Many of alignments terminate at the two arrowed regions, which suggests an assembly error. The revised contig perfectly matched the ce10 reference in the x-axis.

| Assembler, read set, and contig with an error | Revised region | chrI | start | end |
|---------------------------------------------|---------------|------|-------|-----|
| FALCON, PacBio, 000005F                     |               | 4,400,693 | 4,425,111 |
Alignments of raw reads to the focal VC2010 contig are partial in the arrowed region, implying the presence of an undesirable region in the contig. Indeed, the contig before revision has false positive duplicated regions, while the revised contig perfectly matched the ce10 reference in the x-axis.
Blue disks in the arrowed region show insertions into the contig, implying a missing part in the VC2010 genome. Indeed, the contig before revision had a missing part, and the revised contig perfectly matched the ce10 reference.
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Alignments of raw reads to the focal VC2010 contig are partial in the arrowed region, implying the presence of an undesirable region in the contig. Indeed, the contig before revision has false positive duplicated regions, while the revised contig perfectly matched the ce10 reference in the x-axis.

|   | Assembler, read set, and contig with an error | Revised region | chromosome | start | end |
|---|-------------------------------------------|----------------|------------|-------|-----|
|   | miniasm, Pacbio, vc2010.miniasm.quiver.017 | chrII         | 9,919,928  | 9,926,945 |
Blue disks in the arrowed regions show insertions into the contig, implying a missing part in the VC2010 genome. The revised contig had a tandem repeat expansion longer than that in the ce10 reference in the x-axis.
Blue disks in the arrowed region show insertions into the contig, implying a missing part in the VC2010 genome. The revised contig had a tandem repeat expansion slightly shorter than that in the ce10 reference.
Blue disks in the arrowed region show insertions into the contig, implying a missing part in the VC2010 genome. The revised contig had a tandem repeat expansion longer than that in the ce10 reference.
Blue disks in the arrowed region show insertions into the contig, implying a missing part in the VC2010 genome. The revised contig is identical to its corresponding region in the N2 genome and has separated tandem repeat expansions.
Alignments of raw reads to the focal VC2010 contig are partial in the arrowed region, implying the presence of an undesirable region in the contig. Indeed, the contig before revision has false positive duplicated regions, while the revised contig perfectly matched the ce10 reference in the x-axis.
The revised contig perfectly matched the ce10 reference in the x-axis.
Alignments of raw reads to the focal VC2010 contig are partial in the arrowed region, implying the presence of an undesirable region in the contig. Indeed, the contig before revision has false positive duplicated regions, while the revised contig perfectly matched the ce10 reference in the x-axis.
Blue disks in the arrowed region show insertions into the contig, implying a missing part in the VC2010 genome. The revised contig perfectly matched the ce10 reference in the x-axis.
Alignments of raw reads to the focal VC2010 contig are partial in the arrowed region, implying the presence of an undesirable region in the contig. Indeed, the contig before revision has false positive duplicated regions, while the revised contig perfectly matched the ce10 reference in the x-axis.
Alignments of raw reads to the focal VC2010 contig are partial in the arrowed region, implying the presence of an undesirable region in the contig. Indeed, the contig before revision has false positive duplicated regions, while the revised contig perfectly matched the ce10 reference in the x-axis.
Alignments of raw reads to the focal VC2010 contig are partial in the arrowed region, implying the presence of an undesirable region in the contig. Indeed, the contig before revision has a false positive insertion, while the revised contig perfectly matched the ce10 reference in the x-axis.
Alignments of raw reads to the focal VC2010 contig are partial in the arrowed region, implying the presence of an undesirable region in the contig. Indeed, the contig before revision has a false positive insertion, while the revised contig perfectly matched the ce10 reference in the x-axis.
Blue disks in the arrowed region show insertions into the contig, implying a missing part in the VC2010 genome. The revised contig had a longer tandem repeat expansion in the first half and one more genome duplication in the latter half than the previous version had.

| Chromosome | Start     | End       |
|------------|-----------|-----------|
| chrX       | 1,663,381 | 1,712,186 |
Blue disks in the arrowed regions show insertions into the contig, implying a missing part in the VC2010 genome. In the revised contig, tandem repeat expansions are corrected properly.
Blue disks in the arrowed region show insertions into the contig, implying a missing part in the VC2010 genome. In the revised contig, tandem repeat expansions are corrected slightly.