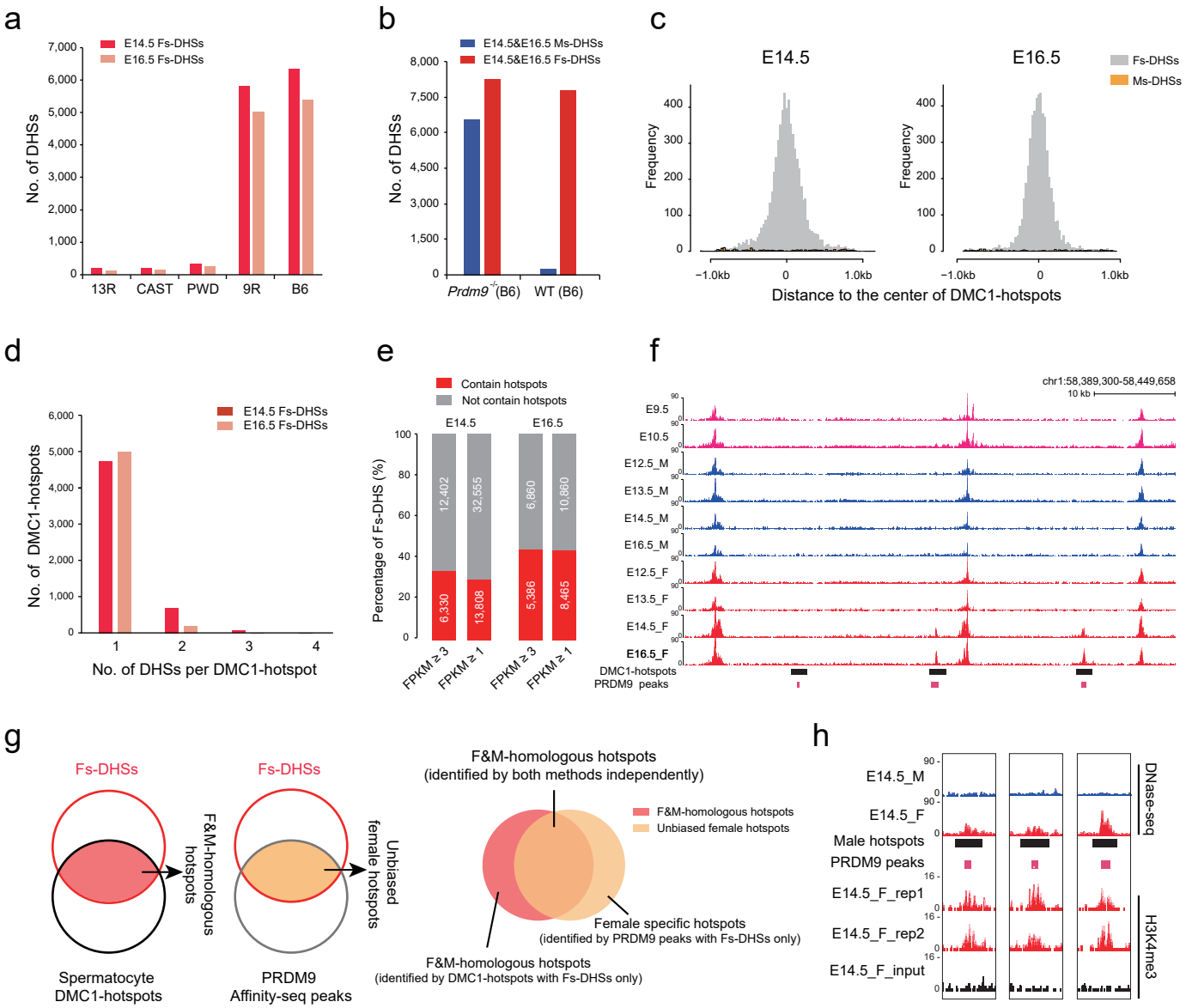

Fig. S4 See next page for caption.

Fig. S4 Identification of female recombination hotspots. **a** E14.5 and E16.5 Fs-DHSs are colocalized with spermatocyte DMC1-hotspots in a strain-specific manner. **b** The number of E14.5 and E16.5 merged Fs- and Ms-DHSs colocalized with *Prdm9*$^{-/-}$ and wild-type DMC1-hotspots. **c** Distribution of E14.5 Fs- and Ms-DHSs, E16.5 Fs- and Ms-DHSs around the DMC1-hotspots. **d** The number of DMC1-hotspots overlapped with one, two, three or four E14.5 and E16.5 Fs-DHSs. **e** The percentage of E14.5 and E16.5 Fs-DHSs colocalized with DMC1-hotspots. DHSs were filtered by signal values FPKM ≥3 or ≥1 respectively. **f** Genome browser view of DHS signal enrichment in mouse PGCs from E9.5 to E16.5. Positions of DMC1-hotspots and PRDM9 Affinity-seq peaks are also indicated in the corresponding genomic regions. **g** Model illustrating female recombination hotspots identified by Fs-DHSs with spermatocyte DMC1-hotspots or PRDM9 Affinity-seq peaks, and the relationship between two methods. **h** Genome browser view of DHS and H3K4me3 signal enrichment in selected female hotspots in E14.5 PGCs. **i** Bar plot shows the number of human 21W Fs-, Ms- and F&M-DHSs colocalized with human male hotspots. **j** Some human male hotspot-representative motifs in 21W Fs- and Ms-DHSs. **k** The relative expression levels of PRDM9 in four types of human female PGCs and four types of human female gonadal somatic cells identified in previous study[6]. The percentages of female 20W, 23W and 24W PGC samples in each group are indicated.