***Relation between nonparental and asymmetric sites.***

Biologically, the nonparental sites are defined as recombination hotspot sites in F1 hybrid genome, which are reactivated in meiotic prophase because of the mutual presence of two (evolutionary distant) genomes and heterozygous PRDM9, while these sites are not activated in the parental genomes. Thus the nonparental sites should be the sites with an extreme extent of asymmetry. Indeed, 66% of nonparental sites (aggregated H3K4me3 enrichment) in the (PWD x B6) dataset (Davies *et al.* 2016) have an “extreme asymmetry” defined hereafter as proportion of B6 reads within 0.00-0.01 or 0.99-1.00 ranges (Figures S1 and S3). Conversely, in the dataset of sites with this extreme asymmetry, a majority (56% by H3K4me3) of sites are nonparental. Measured by DMC1 heat, and thus also considering the time to repair, 73% of DMC1 reads in nonparental sites have the extreme asymmetry, while 58% of DMC1 reads in extremely asymmetric sites are nonparental. Note that, while the extreme proportion of 0.00-0.01 or 0.99-1.00 represents only 2% of the possible asymmetry spectrum, the proportion of hotspot sites with extreme asymmetry is substantial (29% of H3K4me3 reads). In addition, the proportion of DMC1 reads in extremely asymmetric sites is 42%, showing particularly longer time needed for their repair as well as highlighting the importance of the extremely asymmetric and nonparental sites.