

# Single-cell copy number variant detection reveals the dynamics and diversity of adaptation: S2 Text

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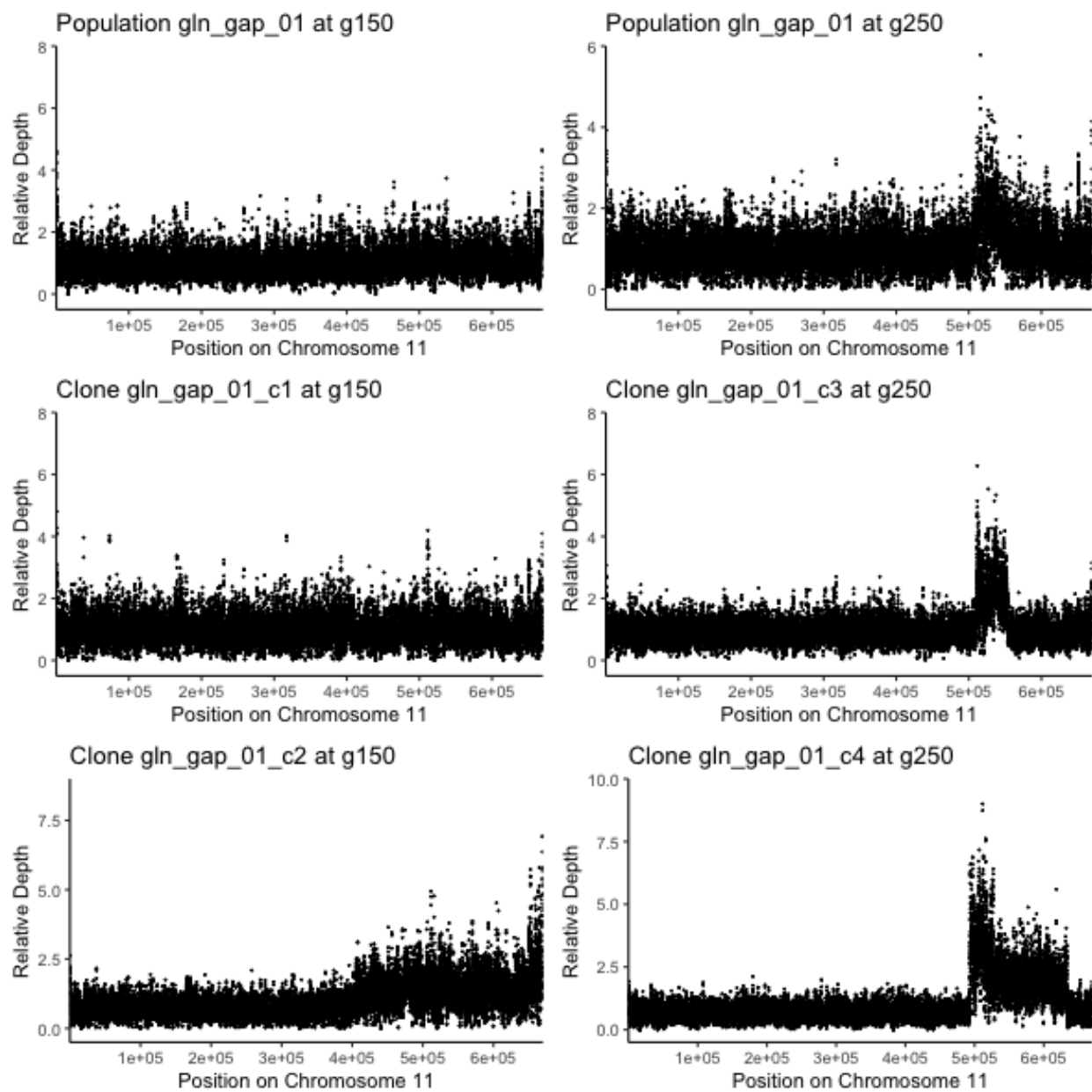
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**18 Urea-limited population 07****49****19 Urea-limited population 08****53**

The relative read depth at generation 150 and generation 250 is plotted for all glutamine-limited populations and for urea-limited populations with DUR3 CNVs. Sequenced clones from their respective populations at generation 150 or 250 are also plotted. In each case, the relative read depth across the chromosome (chromosome 11 for GAP1 and chromosome 8 for DUR3) is shown, with reads randomly downsampled for presentation purposes.

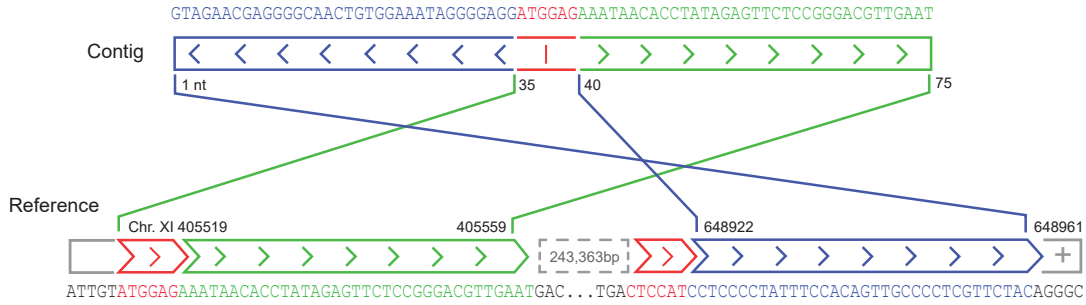
For several clones, nucleotide resolution of breakpoints was determined using a split-read approach (see methods). Each figure depicts a breakpoint assembly contig that was generated by local assembly of split reads and mapped to the reference genome. In some cases, only one breakpoint was resolved, but in other cases two breakpoint maps are shown for a single clone. These maps depict two independent events that occurred on the left and right-hand side of either GAP1 or DUR3. Mismatches in alignment are denoted with dots. Inverted repeats are shown in red. Sequences in the reference genome (blue) are inversely oriented in the assembled contig, suggestive of an inversion.

# 1 Glutamine-limited population 01



Sample: Gln\_01\_c2  
 Contig: 1 of 1

Locus: HCS1, FLO10  
 Supporting Split Reads: 32  
 Proposed Event: Segmental aneuploidy



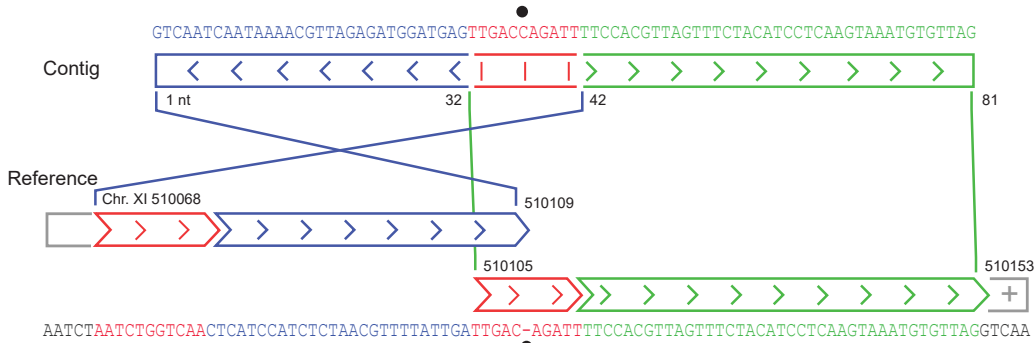
Contig  
 GTAGA ACGAG GGGCA ACTGT GGAAA TAGGG GAGGA TGGAG  
 AAATA ACACC TATAG AGTTC TCCGG GACGT TGAAT

Reference  
 ATTGT ATGGA GAAAT AACAC CTATA GAGTT CTCCG GGACG  
 TTGAA TGAC ... 243363 bp ... TGACT CCAATC CTCCC  
 CTATT TCCAC AGTTG CCCCT CGTTC TACAG GGC

Key	
	Section A
Blue	
	Section B
Green	
	Inverse Repeat
Red	
aagaacccta lowercase	Low complexity region (DUST)
	Mismatch between contig and reference
ATG [ 42 bp ] Black	Unmatched internal reference sequence
	Unmatched flanking reference sequence
ATG	

Sample: Gln\_01\_c3  
 Contig: 1 of 2

Locus: CAF4  
 Supporting Split Reads: 6  
 Proposed Event: CNV, ODIRA



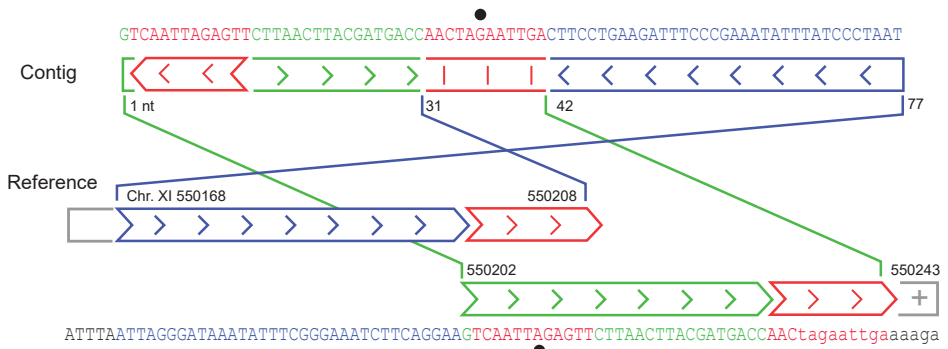
Contig  
 GTC AA TCAAT AAAAC GTTAG AGATG GATGA GTTGA CCAGA  
**TTTTC** CACGT TAGTT TCTAC ATCCT CAAGT AAATG TGTTA  
 G

Reference  
 AATCT **AATCT** **GGTCA** **ACTCA** TCCAT CTCTA ACGTT TTATT  
**GATTG** **ACAGA** **TTTTC** CACGT TAGTT TCTAC ATCCT CAAGT  
**AAATG** TGTTA GGTCA A

Key	
	Section A
Blue	
	Section B
Green	
	Inverse Repeat
Red	
aagaaccCa lowercase	Low complexity region (DUST)
	Mismatch between contig and reference
	Unmatched internal reference sequence
Black	
	Unmatched flanking reference sequence
ATG	

Sample: Gln\_01\_c3  
 Contig: 2 of 2

Locus: TRM2  
 Supporting Split Reads: 8  
 Proposed Event: CNV, ODIRA



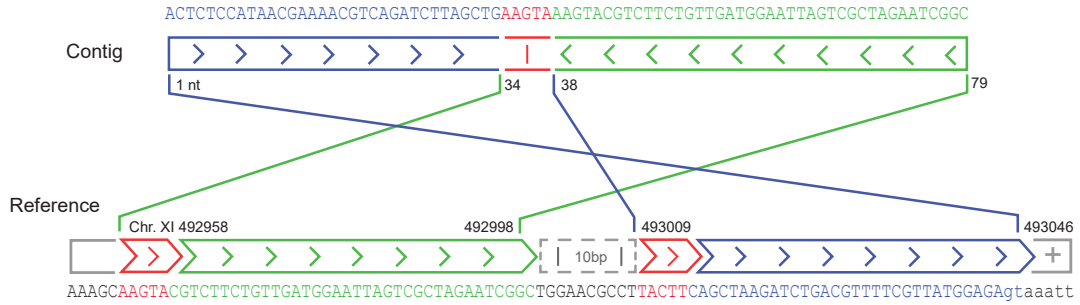
Contig  
 GTCAA TTAGA GTTCT TAACT TACGA TGACC AACTA GAATT  
 GACTT CCTGA AGATT TCCG AAATA TTTAT CCCTA AT

Reference  
 ATTTA ATTAG GGATA AATAT TTCGG GAAAT CTTCA GGAAG  
 TCAAT TAGAG TTCTT AACTT ACGAT GACCA ACtag aattg  
 aaaag a

Key	
	Section A
Blue	
	Section B
Green	
	Inverse Repeat
Red	
aagaaccCa lowercase	Low complexity region (DUST)
	Mismatch between contig and reference
	Unmatched internal reference sequence
Black	
	Unmatched flanking reference sequence
ATG	

Sample: Gln\_01\_c4  
 Contig: 1 of 2

Locus: BCH2  
 Supporting Split Reads: 9  
 Proposed Event: CNV, ODIRA



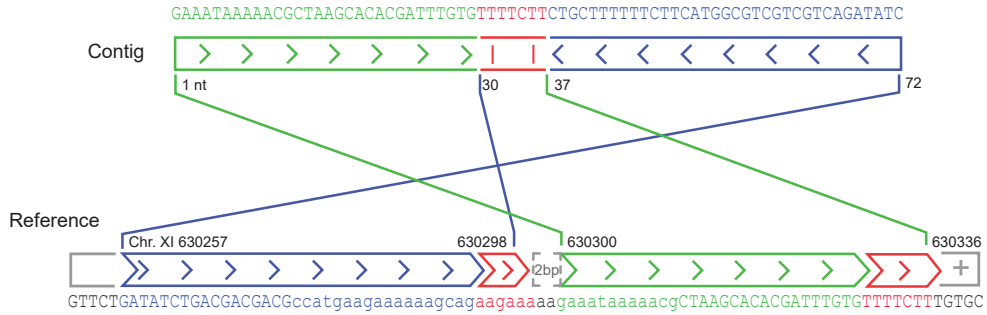
Contig  
 ACTCT CCATA ACGAA AACGT CAGAT CTTAG CTGAA GTAAA  
 GTACG TCTTC TGTTG ATGGA ATTAG TCGCT AGAAT CGGC

Reference  
 AAAGC AAGTA CGTCT TCTGT TGATG GAATT AGTCG CTAGA  
 ATCGG CTGGA ACGCC TACT TCAGC TAAGA TCTGA CGTTT  
 TCGTT ATGGA GAgta aatt

Key	
AAG Blue >>	Section A
AAC Green >>	Section B
CCA Red >>	Inverse Repeat
aagaaccCa lowercase	Low complexity region (DUST)
C T	Mismatch between contig and reference
ATG [ 42 bp ] Black	Unmatched internal reference sequence
+ ATG	Unmatched flanking reference sequence

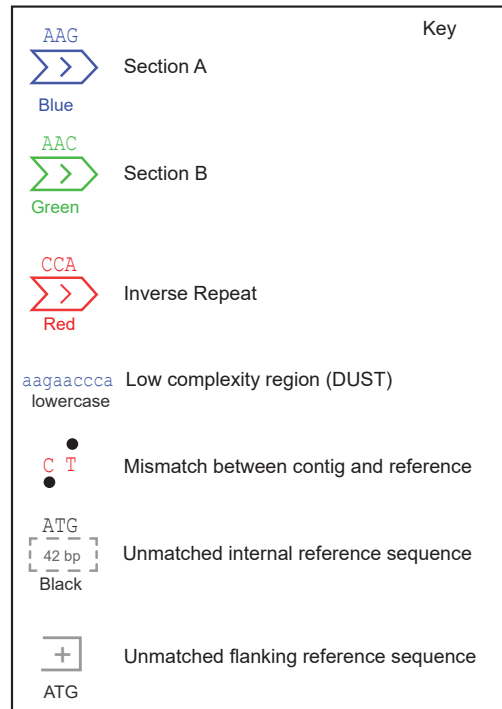
Sample: Gln\_01\_c4  
 Contig: 2 of 2

Locus: ESL2  
 Supporting Split Reads: 4  
 Proposed Event: CNV, ODIRA



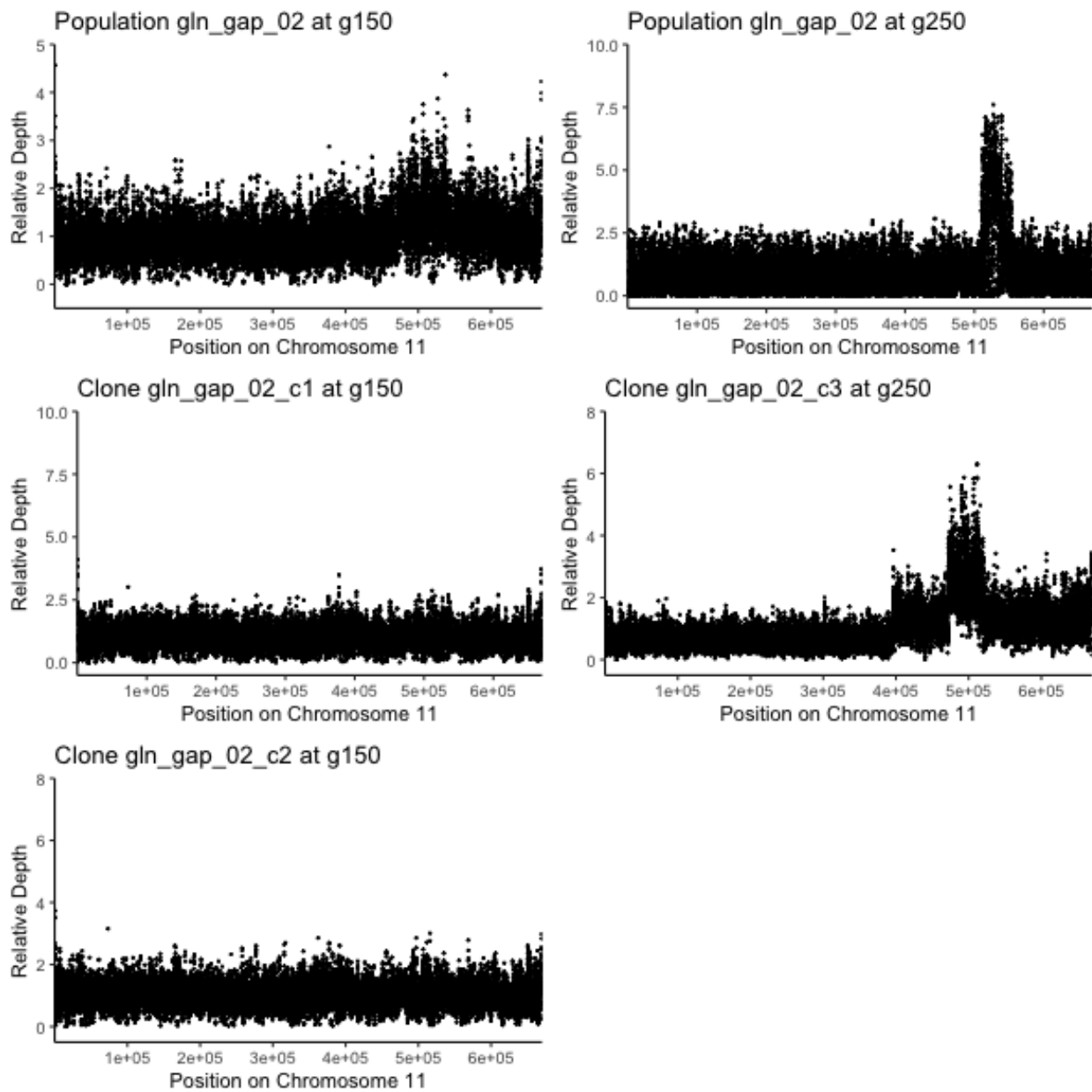
Contig  
 GAAAT AAAAA CGCTA AGCAC ACGAT TTGTG TTTTC TTCTG  
 CTTT TTCTT CATGG CGTCG TCGTC AGATA TC

Reference  
 GTTCT GATAT CTGAC GACGA CGcca tgaag aaaaa agcag  
 aagaa aaaga aataa aaacy CTAAG CACAC GATTT GTGTT  
 TTCTT TGTGC

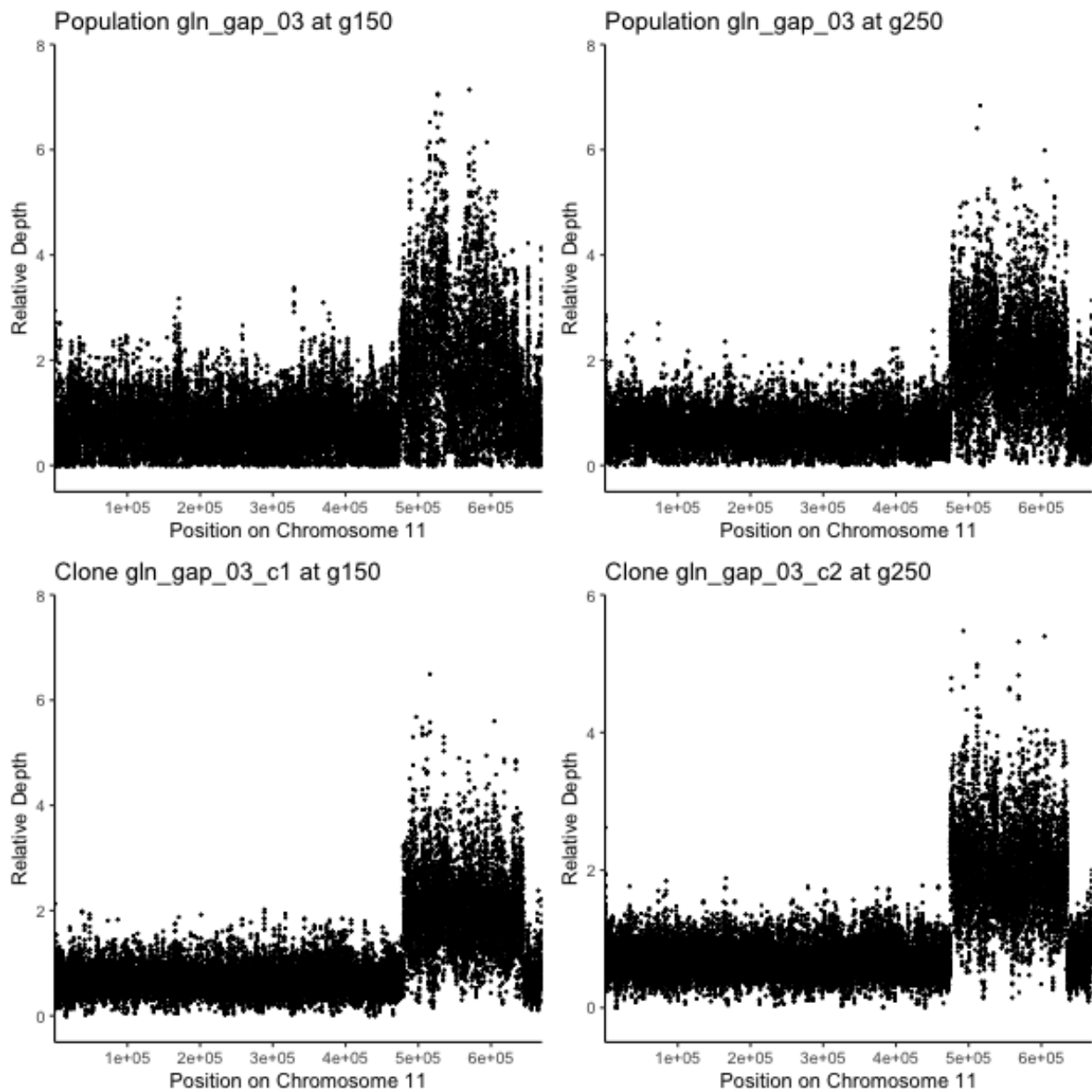




## 2 Glutamine-limited population 02

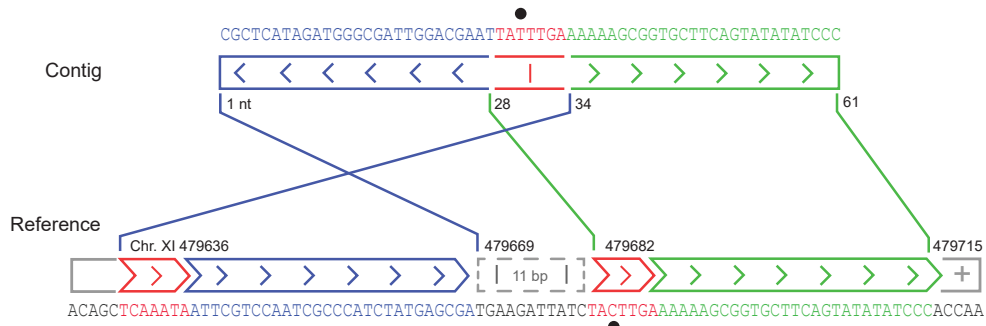


### 3 Glutamine-limited population 03



Sample: Gln\_03\_c1  
 Contig: 1 of 2

Locus: ALY1  
 Supporting Split Reads: 8  
 Proposed Event: CNV, ODIRA



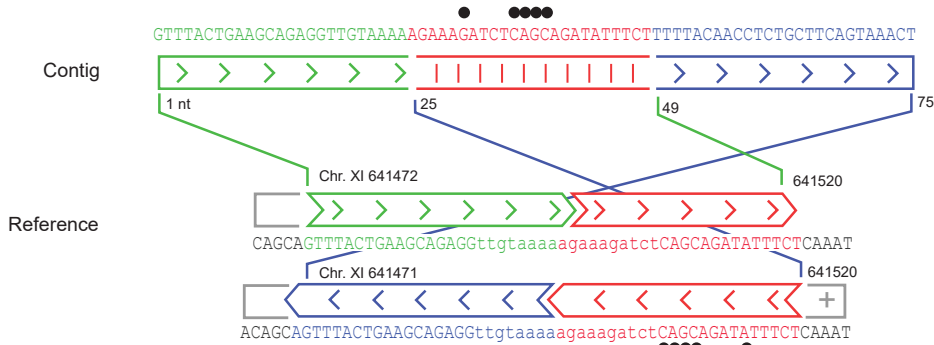
Contig  
 CGCTC ATAGA TGGGC GATTG GACGA ATTAT TTGAA AAAAG  
 CGGTG CTTCA GTATA TATCC C

Reference  
 ACAGC TCAAA TAATT CGTCC AATCG CCCAT CTATG AGCGA  
 TGAAG ATTAT CTACT TGAAA AAAGC GGTGC TTCAG TATAT  
 ATCCC ACCAA

Key	
AAG [Blue Arrow]	Section A
Blue	
AAC [Green Arrow]	Section B
Green	
CCA [Red Arrow]	Inverse Repeat
Red	
aagaaccCa lowercase	Low complexity region (DUST)
C T [Black Dot]	Mismatch between contig and reference
ATG [42 bp Box]	Unmatched internal reference sequence
Black	
[+ Box]	Unmatched flanking reference sequence
ATG	

Sample: Gln\_03\_c1  
 Contig: 2 of 2

Locus: SIR1  
 Supporting Split Reads: 10  
 Proposed Event: CNV, ODIRA



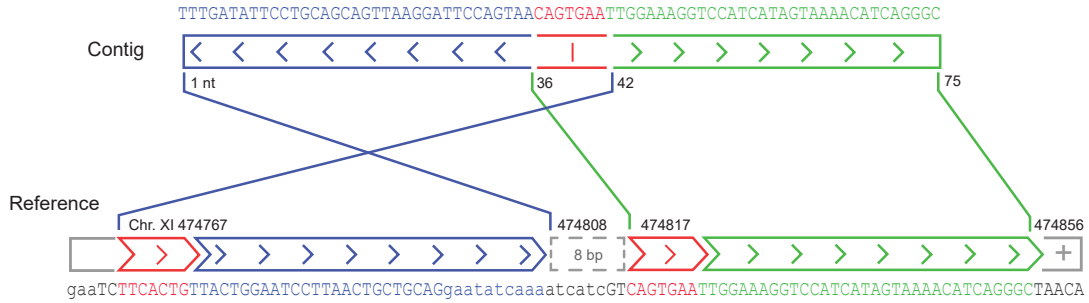
Contig  
 GTTTA CTGAA GCAGA GGTTC TAAAA AGAAA GATCT CAGCA  
 GATAT TTCTT TTTAC AACCT CTGCT TCAGT AAAC

Reference  
 ACAGC AGTTT ACTGA AGCAG AGGtt gtaaa aagaa agatc  
 tCAGC AGATA TTTCT CAAAT

Key	
AAG Blue >>	Section A
AAC Green >>	Section B
CCA Red >>	Inverse Repeat
aagaaccCa lowercase	Low complexity region (DUST)
C T •	Mismatch between contig and reference
ATG [ 42 bp ] Black	Unmatched internal reference sequence
+ ATG	Unmatched flanking reference sequence

Sample: Gln\_03\_c2  
 Contig: 1 of 2

Locus: YKR018C  
 Supporting Split Reads: 11  
 Proposed Event: CNV, ODIRA



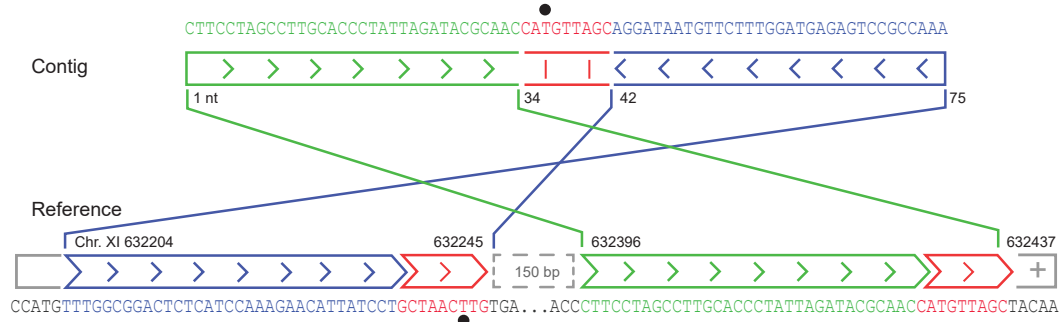
Contig  
 TTTGA TATTC CTGCA GCAGT TAAGG ATTCC AGTAA CAGTG  
 AATTG GAAAG GTCCA TCATA GTAAA ACATC AGGGC

Reference  
 gaaTC TTCAC TGTTA CTGGA ATCCT TAACT GCTGC AGgaa  
 tatca aaatc atcGT CAGTG AATTG GAAAG GTCCA TCATA  
 GTAAA ACATC AGGGC TAACA

Key	
	Section A
Blue	
	Section B
Green	
	Inverse Repeat
Red	
aagaaccCa lowercase	Low complexity region (DUST)
	Mismatch between contig and reference
	Unmatched internal reference sequence
Black	
	Unmatched flanking reference sequence
ATG	

Sample: Gln\_03\_c2  
 Contig: 2 of 2

Locus: PCK1  
 Supporting Split Reads: 23  
 Proposed Event: CNV, ODIRA

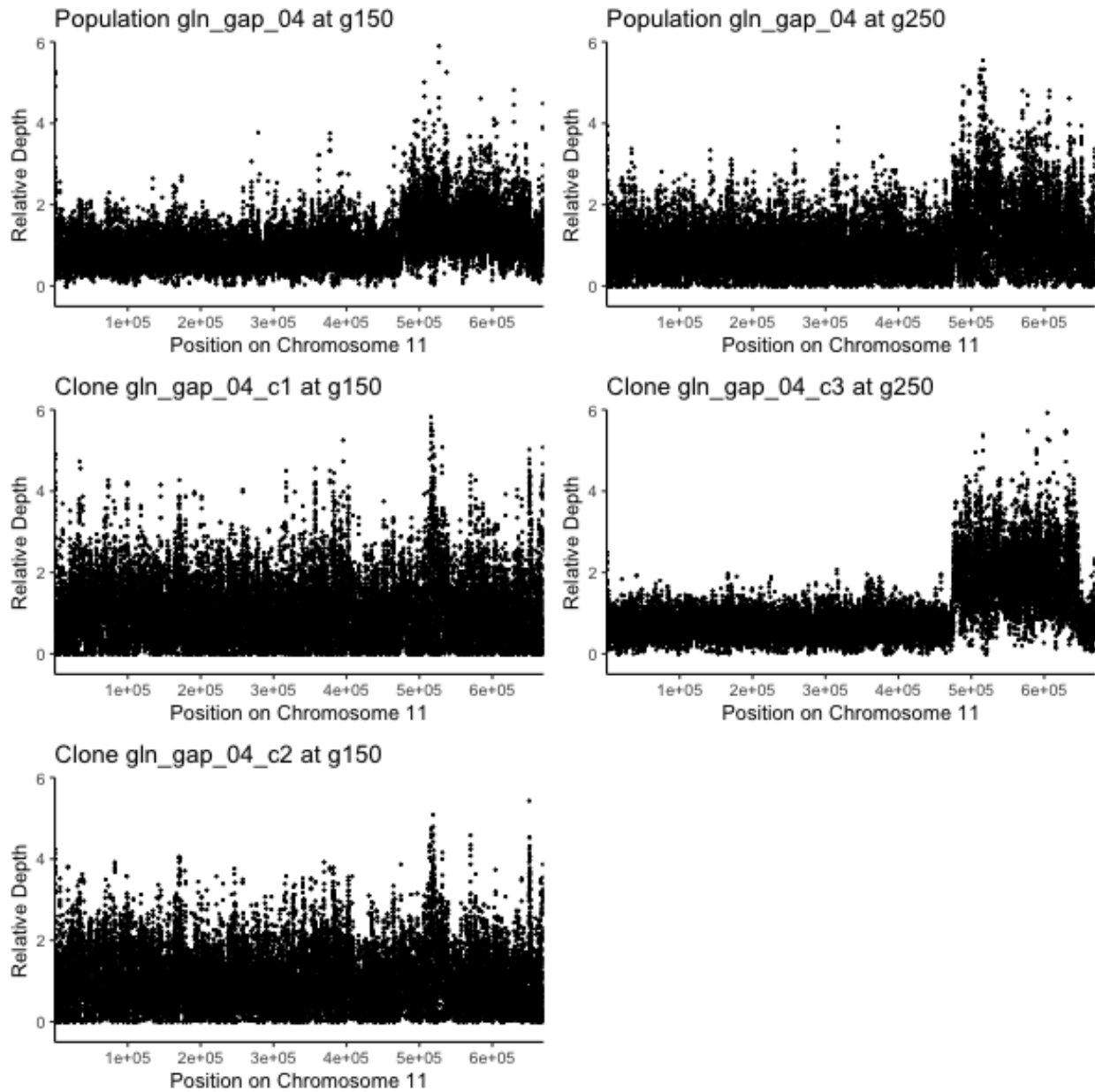


Contig  
 AATAA ACTCT TCCAA CTCTG ttttt ttCAA AGCTA GTGGT  
 GCATT TACAC GGTCA GCTTT ATGAT ACCGC TATTG

Reference  
 CCATG TTTGG CGGAC TCTCA TCCAA AGAAC ATTAT CCTGC  
 TAACT TGTGA TGCTT CGGGT GTTTT ACCAC CAGTA TCTAA  
 ATTGA CTCCT GAACA AGTCA TGTAC CATTT CATCT CTGGT  
 TACAC TTCTA AAATG GCTGG TACTG AGCAA GGTGT CACTG  
 AACCT GAACc aacat tttca tcttg TTTCG GACAA CCCTT  
 CCTAG CCTTG CACCC TATTA GATAC GCAAC CATGT TAGCT  
 ACAA

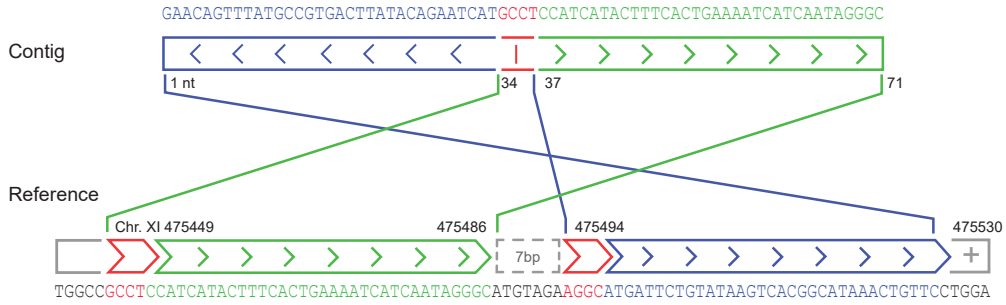
Key	
	Section A
Blue	
	Section B
Green	
	Inverse Repeat
Red	
aagaaccCa lowercase	Low complexity region (DUST)
	Mismatch between contig and reference
	Unmatched internal reference sequence
Black	
	Unmatched flanking reference sequence
ATG	

## 4 Glutamine-limited population 04



Sample: Gln\_04\_c3  
 Contig: 1 of 2

Locus: YKR018C  
 Supporting Split Reads: 6  
 Proposed Event: CNV, ODIRA



Contig  
 GAACA GTTTA TGCCG TGACT TATAC AGAAT CATGC CTCCA  
 TCATA CTTTC ACTGA AAATC ATCAA TAGGG C

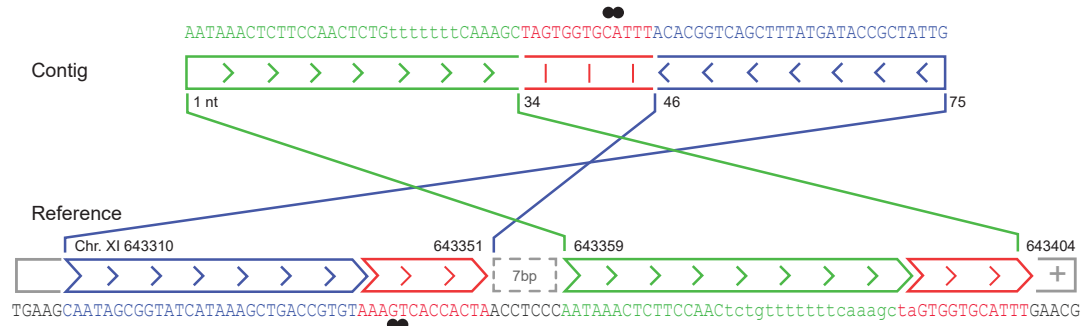
Reference  
 TGGCC GCCTC CATCA TACTT TCACT GAAAA TCATC AATGG  
 GCATG TAGAA GGCAT GATTC TGTAT AAGTC ACGGC ATAAA  
 CTGTT CCTGG A

Key	
AAG Blue >>	Section A
AAC Green >>	Section B
CCA Red >>	Inverse Repeat
aagaaccCa lowercase	Low complexity region (DUST)
C T	Mismatch between contig and reference
ATG [ 42 bp ] Black	Unmatched internal reference sequence
+ ATG	Unmatched flanking reference sequence



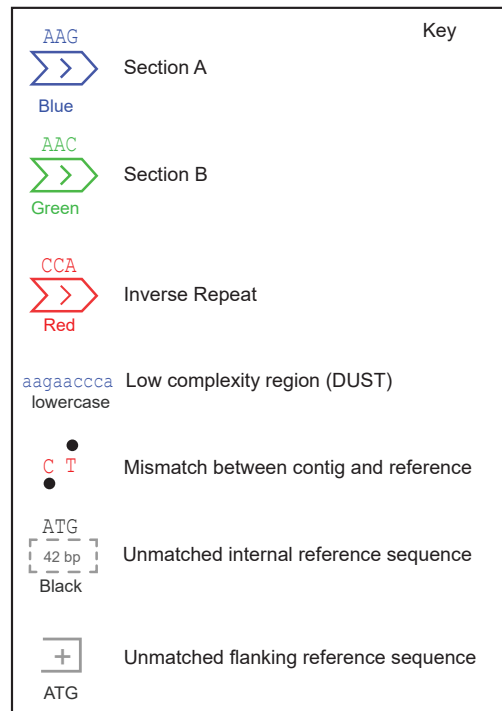
Sample: Gln\_04\_c3  
 Contig: 2 of 2

Locus: Intergenic SIR1, FLO10  
 Supporting Split Reads: 5  
 Proposed Event: CNV, ODIRA

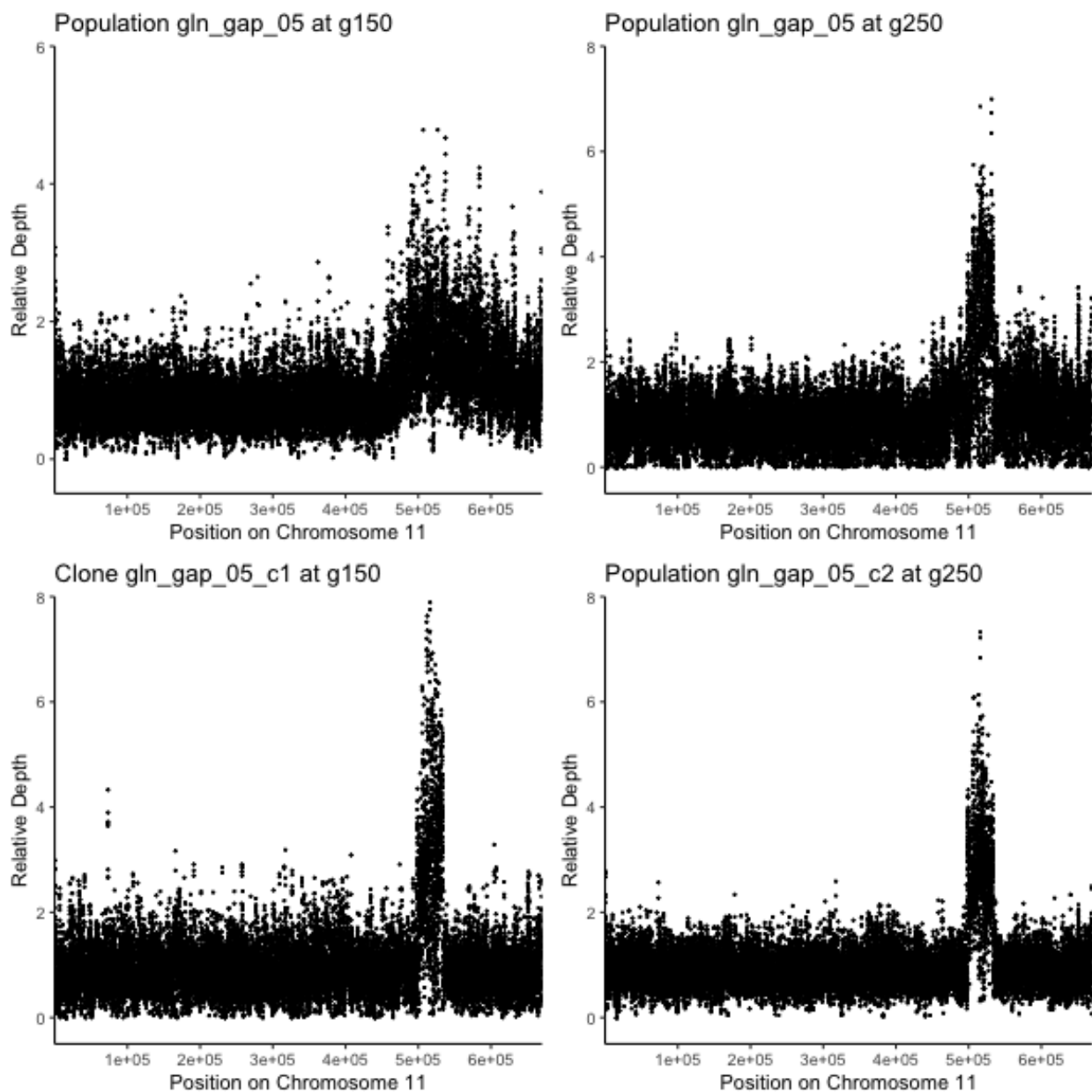


Contig  
 AATAA ACTCT TCCAA CTCTG ttttt ttCAA AGCTA GTGGT  
 GCATT TACAC GGTCA GCTTT ATGAT ACCGC TATTG

Reference  
 TGAAG CAATA GCGGT ATCAT AAAGC TGACC GTGTA AAGTC  
 ACCAC TAACC TCCCA ATAAA CTCTT CCAAC tctgt ttttt  
 caaag ctaGT GGTGC ATTTG AACG

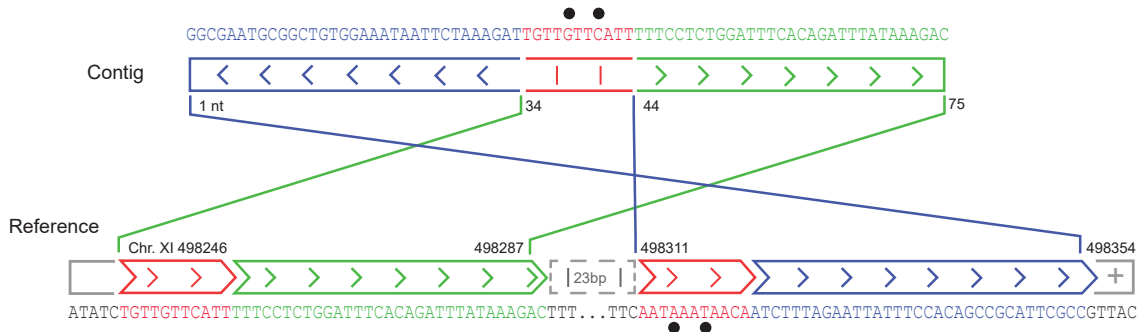


## 5 Glutamine-limited population 05



Sample: Gln\_05\_c2  
 Contig: 1 of 2

Locus: SET3  
 Supporting Split Reads: 10  
 Proposed Event: Unresolved



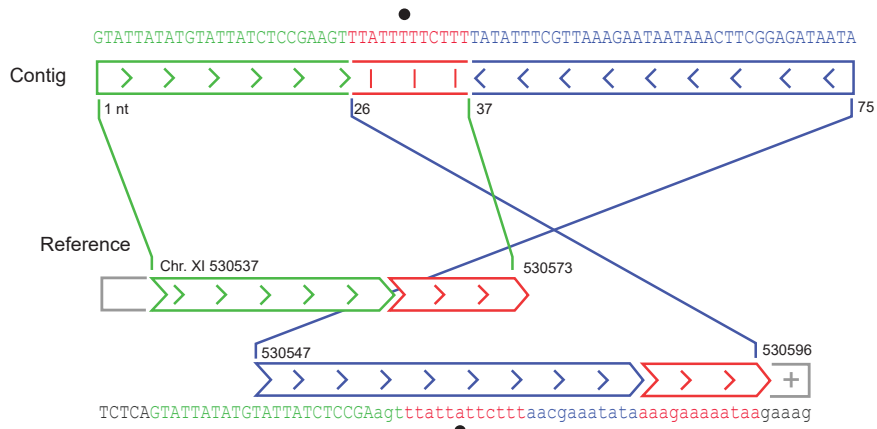
Contig  
 GGCGA ATGCG GCTGT GGAAA TAATT CTAAA GATTG TTGTT  
 CATTT TTCCT CTGGA TTCA CAGAT TTATA AAGAC

Reference  
 ATATC **TGTTG TTCAT TTTTC CTCTG GATTT CACAG ATTTA**  
**TAAAG ACTTT GCGCG TATCT CTCA CTTC AATAA ATAAC**  
**AATCT TTAGA ATTAT TTCCA CAGCC GCATT CGCCG TTAC**

Key	
	Section A
Blue	
	Section B
Green	
	Inverse Repeat
Red	
aagaaccCa lowercase	Low complexity region (DUST)
	Mismatch between contig and reference
	Unmatched internal reference sequence
Black	
	Unmatched flanking reference sequence
ATG	

Sample: Gln\_05\_c2  
 Contig: 2 of 2

Locus: Intergenic TRK2, YKR051W  
 Supporting Split Reads: 8  
 Proposed Event: Unresolved

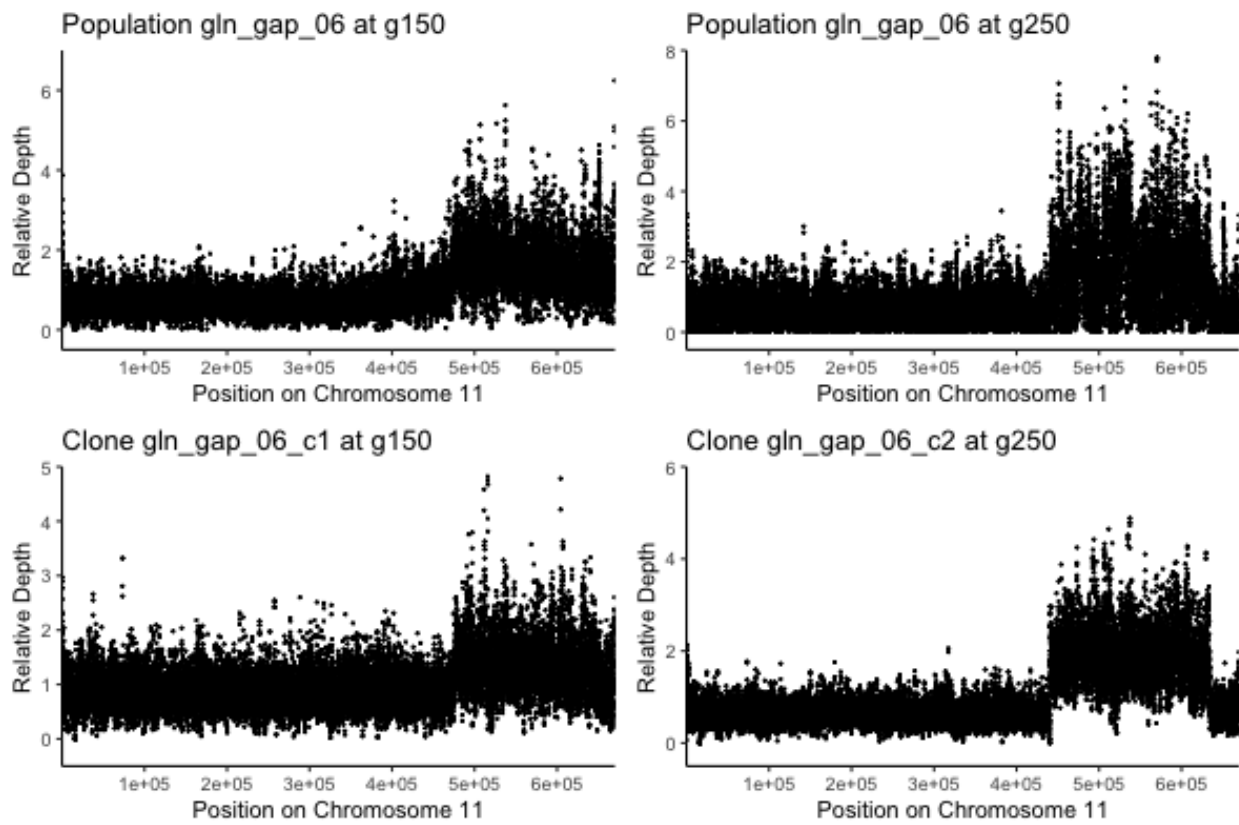


Contig  
 GTATT ATATG TATTA TCTCC GAAGT **TTATT TTTCT TTTAT**  
 ATTTT GTTAA AGAAT AATAA ACTTC GGAGA TAATA

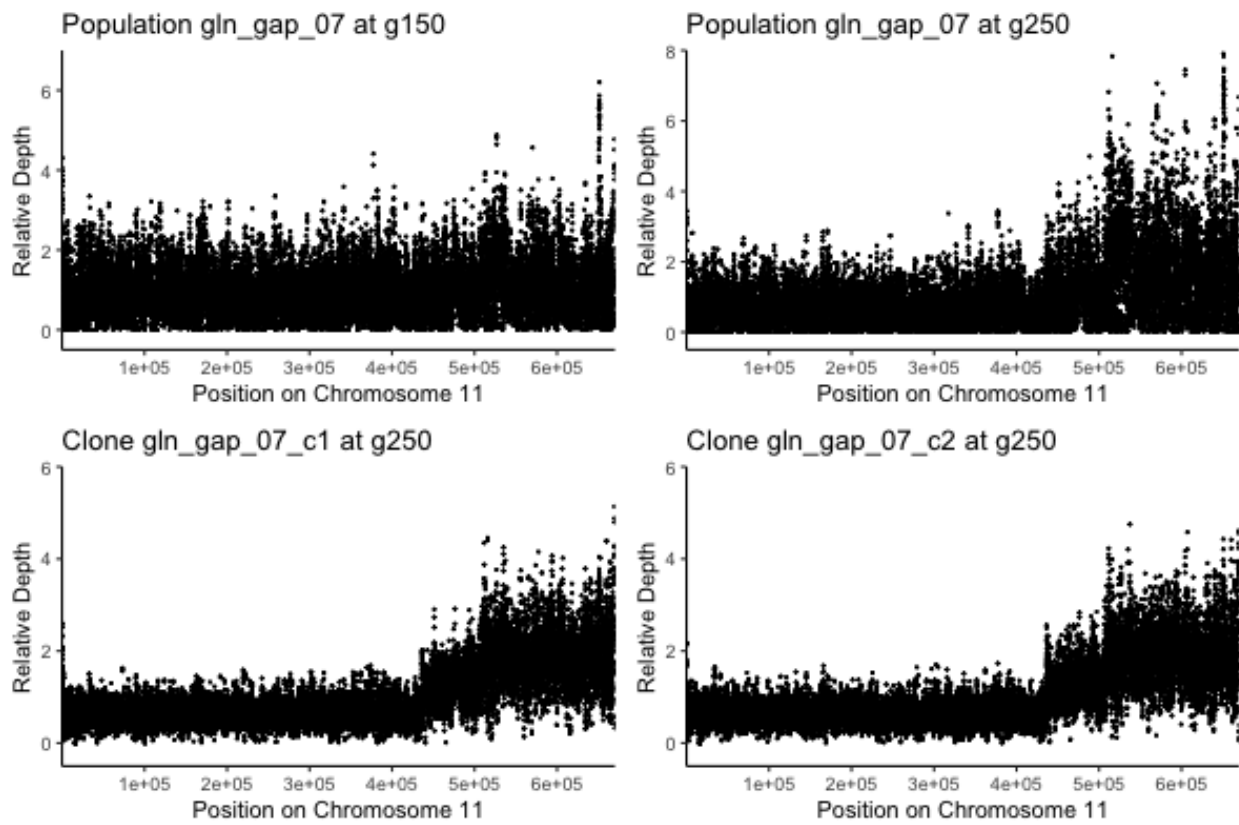
Reference  
 TCTCA GTATT ATATG TATTA TCTCC GAagt ttatt attct  
 ttaac gaaat ataaa agaaa aataa gaaag

Key	
	Section A
Blue	
	Section B
Green	
	Inverse Repeat
Red	
aagaaccba lowercase	Low complexity region (DUST)
	Mismatch between contig and reference
	Unmatched internal reference sequence
Black	
	Unmatched flanking reference sequence
ATG	

## 6 Glutamine-limited population 06

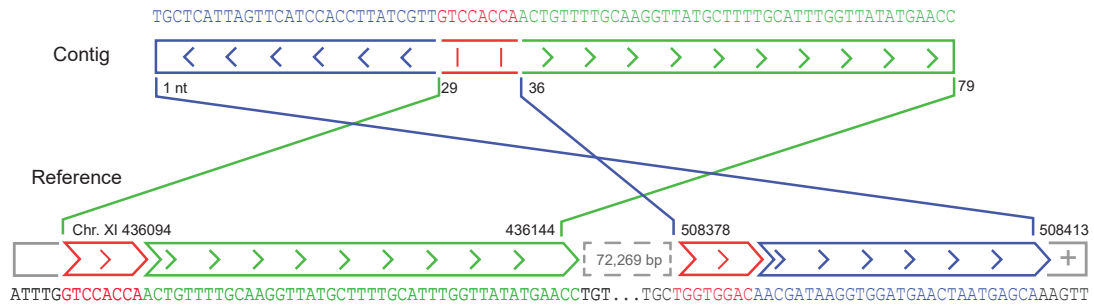


## 7 Glutamine-limited population 07



Sample: Gln\_07\_c1  
 Contig: 1 of 1

Locus: DID1, AUR1  
 Supporting Split Reads: 14  
 Proposed Event: Segmental Anueploidy



Contig  
 TGCTC ATTAG TTCAT CCACC TTATC GTTGT CCACC AACTG  
 TTTTG CAAGG TTATG CTTTT GCATT TGGTT ATATG AAC

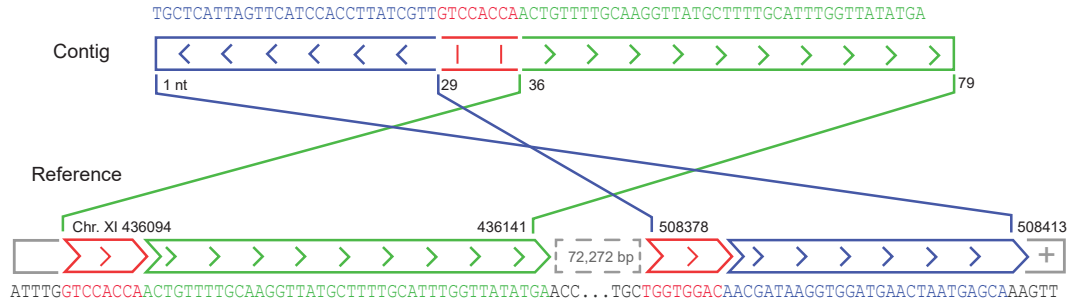
Reference Chr. XI 436094 - 436144  
 ATTTG **GTCCA** CCAAC TGTTT TGCAA GGTTA TGCTT TTGCA  
 TTTGG TTATA TGAAC CTGTT T

Reference Chr. XI 508378 - 508413  
 ATTGC **TGGTG** GACAA CGATA AGGTG GATGA ACTAA TGACC  
 AAAGT T

Key	
	Section A
Blue	
	Section B
Green	
	Inverse Repeat
Red	
<b>aagaacc</b> lowercase	Low complexity region (DUST)
	Mismatch between contig and reference
	Unmatched internal reference sequence
Black	
	Unmatched flanking reference sequence
ATG	

Sample: Gln\_07\_c2  
 Contig: 1 of 1

Locus: DID1, AUR1  
 Supporting Split Reads: 12  
 Proposed Event: Segmental Anueploidy



Contig  
 TGCTC ATTAG TTCAT CCACC TTATC GTTGT CCACC AACTG  
 TTTTG CAAGG TTATG CTTT GCATT TGGTT ATATG AAC

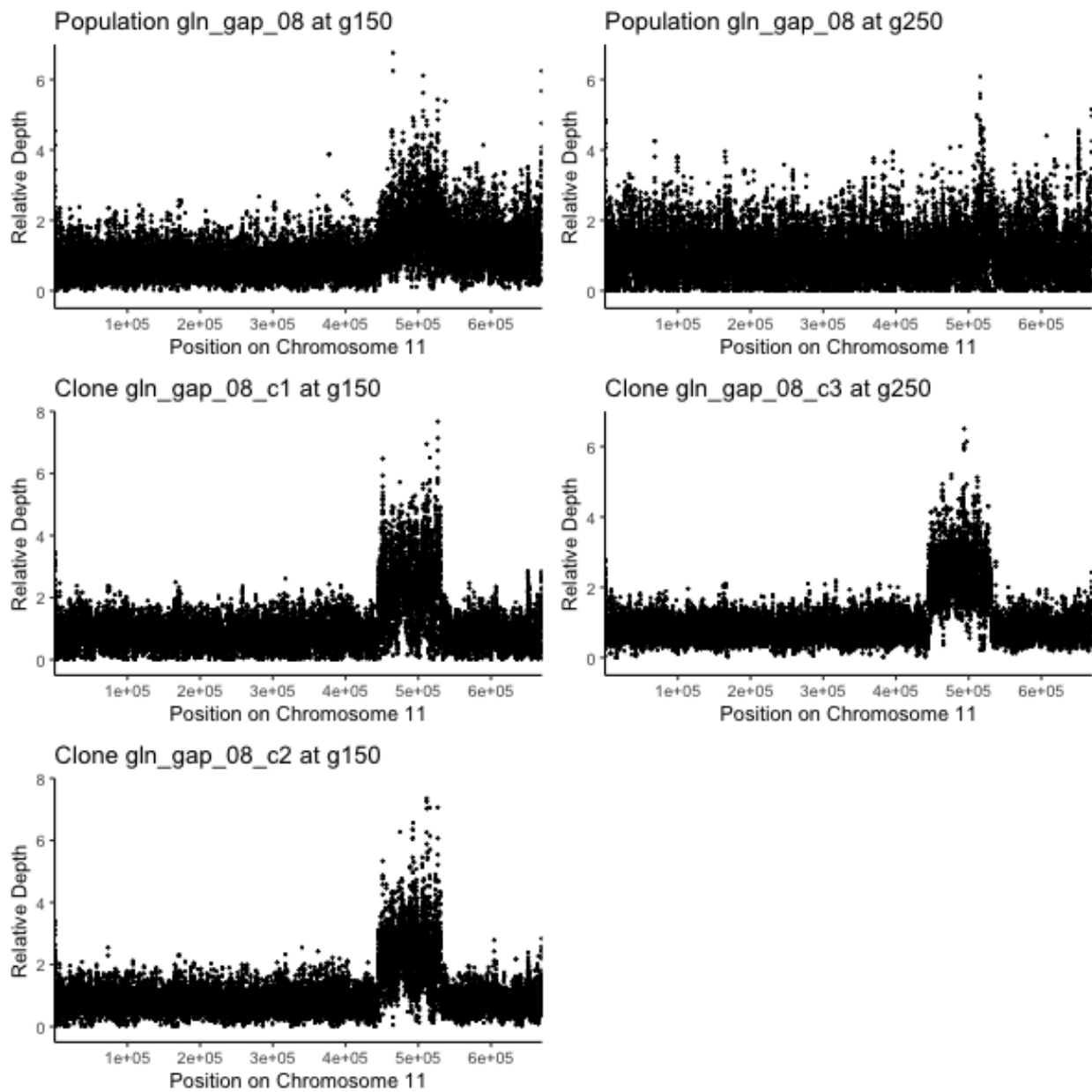
Reference Chr. XI 436094 - 436144  
 ATTTG GTC CAAC TGTT TGCA GGTG TGCT TTGCA  
 TTTG TTATA TGAAC CTG

Reference Chr. XI 508378 - 508413  
 ATTGC TGGTG GACAA CGATA AGGTG GATGA ACTAA TGAGC  
 AAAGT T

Key	
AAG [Blue Arrow]	Section A
AAC [Green Arrow]	Section B
CCA [Red Arrow]	Inverse Repeat
aagaacc ca lowercase	Low complexity region (DUST)
C T	Mismatch between contig and reference
ATG [42 bp] Black	Unmatched internal reference sequence
+ ATG	Unmatched flanking reference sequence

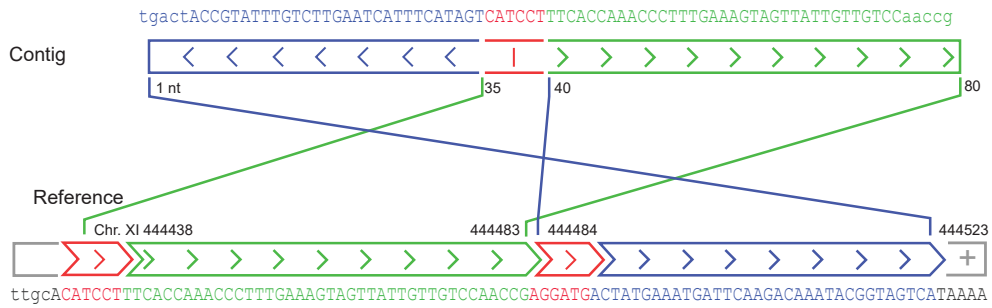


## 8 Glutamine-limited population 08



Sample: Gln\_08\_c1  
 Contig: 1 of 2

Locus: PAP1  
 Supporting Split Reads: 16  
 Proposed Event: CNV, ODIRA



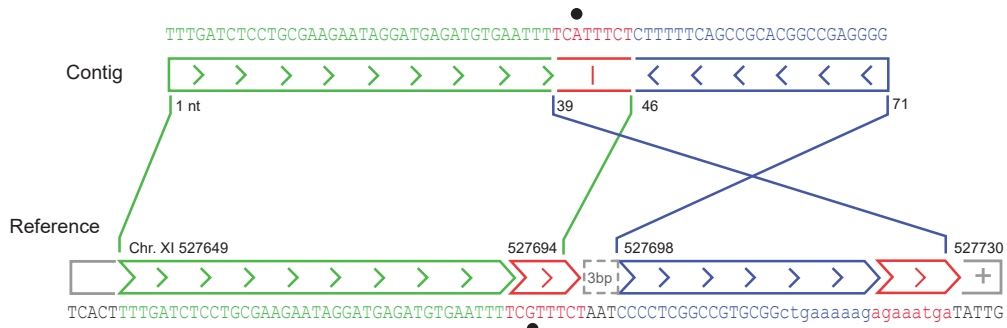
Contig  
 tgact ACCGT ATTTG TCTTG AATCA TTTCA TAGTC ATCCT  
 TTCAC CAAAC CCTTT GAAAG TAGTT ATTGT TGTCC aaccg

Reference  
 ttgcA CATCCT TTCAC CAAAC CCTTT GAAAG TAGTT  
 ATTGT TGTCCA ACCGA GGATG ACTAT GAAAT GATTC  
 AAGAC AAATAC GGTAG TCATA AAA

Key	
AAG Blue >>	Section A
AAC Green >>	Section B
CCA Red >>	Inverse Repeat
aagaaccCa lowercase	Low complexity region (DUST)
C T	Mismatch between contig and reference
ATG [ 42 bp ] Black	Unmatched internal reference sequence
+ ATG	Unmatched flanking reference sequence

Sample: Gln\_08\_c1  
 Contig: 2 of 2

Locus: Intergenic FMP46, TRK2  
 Supporting Split Reads: 16  
 Proposed Event: CNV, ODIRA



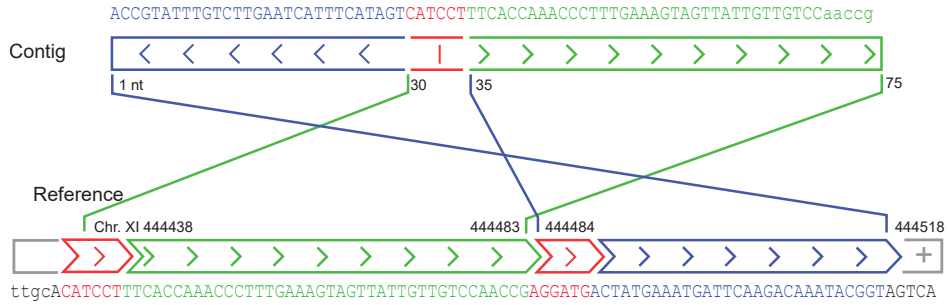
Contig  
 TTTGA TCTCC TCGCA AGAAT AGGAT GAGAT GTGAA TTTTC  
 ATTC TCTTT TTCAG CCGCA CGCC GAGGG G

Reference  
 TCACT TTTGA TCTCC TCGCA AGAAT AGGAT GAGAT GTGAA  
 TTTTC GTTC TAATC CCCTC GGCCG TCGCG ctgaa aaaga  
 gaaat gaTAT TG

Key	
	Section A
Blue	
	Section B
Green	
	Inverse Repeat
Red	
aagaacccta lowercase	Low complexity region (DUST)
	Mismatch between contig and reference
	Unmatched internal reference sequence
Black	
	Unmatched flanking reference sequence
ATG	

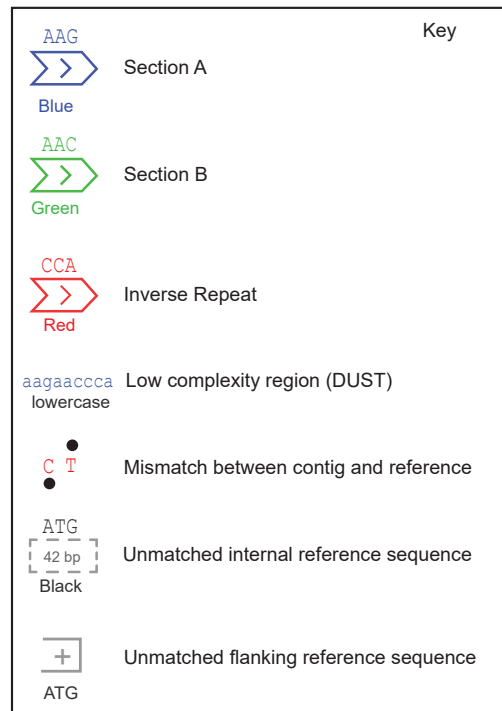
Sample: Gln\_08\_c2  
 Contig: 1 of 2

Locus: PAP1  
 Supporting Split Reads: 15  
 Proposed Event: CNV, ODIRA



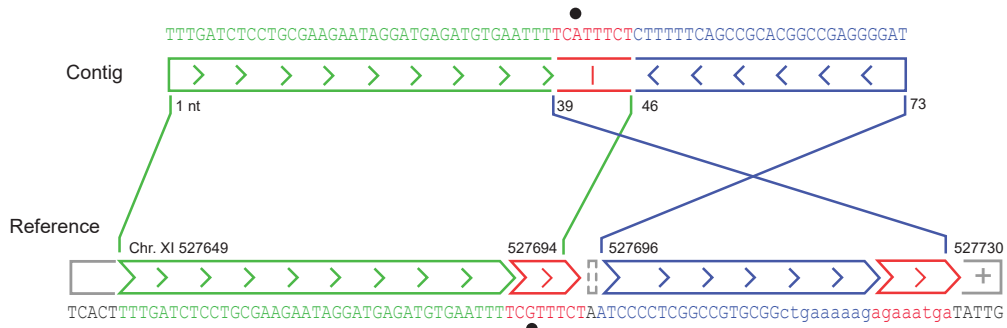
Contig  
 tgact ACCGT ATTTG TCTTG AATCA TTTCA TAGTC ATCCT  
 TTCAC CAAAC CCTTT GAAAG TAGTT ATTGT TGTCC aaccg

Reference  
 ttgcA CATCCT TTCAC CAAAC CCTTT GAAAG TAGTT  
 ATTGT TGTCCA ACCGA GGATG ACTAT GAAAT GATTC  
 AAGAC AAATAC GGTAG TCA



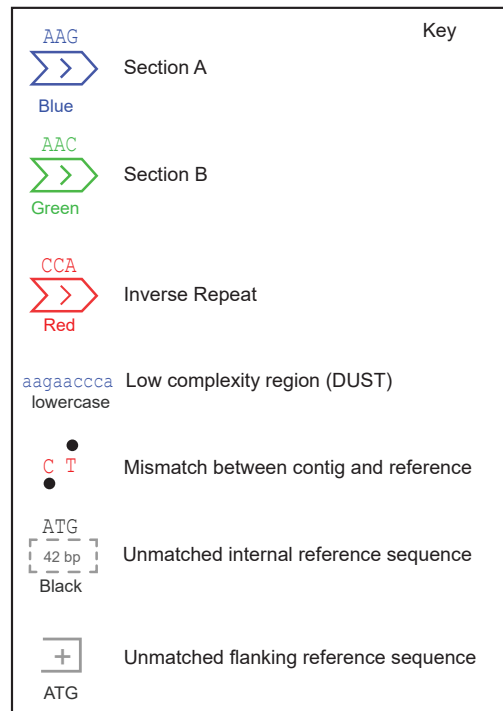
Sample: Gln\_08\_c2  
 Contig: 2 of 2

Locus: Intergenic FMP46, TRK2  
 Supporting Split Reads: 15  
 Proposed Event: CNV, ODIRA



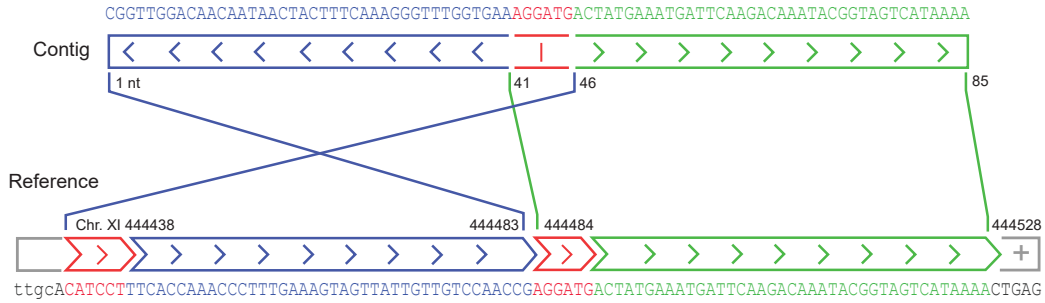
Contig  
 TTTGA TCTCC TCGCA AGAAT AGGAT GAGAT GTGAA TTTTC  
 ATTTC TCTTT TTCAG CCGCA CGCC GAGGG G

Reference  
 TCACT TTTGA TCTCC TCGCA AGAAT AGGAT GAGAT GTGAA  
 TTTTC GTTTC TAATC CCCTC GGCCG TCGGG ctgaa aaaga  
 gaaat gaTAT TG



Sample: Gln\_08\_c3  
 Contig: 1 of 2

Locus: PAP1  
 Supporting Split Reads: 8  
 Proposed Event: CNV, ODIRA



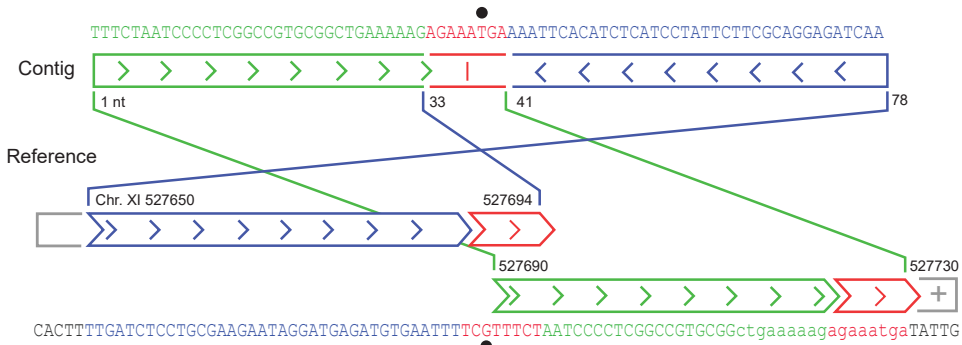
Contig  
 CGGTT GGACA ACAAT AACTA CTTTC AAAGG GTTG GTGAA  
 AGGAT GACTA TGAAA TGATT CAAGA CAAAT ACGGT AGTCA  
 TAAAA

Reference  
 ttgcA CATCC TTTCA CCAAA CCCTT TGAAA GTAGT TATTG  
 TTGTC CAACC GAGGA TGACT ATGAA ATGAT TCAAG ACAA  
 TACGG TAGTC ATAAA ACTGA G

Key	
	Section A
Blue	
	Section B
Green	
	Inverse Repeat
Red	
aagaaccCa lowercase	Low complexity region (DUST)
	Mismatch between contig and reference
	Unmatched internal reference sequence
Black	
	Unmatched flanking reference sequence
ATG	

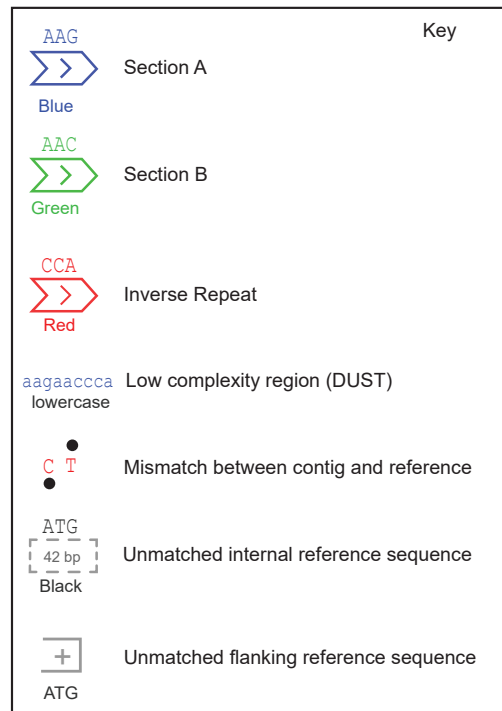
Sample: Gln\_08\_c3  
 Contig: 2 of 2

Locus: Intergenic FMP46, TRK2  
 Supporting Split Reads: 4  
 Proposed Event: CNV, ODIRA

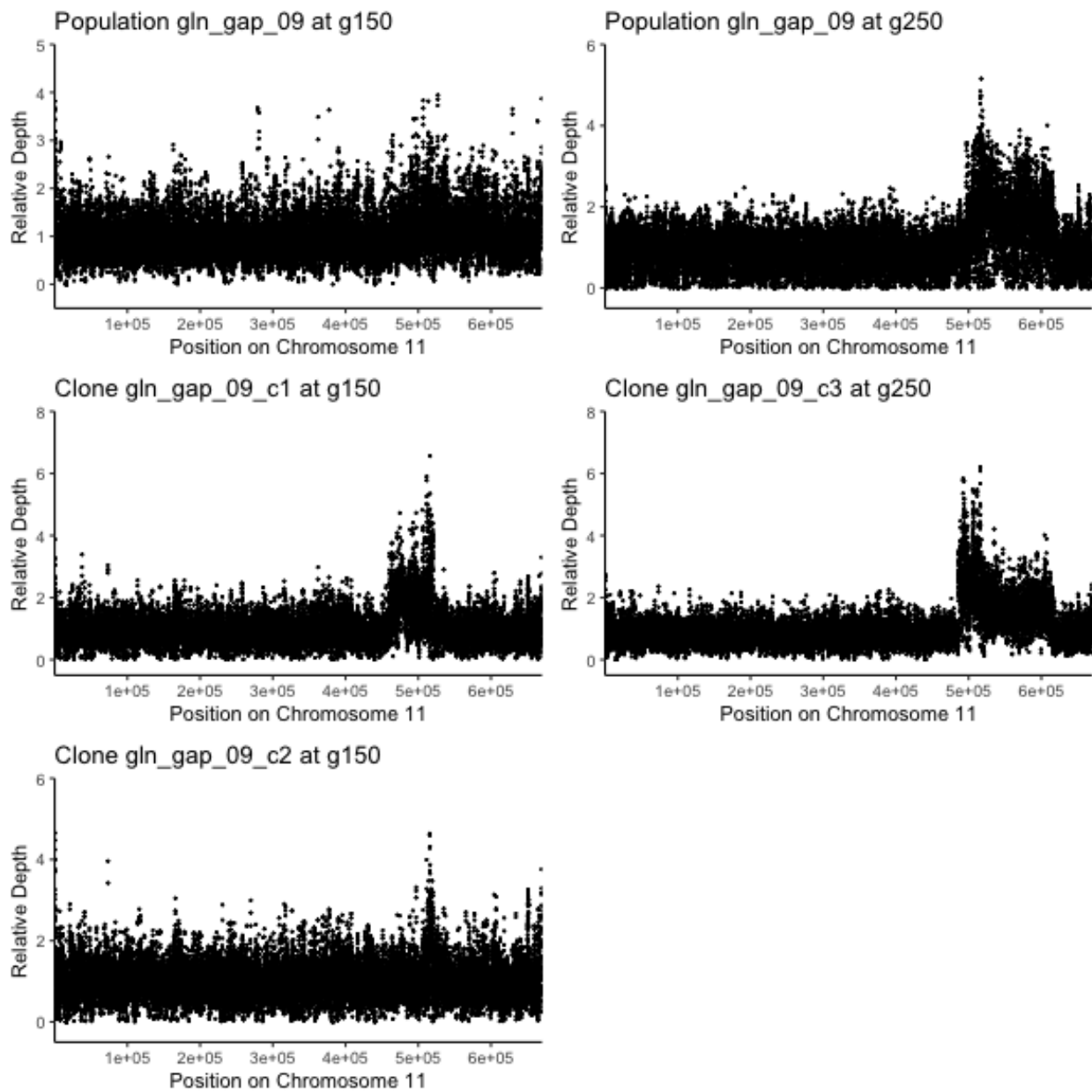


Contig  
 TTTCT AATCC CCTCG GCCGT GCGGC TGAAA AAGAG AAATG  
 AAAAT TCACA TCTCA TCTA TTCTT CGCAG GAGAT CAA

Reference  
 CACTT TTGAT CTCCT GCGAA GAATA GGATG AGATG TGAAT  
 TTTCG TTTCT AATCC CCTCG GCCGT GCGGc tgaaa aagag  
 aatg aTATT G

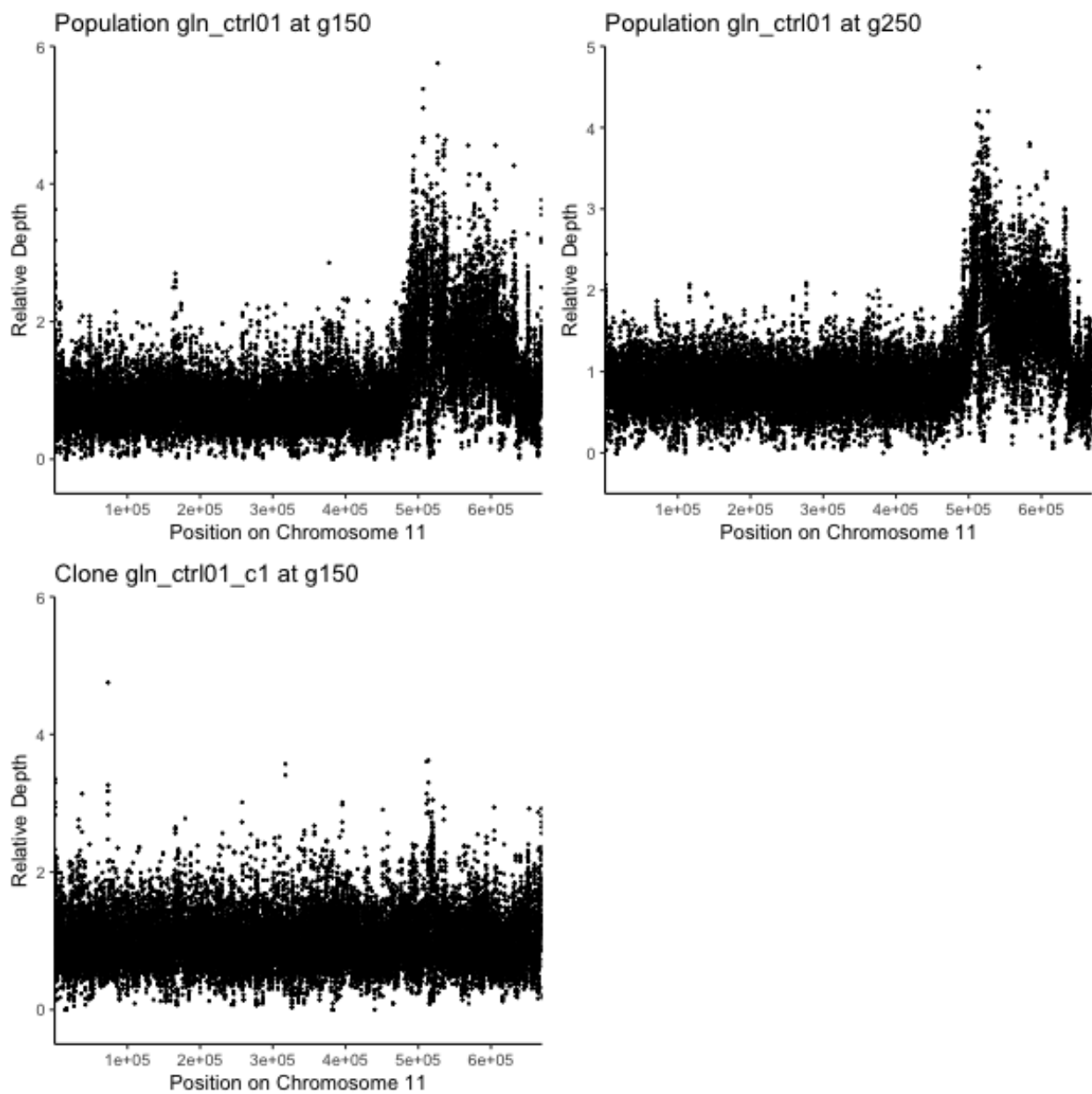


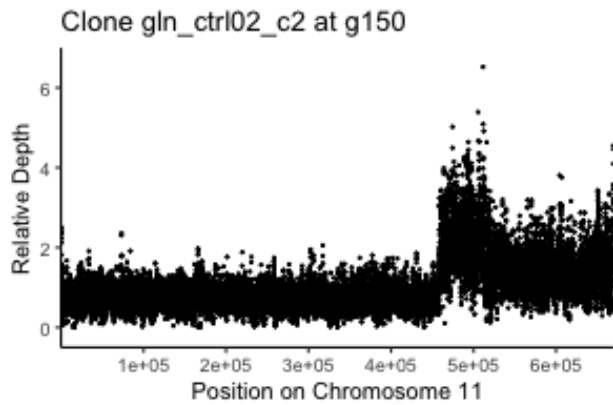
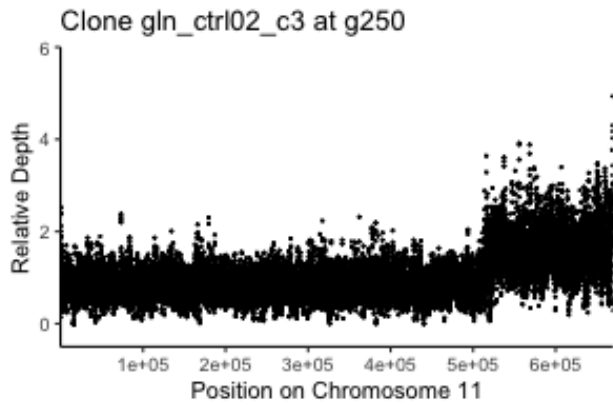
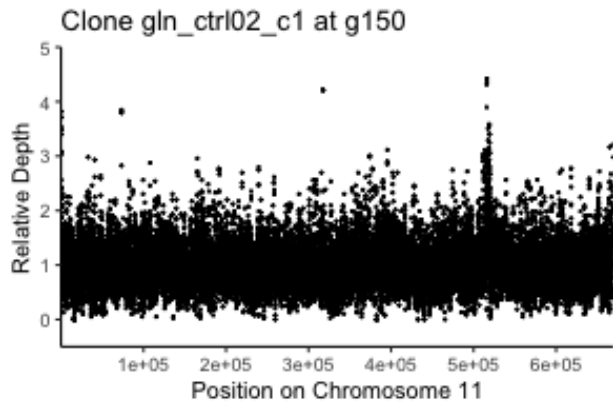
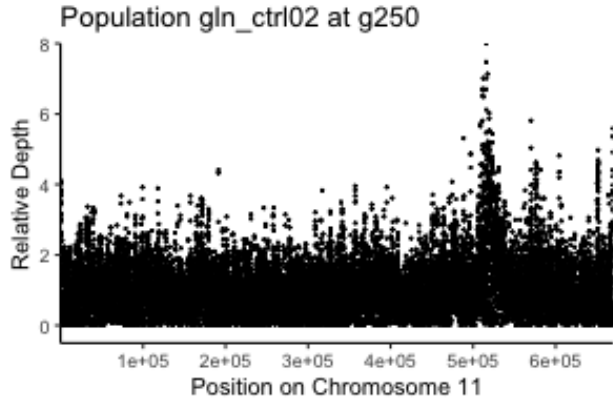
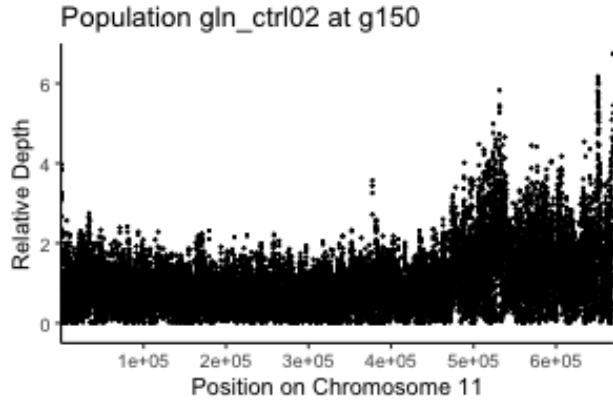
## 9 Glutamine-limited population 09



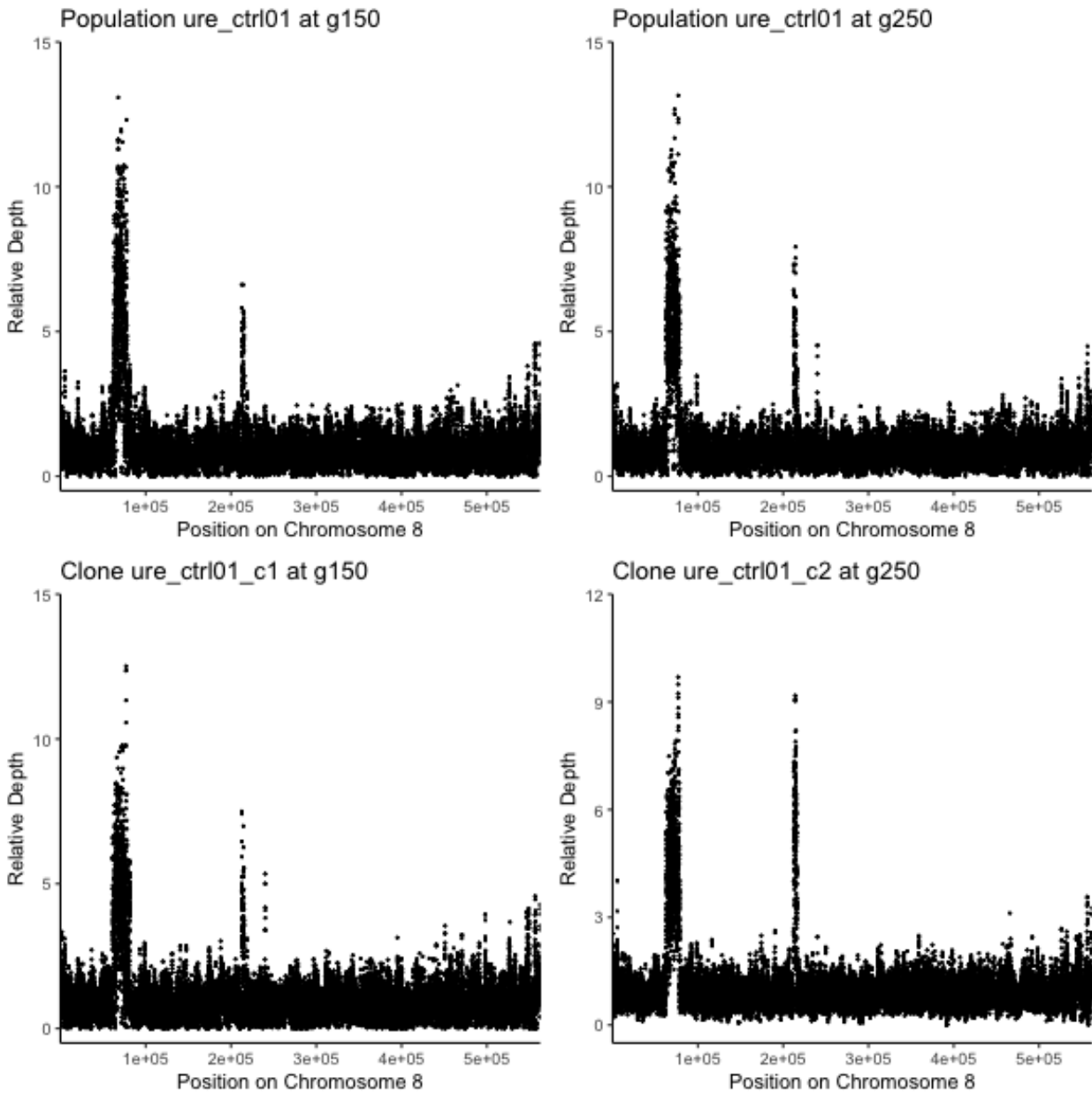


## 10 Glutamine-limited control populations



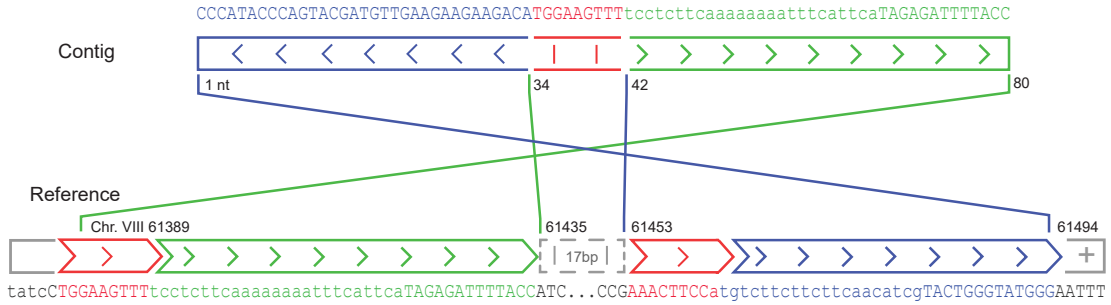


# 11 Urea-limited 1 copy control population



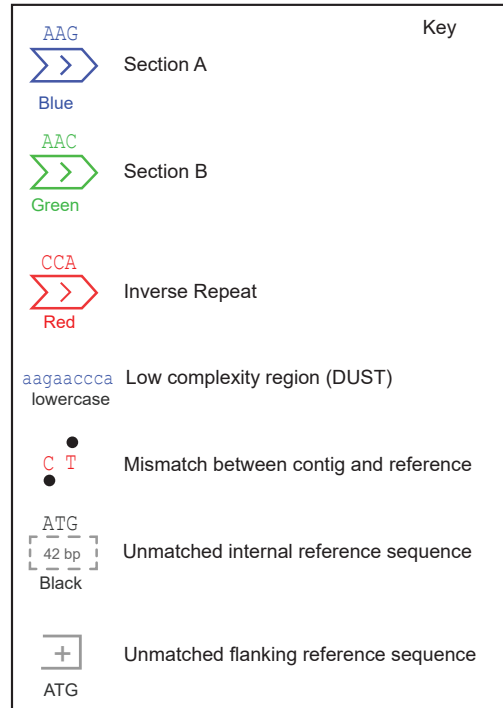
Sample: Ure\_ctr101\_c1  
 Contig: 1 of 1

Locus: NPR3  
 Supporting Split Reads: 16  
 Proposed Event: CNV, ODIRA



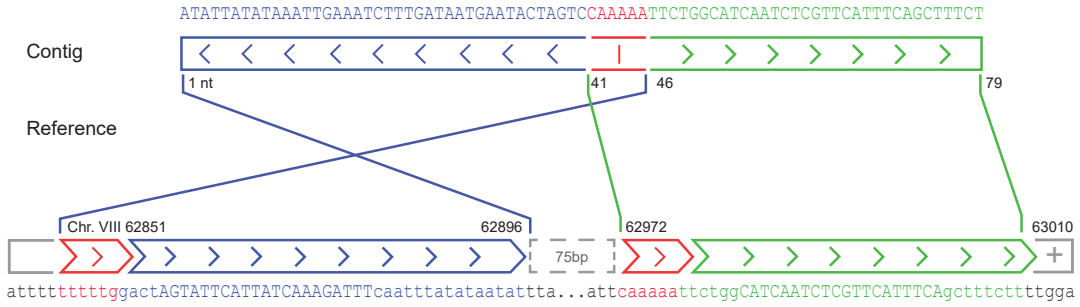
Contig  
 AACAG GTGCT GCGGG CTCGA GCGCT GATCT CTCAC ATCAA  
 TCAAC CGCTG TCGAT GAAGA TTCAC TGGAT ATACC

Reference  
 tatcC **TGGAAGTTT**tctct tcaaaa aaaaa ttca ttcaT  
 AGAGA **TTTTA** CCATC CTGCA ACATT GCCGA **AACTT** CCatg  
 tcttc ttctt caaca tcgTA CTGGG TAIGG GAATT T



Sample: Ure\_ctr101\_c2  
 Contig: 1 of 1

Locus: SPO11  
 Supporting Split Reads: 4  
 Proposed Event: CNV, ODIRA

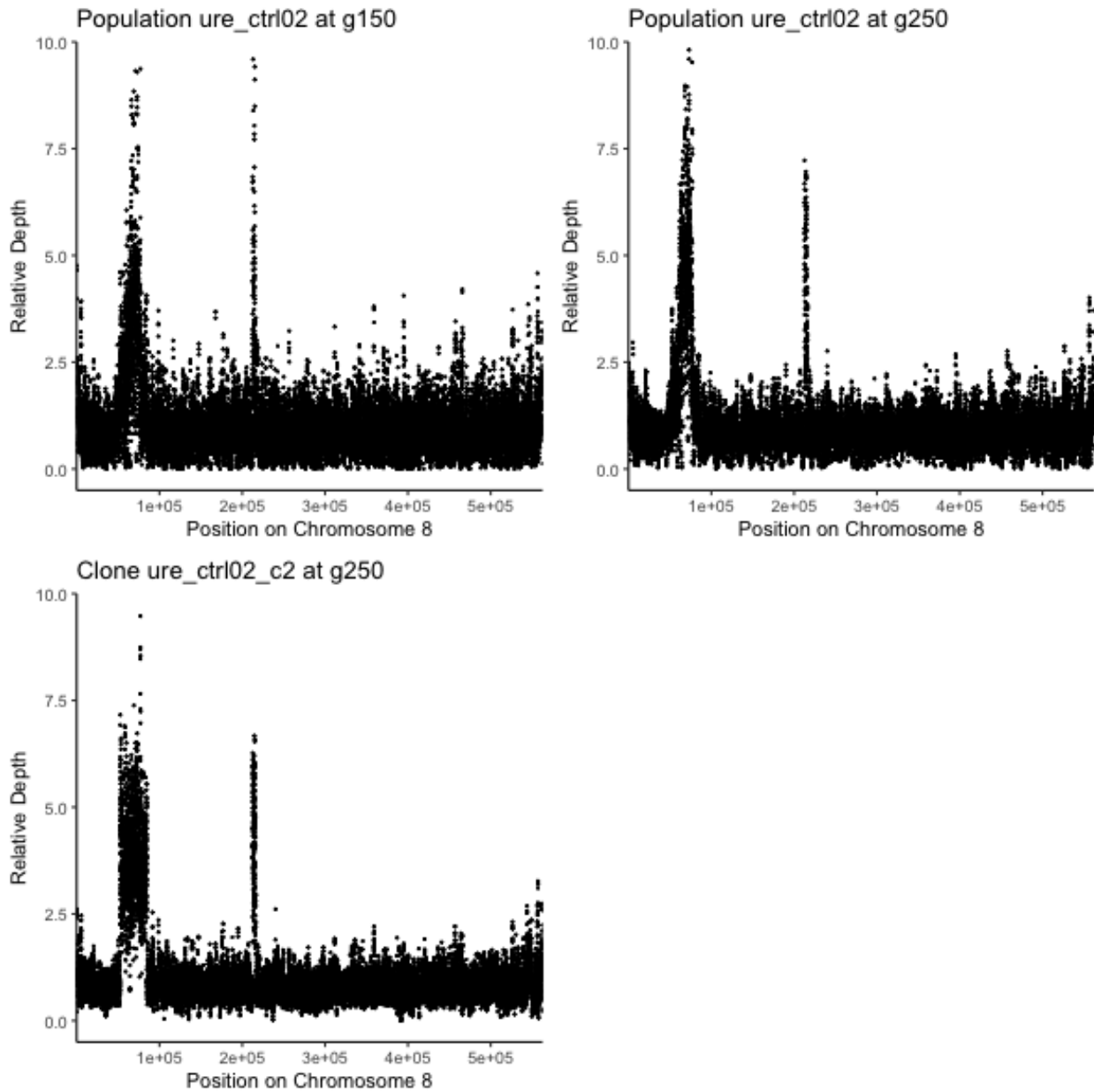


Contig  
 ATATT ATATA AATTG AAATC TTTGA TAATG AATAC TAGTC  
 CAAAA ATTCT GGCAT CAATC TCGTT CATTTCAGCT TTCT

Reference  
 atttt ttttt ggact AGTAT TCATT ATCAA AGATT Tcaat  
 ttata taata tttaa ATGTA ACcgt tttca attct tgaaa  
 aacat ttttt ataaa gCAAC AGCTC CCATT CTTAT TCATT  
 tgtat tcaaa aattc tggCA TCAAT CTCGTTCA TTTCA  
 gcttt ctttt gga

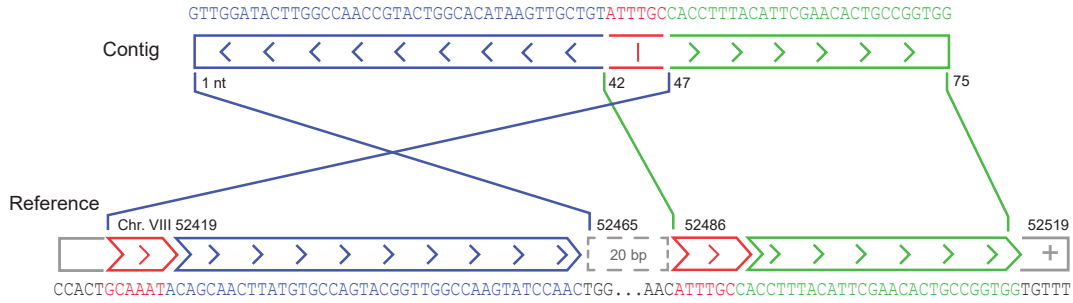
Key	
	Section A
Blue	
	Section B
Green	
	Inverse Repeat
Red	
aagaaccCa lowercase	Low complexity region (DUST)
	Mismatch between contig and reference
	Unmatched internal reference sequence
Black	
	Unmatched flanking reference sequence
ATG	

# 12 Urea-limited 2 copy control population



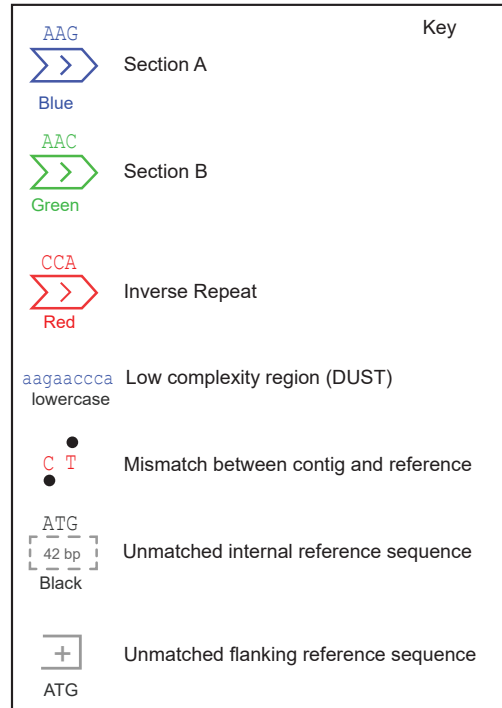
Sample: Ure\_ctr102\_c2  
 Contig: 1 of 2

Locus: Rim101  
 Supporting Split Reads: 17  
 Proposed Event: CNV, ODIRA



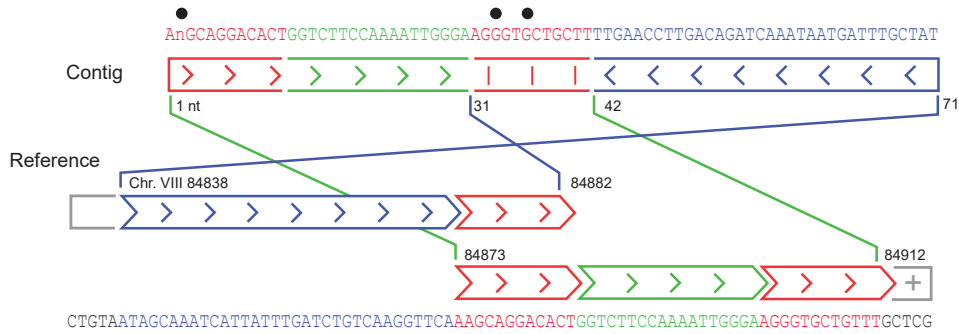
Contig  
 GTTGG ATACT TGGCC AACCG TACTG GCACA TAAGT TGCTG  
 TATTT GCCAC CTTTA CATTG GAACA CTGCC GGTGG

Reference  
 CCACT GCAAA TACAG CAACT TATGT GCCAG TACGG TTGGC  
 CAAGT ATCCA ACTGG TCCTT CGCTT ACTGA ACATT TGCCA  
 CCTTT ACATT CGAAC ACTGC CGGTG GTGTT T



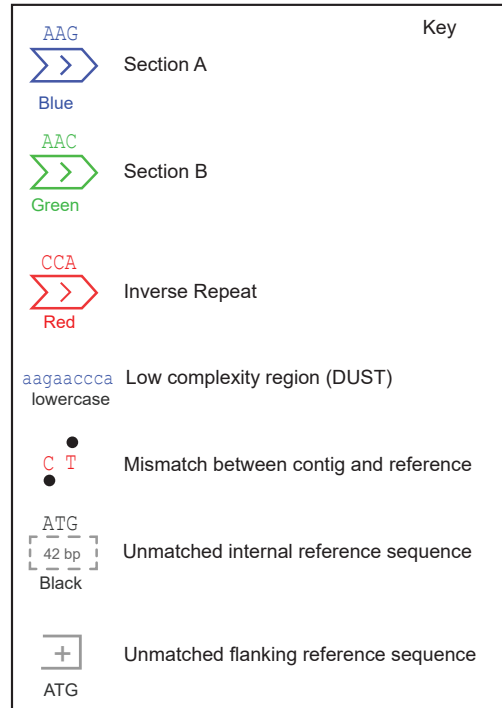
Sample: Ure\_ctr102\_c2  
 Contig: 2 of 2

Locus: Intergenic YAP3  
 Supporting Split Reads: 27  
 Proposed Event: CNV, ODIRA



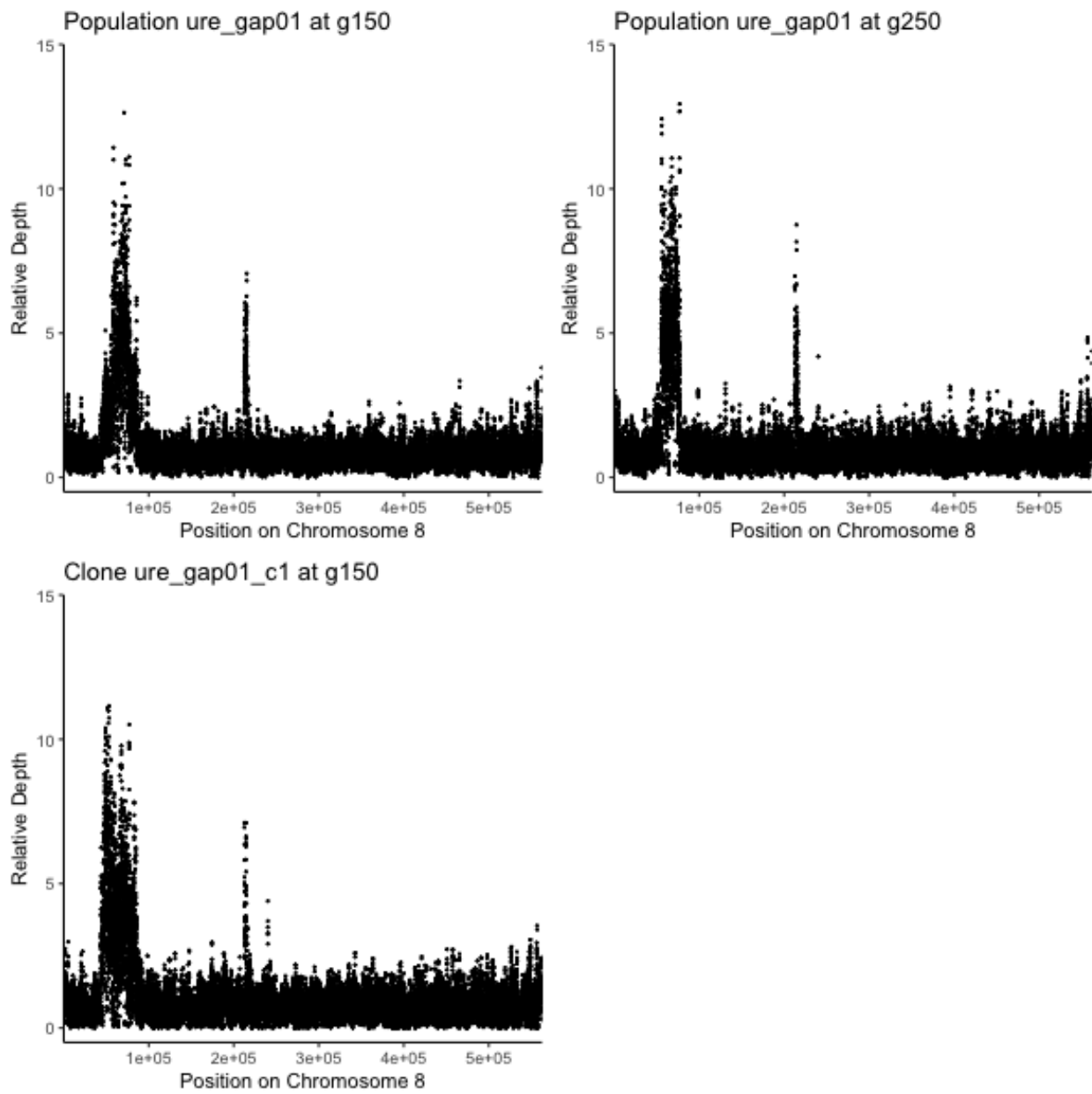
Contig  
 AnGCA GGACA CTGGT CTTCC AAAAT TGGGA AGGGT GCTGC  
 TTTTG AACCT TGACA GATCA AATAA TGATT TGCTA T

Reference  
 CTGTA ATAGC AAATC ATTAT TTGAT CTGTC AAGGT TCAAA  
 GCAGG AACTT GGTCT TCCAA AATTG GGAAG GGTGC TGTTT  
 GCTCG



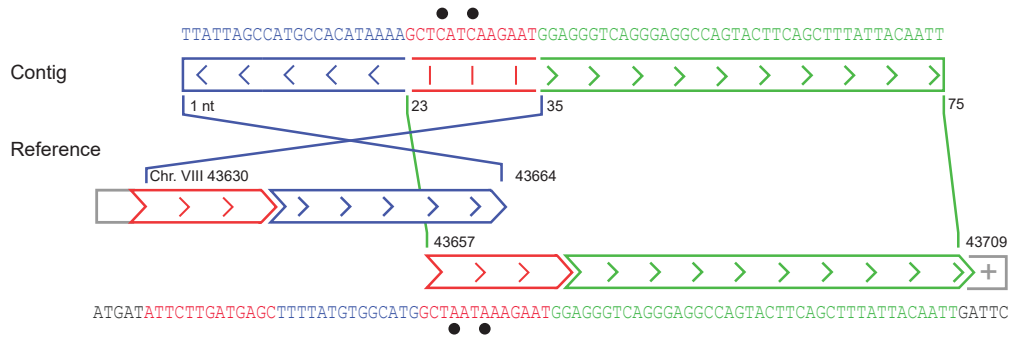


# 13 Urea-limited population 01



Sample: Ure\_01\_c1  
 Contig: 1 of 1

Locus: ECM29  
 Supporting Split Reads: 9  
 Proposed Event: CNV, ODIRA

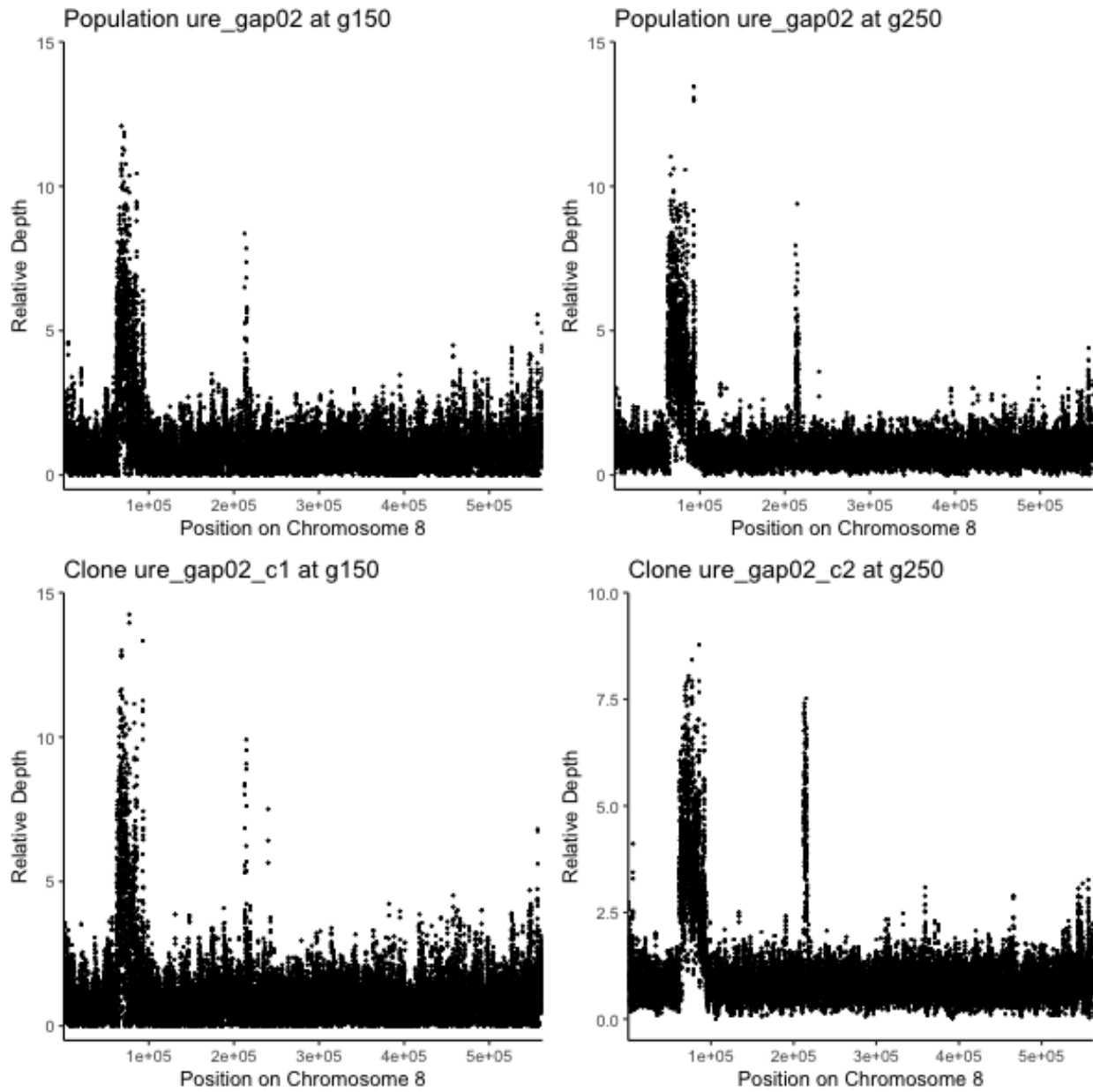


Contig  
 TTATT AGCCA TGCCA CATAA AAGCT CATCA AGAAT GGAGG  
 GTCAG GGAGG CCAGT ACTTC AGCTT TATTA CAATT

Reference  
 ATGAT ATTCT TGATG AGCTT TTATG TGGCA TGGCT AATAA  
 AGAAT GGAGG GTCAG GGAGG CCAGT ACTTC AGCTT TATTA  
 CAATT GATTTC

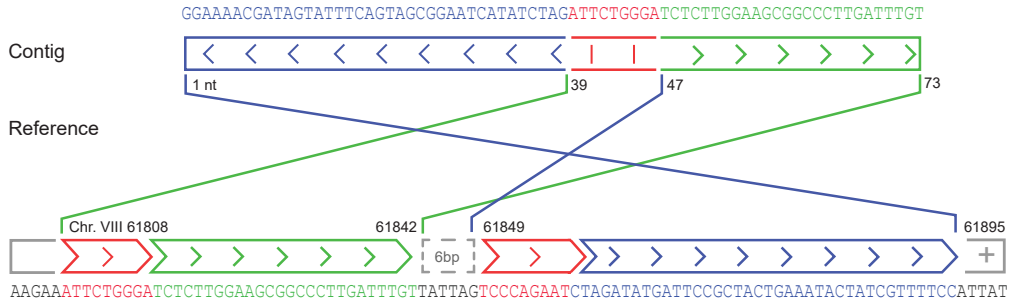
Key	
	Section A
Blue	
	Section B
Green	
	Inverse Repeat
Red	
aagaaccCa lowercase	Low complexity region (DUST)
	Mismatch between contig and reference
	Unmatched internal reference sequence
Black	
	Unmatched flanking reference sequence
ATG	

## 14 Urea-limited population 02



Sample: Ure\_02\_c2  
 Contig: 1 of 1

Locus: NPR3  
 Supporting Split Reads: 15  
 Proposed Event: CNV, ODIRA

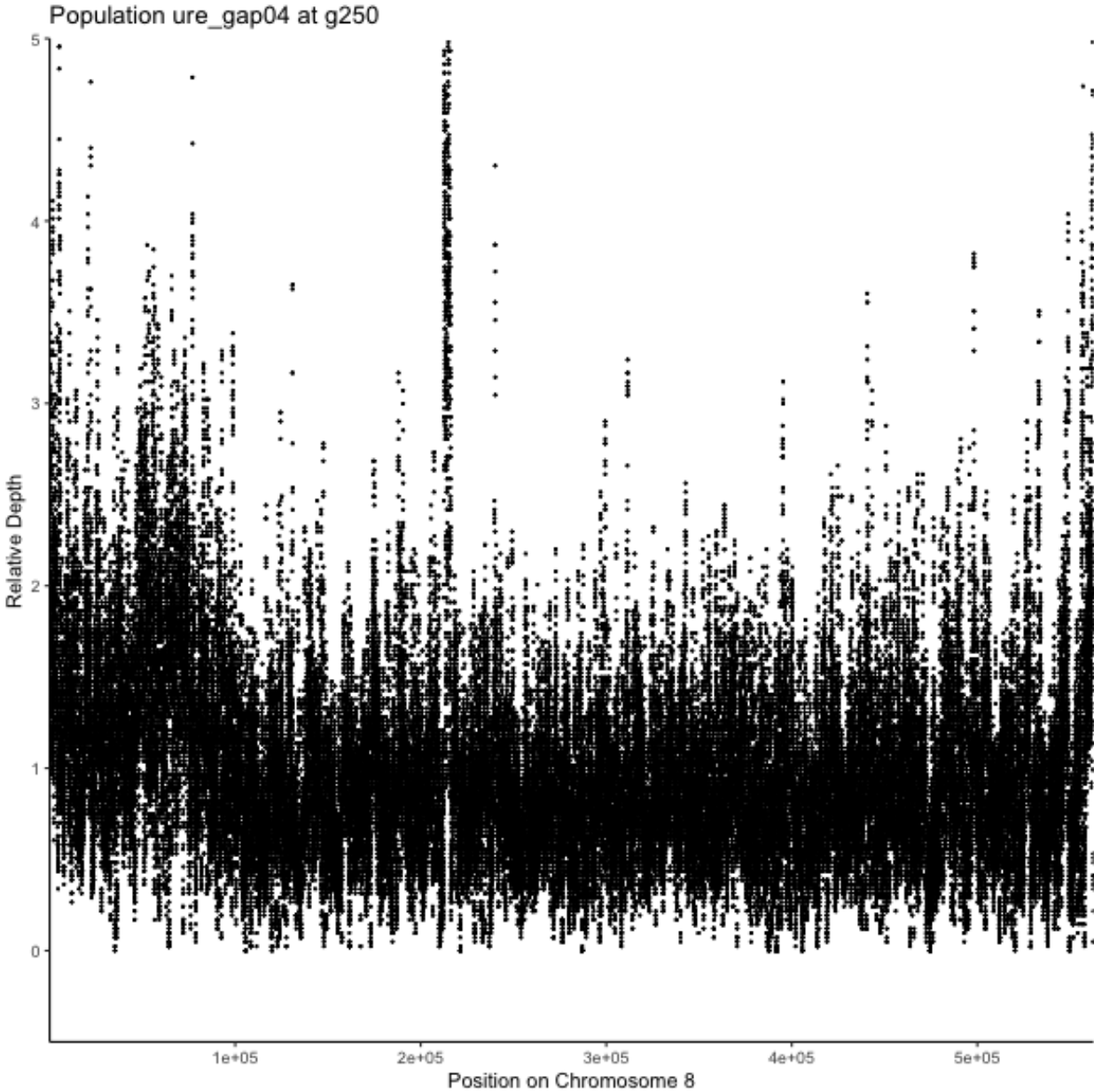


Contig  
 GGAAA ACGAT AGTAT TTCAG TAGCG GAATC ATATC TAGAT  
 TCTGG GATCT CTTGG AAGCG GCCCT TGATT TGT

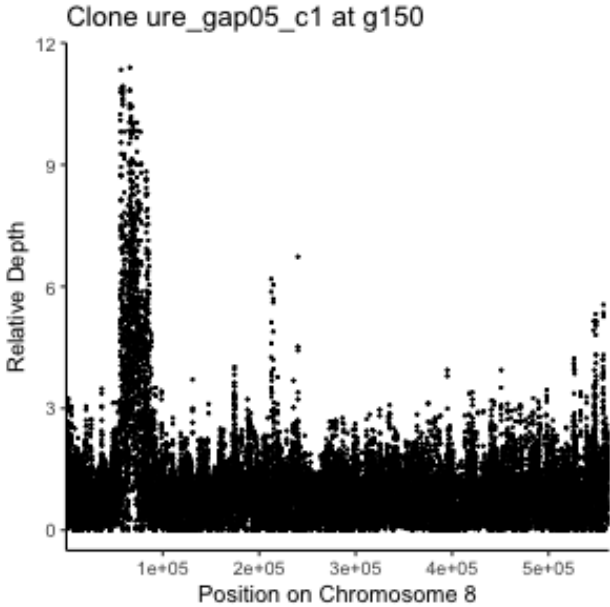
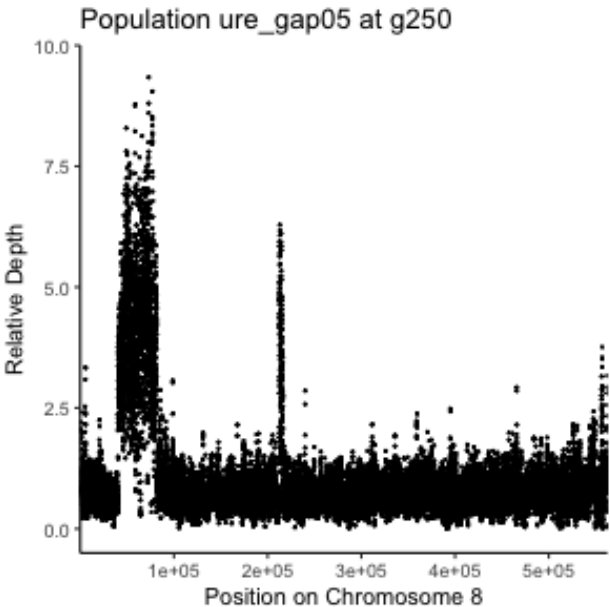
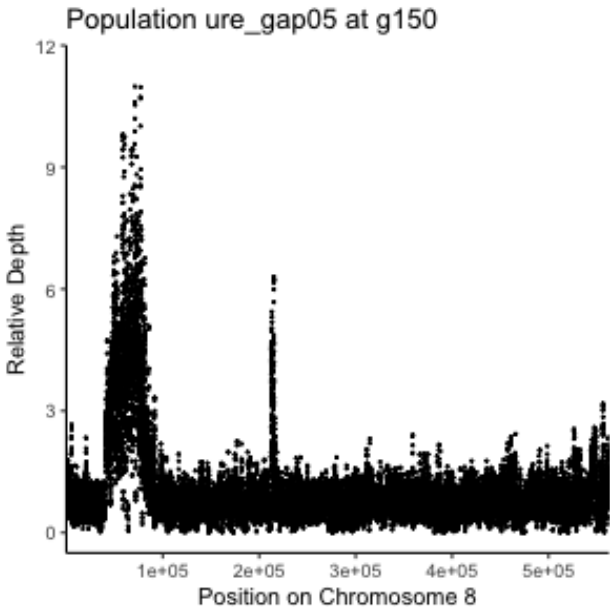
Reference  
 AAGAA ATTCT GGGAT CTCTT GGAAG CGGCC CTGA TTTGT  
 TATTA GTCCC AGAAT CTAGA TATGA TTCCG CTAAT GAAAT  
 ACTAT CGTTT TCCAT TAT

Key	
AAG Blue >>	Section A
AAC Green >>	Section B
CCA Red >>	Inverse Repeat
aagaaccCa lowercase	Low complexity region (DUST)
C T	Mismatch between contig and reference
ATG [ 42 bp ] Black	Unmatched internal reference sequence
+ ATG	Unmatched flanking reference sequence

# 15 Urea-limited population 04

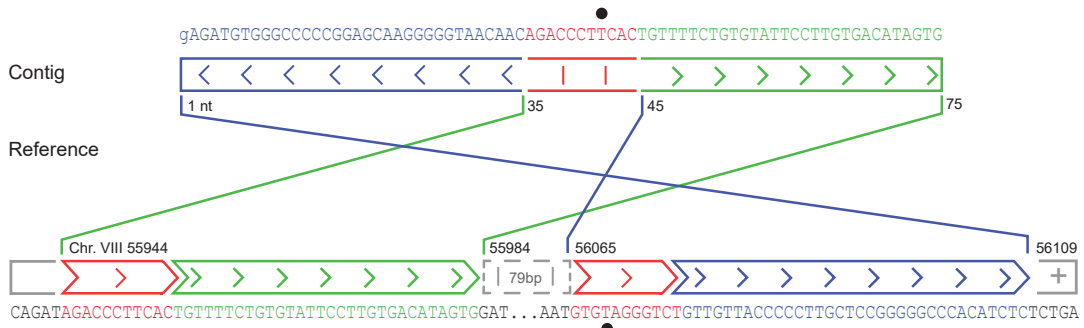


# 16 Urea-limited population 05



Sample: Ure\_05\_c1  
 Contig: 1 of 1

Locus: Intergenic SNF6, RIM4  
 Supporting Split Reads: 24  
 Proposed Event: CNV, ODIRA

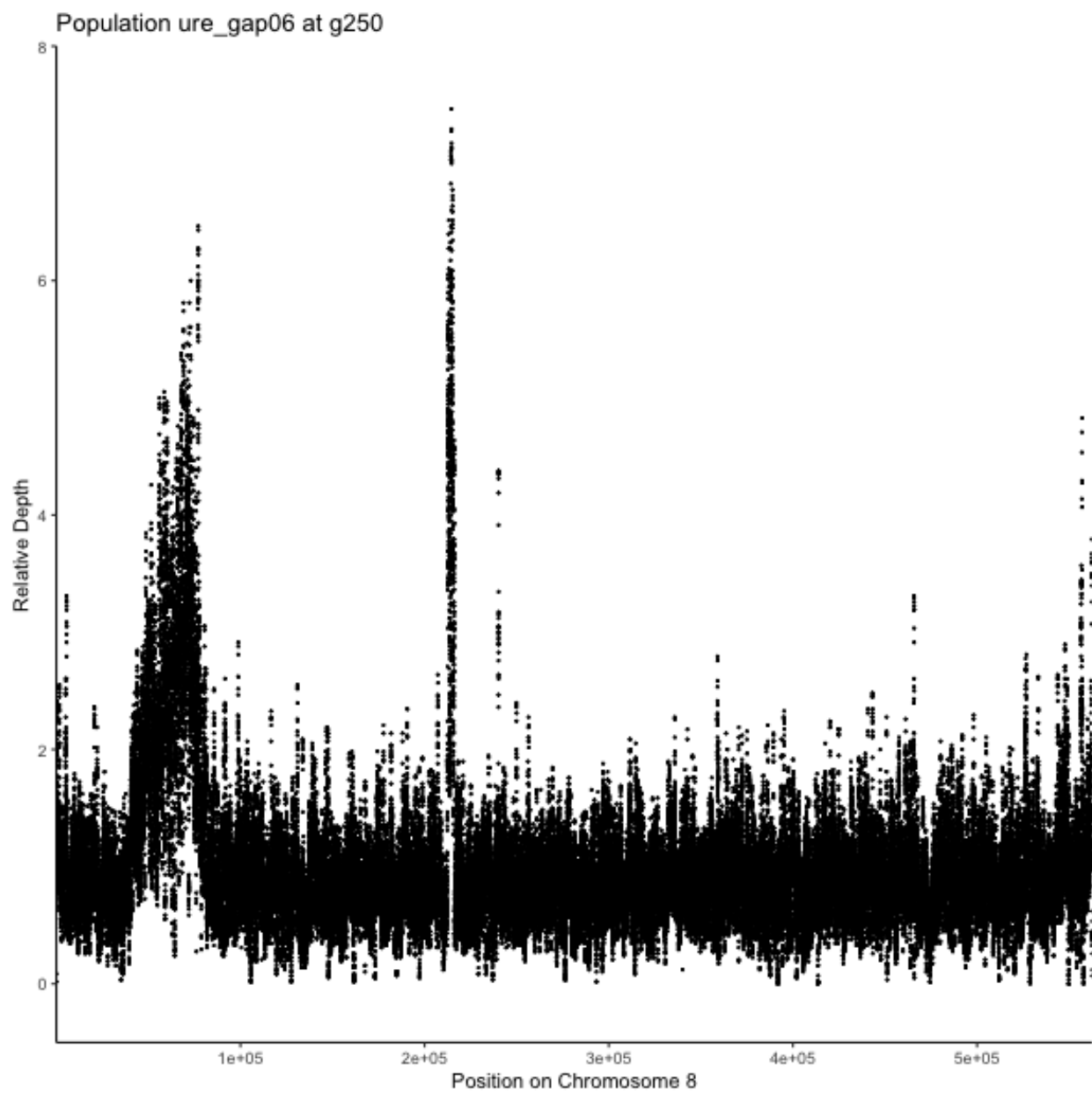


Contig  
 gAGAT GTGGG CCCCC GGAGC AAGGG GGTAA CAACA GACCC  
 TTCAC TGTTT TCTGT GTATT CCTTG TGACA TAGTG

Reference  
 CAGAT AGACC CTTC A CTGTT TTCTG TGTAT TCCTT GTGAC  
 ATAGT GGATT TGTGC AGCTA CTGCT TATAG GAAGC AGTGC  
 CTGCA AAACA ATTCA TTCGT TGGTT GATGT GGCGC GCTGA  
 CTGAA TGTGT AGGGT CTGTT GTTAC CCCCT TGCTC CGGGG  
 GCCCA CATCT CTCTG A

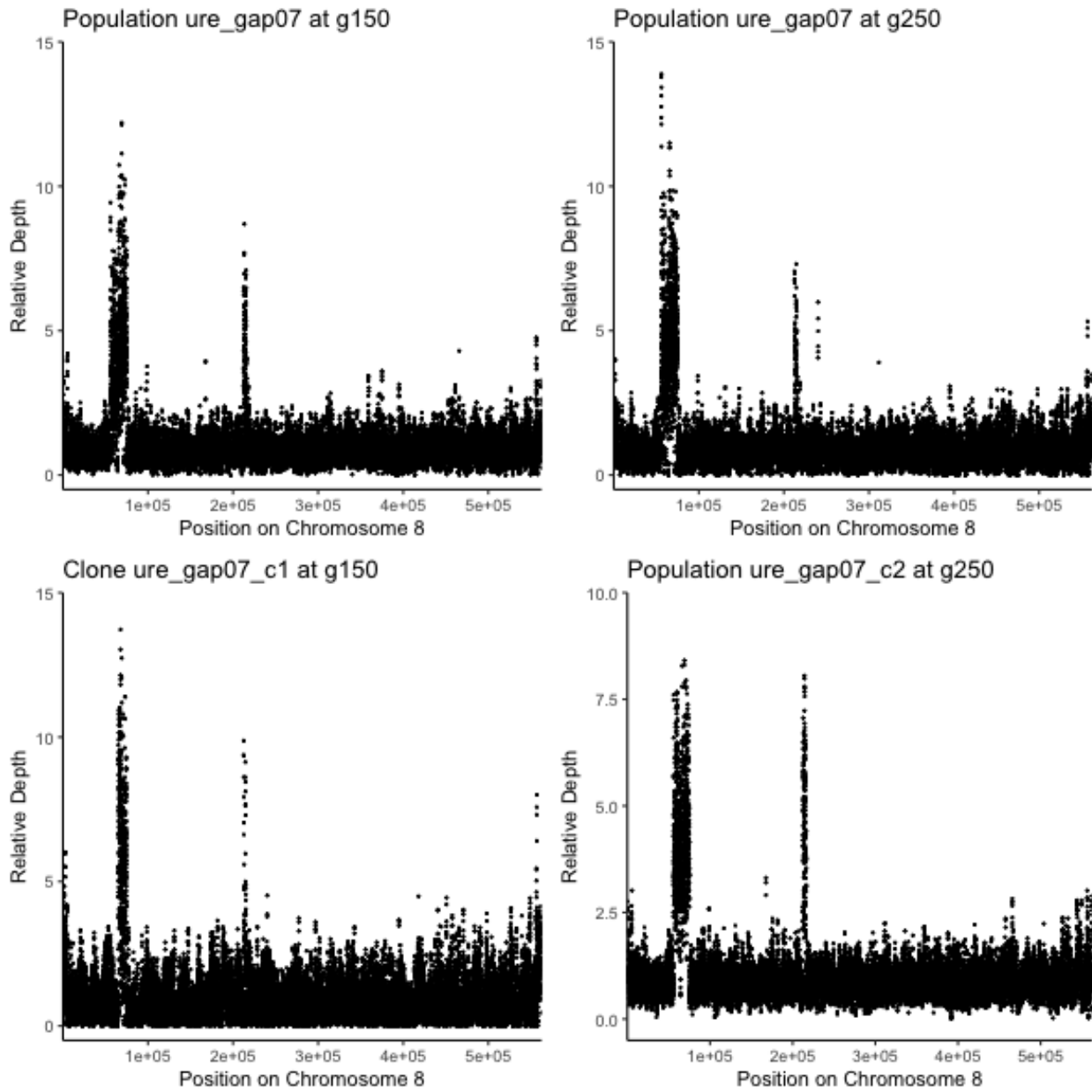
Key	
	Section A
Blue	
	Section B
Green	
	Inverse Repeat
Red	
aagaaccCa lowercase	Low complexity region (DUST)
	Mismatch between contig and reference
	Unmatched internal reference sequence
Black	
	Unmatched flanking reference sequence
ATG	

## 17 Urea-limited population 06



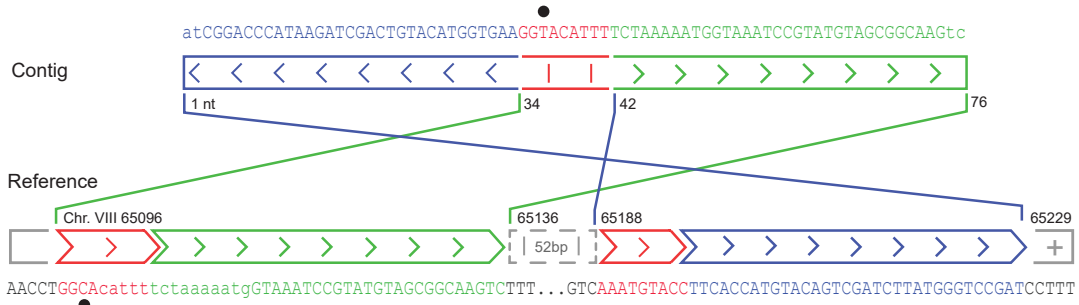


# 18 Urea-limited population 07



Sample: Ure\_07\_c1  
 Contig: 1 of 1

Locus: AIM17  
 Supporting Split Reads: 24  
 Proposed Event: CNV, ODIRA



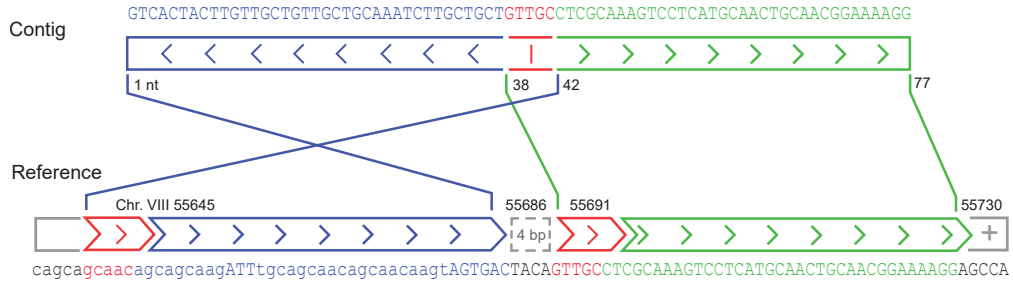
Contig  
 atCGG ACCCA TAAGA TCGAC TGTAC ATGGT GAAGG TACAT  
 TTTCT AAAAA TGGTA AATCC GTATG TAGCG GCAAG tc

Reference  
 AACCT GGCAC atttt ctaaa aatgG TAAAT CCGTA TGTAG  
 CCGCA AGTCT TTATT GGCAT AATGG GCATT AACAC TTGTC  
 GCTTG GGATG CATTC ACGTC AAATG TACCT TCACC ATGTA  
 CAGTC GATCT TATGG GTCCG ATCCT TT

Key	
	Section A
Blue	
	Section B
Green	
	Inverse Repeat
Red	
aagaaccCa lowercase	Low complexity region (DUST)
	Mismatch between contig and reference
ATG [ 42 bp ] Black	Unmatched internal reference sequence
 ATG	Unmatched flanking reference sequence

Sample: Ure\_07\_c2  
 Contig: 1 of 2

Locus: SNF6  
 Supporting Split Reads: 13  
 Proposed Event: CNV, ODIRA



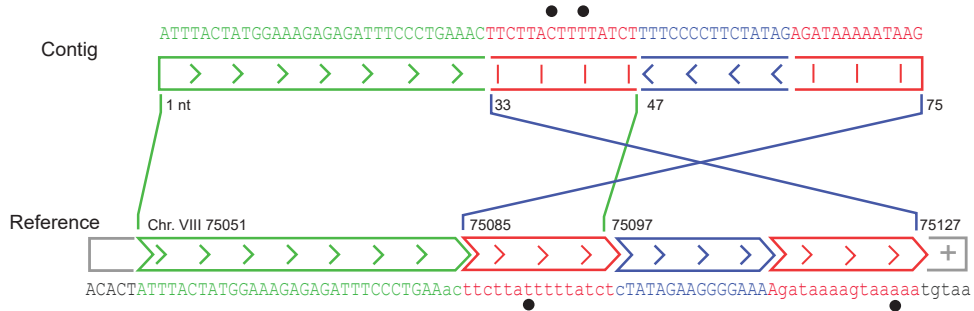
Contig  
 GTCAC TACTT GTTGC TGTTG CTGCA AATCT TGCTG CTGTT  
 GCCTC GCAA GTCCT CATGC AACTG CAACG GAAA GG

Reference  
 cagca gcaac agcag caagA TTtgc agcaa cagca acaag  
 tAGTG ACTAC AGTTG CCTCG CAAAG TCCTC ATGCA ACTGC  
 AACGG AAAAG GAGCC A

Key	
AAG Blue >>	Section A
AAC Green >>	Section B
CCA Red >>	Inverse Repeat
aagaaccCa lowercase	Low complexity region (DUST)
C T	Mismatch between contig and reference
ATG [ 42 bp ] Black	Unmatched internal reference sequence
+ ATG	Unmatched flanking reference sequence

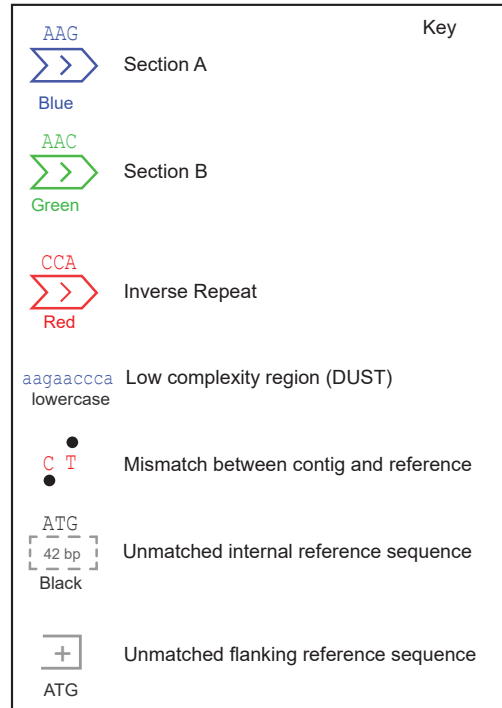
Sample: Ure\_07\_c2  
 Contig: 2 of 2

Locus: Intergenic YHL015W-A, RPS20  
 Supporting Split Reads: 12  
 Proposed Event: CNV, ODIRA

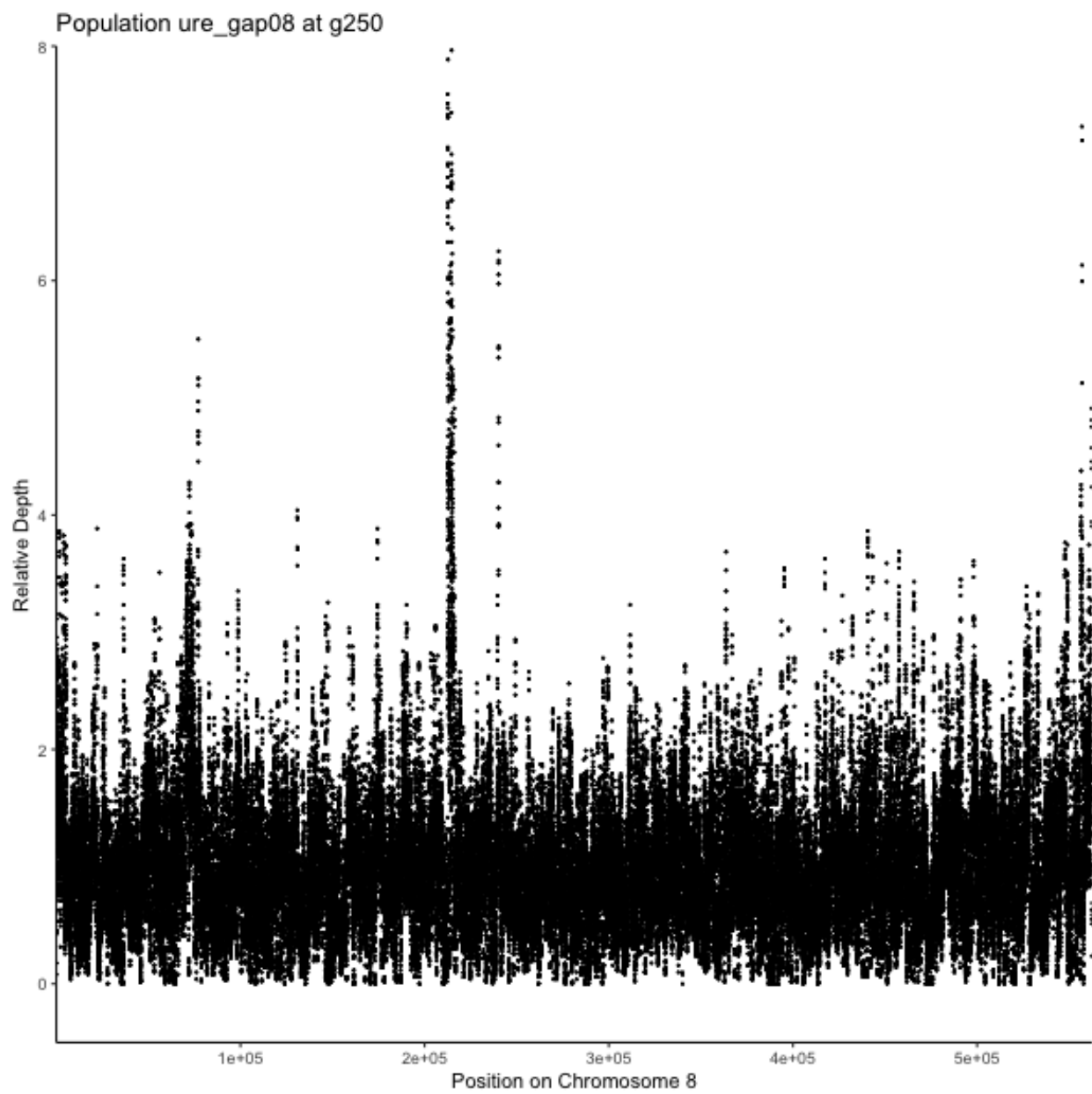


Contig  
 ATTTA CTATG GAAAG AGAGA TTTCC CTGAA ACTTC TTACT  
 TTTAT CTTT CCCCT TCTAT AGAGA TAAAA ATAAG

Reference  
 A C A C T A T T T A C T A T G G A A A G A G A G A T T T C C T G A A A C T T C T T A C T T T T A T C T T T T C C C C T C T A T A G A A G G G G A A A A G a t a a a a g t a a a a t g t a a  
 t t a t t t t t a t c t c T A T A G A A G G G G A A A A g a t a a a a g t a a a a t g t a a  
 a a t g t a a

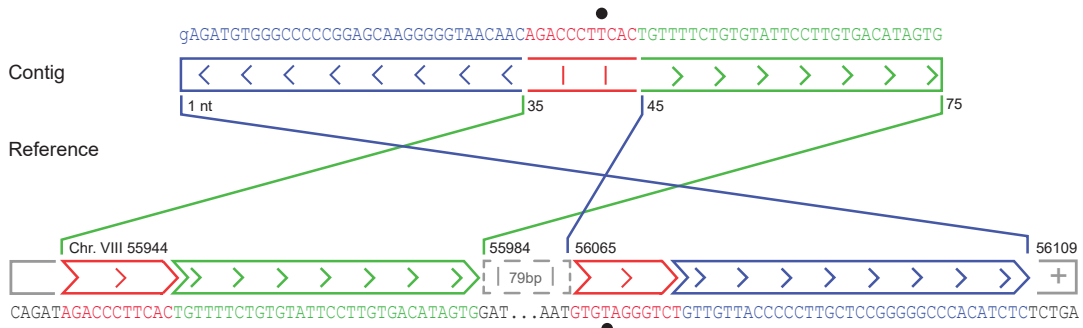


## 19 Urea-limited population 08



Sample: Ure\_05\_c1  
 Contig: 1 of 1

Locus: Intergenic SNF6, RIM4  
 Supporting Split Reads: 24  
 Proposed Event: CNV, ODIRA



Contig  
 gAGAT GTGGG CCCCC GGAGC AAGGG GGTAA CAACA GACCC  
 TTCAC TGTTT TCTGT GTATT CCTTG TGACA TAGTG

Reference  
 CAGAT AGACC CTTC A CTGTT TTCTG TGTAT TCCTT GTGAC  
 ATAGT GGATT TGTGC AGCTA CTGCT TATAG GAAGC AGTGC  
 CTGCA AAACA ATTCA TTCGT TGGTT GATGT GGCGC GCTGA  
 CTGAA TGTGT AAGGT CTGTT GTTAC CCCCT TGCTC CGGGG  
 GCCCA CATCT CTCTG A

Key	
AAG Blue >>	Section A
AAC Green >>	Section B
CCA Red >>	Inverse Repeat
aagaaccCa lowercase	Low complexity region (DUST)
C T	Mismatch between contig and reference
ATG [ 42 bp ] Black	Unmatched internal reference sequence
+ ATG	Unmatched flanking reference sequence