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Erratum

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Thousands of corresponding human and mouse genomic regions unalignable in primary sequence contain common RNA structure

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The authors misunderstood the notation used by MultiZ alignments, which unlike BLAST and many others, does not represent all positions relative to the leading strand. Therefore, they did not scan pairs adjacent to +/+ and +/− alignments; instead, the positions of alignments are relative to the 5′ end of the strand in question. This misunderstanding led them to missing unalignable regions in the vicinity of +/− alignments. The authors note that all the analyses are still correct, and that they're only analyzing the 36,970 pairs adjacent to +/+ alignments, and not the additional 18,956 pairs that are adjacent to a +/− alignment. Also, there are not ~100,000 pairs but ~185,000 pairs altogether between the two genomes. The authors are now in the process of scanning these regions along with the rest of the chromosomes.