CORRECTION

Genome Research **22:** 51–63 (2012)

Death of *PRDM9* coincides with stabilization of the recombination landscape in the dog genome

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The authors have discovered an error in the formula to calculate GC*. In two instances, the definitions of u and v are reversed. The corrected text is as follows:

Page 57 (column 2, paragraph 2): Based on the assumption that the observed substitution patterns persist, we also estimate the equilibrium GC content (GC*; GC* = u/[u + v], where the rate of weak-to-strong [AT-to-GC] and strong-to-weak [GC-to-AT] substitutions are u and v, respectively) (Meunier and Duret 2004) and predict that the GC peaks will be further reinforced in the dog but that they will vanish in the panda (Fig. 6).

Page 62 (column 1, paragraph 3): We calculated the average GC* (GC* = u/(u + v), where the rate of weak-to-strong [AT-to-GC] and strong-to-weak [GC-to-AT] substitutions are u and v, respectively) in the dog as well as the panda, across the GC peak–centered, 18-kb windows described above using a 500-bp sliding window.

The authors apologize for any confusion this may have caused.