

GENETICS

Supporting Information

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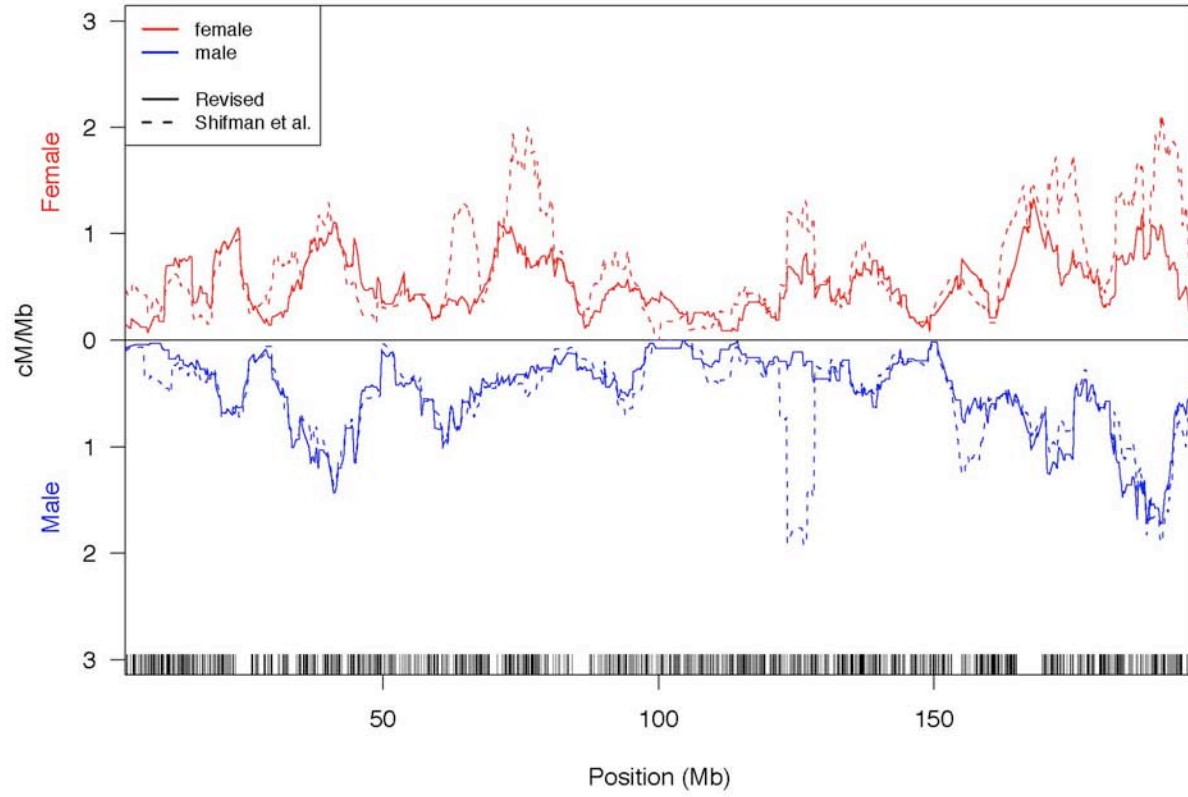
A New Standard Genetic Map for the Laboratory Mouse

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Jordana Tzenova Bell, Gudrun A. Brockmann, Jon E. Wergedal, Carol Bult, Beverly Paigen,
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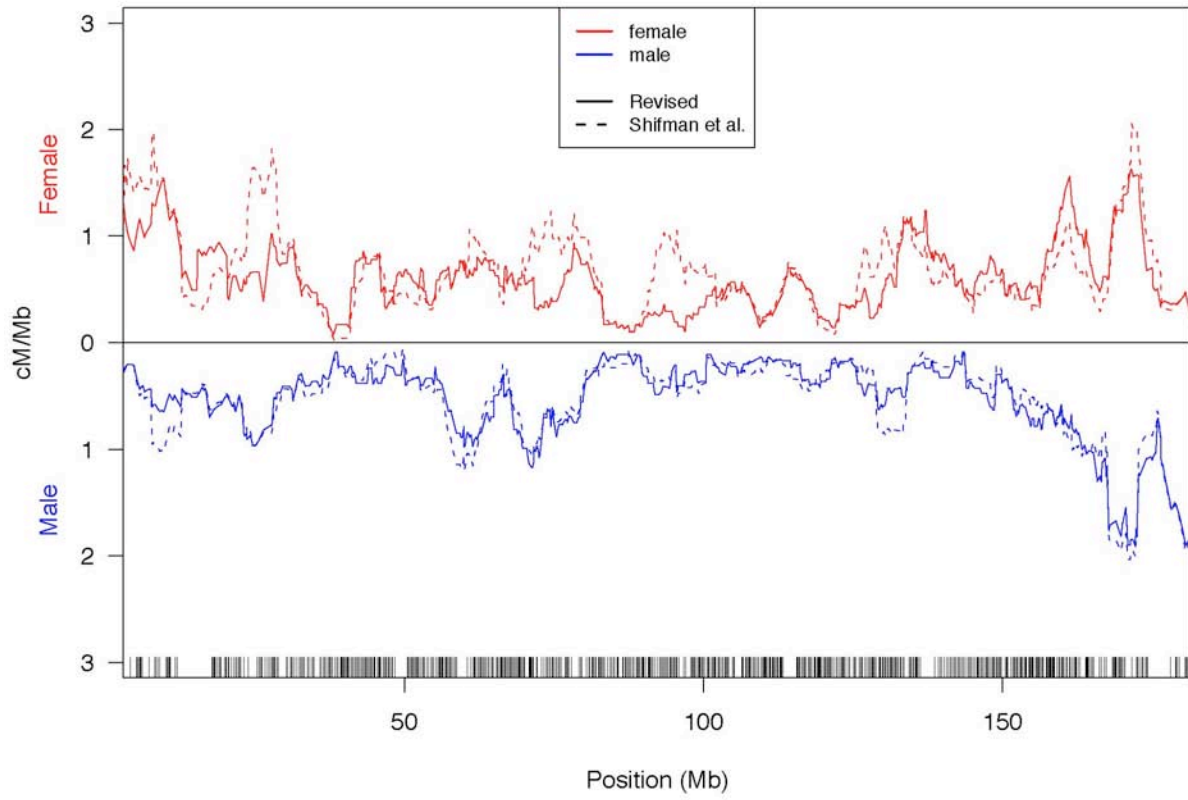
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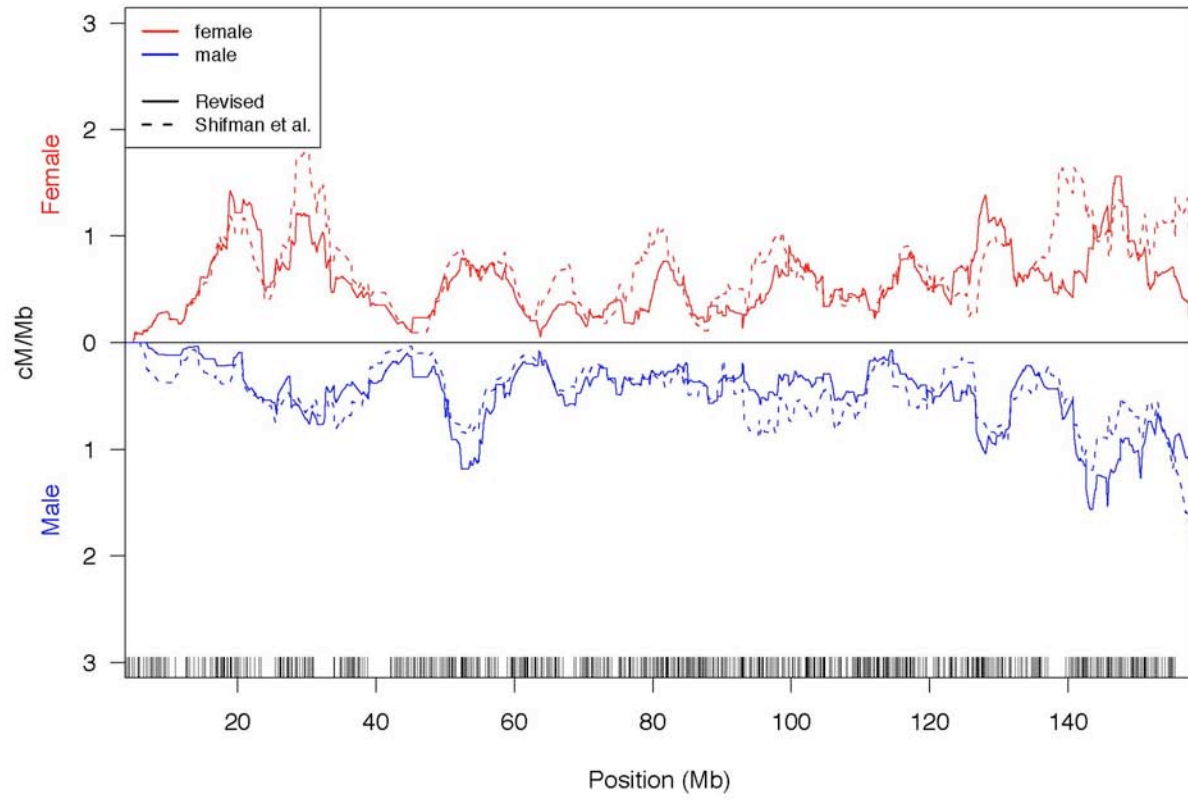
FIGURE S1

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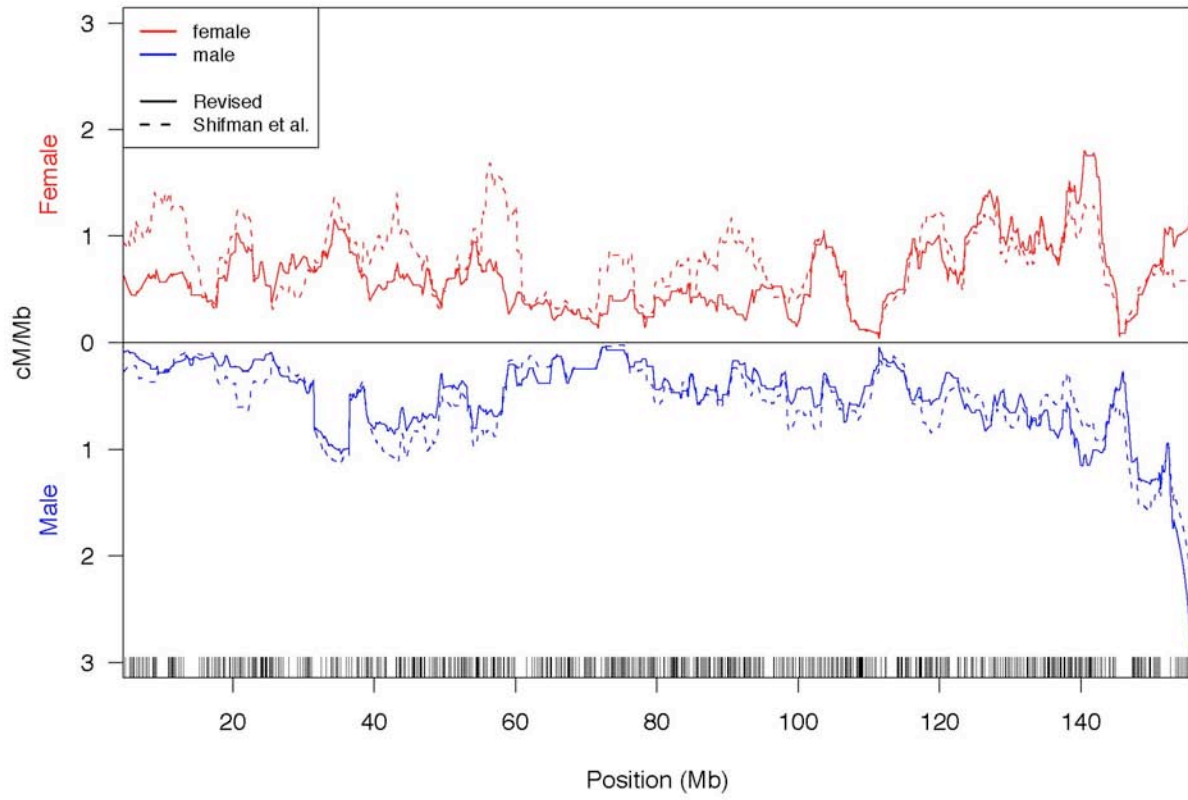
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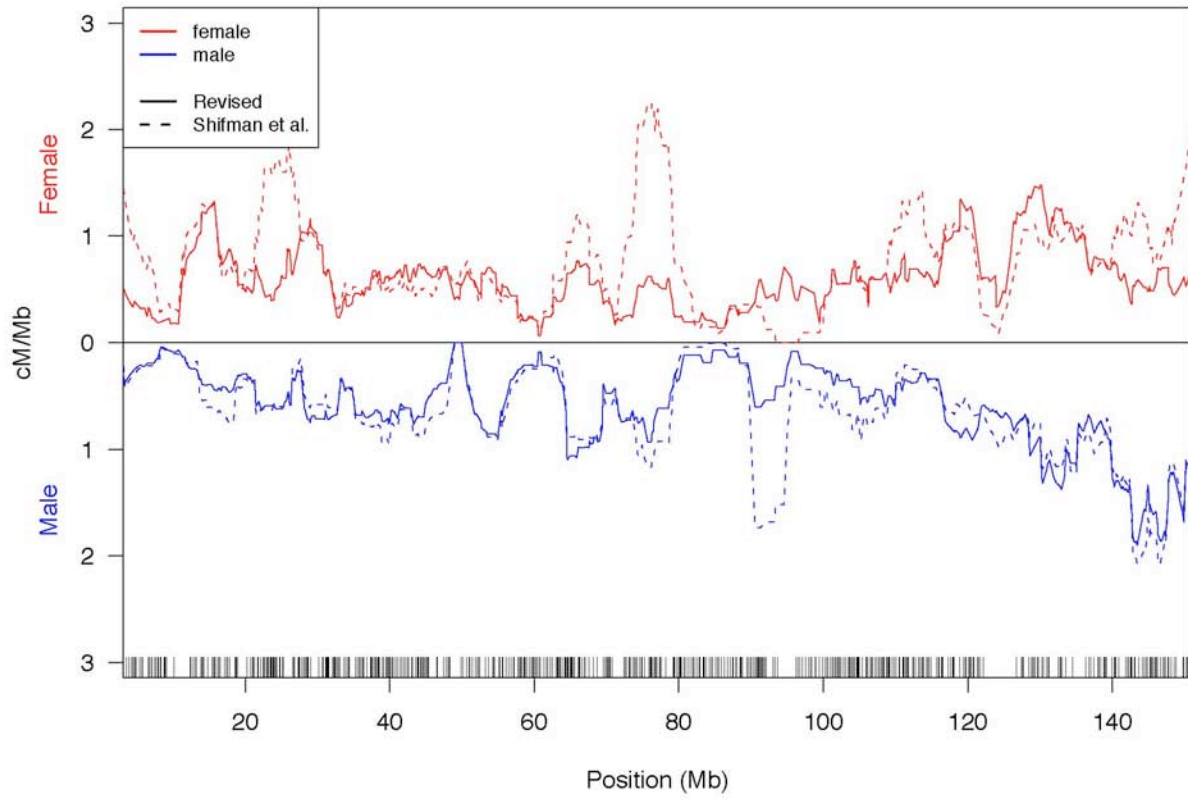
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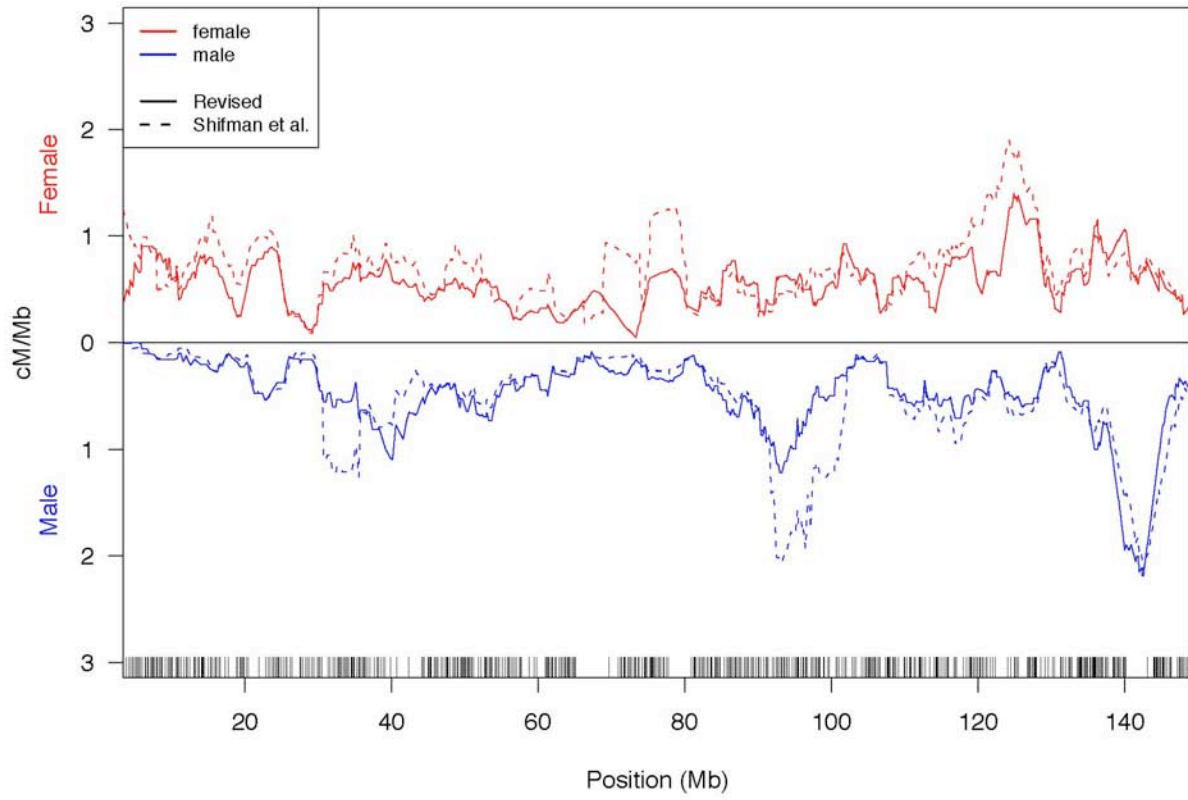
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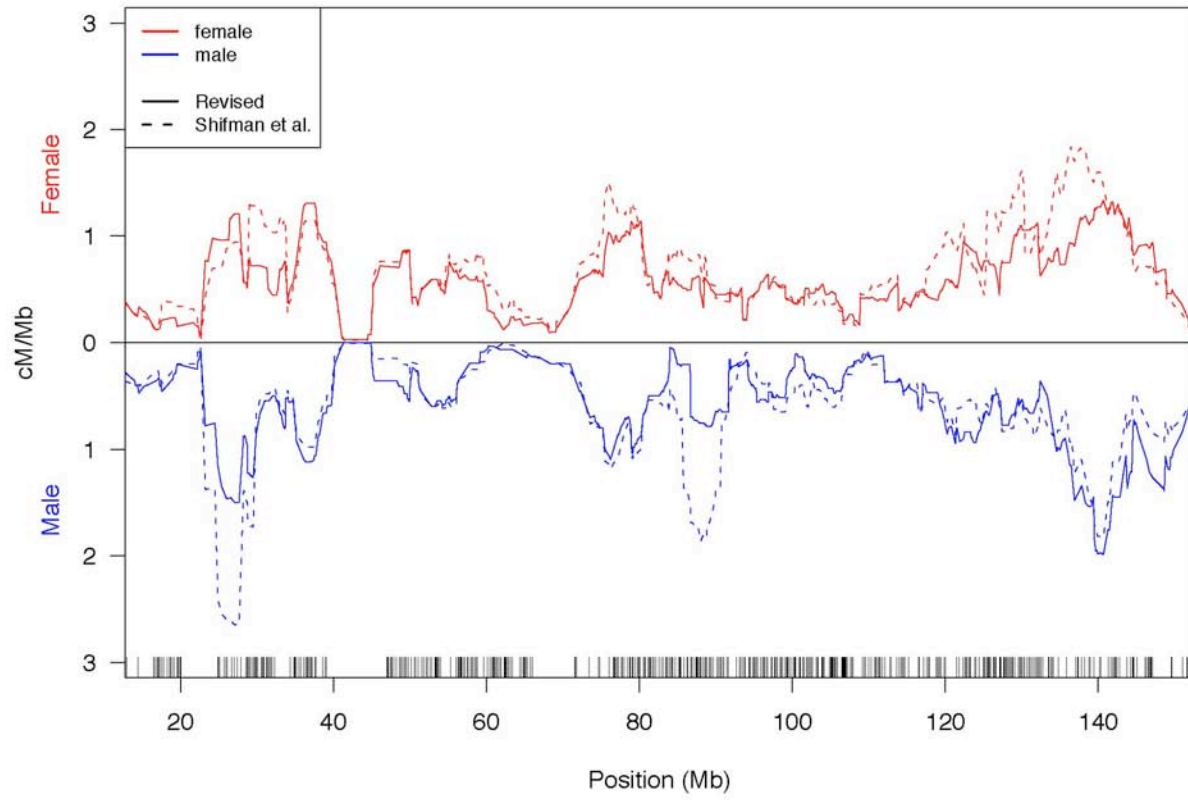
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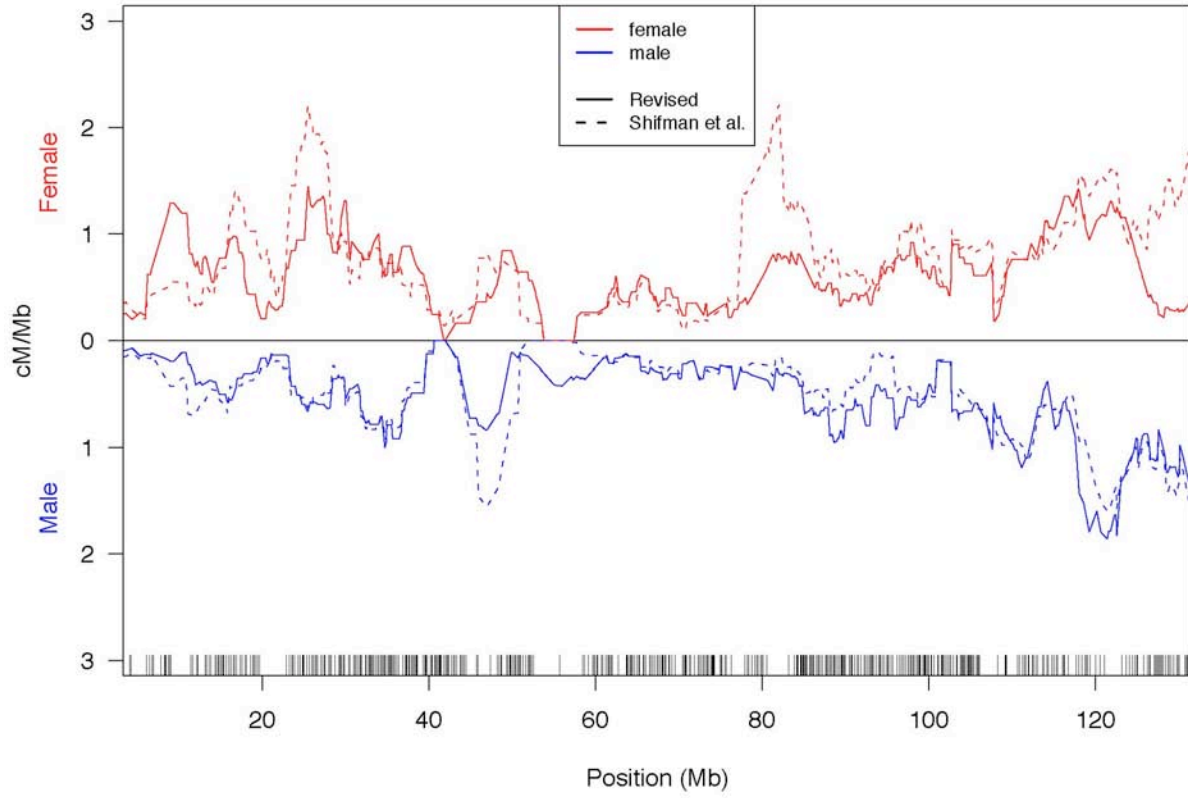
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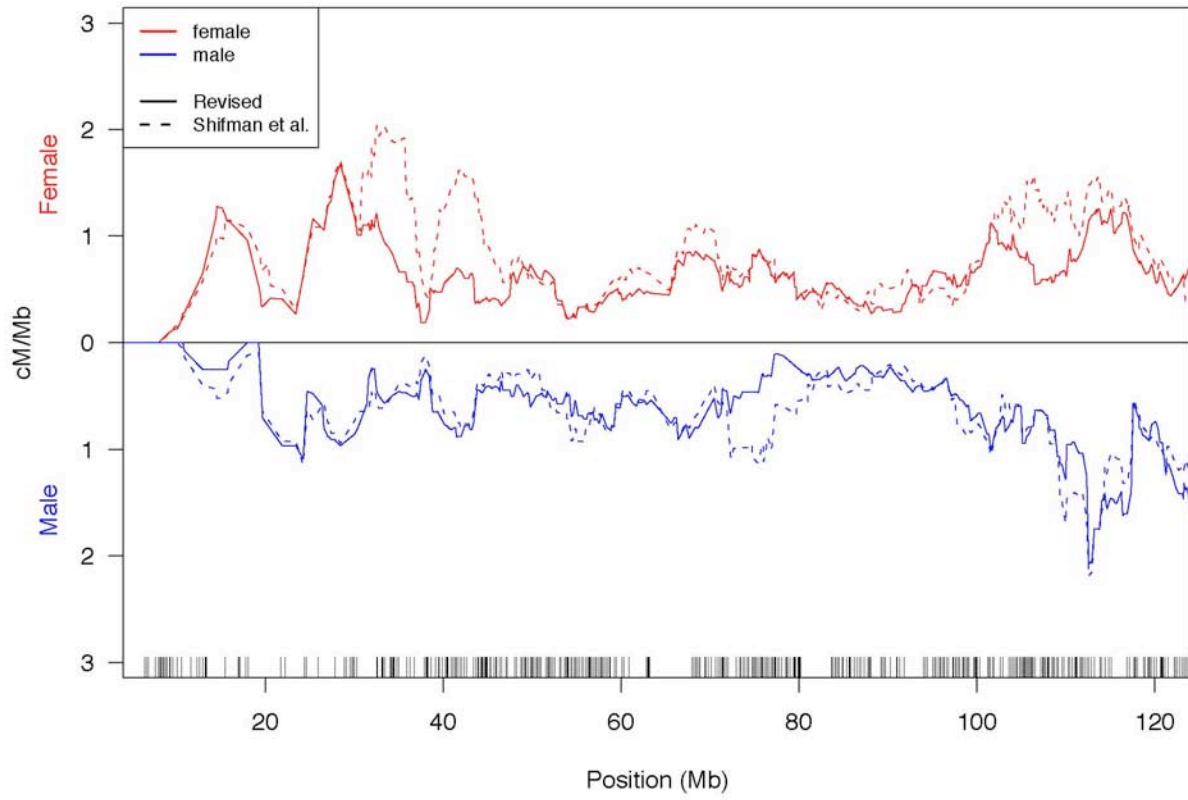
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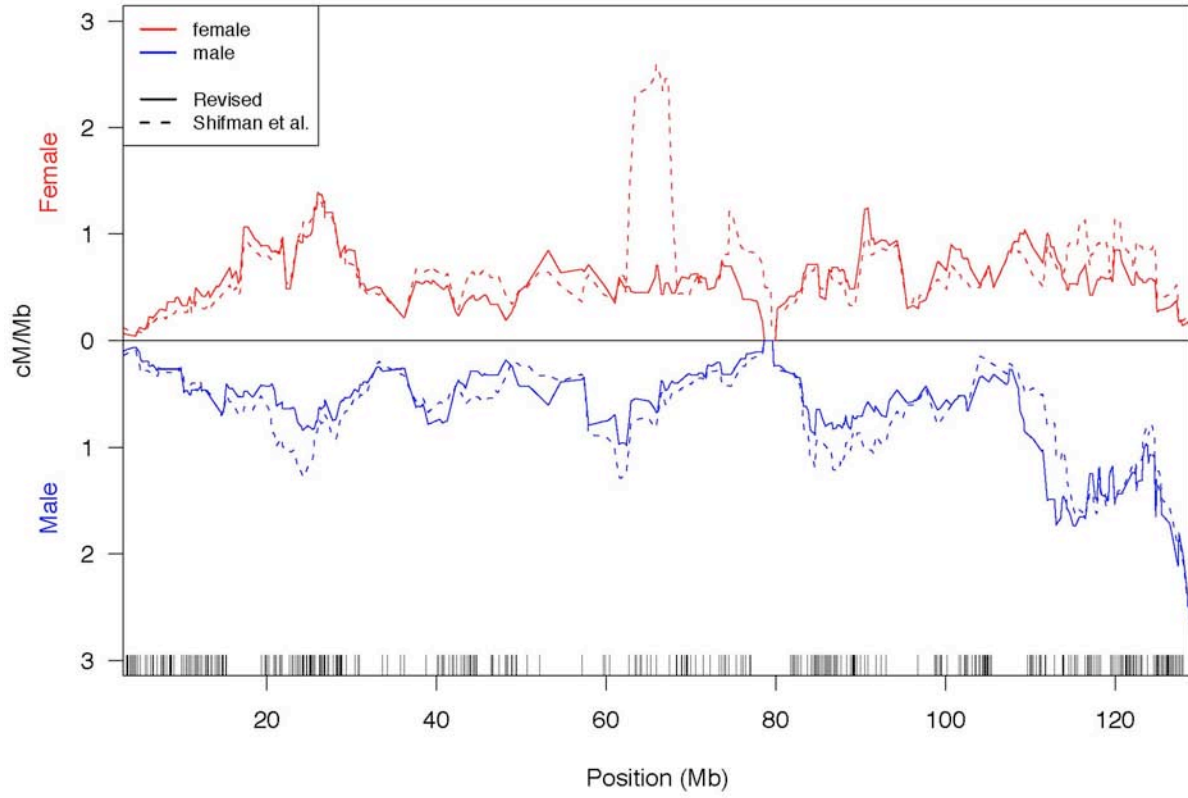
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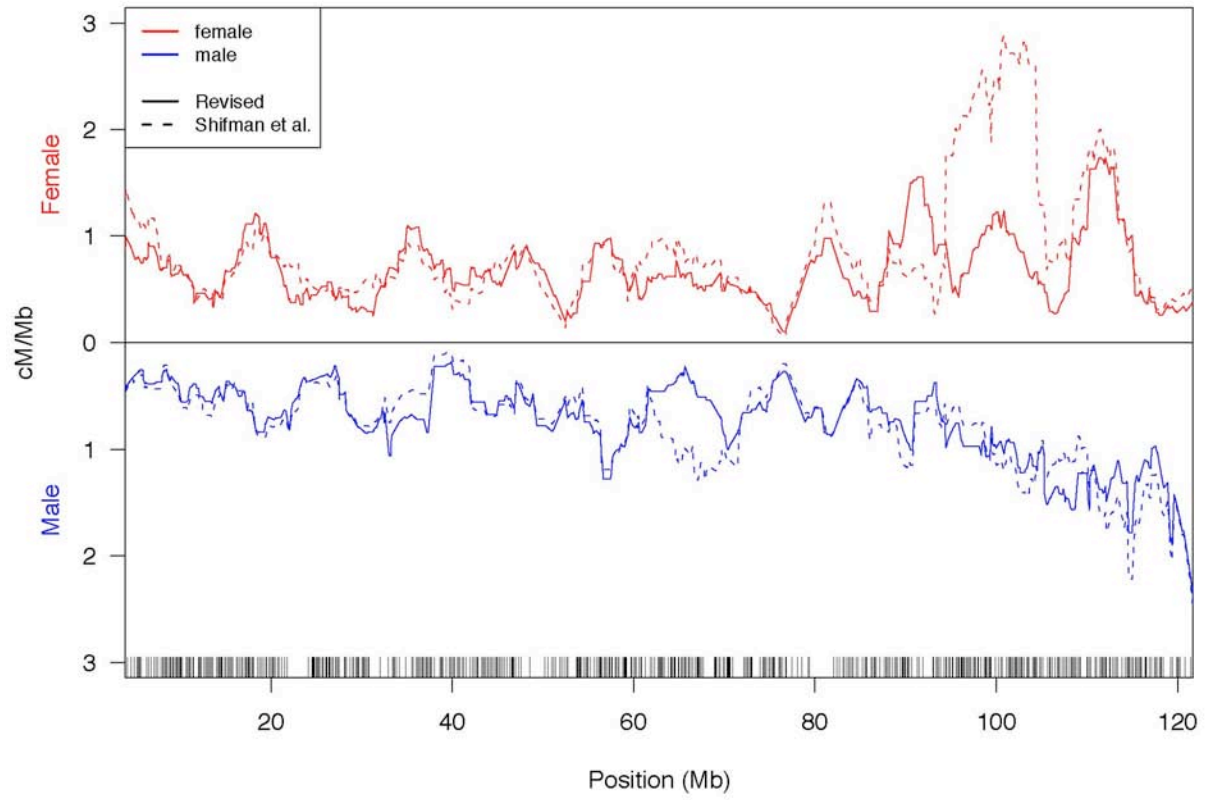
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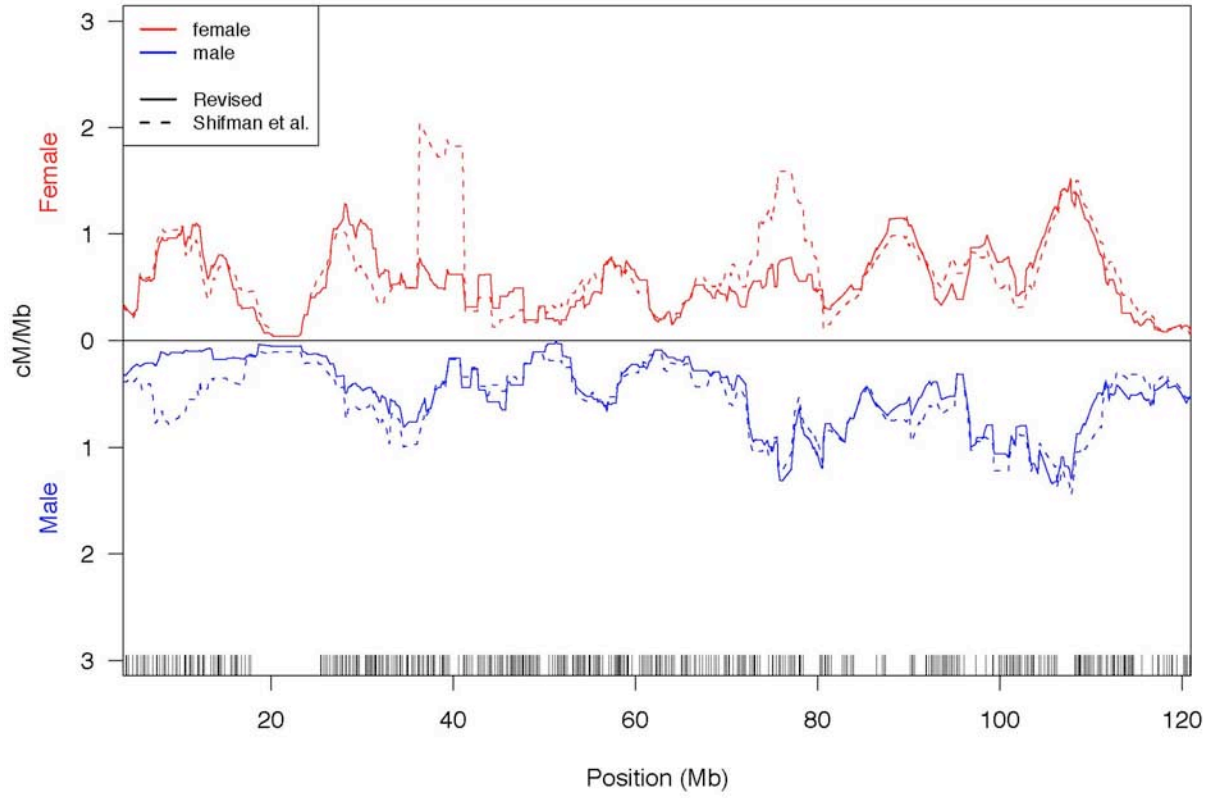
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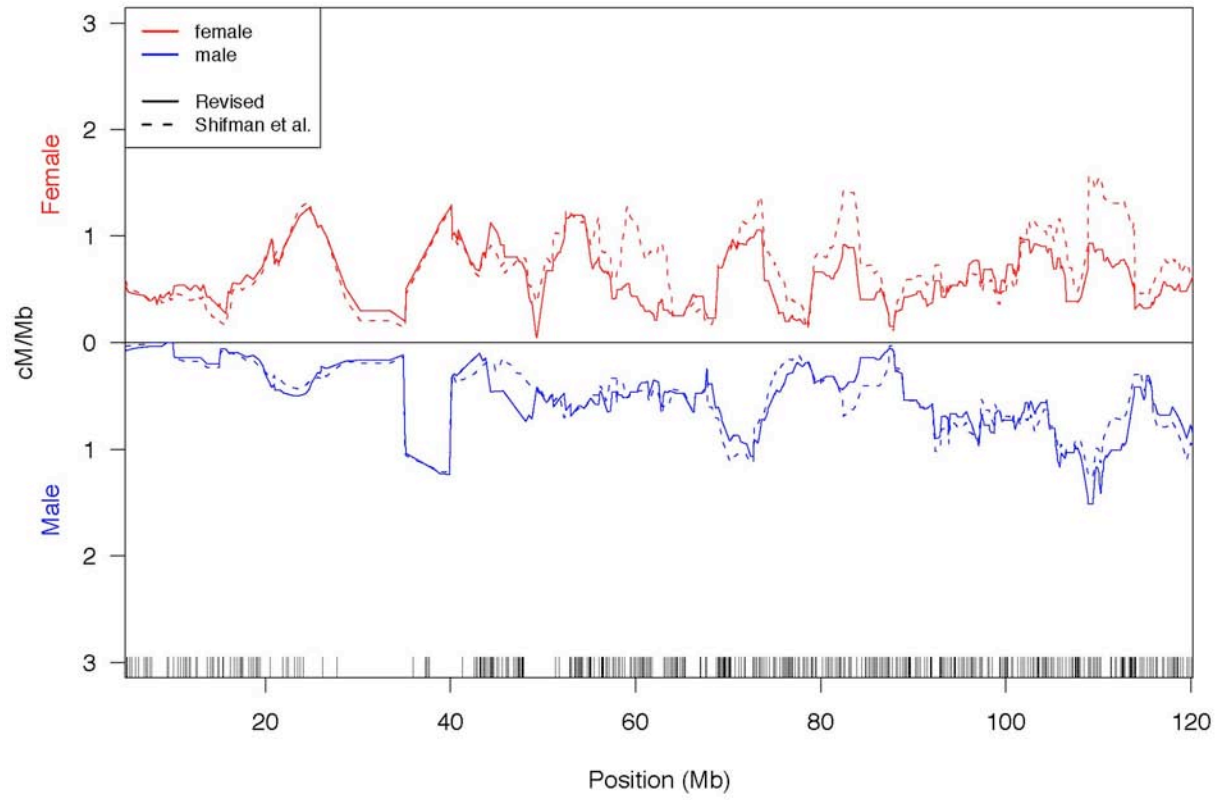
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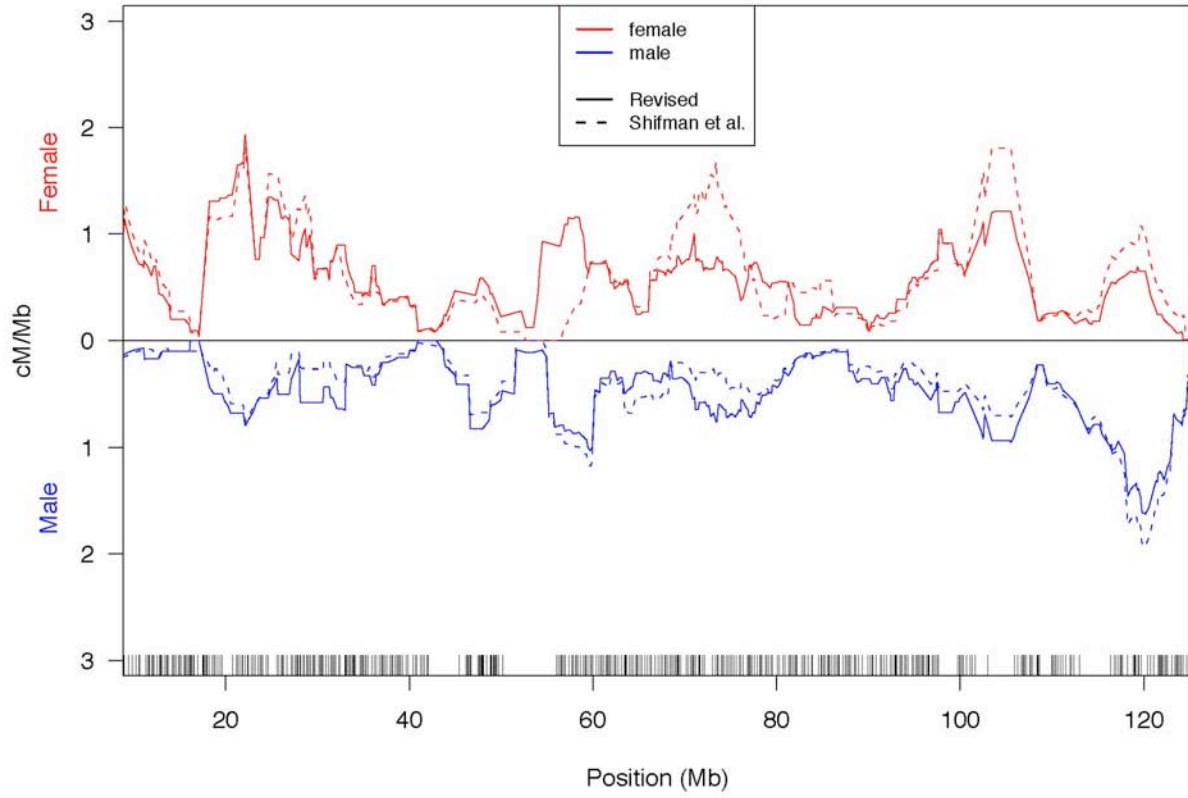
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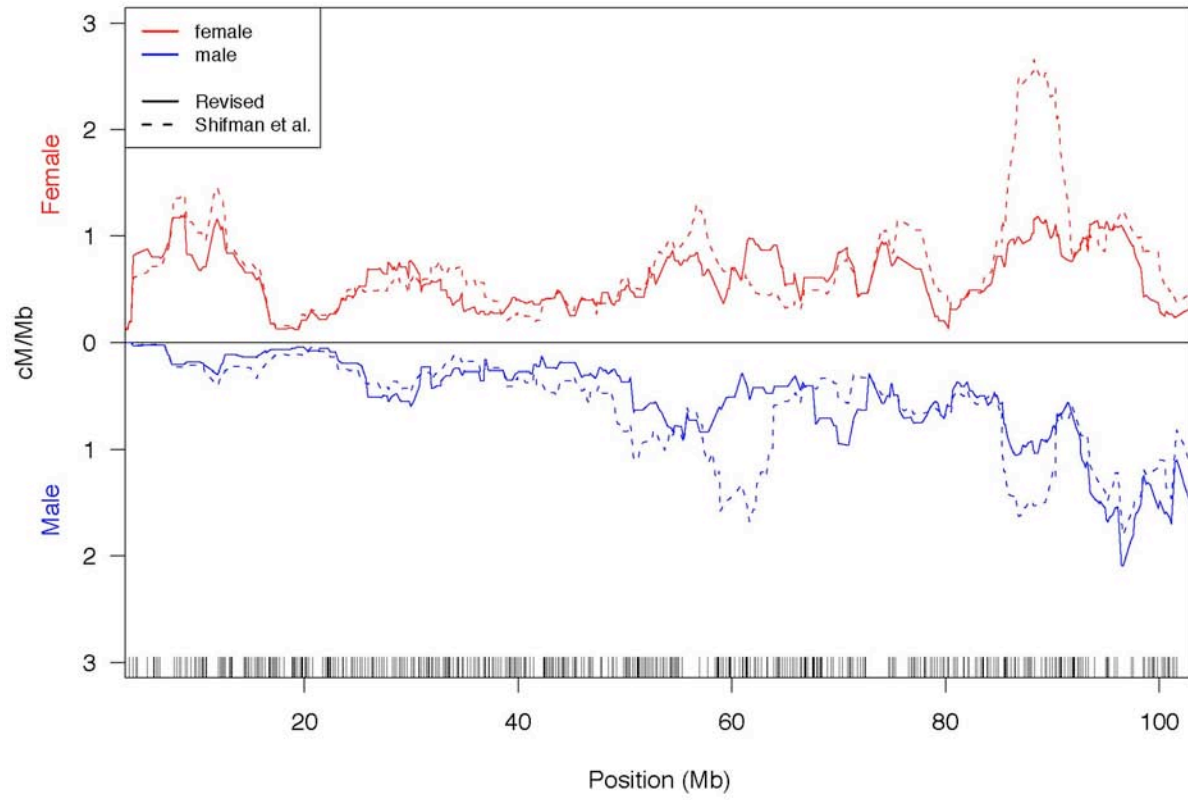
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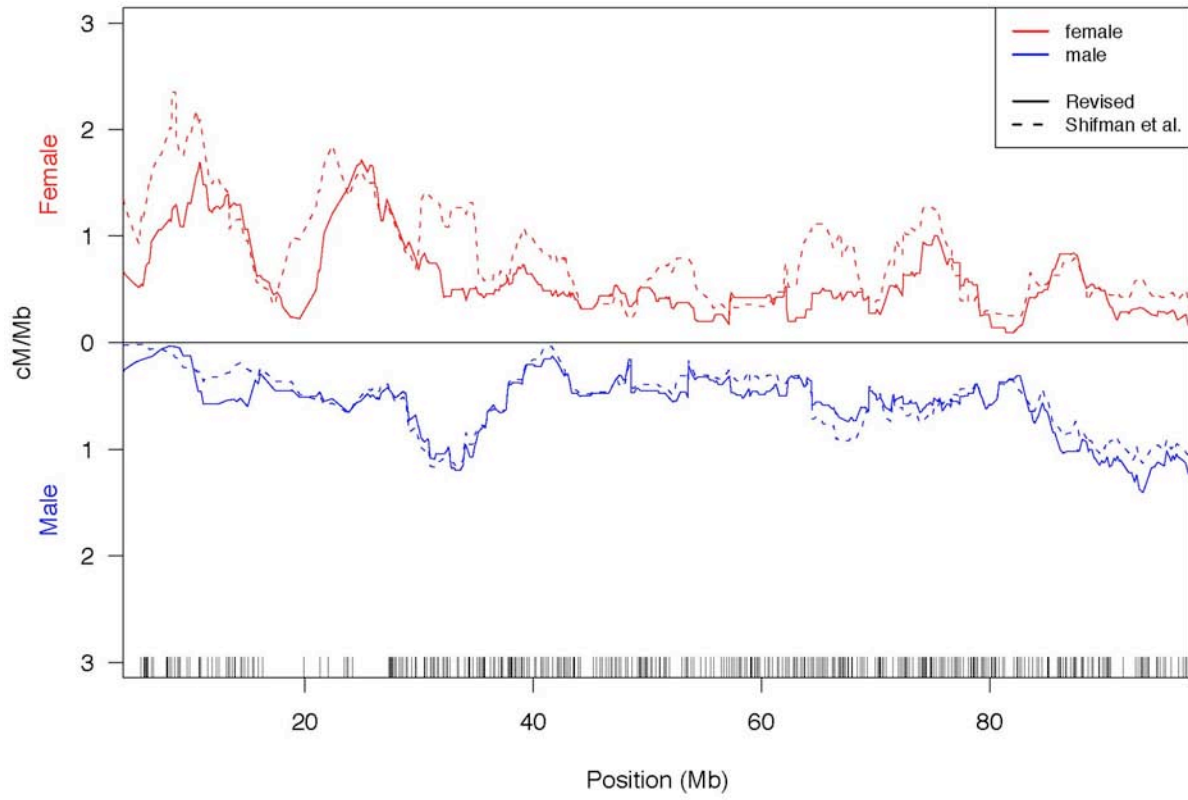
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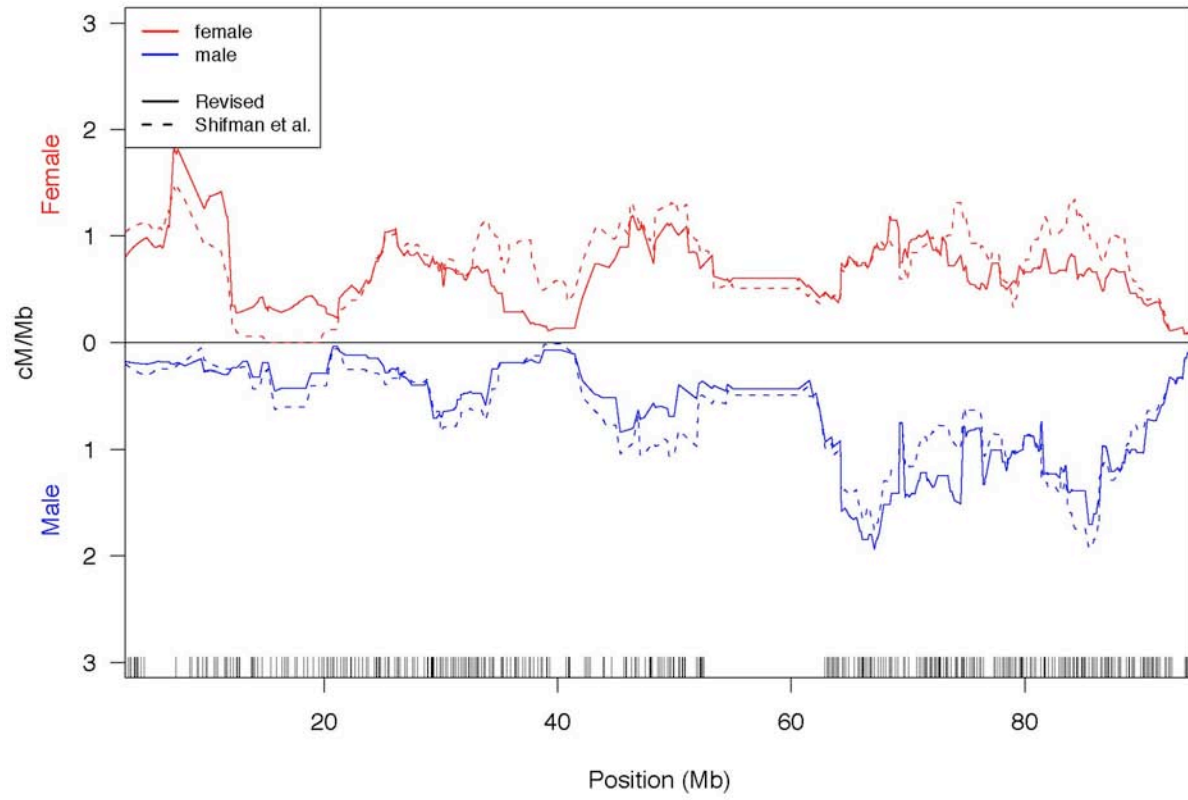
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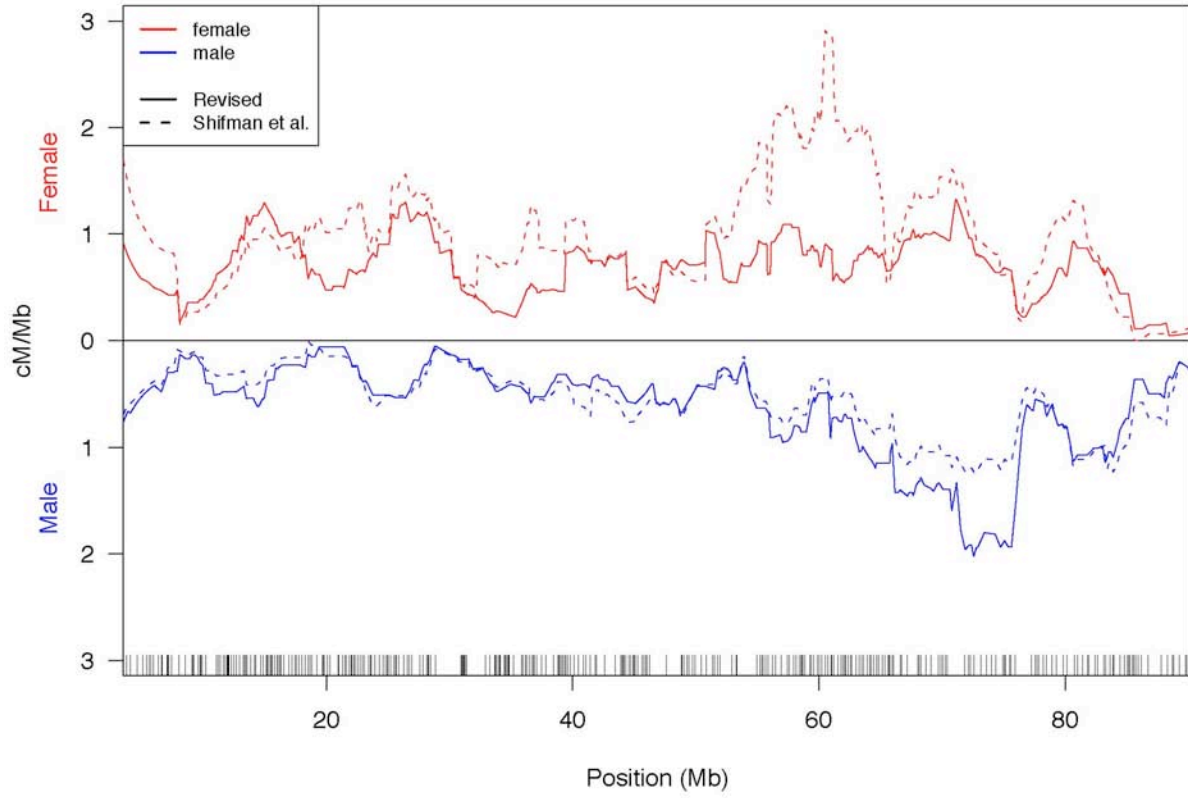
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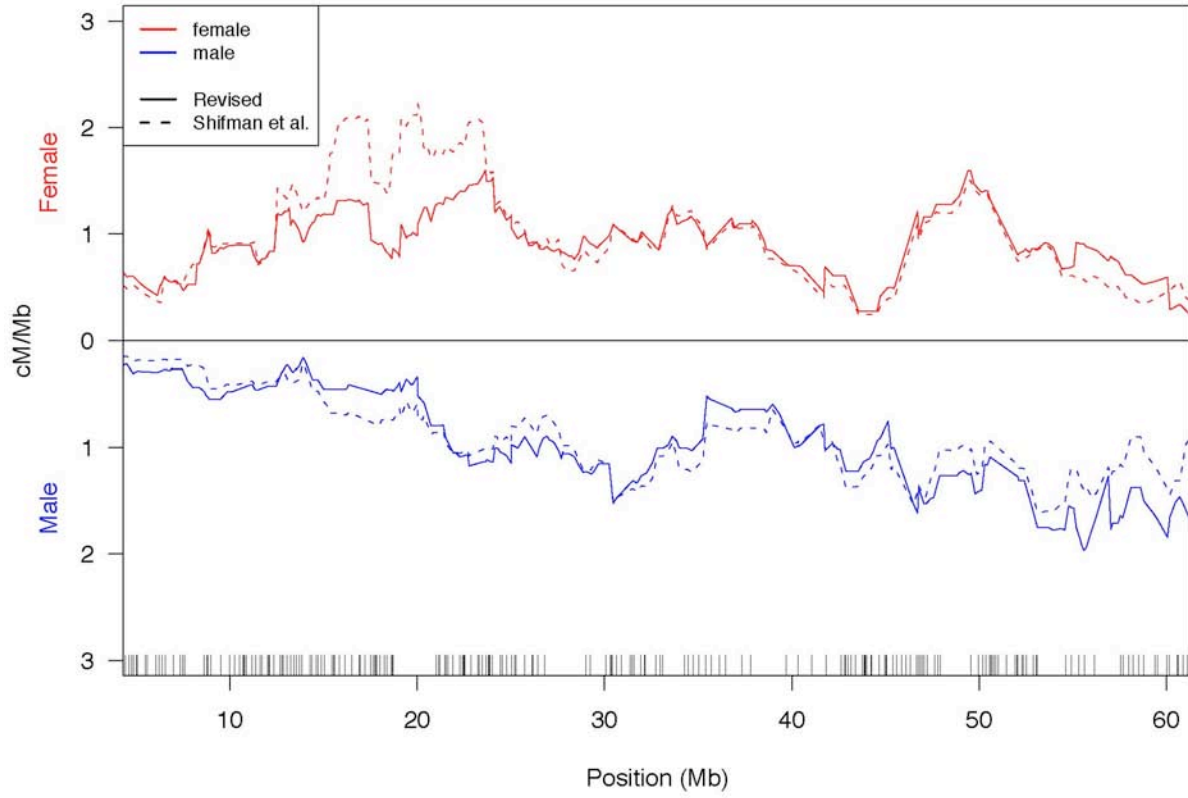
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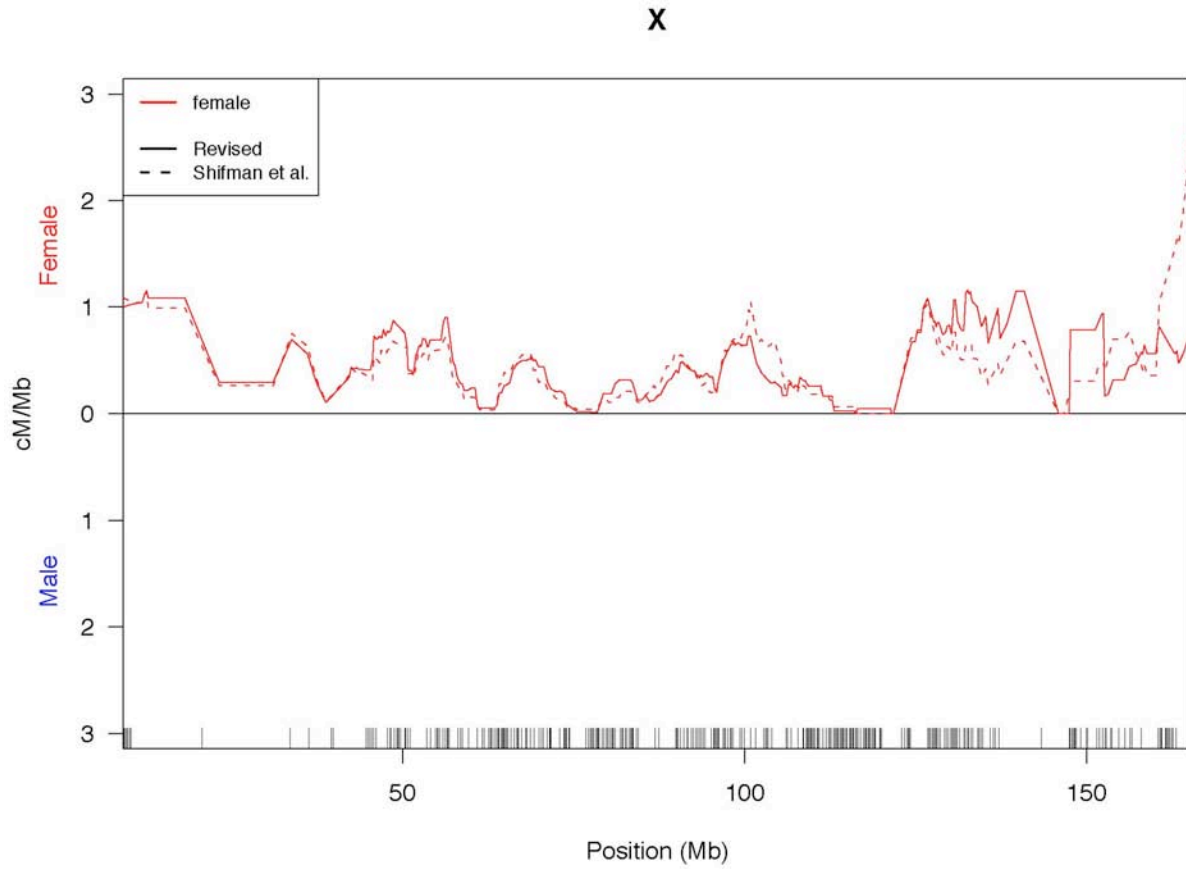
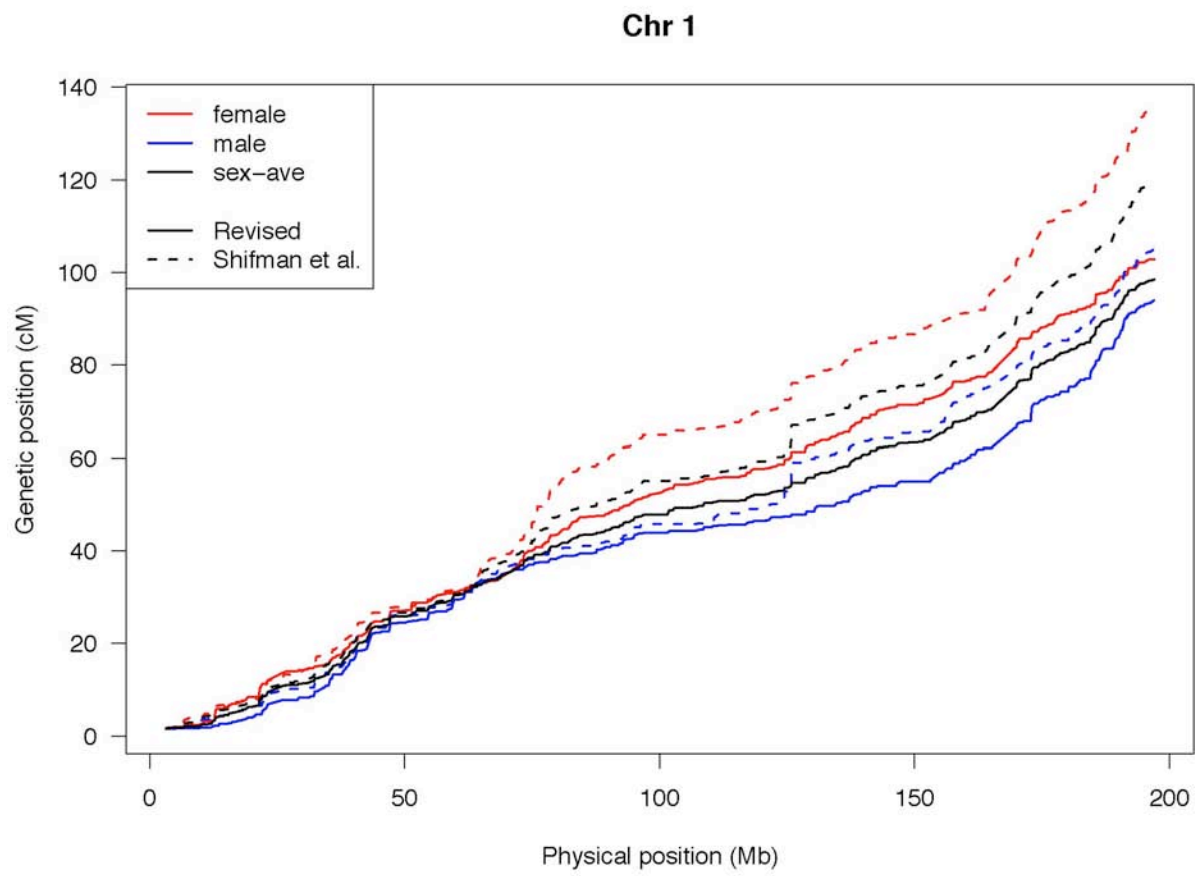
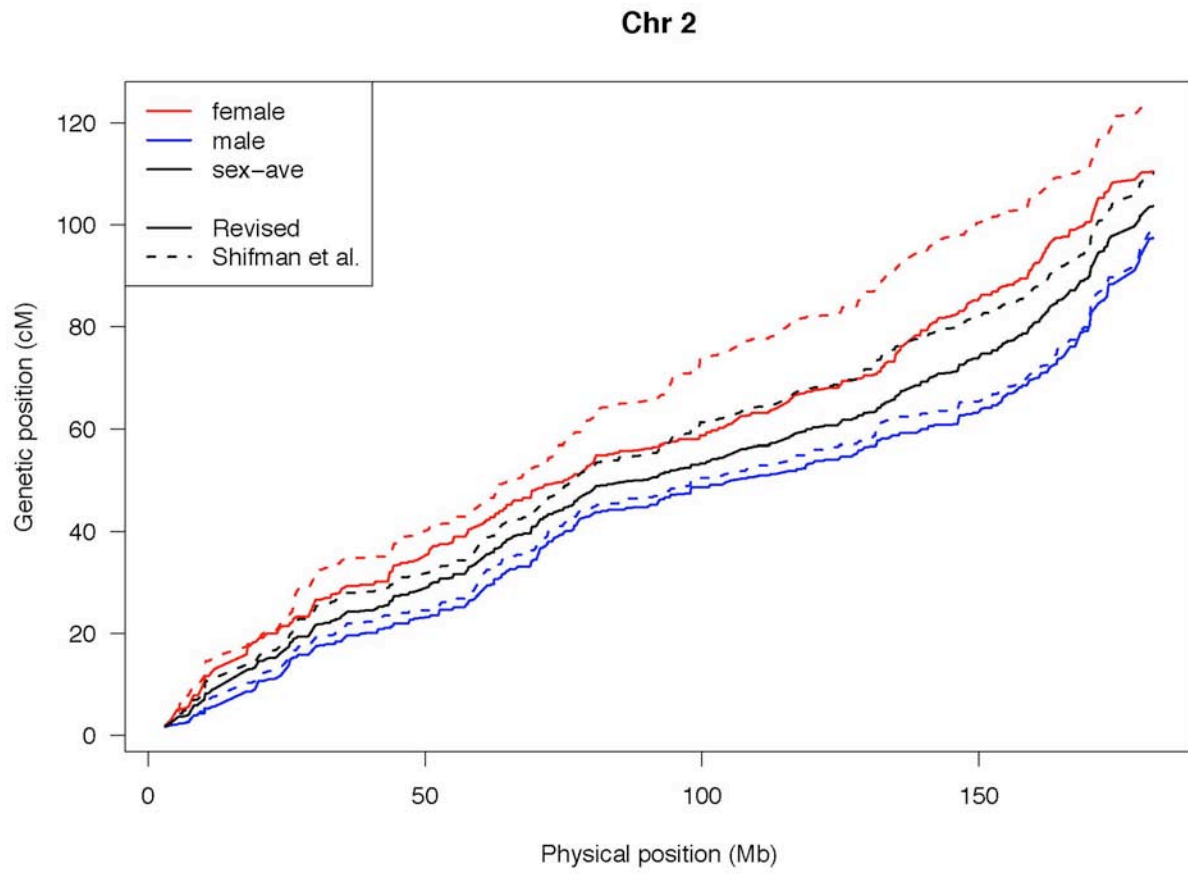
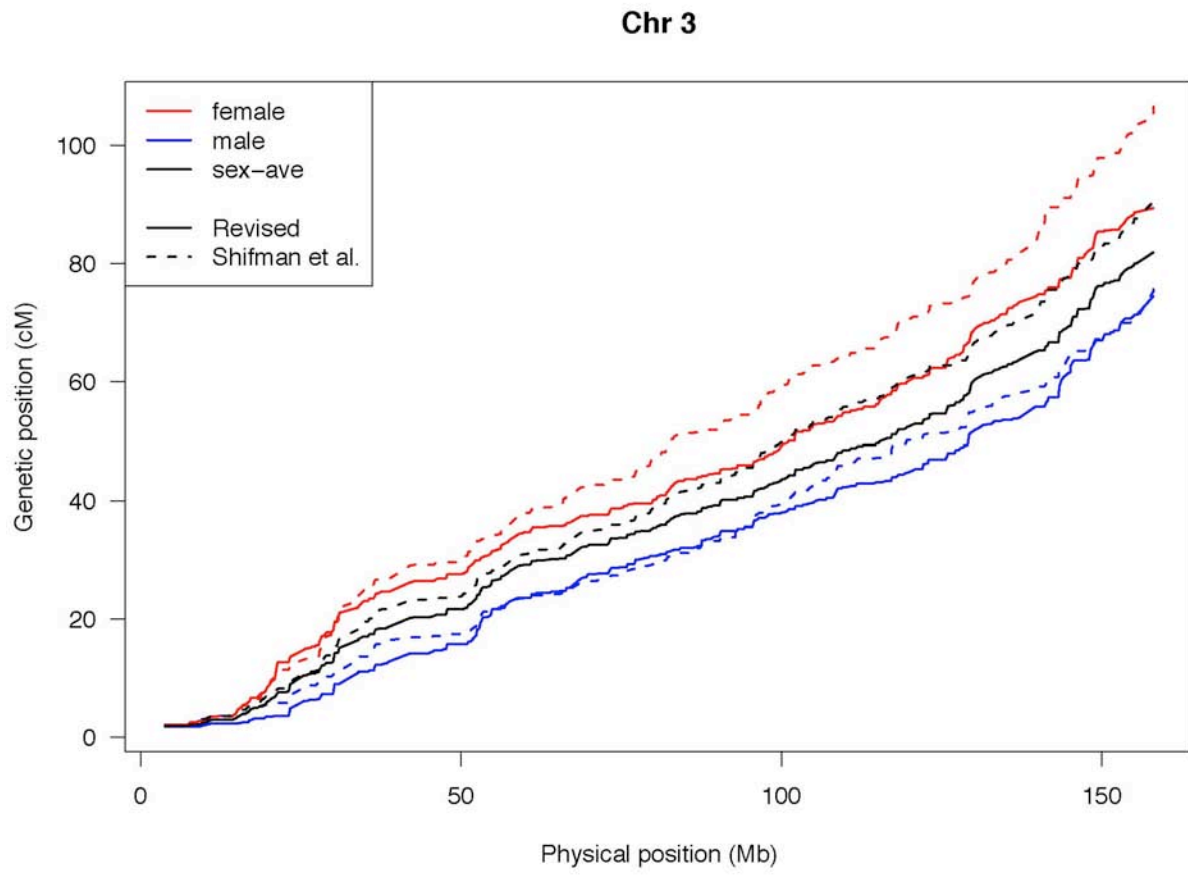


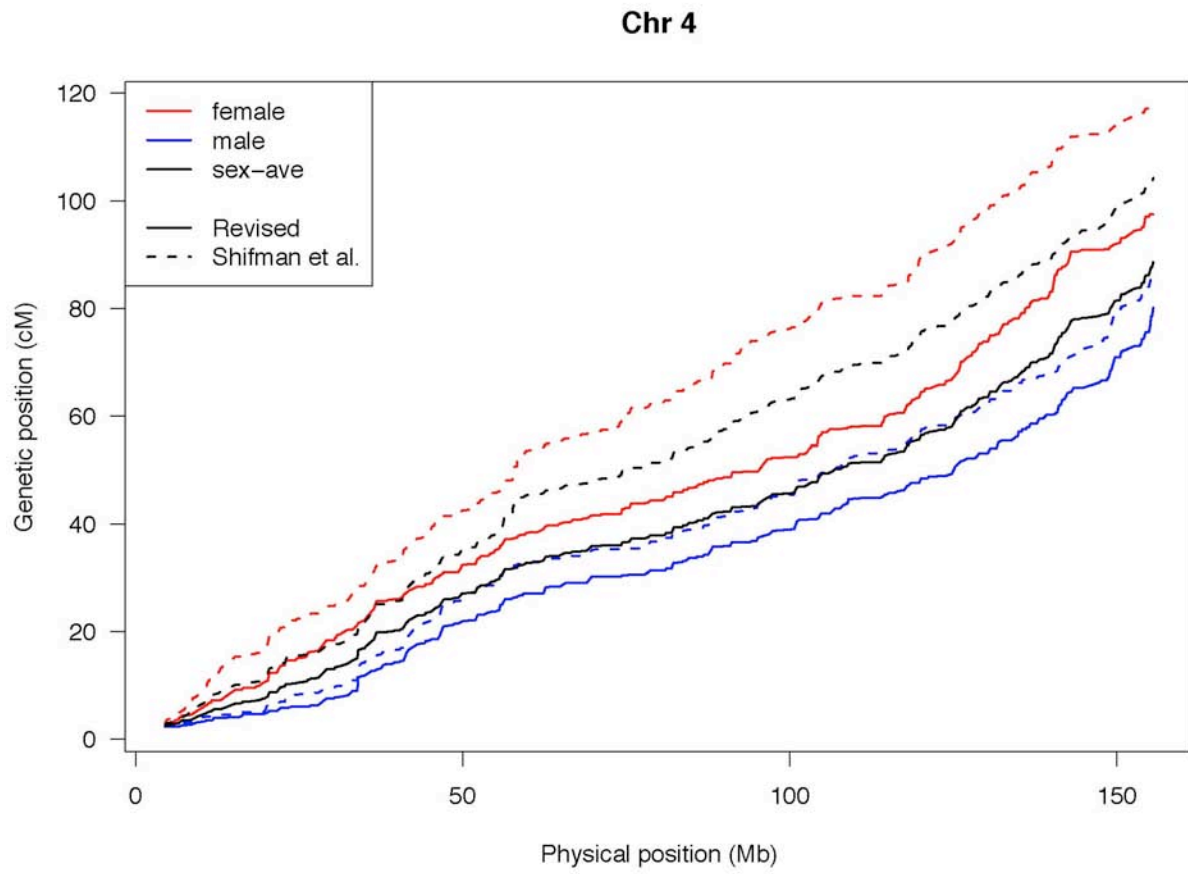
FIGURE S1.— Recombination rates in the original and revised genetic maps. Sex-specific recombination rates for the original and revised genetic maps of all Chromosomes. Maps are based on data from Shifman *et al.*, (2006) as described in Methods.

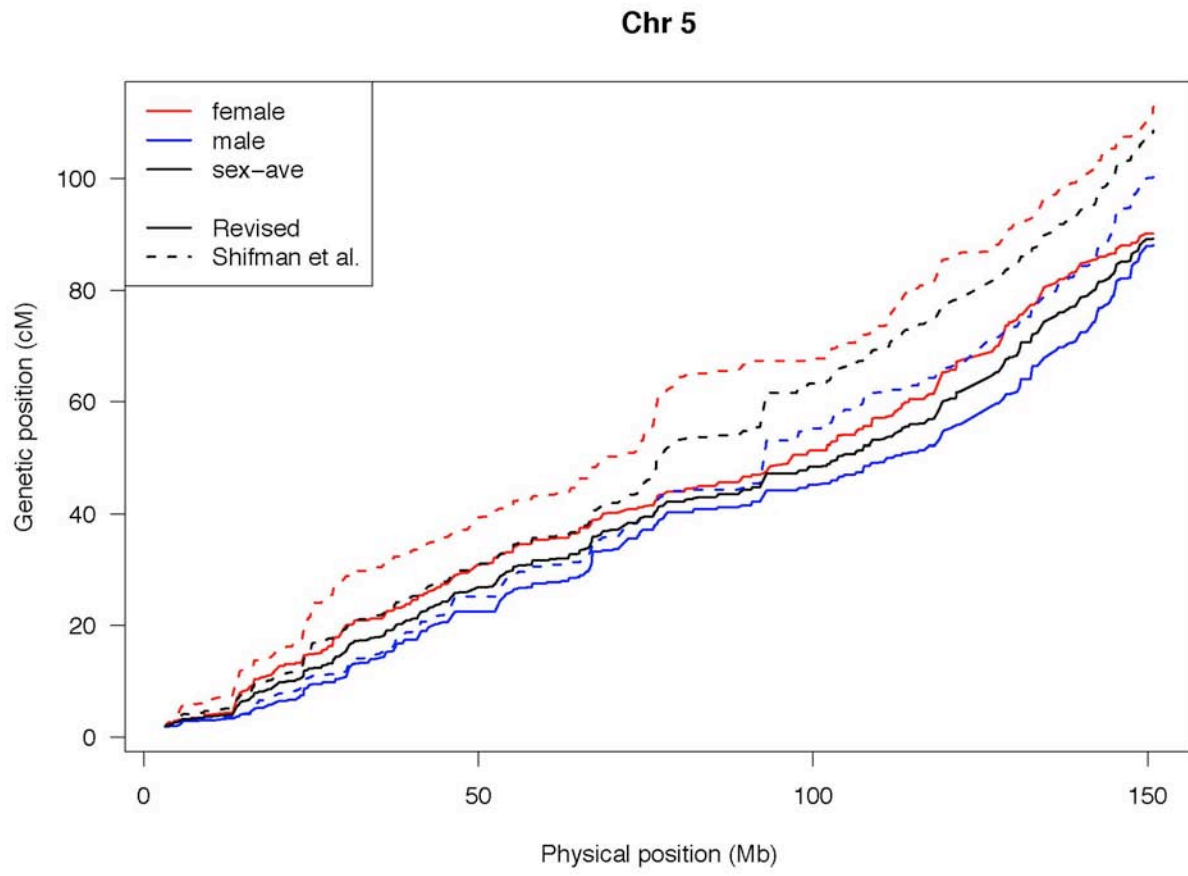
FIGURE S2

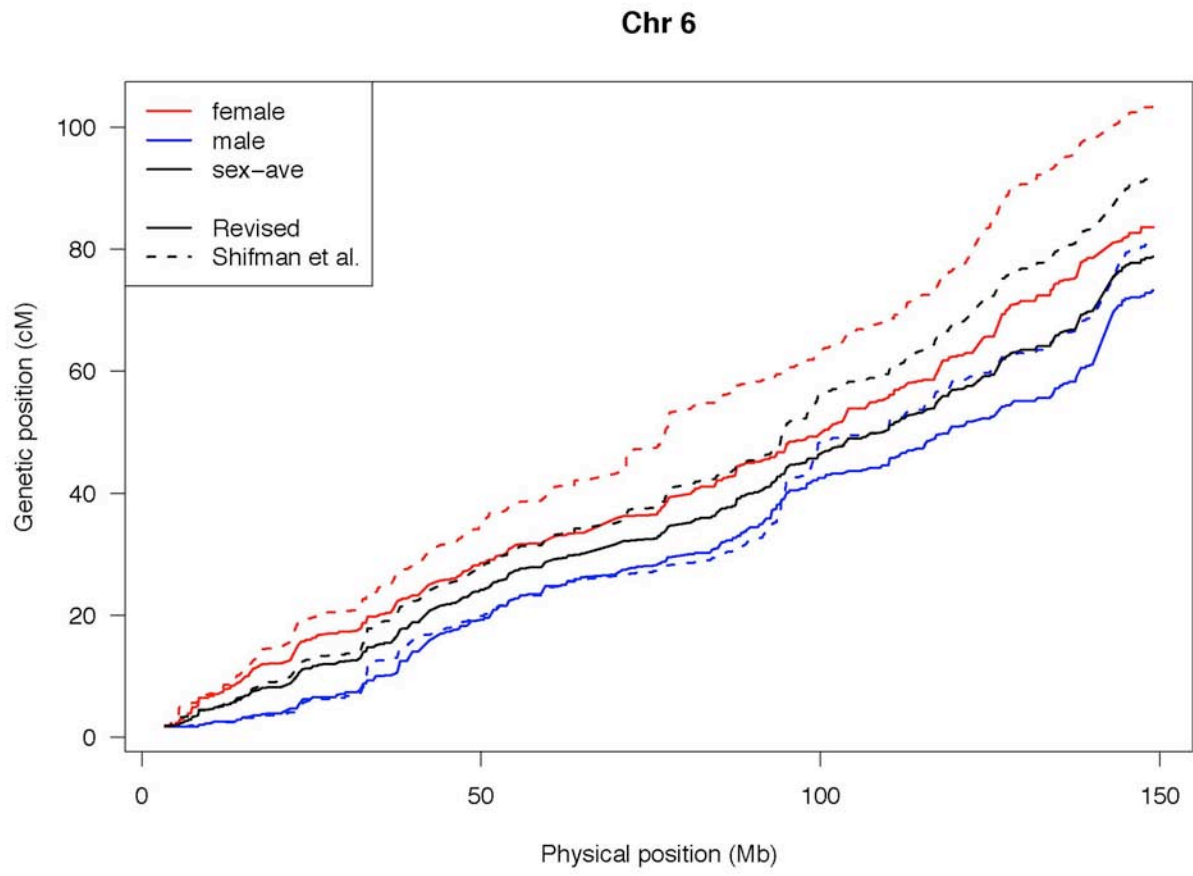


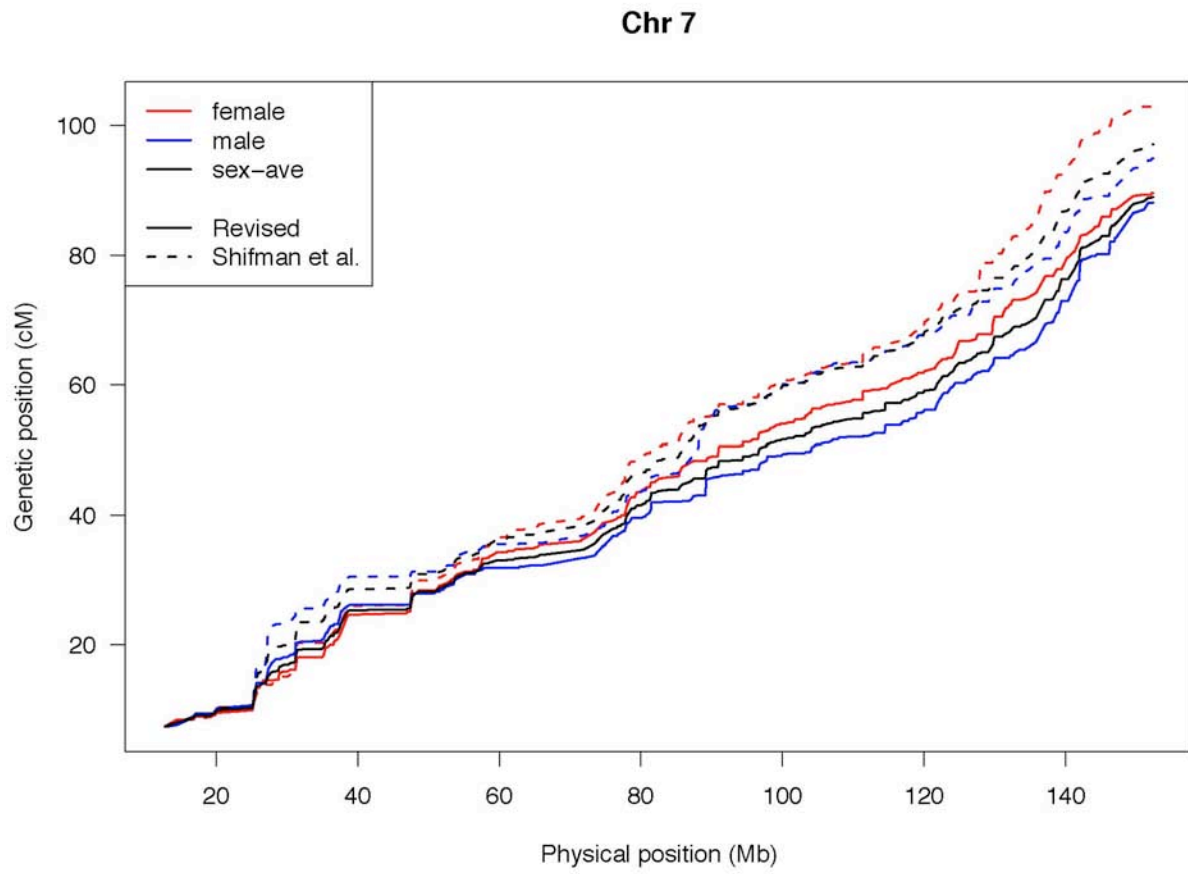




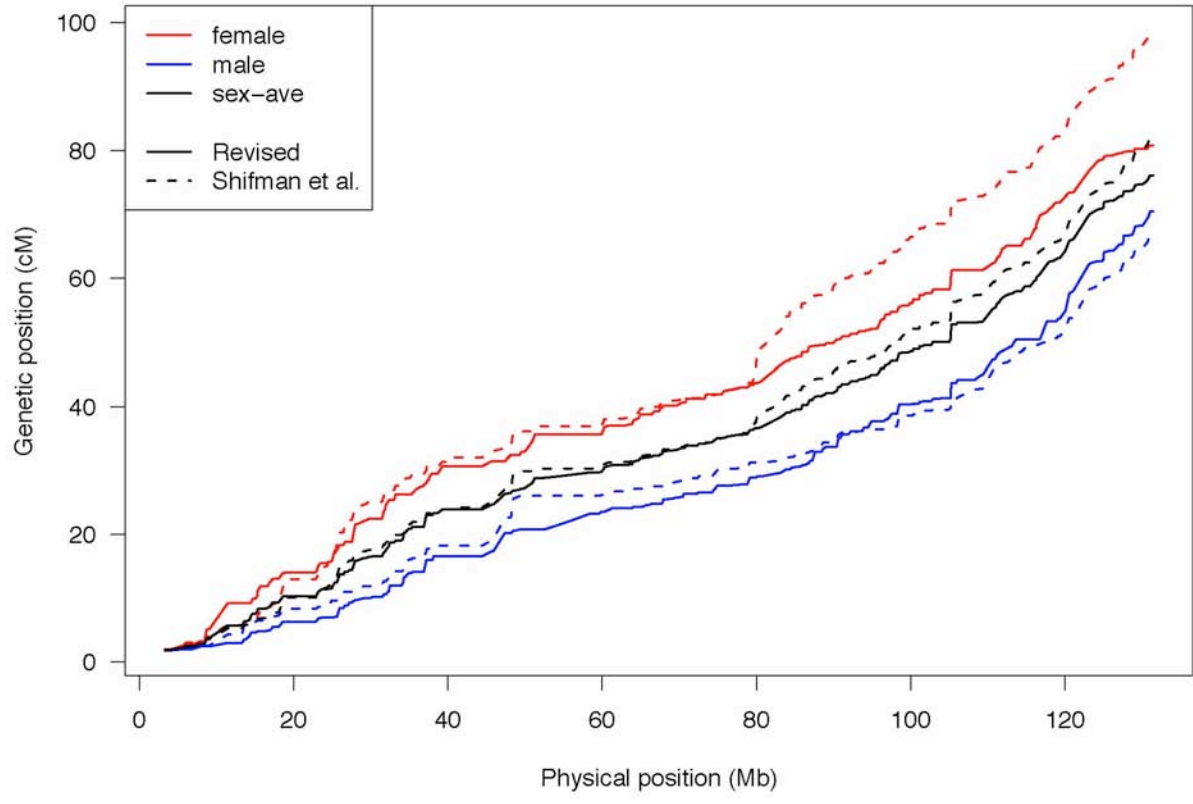


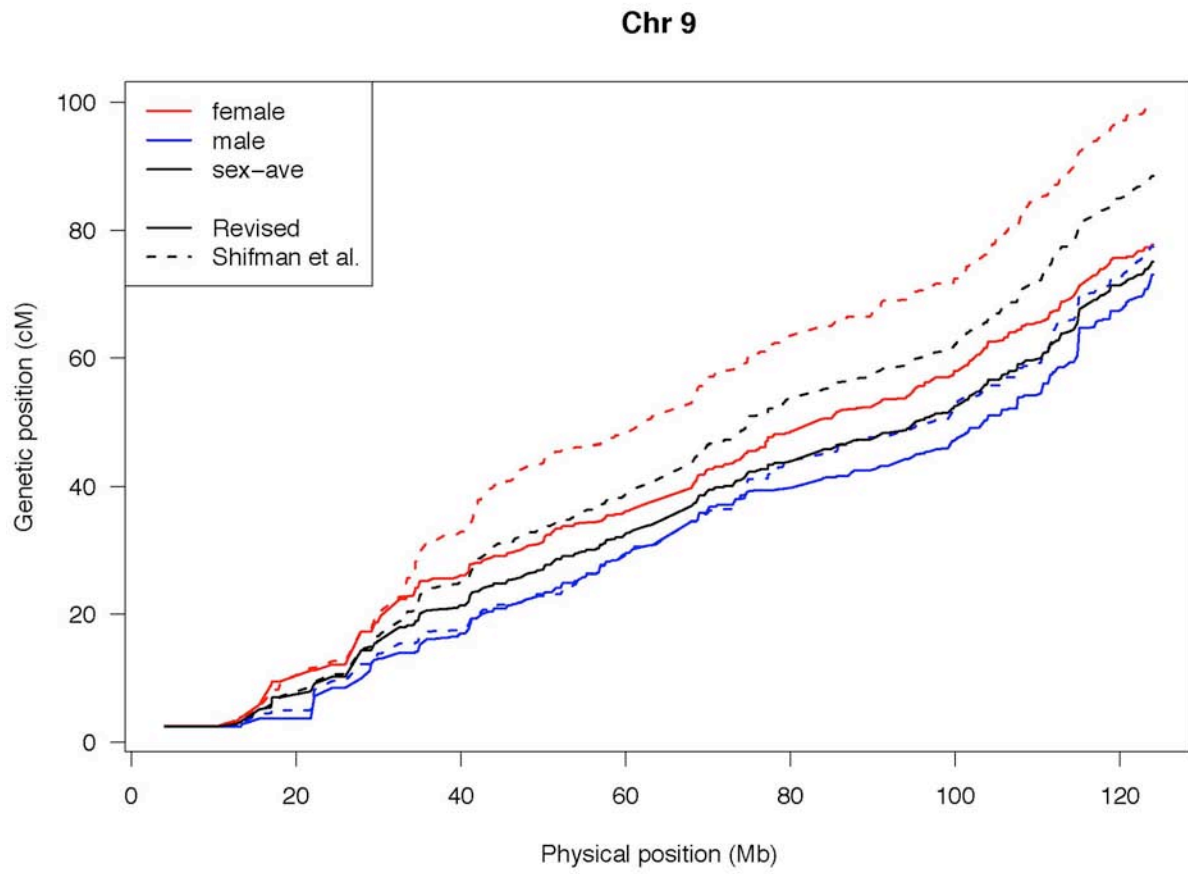


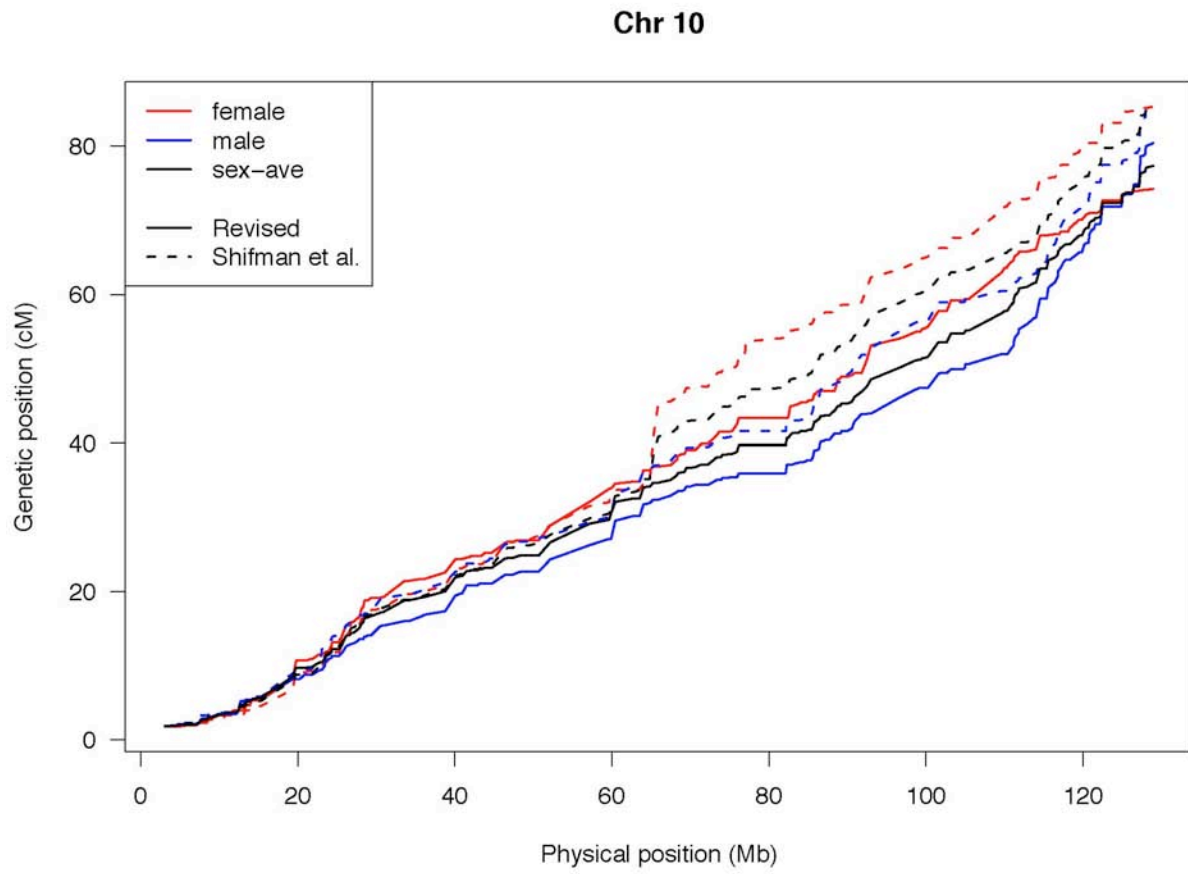


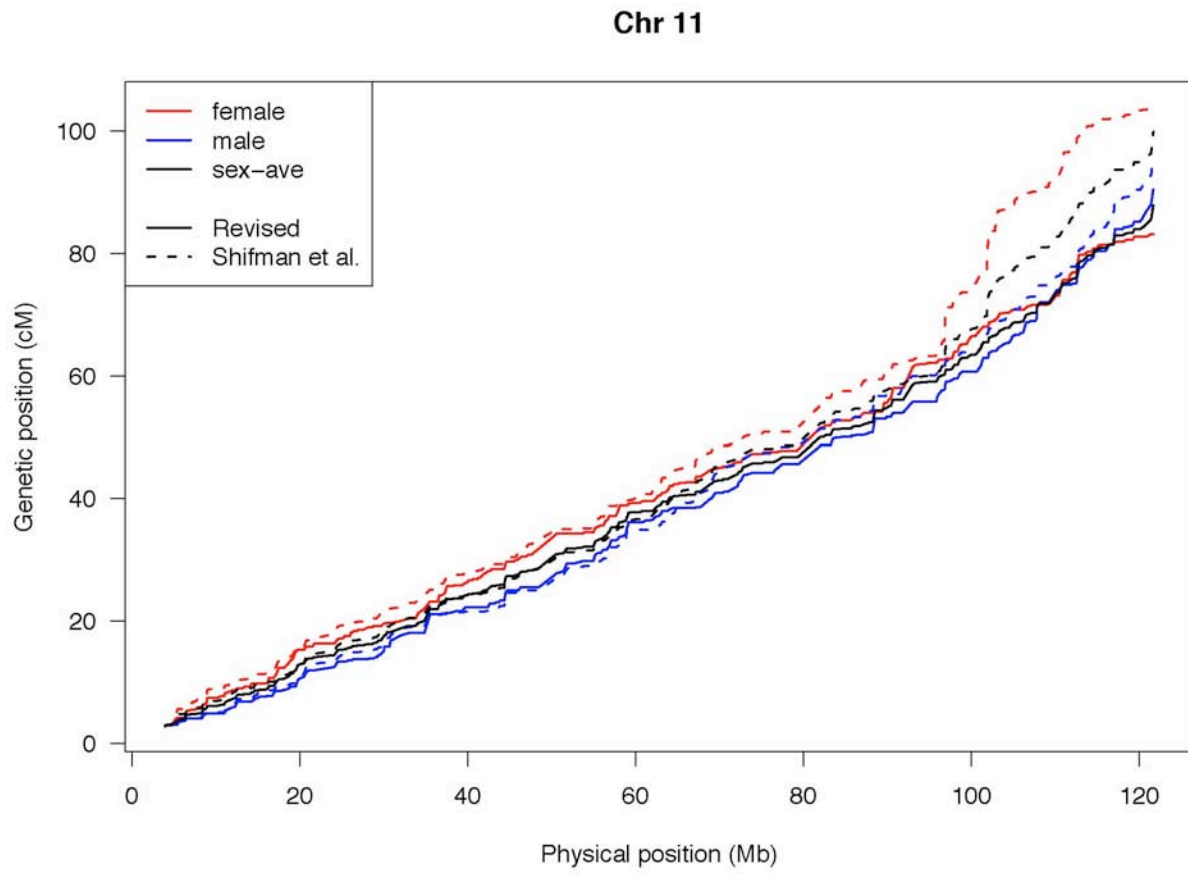


Chr 8

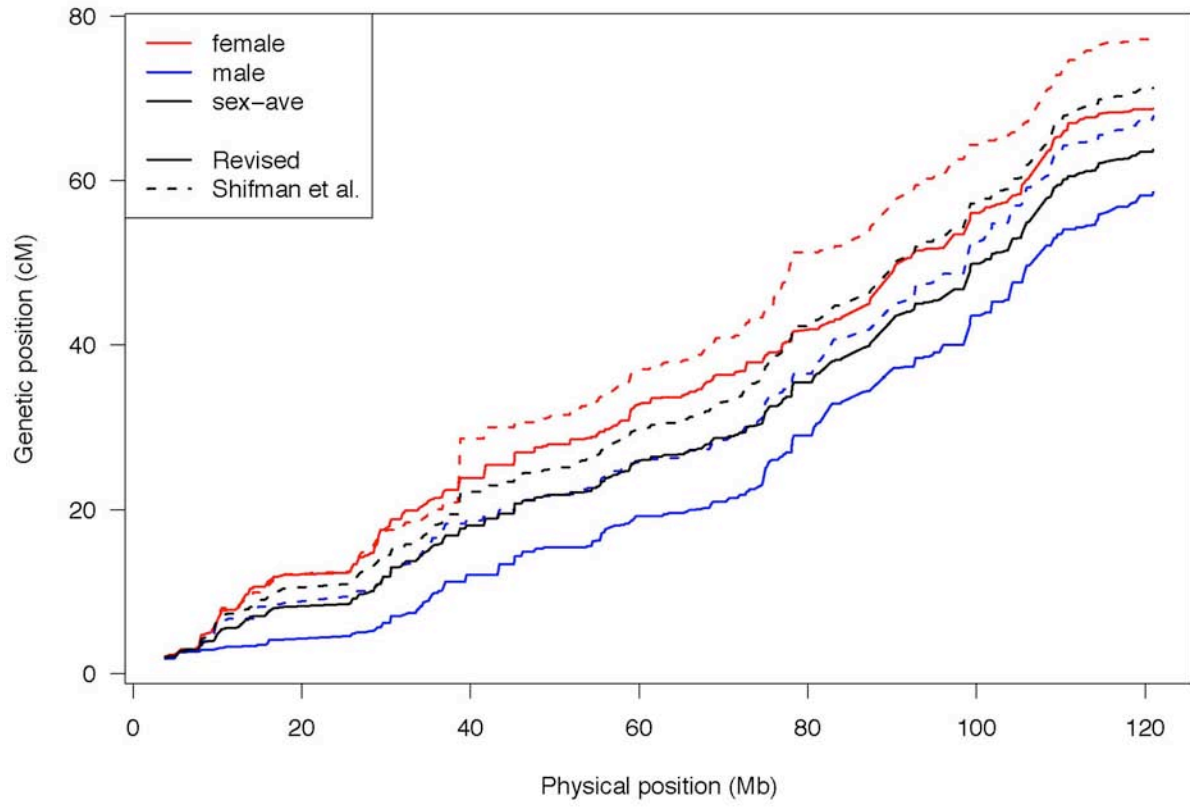


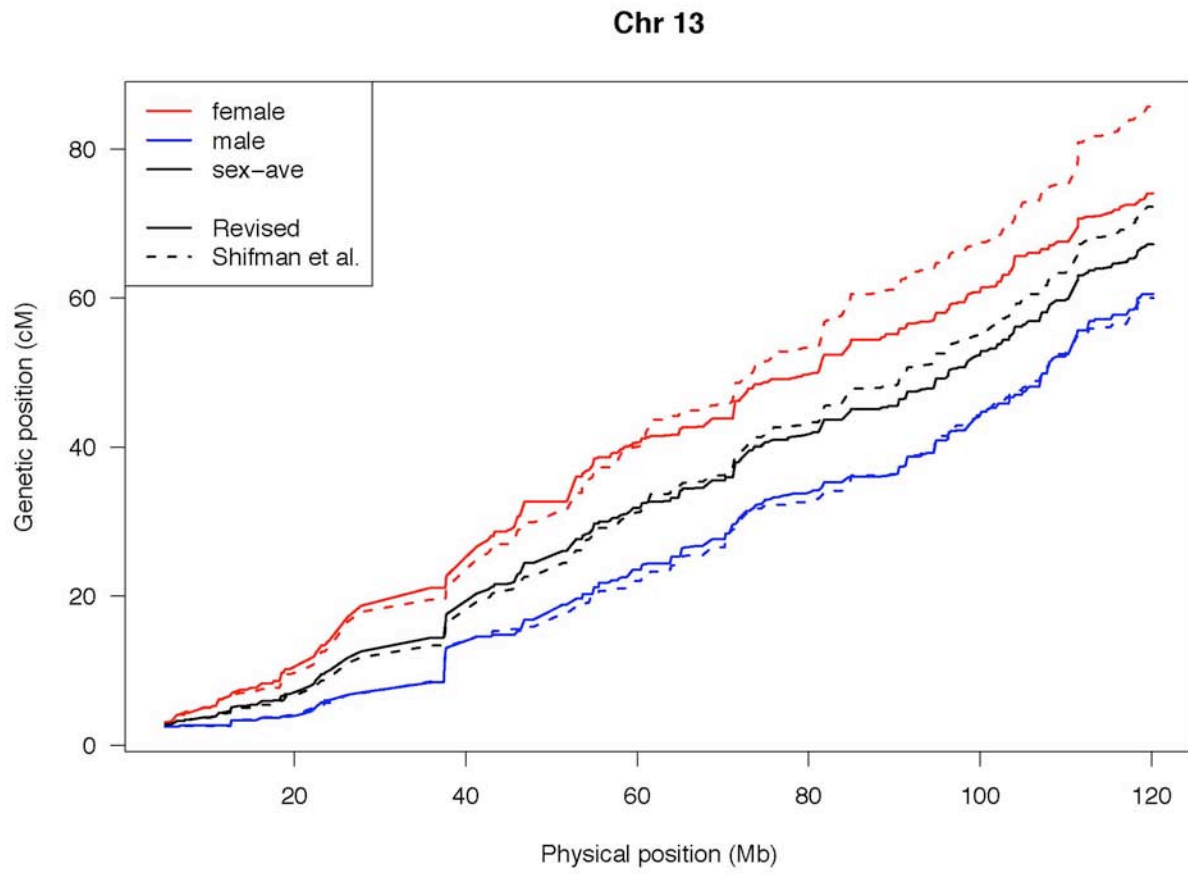




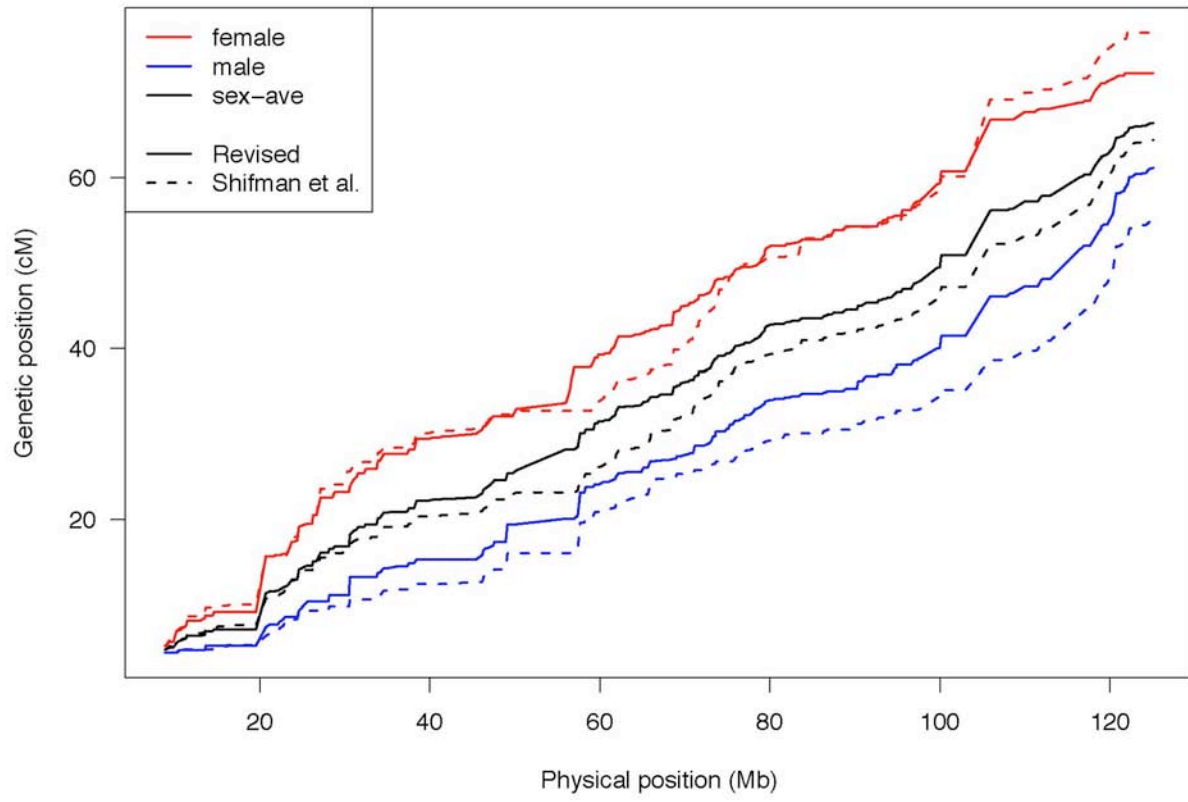


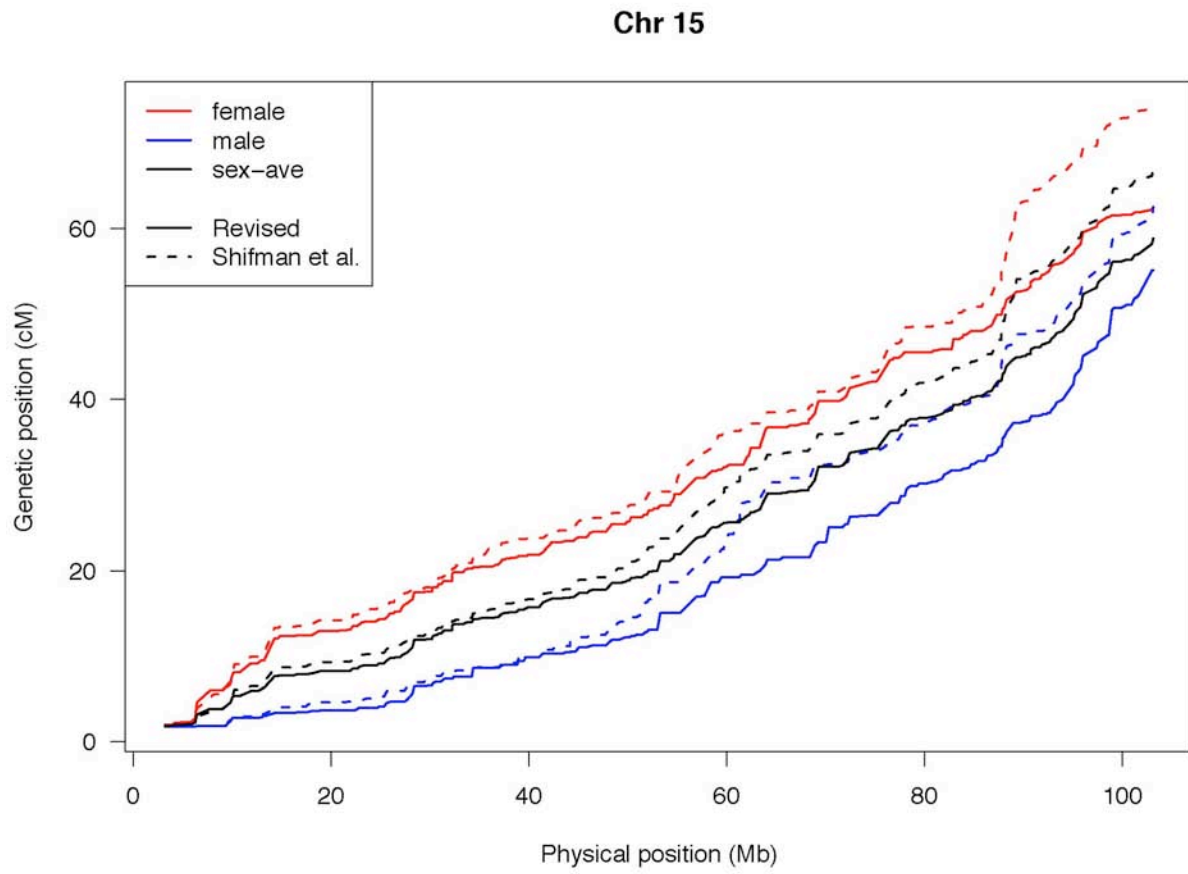
Chr 12

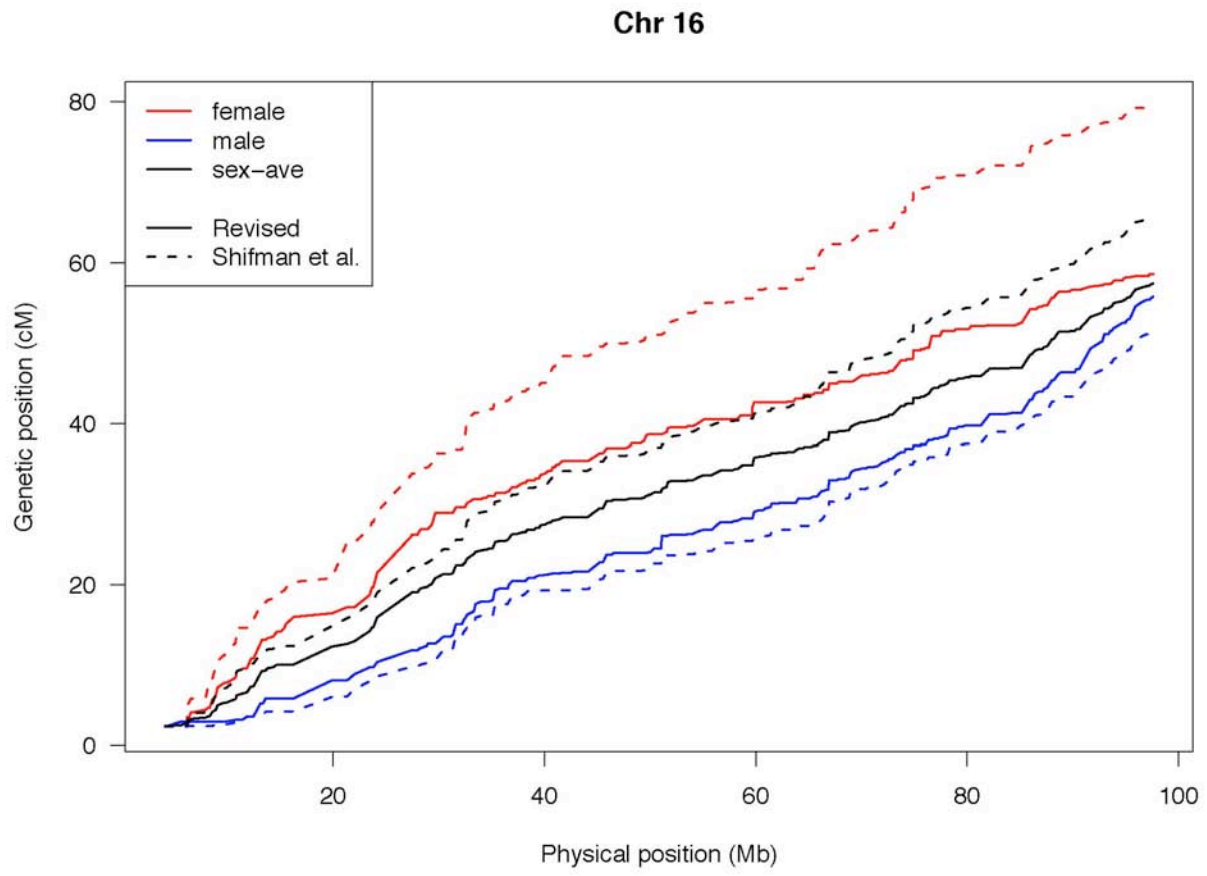


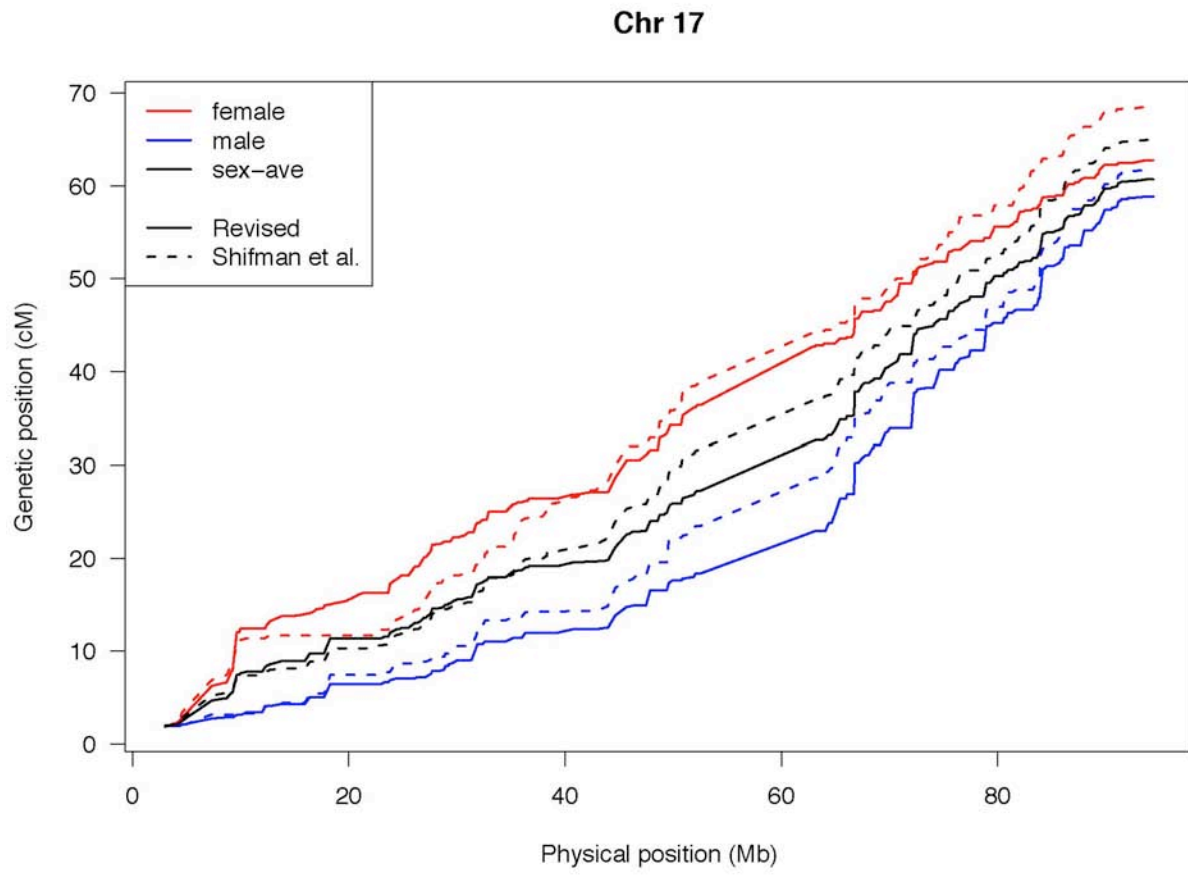


Chr 14

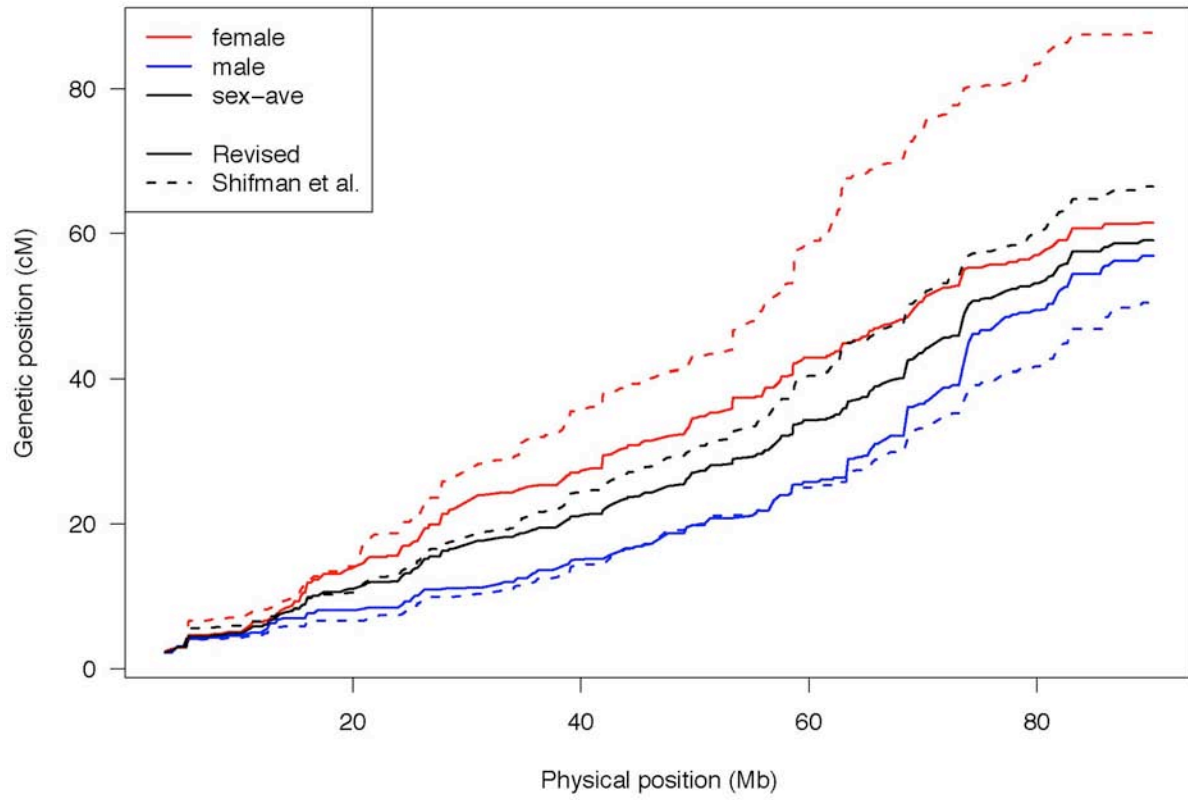


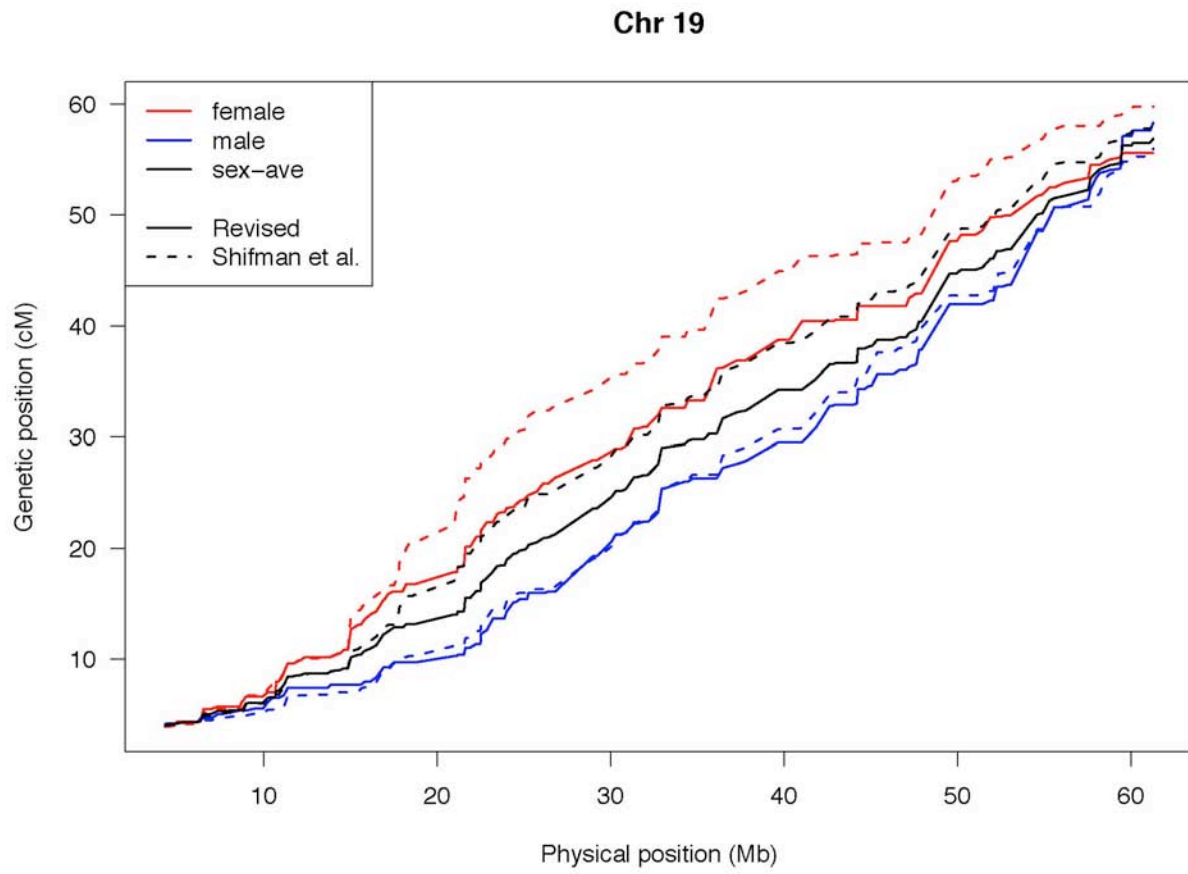






Chr 18





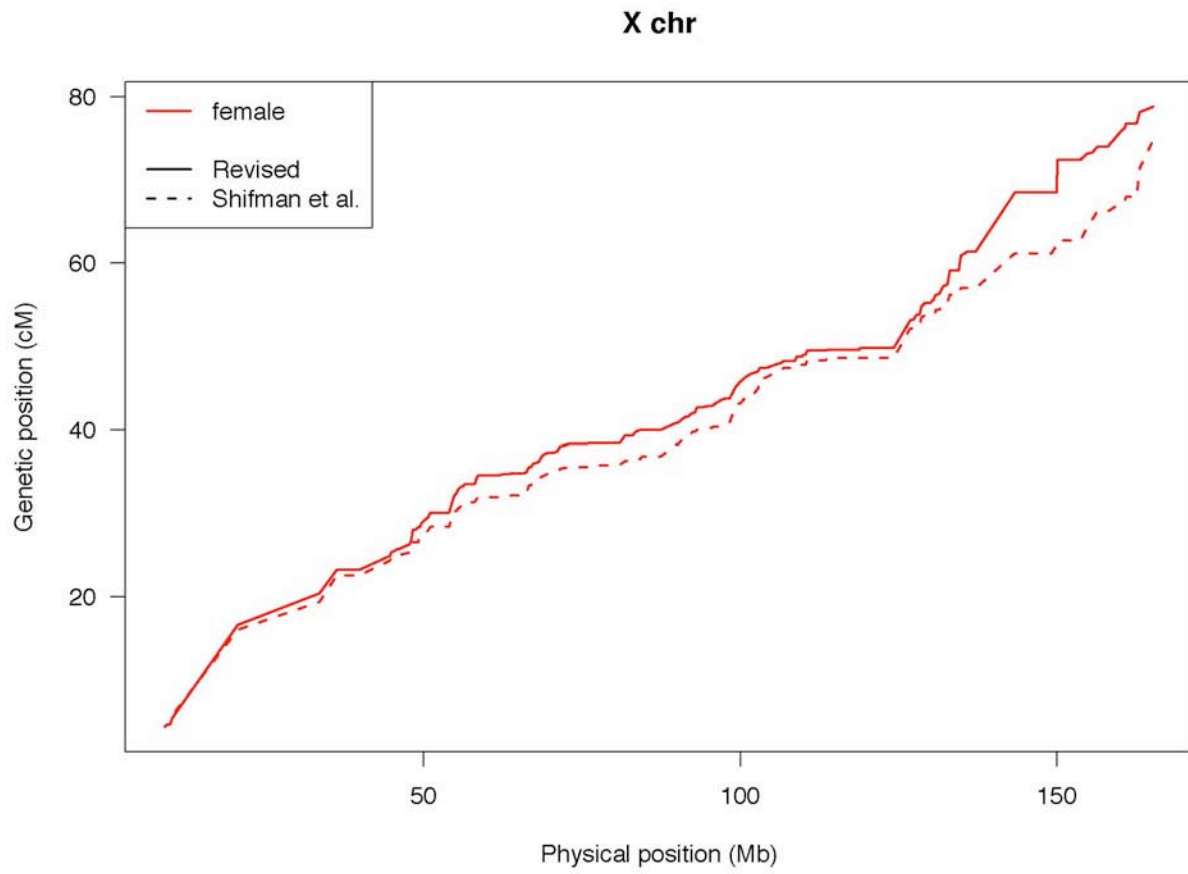


FIGURE S2.—Cumulative genetic maps. Cumulative genetic maps are shown for each chromosome.

TABLE S1**SNPs that mapped to multiple locations in mouse genome build 37**

snpID	chr	Position_Build37
rs13483060	17	62204189, 62383134
rs13475989	1	95771627, 95837777, 95906063
rs13477670	4	42215061, 42803507
rs6177140	4	31468011, 31651727
rs3659566	5	128862845, 129018189
mCV24704879	7	113221222, 113467886

TABLE S2**MIT markers that mapped to multiple locations in mouse genome build 37**

Table S2 is available for download as an Excel file at <http://www.genetics.org/cgi/content/full/genetics.109.105486/DC1>.

TABLE S3**MIT markers that could not be mapped to mouse genome build 37**

Table S3 is available for download as an Excel file at <http://www.genetics.org/cgi/content/full/genetics.109.105486/DC1>.

TABLE S4**QTL peaks that showed significant changes when localized on both old and new genetic maps**

Chr	Peak (cM)*	LOD score*	Peak Marker*	Cross	Phenotype	Type of change
1	62.5	27.50	<i>D1Mit14</i>	B6xC3H	Femoral vBMD	LOD score
	76.0	25.52				
2	60.2	1.75	<i>D2Mit46</i>	B6xCAST	Femoral vBMD	Peak shape
	55.0	1.53	<i>D2Mit15</i>			
2	79.4	4.04	<i>D2Mit48</i>	B6xC3H	Femoral vBMD	Peak shape
	87.0	3.85				
4	63.6	2.64	<i>D4Mit251</i>	NZBxRF	Femoral vBMD	Peak shape
	53.9	2.69	<i>D4Mit26</i>			
4	68.4	3.04	<i>D4MIT308</i>	B6x129	Whole body aBMD	Marker closest to peak
	73.2	2.98	<i>D4MIT42</i>			
4	71.6	2.45	<i>D4Mit68</i>	B6xCAST	Femoral vBMD	Marker closest to peak
	77.9	2.37	<i>D4Mit51</i>			
8	71.6	2.42	<i>D8Mit280</i>	B6xC3H	Ultimate load	Marker closest to peak
	64.0	2.59	<i>D8Mit167</i>			
11	70.7	4.25	<i>D11Mit126</i>	NZBxRF	Ultimate load	Marker closest to peak
	75.1	4.26	<i>D11Mit48</i>			
12	15.5	7.34	<i>D12Mit285</i>	NZBxRF	Ultimate load	Marker closest to peak
	6.0	7.55	<i>D12Mit182</i>			
12	30.2	3.52	<i>D12Mit201</i>	NZBxRF	Femoral vBMD	Peak Shape
	29.0	3.39				
14	4.7	1.92	<i>D14Mit110</i>	B6xC3H	Cortical thickness	LOD score**
14	56.2	3.66	<i>D14Mit170</i>	B6xCAST	Femoral vBMD	Peak Shape
	63.0	3.17				
18	20.5	8.96	<i>D18Mit120</i>	B6xC3H	Ultimate load	Marker closest to peak
	20.0	9.08	<i>D18Mit36</i>			
18	57.5	1.75	<i>D18Mit6</i>	B6xCAST	Femoral vBMD	Peak shape
	54.0	1.94				
19	29.8	2.44	<i>D19Mit11</i>	NZBxSM	Vertebral aBMD	Peak shape
	27.0	2.68				

* The top value is the result from the new map and the bottom from the traditional map analysis.

** LOD change resulted in a failure to detect QTL in one analysis