

Article

**The chromosome-level genome assembly of European grayling reveals aspects of a unique genome evolution process within salmonids**

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Figure S1

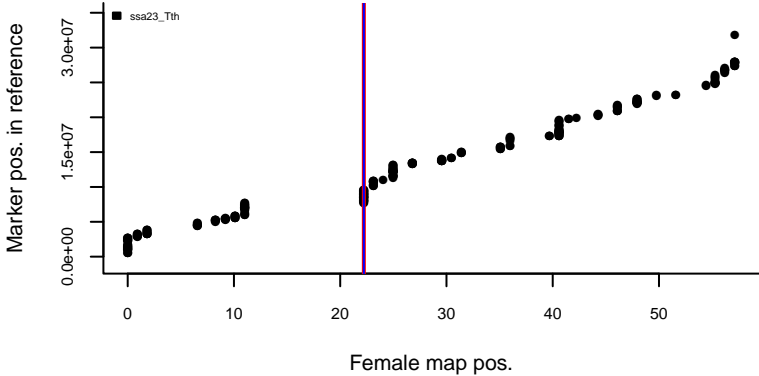
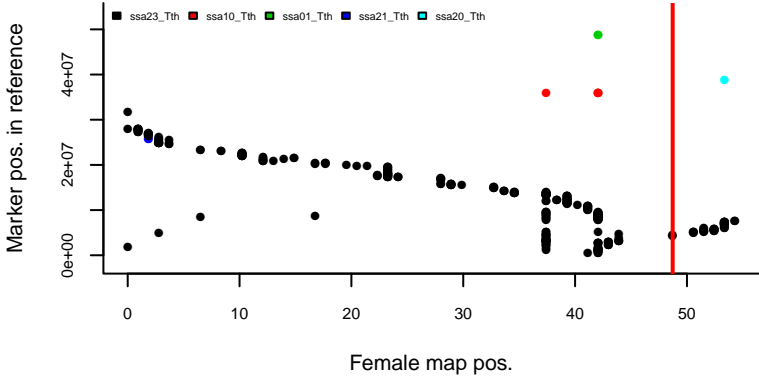
Breaks in the progression of map length increase in the salmonised European grayling linkage groups indicated possible genomic rearrangements between the European grayling and Atlantic salmon genomes.

In each chromosome, figures on the left (A) and right (B) describe mapping positions of the RAD markers in the original and salmonised linkage maps, respectively. Gaps larger than 10 map units (blue) or 8 times the gap size standard deviation of the chromosome (red) are highlighted with vertical lines.

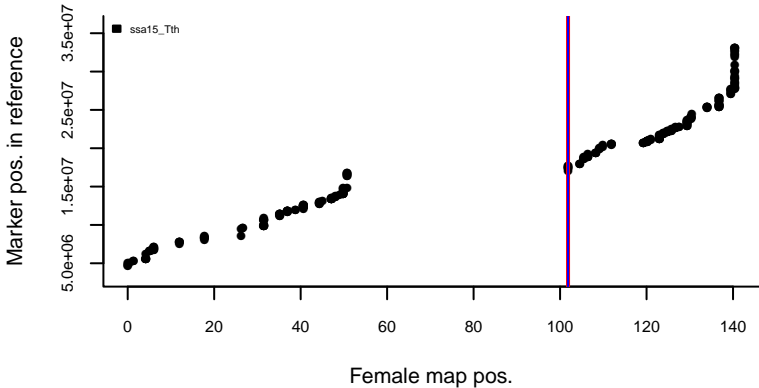
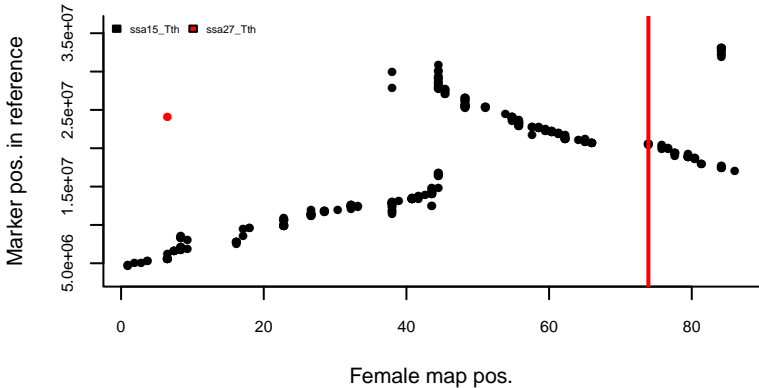
A original maps

B Salmonized maps

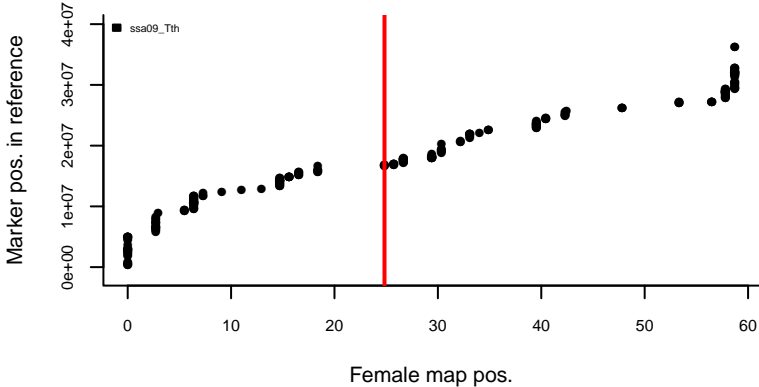
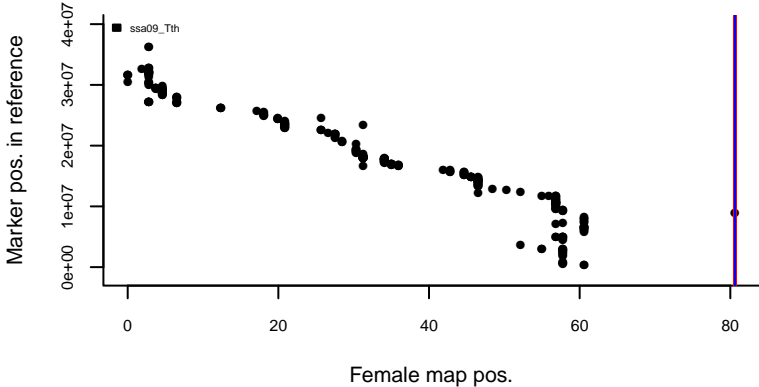
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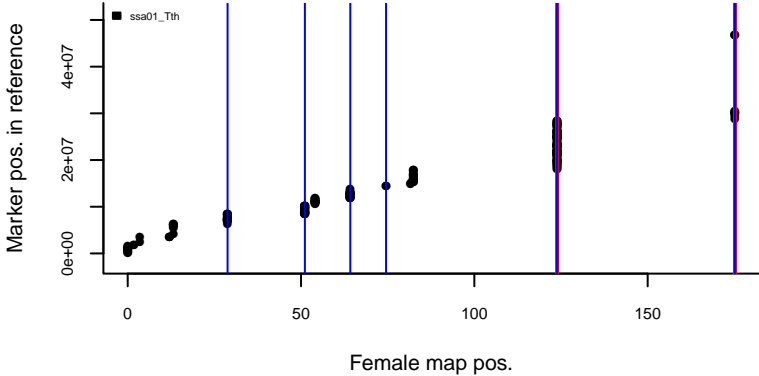
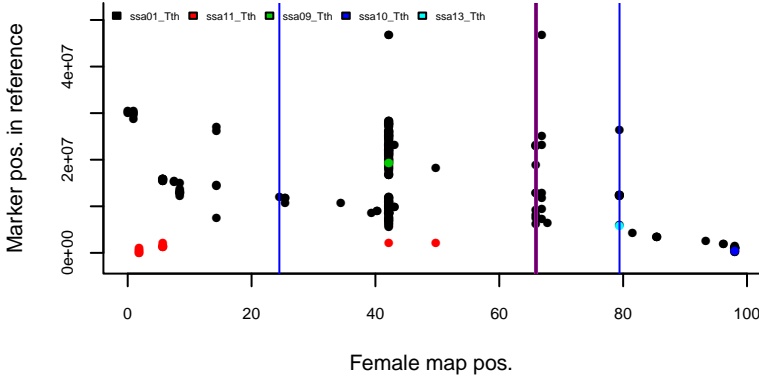
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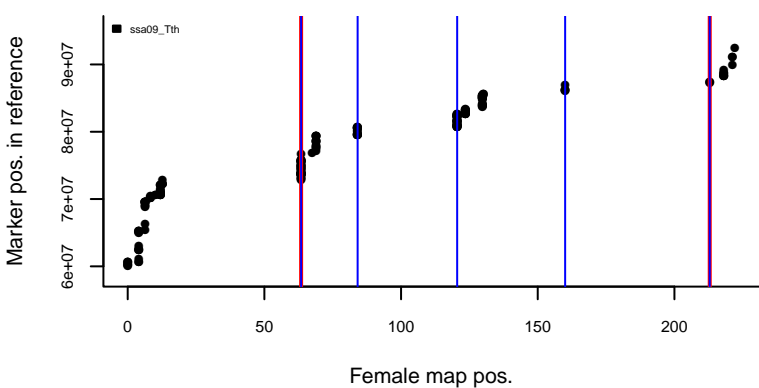
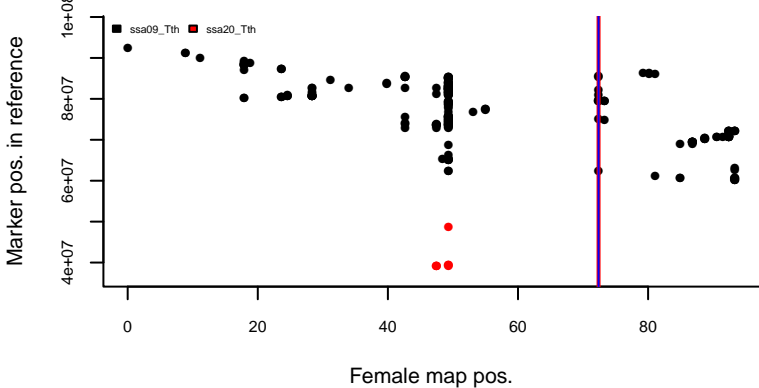
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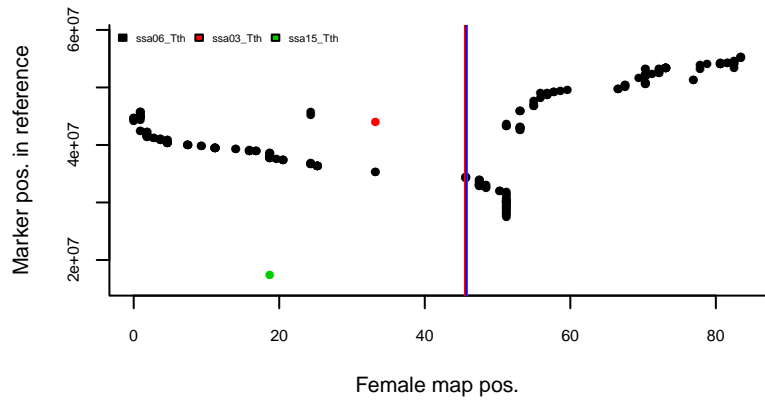


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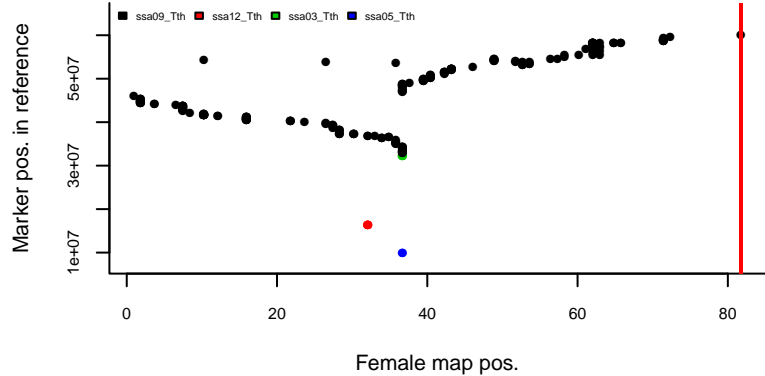
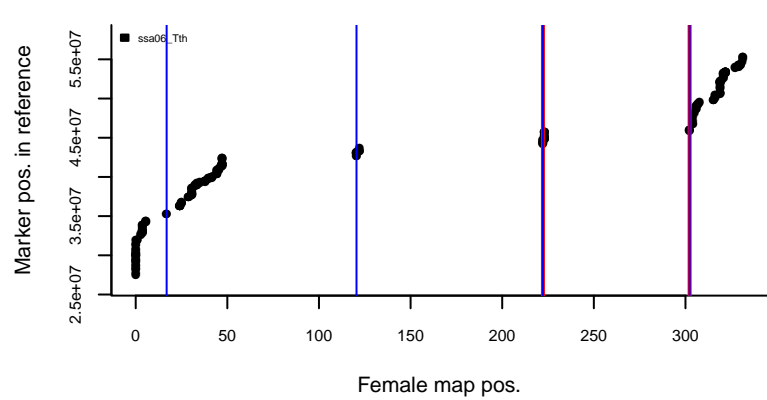


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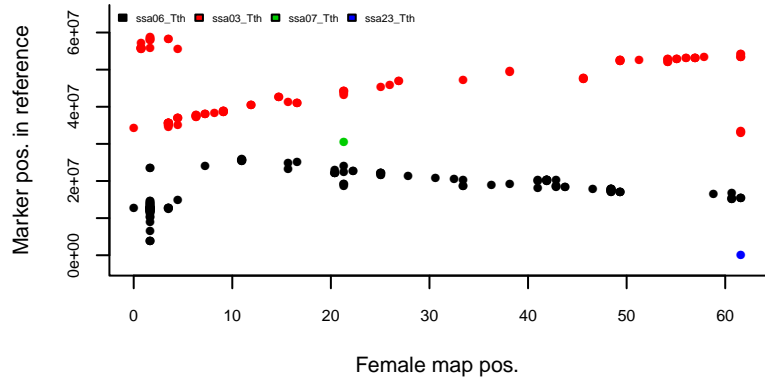
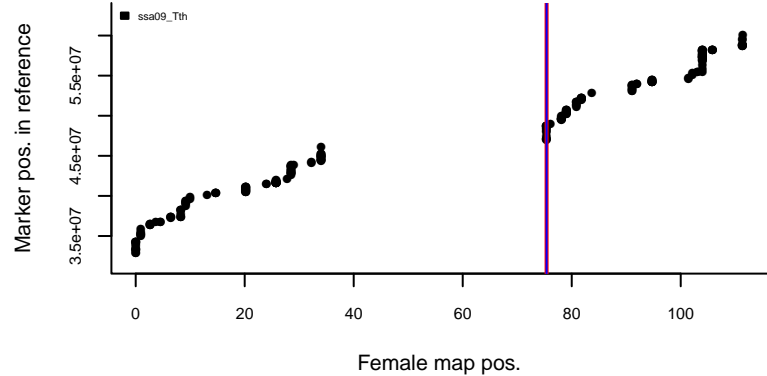




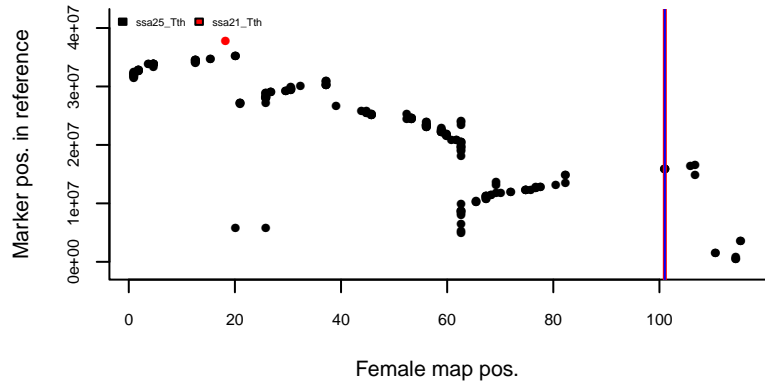
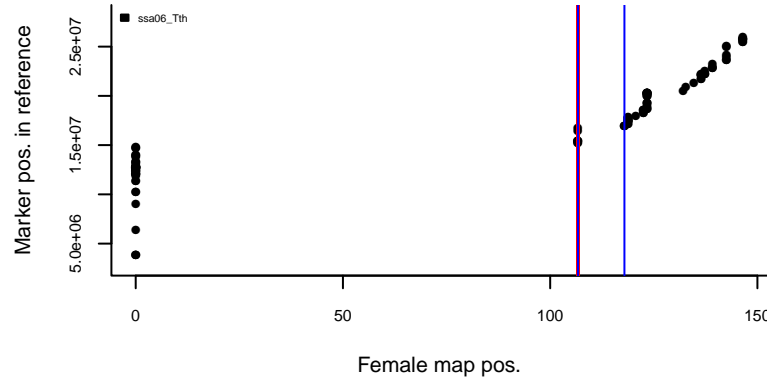
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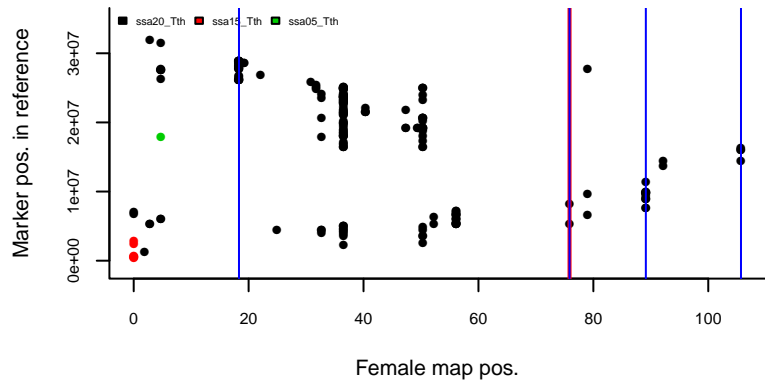
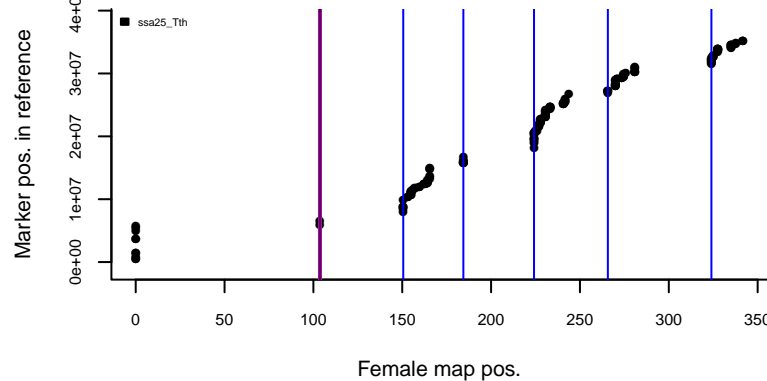
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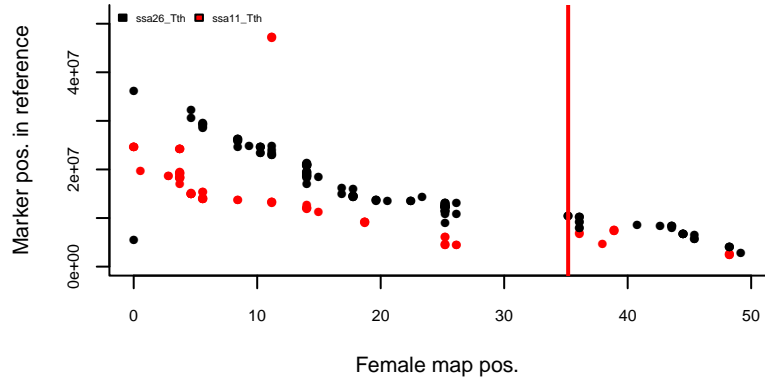
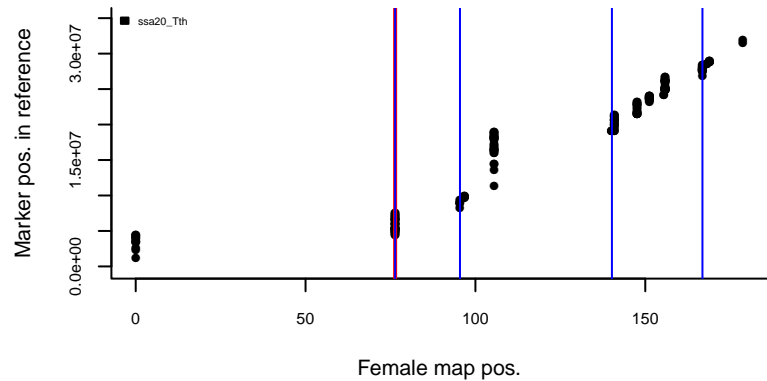
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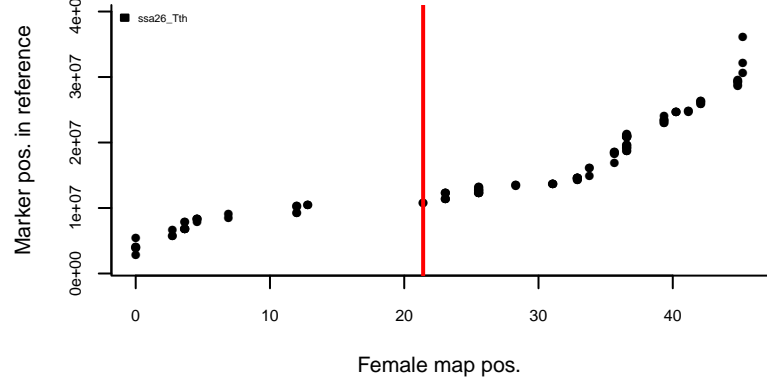
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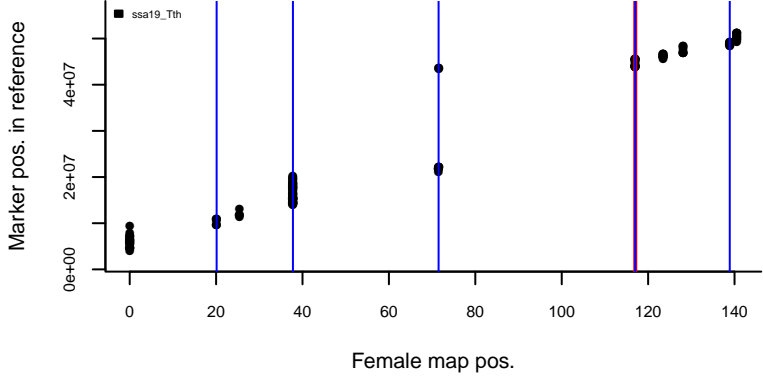
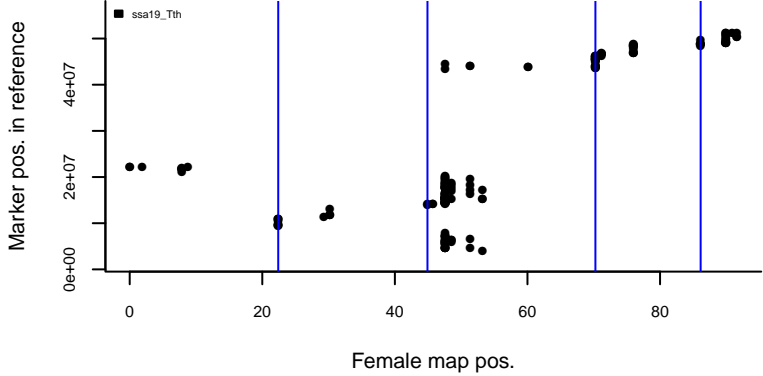
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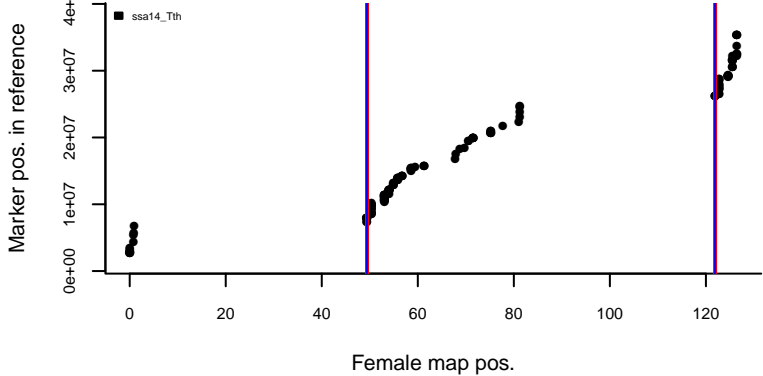
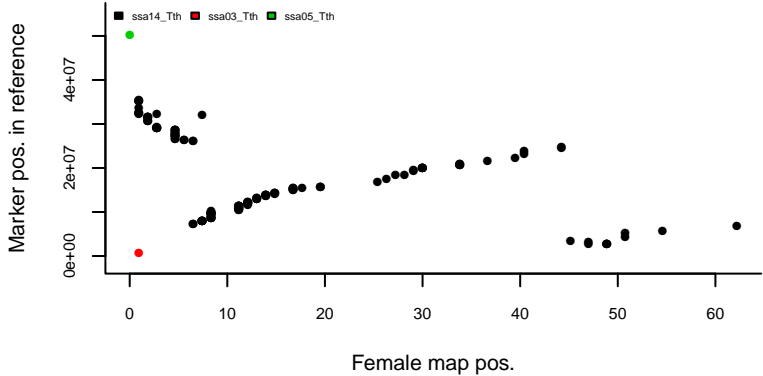
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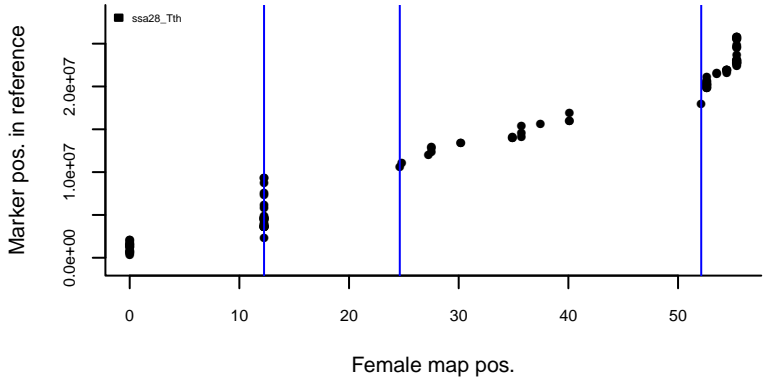
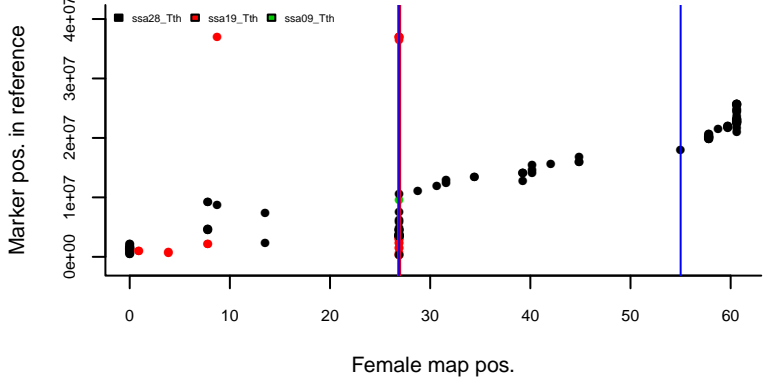
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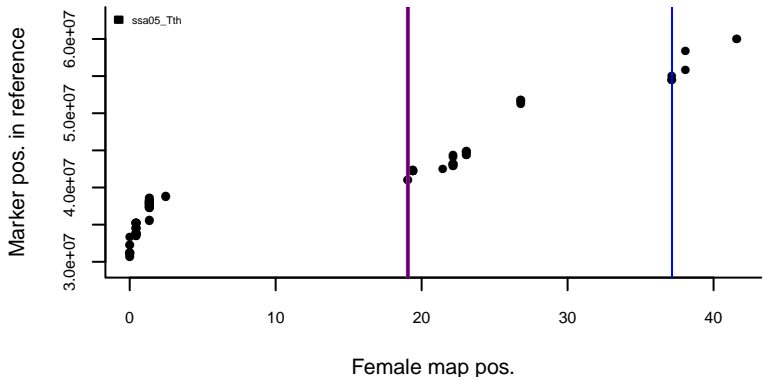
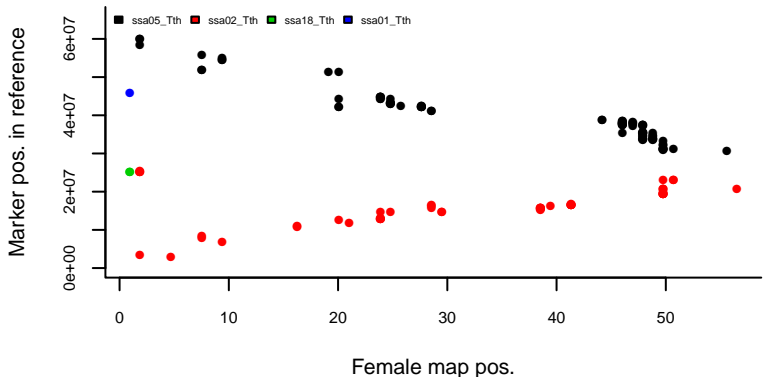
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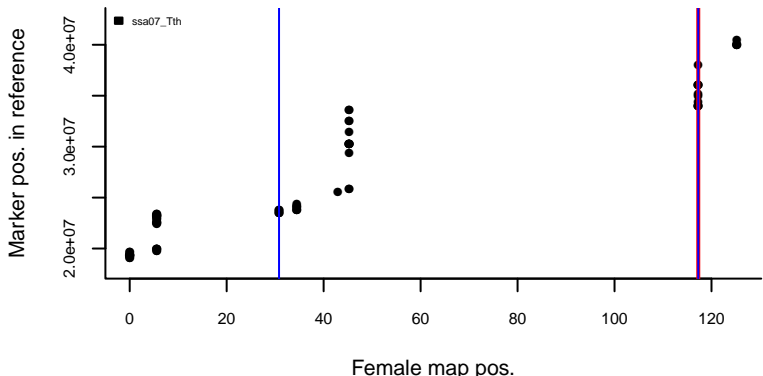
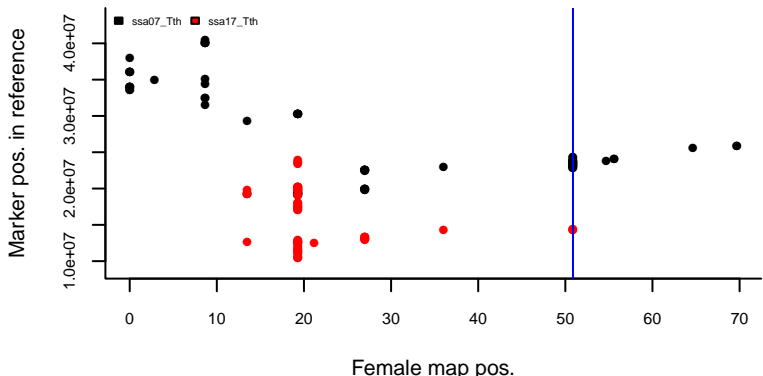
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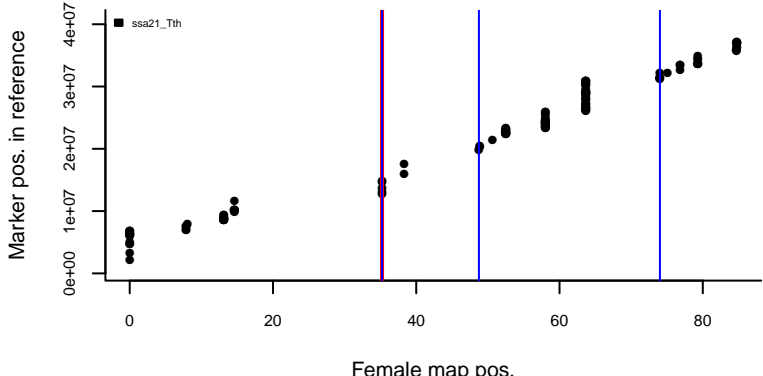
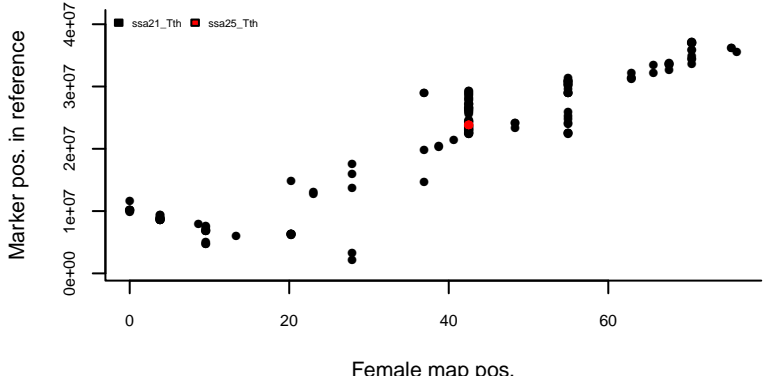
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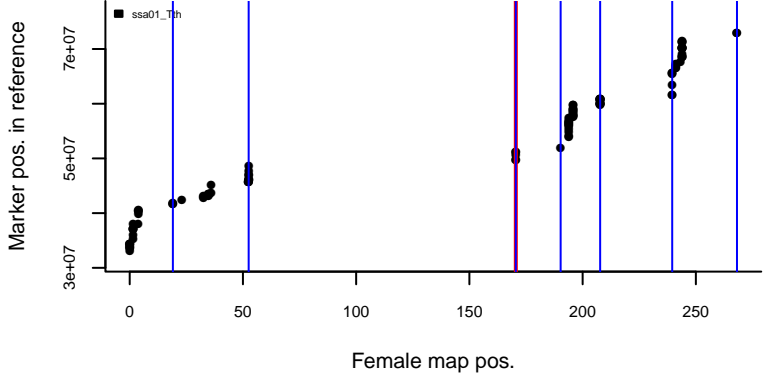
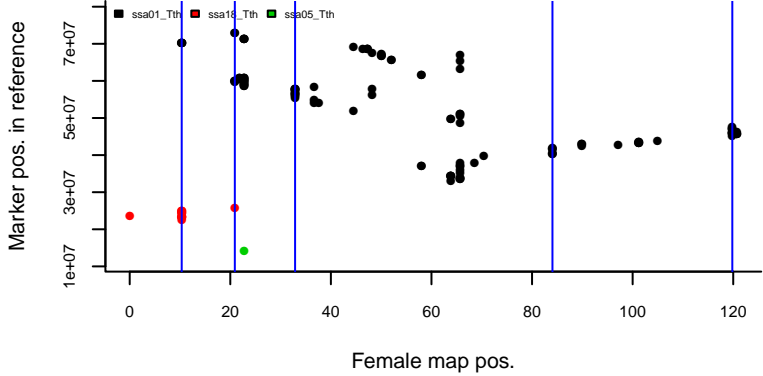
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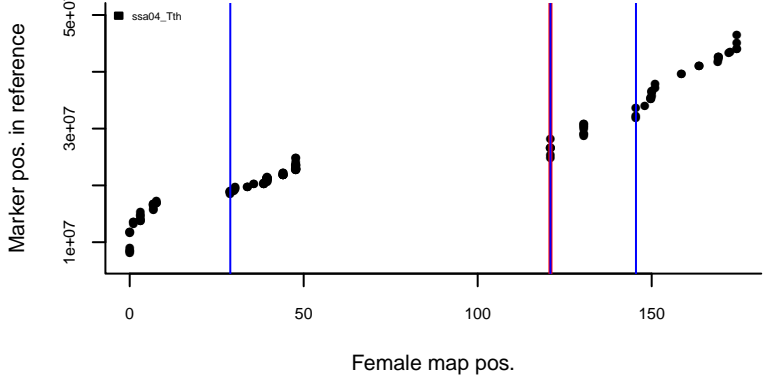
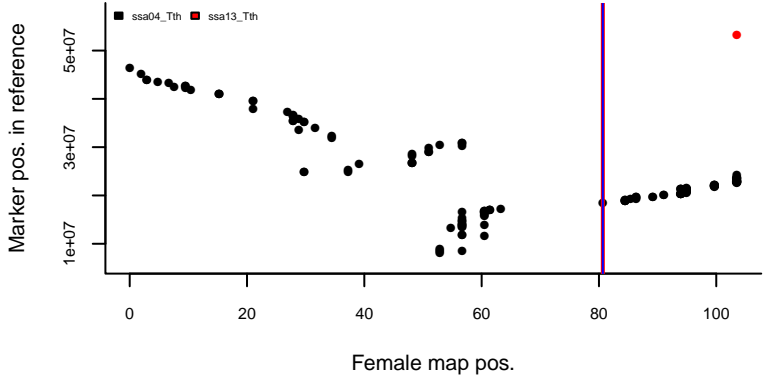
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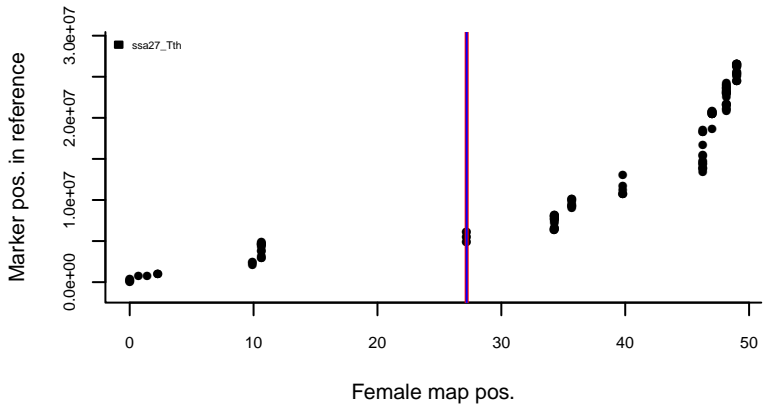
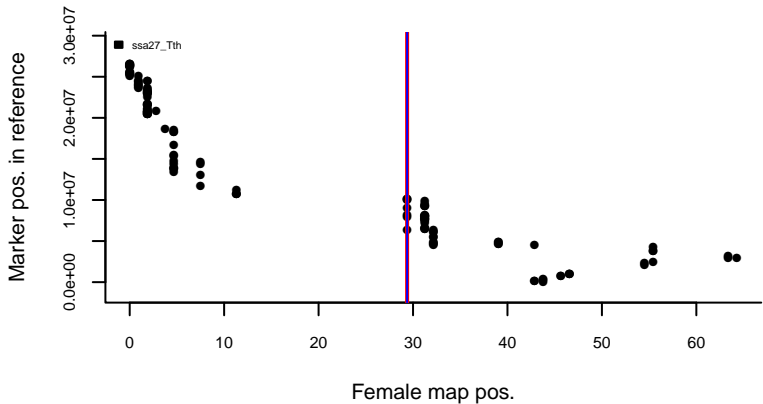
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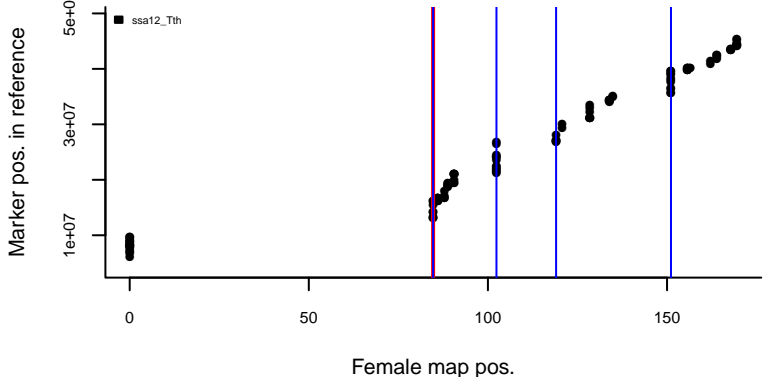
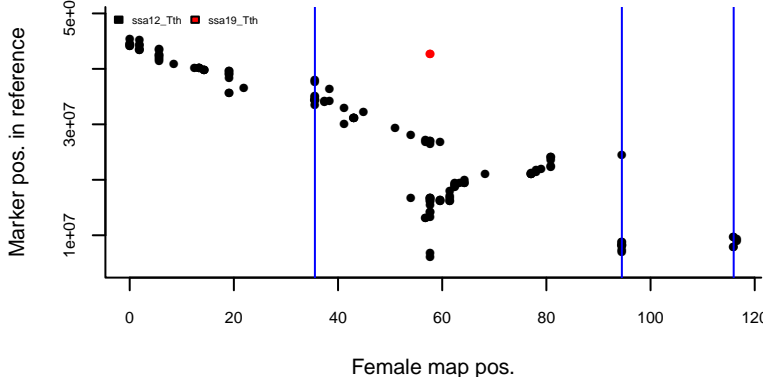
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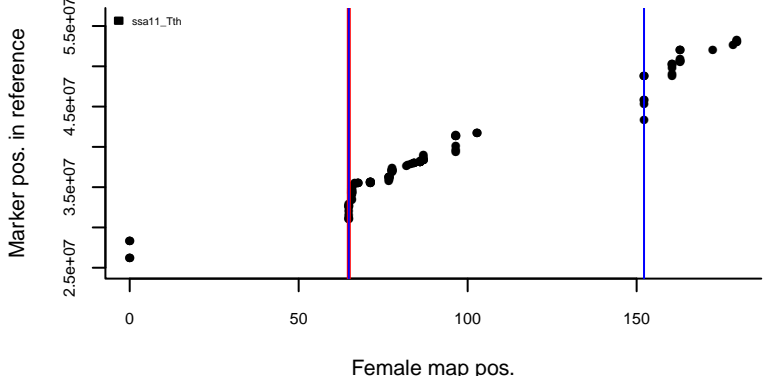
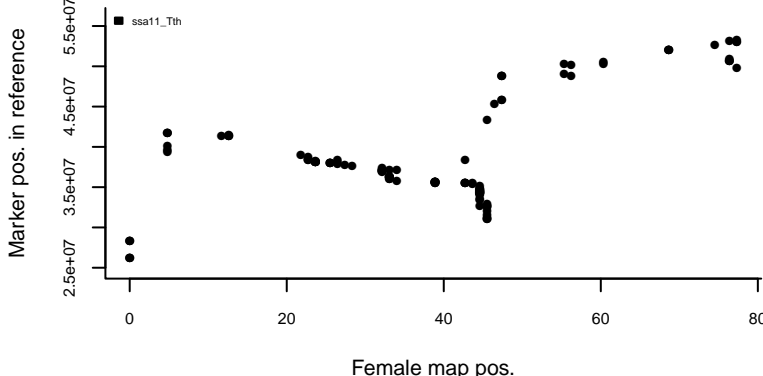
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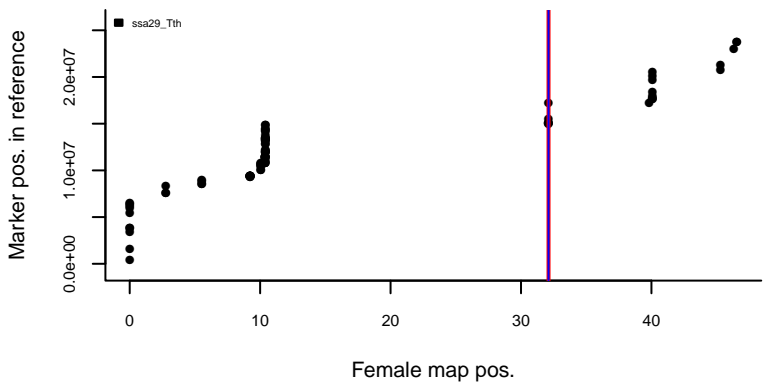
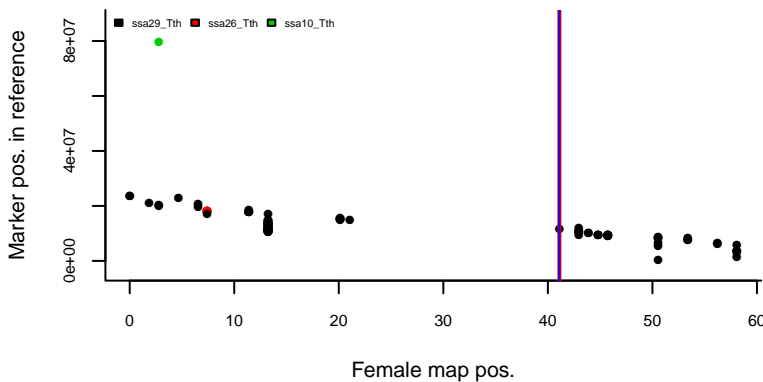
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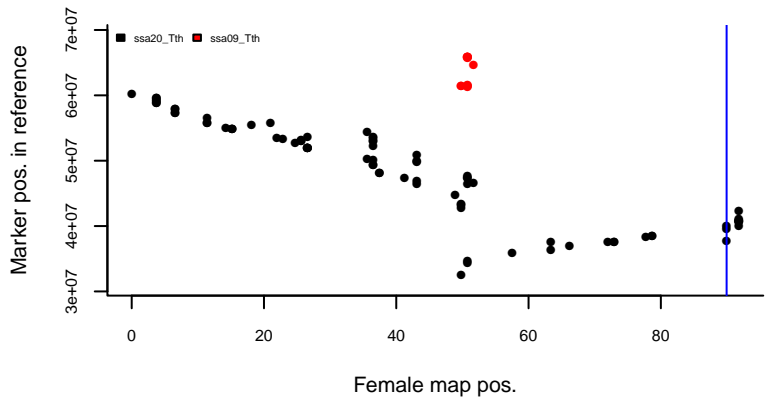


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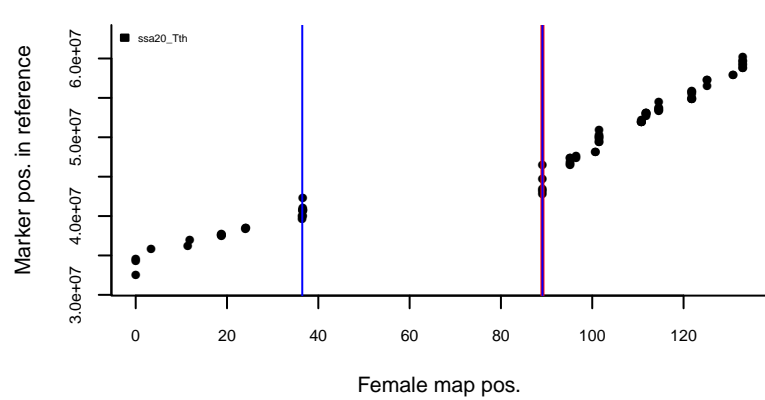


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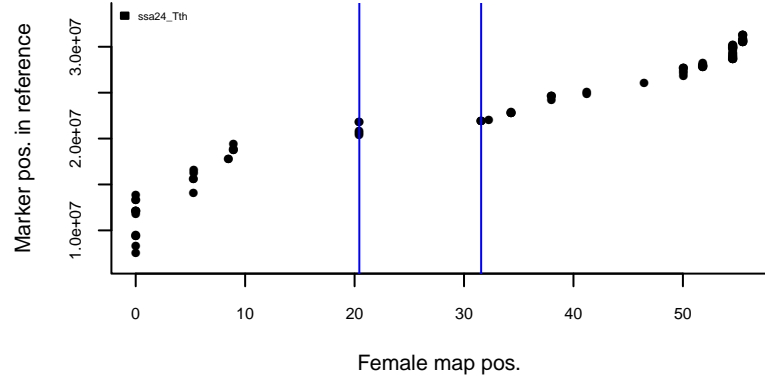
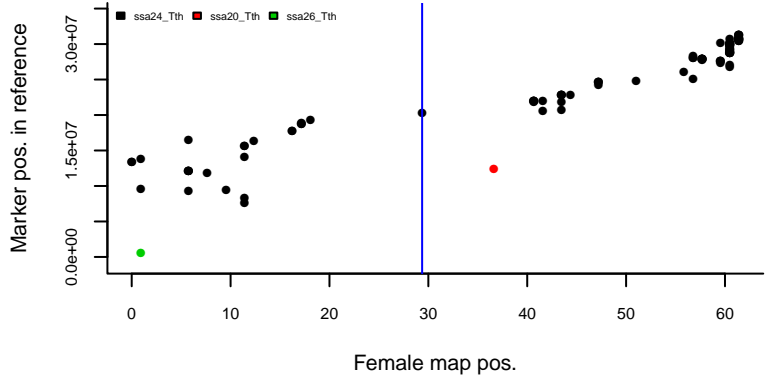




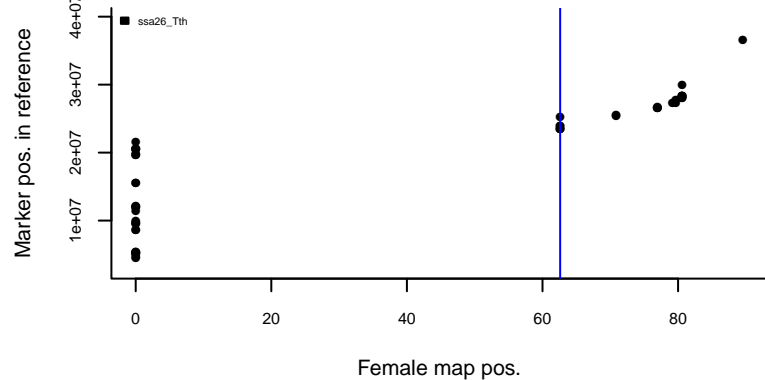
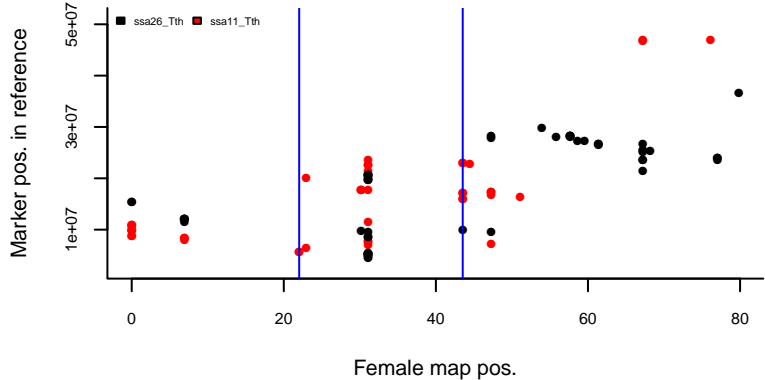
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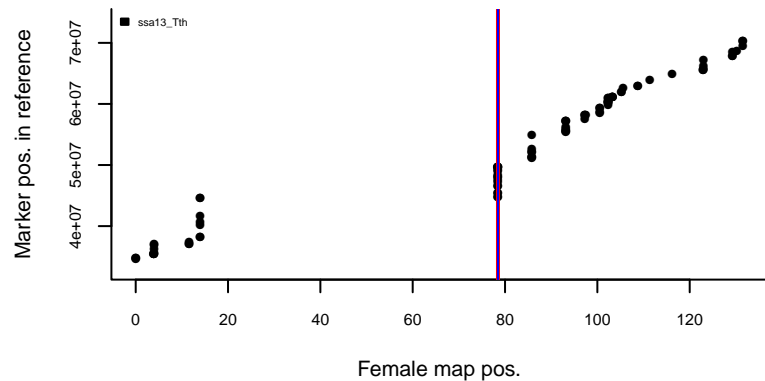
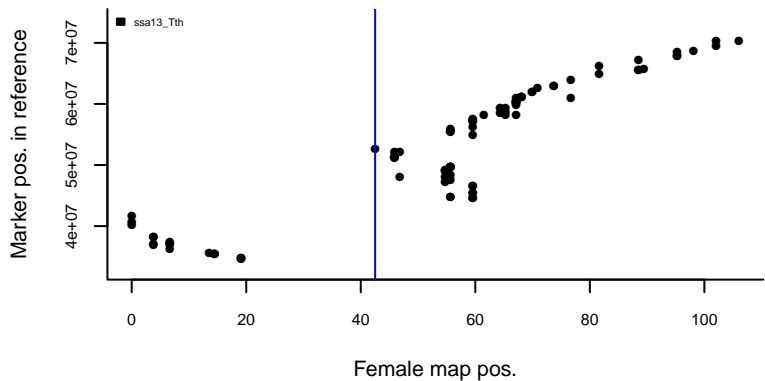
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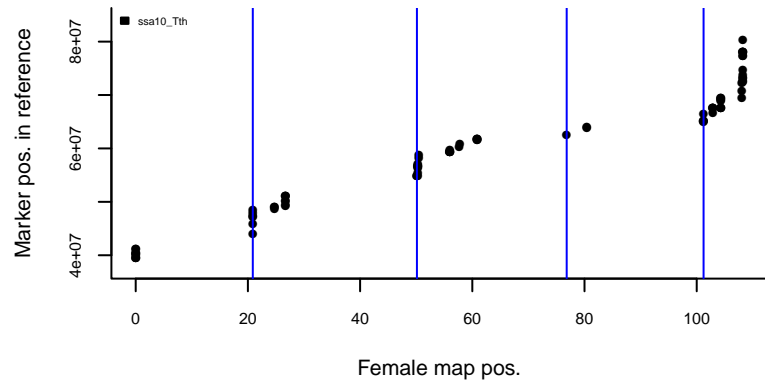
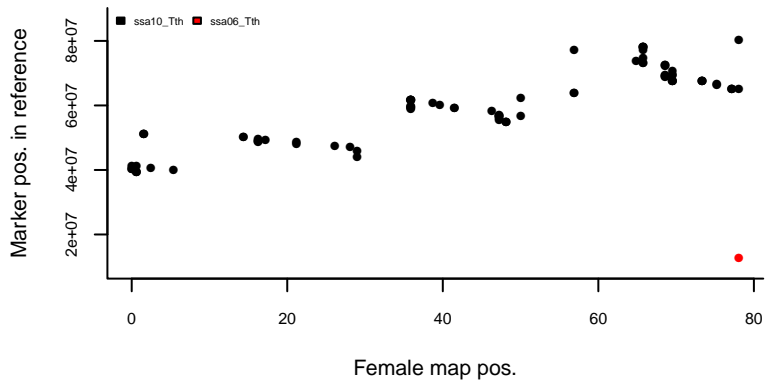
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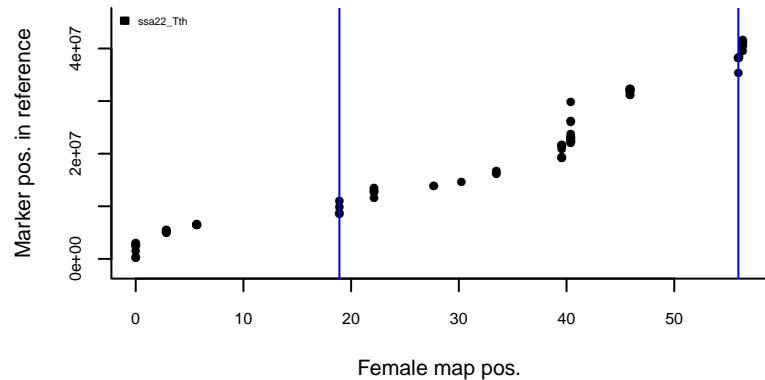
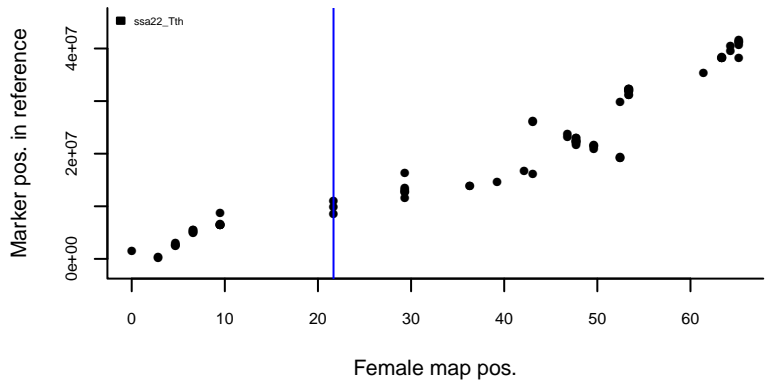
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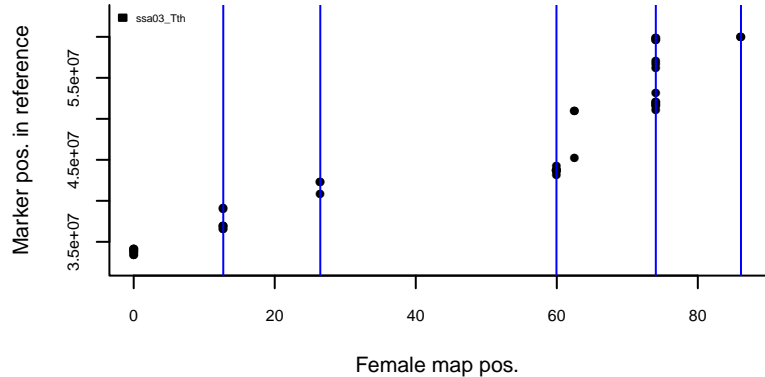
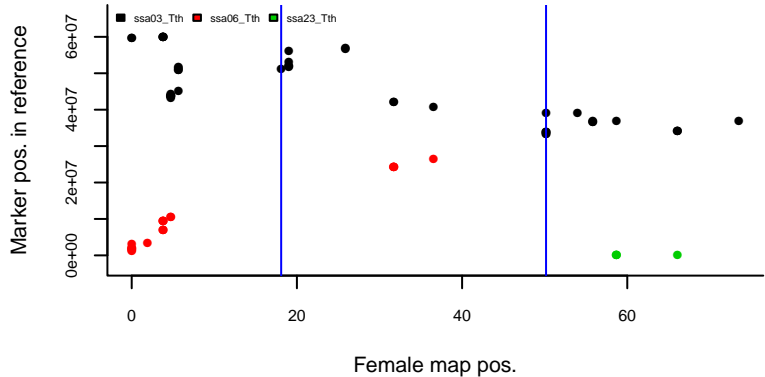
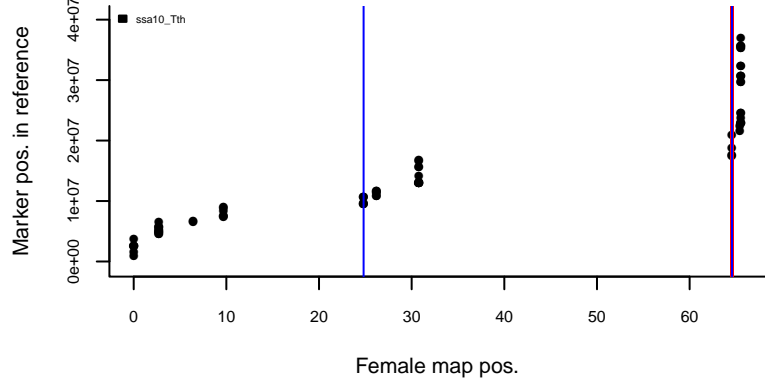
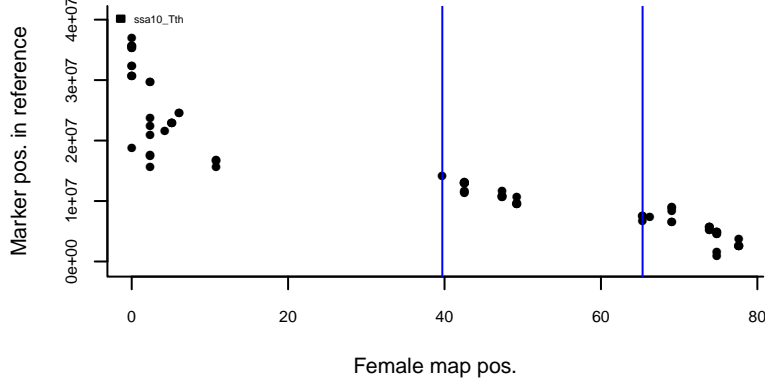
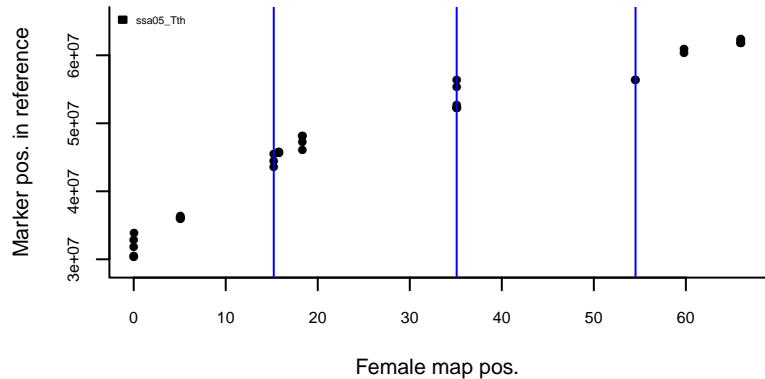
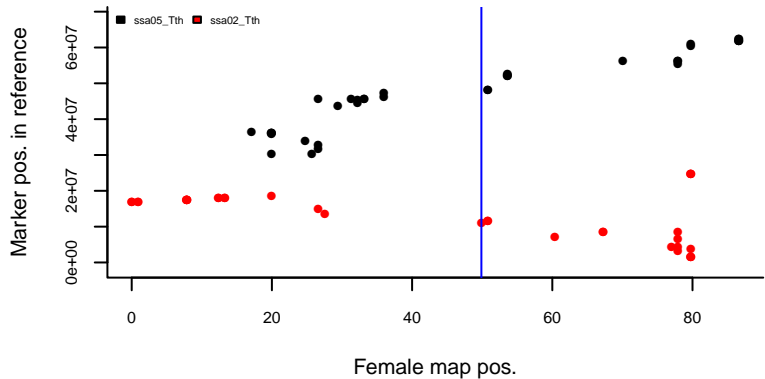
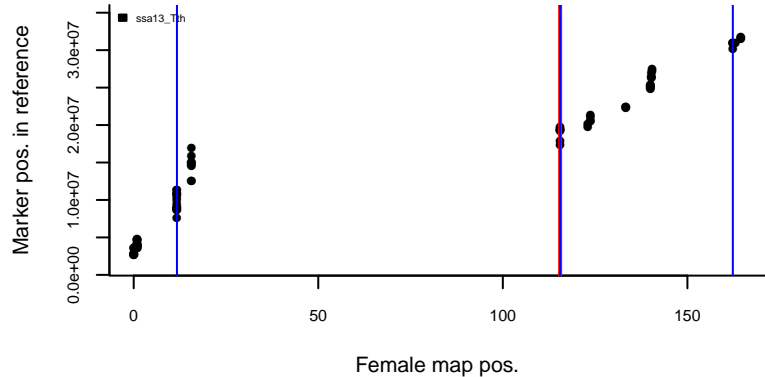
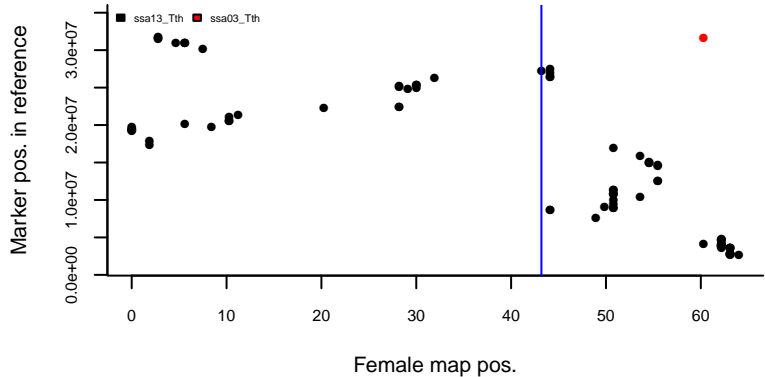
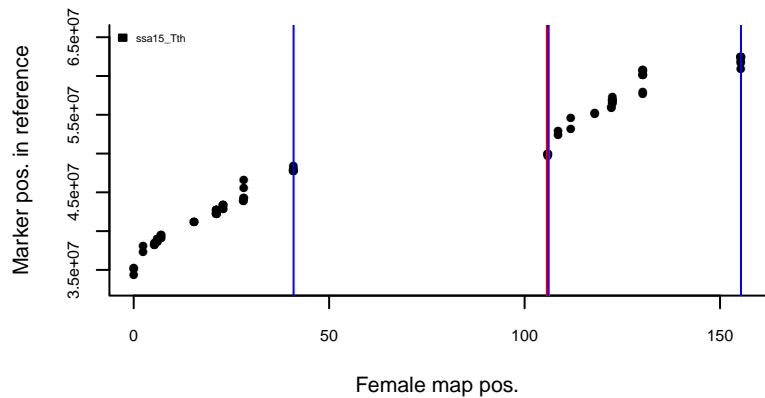
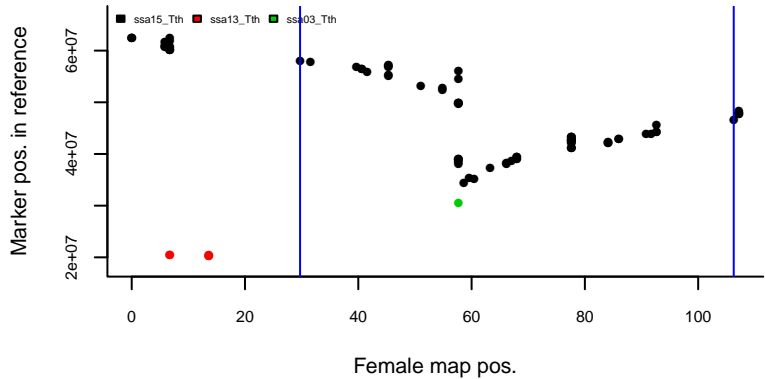
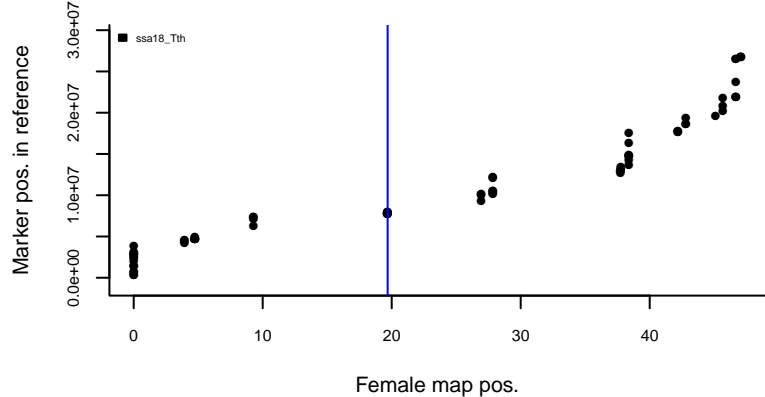
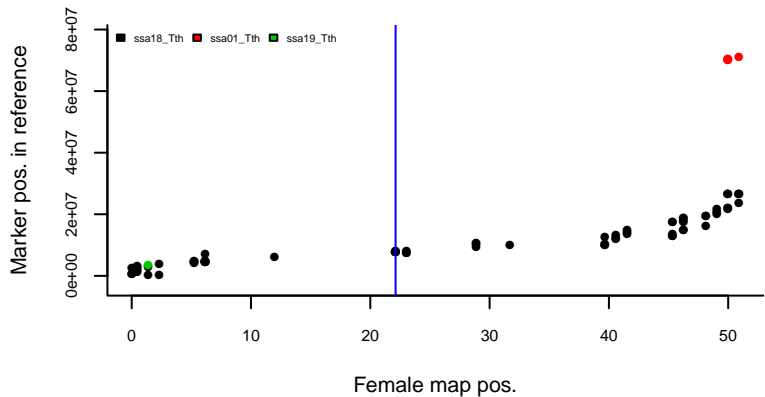


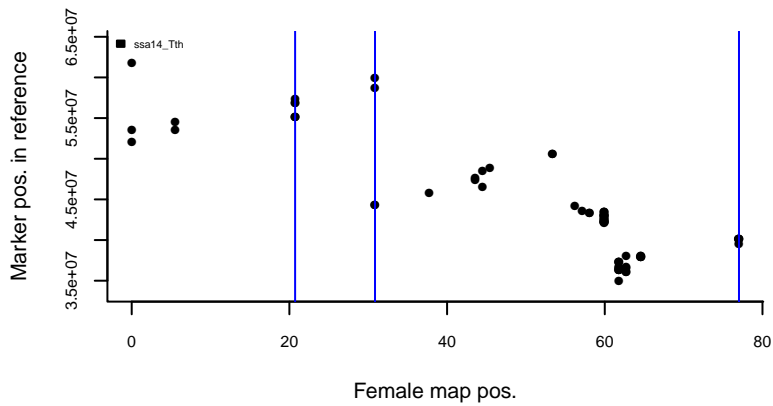
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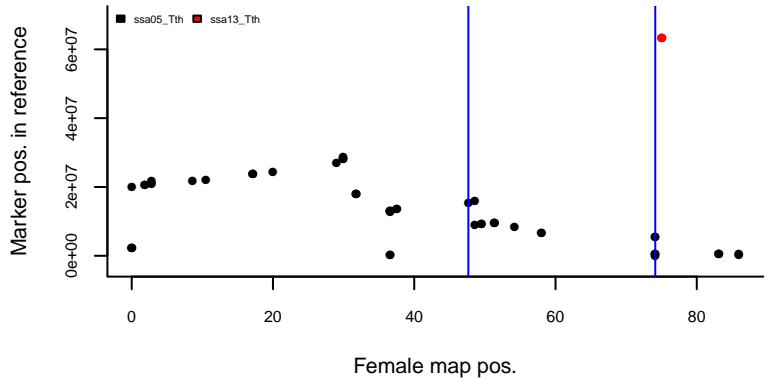
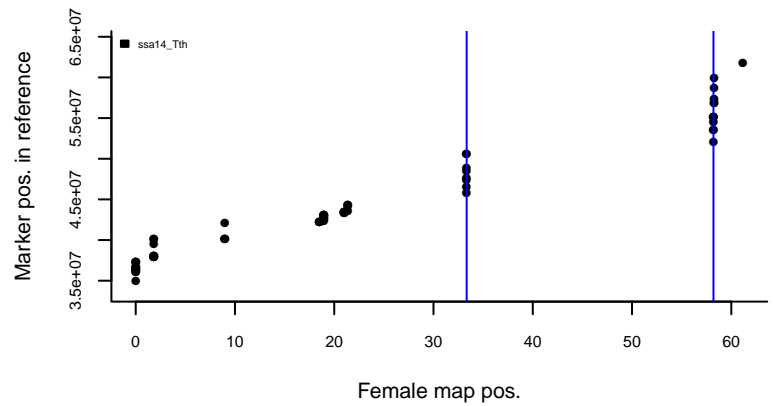
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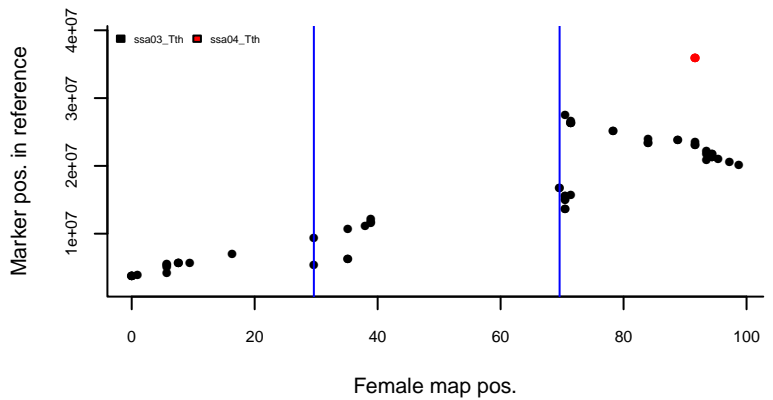
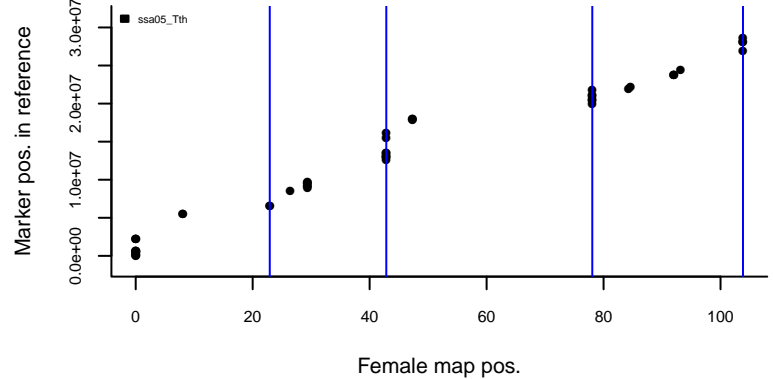




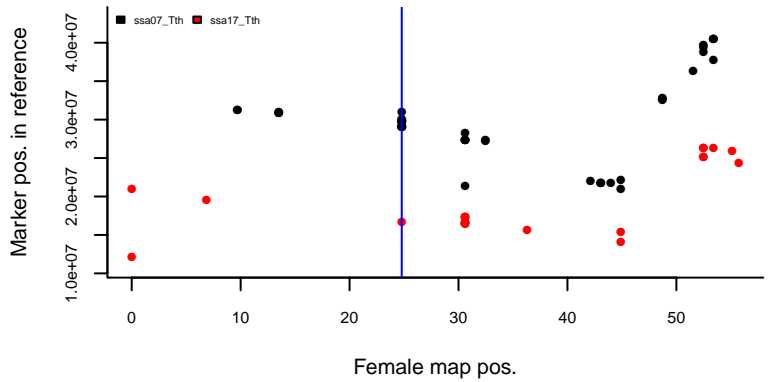
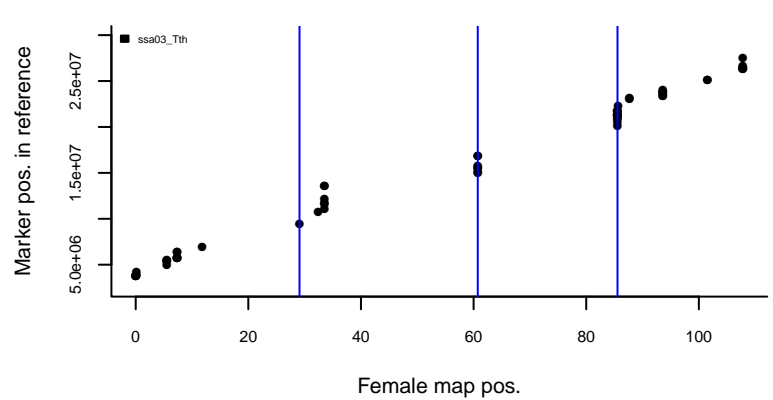
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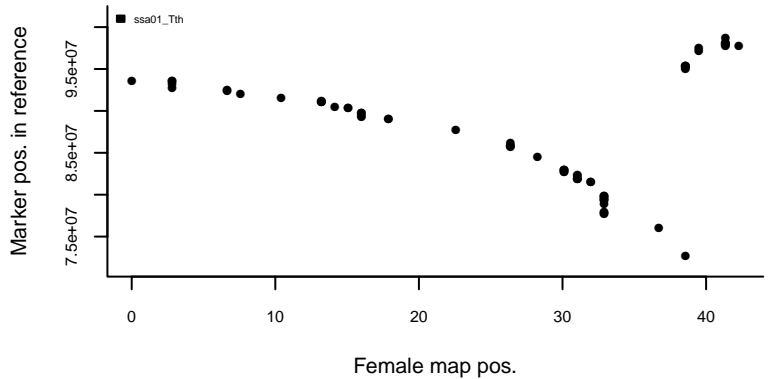
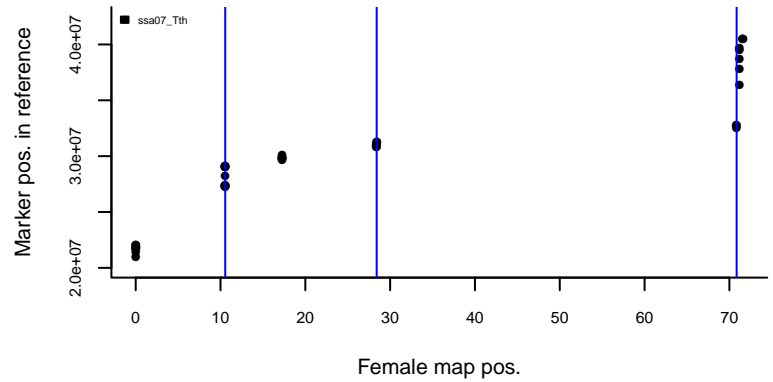
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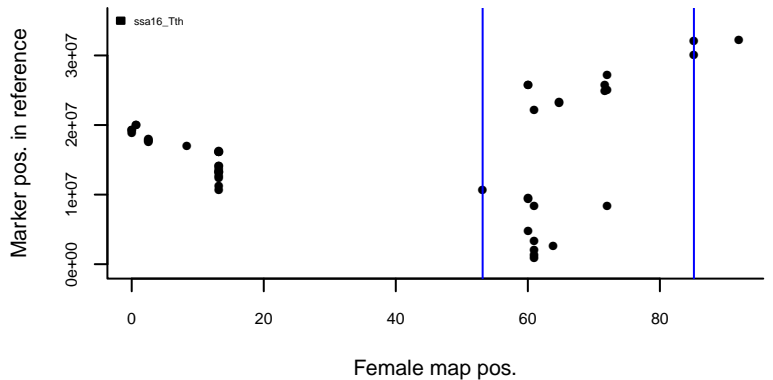
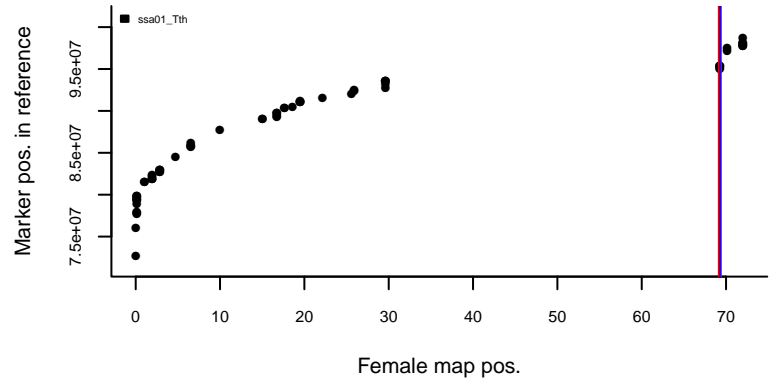
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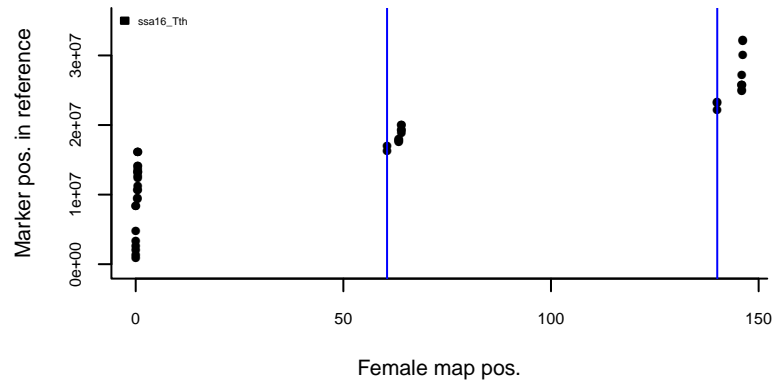
**LG 39**



**LG 40**

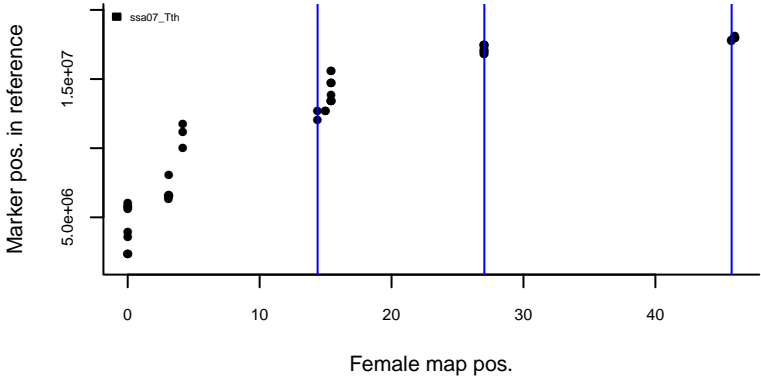
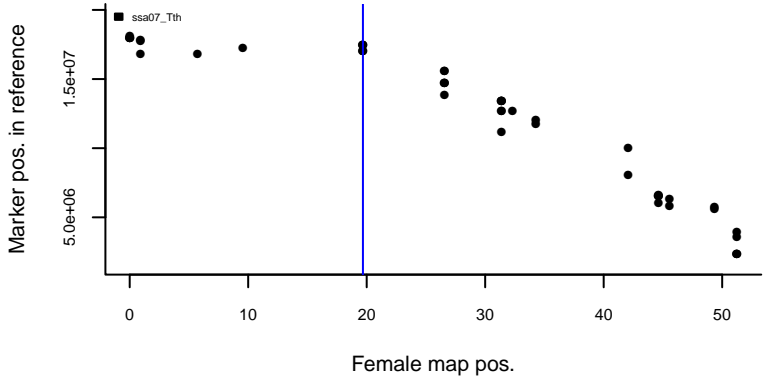


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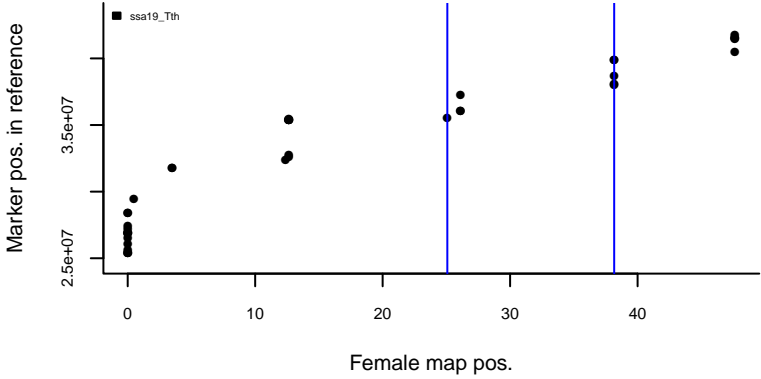
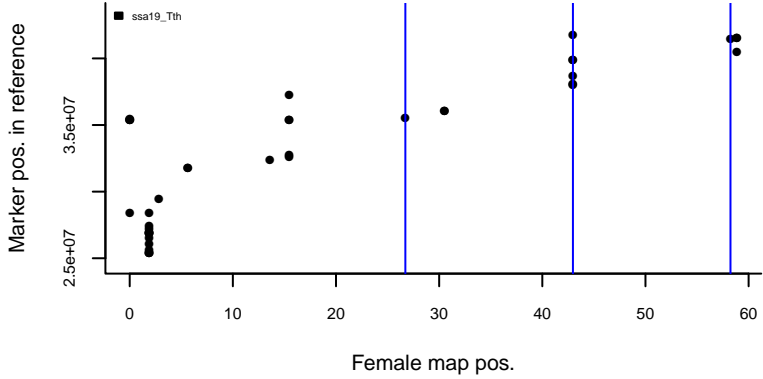




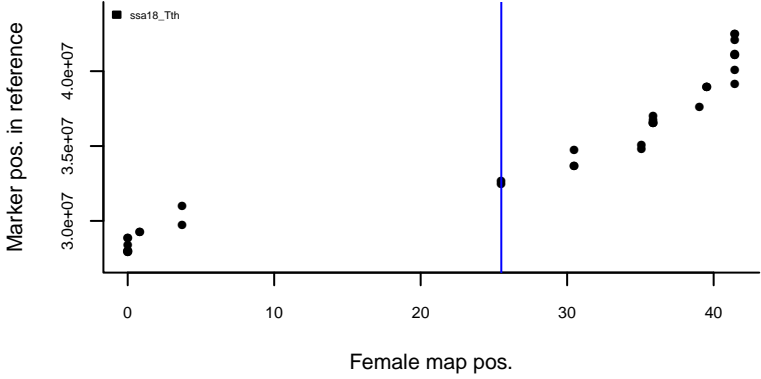
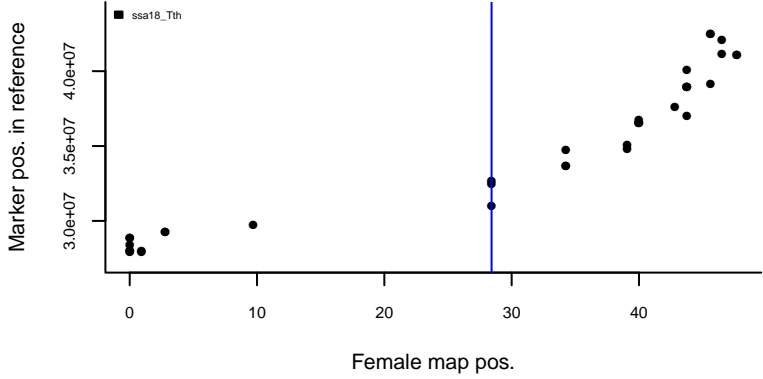
LG 42



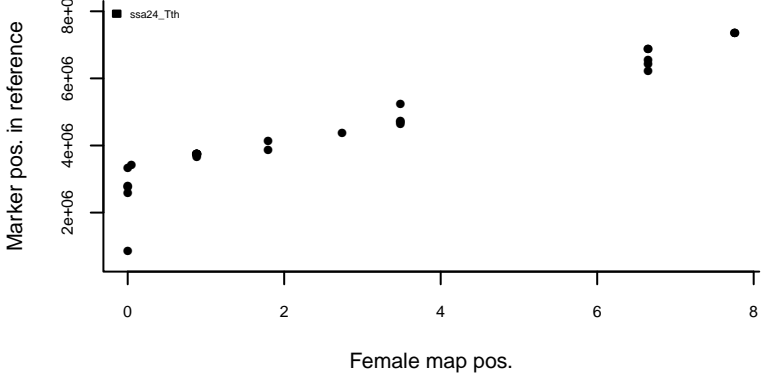
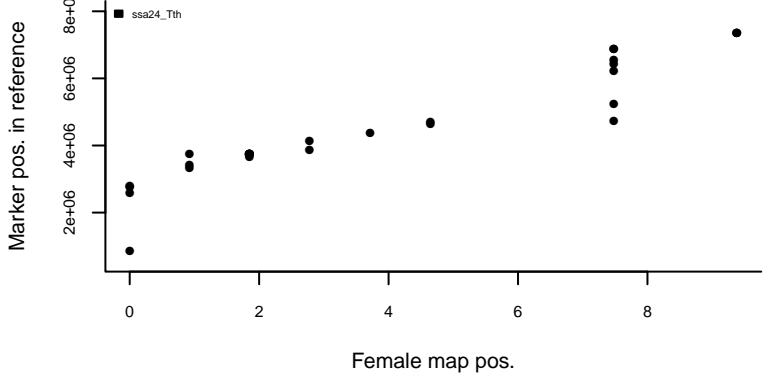
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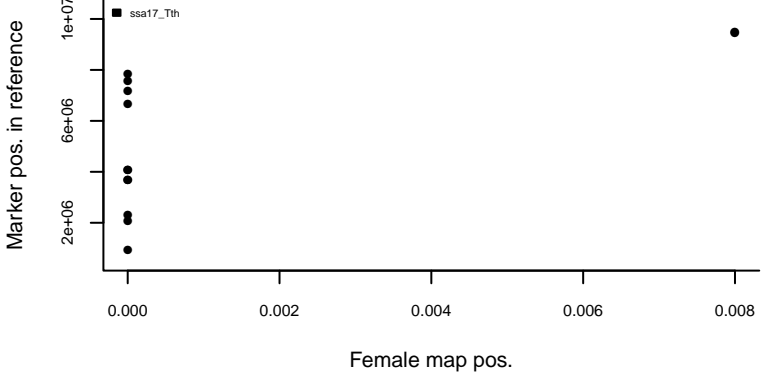
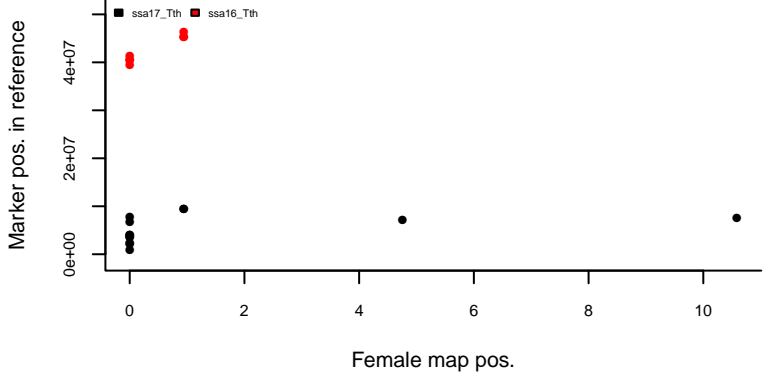
LG 44



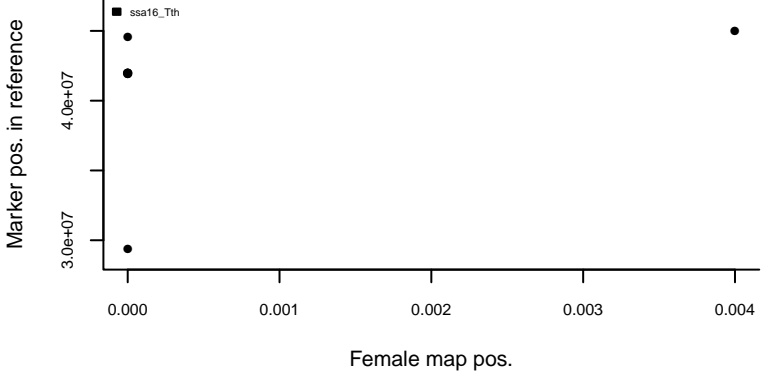
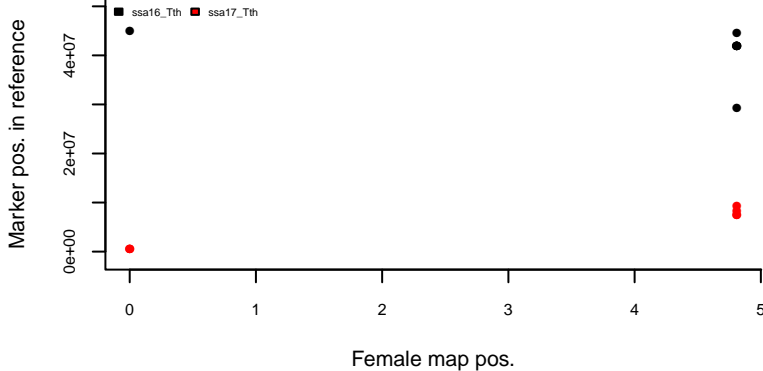
LG 45



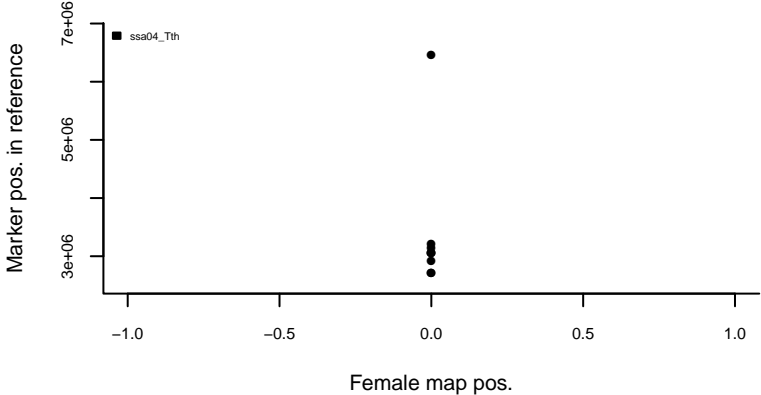
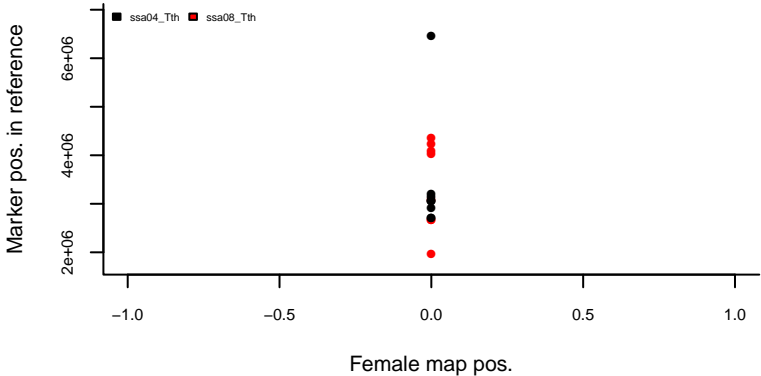
LG 46



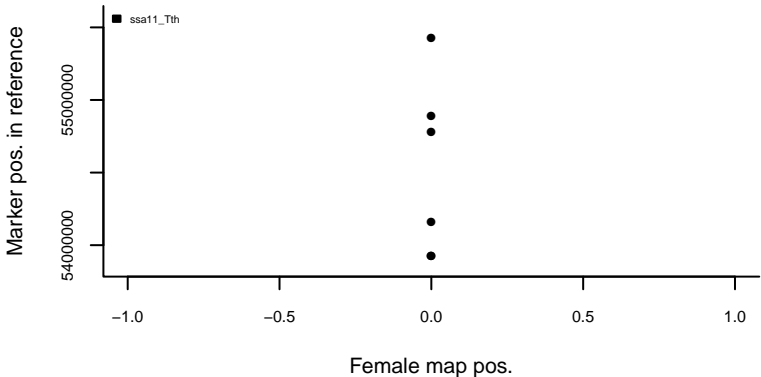
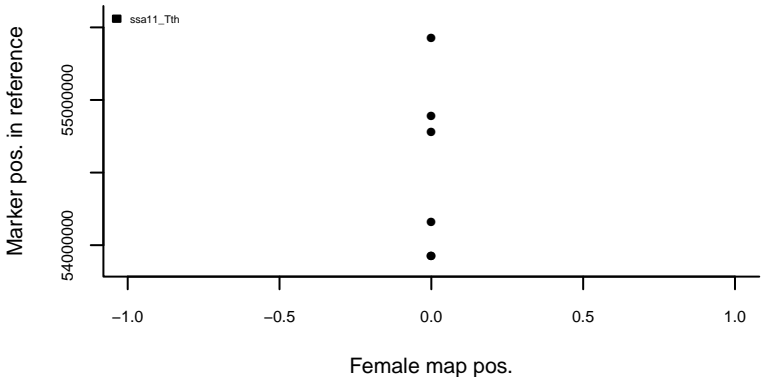
LG 47



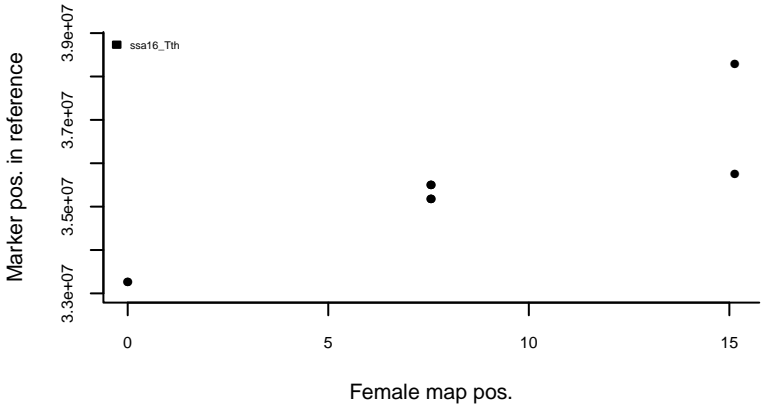
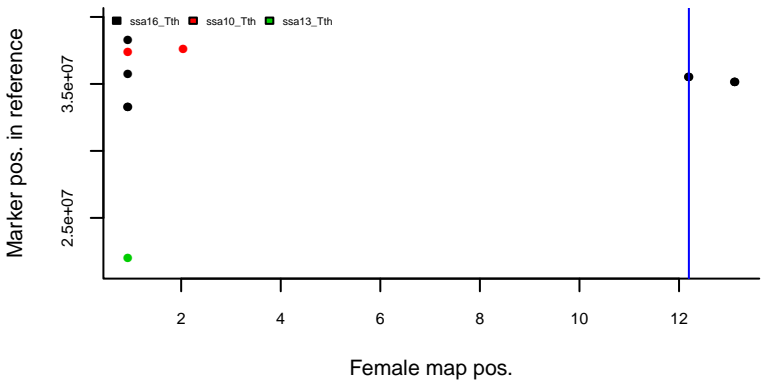
LG 48



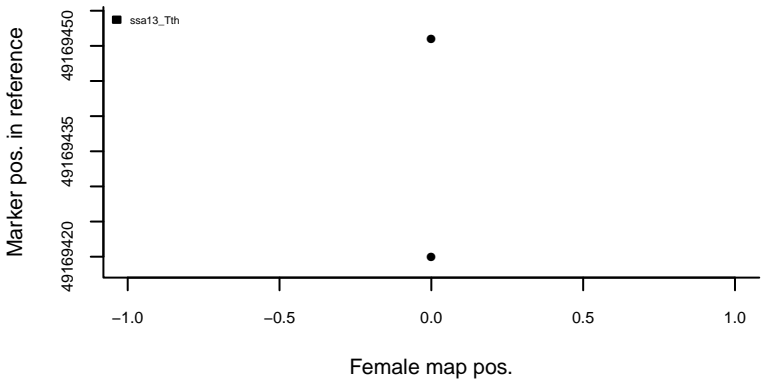
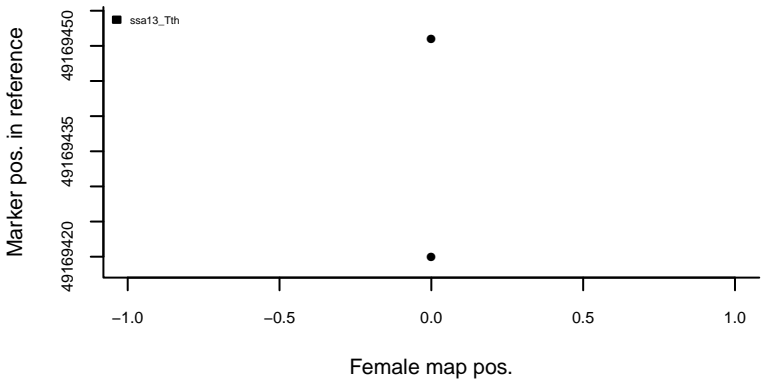
LG 49



LG 50



LG 51



**Figure S2**  
Female-based linkage maps of the European grayling chromosomes (excluding linkage groups for 9A, 9B and 25B where linkage groups could not be derived from the data). See Table S2 for complete lists of markers in the linkage groups.



**Figure S3**

Repeat elements at the European grayling genome. Principal components of element abundance peak positions along each chromosome (A) and element abundancies in the chromosomes (B).

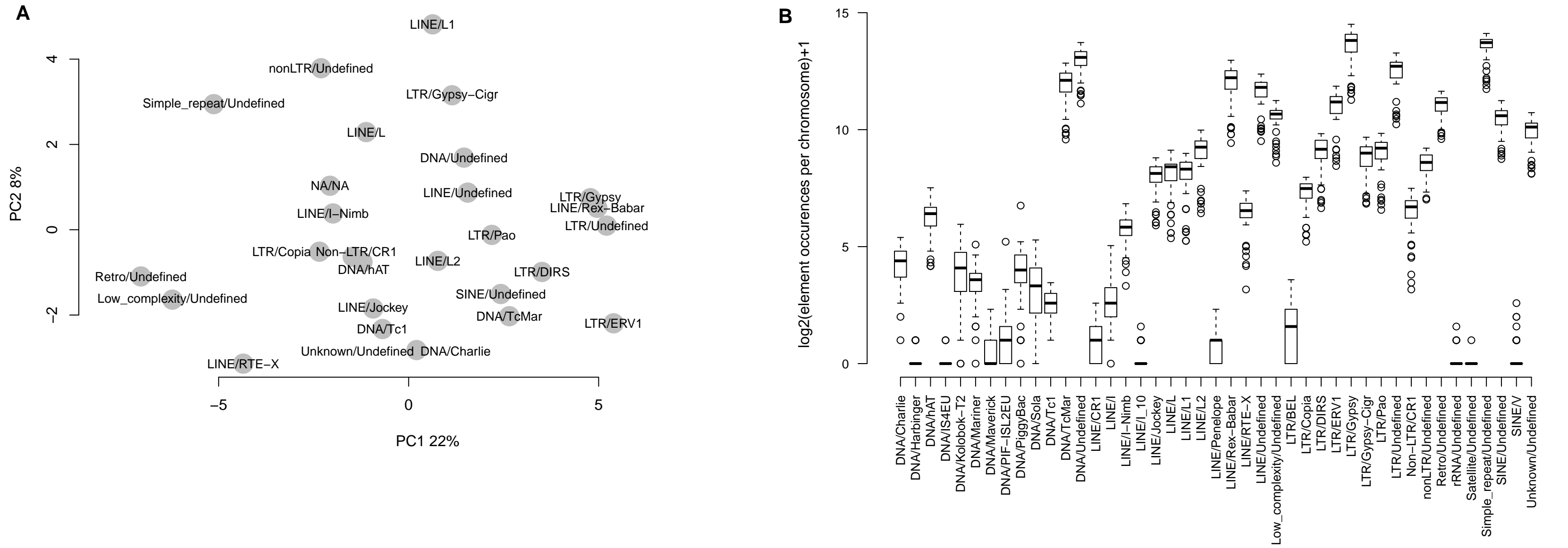


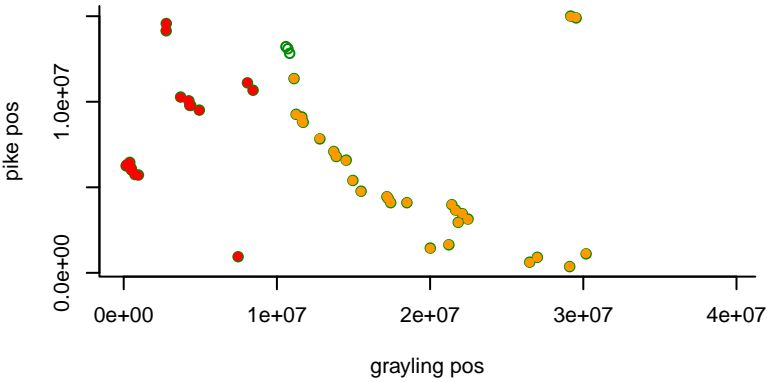
Figure S4

Scaffold positions in 119 synteny blocks in the European grayling vs. Northern pike position comparison (A) and in the European grayling vs. Atlantic salmon position comparison (B).

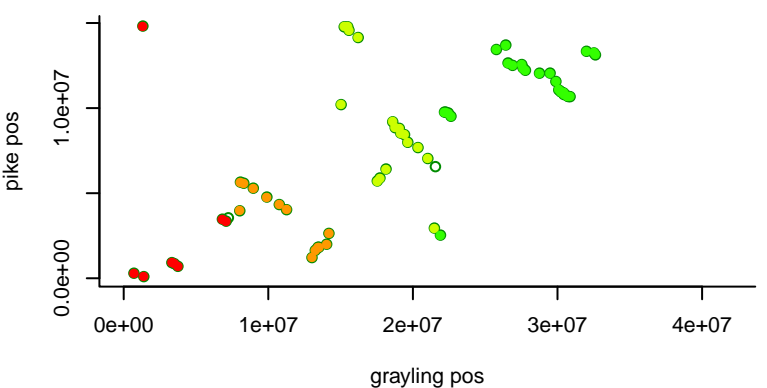
The predicted peak abundance of Tc1-Mariner elements in each European grayling chromosome are marked with purple lines. The block ordering (from 1st to up to 5th block) within each European grayling chromosome are marked in different colors, see color legends in each figure (B). The genome-wide block numbering (from 1st to 119th block) and whether the block orientation is inverted between European grayling and Atlantic salmon are marked above each block in the figures (B).

A Synteny with northern pike

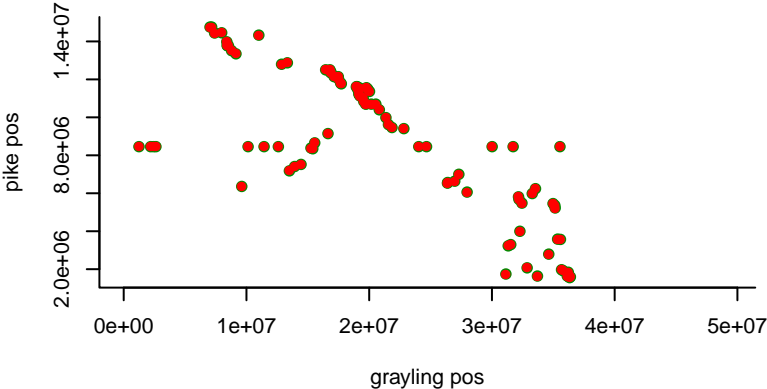
1A



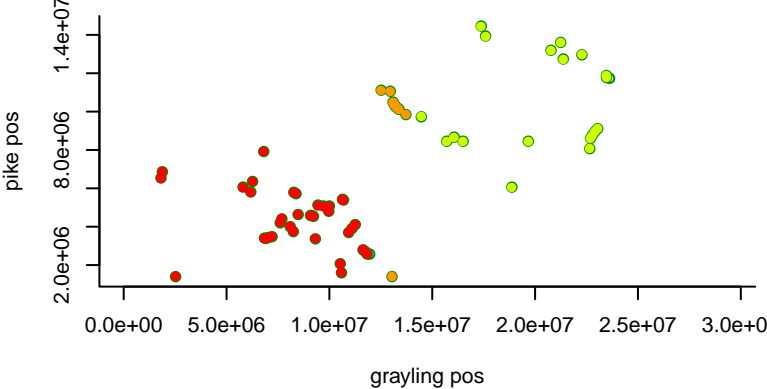
1B



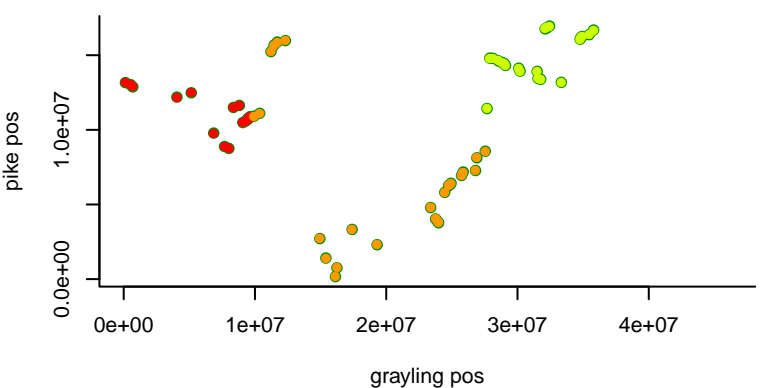
2A



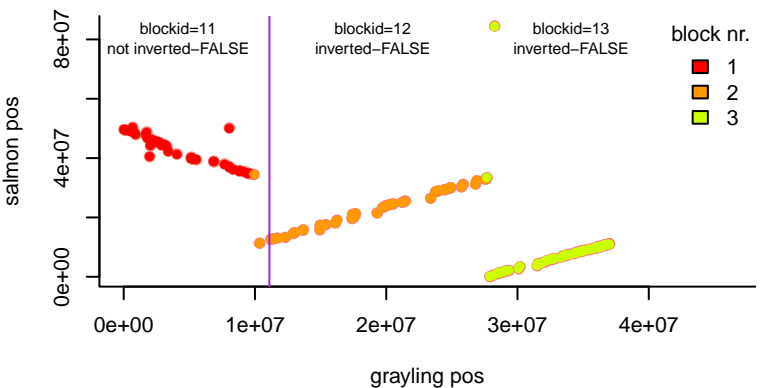
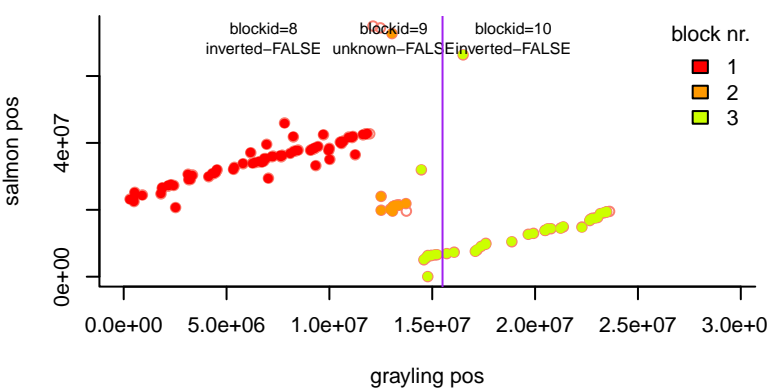
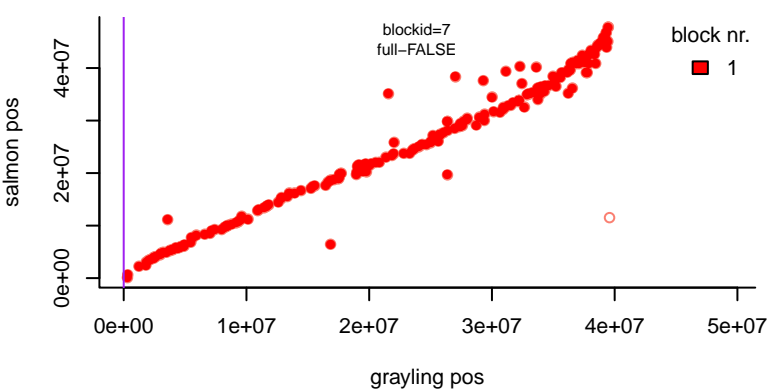
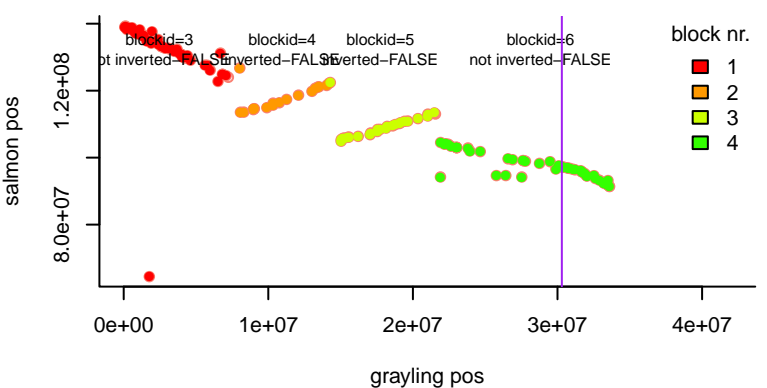
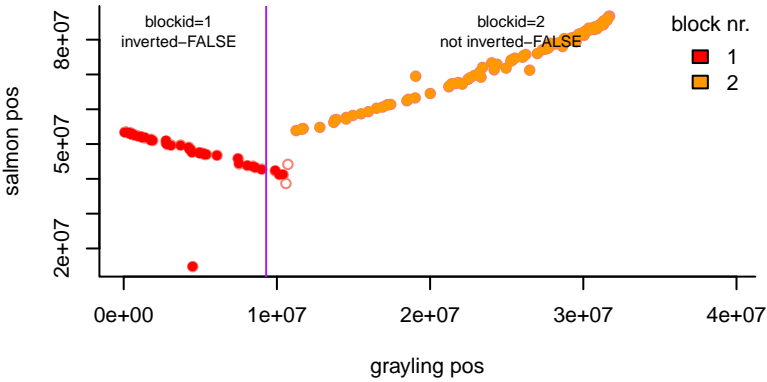
2B

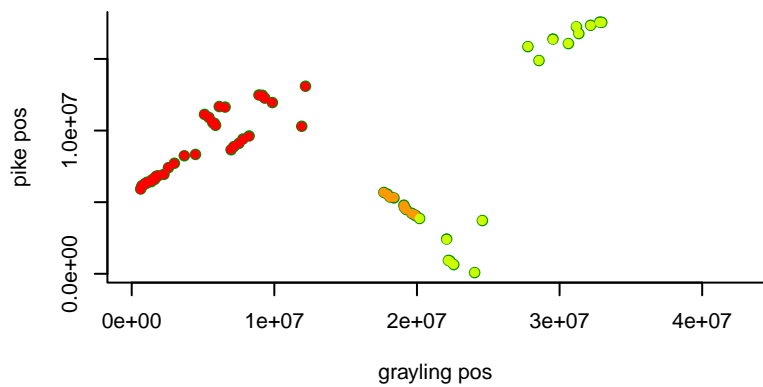


3A

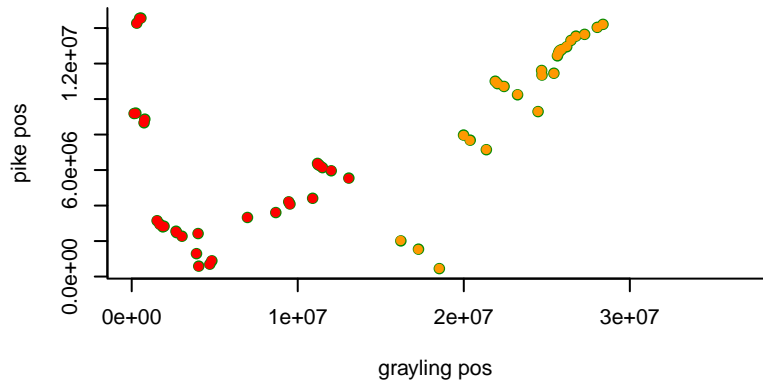
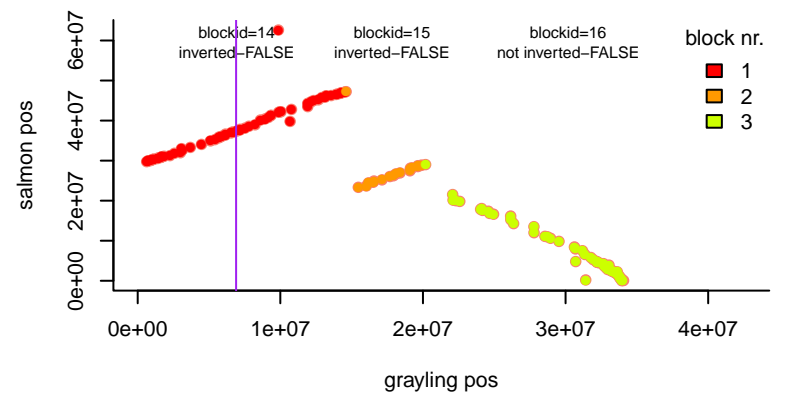


B Synteny with Atlantic salmon

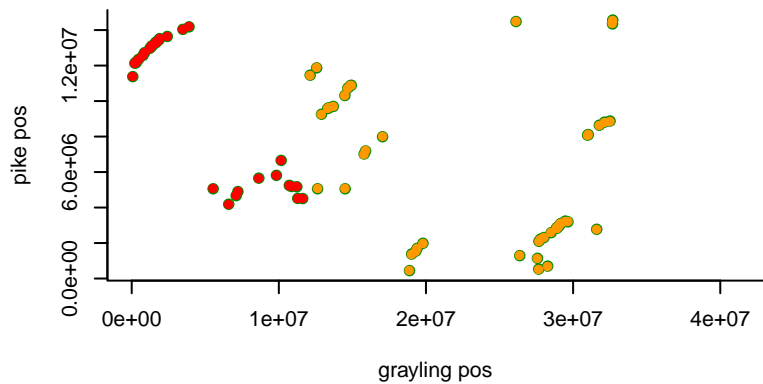
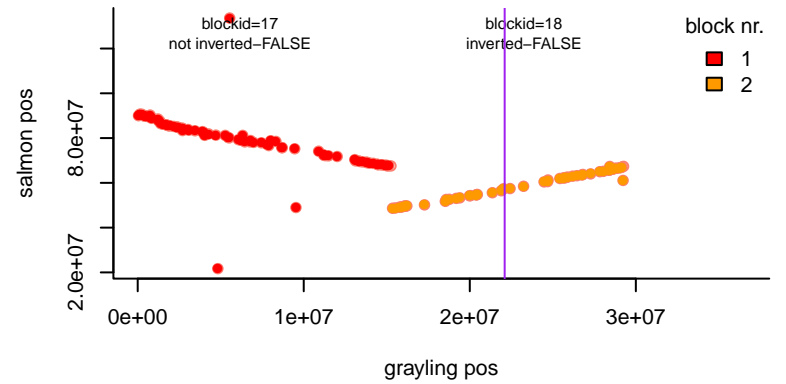




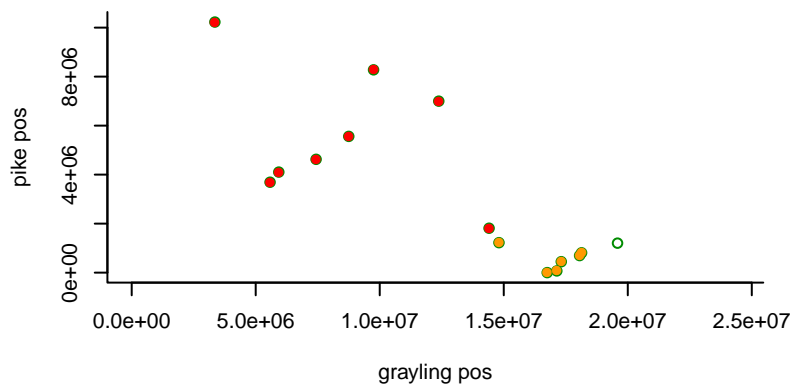
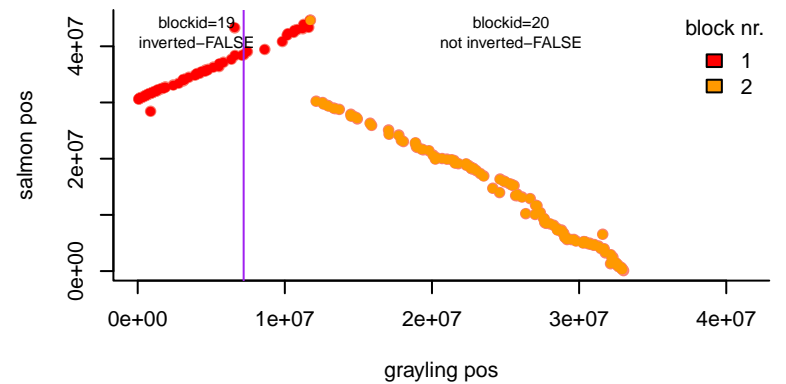
3B



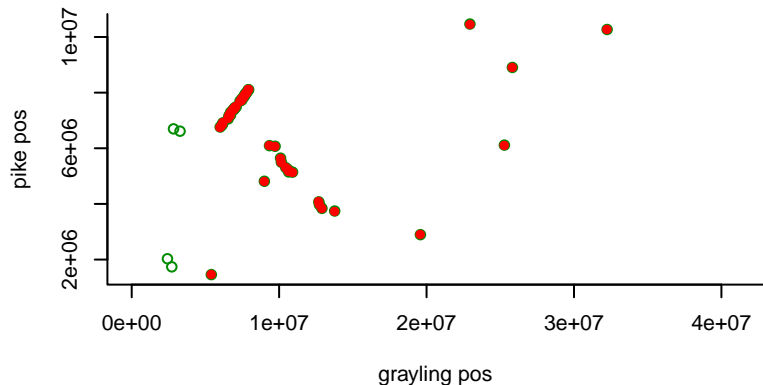
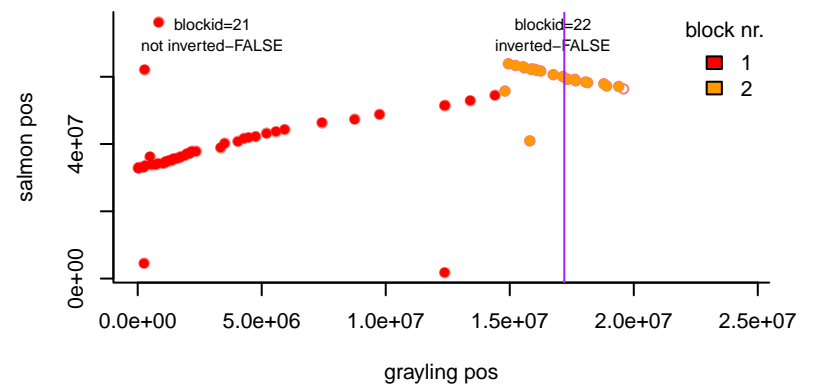
4A



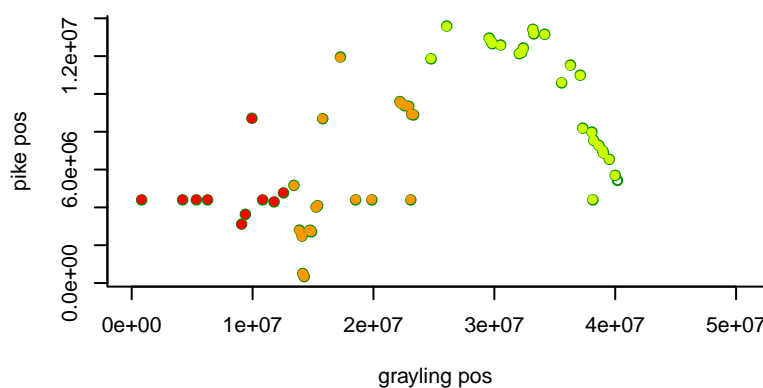
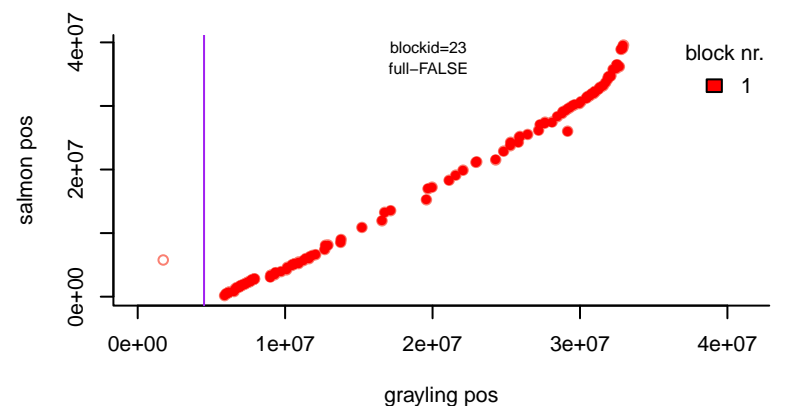
4B



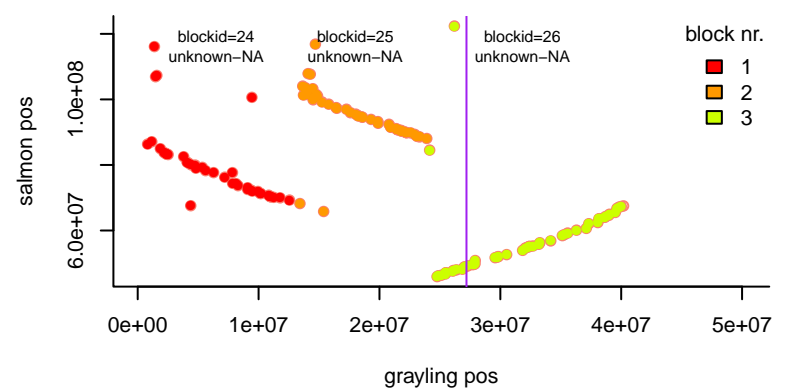
5A

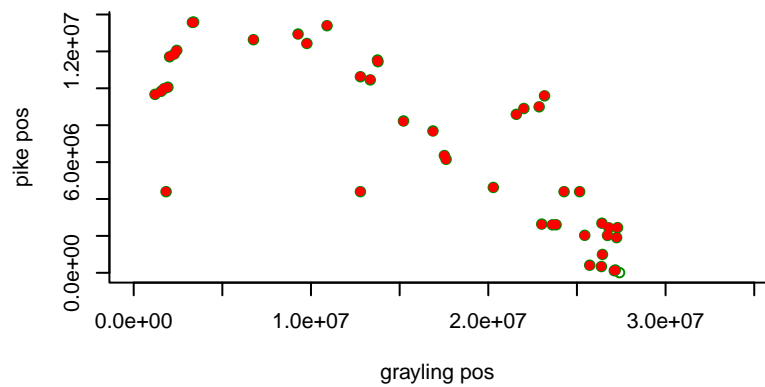


5B

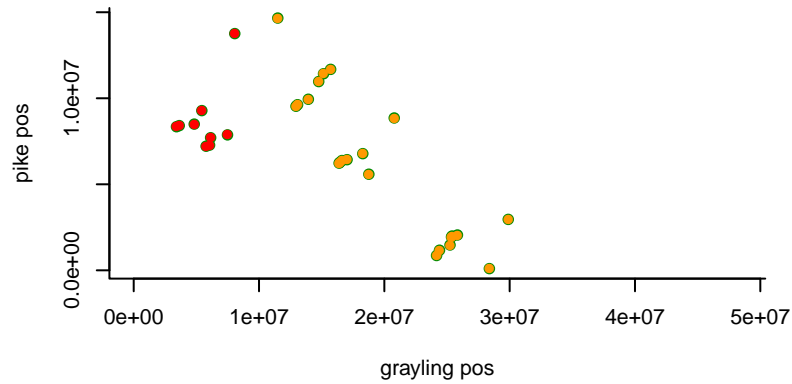
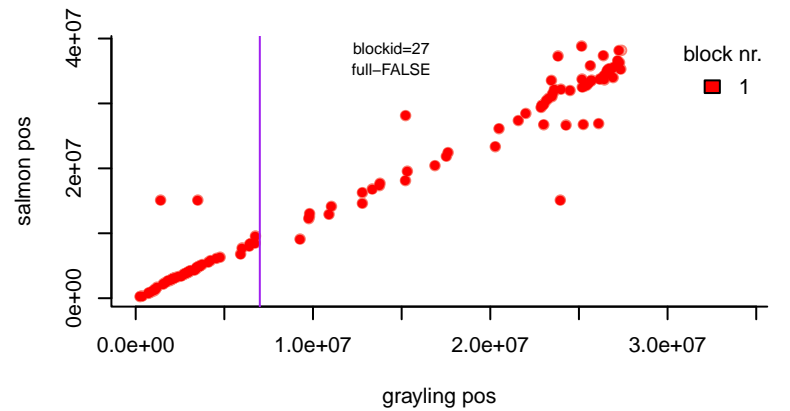


6A

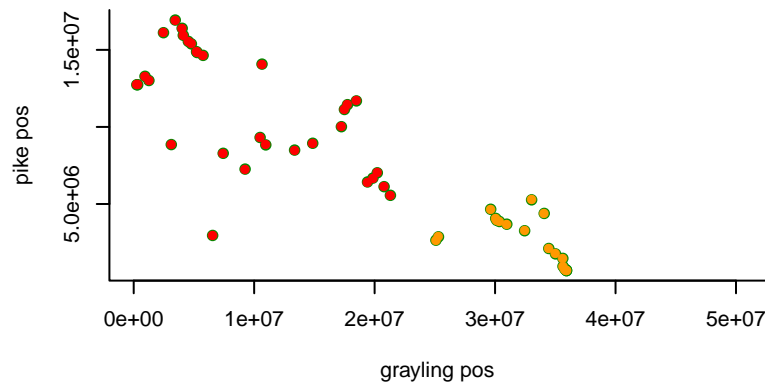
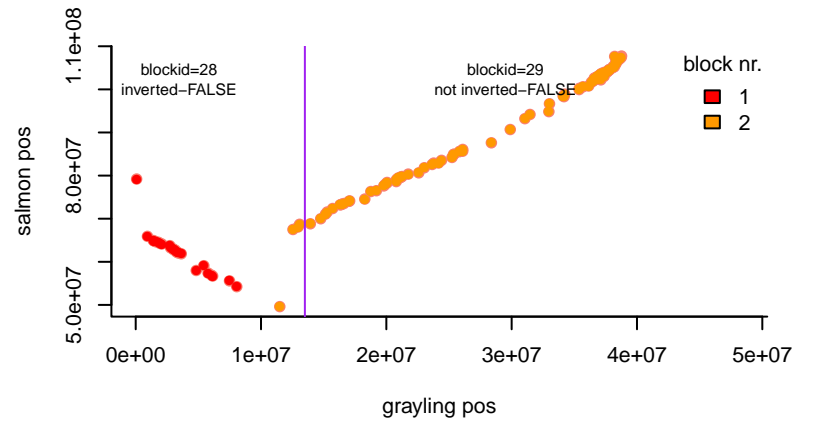




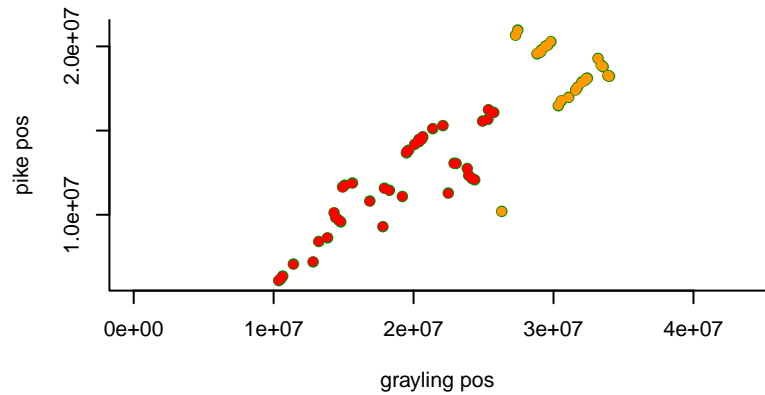
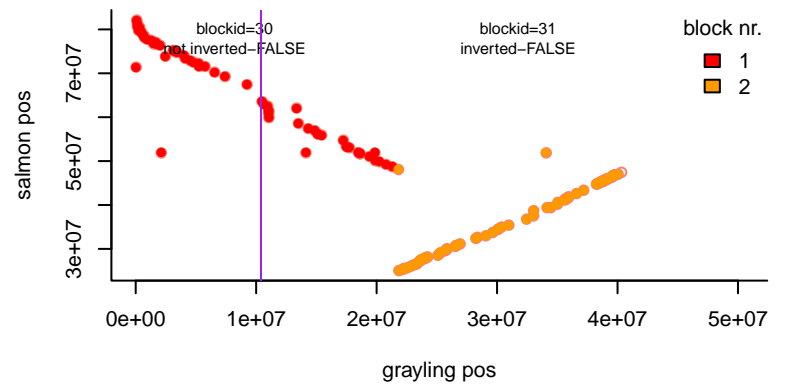
6B



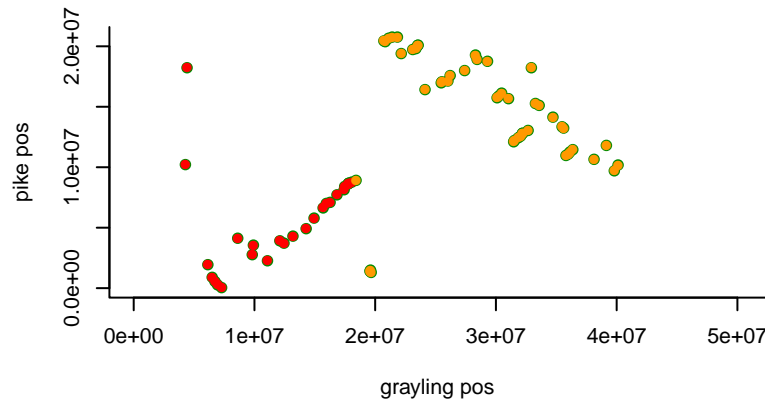
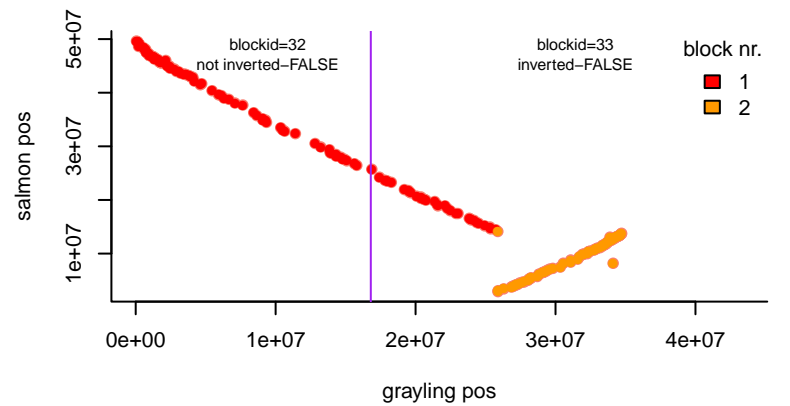
7A



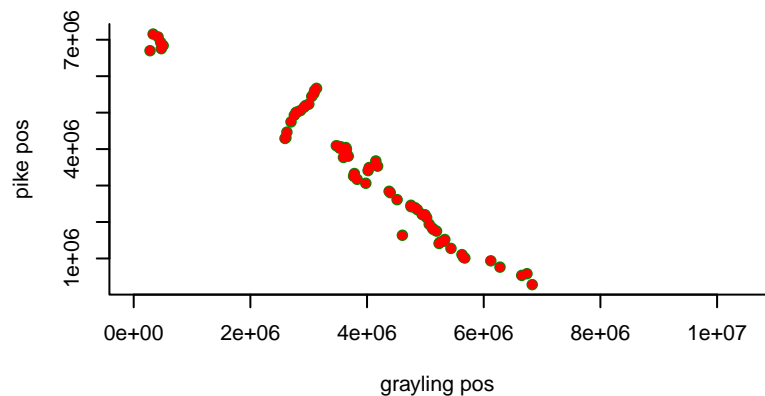
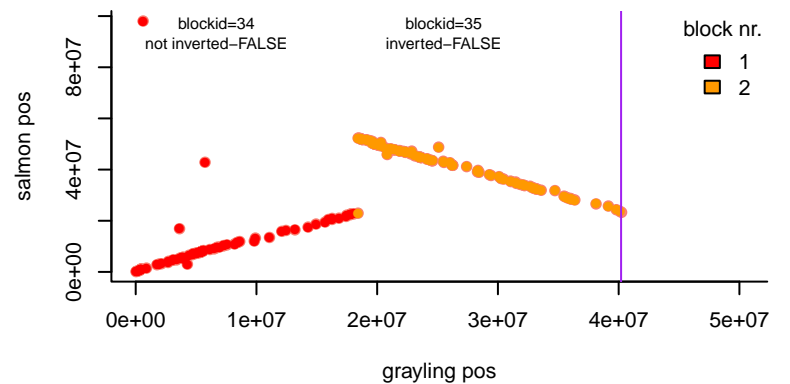
7B



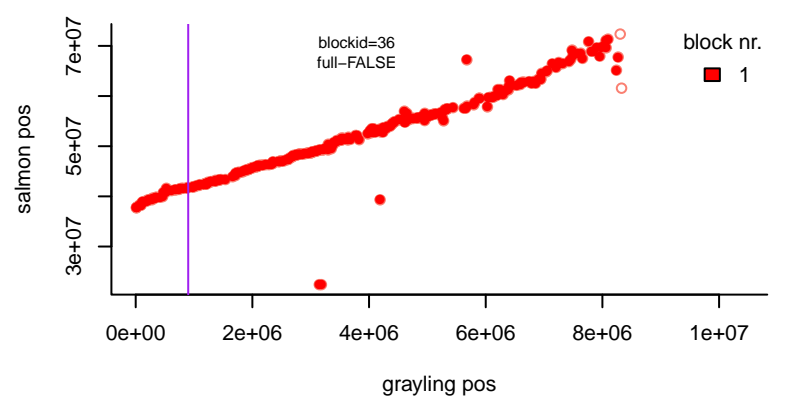
8A

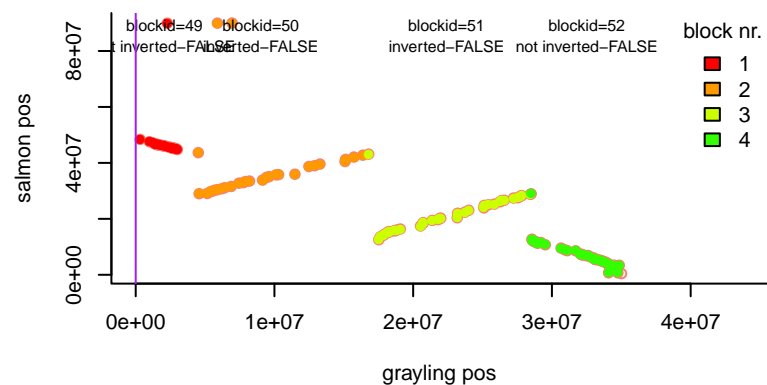
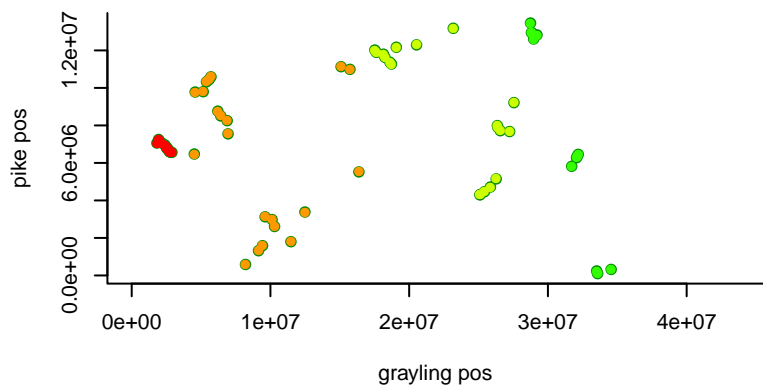
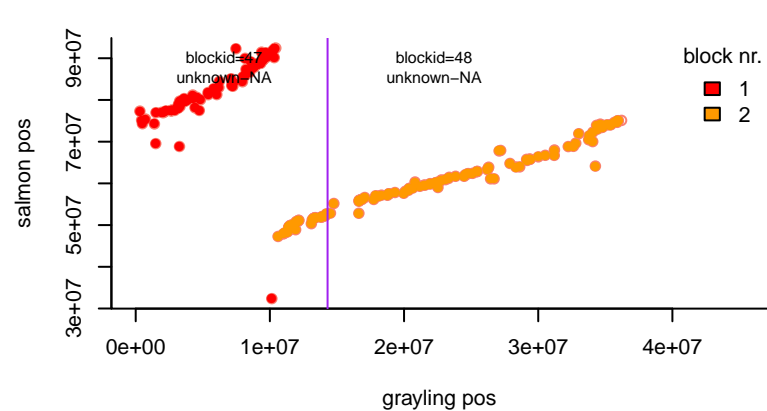
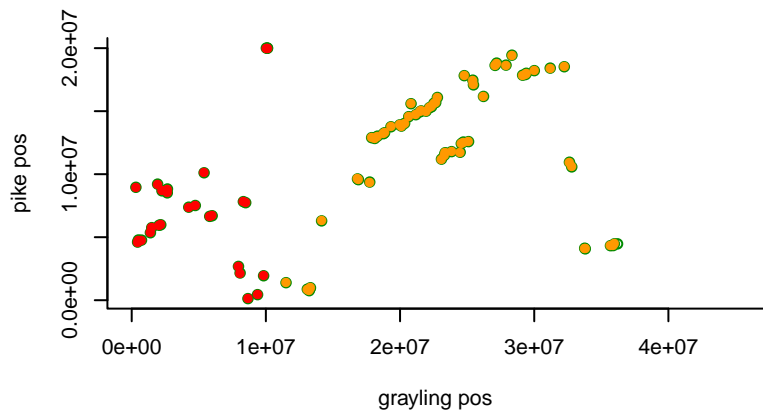
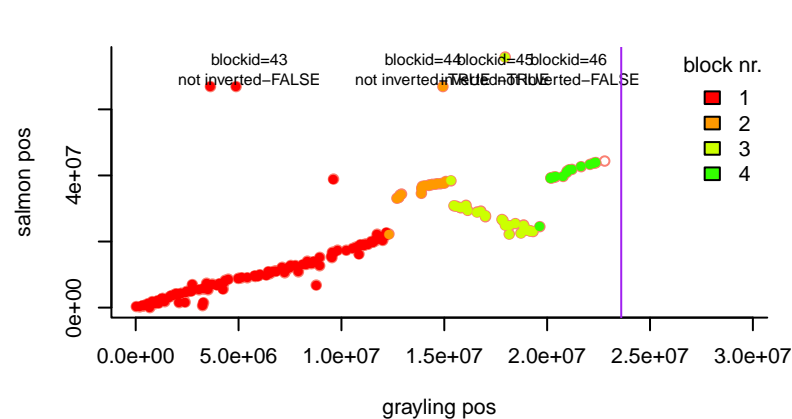
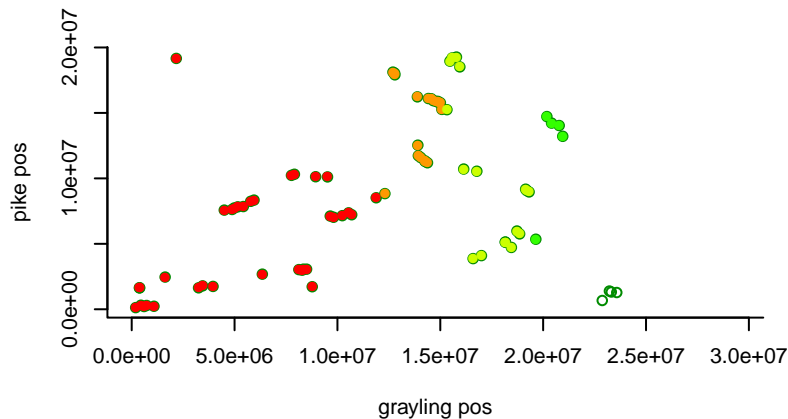
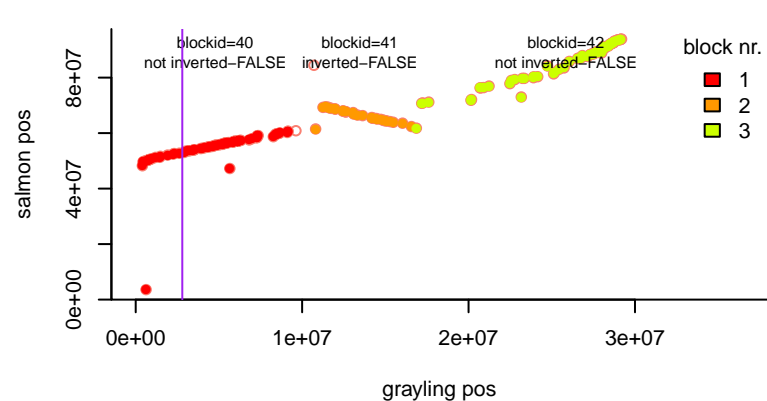
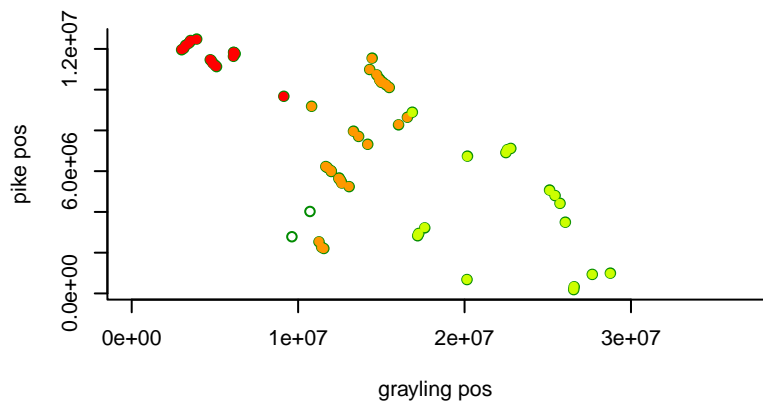
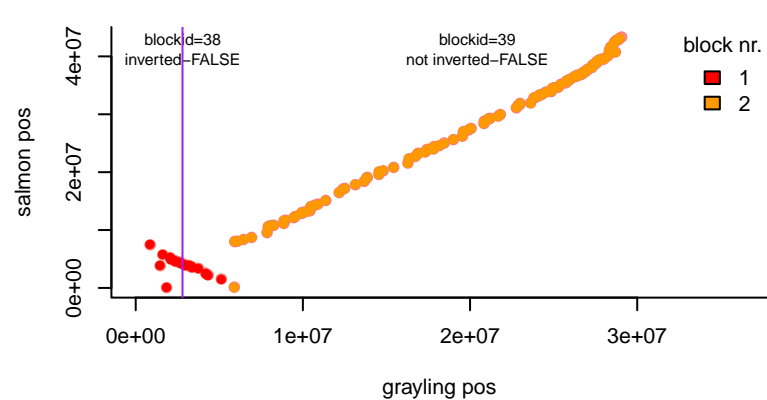
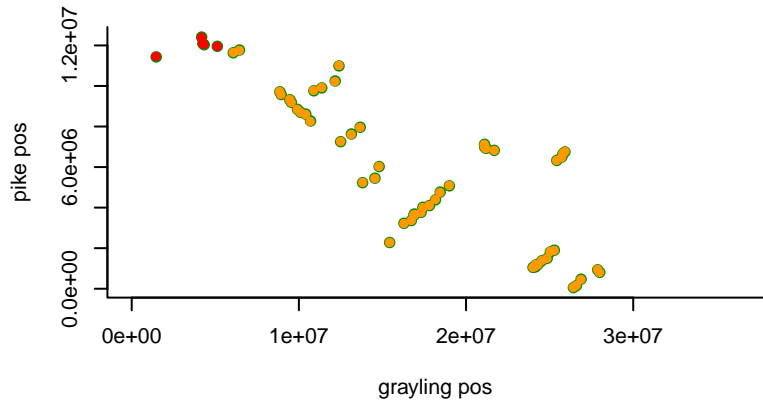
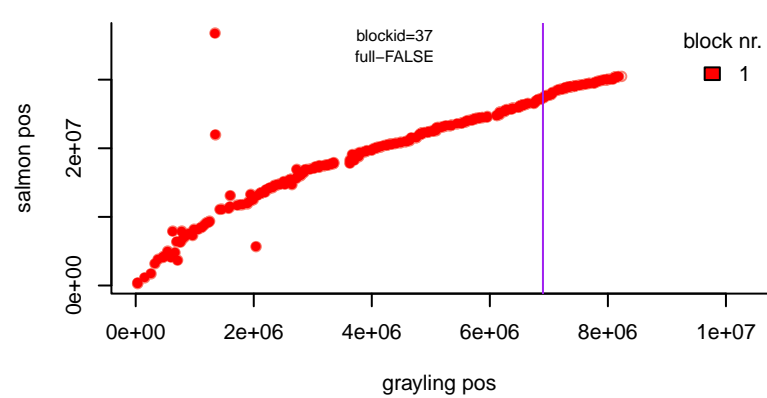
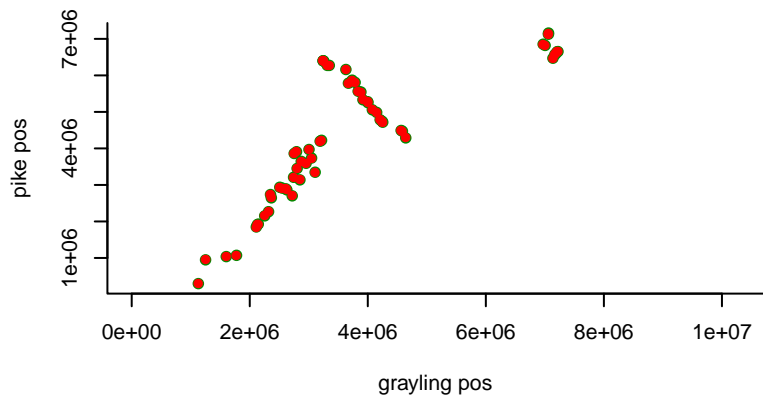


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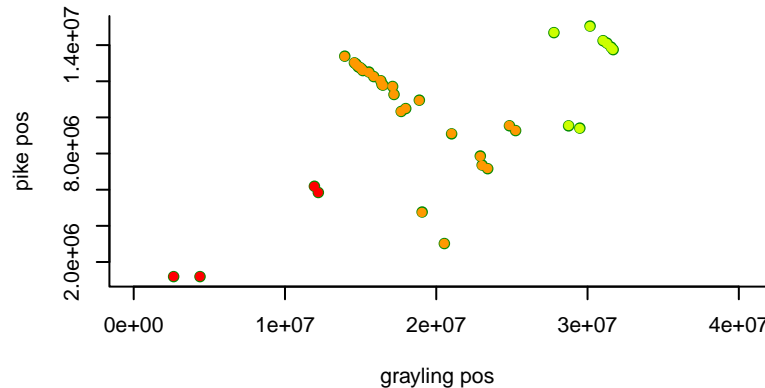
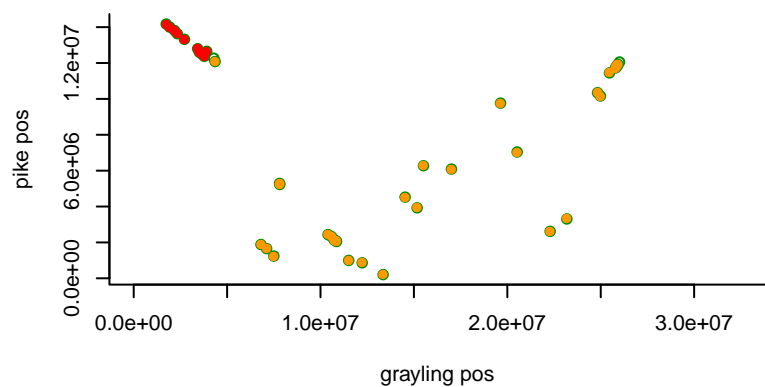
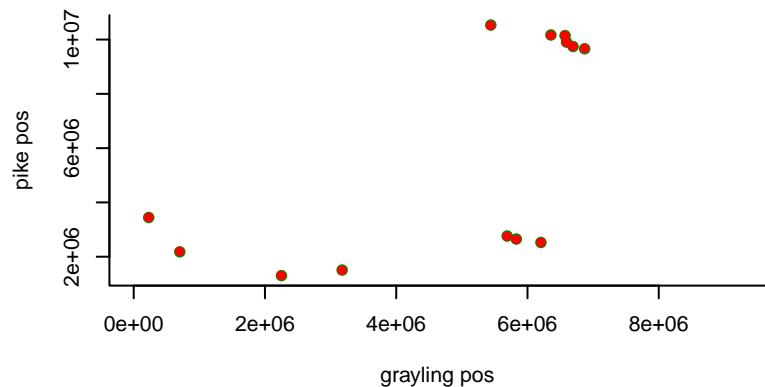
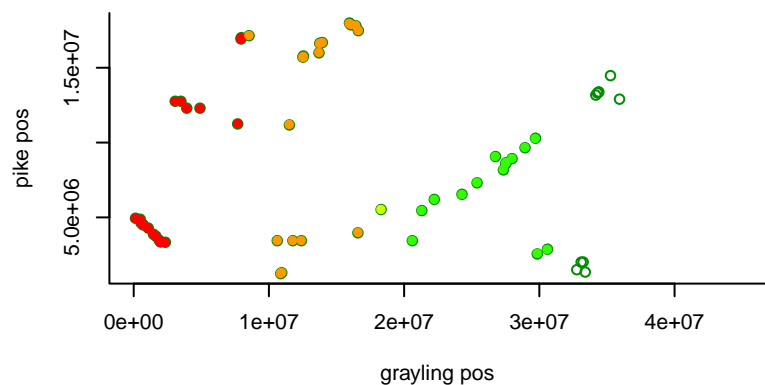
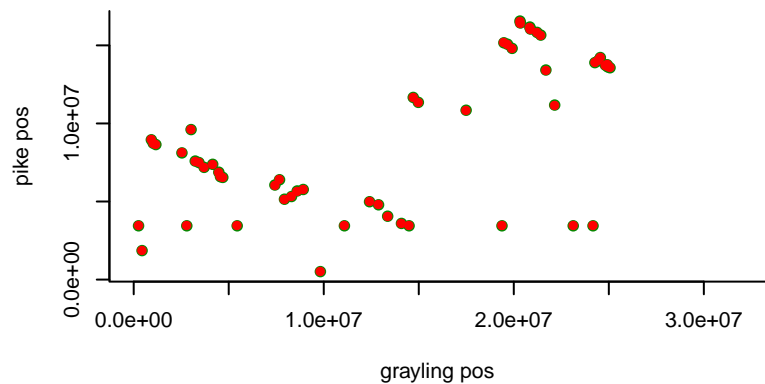
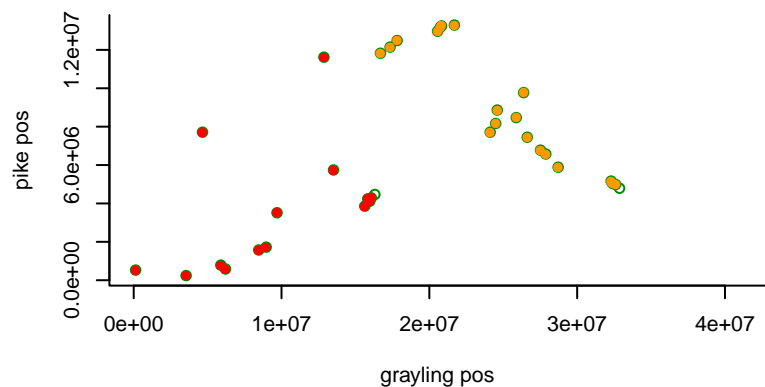


9A

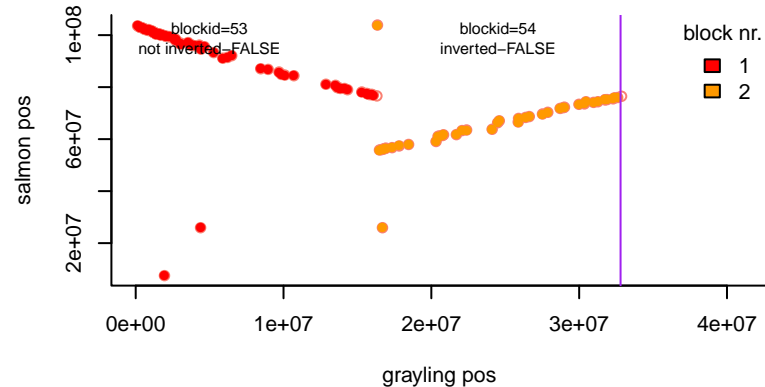




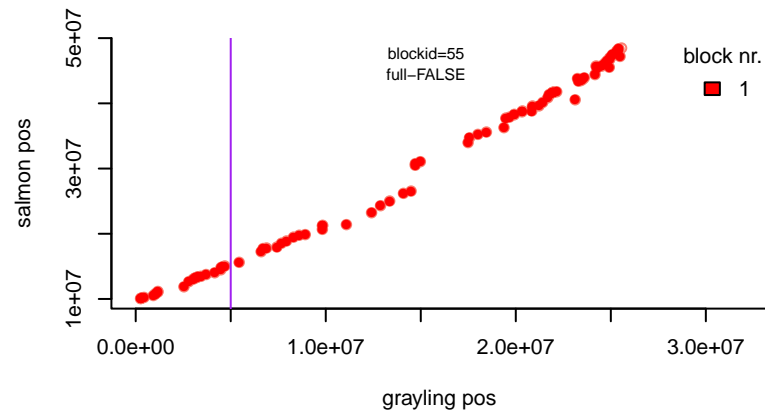




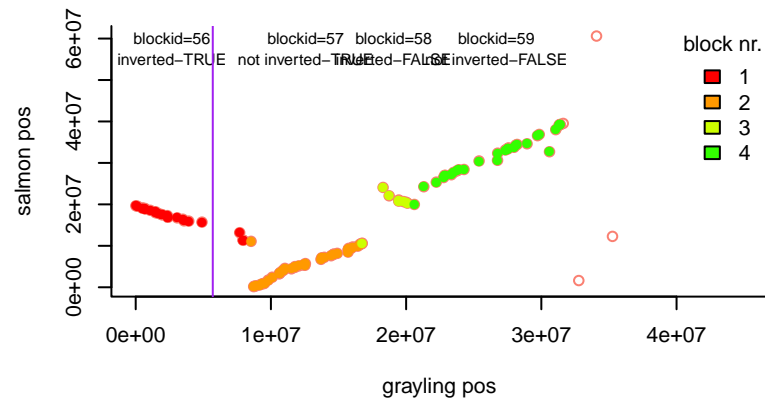
12B



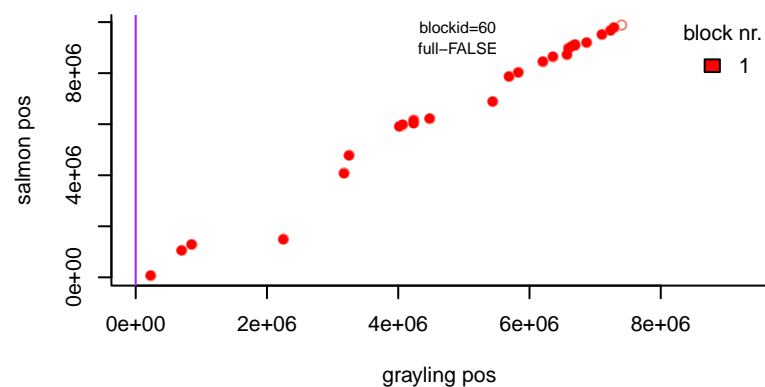
13A



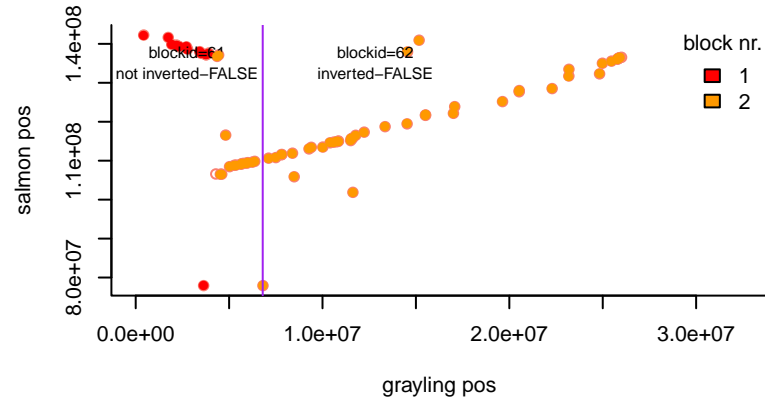
13B



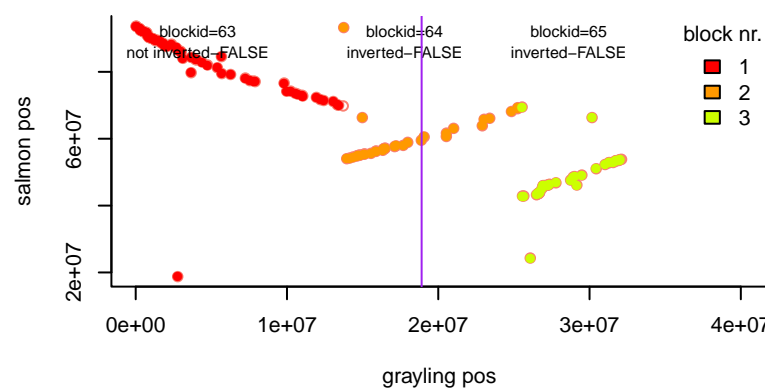
13C

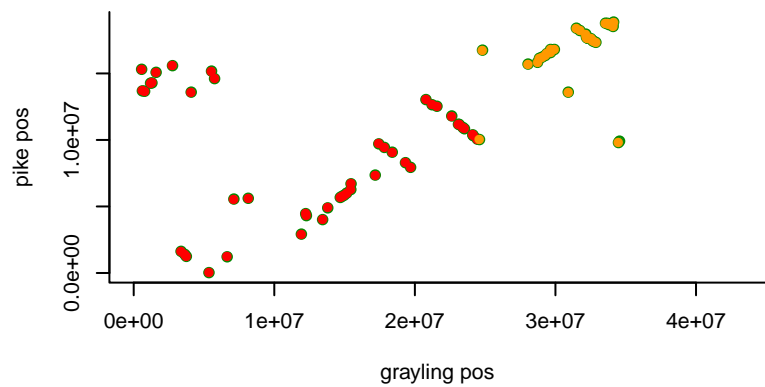


14A

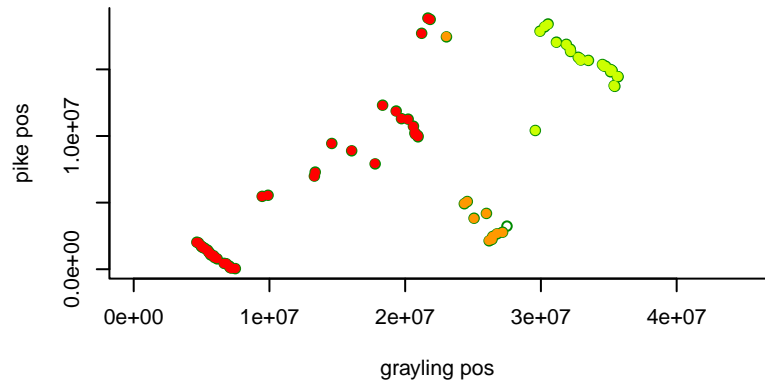
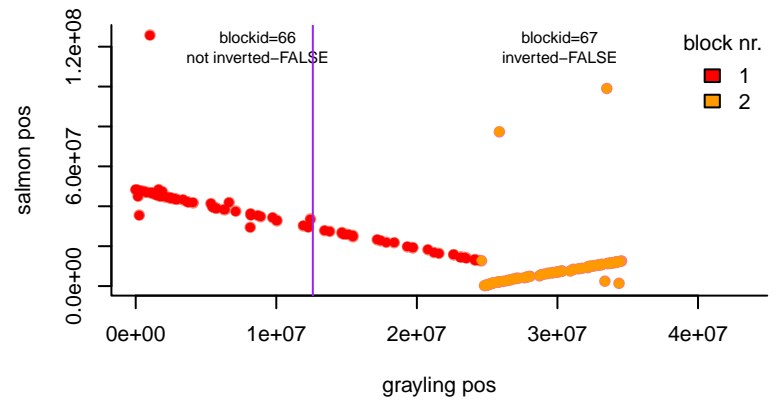


14B

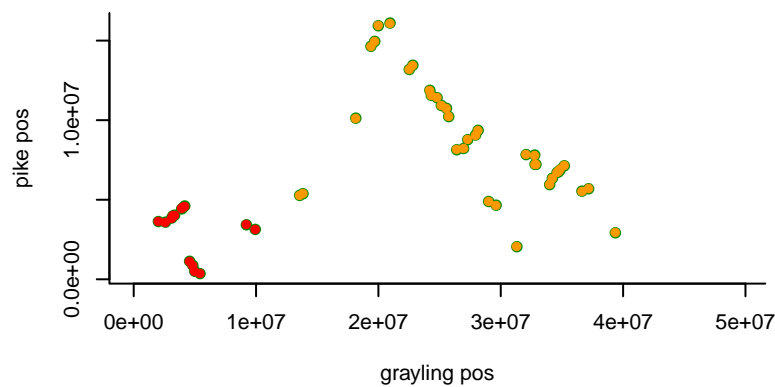
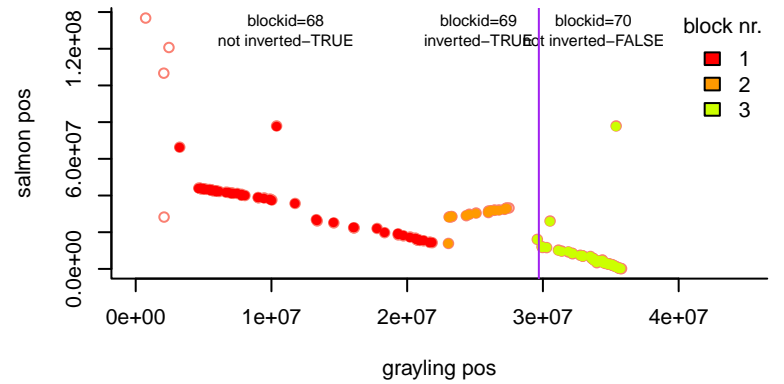




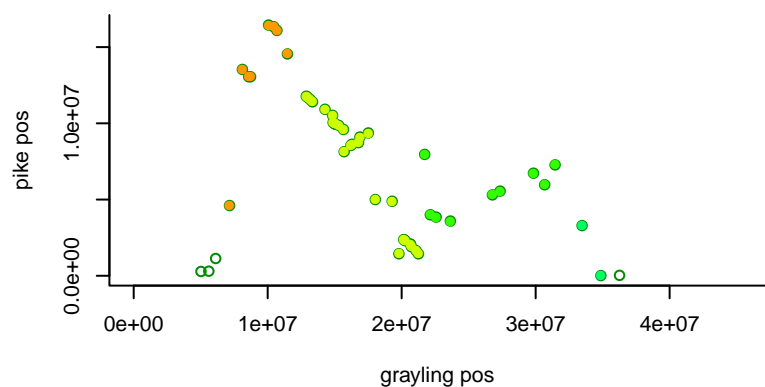
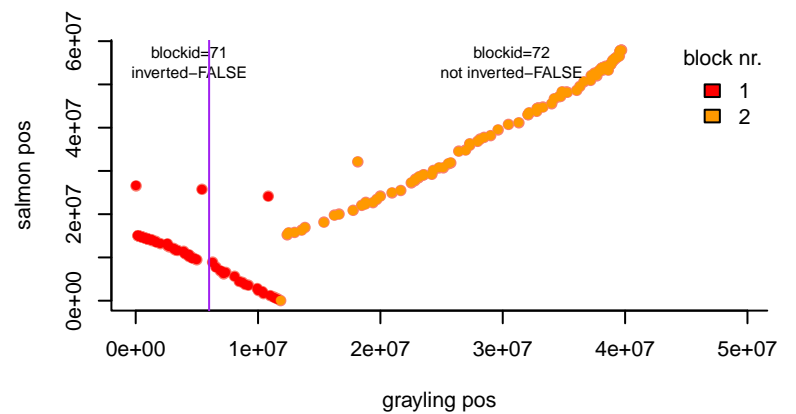
15A



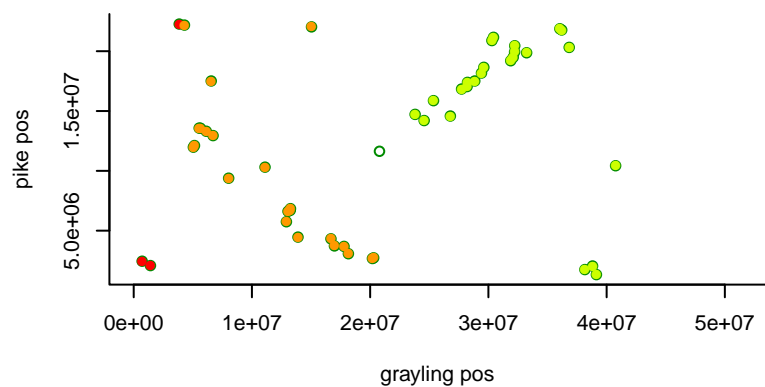
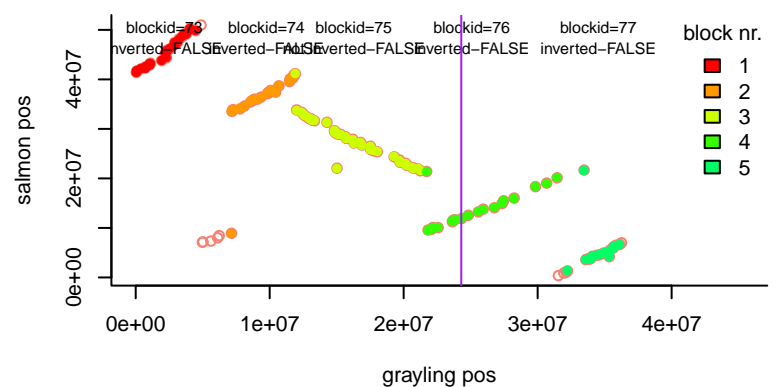
15B



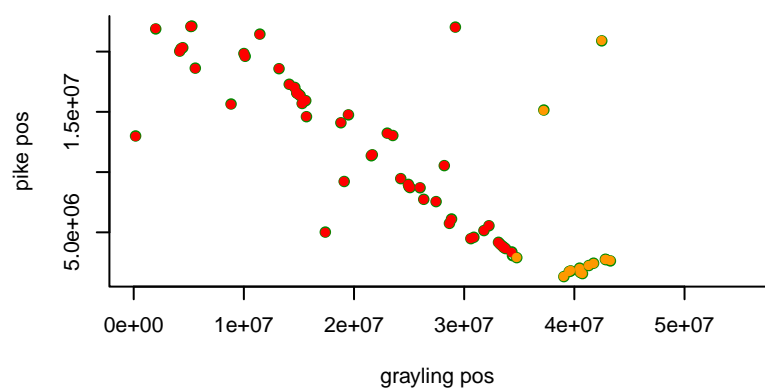
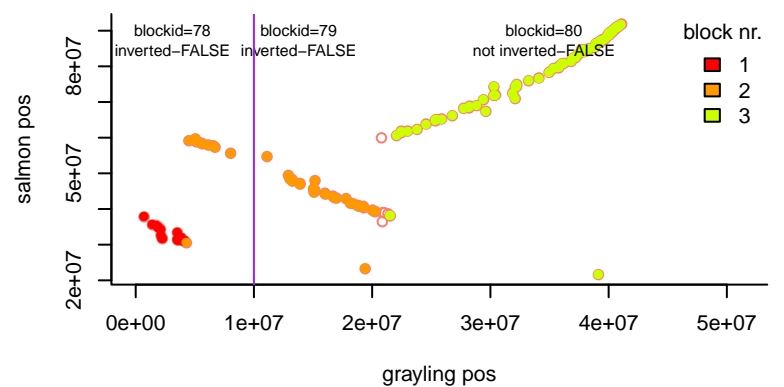
16A



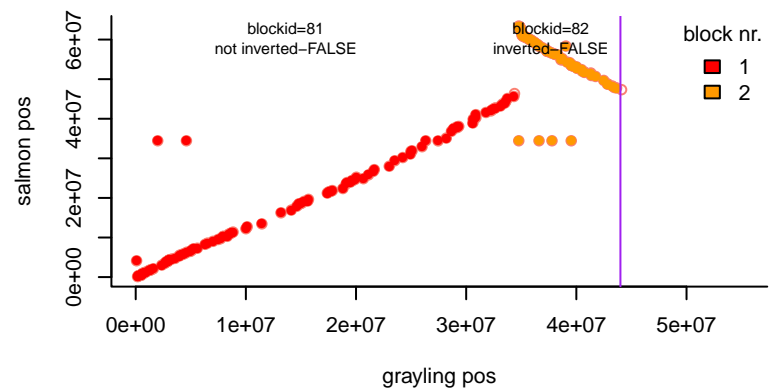
16B

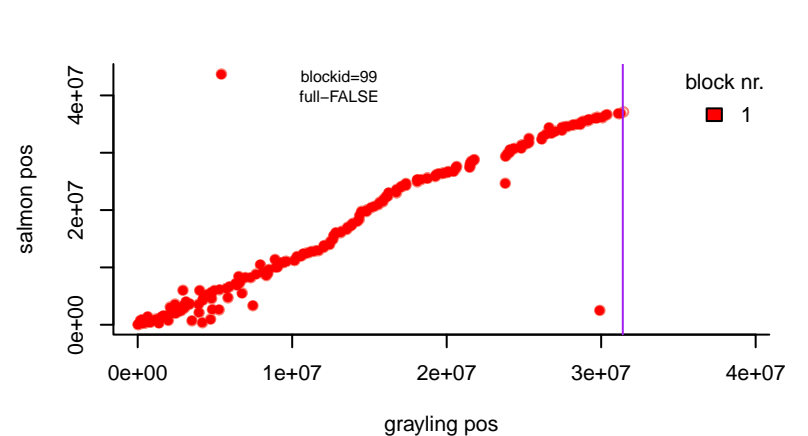
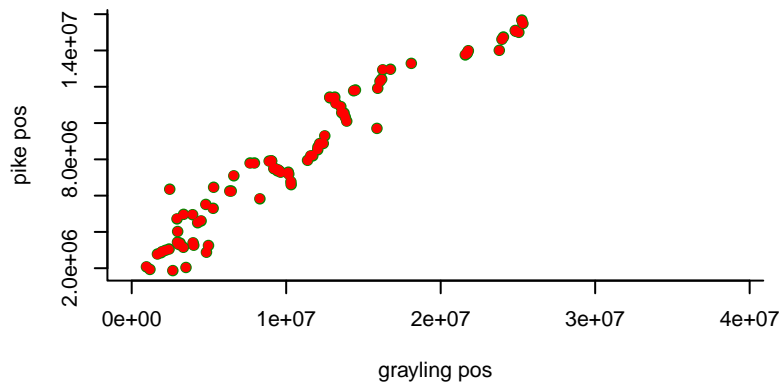
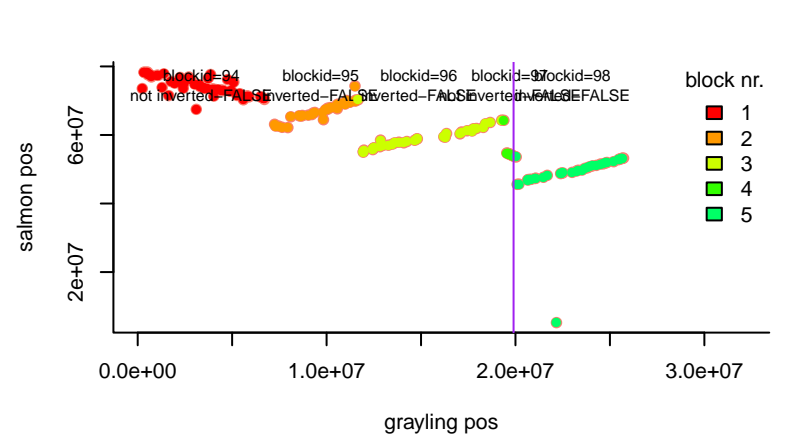
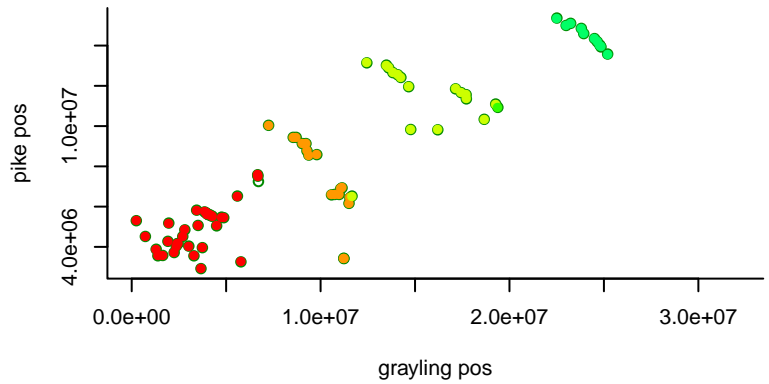
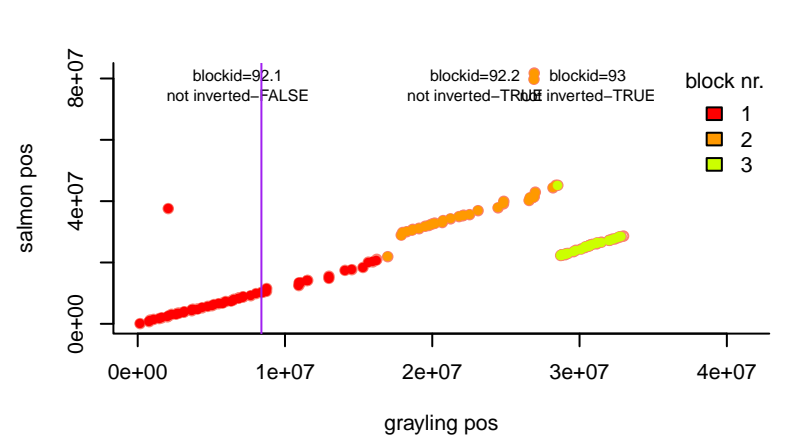
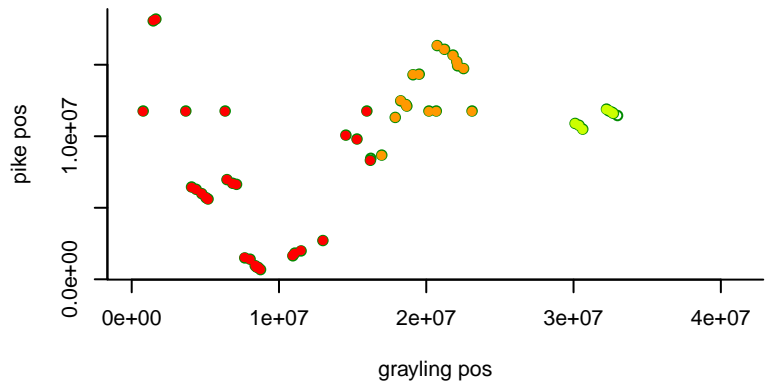
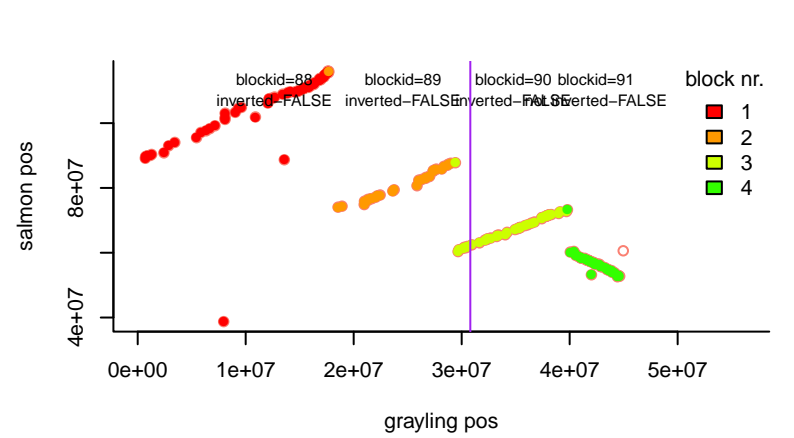
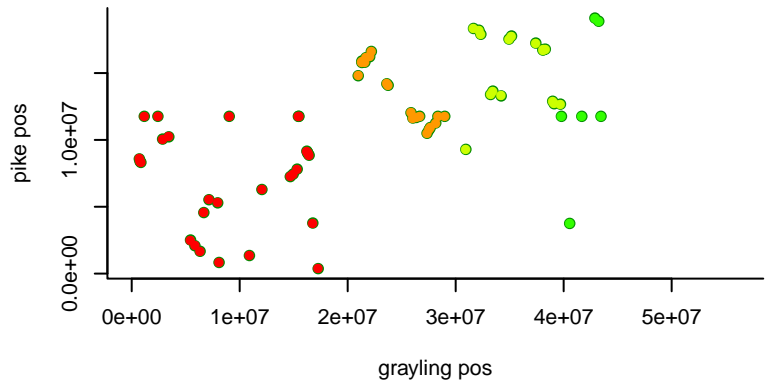
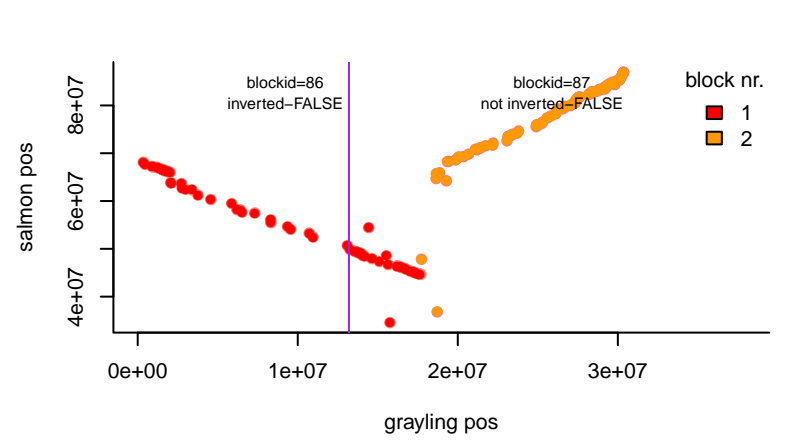
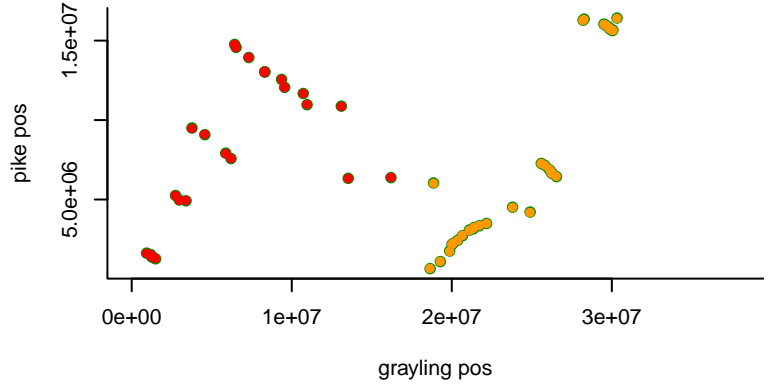
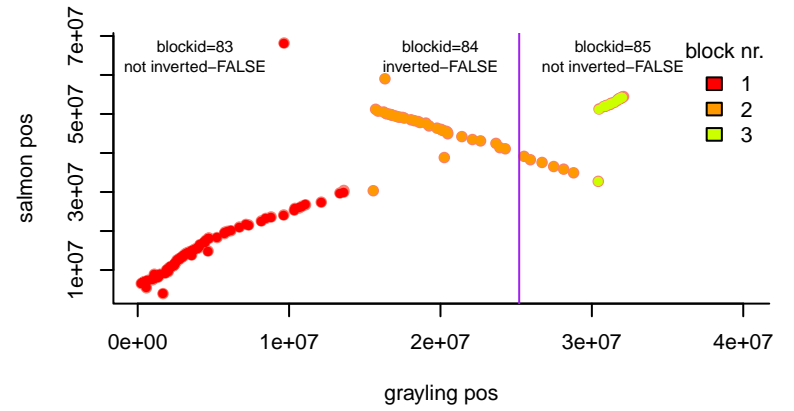
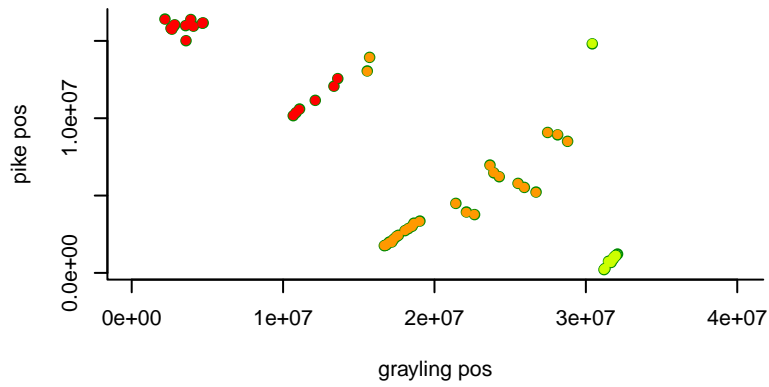


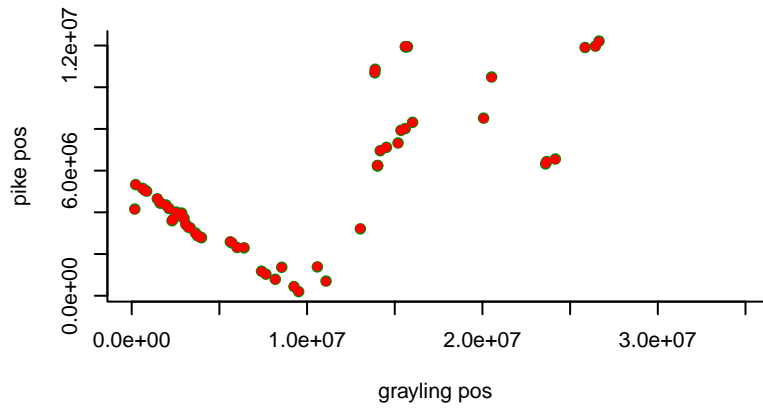
17A



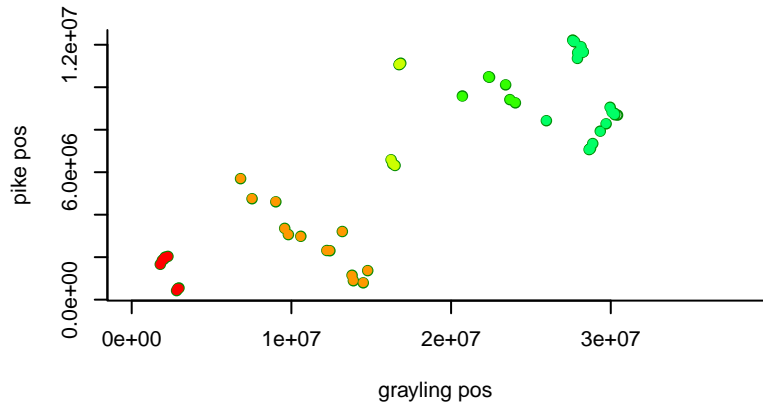
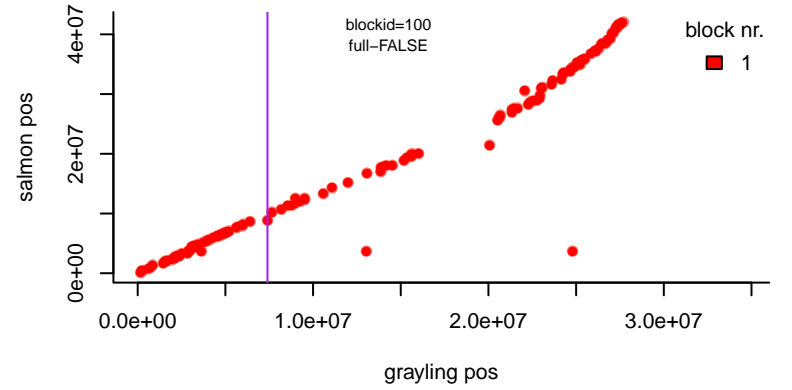
17B



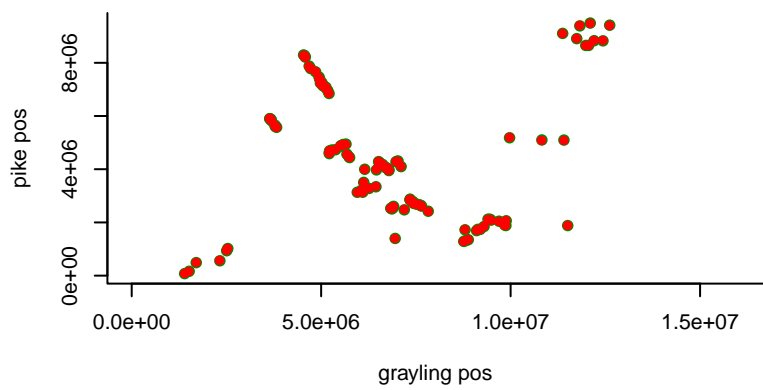
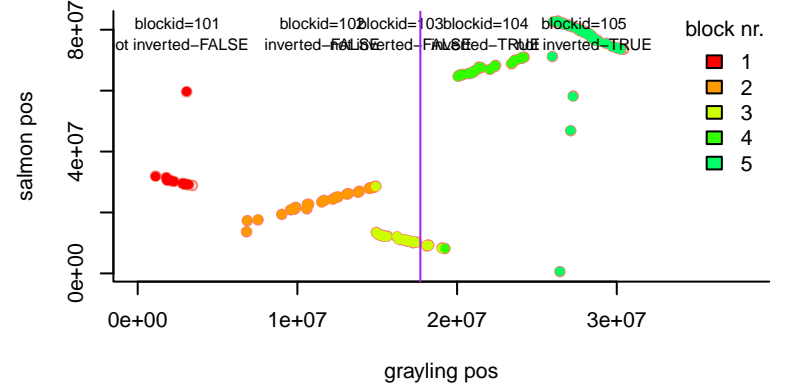




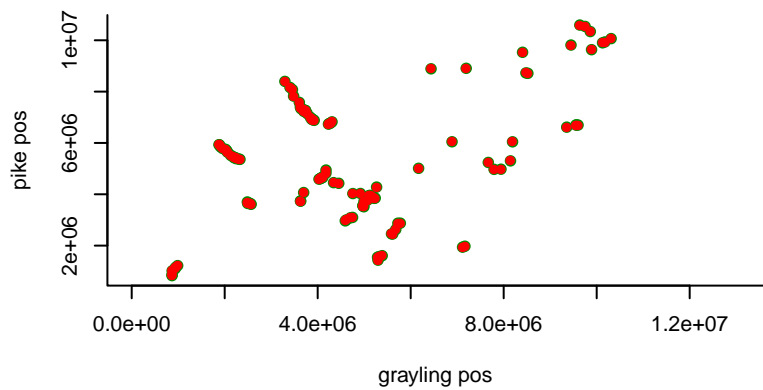
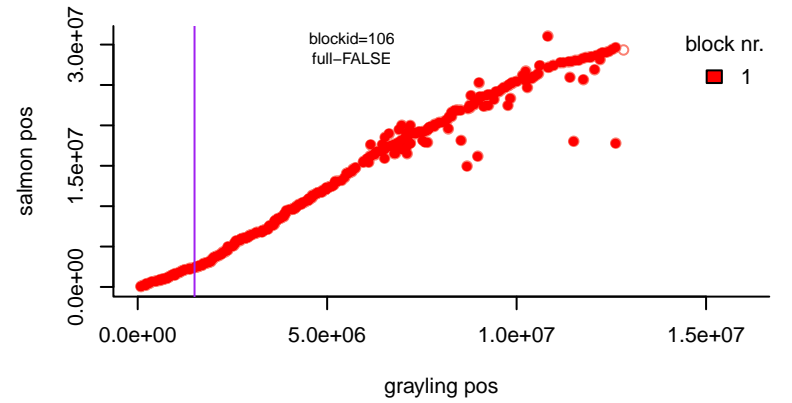
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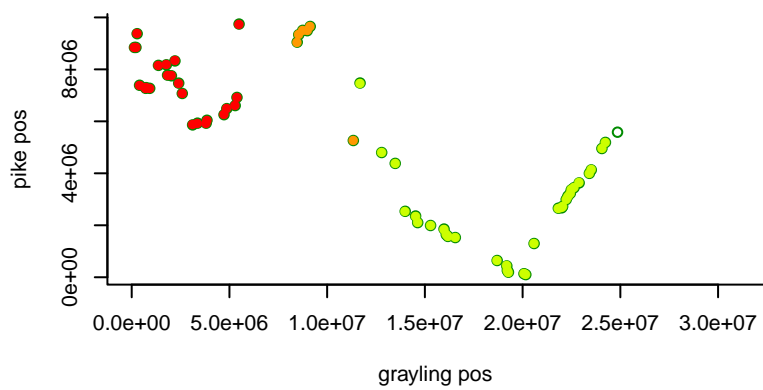
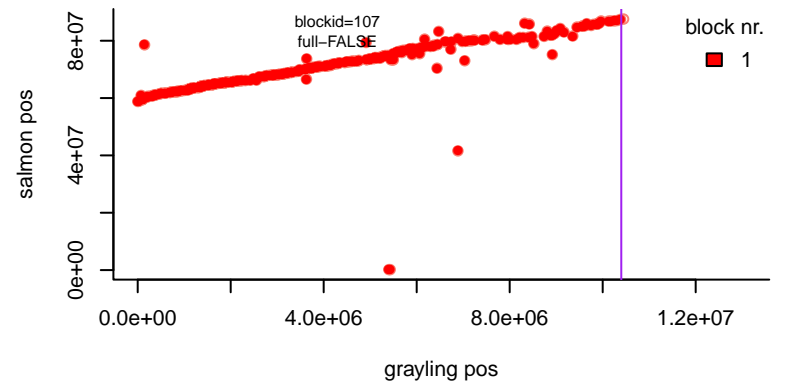
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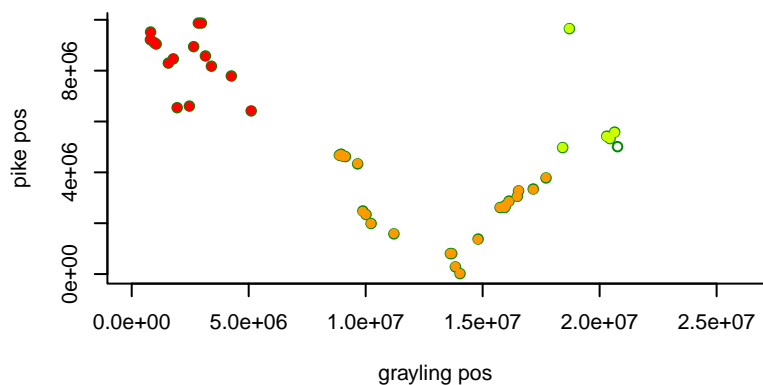
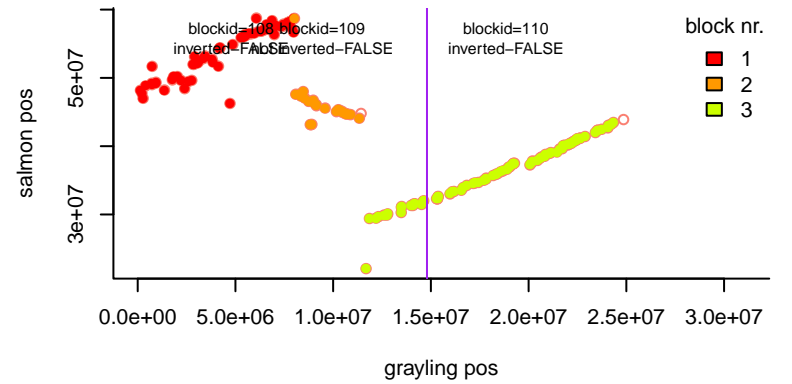
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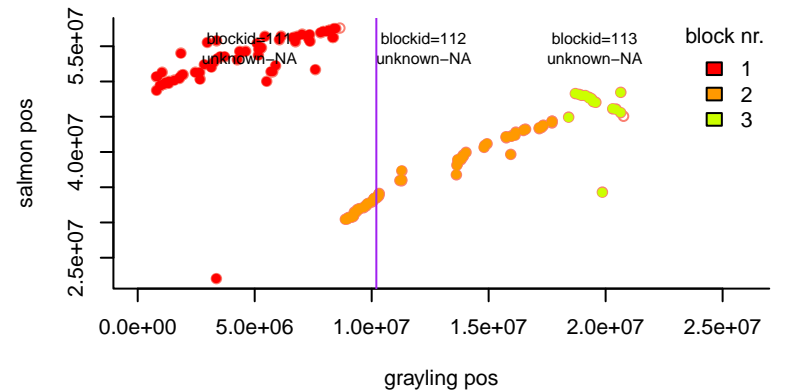
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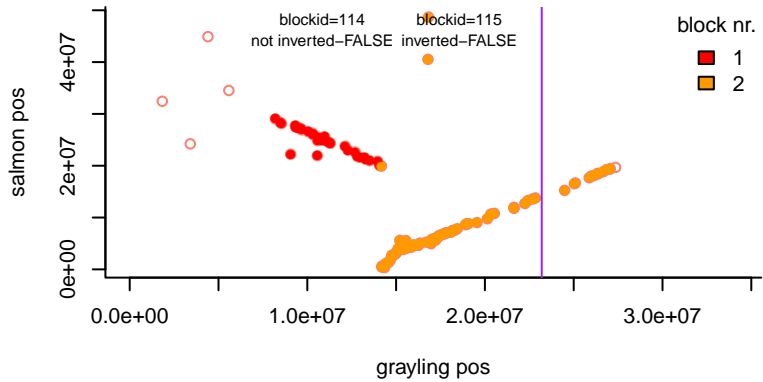
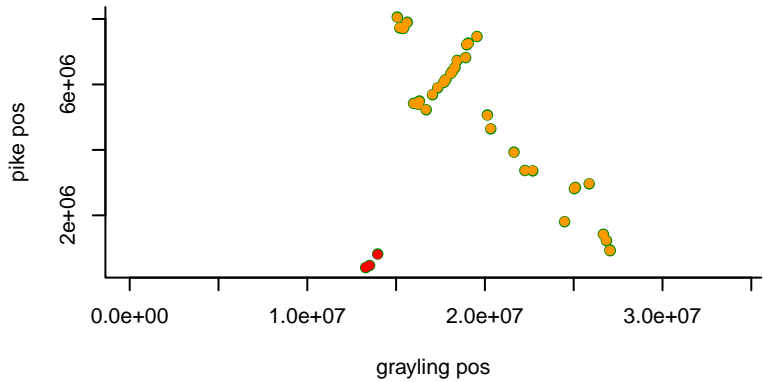
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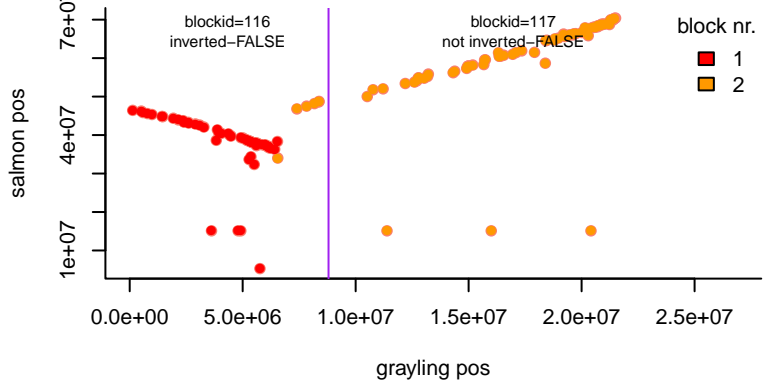
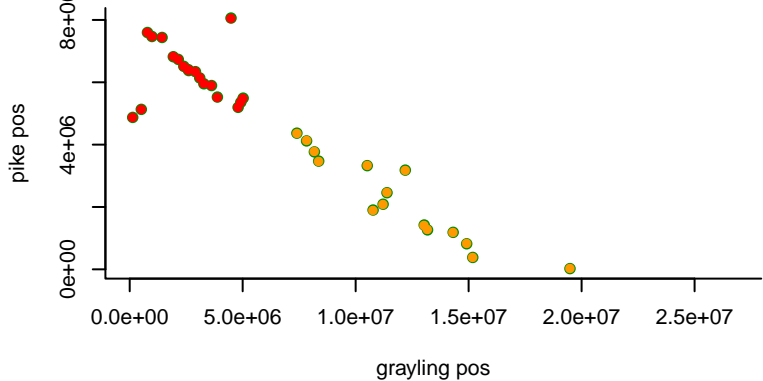
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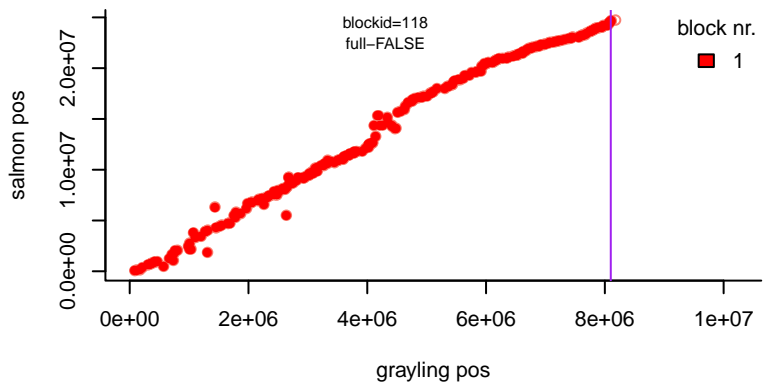
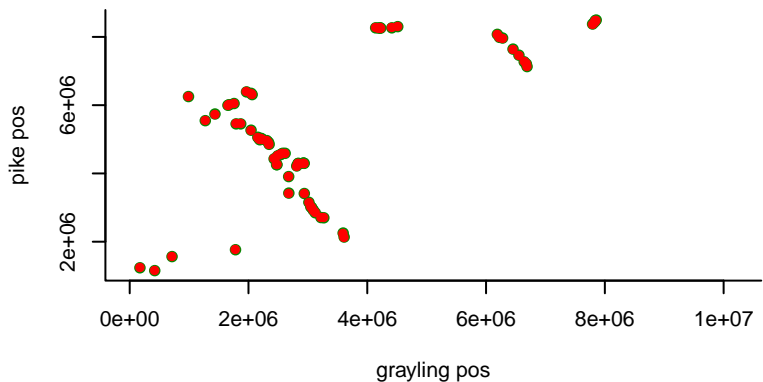
24A



24B



25A



25B

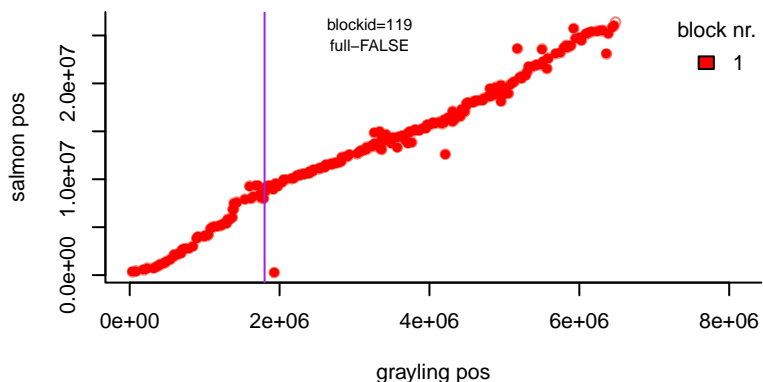
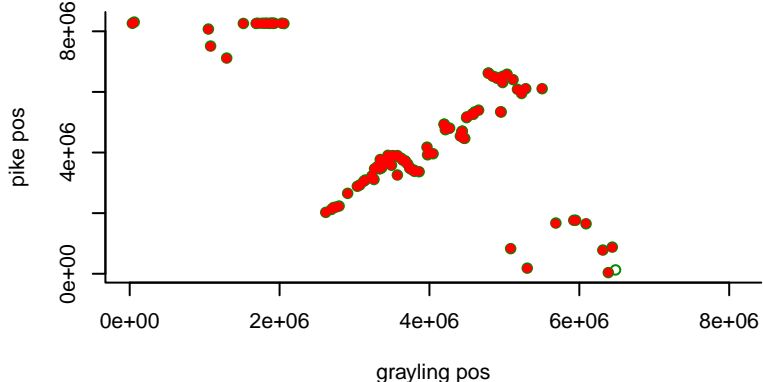
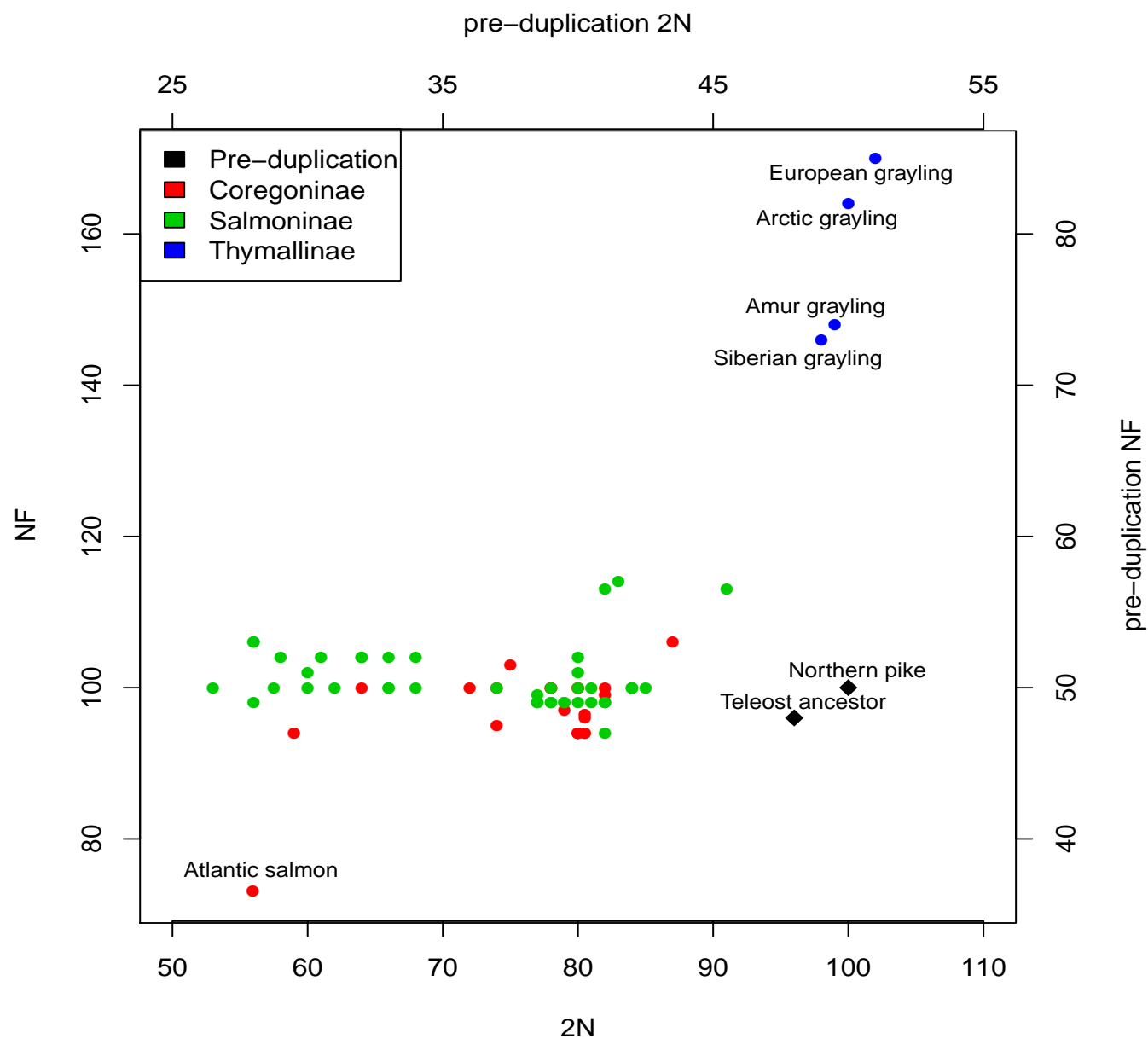


Figure S5

Phylogenetic data of the salmonids combined with karyotypic information. 2N and NF from Phillips & Ráb (2001). Highlighted are the locations of the salmonid species belonging to the Thymallinae subfamily as well as Atlantic salmon. For comparison, the figure shows also the hypothetical teleost ancestor (Phillips & Ráb 2001) and Northern pike (Rondeau et al. 2014), dating prior to salmonid specific whole-genome duplication, are placed in the figure. Axes for the extant salmonids are on the bottom and on the left side, and axes for the Northern pike and hypothetical teleost ancestor on the top and on the right side of the plot.



References

Phillips, R., & Ráb, P. (2001). Chromosome evolution in the Salmonidae (Pisces): an update. *Biological Reviews of the Cambridge Philosophical Society*, 76(1), 1–25. <https://doi.org/10.1111/j.1469-185X.2000.tb00057.x>

Rondeau EB, Minkley DR, Leong JS, Messmer AM, Jantzen JR, von Schalburg KR, Lemon C, Bird NH, Koop BF. 2014. The Genome and Linkage Map of the Northern Pike (*Esox lucius*): Conserved Synteny Revealed between the Salmonid Sister Group and the Neoteleostei. *PLoS One* 9(7): e102089. [10.1371/journal.pone.0102089](https://doi.org/10.1371/journal.pone.0102089).