Table S3. Classification of NCOs based on the inferred initiating PRDM9 allele and predicted hotspot symmetry.

Predicted NCO class	Presence in parental strains	DMC1 dataset*			Hotspot origin*	No of NCOs
		PWD	B6	B6xPWD		
B6 symmetric	parental	-	+	+	B6	62
PWD symmetric	parental	+	-	+	PWD	5
Weak PRDM9 motif, symmetric	parental	+	+	+	undetermined	2
B6 symmetric	parental, incomparable	-	+	-	B6	3
B6 asymmetric	nonparental	-	-	+	B6	7
PWD asymmetric	nonparental	-	-	+	PWD	0
Weak PRDM9 motif	nonparental	-	-	+	undetermined	7
Anomalous, default **	anomalous	+	+	+	B6.$Prdm9^{-/-}$	2
Anomalous, DMC1 negative	anomalous	-	-	-	none	6

* Davies et al. 2016; Smagulova et al. 2016

** includes 1 NCO from (PWD-; B6+; B6×PWD+)