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# HIGH PREVALENCE OF PRDM9-INDEPENDENT RECOMBINATION HOTSPOTS IN PLACENTAL MAMMALS

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## Abstract

1 In many mammals, recombination events are concentrated into hotspots directed by a se-  
2 quence specific DNA-binding protein named PRDM9. Intriguingly, PRDM9 has been lost  
3 several times in vertebrates, and notably among mammals, it has been pseudogenized in  
4 the ancestor of canids. In absence of PRDM9, recombination hotspots tend to occur in  
5 promoter-like features such as CpG islands. It has thus been proposed that one role of  
6 PRDM9 could be to direct recombination away from those PRDM9-independent hotspots.  
7 However, the ability of PRDM9 to direct recombination hotspots has been assessed only in a  
8 handful of species, and a clear picture of how much recombination occurs outside of PRDM9-  
9 directed hotspots in mammals is still lacking. In this study, we derived an estimator of past  
10 recombination activity based on signatures of GC-biased gene conversion in substitution pat-  
11 terns. We applied it to quantify recombination activity in PRDM9 independent hotspots in  
12 52 species of boreoeutherian mammals. We observed a wide range of recombination rate at  
13 these loci: several species (such as mice, humans, some felids or cetaceans) show a deficit  
14 of recombination, while a majority of mammals display a clear peak of recombination. Our  
15 results demonstrate that PRDM9-directed and PRDM9-independent hotspots can co-exist  
16 in mammals, and that their co-existence appears to be the rule rather than the exception.  
17 Additionally, we show that the location of PRDM9-independent hotspots is relatively stable  
18 compared to that of PRDM9-directed hotspots, but that it nevertheless evolves slowly in  
19 concert with DNA hypomethylation.

20 **Keywords** PRDM9 · Recombination landscape · Hotspots · Mammals · gBGC

## 21 Significance statement

22 Meiotic recombination is a key process both to produce gametes and to generate genetic diversity. In many  
23 Eukaryotes, recombination tends to occur at specific loci (recombination hotspots). Two types of hotspots  
24 have been described so far: in humans and mice, hotspots are directed by the protein PRDM9, whereas in  
25 species that lack this gene, hotspots tend to occur in promoter-like features (“default hotspots”). In this  
26 study, we demonstrate that despite possessing a functional PRDM9, most mammals also use default hotspots,  
27 sometimes as much as in PRDM9-lacking species. Interestingly, the widespread coexistence of redundant  
28 recombination-directing systems might explain why Prdm9 has been recurrently lost across animals.

## 29 Introduction

30 Meiotic recombination is a crucial step in the production of gametes for a large majority of eukaryotes. It is  
31 initiated by programmed double-strand breaks (DSBs), that can be resolved in two types of recombination  
32 events, using the homolog as a template: crossovers (COs), where there is a reciprocal exchange of chromo-  
33 some arms, and non crossovers (NCOs), where DSB repair leads to gene conversion around the DSB site  
34 without reciprocal exchange. In most eukaryotes, at least one CO per chromosome is necessary to ensure  
35 correct segregation between homologs and is therefore mandatory for meiosis success (Page and Hawley,  
36 2003; Gerton and Hawley, 2005). In many vertebrates, recombination events are not uniformly distributed  
37 along the genome (reviewed in Stapley et al. (2017); Zelkowski et al. (2019)). Instead, they tend to be  
38 concentrated in so-called recombination hotspots (Lichten and Goldman, 1995; Tock and Henderson, 2018).

39 In many mammals, the position of recombination hotspots is determined by the zinc-finger protein  
40 PRDM9, which binds specific DNA motifs and recruits the DSB machinery through histone methylation  
41 (Baudat et al., 2010; Myers et al., 2010; Parvanov et al., 2010; Diagouraga et al., 2018). This gene is highly  
42 polymorphic and hundreds of alleles have been reported in mice and humans (Buard et al., 2014; Kono et al.,  
43 2014; Alleva et al., 2021). Most allelic diversity is concentrated on residues of the zinc fingers that interact  
44 with the DNA, leading to changes in DNA sequence specificity. Therefore, the position of recombination  
45 hotspots varies within a population and between species (Auton et al., 2012; Smagulova et al., 2016; Alleva  
46 et al., 2021). Additionally, PRDM9 tends to erode its targets through gene conversion (Baker et al., 2015;  
47 Smagulova et al., 2016). As the available targets for a given PRDM9 allele become scarce, its ability to  
48 generate enough COs for meiosis to succeed is compromised. A new allele with more targets will then  
49 be positively selected leading to a red-queen dynamic accelerating the turnover of recombination hotspots  
50 (Úbeda and Wilkins, 2011; Latrille et al., 2017; Baker et al., 2022; Genestier et al., 2023). It has also been  
51 proposed that when PRDM9 binds symmetrically both homologs, it facilitates the repair of DSBs as COs  
52 and thereby contributes to the success of meiosis (Davies et al., 2016; Li et al., 2019; Hinch et al., 2019).  
53 Indeed, experiments in mice and rats showed that an inactivation of this protein drastically reduces fertility  
54 (Mihola et al., 2019, 2021; Brick et al., 2012).

55 Despite its central role in recombination, PRDM9 has been repeatedly lost in vertebrates. (Baker et al.,  
56 2017; Cavassim et al., 2022). Among amniotes, one loss occurred in the ancestor of archosaurs (crocodiles and

57 birds) (Singhal et al., 2015; Cavassim et al., 2022), and another one in the ancestor of canids (dogs, wolves  
58 and foxes) (Oliver et al., 2009; Axelsson et al., 2012; Auton et al., 2013). In dogs and several passerines,  
59 studies based on linkage disequilibrium (LD) showed that recombination hotspots tend to occur in CpG  
60 islands, and more specifically in hypomethylated ones in dogs (Auton et al., 2013; Berglund et al., 2015;  
61 Singhal et al., 2015; Kawakami et al., 2017). Likewise, the DSB hotspots of a mouse whose PRDM9 has  
62 been inactivated through a knock-out (PRDM9<sup>-/-</sup>) also occur in promoter-like features (Brick et al., 2012).  
63 Interestingly, an increase of recombination rate near promoters has also been observed in dogs, birds, plants  
64 and yeasts, which lack PRDM9 (Petes, 2001; Marand et al., 2017).

65 Those observations led to the conclusion that there exist two types of recombination landscapes in  
66 vertebrates. The first one is PRDM9-dependent, fast evolving with recombination targeted away from  
67 promoter-like features, while the second is relatively stable, with recombination occurring in promoter-like  
68 feature such as CpG islands. However, a recent finding in snakes challenged this binary view. In rattle snakes  
69 and corn snakes, which still possess a functional PRDM9, some hotspots are directed by PRDM9, but others  
70 are directed toward CpG islands (Schield et al., 2020; Hoge et al., 2023). It was first proposed that PRDM9  
71 could have a different role in rattle snake and direct recombination towards CpG islands (Schield et al.,  
72 2020), but other observations suggest that the recombination landscapes in these snakes rather reflects the  
73 inefficiency of their PRDM9-dependent pathway to direct DSBs away from CpG islands (Hoge et al., 2023).  
74 Altogether, the two studies concur on the fact that the recombination landscape in snakes differs from what  
75 is observed in mammals, despite the presence of PRDM9 (Schield et al., 2020; Hoge et al., 2023).

76 Most of our knowledge about PRDM9 function and evolution has been acquired in a handful of mammals  
77 (mostly human and mice). In mice, Smagulova and colleagues analyzed the position of DSB hotspots  
78 obtained by ChIP-seq of DMC1 in strains carrying different PRDM9 alleles. They measured the overlap of  
79 these hotspots with the ones of a strain knocked out for Prdm9 (PRDM9-independent hotspots) (Smagulova  
80 et al., 2016). Those strains showed differences in their capacity to target DSBs away from the hotspots of  
81 the Prdm9<sup>-/-</sup> mouse (hereafter referred to as 'MDH', for 'Mouse Default Hotspots'). Some strains show a  
82 significant deficit of DSB hotspots at MDH loci, while others, carrying less dominant PRDM9 alleles, show  
83 up to a 6-fold DSB hotspot enrichment at these loci, even though they represent a small proportion of all  
84 recombination hotspots (~7%) (Smagulova et al., 2016). This shows that even when PRDM9 is present,  
85 PRDM9-independent hotspots can be active in mammals. However, this activity could just be the reflection  
86 of a specific PRDM9 deficiency in some mice strains and overall, we still have no clear idea on how prevalent  
87 the usage of PRDM9-independent hotspots is in mammals. A comprehensive understanding would require  
88 measures of fine-scale variations in recombination rate for a wide range of mammalian species, and ideally  
89 across long periods of time.

90 Recombination hotspots can be mapped directly in meiotic cells (e.g. by chromatin immunoprecipitation  
91 with antibodies to DMC1 in spermatocytes (Brick et al., 2012; Pratto et al., 2014; Smagulova et al., 2016;  
92 Alleva et al., 2021)), but these molecular approaches are tedious and only amenable for a few model organ-  
93 isms. High-resolution recombination maps can also be inferred from patterns of linkage disequilibrium (LD).  
94 This approach is more scalable and provides information on sex-averaged historical recombination activity

95 at the population scale. However, this approach remains laborious and expensive (it requires the sequencing  
96 of at least 10 individuals per species (Auton and McVean, 2007; Chan et al., 2012)), and it is sensitive to  
97 various sources of errors (Spence and Song, 2019; Samuk and Noor, 2022; Raynaud et al., 2023). Hence, for  
98 now, such LD-based recombination maps are available only for a very limited number of species.

99 Alternatively, substitution patterns have been found to be informative about past recombination rates.  
100 In particular, it has been shown in mammals that recombination induces a transmission bias of GC alleles  
101 through the process of GC-biased gene conversion (gBGC). This eventually leads to an elevation of the WS  
102 (AT to GC) substitution rate, and a decrease of the SW (GC to AT) substitution rate (Nagylyaki, 1983;  
103 Duret and Arndt, 2008; Glémin, 2010). The substitution rate matrix can be conveniently summarized by a  
104 single parameter, the equilibrium GC-content (hereafter noted  $GC^*$ ), which corresponds to the GC-content  
105 that sequences would reach if the pattern of substitution observed in that branch remained constant over  
106 time (Duret and Arndt, 2008).  $GC^*$  correlates well with the strength of DSB hotspots in mice (Clément  
107 and Arndt, 2013), with the LD-based recombination rates in humans (Munch et al., 2014; Glémin et al.,  
108 2015), and with the LD-based strength of recombination hotspots in dogs (Axelsson et al., 2012; Auton  
109 et al., 2013). Moreover,  $GC^*$  reflects the recombination activity along the entire branch where substitution  
110 patterns are analyzed, and hence can inform about past recombination events that are no longer detectable  
111 with methods measuring recombination in individuals or populations (Lesecque et al., 2014; Munch et al.,  
112 2014). This provides insights on the long term use of PRDM9-independent hotspots, integrated over long  
113 periods of time, probably encompassing the rise and fall of several PRDM9 alleles. However, variation in  
114  $GC^*$  between species cannot be directly interpreted as variations in recombination rates alone, since  $GC^*$   
115 also depends on the mutation bias towards AT, the repair bias towards GC, the effective population size and  
116 the mean length of the conversion tracts (Eyre-Walker, 1999; Glémin, 2010).

117 In this study, we present an estimator of relative recombination rates based on substitution patterns that  
118 allows us to directly compare fine-scale recombination rate variations in a wide range of species using only  
119 3 genomes (one focal genome, a sister species and an outgroup). We then use it to assess the recombination  
120 activity at MDH loci in 52 species spanning the diversity of boreoeutherians. We reveal a high heterogeneity  
121 in the use of these PRDM9-independent hotspots. We show that PRDM9 alleles in humans and mice  
122 have been particularly efficient at directing DSBs away from PRDM9-independent hotspots but that these  
123 two species are not representative of all mammals. Finally, we show that three species, namely the southern  
124 elephant seal, the ring-tailed lemur and the daurian ground squirrel, have used PRDM9-independent hotspots  
125 as much as PRDM9-deficient canids. This shows that the two kinds of hotspots-regulation mechanisms that  
126 have been described so far in vertebrates are not mutually exclusive and that the fine-scale recombination  
127 landscapes of many mammals are much closer to those of birds and other PRDM9-lacking amniotes than  
128 previously thought. We further show that the recombination activity observed at MDH loci in PRDM9-  
129 containing mammals depends on the conservation of their DNA methylation pattern, which suggests a link  
130 between the evolution of DNA methylation and of PRDM9-independent recombination landscapes.

131 **Results**132 **Conservation of recombination hotspots between PRDM9-deficient mammals**

133 In finches and flycatchers, the fine-scale recombination landscape has been shown to be stable through time,  
 134 as a large proportion of hotspots are shared between closely related species (Singhal et al., 2015; Kawakami  
 135 et al., 2017). To test whether loci corresponding to PRDM9-independent hotspots are also evolutionary stable  
 136 in mammals, we analyzed the overlap between recombination hotspots detected in dogs, which naturally lack  
 137 PRDM9, and those identified in the *Prdm9*<sup>-/-</sup> mutant mouse (MDH) (Smagulova et al., 2016). Among the  
 138 30,929 MDH, 15,009 (49%) could be assigned to one-to-one orthologous loci in the dog genome. Among the  
 139 7008 dog hotspots identified in the LD-based recombination map of dogs (Auton et al., 2013), 34% overlap  
 140 with MDH loci (Suppfig. S1)(compared to 0.06% expected by chance, given that dog hotspots and MDH  
 141 loci cover respectively 2% and 3% of the dog genome). Although this enrichment is very strong, it should be  
 142 noted that 42% of the dog hotspots that could be mapped on the mouse genome occur outside of MDH loci  
 143 (1809/3109) (Suppfig. S1). This number is difficult to interpret because it has been shown that LD-based  
 144 methods can produce a high number of false positives (Raynaud et al., 2023). Moreover, DSB hotspots are  
 145 obtained on males only, while LD maps are sex-averaged. It is also possible that some MDH loci have not  
 146 been identified as hotspots in dogs simply because they did not meet the threshold criteria to be defined as  
 147 such. To avoid the problem of the arbitrary threshold, we computed the LD-based recombination rate in dogs  
 148 (from Auton et al. (2013)) as a function of the distance to the closest MDH loci (Fig. 1A&B) (Auton et al.,  
 149 2013). We divided the 30,929 mouse *Prdm9*<sup>-/-</sup> hotspots into three equally sized categories of strength, based  
 150 on DMC1 ChIP-seq read counts (Smagulova et al., 2016). Respectively 5,266 strong MDH, 4,961 medium  
 151 MDH and 4,781 weak MDH could be mapped on the dog genome. There is a sharp peak of recombination  
 152 centered on MDH loci in dogs. This peak is higher for strong MDH and weaker for medium and weak ones  
 153 (Fig. 1A). This confirms that many recombination hotspots are conserved between *Prdm9*<sup>-/-</sup> mice and dogs,  
 154 but it does not rule out the existence of species-specific recombination hotspots. To explore factors that  
 155 might drive the evolution of PRDM9-independent hotspots, we analyzed their DNA methylation level in the  
 156 germline. Indeed, indirect evidences suggested that recombination hotspots in dogs are associated to germline  
 157 hypomethylated regions (HMRs) (Berghlund et al., 2015). Using HMRs identified by bi-sulfite sequencing in  
 158 dog sperm (Qu et al., 2018), we observed that 74% of dog hotspots are located inside HMRs, which represent  
 159 only 3.7% of the dog genome. In mice, the overlap is even stronger: using HMRs identified in mouse sperm  
 160 (Hammoud et al., 2014), we observed that out of the 30,929 hotspots found in the *Prdm9*<sup>-/-</sup> mutant, 93%  
 161 are located within HMRs, which cover only 4.6% of the mouse genome (see methods for details). This  
 162 indicates that PRDM9-independent hotspots are associated with DNA hypomethylation both in *Prdm9*<sup>-/-</sup>  
 163 mutant mice and in canids. Interestingly, 48% of MDH loci are methylated in dog sperm if we restrict the  
 164 definition of hotspots to their midpoint (7,186/15,009). This shows that many MDH loci are specifically  
 165 hypomethylated in mice but not in dogs. This is consistent with previous observations showing that murid  
 166 genomes have accumulated many new HMRs compared to other mammals (Qu et al., 2018). To test whether  
 167 these shifts in methylation levels are associated with changes in recombination activity, we computed the  
 168 LD-based recombination rate in dogs as a function of the distance to the closest MDH locus, separating

169 those whose midpoints overlap a HMR in dogs (7,186), and those that do not (7,283)(Fig. 1B). There is a  
 170 high and pronounced recombination peak at MDH loci that are hypomethylated in dog sperm (Fig. 1B). In  
 171 contrast there is almost no elevation of recombination at MDH loci that are methylated in dogs (Fig. 1B).  
 172 This confirms that methylation is clearly associated to recombination hotspots in the absence of PRDM9,  
 173 and that many PRDM9-independent recombination hotspots are species-specific.

#### 174 **Equilibrium GC content is a good predictor of past recombination activity**

175 To assess whether equilibrium GC content could be used as a proxy of recombination rate in other species,  
 176 we repeated the above analyses using  $GC^*$  instead of LD-based recombination rate (Fig. 1C&D). Strikingly,  
 177 the profile of  $GC^*$  perfectly mirrors the LD-based recombination rate profile. It should however be noticed  
 178 that the  $GC^*$  peaks are slightly sharper than the LD-based ones (Fig. 1C&D), as are the peaks of DMC1  
 179 ChIP-seq read coverage in the *Prdm9*<sup>-/-</sup> mouse (Suppfig. S2). This suggests that  $GC^*$  is able to capture  
 180 signals of past recombination with a higher spatial resolution than LD.

#### 181 **Estimation of the relative recombination rate in PRDM9-independent hotspots**

182 Following a large body of literature, we showed that  $GC^*$  can be very informative on intra-genomic recom-  
 183 bination rate variations (Pessia et al., 2012; Auton et al., 2013; Clément and Arndt, 2013; Lartillot, 2013;  
 184 Munch et al., 2014; Glémin et al., 2015; Singhal et al., 2015; Figuet et al., 2015; Bolívar et al., 2016; Galtier  
 185 et al., 2018; Charlesworth et al., 2020). However, the height of the  $GC^*$  peak in hotspots is difficult to  
 186 interpret in term of recombination rate because it is also affected by other parameters (the length of gene  
 187 conversion tracts, the mutation bias towards AT, the mismatch repair bias towards GC and the effective  
 188 population size), which can vary between species (Lartillot, 2013; Galtier et al., 2018; Galtier, 2021). We  
 189 thus derived an estimator that can capture the relative recombination rate at PRDM9-independent hotspots  
 190 that controls for those parameters and is therefore comparable between species. Using the probability of  
 191 fixation of AT and GC alleles in presence of gBGC derived by Nagylaki (1983), we obtained an expression  
 192 of the ratio of the recombination rate within hotspots relative to their flanking regions (see details in the  
 193 Methods). This relative recombination rate only depends on  $GC^*$  inside hotspots and in flanking regions,  
 194 and on the mutation bias ( $GC^\mu$ ).

$$\frac{r_{hot}}{r_{flank}} = \frac{\text{logit}(GC_{hot}^*) - \text{logit}(GC^\mu)}{\text{logit}(GC_{flank}^*) - \text{logit}(GC^\mu)} \quad (1)$$

195 where  $r_{hot}$  is the recombination rate in hotspots,  $r_{flank}$  the recombination rate in flanking regions and  
 196  $GC^\mu$  the GC content expected under mutation only. It should be noted that  $r_{hot}$  and  $r_{flank}$  encompass all  
 197 recombination events that can lead to gBGC (potentially COs and/or NCOs).

198 For the rest of the study, hotspots are defined as the 400 bp regions centered on their midpoint, and  
 199 flanking regions as those spanning from 5 to 8 kb upstream and downstream of the hotspots (Fig. 2B).

200 Using the three values  $GC_{hot}^*$ ,  $GC_{flank}^*$  and  $GC^\mu$ , it is possible to compute a measure of the relative  
 201 recombination rate within hotspots compared to their flanking regions, which can then be compared between



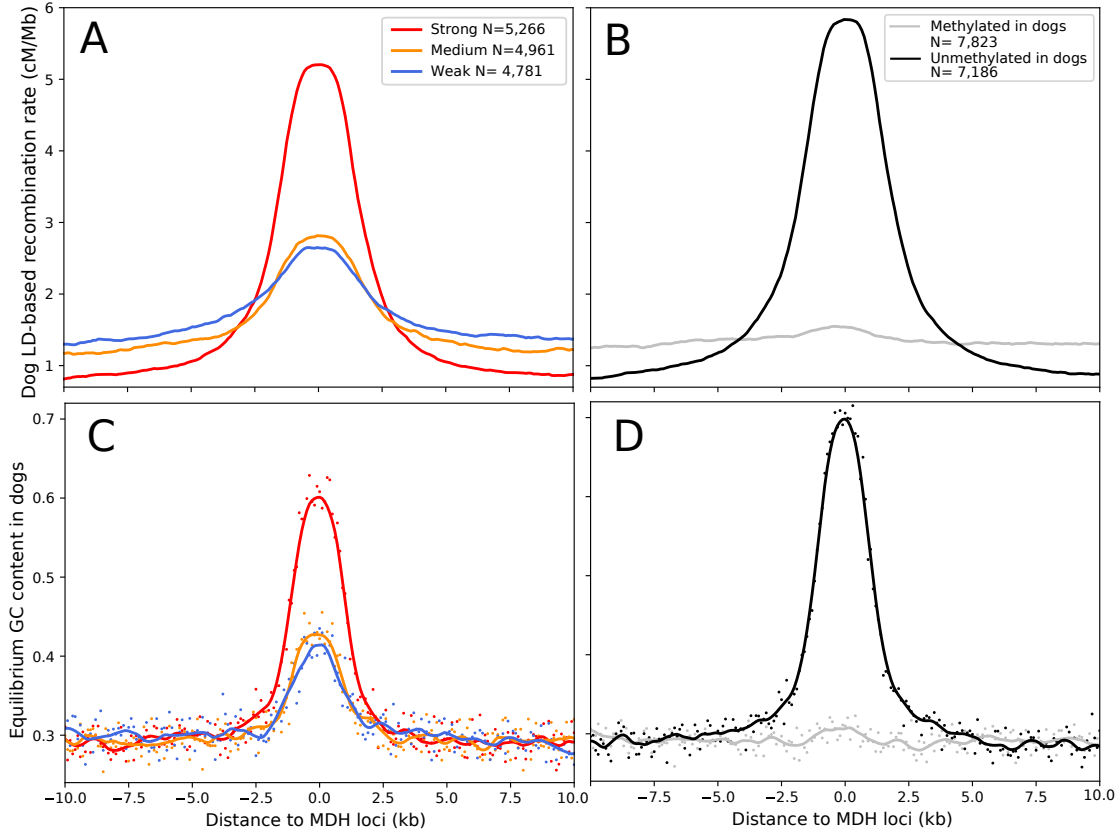


Figure 1: A) Dog LD-based recombination rate as a function of the distance to the closest MDH locus. MDH were divided in three equally sized categories of strength: strong hotspots in red (10-190 FPKM), medium hotspots in orange (5-10 FPKM) and weak hotspots in blue (0-5 FPKM). The line corresponds to the mean value of LD-based recombination rate in a 100 bp window. B) Same as A but MDH loci were divided in two categories depending on their methylation level in dog sperm. MDH loci that are found outside hypomethylated regions in dogs are in grey and those found inside hypomethylated regions are in black. C) & D) Equilibrium GC content in dogs as a function of the distance to the closest MDH locus. Using the same partitions of hotspots as A) and B). Points correspond to the mean value of  $GC^*$  in a 100 bp window. The line corresponds to a smoothing of the data with a loess function.

202 species. Equation 1 holds true under the assumption that the other four parameters affecting the strength  
 203 of gBGC (effective population size, mismatch repair bias, length of the conversion tract and the mutation  
 204 bias) do not differ between the hotspots and their flanking regions (see Methods). As shown in the previous  
 205 section, PRDM9-independent hotspots are often hypomethylated. This implies that the mutation rate from  
 206 CpG to TpG or CpA in hotspots is lower than in the flanking regions, which violates our assumption of a  
 207 constant mutation bias. To avoid this problem, we excluded CpG sites from all the analyses.

208  $GC^*_{hot}$  and  $GC^*_{flank}$  can easily be computed from the substitutions in PRDM9-independent hotspots and  
 209 their flanking region but  $GC^\mu$  is more difficult to estimate. Interestingly, it has been shown that genome-  
 210 wide variations of  $GC^*$  are mainly the result of gBGC, and that  $GC^\mu$  is quite constant along chromosomes,



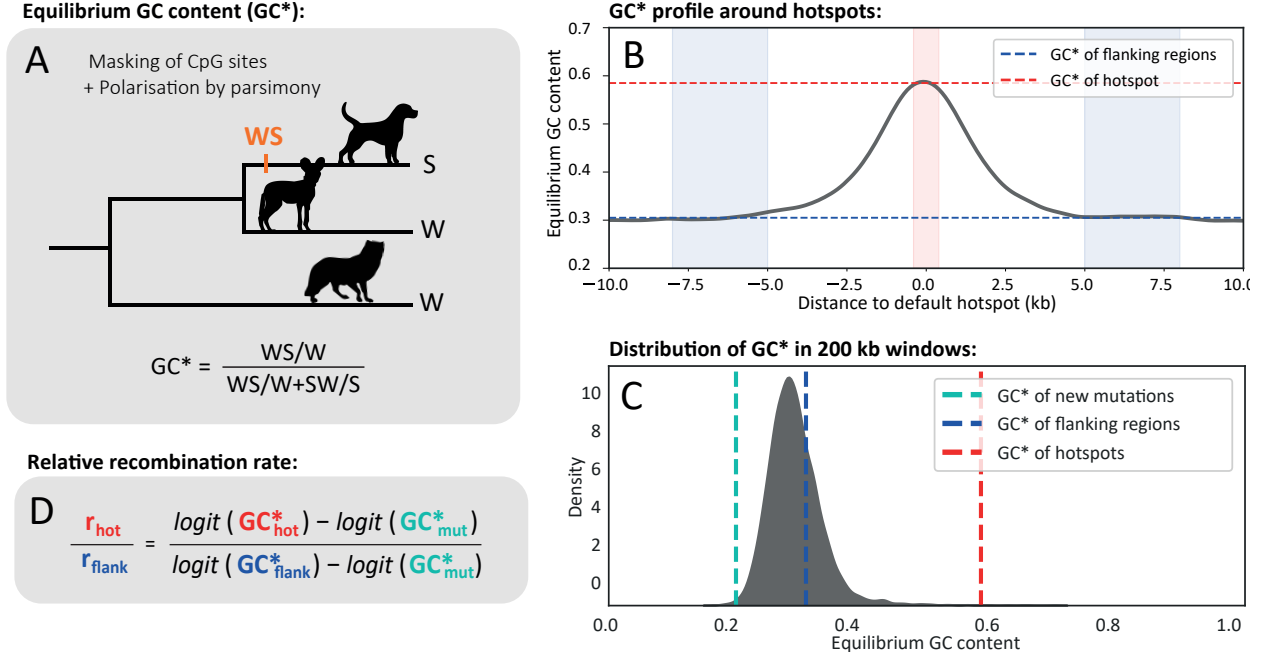


Figure 2: Overview of the method for inferring relative recombination rates in PRDM9-independent hotspots. A) We call substitutions using parsimony on trios of closely related species after having masked CpG dinucleotides. B) We compute  $GC^*$  in 400 bp windows centered on the midpoint of the PRDM9-independent hotspots, and  $GC^*$  in the flanking regions (from 5 to 8 kb upstream and downstream of the center of the PRDM9-independent hotspot). C) We compute the genome-wide distribution of  $GC^*$  in 200 kb windows and take the 1<sup>st</sup> percentile as the  $GC^*$  of new mutations. D) Using the probability of fixation of AT and GC alleles in presence of gBGC derived by Nagylaki (1983), we compute the relative recombination rate as a function of the three values of  $GC^*$  (see methods).

211 despite large-scale variation in mutation rates (Smith et al., 2018). An approach to estimate  $GC^\mu$  consists  
 212 in measuring variation in substitution patterns along the genome, and to consider the regions of the genome  
 213 with the lowest  $GC^*$  as a proxy for  $GC^\mu$  (Lartillot, 2013). Following this logic, we divided the genome of  
 214 each species in windows of 200kb, and defined  $GC^\mu$  as the value of the first percentile of the distribution of  
 215  $GC^*$  to avoid outliers (Fig. 2B) (see methods for detailed justifications). This method allows us to estimate  
 216  $GC^\mu$  for a wide range of species, simply based on substitution patterns in the terminal branch.

## 217 PRDM9-independent recombination hotspots are active in most mammals

218 Using this estimator of relative recombination rate, we assessed whether MDH loci showed an enrichment of  
 219 recombination in other mammals. We identified MDH orthologous loci in the genome of 51 other mammals  
 220 and estimated the relative recombination rates at these loci using the method described above (gBGC-  
 221 based relative recombination rates). Around 75% of the species (39/52) show a significant enrichment of  
 222 recombination in MDH loci compared to flanking regions (Fig. 3).

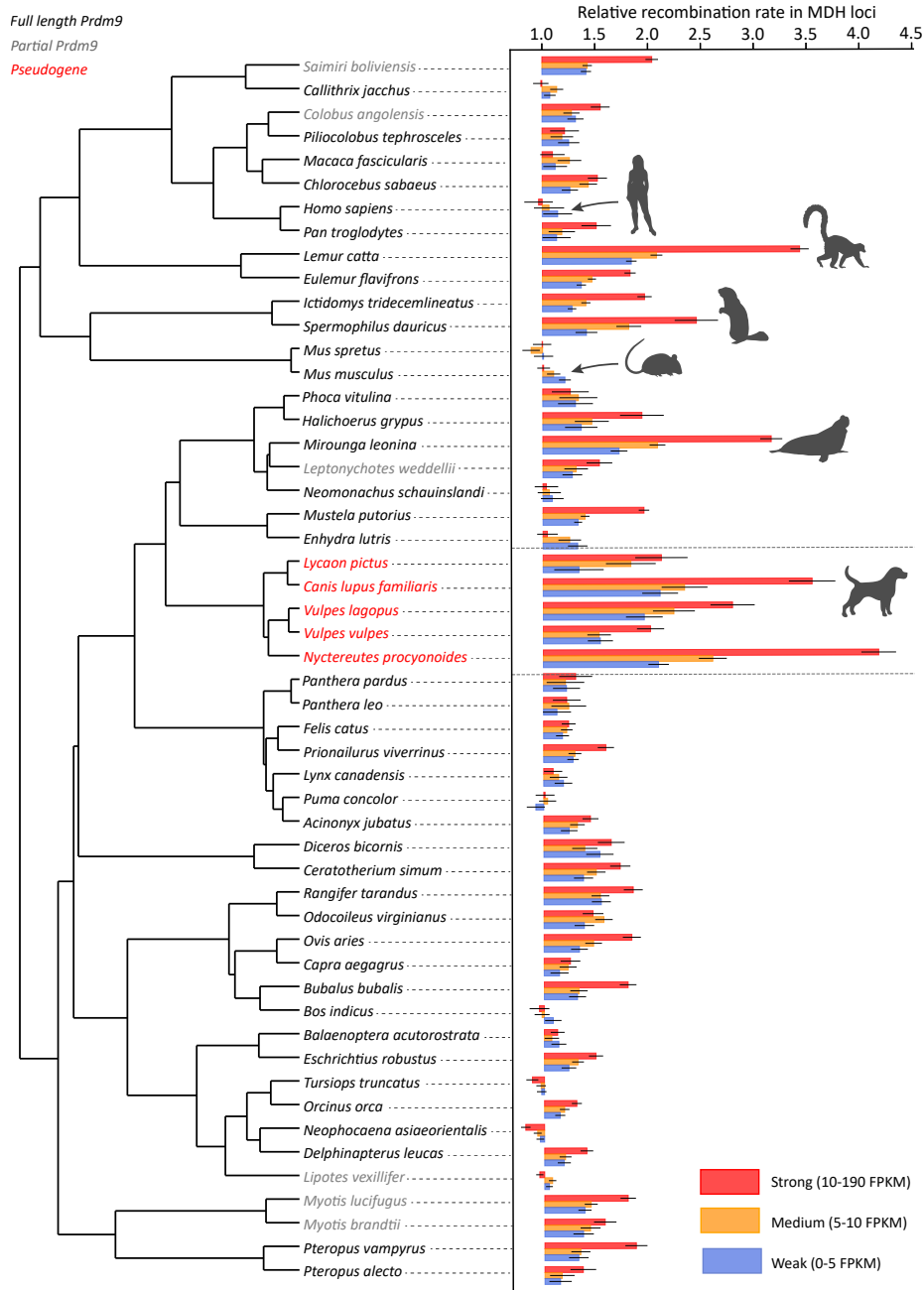


Figure 3: Relative recombination rates at loci orthologous to mouse  $Prdm9^{-/-}$  DSB hotspots (MDH loci) in 52 mammals. MDH loci were binned in 3 equally sized categories of strength based on the number of DMC1 Chip-seq reads of  $Prdm9^{-/-}$  DSB hotspots. The number of MDH loci for each category varied from  $\sim 4,000$  in *Myotis brandtii* to  $\sim 9,000$  in *Mus spretus* (see details in Supplementary Table 1). The tree has been retrieved from TimeTree5 (Kumar et al., 2022). Species with a complete PRDM9 are written in black, in grey species for which we failed to find a complete PRDM9 in the reference genome assembly, and in red the 5 canids (where PRDM9 is a pseudogene). Error bars correspond to a 95% confidence interval obtained by bootstrapping the substitutions for computing  $GC^*_{flank}$  and  $GC^*_{hot}$ . We considered the recombination enrichment to be significant if the confidence interval is above one.

223 In 77% of those species (30/39), the recombination activity at MDH loci is conserved, with strong MDH  
224 loci showing a significantly higher recombination enrichment than weak ones (Fig. 3). The remaining 23% of  
225 species (9/39) show a lower recombination activity in PRDM9-independent hotspots. Therefore, we might be  
226 lacking statistical power to confirm a conservation of hotspot strength in those species (Fig. 3). Interestingly,  
227 in 10% of species (5/52), including mice, there is less recombination in strong PRDM9-independent hotspots  
228 compared to weak ones, which is consistent with the active deviation of recombination away from those sites  
229 observed in those mice having the most dominant PRDM9 alleles (Smagulova et al., 2016). The causes for  
230 this active deviation are however still not clear (Smagulova et al., 2016).

231 To test whether as in dogs, methylation plays a role in determining hotspots in other mammals, we  
232 separated MDH loci in two subsets: loci for which the hypomethylation pattern is conserved between mice  
233 and dogs (and thus likely to be consistently hypomethylated in other mammals as shown in Qu et al. (2018)),  
234 and loci that are hypomethylated in mouse but not dogs (a majority of which corresponding to mouse-specific  
235 HMRs (Qu et al., 2018)). For MDH loci whose hypomethylation pattern is not conserved, we observed a  
236 very weak increase in recombination in all species (Suppfig. S4).

237 Conversely, MDH loci with a conserved hypomethylation pattern, show contrasting levels of recombina-  
238 tion activity: 25% of species (13/52, including mice and humans) show a deficit of recombination at these  
239 loci, 12% (6/52) show no elevation of recombination, whereas 63% (33/52) show a strong recombination  
240 activity. This indicates that DNA hypomethylation is associated with a deficit of recombination in some  
241 species (such as mice and humans), while it is associated with recombination hotspot in others. This latter  
242 group includes the 5 canids (which all lack Prdm9), but also many other mammals with an intact Prdm9.  
243 This shows that DNA hypomethylation can be associated with recombination hotspots even in the presence  
244 of Prdm9.

245 To get further insight into the evolution of PRDM9-independent hotspots in mammals, we measured the  
246 relative activity at loci orthologous to dog LD-based recombination hotspots (DRH for 'Dog Recombination  
247 Hotspots') in the 51 other mammals. We observed a strong correlation between the recombination activity  
248 at MDH loci and DRH loci (Suppfig S5), which is expected since they largely overlap. Nevertheless, species  
249 that are phylogenetically closer to dogs show higher recombination activity in DRH loci whereas those  
250 phylogenetically closer to mouse show higher recombination activity in MDH loci (Suppfig S5). This confirms  
251 that despite a general conservation, PRDM9-independent hotspots are still evolving in mammals.

252 Canids, which all lack PRDM9, dominate the list of species that exhibit the highest recombination levels  
253 at MDH loci, holding top ranks out of 52 (Fig. 4A). This finding both shows that the recombination landscape  
254 is stable in canids as it is in passerines, and validates our relative recombination rate estimator (Fig. 4A).  
255 Interestingly, there are several other mammals that show a similar enrichment of recombination activity at  
256 MDH loci. Notably, three species show a recombination activity at MDH loci significantly higher than some  
257 of the canids: ring-tailed lemurs (*Lemur catta*), southern elephant seals (*Mirounga leonina*) and daurian  
258 ground squirrels (*Spermophilus dauricus*) (Fig. 4A).

259 It should be noted that these three species encode a full-length PRDM9, encompassing the four protein  
260 domains (KRAB, SSXRD, SET and the zinc finger array). The PRDM9 allele represented in the reference

261 genome assembly contains 11 zinc fingers in daurian ground squirrels, and 14 zinc fingers in ring-tailed  
 262 lemurs. For the southern elephant seal, there is only one complete zinc finger represented in the reference  
 263 genome because of an assembly gap within the array. In ring-tailed lemurs and daurian ground squirrels,  
 264 the comparison of zinc finger sequences showed an excess of amino-acid changes relative to the neutral  
 265 expectation, particularly at positions -1, 3, and 6 that are involved in DNA binding, (SuppFig. S6).

266 This suggests that PRDM9 has been subject to positive selection in these two lineages, which is suggestive  
 267 of the red-queen dynamic that is expected when PRDM9 determines the location of recombination hotspots.  
 268 Thus, PRDM9 does not show any sign of pseudogenization or functional change in these three species where  
 269 PRDM9-independent hotspots appear to have been particularly active.

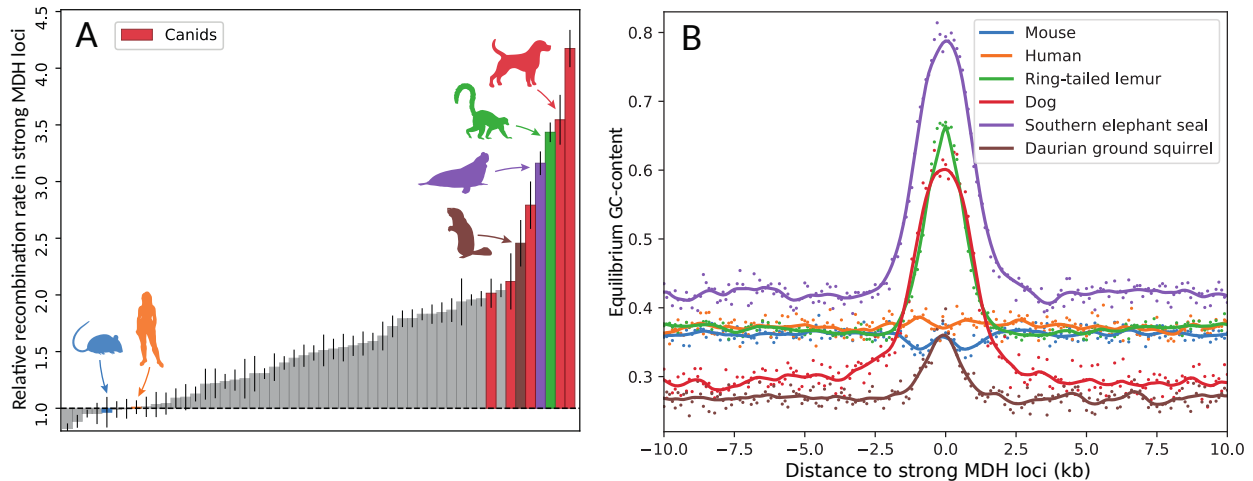


Figure 4: (A): Sorted relative recombination rate in strong DSB hotspots ( $>10$  FPKM) of a PRDM9  $-/-$  mouse in 52 mammals. Error bars correspond to a 95% confidence interval obtained by bootstrapping the substitutions for computing  $GC_{flank}^*$  and  $GC_{hot}^*$ . (B):  $GC^*$  as a function of the distance to the center of the closest MDH locus for humans, mice, dogs, and the three outlier species. Each point corresponds to an estimation of  $GC^*$  in a 100 bp window.

270 As an illustration of our substitution-based approach, we plotted  $GC^*$  as a function of the distance to  
 271 the closest strong MDH loci in dogs, humans, mice and the three outlier species (Fig. 4B). We observed no  
 272 elevation of  $GC^*$  in humans and mice in strong MDH loci, confirming that very little recombination occurred  
 273 in their lineage (Fig. 4B). In dogs, ring-tailed lemurs, southern elephant seals and daurian ground squirrels,  
 274 there is a pronounced peak of  $GC^*$  at strong MDH loci (Fig. 4B).

## 275 Discussion

276 The current paradigm is that vertebrates either possess a full-length functional PRDM9, recombine away  
 277 from promoter-like features, and display a fast evolving recombination landscape, or they lack a functional  
 278 PRDM9 in which case they consistently recombine in CpG islands (e.g. in canids, birds or the swordtail fish)  
 279 (Baker et al., 2017). Our results revealed that there is a continuum between these two types of recombination

280 landscapes and that despite the presence of PRDM9, some species use PRDM9-independent hotspots as much  
281 as canids. We showed that the activity of those PRDM9-independent hotspots is highly dependent on DNA  
282 hypomethylation. This implies that despite a general conservation, PRDM9-independent recombination  
283 hotspots are evolving slowly, in concert with germline DNA hypomethylation (Qu et al., 2018; Berglund  
284 et al., 2015).

285 From a methodological perspective, while signatures of gBGC have been commonly used in studies of  
286 recombination landscapes (Axelsson et al., 2012; Auton et al., 2013; Munch et al., 2014; Lesecque et al.,  
287 2014; Singhal et al., 2015; Charlesworth et al., 2020; Hoge et al., 2023), the approach presented here allows  
288 to quantify gBGC-based relative recombination rates along a branch that are comparable between species.  
289 The analysis of gBGC signatures only requires the genome of three closely related species, and is able to  
290 detect recombination activity at a given set of loci with a very high spatial resolution, even better than LD-  
291 based methods (compare Fig. 2D and 2B). It thus offers the possibility for large-scale comparative studies  
292 of fine-scale recombination landscapes. However, this approach requires a large number of substitutions to  
293 estimate  $GC^*$  precisely and is therefore not appropriate to measure recombination at a single locus.

294 Moreover, it should be noted that our estimation of recombination activity using gBGC does not allow one  
295 to conclude on the nature of recombination events (COs or NCOs) that we detect at PRDM9-independent  
296 hotspots. In humans, there is evidence that both COs and NCOs induce gBGC but in mice, only NCOs  
297 appear to do so (Williams et al., 2015; Arbeithuber et al., 2015; Halldorsson et al., 2016; Li et al., 2019).  
298 This suggests that the type of recombination events triggering gBGC can vary among mammals. Thus, it  
299 is possible that while a large number of DSB occur at PRDM9-independent hotspots in our three outlier  
300 species, COs still tend to be associated to PRDM9-directed hotspots. Altogether, while the enrichment of  
301 recombination events in PRDM9-independent hotspots is very clear in numerous mammals, the way they  
302 are repaired remains to be explored.

### 303 **On the maintenance of a default hotspot regulation mechanism**

304 It had been previously demonstrated that both PRDM9-dependent and PRDM9-independent pathways  
305 coexist in two snakes genera (Hoge et al., 2023). The authors suggested that a change in the binding affinity  
306 of a gene which operates downstream of PRDM9 could explain this coexistence and that selection might be  
307 operating on these genes to fine-tune the usage of PRDM9-independent hotspots in vertebrates (Hoge et al.,  
308 2023).

309 In placental mammals we revealed that the coexistence of both PRDM9-dependent and PRDM9-  
310 independent pathways to direct DSBs is pervasive. We showed that those pathways determine recombination  
311 hotspots with varying proportions across species. Interestingly, these variations do not show a strong phylo-  
312 genetic structure, suggesting that this evolution can be very rapid. Furthermore, the species with the highest  
313 levels of PRDM9-independent hotspot usage have quite contrasted life history traits, which they mostly share  
314 with sister species with lower PRDM9-independent hotspot usage. Thus, it is difficult to imagine that dif-  
315 ferences of PRDM9-independent usage depend on reproductive life history traits. Moreover, in mice, even if  
316 the usage of PRDM9-independent hotspots is quite low overall, there exist substantial variations that seem

317 to depend only on PRDM9 alleles (Smagulova et al., 2016). A plausible explanation for the maintenance of  
318 the PRDM9-independent pathway in placental mammals would be that variation in PRDM9-independent  
319 hotspots usage depends on the efficacy of PRDM9 alleles to recruit the DSB machinery.

320 Overall, proper chromosome pairing can be achieved through the two different pathways mentioned  
321 above (PRDM9-dependent or PRDM9-independent). When the efficiency of one pathway is altered, better  
322 chromosome pairing can be restored either by a mutation restoring the efficiency of the altered pathway,  
323 or by a mutation increasing the efficiency of the other pathway. For the PRDM9 pathway, we know that  
324 alleles inevitably decrease in efficiency due to the erosion of their high affinity targets, which reduces the  
325 probability of symmetrical binding, and thus impairs efficient chromosome pairing (Baker et al., 2015, 2022;  
326 Latrille et al., 2017; Genestier et al., 2023). This efficiency can be restored either by a new PRDM9 allele  
327 inducing a red-queen dynamic (Úbeda and Wilkins, 2011; Latrille et al., 2017; Baker et al., 2022; Genestier  
328 et al., 2023), but also by a mutation increasing the efficiency of the PRDM9-independent pathway. Every  
329 mutation increasing the efficiency of the PRDM9-independent pathway lessens the deleterious effect of a  
330 mutation that reduces PRDM9 efficiency. Conversely, new efficient PRDM9 alleles will lessen the deleterious  
331 effect of a mutation that decreases the efficiency of the PRDM9-independent pathway.

332 Of note, if this dynamic reaches a point where the PRDM9-independent pathway becomes sufficient for  
333 correct chromosome pairing, PRDM9 can be lost without strong fitness consequences. Under this model,  
334 PRDM9 is lost through the accumulation of small effect mutations which reduce its utility, rather than a  
335 sudden loss that would imply very inefficient selection. The continuum in the use of PRDM9-independent  
336 hotspots we observe in mammals could reflect different stages along this path, and despite still having a  
337 fully functional PRDM9, the three outlier species could be on their way of losing it. It is also possible that  
338 their PRDM9 have only been going through a temporary inefficient phase compensated by the PRDM9-  
339 independent pathway, but has now been rescued by a new efficient PRDM9 allele.

#### 340 **The recombination landscape of amniotes**

341 Overall, our results suggest that in addition to PRDM9-directed hotspots, many mammals share some  
342 of their recombination hotspots with other amniotes, (Axelsson et al., 2012; Singhal et al., 2015; Schield  
343 et al., 2020; Hoge et al., 2023), and therefore the fine-scale recombination landscapes of mammals, birds and  
344 snakes is probably more similar than previously thought (Baker et al., 2017). However, the determinants of  
345 PRDM9-independent hotspots usage remain unclear. Interestingly DNA methylation has also been found  
346 to be a suppressor of recombination in a fungi hotspot (Maloisel and Rossignol, 1998), in plants (He et al.,  
347 2017; Choi et al., 2018), and in honey bees (Wallberg et al., 2015), which suggests that local hypomethyla-  
348 tion is a common determinant of recombination hotspots in eukaryotes. However, the association between  
349 hypomethylation and recombination has not been formally established in non-mammalian amniotes and  
350 remains to be tested. Moreover, this association need not be causal, as the potentially diverse molecular  
351 mechanisms of PRDM9-independent recombination in amniotes remain largely unknown. In particular, the  
352 results presented here suggest that despite having lost PRDM9, red foxes (*Vulpes vulpes*) and african wild  
353 dogs (*Lycaon pictus*) have only a mild recombination enrichment in PRDM9-independent hotspots compared  
354 to other canids. It has been previously noted that the number of recombination hotspots varies between

355 PRDM9-deficient amniotes. Notably in finches and flycatchers, only few LD-based hotspots have been re-  
356 ported compared to dogs (Auton et al., 2013; Singhal et al., 2015; Kawakami et al., 2017). Altogether, it is  
357 still not clear what drives the concentration of recombination events in absence of PRDM9, and why some  
358 species have numerous hotspots and others less.

359 Finally, the widespread use of PRDM9-independent recombination hotspots demonstrated in the present  
360 study is likely to have important consequences for genome evolution. In particular, the fact that gBGC is  
361 stronger in hypomethylated regions in numerous mammals and in several passerines provides a convincing  
362 explanation for the widespread GC-richness of CpG islands in amniotes.

## 363 Material & Methods

### 364 PRDM9-independent hotspots and DNA methylation datasets

365 Data on the location of DSB hotspots in *Prdm9*<sup>-/-</sup> knock-out mice, detected by DMC1 ChIP-seq experiment,  
366 were retrieved from the study by Smagulova et al. (2016). The dog LD-based recombination map and the  
367 position of hotspots were retrieved from the study of Auton et al. (2013). We excluded hotspots that were  
368 larger than 20 kb as they do not fit the definition of hotspots. Data sets of hypomethylated regions in mouse  
369 and dog sperm (identified using Bi-sulfite sequencing) were retrieved from the literature (Hammoud et al.,  
370 2014; Qu et al., 2018). Even though methylation data on spermatocytes would have been more fit for the  
371 task at hand, only sperm is available in the literature for dogs.

### 372 Whole genome alignments

373 For most mammals except canids, felids and phocids, whole genome alignments (WGAs) were obtained from  
374 Genereux et al. (2020). In order to get further phylogenetic resolution in canids, and in closely related  
375 outgroups, we generated a WGA of high quality genomes for 19 carnivores downloaded from NCBI (Supple-  
376 mentary Table 1), using the Progressive Cactus aligner (v1.3.0) (Armstrong et al., 2020). We first defined a  
377 "guide" species tree using the topology obtained from TimeTree5 (Kumar et al., 2022). To streamline the  
378 computational process, we ran Progressive Cactus separately for canids, felids and phocids species, using  
379 different "-root" options on the same guide tree. We created a root alignment by running Progressive Cactus  
380 with the inferred ancestral genome of each of the three clades. We obtained the final WGA using the "ha-  
381 lAppendSubtree" command to iteratively include the three sub-alignments at the corresponding ancestral  
382 nodes (Hickey et al., 2013).

### 383 Defining orthologous regions

384 To find the orthologous regions of the PRDM9-independent hotspots in the genomes of other mammals we  
385 used `halLiftOver` (Hickey et al., 2013). We first made a liftover from the mouse/dog genome to the target  
386 genome using the midpoint of each feature and removed multi-mapping features. Then we lifted back the  
387 single-mapping features from the target genome to the dog/mouse genome and again removed multi-mapping  
388 features. This approach ensures that all orthologous loci were one-to-one.



### 389 Hotspots overlap

390 We considered hotspots to be overlapping if their midpoint was at less than 5 kb one from another. This is  
 391 equivalent to a strict overlap for hotspots defined as 5 kb windows centered on their midpoint. Using this  
 392 approach, we calculated the percentage of the genome covered by the hotspots by multiplying the number  
 393 of hotspots by 5,000, and dividing by the assembly size. For the overlap with HMRs we defined hotspots as  
 394 the 5 kb windows centered on their midpoint and kept the size of HMRs defined in the study of Qu et al.  
 395 2018 (Qu et al., 2018). The percentage of the genome covered by HMRs was computed as the sum of all  
 396 HMR sizes divided by the assembly size.

### 397 Substitution mapping

398 We selected trios of closely related species such that the divergence between the three species was low enough  
 399 to avoid double substitutions, but with an outgroup distant enough to avoid incomplete lineage sorting based  
 400 on the guide tree used in the Zoonomia WGA (Genereux et al., 2020). We tried to take trios spanning the  
 401 diversity of boreoeutherians, avoiding over-sampling of disproportionately represented groups (primates and  
 402 artiodactyles). A complete list of the trios used are available in Supplementary table 3. *A posteriori*, it  
 403 appeared that there were substantial variations between the branch lengths used to map substitutions, but  
 404 we showed that the divergence was still low enough ( $< 2.5\%$ ) and did not influence our result (Suppfig.  
 405 S7). Genome quality was very variable. We thus controlled that genome quality (approximated by the  
 406 N50 statistics) did not influence our results (Suppfig. S8). To call substitutions, we retrieved multispecies  
 407 alignment using hal2maf (Hickey et al., 2013). We excluded alignment blocks which size was inferior to 50  
 408 bp to avoid poorly aligned regions, and duplicated regions. We then excluded CpG sites (sites for which at  
 409 least one of the three species has a CpG) to avoid convergent mutations. Finally, we called substitutions  
 410 using parsimony as depicted in Fig. 2.

### 411 Measures of equilibrium GC content

412 We compute the equilibrium GC content as follows:

$$GC^* = \frac{WS/W}{WS/W + SW/S} \quad (2)$$

413 With  $W$  the AT content of the region (CpG masked),  $S$  the GC content of the region (CpG masked),  
 414  $WS$  the number of Weak to Strong substitutions and  $SW$  the number of Strong to Weak substitutions.

### 415 LD-based recombination rate and $GC^*$ profiles around hotspots

416 We cut the genome in windows of 100 bp. We extracted the LD-based recombination rate for each window.  
 417 We also computed the distance between the midpoint of the window and the closest midpoint of a hotspot  
 418 using bedtools closest (Quinlan and Hall, 2010). We then made bins of distances to the closest hotspot  
 419 every 100 bp. For  $GC^*$ , we repeated the same procedure, but we computed the counts of WS and SW

420 substitution for each window, and then computed  $GC^*$  using the total substitutions count for all windows  
 421 in each distance bin as described in the previous section.

#### 422 Estimation of the mutation bias

423 Germline mutations rates have been measured by sequencing parent–offspring trios in 36 mammalian species  
 424 (Bergeron et al., 2023). However, for most species, the number of detected mutations is too limited (typically  
 425 less than 100 de novo mutations) to estimate  $GC^\mu$  accurately. Thus, measures of  $GC^\mu$  based on empirical  
 426 data are associated with very large confidence intervals (Wong et al., 2016; Milholland et al., 2017; Wang  
 427 et al., 2020). Even when there is enough statistical power, the results vary substantially between different  
 428 datasets (Wong et al., 2016; Milholland et al., 2017). In addition to the issue of reproducibility, it has been  
 429 demonstrated that the mutation spectra can vary rapidly within human populations (Harris and Pritchard,  
 430 2017). Therefore,  $GC^\mu$  estimated from living individuals may not necessarily reflect the average  $GC^\mu$  in  
 431 the terminal branch. We therefore took a similar approach to Lartillot (2013). We divided the genomes in  
 432 windows of 200 kb and took the value of the first percentile of  $GC^*$  as an estimate of  $GC^\mu$ . To ensure that  
 433 our results were not sensitive to our estimation of  $GC^\mu$ , we used different thresholds to compute it (Suppfig.  
 434 S3B&C), and recovered the same results. We also controlled that our gBGC-based relative recombination  
 435 rates were not correlated to our estimations of  $GC^\mu$  (Suppfig. S3A).

#### 436 Estimation of relative recombination rates from $GC^*$

437 Using a Wright-Fischer diffusion approximation and assuming that mutations are selectively neutral, the  
 438 rate of Weak-to-Strong substitution in a given branch can be written as follows (Nagylaki, 1983)

$$q_{WS} = 2Ne\mu_{WS} \frac{2b}{1 - e^{-4Neb}} T \quad (3)$$

439 where  $\mu_{SW}$  is the mutation rate per generation from W to S,  $b$  the gBGC coefficient,  $T$  the divergence  
 440 time from the ancestral node in generations, and  $Ne$  the effective population size.

441 The gBGC coefficient is directly linked to the recombination rate, with  $b = b_0 r l$  where  $r$  is the recombi-  
 442 nation rate per base pair per meiosis,  $b_0$  the repair bias, and  $l$  the length of the conversion tract in base pair.  
 443 It should be noted that  $r$  encompasses all recombination events that can lead to gBGC (CO and/or NCO)

444 Similarly, the rate of Strong-to-Weak substitutions can be written as follows:

$$q_{SW} = 2Ne\mu_{SW} \frac{2b}{e^{4Neb} - 1} T \quad (4)$$

445 The equilibrium GC content can be written as follows:

$$GC^* = \frac{q_{WS}}{q_{WS} + q_{SW}} \quad (5)$$

446 Thus, we can write:

$$\frac{GC^*}{1 - GC^*} = \frac{q_{WS}}{q_{SW}} \quad (6)$$

447 Simplifying the previous equations we obtain:

$$\frac{GC^*}{1 - GC^*} = \frac{\mu_{WS}}{\mu_{SW}} e^{4Neb} \quad (7)$$

448 Thus, the population-scaled gBGC coefficient. ( $B = 4Neb$ ) can be written as:

$$B = \log\left(\frac{GC^*}{1 - GC^*}\right) - \log\left(\frac{\mu_{WS}}{\mu_{SW}}\right) \quad (8)$$

449 or:

$$B = \text{logit}(GC^*) - \text{logit}(GC^\mu) \quad (9)$$

450 where  $GC^\mu$  is the equilibrium GC content under the mutational bias only ( $GC^\mu = \frac{\mu_{WS}}{\mu_{SW} + \mu_{WS}}$ ).

451 Let us note  $B_{hot}$  the population-scaled gBGC coefficient within hotspots:

$$B_{hot} = \text{logit}(GC_{hot}^*) - \text{logit}(GC_{hot}^\mu) \quad (10)$$

452 And  $B_{flank}$  the population-scaled gBGC coefficient in their flanking regions (defined here as 3kb-long  
453 segments, located at 5-kb of the hotspot center, Fig. 2A)

$$B_{flank} = \text{logit}(GC_{flank}^*) - \text{logit}(GC_{flank}^\mu) \quad (11)$$

454  $B$  depends on  $b_0$ ,  $N_e$ ,  $l$  and  $r$  ( $B = 4Nerb_0l$ ). The first three parameters ( $b_0$ ,  $N_e$ ,  $l$ ) are not expected to  
455 differ between the hotspot and their flanking regions. Thus, the ratio between the recombination rate within  
456 hotspot ( $r_{hot}$ ) over the recombination rate in their flanking regions ( $r_{flank}$ ) can be written as:

$$\frac{r_{hot}}{r_{flank}} = \frac{B_{hot}}{B_{flank}} \quad (12)$$

457 And thus, under the assumption that the mutational bias does not differ between hotspots and their  
458 flanking regions (i.e.  $GC_{hot}^\mu = GC_{flank}^\mu = GC^\mu$ )

$$\frac{r_{hot}}{r_{flank}} = \frac{\text{logit}(GC_{hot}^*) - \text{logit}(GC^\mu)}{\text{logit}(GC_{flank}^*) - \text{logit}(GC^\mu)} \quad (13)$$

#### 459 Annotation of PRDM9 in mammals

460 We investigated the presence of PRDM9 homologs in each of the 52 species analyzed. The full-length PRDM9  
461 isoform encompasses four domains (KRAB, SSXRD, SET and the zinc finger array). It is encoded by 10  
462 exons (corresponding to exons 2 to 11 of human PRDM9, exon 1 being within the 5'UTR): exons 3 and 4  
463 encode the KRAB domain, exon 7 encodes the SSXRD domain, exons 8-10 encode the SET domain, and exon

464 11 encodes the zinc finger array. We first searched for PRDM9 homologs by sequence similarity (Camacho  
 465 et al., 2009) against mammalian proteins annotated in RefSeq (<https://www.ncbi.nlm.nih.gov/blast/>), using  
 466 the human protein (NP\_001363829.1) as a query. We performed a multiple alignment of the strongest hits,  
 467 to assess their completeness: homologs were considered as complete if they encompassed the 10 protein-  
 468 coding exons, from the start codon, up to the beginning of the zinc finger array. By this approach, we  
 469 identified complete PRDM9 homologs in 16 species (Supplementary Table 2). For the 36 other species, we  
 470 further analyzed the corresponding reference genome to identify potential PRDM9 homologs. We performed  
 471 a TBLASTN search against reference genomes, using the 16 previously identified PRDM9 as queries, and  
 472 extracted loci presenting hits with the zinc finger domain and with at least 2 other PRDM9 exons, within  
 473 less than 100 kb. Then, for each candidate genomic fragment, we used GeneWise (Birney et al., 2004) to  
 474 annotate protein-coding regions by similarity with a representative complete PRDM9 protein taken from a  
 475 closely related species. Of note, GeneWise does take frameshifts into account, and is therefore appropriate to  
 476 annotate both genes and pseudogenes. In most species we identified one single candidate locus per genome.  
 477 When several loci were found, we retained the one(s) encoding the most complete protein. By this approach,  
 478 we identified PRDM9 loci in all 36 species, 25 of which encode a complete PRDM9 protein. Thus, in  
 479 total, we identified complete PRDM9 proteins in 41 of the 52 species analyzed. In agreement with previous  
 480 reports ((Axelsson et al., 2012; Auton et al., 2013)), we found PRDM9 to be pseudogenized in the 5 canids  
 481 (*Lycaon pictus*, *Canis lupus familiaris*, *Vulpes lagopus*, *Vulpes vulpes*, *Nyctereutes procyonoides*). In the 6  
 482 remaining cases, we failed to annotate a complete PRDM9 protein: either several exons were missing (*Myotis*  
 483 *lucifugus*, *Myotis brandtii*, *Leptonychotes weddellii*, *Colobus angolensis*), or the gene contained one exon with  
 484 a frameshifting mutation (respectively in exon 8 in *Saimiri boliviensis* and in exon 10 in *Lipotes vexillifer*).  
 485 In absence of data from more individuals, it is difficult to state whether these cases result from sequencing  
 486 errors or assembly artefacts or if they correspond to bona fide pseudogenes. We therefore tentatively annotate  
 487 these 6 cases as ‘partial’ Prdm9. The number of zinc fingers in the annotated proteins vary from 0 to 14.  
 488 This number should however be considered with caution because the zinc finger array is encoded by a highly  
 489 polymorphic minisatellite repeat, which is prone to errors during genome assembly. The detailed list of  
 490 PRDM9 sequences is given in Supplementary Table 2 and the corresponding protein multiple alignment can  
 491 be found at <https://zenodo.org/records/10149667>.

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 499 **interests:** The authors declare no conflicts of interest.

500 **Data availability**

501 Analysis scripts and documentation for whole genome alignments are available at  
 502 <https://github.com/AlexandreLaverre/CANCGI-WGA/> The hal file of the Carnivore WGA, along  
 503 with analysis scripts and documentation for PRDM9 annotation and the study of positive selection can  
 504 be found at <https://zenodo.org/records/10149667>. The remaining analysis scripts and documentation are  
 505 accessible at <https://gitlab.in2p3.fr/julien.joseph/defhot>.

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