG[C/T]G
GAATAAGAATGGATAAGATTCATACGTTTGTGTTTTCAGT TCT

Alignment51795:480-618

GCGTCAGTGAACTAGTGAAAAGTTTTTTTCGCCGCGCGGGGGACCACCCCTCGACGCCGAAAAAAT
CACCCCTCGCGTCCCGCGCCGCCCGCC[A/G]CCGAATTTTCATTCACCGGGGAAAAAAGTGTGGCAAGGC
AGG

Alignment52218:675-768

CGTACGTGAAGTAAATAAGGAGAAGGTCACATCGGCGAGACCAACTTATGCC[C/T]TGCCGCGAGCAAA
AACGAGACGCAATGAAAACAAATCAAT CTC

Alignment52436:354-488

GTAATAAATAGATGTTAAATAACTTCGGATTTGGTTTCTACTATACAGAGATCAAACTTTTAACCATAC
ATTGAAGTAAAAGAAAAATGCAGATT[C/T]GCTTTTCTATAAAAAATTACCATACACATTTTCATTATC TCT

Alignment52975:1127-1268

AGCCCAACGTGTCGCTGCTGCGGCCGCGACCAGAGGCCGAACGAGAGCGCAACGCCTACGTGGAAGCTCC
ACGGCGAACGCACAACGCGCCCGCGGCATC[C/T]CACGCTGCTGCGCAGCCGCTCAAACCGGTGACAACACAGC
CTC

Alignment53072:37-178

TCCGTGCGAGTGAGTAATGAGACCATATCGCCAATGTATG[A/G]GGAAGCGGTGGTGTGAGTGCGTGG
TACAAACGGGGCATCCGTACGTAGGGAGGTCTCGGGTTGGGCGGCAGCGGCGGACGAGTTGCCGCGGAGCTGC
AGG

Alignment53305:88-229

TTAAAAAATACGAGCACGCCGAGCGGCATTAATTA AAAATTCTCGGTAGAATATTCAAAAATAGAATT
CGCATTCGAACGCTCCTTGTACGGATCCCAA[C/G]TTTGAATTTGGAAGGAACAAAAGAAAGAGAGCGCGGGAG
C GGC

Alignment53484:36-170

GTATACCATTATACCAGCGCATTAAATCGGTTGGA[A/T]TCAACCTTATATTTAATGAAAAGTGATACGT
TATACAGAATTTCTTTGAAAAGGAACGACTACATTCGTATACGTTTAGATCCTTTCAGATATACTTA TAA

Alignment53591:15-120

ACGTCGTAAAATCGTACGGTGAAAACCTTATTGGAGAGGCCAACTTTATTGCCTGTATCATGACAT[A/G]G
CTGATCCCTCATAAAAATATGTATCGATATTGTAAGAAA AGA

Alignment53592:195-286

GAGCGGGCCGAGGTGGTTCGAGGGCGTGAGAAAAGTTGCGAAGCTGCAGCGG[C/G]CTCGGAAGCGCTGGC
GCACGCAATGAAGTGCAATTTAC GCC

Alignment54021:81-165

CTTCGACCAAGTTTTTTGCCCCCGTACCCTGTA[C/G]TTTGCGTTTTTCTAATCGCTCCATTGAATGTTTC
AAGTATTCCCATCGACT GCC

Alignment54097:425-514

TGATTATCCAAAGCTACAGAATAGGTATTATCAC[A/G]TCGTTTGTTTGTTCGCACGCAATTAGAACCCT
CCTGGCTCATTAGCACTTACGA AAG

Alignment54560:158-272

TAAATAGAATGGGCGAACGCTACGGCGACCGGCGTGCCATTTACCGGCCGTGACTCACGAATTAGATCT
CCA[A/C]GGCTACCGAGATCGTAATTATATCAACAATTTTCGTGC CCA

Alignment54621:923-1007

TCGGGGAGGGCGCAATGACTGAATTATTTAC[A/T]ACCAACTTTGCCAAACATTTATTTTTAATGTAAA
ATGACTTTTATAGCATAC AAT

Alignment54919:1520-1660

ACAAACGGCAATCACAACAAAGGTTCACTTTACATTCTAACGCGTTTTAAACTAACAAAGGGATTGGAA
TAAACAGTAAATCGTGCACCCTTTGACCGA[C/G]TGGGCAATTTCCACCTTTGGCGGGAAAACCGAATGGAAAT
GGC

Alignment55677:5652-5742

TAATAATATTACTTAAAGATTAATAGCTTCAATTGTAACTATGTAATAAAATTAT[C/T]ATTATTTT
ATTATTGTACCAACGCGTATACAT TTC

Alignment56329:917-1006

CGCAAGAATACAAATATTATTATCCAGCCCCTTCACAAATATCAATAACGTATTACCC[A/T]GCCTCGAG
ACAGATTTAAAAAGTTAACGAT AAT

Alignment56517:228-326

ACAGGATACGTTTTGTATGTTGTCATCGTAATAAAATATG[A/G]CTCTCATTTACAATCGGTGTTAATT
GTTGAGCAATAATTTATTGCTCTTTTCGTAA AAG

Alignment56633:357-451

TGTTTGTCTTCTAAACTTCTTTTAAATGAGTTGATTAATAGGGCGTTGCTTCA[A/T]GTTGATTGTTGCA
TTTTATGAGGCCAGAGACTTTATAC TAA

Alignment56755:80-220

CGGGCATGGTGCCGGGCCGGTAGCGCGCGGGCGGCCTGCGCAGGCCCATCCAGCACCCGCGTGTGT[C
/T]CCCCAGCGACGTCTATGGCCGAGCAACACGACGCACCGTCCGGCGCACTCTGCACTATCGAGAGAGTCCAA
TCT

Alignment57504:670-774

TCCCCTCAGGACCCGAGAAGCCCCTCGCAGTCGTT[C/T]GACGAGAGCCCTCACTCCAAGTTCCTCAAGTA
CACGGAACCTTGCGAAACAGCTGTCGAGCAAATACGT CCT

Alignment57687:106-247

ACATATTGTATAGCTCAGCAGCATTGTGTTGTCACCCCTAATTATACAGGGCCGCTGATATGAGCAGATT
AGGCGCTGGTAATTAACGTAATGCGAGTGG[C/T]GGATTTAAATTGCCCGATTCTCTGTGTACCCTCTCTAT
CCT

Alignment57923:245-385

GTACATATAATCTGTGATTGTTTCTCGACATTGTCAAGGTACTTCTCGTCAGTTTAAACGTAGCGTAGTTT
GAGGCCATTCTGTTGAGTAACTCCTCGT[A/T/G]AATAGTTTAAAGTTTACATAGAAGTGCCATCGTAGCTGCAG
AGT

Alignment58107:590-690

GCAACATCGACACCGGATGTCGCCAGAATCGTTAAACTATAATTGATGCAAAAGCTAATGAAGCGAGCG[
A/T]CTATTAAGCCGTTTATATGATGGAGCCGCG TTA

Alignment58126:376-476

GAGGCAGATGCAAAACAGTTTGACAGTGTATTGAAGTTATATCCACAAGCGATTAAGCT[A/T]AAAGCA
GAGCAGAAAACAAAGAAACCAGAGGAGCTGATAA AAT

Alignment58315:400-504

AGTCTCTAATTAATTCGAAGCCGAGACATTAATAACCCCCTCTAATTGAAGACATCTTTTGCCGG[C/T]
TTCATCTTTAACTCGCGATTATGTGCAGCCAGGCGCG TCC

Alignment58956:256-358

CAATAGTTATTACACCATAGATGTTGCAAATAGCTCTGTA CT TATCTTCTGCATTTTTTACA[C/T]TTCAC
ATAATATTGTTTGATGTTATCCAAAGATTCTTCTT CTT

Alignment59171:2906-3012

GAAGAGTTCAATGCACAGCTTTCAACTACCCGTAACGGTAGGGAGATGCCATCAGTGCGAACAATAAAA
AC[T/G]GTTGACGACGCGATGCTATCGACGGCGGCGTCTC TGT

Alignment59323:9-137

TCCCCCTCTCGAGCGCTCATTACGTTAAAAAGTGTATCGGAATGGCGGCGGCCATAAATAACGCGAGCG
GTGCGGTATTTTACGCGC[A/G]CGCGACGGAAGATAATTAANA ACTCGCCTGGAATATTCACA GAG

Alignment59604:272-372

GGTTATCCTATAATCTCGTCACGATACTAACAAGGAAACCCTTAACATAGAAACACCTC[C/T]AACAATG
ACTGGACAGTTTGCAGCGATAGTTGTGATATCA CTC

Alignment59693:2931-3032

AACGTTTAACTTTCATAGAATTTCACTCATTCTGTGTAATTGCCATCCAGTCCATTATC[A/G]CATTTA
AACTTTTGCTCGCAAATGAGGATGGAGCTGTTTG AAG

Alignment60078:212-353

TCCGAATCCACTCTCCGTATGCAACTTCGTTCTTTTCGAAATAAGAAAATTACA ACTTGCGAAATCCATTT
AAAACATTTTCTTTTACGAGTGTCTGCTG[A/C]ATGAAAGAGTGAACACGCCACTTATTGCAGTACAAACGGC
CCA

Alignment60306:20-115

TCTAGTGCGGGCGTAACGAAGGGCGAAAGCAAAGGGTAGGTCGGCGGGTTGGGG[C/T]GCGGGGCGCTT
TGCCACTTCTCAAATAAATTATAATTCG CCT

Alignment60725:3-108

GGTGGATGCTCACTTGCCGAGCAGGATCTTGCG[T/G]CCAGCGCCCATGTTCTGGCCAGCCTGGGTGGCG
CCCTTGTTGGAGCCAGCCTGGAGACCGATCACGGTCTT TGG

Alignment60920:5209-5310

GCCAGAGACATCGACACGATTTATCGACTCACTAGCCAC[C/T]ACTCATTCTGTATTTCCCAACGGAAT
AAATTTCAAATAAACAACCGAAATGATTGAATAC TCT

Alignment62535:179-293

AGATATTA AAAATAAACGTAGGACAAACATG[C/T]TATTA ACTTTTAGATTGCAAACAATAAAAATGTGC
CAATACGCTATGAATAGCAAGTGGGTAGCCAATAATGGCTTGAATAT TCT

Alignment62584:159-268

TTTTTGTGTCATATAGTCAGCATATAGCCG[A/C]AGGATCGCCTTCCATAGTGCAAGCTATATTATCTAA
TTTATGAGCTAAGTGCATTTTGTGCTAAGCCTAATATAAT CAA

Alignment62688:412-541

TTAGAAGAGGCCCTCCACCTTCCGTAAGTATGTGAGAGAAC[A/G]ATCAGGCTGCTTAGACTACTGGCCGG
CGTGTAATACCTCTGGTATTTGATTTCTGTCATTTTGGTTTCGCTTGCAGACTGTTGTCTG AGA

Alignment62874:274-393

TTGCTATTTTCAGTAAACATTTTGCTGTTAGCTTTTATTTT[A/G]AATATTGTGTAAATTATTGATGACA
TGTTGTAATAAGTATAATTTAATGATAGCCATAAAATTAAGTGTGTTTATATAAC GGA

Alignment62877:204-320

CCAGTTGTAGTATGATTTATTGATATATATTTTATC[A/G]CGATACGATCTAAATACGGCATCATAATT
GATGACAATTGCTCTGTATACCGTGTAGATATTAAGTGTGATAGGCATGG AGA

Alignment63018:1301-1409

GTCGATATTATTCAACGAAAGTAAACAGCTGCTATTG[A/T]AGAATAACAATTAGCGTTAACGCGTCCA
GTCGACGTGCTTGATGCATTAATTTCAATCTATTCTCGCTC TTA

Alignment63431:4-97

TGGCATTATGAAAATAAAGTGACGTTTCAATACCATCCGTTCCGGTGAACG[T/G]ACGTCTTCGTAAAC
CACGTAAACAATAGCTTACCGGTCAA GTG

Alignment63667:905-996

AATTACAAAGGTGTCCGCACTGGCGCCATATCTTG[C/T]AATAAATCAGTTGAGCGCGATATAACAATT
AGCCGGTATGATAGCAATGTTAATT TCT

Alignment63706:2911-3006

TATCCATAAAGCTTAAGATTTAGACACTACATATAAATATGAGATACTCAATG[C/T]GGTGACATACA
AAATATATCCATCTTTCGCAATCGAATTT CCT

Alignment63853:451-592

GAAAAACAAGTGAGCACCGTGAAAGTAGCTTGAAAATCG[C/G]TGGAAGTTCGATTGGGCTTTGTAAA
GACGATTCGTTTGGAGTAATTTCCGCGGTTTTTGAACGATTTCCGGTGTGACCACGGCTTTCCGGTCCGAT
CGG

Alignment64026:459-571

TGGGTGGTAACCGGTGACGATATTGTCTCGG[A/G]ACATAACAGCTGGGTTTACGATCAAATCGGCGCA
GTTGGTGCTTAATGTGAAACCAGTTTAAATATACTCGTAAATCTCT GGA

Alignment64329:2491-2586

CCCGATGGAATGCTCCTCGGACCCCTATTTTCGC[C/T]ATTAACAGCGACACTTCTGCTGTTCGTAAAT
TATTATCAGCGAGCGCTTTCATTACTCG TCC

Alignment64529:3987-4121

AAATACATTTTCGCTACAAATTCGAATGCGAAAGCTCGCAATTTTGTTTAAATTTTAAACTCGAAATTC
GATTTGATTCTGTGCGAATAAGC[C/T/G]CGCTCCGTAGTATTTCTCTGGTGCGAATTTGATTTAAGCA TCG

Alignment64595:5376-5469

CGGGGCATTTGGAGGAATGCTCAATTTACTTAGAAGGGT[C/T/G]GAGAGCTCTCGCTGTGATAACAATA
CTCAAAGACAGTGCCAGTAAAAATGC GGT

Alignment64618:71-192

TAAATTATGCATGCTGTTCTAAATTTATTTTCCAAATTAT[A/C]GTTACAAGTACAATGTAATGTATTT
TGCAGGATGATACGAAAGGGACTACAAACGGGTGTTACTCACTCTTGTTCGTA CCA

Alignment64725:17540-17656

CCCTGA[T/G]CCAGGGCTTATCCTGATAATTATTTCAATTGTTTGCCCT TGT

Alignment64835:1339-1432

TAAAATTATCATAAGATTCATAAGCT ATT

Alignment64890:1822-1943

AGGTTATTCTCGGGGAGAGTGATATTTAATTGTACGGGTAACCAGGTAACGAA TTC

Alignment64992:3590-3697

GCC[C/T]CAACAAATTGTGCGACTACACAAATCGAAAATAAA TTC

Alignment65193:227-310

CGAAGAATAACGGCGG GGA

Alignment65418:230-330

CGTATCTTAATTGCTTTTCATTGGCGAAATAAAA ATA

Alignment65503:19-115

CATTGAACTTTATAAATTATTATAACG GAG

Alignment66079:81-219

CCT

Alignment66101:52-160

G]AGGATACTCGGGAAAACGTGAGGACTTCATTCTTTGAAC TGG

Alignment66274:6-144

]TTCTCAAGCGAACAGCTCTTTGGTATCACGCCACTATTTTCCCTCTCGAATCTTCAGGAATGCAATGTC TCC

Alignment66526:66-168

TGCAGTGCATTTGTGTTGCAAATTTTTCGGTTA GGT

Alignment66645:632-742

CTTG[C/T]CCTTTTATTATCTTTGTGTCCTGCGGCTTGATTAT TCT

Alignment66794:43-136

GCCACCTGTAATCCCCAGCCTACCCGATAAGAACTTTC[T/G]CGCCACTATCCCGCGGGAGTCATCATT
TGACCGCACTTTTCCATCTTGCCCCG TGT

Alignment67191:234-375

ACAAGAGAGCGCTGAAGGATATTGAAGACTTCTACCACACTACTATTACTGAAATGCCAGCGATGTGGC
CAACCTCATCTAAGGGCCTACGCTTCCCG[A/G]TTTATACTTTGTGTCTGCGTTCTATTGCGATATTTATAA
GGA

Alignment67219:146-238

AAAAAAGCCTCGCATTGAAATGTAGATTTTGAATATTATACACGTAGG[T/G]TTCCAAAAGTCTTA
AAAATTGTCGTTATTGTATAATTATG TTG

Alignment67225:266-354

ATATCGTCACGAGCCACCTAGCTATTGATATCACATG[C/G]AGCAGTTGGGCGTATGACGCTGGATCCAG
CTGCGCCACGACCTTCACAAT GGC

Alignment67704:112-245

ACTAAGTTGCCATAATTGTGATACCAAAATGT[A/G]CTTTAAAAGTACAAGTCGCAAGCGTTTCGTTTG
TTATTTAGTTTGTTCATAACGATTTTATTTGTGTGTATAAATACGAATACGAAGTTACCACGAT AAG

Alignment68204:283-420

AAAAACATTTTATTAGCAAATAACGTAGGAAAGTA[A/T]AAAATATAAGAAATTCATTACAAAAGTGT
AAATGTTGTAATAATATGGTAGCTACGTATCTCTTTTATTACATTACACCATAGTGTGATACTGATTACA
TAA

Alignment68290:39-139

ATGAAATAACATAACTAGCTCGCGAAGTTGGTCTAGTGCC[C/T]ACTGGATTGACTCTTCCGGTAGTAA
TGAATCACATTGAAAAAATTGACAAGCGCAGCG CCT

Alignment68438:77-186

CAGTAAATGCTGGTACGTTGTCGTTTATATCAAGCAGTTG[A/G]ATCTTCACCATTGCAGTCGTGGACAG
GCCCCCTGCGAATAAATAAATAATTGGTCTCTTGATTGTTG GGA

Alignment68443:124-237

CTTAGAAAGCCGCATTGCGTTATATTTTCGCGCCACTGGAT[C/T]CAGGTAAAGCACTTCATTAATATTA
ATCTGTGTTGAAAATACAACGTTAATTTGATAGCTCGTACCATGTT CTT

Alignment68997:102-195

TGCACAATGTAATTTGCACGGGTTATGCGCAGGCGGCGGC[T/G]TTCTGGCGGGAGAAAGTGCACCTAACCC
GTTGCTCCACTTTCCACAGACAAACA TGT

Alignment69066:68-181

CCCCCTAGTTAAGTTATTTTCTATGTATAGTTAGTTATA[A/G]GTGTAAATGAGTTAGCACATAAATT
TGATGCATGATGATAATGTTAATAAAAATATCCACAATAAAAATTCAA GGA

Alignment69227:168-265

ACATTTTATGAGGACAAATGACAAAAATACTCAACGTTTCATTGTGAACTTGGGA[A/G]CGAACATTT
TTGTGCGCCCTCAGTACTTTCCTATACATGT AGA

Alignment69453:1583-1723

TTAGGAAGAAGCGTGCGGGTAGTGTGCGGGGAATCAATTGAATTACGAAGCATTATGAGGCTCCGGTTAC
GGCACGTCCGCGCCCCGCGGGGCTGACGCA[C/T]TGCTCTTGACACCTATTCATTCCGCTACTTTAGTTAACA
CTT

Alignment69681:115-210

AGGGTCTCAGTGCATTGAAAATACGTGCTC[A/T]GCCATTCCAGTGCCAACACCACAACACCAATACCAG
ACAAGCCGTTACCTGGCAGCTGCTGCCT ATT

Alignment69790:219-351

TGGACAATTTCTGTTTACAGTATATTTACAA[A/T]TTCAGTATCATAATATAATTCATTCTAGGTCTAG
GGTAATGCTTTTAGGAGTAAATTACTGTATATTCACAATAATTACGAAGACCTATAACAAAATCAT TTA

Alignment69933:203-344

GTCTCATGACTTGCACCAGCGCTAAGGCTACAATTTATTC[A/T]CCGGCGCGGGTGATCGATGGCCGCC
GAGGCTTGTCCCGGCCACCGAGACAACGCGGACCCGCTGCCGTTCTAAATTCAAAAATATTTTACCACGCTCT
TTA

Alignment69983:5964-6055

ATACAATCAATAAGCGATGCGGCATCGCAAACCTGCTG[C/G]CCATTTCATATCCAGTTAGCTGGGCTATT
GTTAGTTGCTTAGCGCTGCAGGAA GCG

Alignment70506:358-456

GGGGCATTGTGCTACACAACCTTACAAGCGTTATGCAAAATACGAAGCGCCTCTCGATT[C/A/T]GCGATAT
CTATAAATCTAGACGACCGATCGTGGGATCG ATT

Alignment70978:1-99

CTGCCGTTAGTGTTTAGTCCAAATTATCATGTAAACG[T/G]ATTCGATTATACATCTCACTCGATTAGCA
TCGGCTAGTGTTCTATACAATACATCTGCAA GGT

Alignment70987:397-514

CGACCACCTACCACCCGGCGCAAGCTATGCCTGTGTCGTGAATTAGTTTGCCAACTCTCTGTCTATGGCG
GAGCTC[C/T]GAGGCTGTAAGTATGGACGGCGGGCTGAATAATCGATAAA TCC

Alignment71464:111-246

TCTCGCGCCCCGTGTCCTGCCTGCTCACCATTGTGCTTACTAATGATTTTATGCAAATGCAGCCTCTTTA
GATCGGAGTCTTAGCGCGATCTC[C/G]ACCGTCAGGTACCGGGCTCATTATTAAGTGTGAAATAT GGC

Alignment71551:111-214

TTGCTGTATACGTGCGGCGAGGCGAGACACAACAAGTTGTGTTTGAAGCGATCGACGACGC[C/T]GACA
ATTCAAACGAGGCAGTGCCCAATCAATACTCGCCGA TCC

Alignment72244:232-332

AGCTAAGTGTAGGAAAATGAGGTGCGACGTTTTGGTTCCAAAGAGGCTGCGATACAGCG[A/T/G]CGCT
TGACCCAAATTTGTAGCACGCTCGTCCACTTTGCC TAG

Alignment72604:1453-1553

CGCTAAAAGGAATGGAAAAAGTTGCCGAACACATCAATGA[A/G]ATGCAACGAATACATGAAGAATATG
GTGCTATATTTGATCACTTGTGTTAGGCAACACCA GGA

Alignment72699:181-269

CATAAAGGGGCATACACATCAATTACGTATTGGTAAATAAGTGCGCATTGT[C/T]TCGGGGCCGCGTG
AACGGGCGACCTCTCGCCTCCG TCT

Alignment72943:128-229

CGCGCAAACCGACCGATTTCATATTTTGTTCGACCGCCAATTTATATCTGTTACAAATGG[C/T]TGTTCCG
CGATTGGATGGCTATTGGAAACAAATGACAGTAG TCC

Alignment73017:279-362

ATGACTGAAACAAGGCGAACGCATTTGCATCT[C/T]GGGAAGTGCATCGAGGACTTGGACAAACTGCAC
AATGTTCCAGATTTGAA TCC

Alignment73219:762-867

GTGAACTTGAAGTATTTAGTGGAGAAATTAAGGACAAATTTTGGGGGATTGTCTTTTTGTGGC[C/T]G
AGGTTAATTGTTCTTGTTCGCTTGTGTAACCTGCCAGC TCT

Alignment73240:51-187

GAGTACGCCCCGTGAATATTTTCGTTCCGGCCGTCATCCCCTTCTGAAGAAGAATTATTAAGTTTC[C/G]C
CGAACTTCGCAATTATGAAAGTTCGAATAGCTCTCGCAAGACGGCCTCTGAATTTATAGATGAATGTGT CGC

Alignment73276:1298-1421

TAATGCTTTCATTATTTTTATCTATTATTTAAGTATAATAACAATTTTTAAAGAATGTGCTTTTACAA
GATCTTACTAATT[A/G]ATAAGCCACATTGAGATGTTAATCAGCTACTAGTTTTAG GGA

Alignment73571:721-826

GCGTCGACTGGTGGTTGTTCCATCGCAGACAAAAGTCTG[A/G]TCGTTCGTCATCGTACCGCGTGTCT
GACCGCTCCGCGCCCGCAGCCCTACGACAAATCACACT AGA

Alignment73848:704-808

CGGTTATATAGGTAGTTACGCGTATAATGCGATGGATTTTTTTAGCGATCGATTGAGGTTTG[A/C]GG
CGGCCCCGCTTGGGATGCAAATGTGCTGTTTACGAAGTC CAC

Alignment74248:182-297

TACTTTATGAAAATGCGTTCCCACAGGTTAGCGAGGGTTCATCTGATCGGGATCGATTATAGATCAAGA
GAAAATATTGAAC[A/G]AGATGAGCGAAGATAATACTATTCTCCTTATG GGA

Alignment74430:170-306

TCATCGACATCGCTGTTTTACCTTAAAAGGTTTTCACTCA[A/G]AACCGATCGAGTGAAAATTTAATGAC
TGCTTTCAAATTCGTATTAATTCAACTTCACACGCGAGTGTGCAGCGAAGGTGGAAATCATAAACTCG AAG

Alignment74444:1452-1582

ATTTTTATTTAATGCGATAAGTCTGACTGTAAAGAAAATATTATGGTGACGATTTGTTAC[T/G]TTGTA
ACATTGTATTGTATTATTTGTTCTTAATTGCTTCACCGTACTTAGACAATGTTCCGAGCGATCG GGT

Alignment75079:214-306

AAGCCGCGTGAGACAGCACATTGGAGTTTTATAGTTGGTTTTATTACGTATAAATGAGACT[A/G]TTAA
ATTTATGATTCCTATGATTAAGTTTA GAA

Alignment75111:473-589

AGTGCCATAAATATCGATCCGGACCTAAAAGTGTT[A/G]CTGAAAACGTGTACAGTGATAGTGTGGGGT
GAAAGAACTGTTGGGAAAAGCTAAATTTTCGGTTACCGGATGTGGACGT GAG

Alignment75124:114-202

AAAACGCCATTTATTTTGGCGAGTCCCCGAATAGCGTACTCCTTATAATTT[C/T]GGATGCCTAATAACA
AATTGTTGGGGTACTTCGTG CTC

Alignment75174:119-260

TGAGCAGCTCACATACGCACATACATTACACACACAAACACACCGCGACCGGGCTGCATTGCATATAA
ATTATACTTATATAGTCCTTATAAATTATT[A/T]TCAGTCTATTTGCGCTCTCCTCGTCCGCACCGGCCACGCA
ATT

Alignment75257:1795-1900

AGTGCGAGTATTTGCGCAAAGTGCAGTTTCATTTGATTCTAAACGCTGCGGGAGCGACACGAAATGAG[A
/G]TTTTTCATGTTTCATTTCTTTTGCCATATCGGATTTT AAG

Alignment75288:161-300

TTGTTTTATCATTTTATATTACATACATTTGTGAGAAGTGTATAAAGTACTATAATTGACAGTAATTT
AAAATATTACACTTTTGTGTATAGGTAAG[A/G]ATAAAGTTCTAACTTAAATTTAGCCATATCAATATCTATT
AGA

Alignment75522:16-124

ATGGATATGACTTTCGTTTTTTATTGTCCGTCTGCGCTTG[T/G]AAGAAAGCTTGTTTTCGATTTGGTTA
ATAGTACTTTCGCGTTCGTTTAGATATGTTATTGAAACGAA GGT

Alignment75598:109-210

CTTTATTGAATTTGATTTACGCGCCAATTTTTCAGGGCTTCGGTTTTTATAAACTGACCTC[C/G]GCGTC
GATGTAATCTTAATTGAATCCCCGACAATAGGCG GCG

Alignment75794:245-339

TTTGCTCGTTTTTCATTCGTCACACACACG[A/C]CGTCAAATGGAAGTTTAATTTTTAAAATTGGATTTT
TATTGCCTTTTGTACCGGAATGAAAAC AAC

Alignment76195:47-132

CAGCAATAAATCTATAACGGTTTTGTAATATC[A/G]TGTAATTATTATTTAAAAACATGTTTGGGTAAT
AAAGTTGCGTAAAATGTAC AAG

Alignment76638:427-559

ATGTGTGCTTTCTAGGAGTGGTGAGCGGCTAAAAGACCTGCCAGGACCGGGCTCCGCGCGC[A/G]AGGTC
AGGTTGCGGCGCTCCGCTCCAAGAAACCATGGAGTGCTGCATGTCAGAAGAAGCCAAAGAACAAA GAG

Alignment76840:56-158

GTCGTGCCATAAATTCAATTAACGTCCTAATAGG[A/C]GCATTATTTAAGGTGGAGATCTTGACAAAGT
AATGTATTCGTTGAGCGACGATGACGCCCCGTCGCT CAA

Alignment77203:1233-1329

TTGTTTTGCTTGATGATATTTGTGGGCGAGTTTGCTTCTGGTTCATGTTGGTTAC[A/G]ATTCATGACTA
GATCCATACTCGTCTGCAGCCATCAACTC GGA

Alignment77723:117-225

CAGTACGCATCCATTTTCACCGGCACGCACATTTTATAGC[C/T]GTTACAGACACGCACTTCATGCAGTA
TAAACGTCAAATTATTTAAAATTAAGGCAATTCGTGAACCGA TTC

Alignment77923:163-279

GCTAATAGGTTCCCAATCCCCTTGCAATCCCCTCAATAGTTTACGAAGCTAGTGTTAGGGTGACAGGTGA
TTCAAG[A/C]CCCTATAAATCAGAGGTCTTGTAACGCTTAACACTATC AAC

Alignment77943:58-199

AAATACCCTAGCGGTCACCACTCAGCTCGCTCTCACTTAACGTCATAAATAACTTTGTCAATCTGCTAAC
TTAATAGCATAATTTAACCGTCGCAGGACA[A/G]CATAACGAGCAATGCCGATAATAAACCAGAAAAGCCATGA
AGA

Alignment78165:115-231

TCTGATGACGGATTTAACGAGTCGACCAAACAACGTCCTCACAGAAATCTTTCACCTGAATATTTAGCTC
TTTGA[C/G]TAAAAATAAATCTTTCGTTTCTCGGAATAACAACAGTGT CGG

Alignment78455:184-325

TAATGACGGACACGAGACGAAGAGTAAAGCTTTATGCTCTGAATGCTGACCGGCAATGGGACGACAGAG
GAACAGGACATGTATCTTCATGTTATGTGGA[A/G]AGGTTGAAAGGCACATCTCTGCTTGTAAGGGCAGAGTCA
G AGG

Alignment78482:373-464

CCGATTGGTAGGCCATAGGGAATCCAATAAGCGCTGCCCCACTTCCAC[A/G]CCGATGGCTGTTTCGAG
ATTCAAAAGAAGCCCCGCTTTGAA GGA

Alignment78589:892-980

AGTACTGAGTAATATATCCTTATTGCTATTACATTGATTAGTATTCCGCGTAGT[A/G]GTCTACTAAACG
AACATACCTATTGGGTTCCGT GAG

Alignment78643:53-158

GCTAGAATCGAATTCAAAGAGGTAATAAGGCAATTTTCT[C/T]GAAAATCCCTAAACGTAATAATGTTC
CGAAAACGTTTTCTAAATTTACACATATTGTGCTCTGGT TCT

Alignment78664:154-295

AAGCTTAACATACATAAAGATTAAGCATCTCTGCACCTTA[A/G]TTATATAATAGCCATTCAAATTAAC
TGCAGATTAATAATCTCATCTTAAAAATAAAGTCTTAAACATTAAACTATAAAAGACTCGTAAGTTACGAAAC
A AGG

Alignment78726:116-217

CACAGGTGTAGATTATTATTTTCGCTCCGAGTAAATATGGC[C/T]GCCGTATGAATTATAACCGGAAGTTG
ATACTGTAAGTTGGACATAATTTAAAGGACAATA CTT

Alignment78854:479-578

TGGGAGCCACCATCACAGGCCTAATGTAAATTGATTGACACGCTTTTTTAAGCGGCTAG[A/C]GCTCGCGT
GGCGGGTATTTTTGGCGTAATGGGCGCACTGA CAA

Alignment78859:95-180

CTCGGTGATCACAAGACCTTTCATAGACAAAC[A/G]TCTATCACCCAGTTGTCTTCTGTCATCAGGTGAT
TTGGGAGTAAAAACCTAA GGA

Alignment78944:844-942

ATTGCACTTAATAGGAGAACATAAGTAATCGGGCAAAAACAACGCACATATCCGTTTCG[C/G]CCGGAGTT
TGCATGCAGCGTAGTTATTATTTCTTAGCTCC CGG

Alignment79145:2900-3003

CTCGCGGAAGTCCATAAAGATGGATTTAAGAAC[A/T]CATAAACCGAAGCATTCAATAAAGTAAAACT
GATATCTCTATAATTTTTTCGCTACAAATTAAAGGATT TAA

Alignment79238:65-184

ACGATATCATTTTCGTCAAAATTCACAAACAAAAAAACC[A/G]AAGTAACGAGAGGAAGCGCATCGTT
CAAGCTTCAAATATATACTGACAGCCATGCTGCTGATGAGTCCGTCTTTATTC AAG

Alignment79289:189-323

GAGACATTTGTAATCGAAATTCATCCCTCAAACAAATGAAAGAATAATTGAGACGATGAAATATTCATT
GTTTGACCGAAAGTAACGAAAAC[C/T]GAATACTGACTCGAATACTCGAACTCGAATAGAAATTAT CCT

Alignment79350:87-181

TCGTCTCGCTTACCGTAACGAGTTCACGAGTGCTCTTTTATTAACCCGCT[A/G]CCCTTATCTCGGC
GTTACGAGCGAGAAATTAATTTGTAA GAA

Alignment79586:266-400

CGGGTACACGACCGGATCAACATACGGCATCGACGGCAGATTGAACGATAGTTCCCGAGGAAC[T/G]GGT
TATCGTTATGGGGCGACTGGCGGATGAAATTTATTGGCAGCGCGTTGGAGAAATGTAGCGAGCGGAA TTG

Alignment79674:3475-3578

TTACGATGCCGCTGGCGCTAGCAGGACAATGCATTATCTA[A/C]ACGCAGACAAAAACAAACAGGGCATC
TCGACATTACACCGCAATGGGCAAAAAATGACAGCT CAA

Alignment79885:980-1101

TCGATCGCGGAGGTTGTCCAATGTTCAAGAAATGGTGTCAATGCTCGCTGCGGTTGCAGTGTTCGAAA
TTATGTGTTGAGCAA[C/G]AGTGCGCGGACATGCCCCGGCCAGCGACCCACCGG GGC

Alignment80071:58-182

AAGAACAACAGGCCAATCAGGAGAGGCTTATTGCGGGATACATTCCAATTTAAAGTTGCTTTCAATCC
GACAGTAGAGGCG[C/T]TCTAAAACCAAATGTTGGTCCATGCTTTAAAGTCGATTTT CCT

Alignment80278:5719-5831

CGAAAATAACACAGCGAATCGAGGCAGAAACCATAGCAGG[C/T]CGATGACGTAAAAGGATGTTTTTCAG
CGGGGCGGCAACAGCGTCTGTTTATCGTCGGAGCACAGTTAGAGCT TCC

Alignment82228:38-133

CTGAATGAGCTTGTGTCTGCGGAGCCGAACGAGAACTTA[T/G]CAATATCTTCTTTGGGAAACATCTCT
AATGTATATCTAATGAGGAATGAATACC GGT

Alignment82425:10-105

CTGAACAACGCCGCGGGCAACGAGACCGTGGTGATCCAGTCTCCGGGCAGCGACCC[C/T]GAGACCATCT
GCATGTCCGTGCCGTCGTTTCGTGGCGGG TTC

Alignment82447:1066-1201

CACCGTAGACTATATTTTGTAAATAAACTTGAA[A/G]TATTTATCAATAATCAATAAGTACATTATAA
TAATTGAATAATTAGTATTTTGTTCATAAGAGACTAGCATTACAAATAAATACCTTCAGCTATACAA GAG

Alignment82447:1201-1317

ATTTAATGTTTATTTTCTATTTTAAACATTTTGAAGATGTTTAAAGTGGACTACGTCGGTTTTTACACA
AGAATA[C/T]AGTGTACAGTCTTGTATAGAACTTTTGTAGTTGAATGCC TCC

Alignment82706:217-358

TGAAACAAATTTCAAACGTTCCAGTCTGAAGTGTGTAGCTAGCTCGATATAACTGTCAATTTGGGTGTA
GAAATTTATTTTGTAAATTTTCACCGGCTCTC[A/G]TGTGTAATTTCCAAATGTGTTAGACTATTTTTGACCTAGG
GAA

Alignment82726:257-380

AATGGCAGCCACGTACGAAGATCGGGGACCTATACAAAATTTTCGAATAGAAATGTCCATATTTTATAT
AGTTTACTTTGTGGTGTTC[A/G]TTCTTCTTTGTTAACATATTCGTAGCTCTGAT GGA

Alignment82875:169-296

CAAATGCAAATTTGGGAACTGTAAATAGTTATATATGTTTAAAAGATAAGGTCTTAACAAGGTTGATT
TTTGTTGTTACACAACTTCTT[A/G]AAAAATAAACATTTTGTATGTGTGAATTTTTGTTC GGA

Alignment83207:146-257

AAAATCTCTGCTGCCATTTTCTCCTTCGAGAAACAGACGCCATTTTGCAAGCGTCACTTGGCGGCGTGTT[
A/G]GGTTTCTGCATTTACATCGGTAATACGGCCACACAAAAT AGA

Alignment83238:446-540

TGTGAGCAACAGGTTATCTGTCATAATCCGAATTCGCGAATAGCCTTTCTAGA[A/T]TTCCACTCATGTT
TTTGTTTGCATACGGTCAGAGTTCCTT ATT

Alignment83811:467-565

TTTTTGCCTATGTCTACCGGCAGACACCTTCCAGAAATCTTTAATAAAACTTAA[C/T]AGAAAACAA
TCTTCACTAAACATTATTGCTTTCGTAATAT CTT

Alignment83816:1346-1477

AACTAGAGCTGAAATGTATTAGAATTAGTATGTA[C/T]GAAAGCGATAAAATTTGCCTATACCTGATGA
AGTGTAGTTTGTGCTGCCGGCTCGCTGAGCAATAATGGATAGGCAGAAGGCTTCCGCATCACC TTC

Alignment84228:3488-3619

GGACAGACGGCAAAGGTCAATATTAGGGGATTAATCCGGTCTCGTTGGAACCTATCGATTACTCGATTC
AGAGGAGTCGAACACTCGAGGCGGCCGTCT[A/G]TACGGTAGTGGAGTGTGGGTAATTGTACCA GGA

Alignment84311:4632-4753

CCGTTTTTCATTTTCGATTCCTGCGTCTAAGAGATAGCACATTGGCTAGTAATTGAACCGCAGCCGTCTT
TGATATATCG[T/G]CTCTTTTATCGGATTGGACGGACGCAATAACAGACCGTTG TGG

Alignment84395:150-236

TCGTGCGCCGCCGCCGCCGCTCCGAGCACCTGCCACCCACTTCACCCT[C/G]AACGACCTCATCGGCAA
GCTGCGCCCGTCGTCGCT GCC

Alignment84476:99-190

CGGGGTGCGGAAGCCCGGGTCAGTGGGTGCGTCGCGCAGCCTCCCAAAGCGTTCCGGGA[T/G]AGACGC
GCCTCTATCGACCGCTTGACGCCA GGT

Alignment84611:123-220

TTTATAACAGAATATCATGAACTACATGCAGAGATACGATAACCAGACCCATTGTA[C/T]TTTCCCCGCA
GCATTGTTTAGGTAATCTTATGTGATTAAC TCT

Alignment84873:123-216

TGGGCAAATAAACGCAATTTAGGGAAAAAACGG[C/G]CGTCCGCGGACTAACAAAGGCGGATTTCCATA
TATAAAAAGCATAAATAATTTTGATTG CGG

Alignment85128:184-319

GGCGTAGATTTTATCAGAGCATTAAATCGCTTACGATTTATTATCAGTAAGAGTTTATTACCTTCAAATA
ATTATTTTAATTGTACAGTATTTTT[T/G]TAATGAGTATTTTATGATTGATTGCGATGATCGATGTTCT GTG

Alignment85229:167-273

TGATAAGTTAACATTATTTTCGATTTGAGAGTAATATTTTA[C/T]CTTAACAACAATATTAGAAGCGATC
TGAAAAACGTAATGCATGATGATTTCGACGAAAATAGACGA TCC

Alignment85277:375-505

GAGATAACTATGTATAGTGGGTTTAGCGCGCCTTTGTCAC[A/G]AGGACTGAACTAATTTTTTCATCATAC
GGCCCACGACAGTTACAAATGCGGCCCCGAACTGTCTCTTTCTTAATAATACTTTTTATATAT AAG

Alignment85363:727-868

TCTTTGTGCCATTCTTCGCATACCAATAAGAGTATATTCTTAAAATATACTACCAAATTAACCTTTTTATC
AAAATTCGGCCCTTCACTTCTTCTTCGTCC[A/T]CCGTTATAGGTAAGTGAAAATAATTTTCTAAGTGATTTTC
TTA

Alignment85399:63-164

TATTCCAATTAGAAGTGTATCAAGCTTTTTGCC[A/G]CTGCGCTCGCTCCCAGGTTCAACGGCCAGACGC
TCCGAATTGTTGATTTTTTCGCGTGATCGCATTG GGA

Alignment85634:503-632

ATGAACCGCAAAACAACATCCGAAACAATAAACCAGCAAATTATTGTGCGACAAGAAATAGCGTGGGAG
CCAATTAATTTTTGCTGAG[A/G]CTACGGTTTATGTTCTCCGGGATAAATAAGGAGATTTAGC AAG

Alignment86004:89-172

AGATTAAAGTAATTTGCTTAAATTGTTTACATCAAAGTCGTGACCGACTG[A/G]CTATAGGCTGGTAAT
AGGTGTCCTAGAATATC GAA

Alignment86287:1728-1811

GTGCTTTACGGAAGATACAGATGATATGTTCA[A/T]AGTTTGAGCATACTGAGATTGATTGCGGTTTCCG
ATGTACCGATTCTGAAA ATA

Alignment86393:2434-2532

GATACATAAATACGTAATGTTGACTAGTATAC[A/T]TTTATTGTTACAAACAAAATTAATTAATATCA
CTAGATAATGTCACCTGATTAGCTGACAAAAG AAT

Alignment86487:1464-1586

GTGATGAGGAACGCGCCCTTGCACAGGAAGTG[C/T]TCCGAGTCCGAAATGTCGGACTCGCTCTCCCCGC
CCTTCATGAGGGTATGGATCTGCTCCTTCCACATGTATGACTCTGACATCTGAAG TCT

Alignment86520:54-144

ATTTCCAGAATAGATAATCTAGGGGCGTGCTAGA[A/C]GCGTGAACGGAGGGCACACATAACGAAGATA
ATGGTGCTGTAAAAACGTCCACGC CAA

Alignment86773:124-216

TTTGCAGCGCTGCAGCGCAATCGTAGCGGGC[A/G]TAAAGCCGCTGCCACTCCTGTTATCCGGGAATGGA
AATAATAAGATTTTTTAAAGCTCCA AGA

Alignment86822:482-600

GCTCGCTCTTTGAAAGAGGTTGTAAACAGCATCCGTTGAATGCGGGCAGAAAGTGAGCAAACGCCGTGTC
ACATTCT[C/T]AATTCAGCTAGTGCATAATGTAACTTGACCCCACTGAAC CTC

Alignment87144:285-377

GAAACTCGAAAGACAAGGATCTGGGCAGGATTTATTACCGCAAAAACGCTTCG[C/T]TTCGCATTCTGC
TTCTTCATTTACGCATAATGAACTA CTC

Alignment87496:1423-1518

ACGAAAGCAAATCTGCCCGAGTGACGAAGTC[C/G]CCGTCTCGGTGACTGGTATATAGTTACTTATTTTT
GTGATAAGCGGAGCGCGGGGGCCTCGCG CCG

Alignment87653:1628-1761

TCGTGTTTACACGTCCTCGGCGTGAGACGTTCC[C/G]AGTAATAGGATTAATGTGGGAGCTTTAAGTGGG
ACGTTTTAGGGAAATTGGTATTTTTGTATGAAATTATGCGTGACGAGATTGAAGTGAAATATCTACT CCG

Alignment87996:51-142

CCTAAGCCTTCATGGAAATTGCTTCAAACCATGCATAAATATCTATTAAG[A/C]GCGAGATTAATATTTT
TCAATGGCTGCATGAGGGATTCCG ACC

Alignment88144:121-219

TTTTACGTTAAGTAGTTATAATGAAGTATTGTTACCTTTCTCAAGAAGACGTCAGA[A/G]CGCTAGTA
TGGGCATCTTAATGTAACATTTCTTAACAAGG AGA

Alignment88315:60-197

TTTTATACGTACATCCTTGGTACTTACAGAACAGCCTAACTCATACAATCTATCCCTCATCTGATAAGTA
TTGTGATGAGCAATAAAGACTAGTGT[T/G]GGGCATTTTCTGAAAAGCATATTTACCACAGTTAATGCC
TTG

Alignment88319:161-259

CAGTTTGTCTGTCAACTTCTGCAAACACGACCGAGAATA[A/T]ACTGGATTTGTTTCGGAAGAGACTTG
AATTTCAACTATCGAAACGTATTCGGACAA ATT

Alignment88333:271-361

AGTGGGAACAGCAATGTAATTAACCTGCATAATGG[C/G]CAGTTATTAAGCAATTTCTGCGCTAACATG
GCGGATATGTCATGTAACCTCAGGC CCG

Alignment88337:719-860

TCACACTCAGCCTAGACACCCCGTACACCATCAATTCGGAAATTAGAAAGGGACGACGCTCTAGAGACGA
CAAGGACGCGGATCGATCGGACGTCATCGC[C/G]AAGTTAAAAGCCTGCGTTCGTTACATGGCCCGTAATAGGCG
GCG

Alignment88391:49-190

GGCTGATAGTACGAGGTAAAGTGAACGTTACGTTAGCCACGTGGTGACAGGGAGTGATATATTTACGGC
AATCTGCCGCTCGCAGTTTTAAGAAAATTC[C/T]AGCTTTCGGCCAAGCTTGTTTTACGATAGCGACATTTGCT
TTC

Alignment88794:475-572

CCCGAACCAAACAGGTCTCCTAATAAATCTTC[A/G]CCAAGAAGACTGAATCCTGTATAATCAGCGCCTT
CTACGTCGTTGATAGCGTCGAGGTCACCTG GAA

Alignment88921:17-150

GATTAACAATAAGGTACATCTAGTCAATCAGATTGTTTTATTAGCAAATGTCAGTGAAGTTATCAGAAC
TGTAATAAATAAGATTTATTAATTAAT[A/G]TGTAAGTGCTTGCCAGTTTTTAGAACGGACTTTATT GGA

Alignment89180:286-398

CTGCAGAATGGCGTGAAAGACTTCGTAATTTTAGAAGCGAGAAATCGTATCGGTGGCAGAATCATATCT
AT[A/T]CCAATGAAAACCATAAGGTGGAAGTTGGAGCCAACTGGA AAT

Alignment89296:4215-4345

TAGTCGGTCTTGGTTGAACAGAACTCCATTCCTTTACTTCAGTTAGTCTTTTCTAACTTGAACAGTGC GA
CGTCGTACAAGGGCAGGTG[T/G]AACTCACACCATTCAATTTAAAAGAAACTGGGCGCGTGCA GTG

Alignment89393:1015-1156

CCAATTTTCATATTTCCACGCAGAGGGCTCGCCAAGATATCTAGTAAATCGCCCCGTGATATTTTTATG
AATCCAAATTGATTTACAGCACTTGATACC[A/G]AGAAATATCGGTACAATTTTCGTGTAAGCCTCGTGAAATC
GAA

Alignment89479:152-280

GGCCAATCCACGTCAGGCAGATGTCCTACCCCGGGGTCAGCTTCAATGGGGCATACTAATAGGCGTCCCA
CCCTATTAATTGTGTCG[A/G]CGAGAAAATTTCAAGGCAAGAAATCCTCACCATCAGACTT AAG

Alignment89637:176-277

ATCGGCGCTTGCGCAACATAGAAAGCCGCATAGA[C/G]CCGGCTGCACTCGGACGCACTCGCTGCATAAC
CCGCTTTATTAGAATCGTAAACTAATGCAACAAC CGC

Alignment89644:726-822

CGGAGAGCCGCGAAATTGTTTAGTTTACAATGTTTTTATGCAAAGGTAATAAAGT[A/G]ATATGAAGAA
AAAACCAGTTTAATTTGTGCATGCTTGGA AAG

Alignment90003:178-284

CTTACAATACATCTGCACATGAAAATGGATTGATTTGGCAGCGATAGTGATCATTCTGGTCAAGG[A/T]
TTTATAAGTCGCAAAGCTTCTCACTACTGTGTCTTATAAT ATA

Alignment90066:131-245

CAATAAACCATCGTGGATTTCGCATACAAATTTGCATAATTAATACTAATTAATGCGAAAAAAGTTTG
CCGTCAG[C/T]GTAATAACAGTGTGGGATTGAACTGCTTTACCAGCGA TCC

Alignment90066:249-337

TTTTTTTCTCGCGGACGTGTGGAAAGTGGAATTCCTG[C/T]AGAGAGATGTTTGATTTTCTTTGTAATT
ATTAGGGGCTCCGATTGGTTAA CTC

Alignment90159:205-317

GAAGCCATTCAAACACACAAAGCCACACTGTCTAAACAAT[C/T]AAACGAGACCAACAATAAATACTAA
AAGAGCGGAATCCTCGACGCGAATAAACATAAATTGTGTTTTTATTC CCT

Alignment90279:2604-2710

CCTCATTATGCGGTGACATCTCTGTTCTGTTTATACTCTGTGGTTGCGGTTTCGTGCCATAGATTATTA
TAG[A/T]CTGTTACAGATAGGACGTCTCCATTCAAATTG AAT

Alignment90584:153-291

GGAGGGCGGCTCCATTCTGCCGCTCGCCTCCGCAATCTTGGCGCGCTGGCTGCGTTTGACATTAAATAATT
GTTGGGCGCCCGCCCGCACCCCTCGCT[A/G]GAACCGGGTAGAACTGGCGCGTTTATTTTGAATTTGGAAG
GAA

Alignment90642:3760-3858

CGGATTTGGTACGTCATGTTCAATTGCGCGGAAAAGACTGATGCGTTTATAATTGGC[C/G]GCCACAGAC
GGTCGTATTGTGTCTACTGTAATTGTTTTAT GGC

Alignment90793:121-217

GGCCGCTTGAACCTCCGTAATATCTCTTTGACAAATCGTTG[A/T]ACACGGAACTTCGTTGTTGTTTATTT
ATAAGGCATAATGCGCGAAATAATTTACG AAT

Alignment90949:2720-2836

GGTTTGTGTCAGTAATTTTGTGTTGAAATCTAGAGCGGCGTACCGGCGTACTCCTTTTTTGTGTTCCGA
TATGTGTAAGAGAG[C/T]GATGTTGACATGTTTGGCCGATTATTTTAC CCT

Alignment90956:189-330

TTCGTTGATTAACAGAGCCACGGCCGCAATGCGTATGCAAGCGGACGGACATATTACCAGGGCTCGAAT
TCTGATTGTTAGAGAATTTATTACTCCCG[C/T]GCCTTGACAGTTAATTGAATTCGCCTGTAGAATAGGCAC
TTC

Alignment91408:928-1019

TTTTGTTATTTTAAAAGGAGACATGATGGATCAGTTTCAACACGTATTCG[C/T]CGGTGCCTTTGTTGTT
TGGTTTATGGCTTTGTAATGTGTT TTC

Alignment91576:157-245

CCCCTCGCGGGCATTATCAGAGACTTTG[C/G]TTGTGCTAATTGCAGATGTCTTGTCATTGTCTCCTC
TTATCTTCGCGTTTGATTTAT CGC

Alignment91629:341-474

CTCGTGACGTAAGTAATATTGGCTTGGAAAGGC[A/G]AGCTTCAAAGTTTTGATGTGGCGTATTAGCTTG
CAAATATAGAACCCATACAAAACACTTATTGATCGAATGTTGCTGGTGCAAGTTGCAAACCTGAAATT AAG

Alignment91740:1484-1585

CAACCATAAATACACCAAGAAATCGGGACCATCCCCATAAATTCCTCTCGTAAAAGGCTC[A/T]GCGATT
ATGTTAGAGGGTGGTATTAGCAAAGTTTGTCCGA TAT

Alignment91961:1168-1281

CGGAATTAAGGCTAAACTTCGTTACGACGAGTTTTGTCCGTCGAATTGAAAGAACTTGTTACGTCGTC
GT[A/C]GCTATGATTTCAATTTCAAAGCGGATCCGACACCTTGAT ACC

Alignment92241:103-215

GGCAATAATCTGCTAATCTGGTTGGTTTTCCCGGCC[A/G]TAAACCGTAAAACGCTCGTAAAGGCTCACT
TTAAAATTCAAACGAGATTTAATATCGATTGTTTCGACAATATGT AGA

Alignment92664:244-337

GTGAGTTCAACCTTTTTGAGGGCGGGGTGACATAAAATTGAAATATTTCTATTTTATTGT[C/T]CGTAA
TATTTATTTGATTGTTGAATAAATACG TCT

Alignment92779:677-771

GATAGAGCCACCATGACGGCTCAAAAATGTGTGGTTGAAGGCTGCAATCTCGA[A/G]TACGATGTTATT
TGCAGCTTCTCCTTTTACAAGTAAGTGT GGA

Alignment93077:158-252

TTACAAGAAAATTGTAATTTTATTTAGGTATG[C/T]AGCACTTTTTACACTTTGCACCAAATTAGGGCA
GTAATTACAGCTCGTATAATTTACATAT CCT

Alignment93077:351-433

CGCACTTATTCATTGAGAGCATTTTTTTACAC[A/G]AGTTTTTATCACCAACTGACATCATTGTGTTCACT
TTCGTAGCAACGGAA AGG

Alignment93246:54-186

AAAAAACGAAATAAGGAATTAATTA AAACTG[A/G]AAATTA AAAAGGCGTTTTTCGTCAATTAATTA AAC
AAGGAAAGGGCTCGTCCTAAATAATATAAAGGTCGTTAGGGTTGAGCACAGCCAAAGCGTCATTAT AGG

Alignment93826:100-205

AATAAGGCCGTGAATGCATTTTTAATTTTCTCGTTATCAA[C/G]TTGGCTGCGCTCGTAATTTTCAGCGAT
GACAGTTGGTAAATGCCATTTATTTTTTCGTTTACACT CCG

Alignment93980:900-991

TCTATTTTTTTTAAATCACATTAAAGAATCGAATATGGTGGACGTTTTTTTTGCGCGGCC[A/G]GTGCGTG
CGACGCGATTTATTTATTTGCGGG AGG

Alignment94038:404-543

AGAGCTATGCCCGATCTAGGATATCCGGACCTCAAAGA[C/T]GGCTTTTGTGACCCTCTCCGGATCTTT
TGGCTGAAACGACGGTCTAGTAATTTGGGACTTTCGGAGATCCTCCGGAAACATTTGAAATTATTCGATGAT
CCT

Alignment94187:97-238

TGATTTGGATTTTGGCTTTAGTAGATTGATGATAGATTTTACCATCCCAGTAGACTCACTCATACTTACC
CCTTAAGCTAAGATATATGATATATTGTAT[C/G]CGATATGTAACATTAAGTCAATAACCATAATCTTTTTACT
GCG

Alignment94318:579-683

GTCCAGGCACCCAAGCAACCCACACGGCACCCATTAATTACTTAAATTTAATTCATACGACCC[A/G]CCA
CTATTTACATTCAAAACGTACCCCAACCCGCATCGC GAA

Alignment94468:407-508

TGTAAAAACGTCTTTAATAAAAATTCAATTATTTCTCTTTCTATACGAGCTTTTGTAAACAGTTGGA[A
/G]CGGTCCGGATTTTTTATTACATCTCCTTTGTC GGA

Alignment94784:73-170

ATATTTGTAGGTAGGCCAGGTAAAATGTTG[C/G]CGGATAAGATTTGTGCGCCACTTAACGGACACGA
TGGGCCAGGAGGCCAAATGAAGATAACGT CCG

Alignment95227:805-892

TGTGTTGATTTGAGGATAATGTAAAAGTTTACTAA[A/C]TTGTTGAATGTACTTATAGA ACTGAAAATA
ATGTATTTTTTTTATTTAATT AAC

Alignment95385:547-683

GACGCACACTACGATAGCCAGCATCACTTCGCGGTCGCACCGCTACTCGATATAAGTATATTATACTCTT
AAATACCTTAAGGTTCTATCGATA[C/T]AATATAAAAAATAATATGGTAATAAAATTAACATCATATT CCT

Alignment95516:174-276

ATTATGGTAAACATCCTGTATAATAGATTAGGAATTCCTAACACATTAGGACTTCCCAACT[A/T]GCGCC
CGATAACGCTCCATTCAACTCCTTCTCCGTCCAAT AAT

Alignment95727:2361-2502

CTGGAGTGTTTATCCCGCTCGGCGGATCAATACCGGTGGCGCAGTGGCGGTGACTAGGCGGCGGCGCAG
CGACGGCGCGTGCCTTTAGCTTTAGGTACT[C/T]ACCTCGCTCGAGTCTGTGAGATGCTGTCAAGCCGACCGGT
CCT

Alignment95968:132-273

CTCGATATCTAAAATTACAAGCCTGCACAGTGCCTATCTG[T/G]GCCTCACCGGCACACCGCTCTCCATT
CCTTTATGTTTCAGCTGCCACTTTCAGACATACTTCCATTCAAATATGCCCCAGACGTTACTTTATGCGTAA
TGG

Alignment96361:1153-1282

AACGAGAGTTTATAAGCAATAAACGGGCAAACAGACGTTT[C/G]GGCGTAACATAAAATCAAATCAACA
GTTATCCTGTGAGCCTACATCACAATCAGGTTAATCGCGTATGTGACAAGTTGGCTCGTTTCG CGC

Alignment96549:758-891

TCCCGCTGGTAAACAAAGCACCTCTCCAGTGG[A/C]ATTCTCAAGACGGAGGCAACGATCGTGAAAACG
GGCCGGACATGTGTGCCGCGCCGTGACCGAGTTACAATCACTTTTCAATTAATAAAGAAGCAAGC AAC

Alignment96718:5282-5394

CCATTACGTCAAAAAGGAGAATTTAAAAAGAATTGATCAGTATGGCAATGACCGTAGACGTTGCAATTG
ACCGCATCG[A/C]GCCACGTGCGAGACGAAACGAGCACTTCTTCT ACA

Alignment96866:816-929

AAAAAGTGCAAAATAACGCAGGTAAGCCGAGTGGTCCAATCATACCATAATCCATTAAGATTTTGCTTC
GCT[C/T]CGGCCAACACACTTCCAAACTCCCCAGAGGTAATATCCA CTC

Alignment97131:305-399

TTTGATGTCTGCTTTTCGTTTCGTGATCGTAGTTT[C/T]GTTCCCGTTTAAAGTGTTTACGAAAATGGTAAA
GGAGAAGCCAAACTCTATCAGGATTTA CCT

Alignment97466:52-155

GGCTATTTGTATCCCCGCACTTTTGTGTCAGGGGAAATCATGTCTTATATTTATAGGGACATAGCCTAATA
C[A/C/T]CCGTTGCCTGGATATCGTTGCGATGGTGACC TCA

Alignment97697:2964-3072

GCAGATTTGTGAGTTCTTTAAAGATTTTCTTATGTTCCAGGCTGCTCGATCTCGGGCCCCGAGGGCTGC
AA[C/T]CTCTTCATCTACCACCTGCCCCAGGAGTTCGGAGA CTT

Alignment98175:1556-1668

GTATGAACCTCCATAAAGTGAGCTCATTACATCTCGGTTTATGGTTGCTGTTAGTTACCTACAGTACTTA
C[C/T]CTGGATTTAATAGGTGCAGGGACAAGAGGTGTACAAAATA TCT

Alignment98409:68-174

GAATCTTAATTGAAATTACACTTTGCATGAACACTAATACATATTCATGTTACAATGATGAAAA[A/G]
TGGCGATTCATTTTTACGTCAACATTATGAAATCGTTAAA GAA

Alignment98493:849-982

TTATTTTCTTTTATTGCCGCAAATTGCCGGGA[C/T]GCATCTAGACAGTTATCGATATGTTGTAATTATT
TATTGTTGGCTGTTGAAACCGTGGCGGATGCGAGTAGTTTGGCAGATAATATGCGCTGGGTAGT TCT

Alignment98601:885-978

GCCACCTTCGTTCCGGCTCTCATAAATAATTCAACGGCATCGTGACGTCACA[C/G]TGCAATGGTGGTTT
GATATCGCTGCAGGTTTCATATTTAC CGG

Alignment98690:15-109

AAGTCAGCAAAAACCTTCAGTAGGCGCTCGTGACAGTCGAATAAGATATCAAAGCAA[A/T]GGAATCCGC
CGTCAAACCTTGTCGATAGATCGATTACT TTA

Alignment98729:275-391

TTTAGCGAGACGGTCCAATCTCATTATGGAACCGATCTTCCTTGTCGCTCTTAAAGCATAATCACCATAA
GTTAG[A/C]GAGCAAGTGAAGCGTGAGAGATGCGATTATAAAGTGTTC CAC

Alignment98842:127-221

CGCCATTGCCGACTCCGCTATCATAACATTAATTTGGATAAAACACCCTTGTA[C/T]AAAGAGTCAATAG
ATTTTTTAAGTTGCTCATTAACTTAAA CCT

Alignment98975:2854-2952

AGAATAGTTTCACGTGCCGGTGGCGCCGATAACCGTTTATGCCAGCAATTAATGCTGCGC[A/G]TACGCA
CCGAATGCATGATAAATGTGACAGTTTACAA GAG

Alignment99125:326-449

ACTTCAAGGATGTTTTGATGGAGTGGGCCGTCAATTAATAGGAGAGGGTTCAGACGTCTCC[A/G]ATG
TGATTGAGTGCACGTGATGCAGATTTACTTTGATGATACGGTTTTGTGTGGGCGAGAC AGA

Alignment99181:136-229

CCGCGATTTGTCCAAATGAAAAATTAATTTGCCAATGATTAATATAATGGC[T/G]GGCAATCAGCGTA
ATCGTTGTCCAAACTTTTTACATCTT GTG

Alignment99451:61-146

TTTTTGTACAGCAAACGAGTATTAGTAATAGTT[A/G]TAATATGACATTAAGATGATGAAATTATGCTA
AGTCTAACTCCAAAATTA AGA

Alignment99456:1526-1642

GCAAACTTAAATTCGTCCCCCAAGAAGAAGGCTGGACCGACGGCTCCAAATTCGTATGTTAATACAGG
GGGTA[A/T]TACCCTCCTCCACCGCACCTCTGGGAGGGCCGAACAT TTA

Alignment99669:54-145

ACCAGTAAATTAACGCTAGTTTCATTTGCGTTACAAAGTGAATTATGTG[T/G]TGGTGTCTTAGTTCT
GTCACCGCAAAGTTACTACGGTTC TTG

Alignment100029:1957-2077

AAGATAAACAAAACCAATTTCTACGCAAATATGTCAGCGATTGCAGATATTGTAGTAGATTTATTTGAA
ACCGAAGGCGTTGGTGGAG[C/G]AAAGTAAATATAGGGTGAATAAATAACAAA GCG

Alignment100245:372-510

GGCCGTTAAGTCTGTGTTATTTAGTTGATCATGTTAGTTAAGGCCTCTTGTGTTGCTGTGCATTTCT[A/
G]AGCATTGTATGTATGTCTGTTTATATATTGTAAATAGCTAAGATACATTATATTTTTACGAGTAGAATAC
GAA

Alignment100351:60-158

CGTGTGGAGCTATTGCAATCAGTTCAGGCGAGTTTCACTGCGAGTATTCGCGCTGTTACTTTT[A/C]CAA
CGCGCGACCGCGCACGACAACGCTCTGTTTG ACA

Alignment100794:260-393

GCACACTTTGATATAAATATTATCACAATACAGTATGTCAGATATGGTGTGCATCCCTTCTCTGGACGTAT
CTAGAATACAAATCGCCTGCTA[C/T]GCTACTTAGTGTTATTATCACAGTTGTTTAGTAGAGGTGG CCT

Alignment100824:102-200

GAAAAAACAACCTTATCTATCTGCGATAATAAAAGTTTCAAGGATGCGAACACTAGAGTTCA[A/T]TGT
ACCGATGACTTTGCCAGTGCACTAATGATAAA AAT

Alignment101177:247-333

CTATAGTGTAATTTGATCCAATGCTGCGTGCAAGTTTTTCTGATGGAGAA[A/C]AGACGGTCAGCAGAA
AACATAATCTGGGATCTGAG CCA

Alignment101743:698-833

GCTAAAACGACCTCTTATCATGTGGACAATTACAAAGCAATTACTGAACAGTAGAGCCCATTAC[A/G]GC
GGCTAATCTTTGCGTGACGTAACAGCGCATGGACAGGAAGCCTGAATTGAGATATTAGCAGCAACGGG AGA

Alignment101778:1379-1489

AGCAAAATCACGCCAAAGATAAATTACTTAG[A/G]CTGAATGAAATTGGTGCCTTTTAGGCGTACATTAA
CCACTTTAATTATTAATCTCCCAATCTACCCCGAAAGAACTC GAG

Alignment101842:119-210

CGGCACTCGGCCGATCCGGGATCATTGCTCGCCT[C/G]TTGTTTCGAGTGCGCATGCGACTGTTTCGCAAC
TCTACCTACTGAATGATTGATGCC CCG

Alignment101857:585-691

TATAATCGCCCTTATGAGGACGTGCGAAAAACAATTTTC[A/G]TAAAGTAATTCATATTGATTTATGGG
CGTTGTTTATGATTAATGCCAATTCAGATAGGGAGATGG GGA

Alignment102223:2700-2789

GAGGAAAGTAATAGGAAGCTCGCTCGCACACTGACCCATTGATAGACTAGT[A/G]GCACACCAGTAGAC
TAAAAAGGAAATCCTACTTGCGC AGA

Alignment102391:112-211

CGCCGCTCGGCATTACTTGTGTCACTGCATTGAATATATCGGCCTTTGCCTTTGTGC[A/G]GAATATTG
CTCGTCTTTTGTGCAATGAACGTTAGCCAACG AGG

Alignment102557:42-159

TCGATACACATGTACCGACTATTGTATTGAAAATT[C/T]AGATTATTCGGTACATACGAATAACAACGA
ATAGGTAATTACGAATAAGACCGAATACGAATTAACACACATTCGTGTAT CCT

Alignment102848:357-477

TAAAAAACTCAATCCAGACTACAAGATCATTATTCTAATATGTTTCATCTTTTATAAAAAATTCAACAAC
ACTTATTTTA[C/T]TGTGGAAGTGTTCACAAGTCTCTATTGTGTTAAAAAAT TTC

Alignment103440:394-498

AAGCTGCGATTTCGTAAGTAAAGTTAATGGTTCACCTATTACGAAACGTCAAACCTGTGGTTA[A/T]TA
TTCGCCGGGCCGTACTGCACTACGTGCGGTTTCGCTCGC TAA

Alignment103838:170-257

TACCTCATTGGGTTTAATACCTGAGTTCATTTTCATTCTACAAAGTAAAGTGG[C/T]AATGAAACTGTAA
GAATCTTACTTTATGAGGAGT TCT

Alignment103916:30-122

AATAATTCTAGGTCACAGGTCATTTTGTATTCCGCCTGCC[C/T]GTGTCTAGACATATTGCATGGTCGAA
TTTTAAGCGAATGACATCGCATTAC CTT

Alignment103990:162-286

CCGCTCCGCCCAAATTATATTCAAATATTAATTT[C/G]ACGAAGAAAAGCCTTTTTGAGAGCACTTAAT
TAAAATTAGACAAAATCATAATTGAAAGTTCTCCTCGAGGCGTGAAGAGGGGGGAGG GGC

Alignment104018:952-1043

TCACACATCCTGGCACACGTTTAGACGCAGTTTAGGTTGTTGTGTCCAG[C/T]GTCTTGGCGCCACCTG
TGTTTATAAGAGATGCACGCTCCA TTC

Alignment104106:575-671

GATGTTGTTTTGATATATTCACGTTATCAGTTGAGATAAA[C/G]CTTAGAACAAAGACGATAAGGCGCG
ACCATCAAATTAGGAGATCGACAACCGGCC GCG

Alignment104110:491-600

TGCCACAATTAAGTATTGTTATTAGTTTAAACATAAAATTCCTAATAAGTTTCCATTAGATTTTAAACGG[C
/T]CATGCATAATTTATGAGCCGCCCATATTGTTTCCAAAAC TTC

Alignment104209:1038-1129

GAAGATTTGGTATGTCGAAGTTGGAAAAGTGTGTTTGTTC[C/G]TTACAAGAAAAGTATTTCAGGAACT
ATTAAAGTTAACCAAGAAATTAATT CGG

Alignment104282:488-582

AAATTGGGGGCTTATTATGTGTGGCGGGGCAGCGGTGCGC[A/C]CTGGTCGCACAGAGAGCGGCGGGCGG
GCGCGGCGCAAGCGCTCCGGGCCCCG CAA

Alignment104563:132-261

CGCGCATTGTTCAAACGTTCAACCCTTGGCGCGGTTCCGCTGAATCATCCCGGTTCAATTAATAT[A/T]
GTTTAATGTTGTATCTAGATCCCGACGGCGTATTACAGGAATTATAACGTTTCGGGAGTCAG TTA

Alignment104563:296-390

CGTCTGTTTTGTTTGATCAGTGAAAGAAATAGCGTGACATGAATATGCGAGTAGGAAACATAT[C/T]TC
GATACTGTCTAAATAACTGTCTCTATAC CTT

Alignment105021:2570-2669

GTATTCAAAAGTGAATATGAATGCAAAGTCCCGGCGAA[C/T]GGGCGAAATGGCGAAAATCAAATTAGG
TATGGCGTGAATACTTACGGCGACGTCGGGAA CCT

Alignment105060:2734-2850

AAGCGCCTTCCAAGTTTCAATTCCCAGAAATCCCTTAATCAACTCACAAGGTACTIONTACGACCTAATCTTAT
CCTCG[A/G]CCCATTACCGGATATCAGATAGAAAAGGCCATTTTCAGTC AAG

Alignment105419:299-401

ATATTTTACATGTGGCGGGCGCCCGACCGTG[C/G]CCCGGACTCGAATTAATACTAAATTGAAATTGTAA
AAATGGAAATACAATTTTCACTTTGTAGCTACTCA GGC

Alignment105606:726-824

TGGTGTGTGCAAGCGACATGTAACTATCTATTTGCGTGGCAGCTGTTGATACAACCTC[C/T]AGCAACAAT
TGAATATGGCTGTAAATCAGGGAGATAGTAC CTC

Alignment105650:19-116

ATGATACCATATCCTGCTACGTTAAACCTTGCTAGGGTTAGGTCGCGCACGCGACG[A/T]TAAGTATTTTC
GAAACTCTTTGCCAATTTAATTATTTAGGT TAA

Alignment105650:168-309

ACTTAAGTATACGCCAAACGTCTTACGTTTCGATTAGAGTAAGAGAATATTTTCAAATATTGCCTTTAG
GTGAAGTTGATTGGTTGTTGTGCGGTGAGCG[A/G]CCGCGCTTATCTTCCACACTACGTTGTAATTCATTTTCG
AGG

Alignment106265:293-383

GGACCAATTTAGATAAAAAGGAAAGAGCTTTCTCCCTG[A/G]AACACCATAGATAGCAGTCTTAACTATC
GCAAGTTAGGGCAGTTAATCCGAG AGA

Alignment106399:109-250

TCTGAGGATGACGTCTCTGTTTCGAGCACTCGTCGAGTTTCCTTTGTAATTAATATTGAAATTAAGAAA
TGAACAGCCGCTAATTACAAGAGGTTGTCCC[C/T]CGAGGGCGCGGTGCTGATTACGCCCAACATTCGCAGAAA
TTC

Alignment106400:493-620

TCATTGTCCAACCGTAATTATAATGTAATTAATGTAC[A/G]GTTTAATTAACCCATCAGATAAGTCGCC
ATTGCAGCTTATTGATGCACCAATTAATGTAATTAAGCCATCGATCGTAAGAAGATAC AAG

Alignment106638:161-247

GCCAAAATAATGTTCAAAGCAGAACTCGAAGAATCAAATAATGAAAGGAA[T/G]TCGGAAAATATGGTG
ATGATAGTACAGCAGCCTCT GTT

Alignment107322:69-160

CTTCTAGTTCCACTGCAGTGAACAAGATTATAATGAGTA[C/T]ATGTGGACTATGAGAAAGGATTTTG
CTGAGCCAGAGCCATCAATAATTGT TTC

Alignment107590:158-260

CGCGGTGCGCCGCTGAAAATATATAATATTGAATACAATGTTTCCGCAATAAACAATGTAG[A/G]AAAA
ACACAATATTGCTGTGAAAATGGCAGCGACACGCG AGG

Alignment107810:267-382

ACTGGGTATTGCAGAACAAAGTCTAAATTTGTTTTGATATTTGCTTCCTAACTTTCTCACGGTGGCG
GTGT[C/T]TAGGCCGAGTAGAACATAGTCTAAACTAGACGGAATGACA TCC

Alignment107810:634-725

CCGCATCATCATTCCAACCTCCAACCGTCTAAGACTGTCCAATGGAATTTT[A/G]CAGAAAATCGACGTTCCGTAGCGCGCTATCGGCCTTCATA AGG

Alignment108129:264-355

AGATCGCTGCCGGCAAAGTGTACCAATTTATTTATCACTTCAACCATTTTGCACGAGCGC[C/T]CGGCGCCGCAGTCTGTTTTATTATTGTGC CCT

Alignment109093:791-895

CCCGTTTAAAAAATCTAATAAAAAACAAGTTATCGAACTATCTAAGAATATCGACTTTTATAAAAAATGTTA[A/T]TTTACAATGGCAGTCAACTGTGTCACAAATAT TTA

Alignment109291:701-796

ATGTAAGTGGCCAAATCTCTGTAGGGAAAGC[C/T]GGTTTCAGCCAATTTGGCTGAATGTTGACATTATGTTGAGATAACTGGAATTCGTGTAATCGC CCT

Alignment109338:877-1018

TCTACTGTGATATTAATAATTCTATTTATTATTTTCTAGATTATTATTTATAACTTTAGTGTTGAATGTGAACGTGTGTTATTTACTGAAGTTCTAGA[A/T/G]TAGGCAATGTTATTTTATATTGTACCTAATGCTAAAA GGT TGA

Alignment110317:244-385

CATGAAGGTATTATAGAATTTACTGTAAAAACCTTAACTTTATTGTATTTACTTAGATCTATATCACTAACCAAGGCTTCCACACGCTTTAGTGTGATT[C/T]CCTTACTATTTTCAACCTTCAAGATATTTTTAGAAATTAACCT

Alignment110862:37-178

AAGACAATTGGTATTTCTTTAGCAGTTATAGCAGTAGCCT[C/T]GCTTACAGCTGCTTATCTCTTAAGTCCAGCTTATGCAACTTTTGTGGTACAGTTGGAACAAAAGCTGCAACACTTGTTAGTCCTGCTATTACTGCAATG CTC

Alignment110908:677-818

TGGGCAAGGAGAGAGAAAAGAGAAATCGTACTTAGTTGCTGGAAGAGAAAGGGCAACAAAACCTTACTATCTCTGGACGGCGCATTGTCAACTGCATAGCT[A/G]CCCATGCTCCAAAAGAAAACCGACTATCCAAATTGGAACAGA

Alignment110919:477-618

CAAGTCTGGTACAAAGTCCAATCATCTAGCAGTACCAAAGGAACAGCAACTCTCTATTGATTTAGGTAA TAGAAAAGTTTTTGGTATCATAAATAAGATT[A/C]TGTATTGGATAGAGAATAATTTTACTTATTTTTTTCCACG CAC

Alignment110981:322-463

TCCTCATTGATTTTATCGACTATCGTCTGTGGTGGATCATCTCCCATCCTGAATATAAAAATCTCTCCATAATCTGCAACATCTATAGAGCCAGTTCTAC[C/T]TTTTGCCAGAAACATTTCTCTTTTATCTTTATCAACTAAT TCC

Alignment111062:661-802

TGAATTTCTTATCATAGCATCTGTCAATCCAGTACCCTGGAATGACAGAAAAAGAACACTGAATTAATAACAACATACCATCTTATATCTTAATACTG[C/T]ATAATACCTCGATCATAGATTGATTAAGGACACCTTGAGT CTC

Alignment111068:339-480

GCTATTGCTGCTCTTCCTGATTGTGTAAGAATTGACACCT[A/G]TGATGAGTTTGAAGGCTTATATAA
TATATATTCAGGATTTGGAAAATTTTTGTCCAAAAAAAATGAATTTTGCCTAATTTTTGTTGCAGTATTATT
T AAG

Alignment111099:1033-1174

GTAGCATCAACTACCACTGCACCTACTTCTACAACGAGTAGGCCTTCAACAGAGTCAACAATTCAAACAA
GTACAGTAACAGTGGGGCCAACAACAGTAG[C/T]AAAAACAACACTACTCCACAAGCGACCACAGTTGCTACA
CCT

Alignment111164:937-1076

ACTTCAACTGTTGTATTTTCCTCAAATCTCTCATAGCTTTTAGTTTGATCTAAAAATTCTAATACATCAG
CTTTGATGATACGACCATATGGACCTGTAC[C/T]TTTAAATCGCTTATATCAACACCTTCATTTTGAGCTA
CTC