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High-throughput biochemical analysis of in vivo location data reveals novel distinct classes of POU5F1(Oct4)/DNA complexes

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In the author list for this paper, author name William Fairbrother should have appeared as William G. Fairbrother.

The authors apologize for any confusion this may have caused.

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Mapping DNA structural variation in dogs

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The authors have discovered minor changes in the data, which affect one sentence in text and one species row in Table 2.

On page 501, the fourth sentence beneath the heading “aCGH of pedigreed dogs” should read:

We identified 152 CNVs—in 57 CNV regions (CNVRs)—at high confidence (Fig. 2; Table 1; Supplemental Table S2).

In addition, the row that displays the data for the Dog species is incorrect and has been replaced. The corrected Table 2 is reprinted below.

Table 1B. Comparison of dog CNV to that reported in other mammals

Species	Total no. of CNVs	Mean no. of CNVs per individual	No. of CNVRs	No. of deletions, no. of amplifications	Amplified avg. (mean)	Deletion avg. (mean)	References
Dog (<i>n</i> = 9)	152	16.9 (385 k oligo aCGH)	57	85, 67	476.5 kb	272.2 kb	This study
Mouse (<i>n</i> = 21)	80	22 (385 k oligo aCGH)				271.5 kb ^a	Graubert et al. 2007
Rat (<i>n</i> = 10, 5 M oligo ^b ; <i>n</i> = 3, 375 k)	643	63 (5 M exon-specific oligo ^b); 11 (385 k oligo aCGH)			5.2 kb (5 M exon-specific oligo ^b); 256 kb (375 k oligo aCGH) ^a	102 kb ^a	Guryev et al. 2008
Macaque (<i>n</i> = 9)	123	14 (385 k oligo aCGH)					Lee et al. 2008
Human (<i>n</i> = 270)	1447	70 (BAC aCGH); 24 (SNP array)			341 kb (BAC aCGH); 206 kb (SNP array) ^a		Redon et al. 2006

^aAverage CNV size, amplifications and deletions combined.

^b5 M exon-specific, non-CGH oligo array.