

Table S1. Summary details of the six hotspots chosen for analysis

Hotspot:	E	F	H	K	T	5A
centre location (GRCh37/hg19)	chr8:137,524,198	chr12:5,749,255	chr3:14,817,625	chr8:94,302,762	chr3:2,426,642	chr5:1,935,700
genomic context	intergenic	intronic (ANO2)	Intergenic	intergenic	intronic (CNTN4)	intergenic
main activating <i>PRDM9</i> variant	A	A	A	A	A	C
CO frequency per sperm (%)*	0.49	0.97	0.13	0.22	1.10	0.54
peak frequency (cM/Mb)	550	1100	180	260	1200	600
95% width (kb)	1.4	1.4	1.2	1.4	1.5	1.5
Informative SNPs ±150 bp from centre (local name) [distance (bp) ; MAF†]	rs2255417 (E6.8) [47 ; 0.372]	rs11063791 (F5.9) [87 ; 0.346] rs386440 (F6.0) [-26 ; 0.277] rs10492181 (F6.1) [-108 ; 0.133]	rs853334 (H7.5) [-29 ; 0.410] rs3899614 (H7.6) [-102 ; 0.457]	rs1374633 (K7.4) [20 ; 0.302] rs1374632 (K7.5) [-4 ; 0.406]	rs9854419 (T7.9) [10 ; 0.346]	rs13355978 (5A7.1) [127 ; 0.238] rs116141470 (5A7.2) [21 ; 0.169]

* in men with two activating *PRDM9* alleles

† minor allele frequencies as determined from 94 north Europeans for hotspots E, F, H, K & T [refs 37,5], and from 74 Africans for hotspot 5A [ref 9].