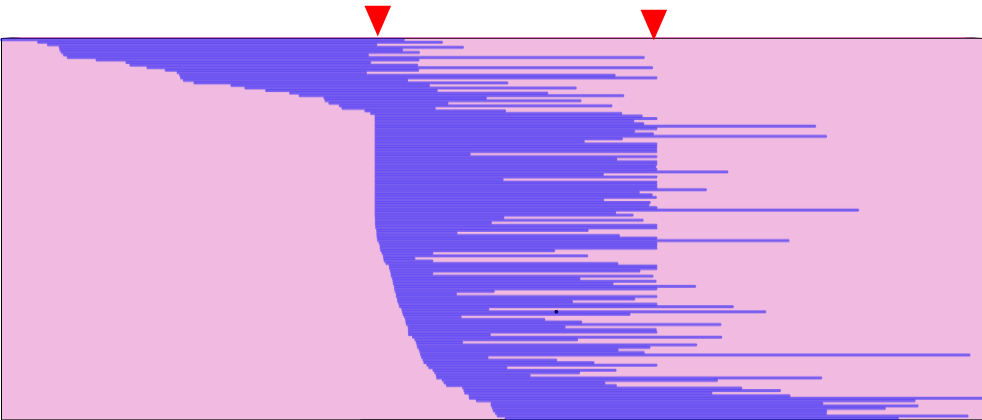


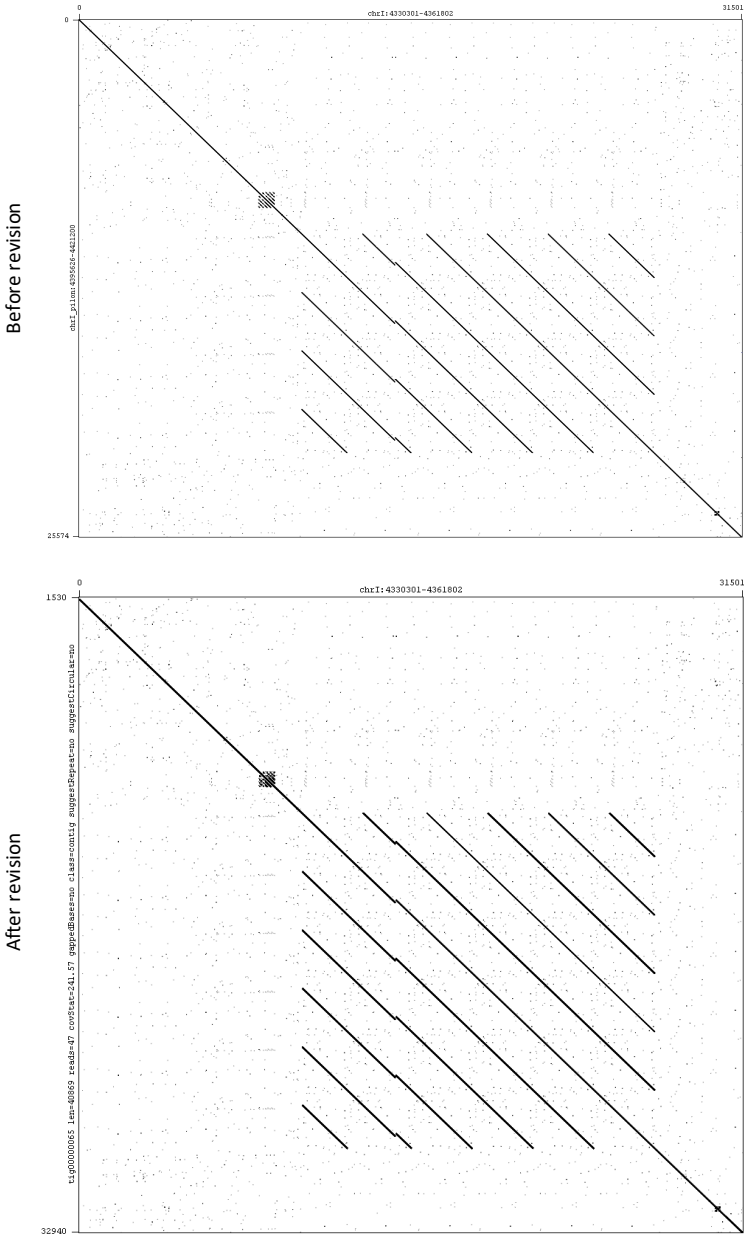
Assembler, read set, and contig with an error	FALCON, PacBio, 000005F
--	-------------------------

Revised	chromosome	start	end
region	chr1	4,400,693	4,425,111

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.



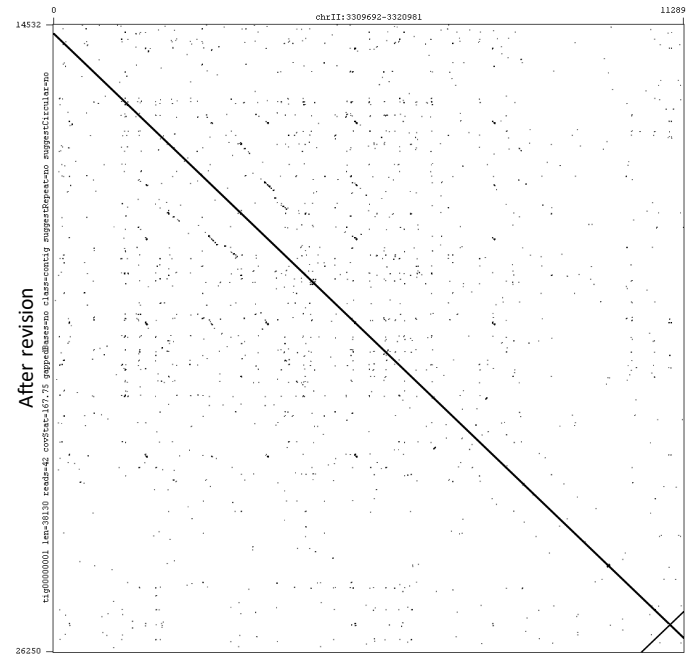
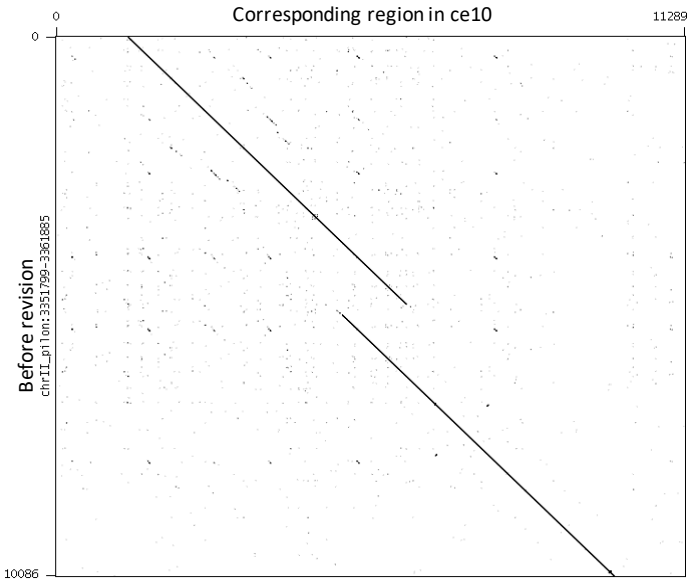
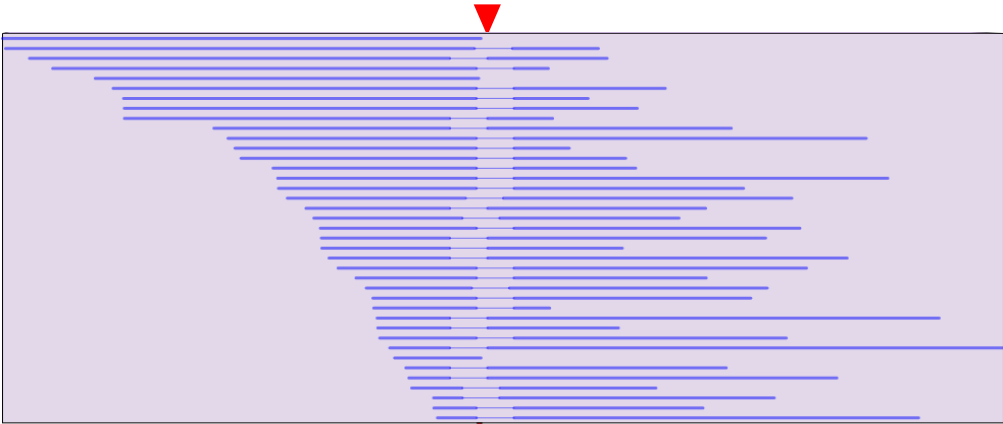
Corresponding region in ce10



Assembler, read set, and contig with an error	miniasm, PacBio, vc2010.miniasm.quiver.002
--	---

Revised	chromosome	start	end
region	chrII	3,352,028	3,360,235

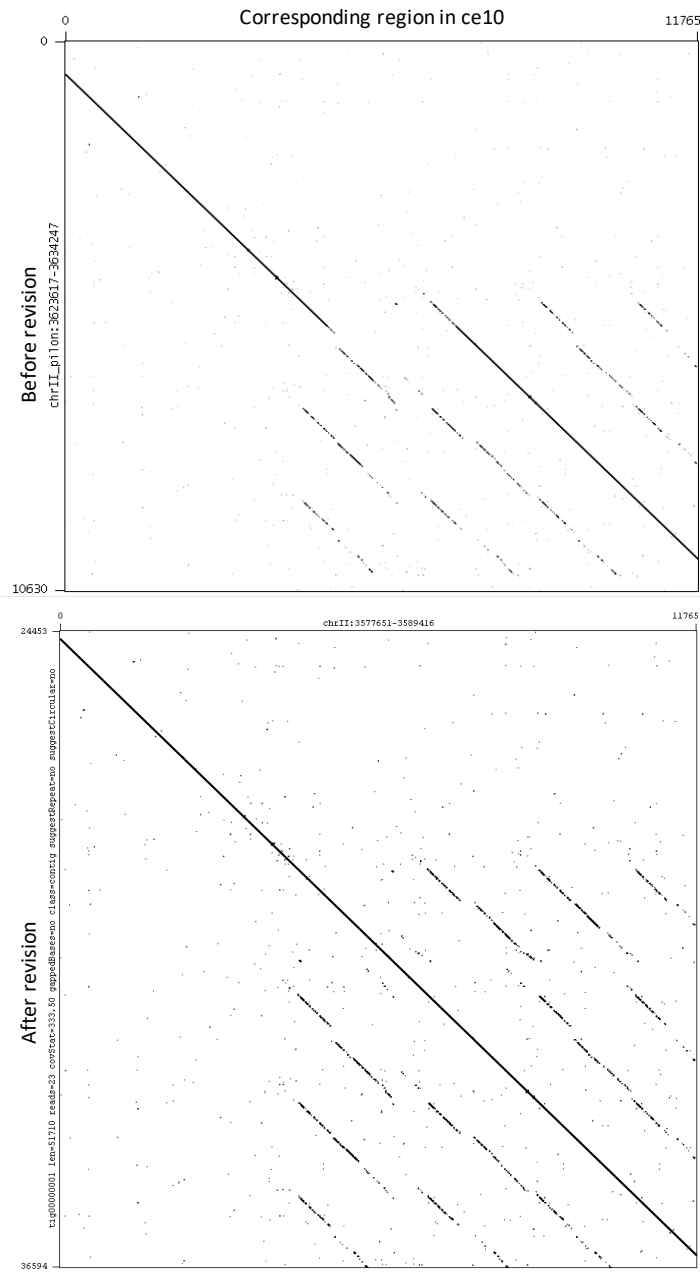
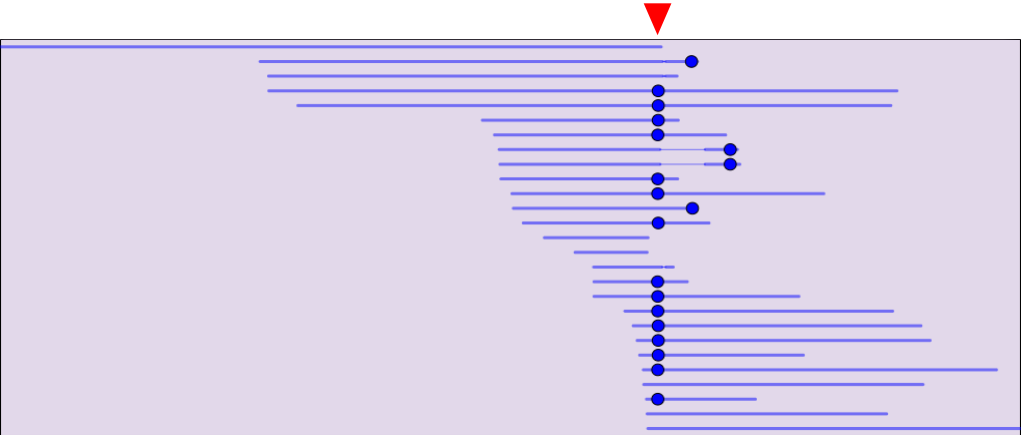
Alignments of raw reads to the focal VC2010 contig are partial in the arrowed region, implying the presence of an undesirable region in the contig. Indeed, the contig before revision has false positive duplicated regions, while the revised contig perfectly matched the ce10 reference in the x-axis.



Assembler, read set, and contig with an error	miniasm, PacBio, vc2010.miniasm.quiver.002
--	---

Revised	chromosome	start	end
region	chrII	3,622,561	3,634,897

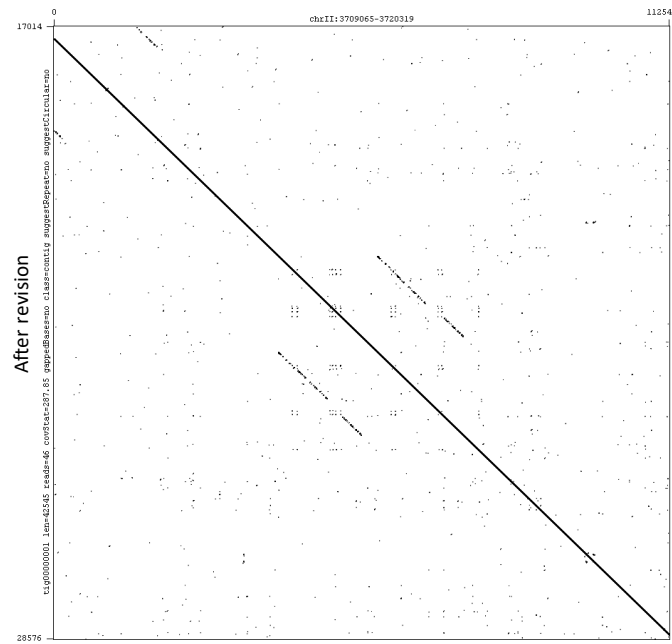
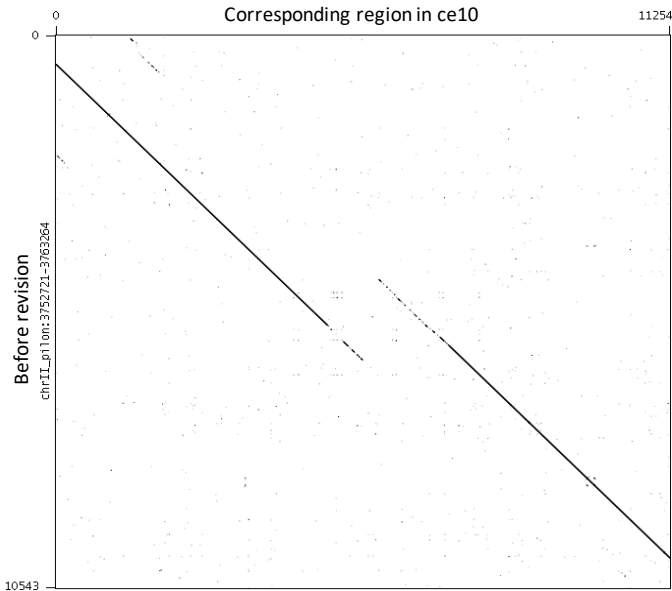
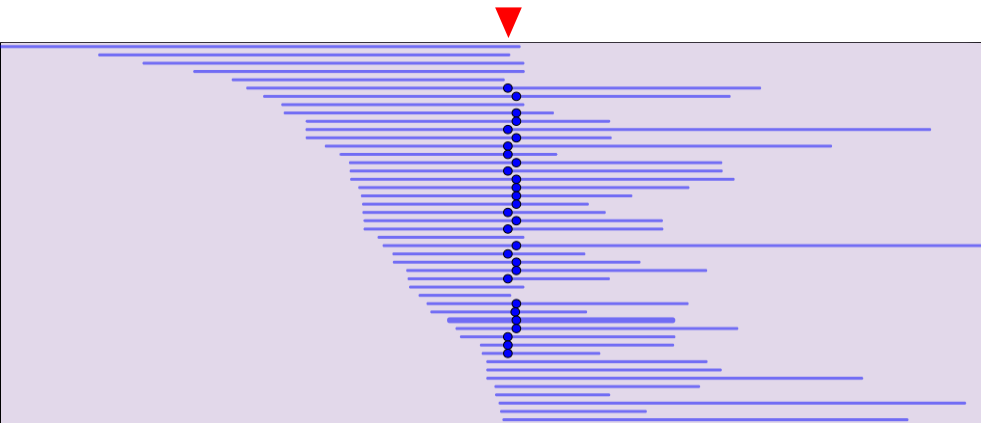
Blue disks in the arrowed region show insertions into the contig, implying a missing part in the VC2010 genome. Indeed, the contig before revision had a missing part, and the revised contig perfectly matched the ce10 reference.



Assembler, read set, and contig with an error	miniasm, PacBio, vc2010.miniasm.quiver.002
--	---

Revised	chromosome	start	end
region	chrII	3,754,297	3,765,576

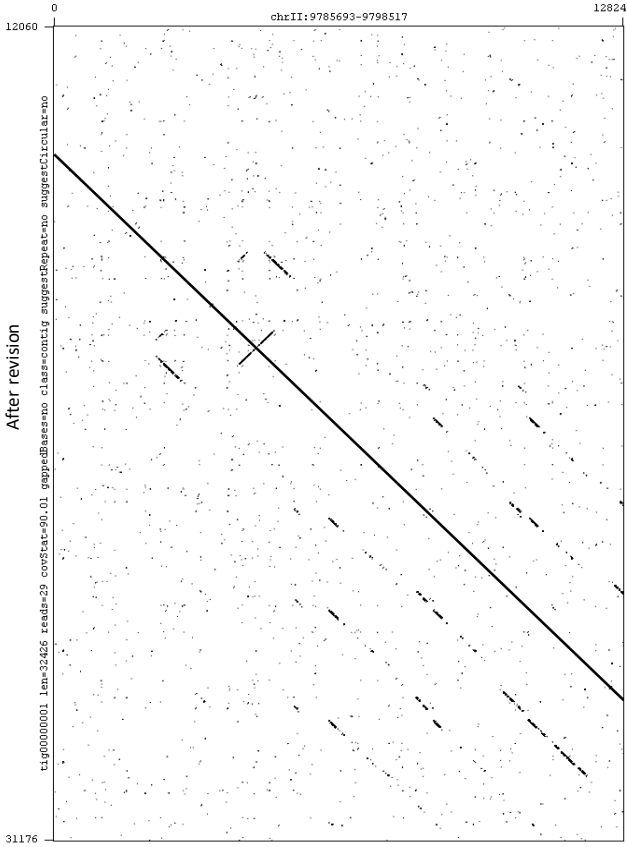
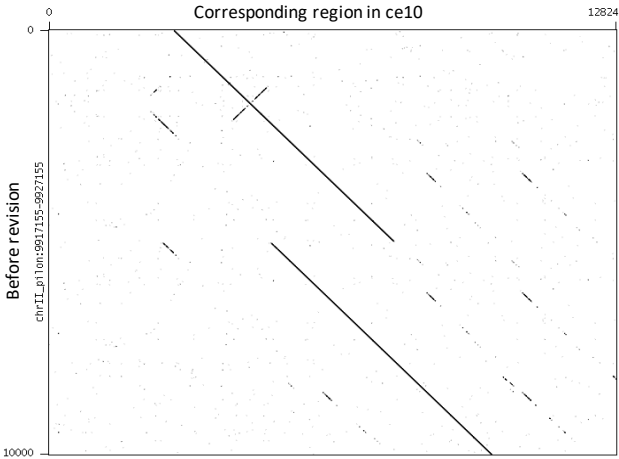
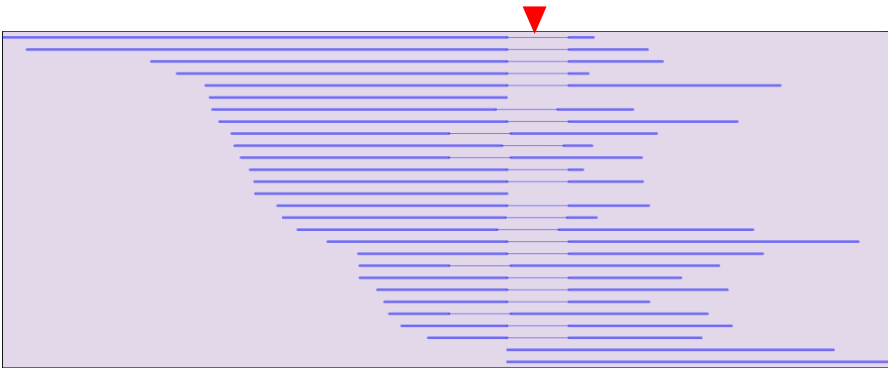
Blue disks in the arrowed region show insertions into the contig, implying a missing part in the VC2010 genome. Indeed, the contig before revision had a missing part, and the revised contig perfectly matched the ce10 reference.



Assembler, read set, and contig with an error	miniasm, PacBio, vc2010.miniasm.quiver.017
--	---

Revised	chromosome	start	end
region	chrII	9,919,928	9,926,945

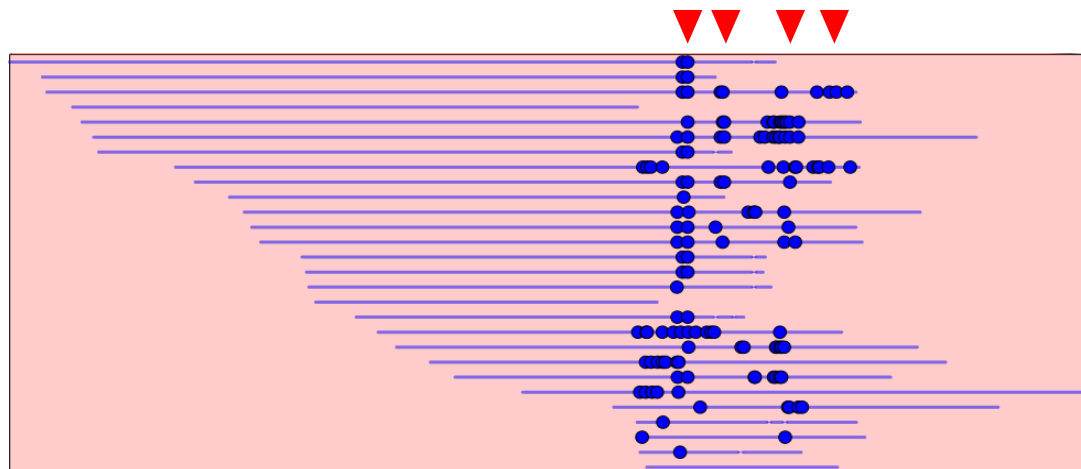
Alignments of raw reads to the focal VC2010 contig are partial in the arrowed region, implying the presence of an undesirable region in the contig. Indeed, the contig before revision has false positive duplicated regions, while the revised contig perfectly matched the ce10 reference in the x-axis.



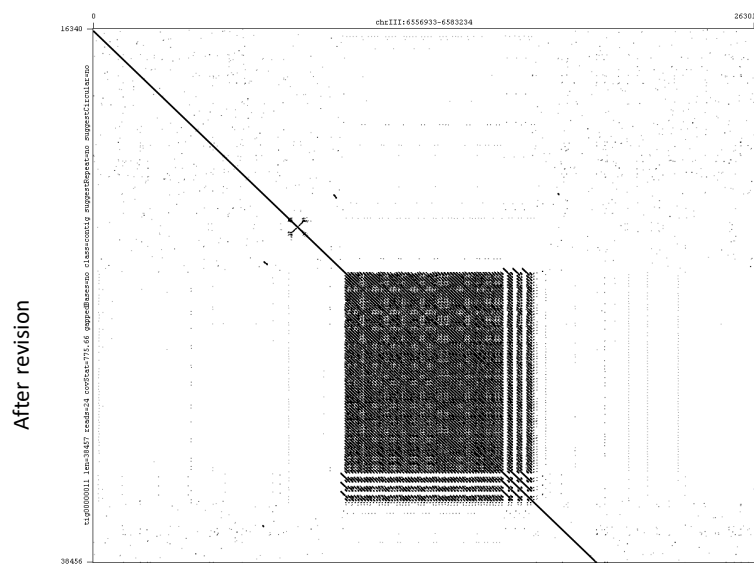
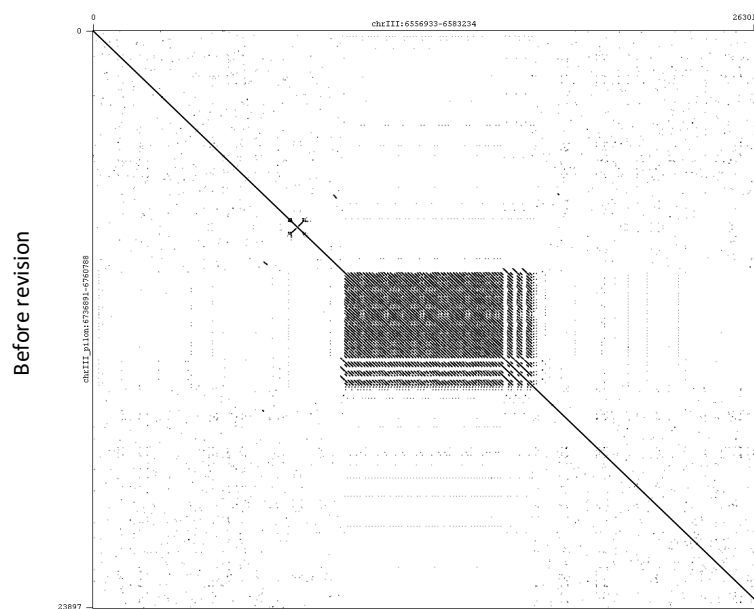
Assembler, read set, and contig with an error	miniasm, PacBio, vc2010.miniasm.quiver.022
---	--

Revised	chromosome	start	end
region	chrIII	6,742,995	6,758,773

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.



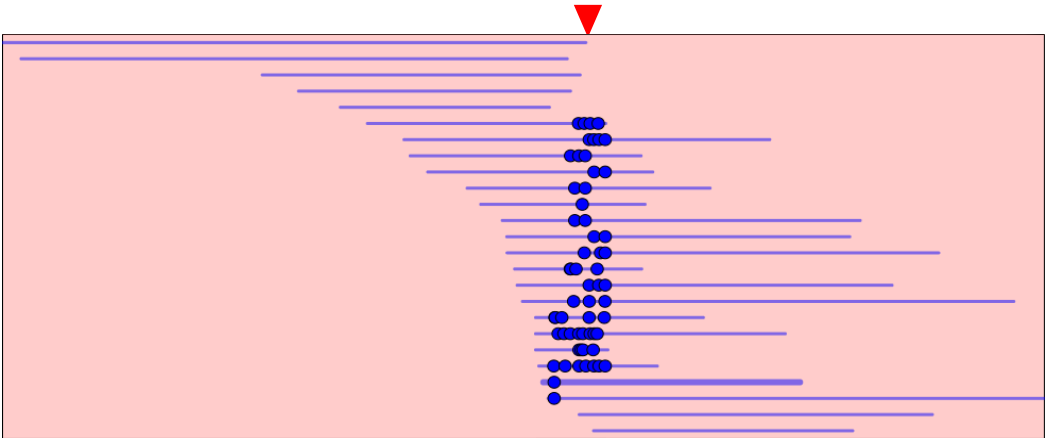
Corresponding region in ce10



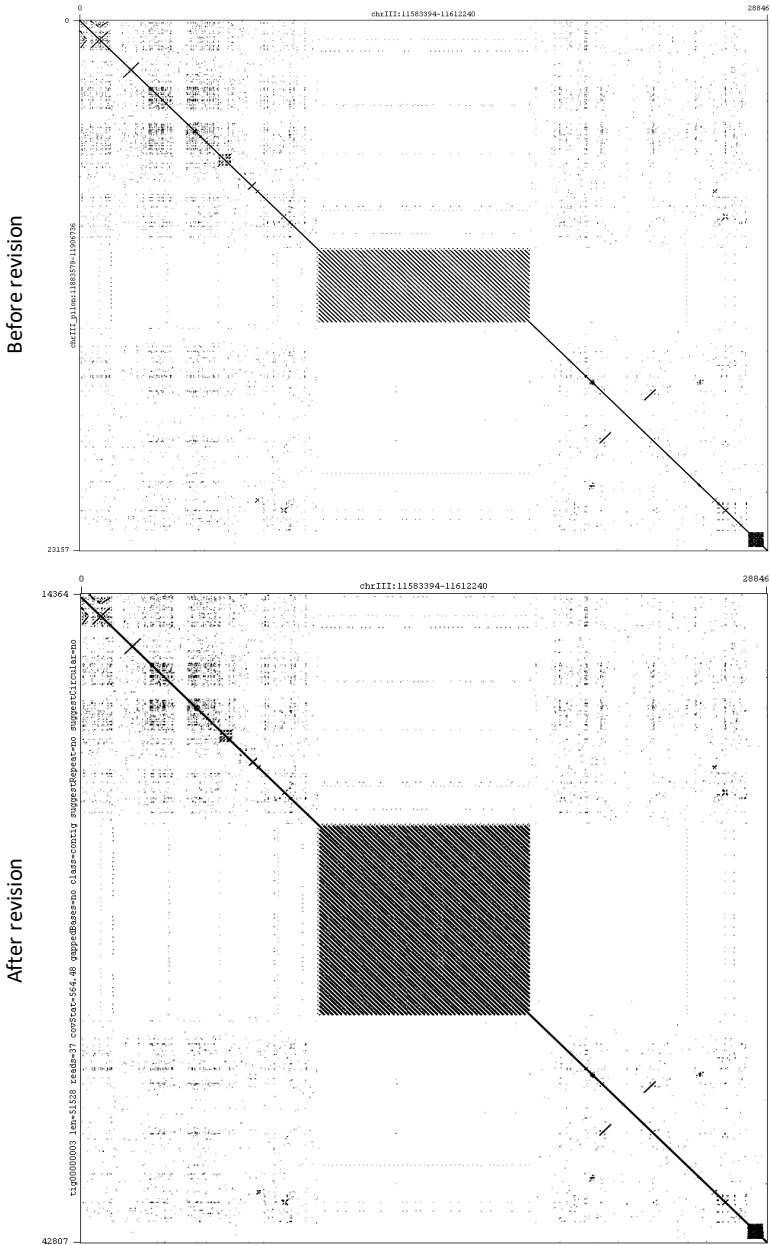
Assembler, read set, and contig with an error	miniasm, PacBio, vc2010.miniasm.quiver.003
--	---

Revised	chromosome	start	end
region	chrIII	11,895,171	11,908,856

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.



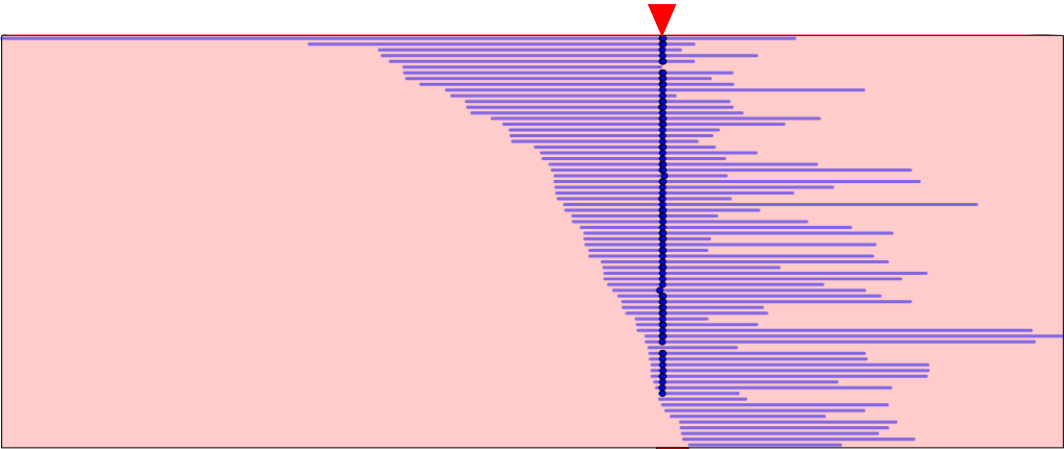
Corresponding region in ce10



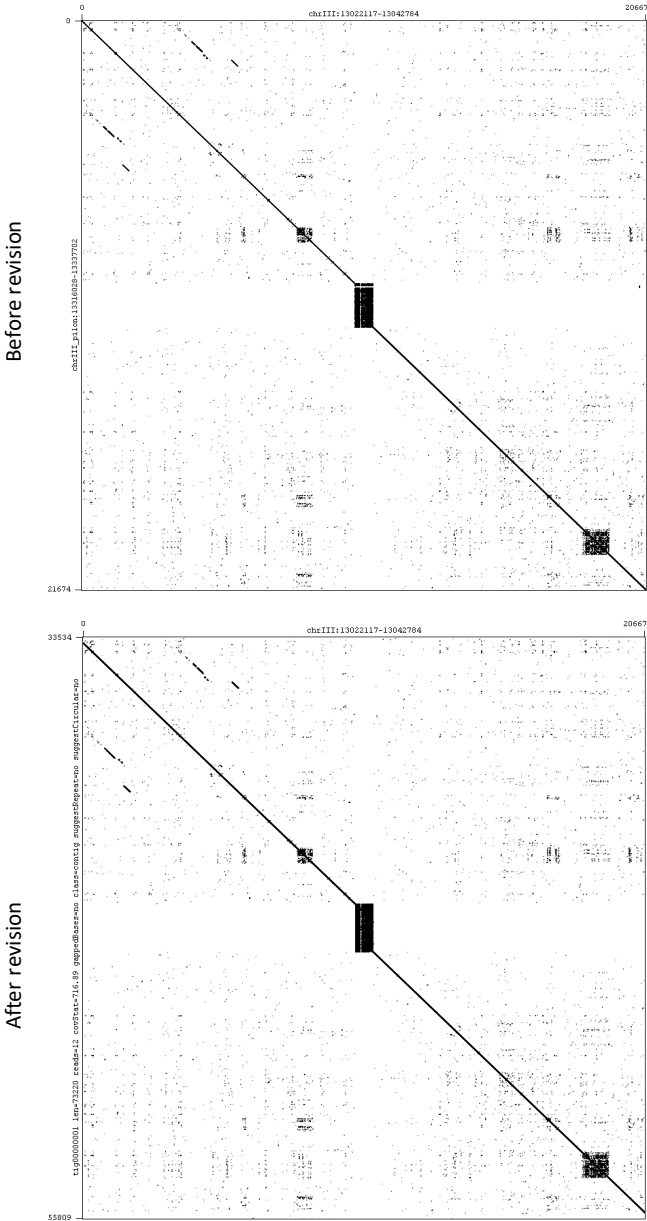
Assembler, read set, and contig with an error	miniasm, PacBio, vc2010.miniasm.quiver.003
--	---

Revised	chromosome	start	end
region	chrIII	13,332,333	13,339,443

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.



Corresponding region in ce10

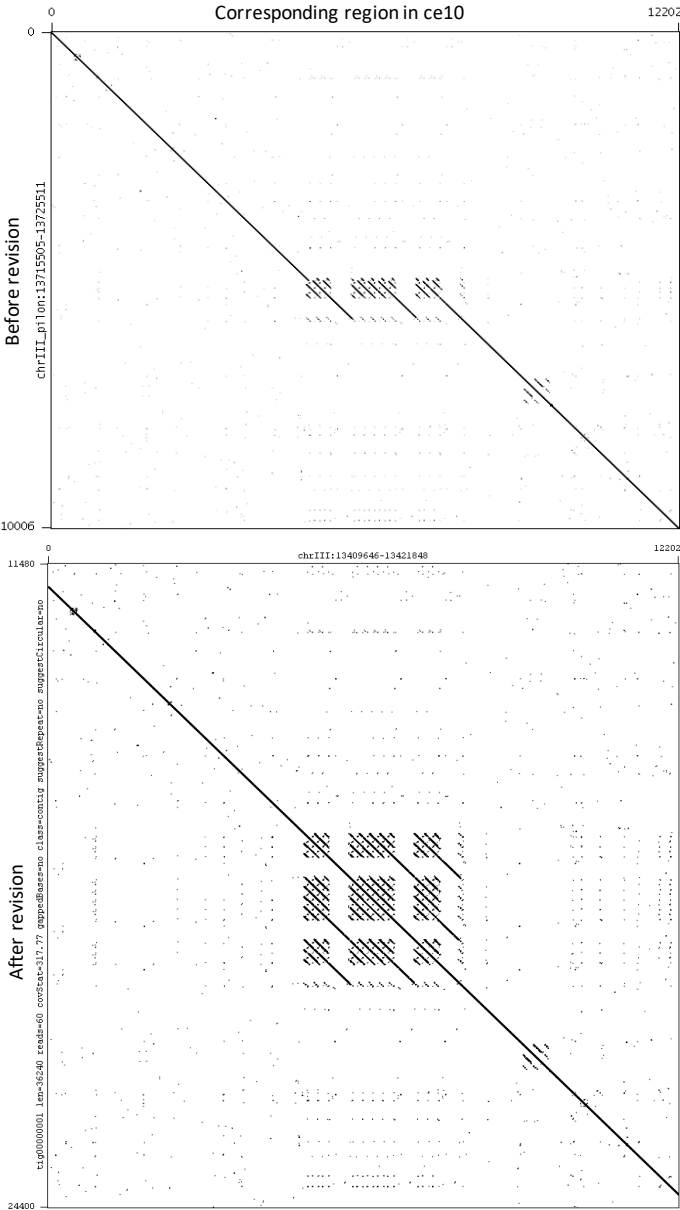
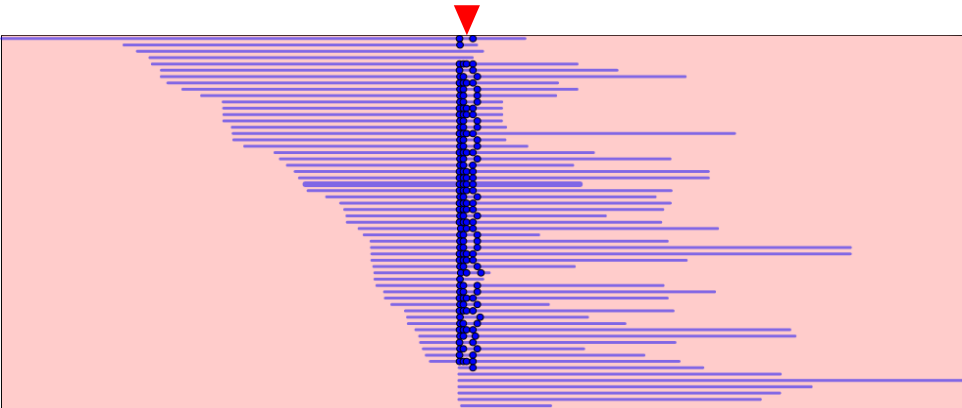




Assembler, read set, and contig with an error	miniasm, PacBio, vc2010.miniasm.quiver.003
--	---

Revised	chromosome	start	end
region	chrIII	13,725,597	13,736,906

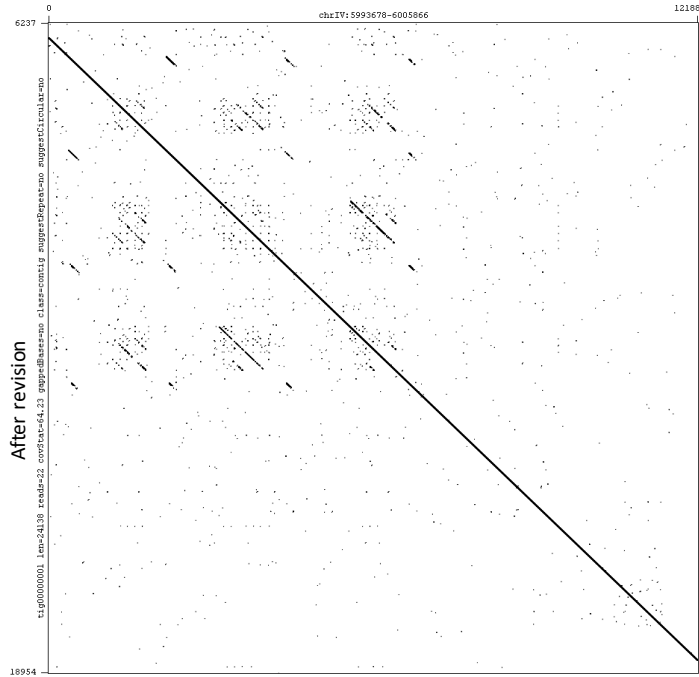
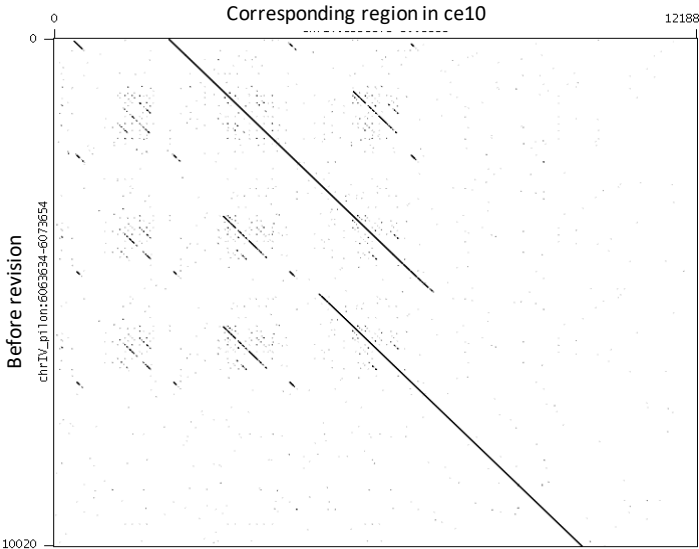
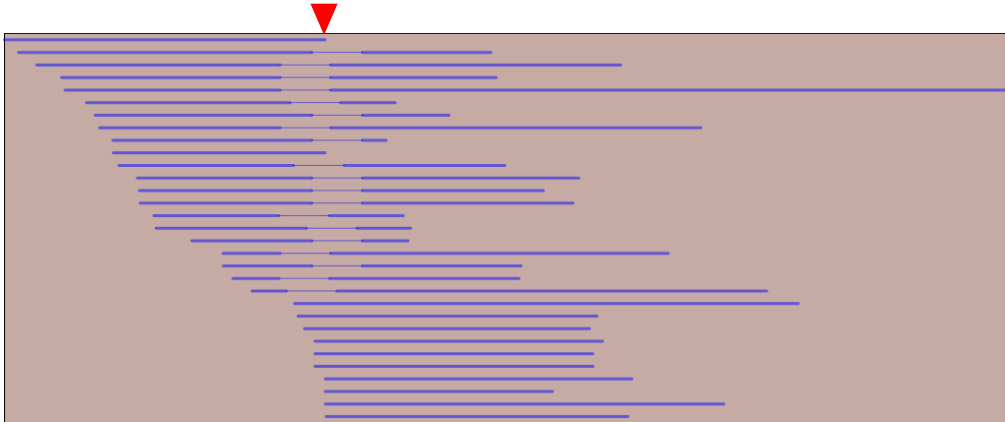
Blue disks in the arrowed region show insertions into the contig, implying a missing part in the VC2010 genome. The revised contig is identical to its corresponding region in the N2 genome and has separated tandem repeat expansions.



Assembler, read set, and contig with an error	miniasm, PacBio, vc2010.miniasm.quiver.006
--	---

Revised	chromosome	start	end
region	chrIV	6,063,597	6,071,178

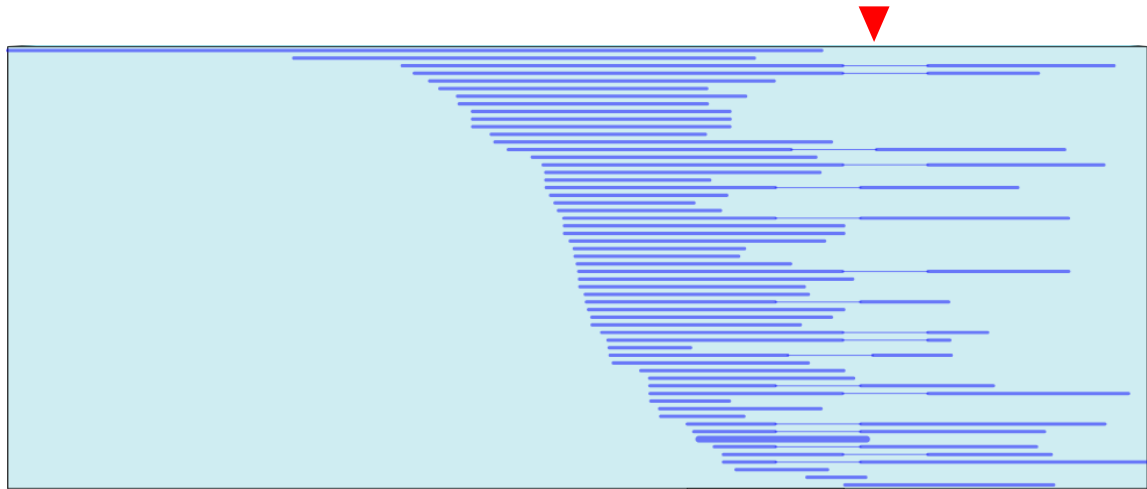
Alignments of raw reads to the focal VC2010 contig are partial in the arrowed region, implying the presence of an undesirable region in the contig. Indeed, the contig before revision has false positive duplicated regions, while the revised contig perfectly matched the ce10 reference in the x-axis.



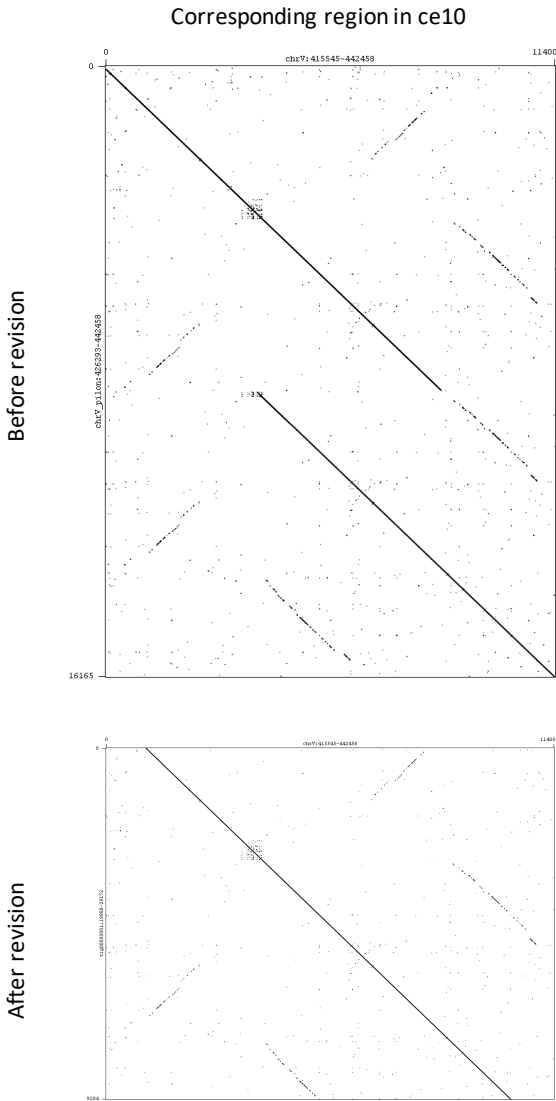
Assembler, read set, and contig with an error	miniasm, PacBio, vc2010.miniasm.quiver.007
--	---

Revised	chromosome	start	end
region	chrV	427,343	436,627

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.



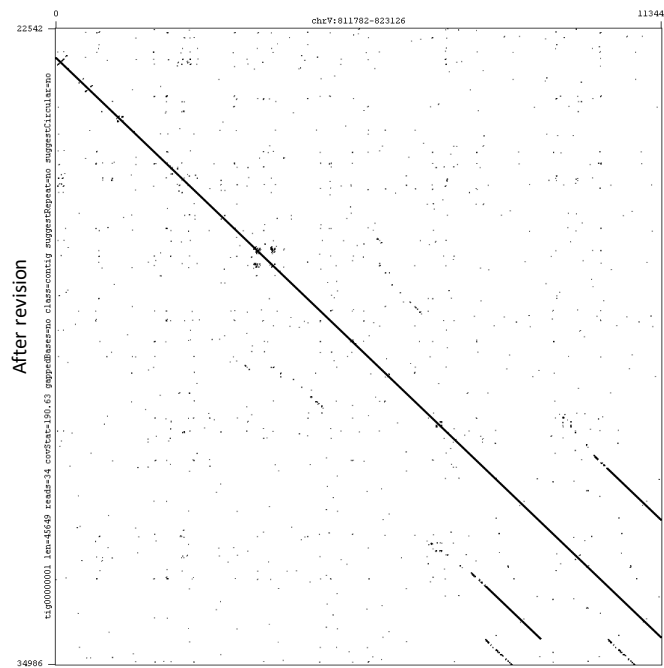
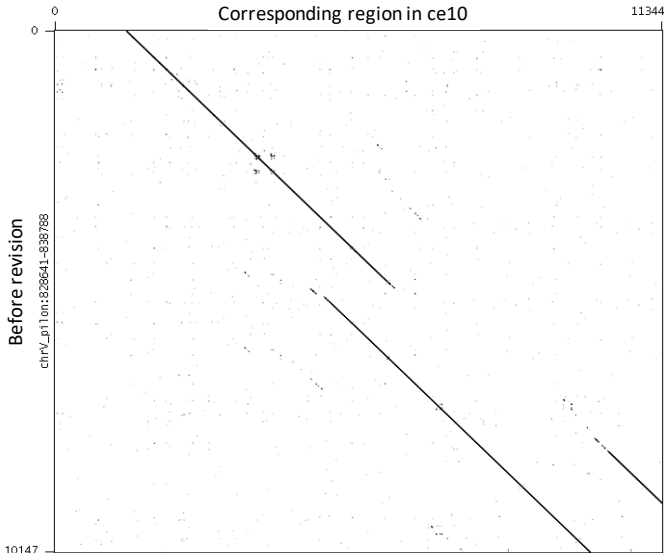
The revised contig perfectly matched the ce10 reference in the x-axis.



Assembler, read set, and contig with an error	miniasm, PacBio, vc2010.miniasm.quiver.007
--	---

Revised	chromosome	start	end
region	chrV	824,103	832,294

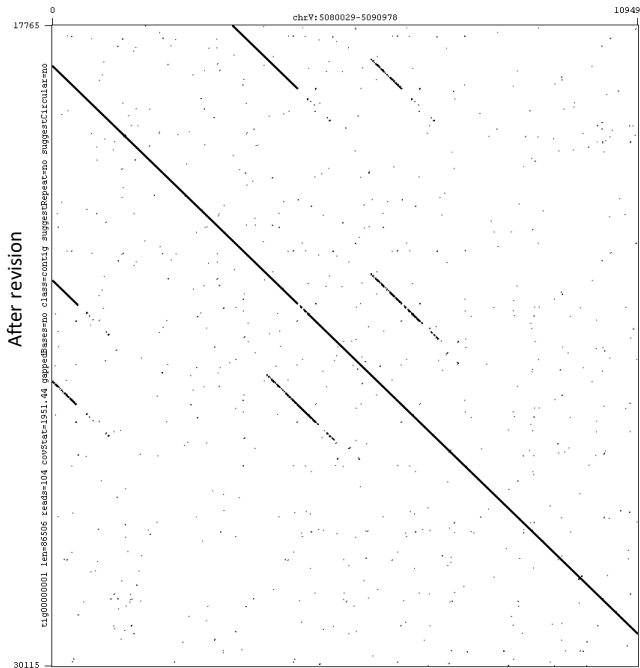
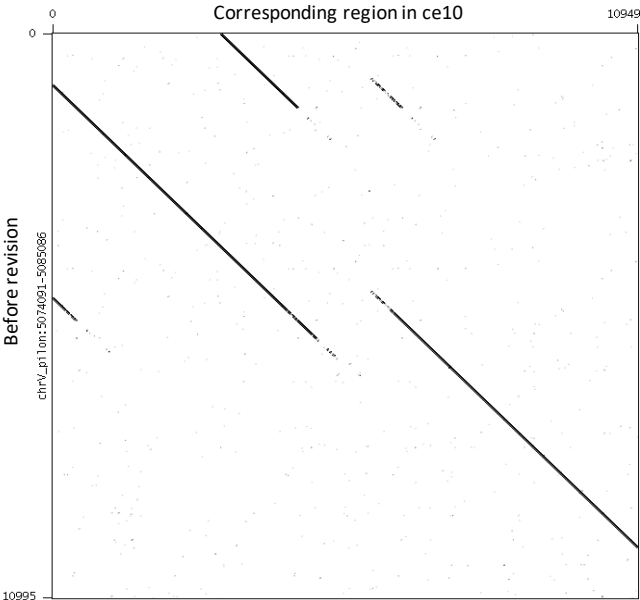
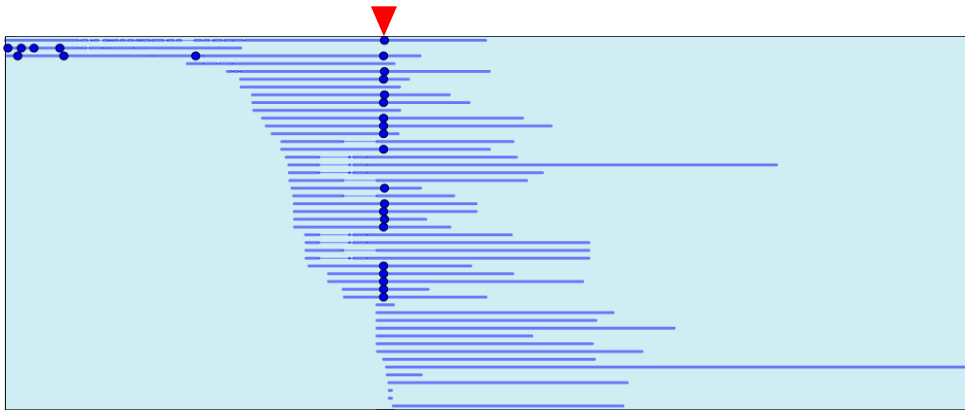
Alignments of raw reads to the focal VC2010 contig are partial in the arrowed region, implying the presence of an undesirable region in the contig. Indeed, the contig before revision has false positive duplicated regions, while the revised contig perfectly matched the ce10 reference in the x-axis.



Assembler, read set, and contig with an error	miniasm, PacBio and ONT, utg0000051
--	--

Revised	chromosome	start	end
region	chrV	5,067,935	5,080,560

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.

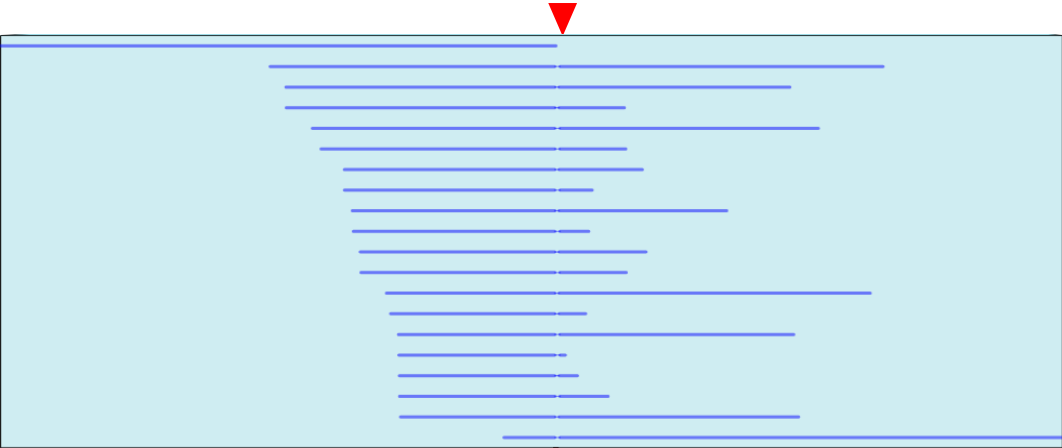




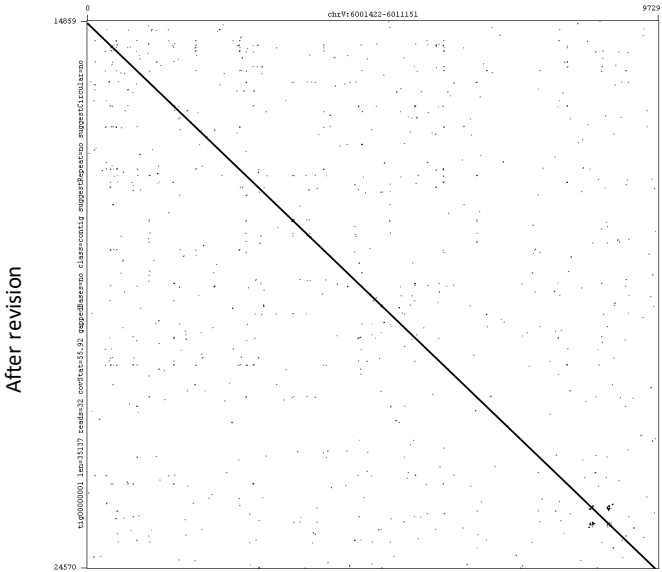
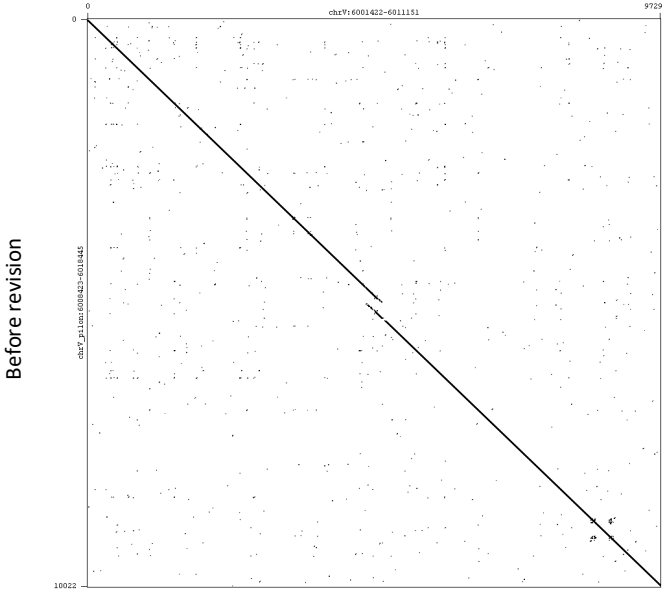
Assembler, read set, and contig with an error	miniasm, PacBio and ONT, utg000005l
--	--

Revised	chromosome	start	end
region	chrV	6,006,957	6,009,592

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.



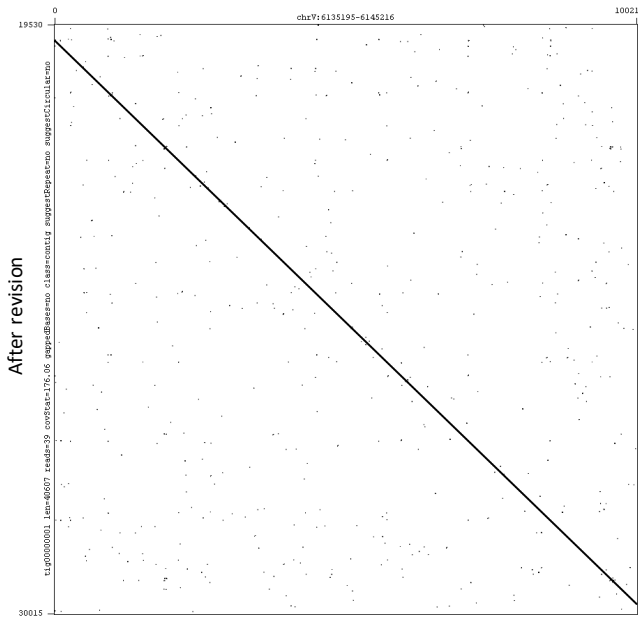
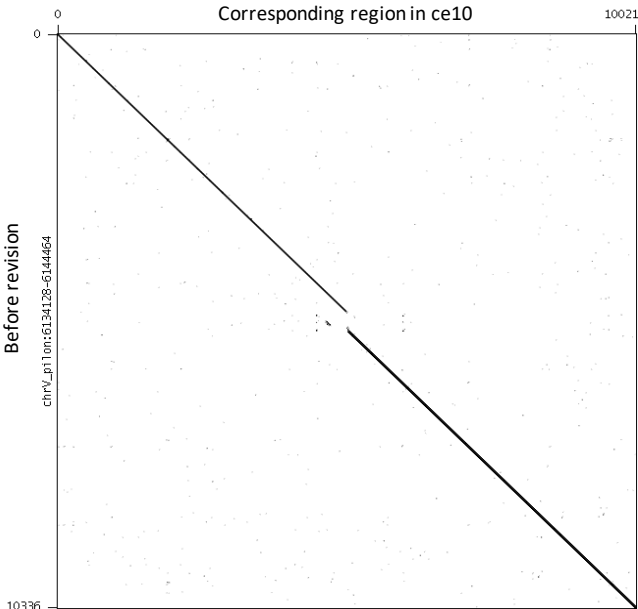
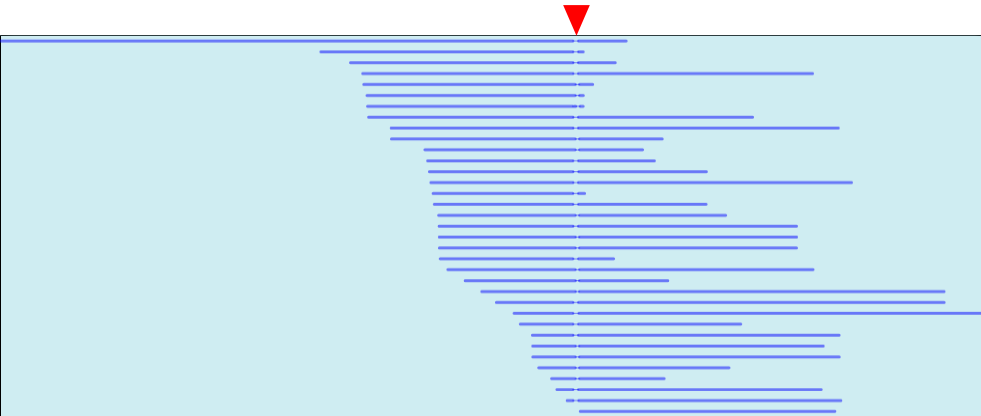
Corresponding region in ce10



Assembler, read set, and contig with an error	miniasm, PacBio and ONT, utg000005l
--	--

Revised	chromosome	start	end
region	chrV	6,129,224	6,138,343

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.

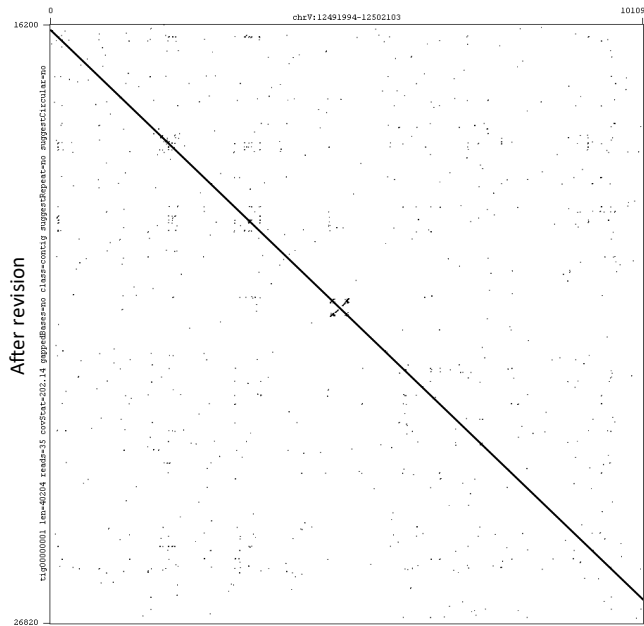
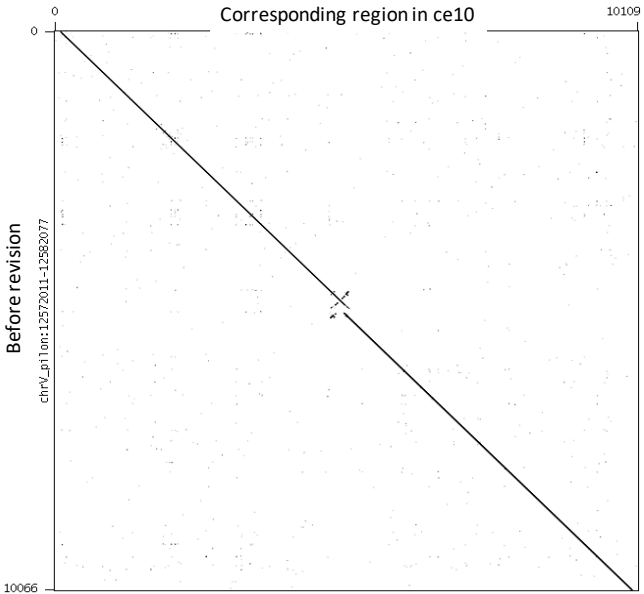




Assembler, read set, and contig with an error	Canu, PacBio, vc2010.canu.quiver.002
--	---

Revised	chromosome	start	end
region	chrV	12,566,583	12,575,930

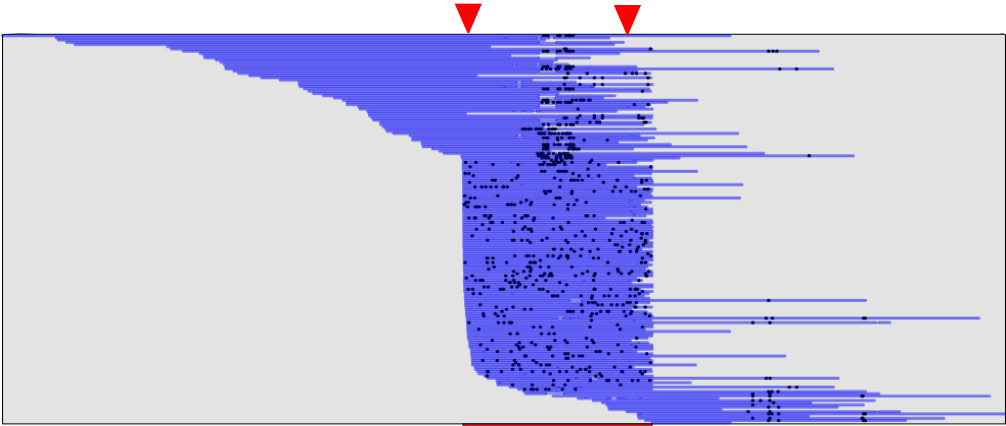
Alignments of raw reads to the focal VC2010 contig are partial in the arrowed region, implying the presence of an undesirable region in the contig. Indeed, the contig before revision has a false positive insertion, while the revised contig perfectly matched the ce10 reference in the x-axis.



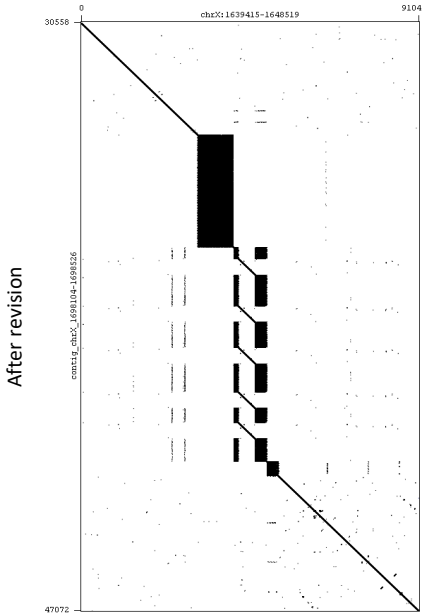
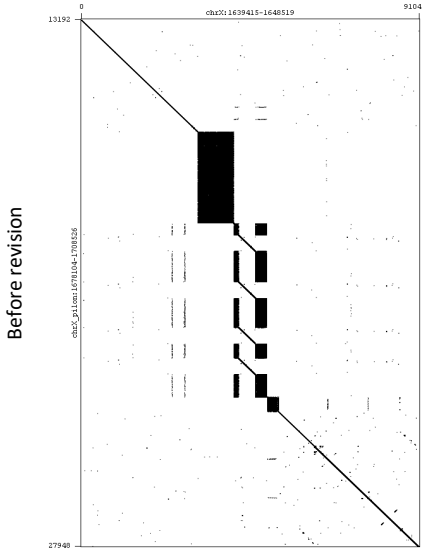
Assembler, read set, and contig with an error	miniasm, PacBio, vc2010.miniasm.quiver.009
--	---

Revised	chromosome	start	end
region	chrX	1,663,381	1,712,186

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.



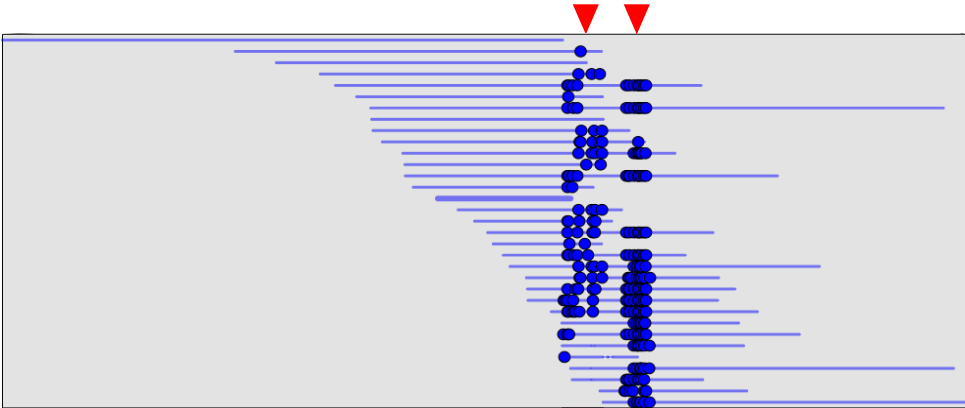
Corresponding region in ce10



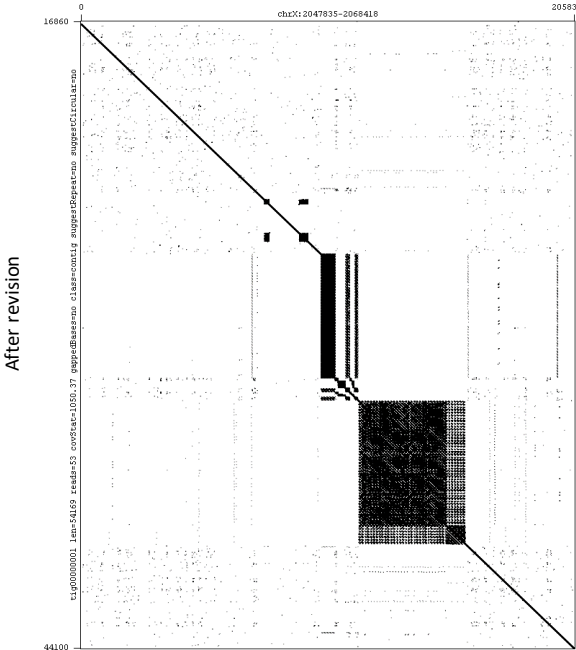
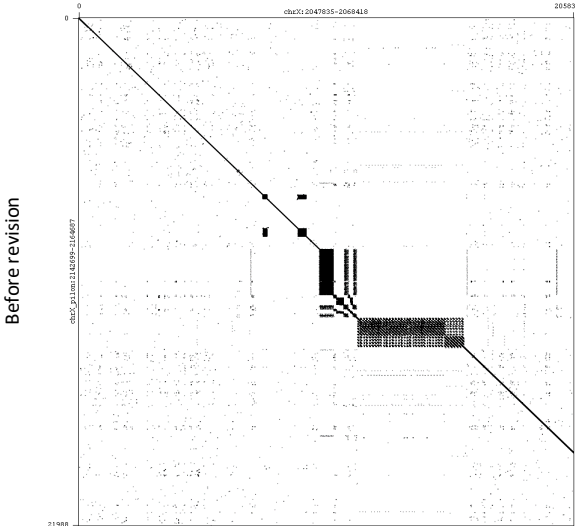
Assembler, read set, and contig with an error	miniasm, PacBio, vc2010.miniasm.quiver.009
--	---

Revised	chromosome	start	end
region	chrX	2,151,788	2,173,448

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.



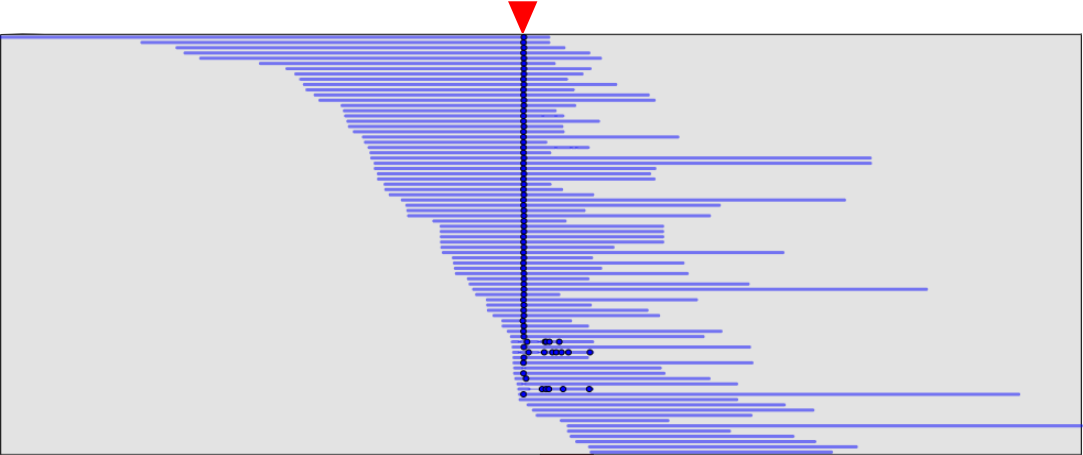
Corresponding region in ce10



Assembler, read set, and contig with an error	miniasm, PacBio, vc2010.miniasm.quiver.008
--	---

Revised	chromosome	start	end
region	chrX	17,683,237	17,691,717

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.



Corresponding region in ce10

