

CORRECTION

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Correction to: Recommendations for performance optimizations when using GATK3.8 and GATK4

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Following publication of the original article [1], the author explained that Table 2 is displayed incorrectly. The correct Table 2 is given below. The original article has been corrected.

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1. Heldenbrand JR, et al. Recommendations for performance optimizations when using GATK3.8 and GATK4. *BMC Bioinformatics*. 2019;20:557. <https://doi.org/10.1186/s12859-019-3169-7>.

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Table 2 Splitting the genome by chromosomes

Chr	Length	Split 2	Split 3	Split 6	Split 12	Split 16		
1	248,956,422	1674883629	1061198324	491,149,951	248,956,422	248,956,422		
2	242,193,529					242,193,529	242,193,529	
3	198,295,559					198,295,559	198,295,559	
4	190,214,555				570,048,373	190,214,555	190,214,555	
5	181,538,259					352,344,238	181,538,259	
6	170,805,979						170,805,979	
7	159,345,973				475,290,588	304,484,609	159,345,973	
8	145,138,636						145,138,636	
9	138,394,717			1015844658			138,394,717	
10	133,797,422	1413386203	1011226850	540,554,070	272,192,139	133,797,422		
11	135,086,622						268,361,931	135,086,622
12	133,275,309							247,639,637
13	114,364,328							
14	107,043,718					323,399,235	209,034,907	
15	101,991,189				496,995,021			
16	90,338,345							
17	83,257,441					253,969,071	253,969,071	
18	80,373,285							
19	58,617,616							
20	64,444,167							
21	46,709,983				514,231,829	220,590,234	220,590,234	
22	50,818,468							
X	156,040,895							
Y	57,227,415				213,268,310	213,268,310		

Horizontal lines segregate the chunks. Numbers indicate the total number of nucleotides in each resultant chunk of data