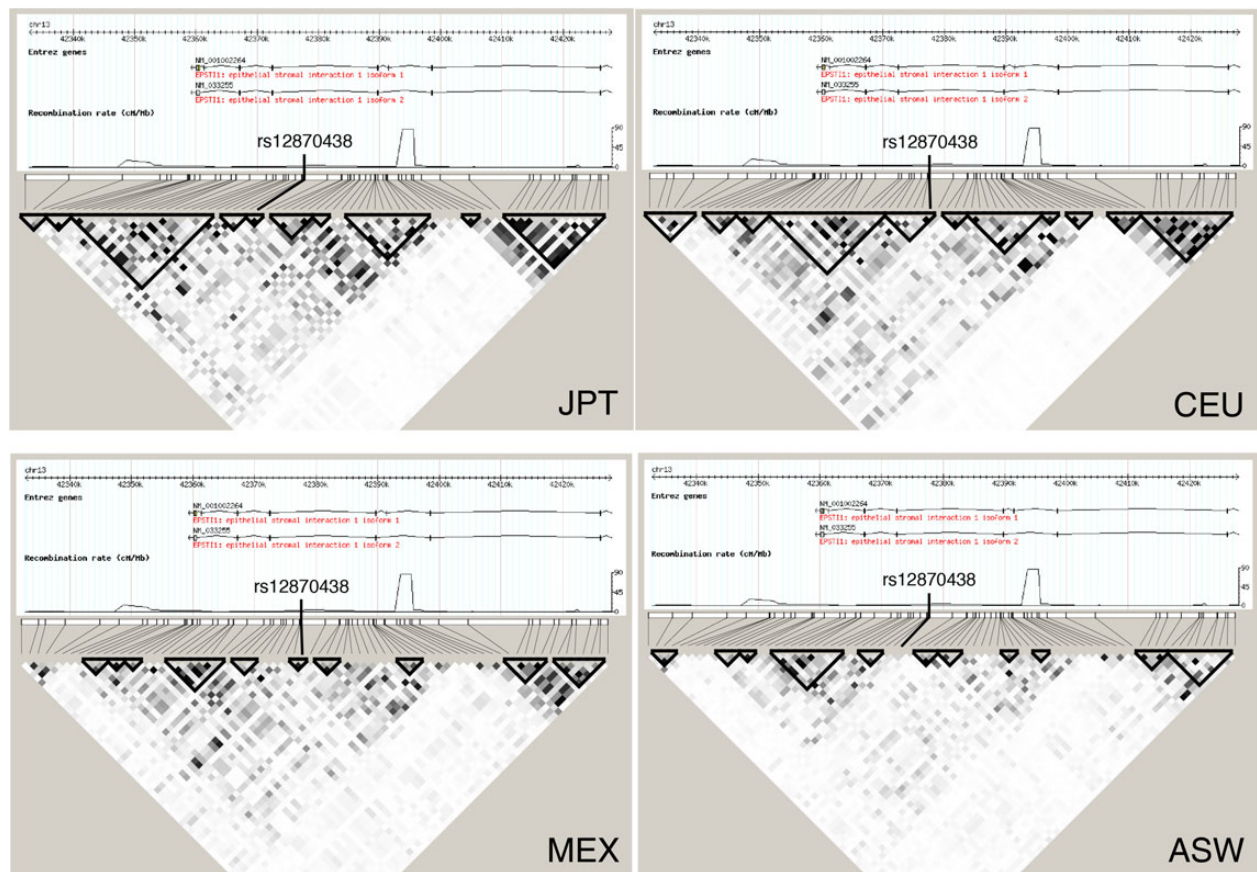
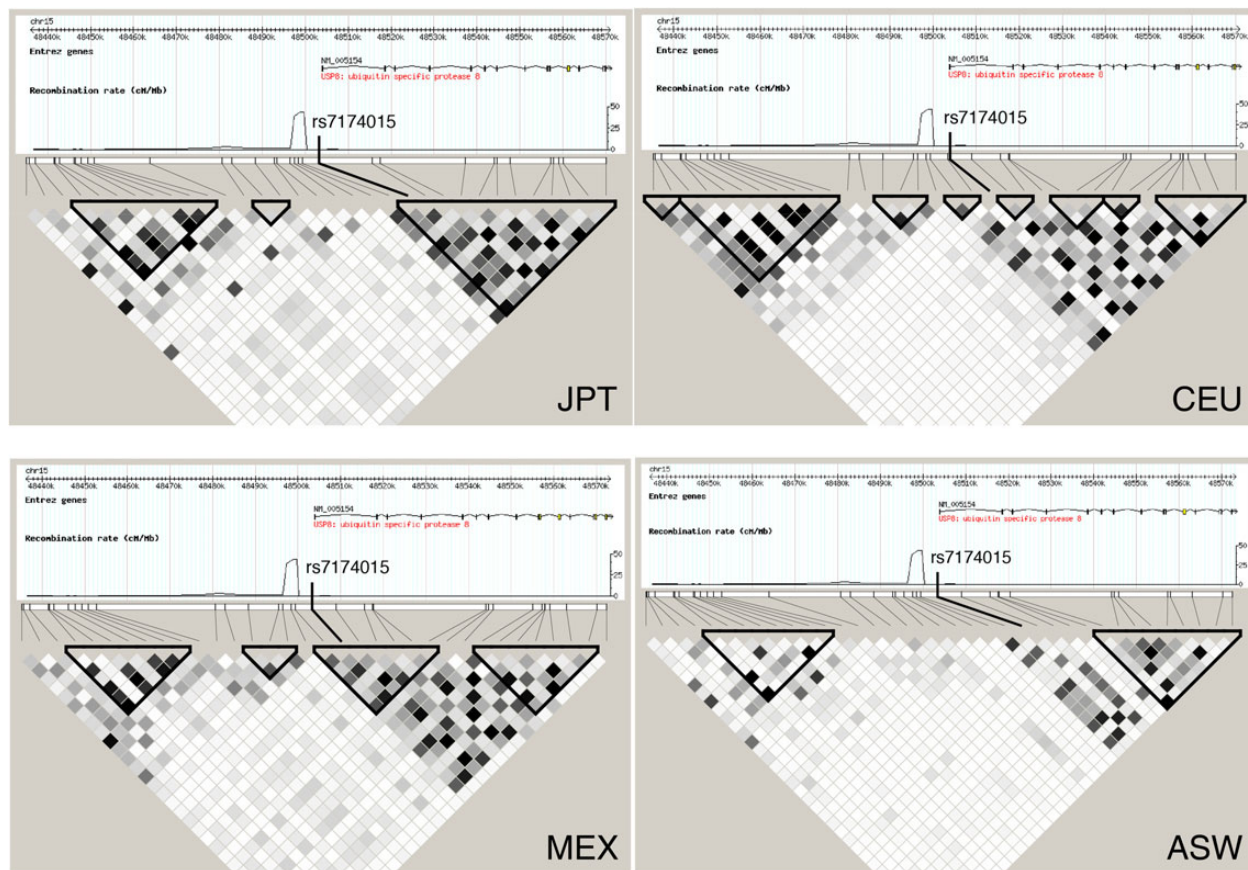


**Supplementary Figure S1** Comparisons of linkage disequilibrium (LD) patterns of rs7867029 for male fertility traits among human populations. The white rectangle with black vertical bars represents a region in and around the fertility trait locus examined. The identifier of the single nucleotide polymorphism (SNP) genotyped and the genomic position are shown. The triangle represents the LD map calculated from SNPs with minor allele frequencies  $\geq 0.05$  in the respective populations: JPT, Japanese in Tokyo, Japan; CEU, Utah residents with ancestry from northern and western Europe; MEX, Mexican ancestry in Los Angeles, CA, USA; ASW, African ancestry in Southwest USA. The color of each square in the triangle expresses the extent of LD: black,  $r^2 = 1$ ; shades of gray,  $0 < r^2 < 1$ ; white  $r^2 = 0$ . LD blocks according to the definition of [Gabriel et al. \(2002\)](#) are indicated by bold black lines. The recombination rates obtained the HapMap database and the RefSeq genes within the region are shown in the panel above.

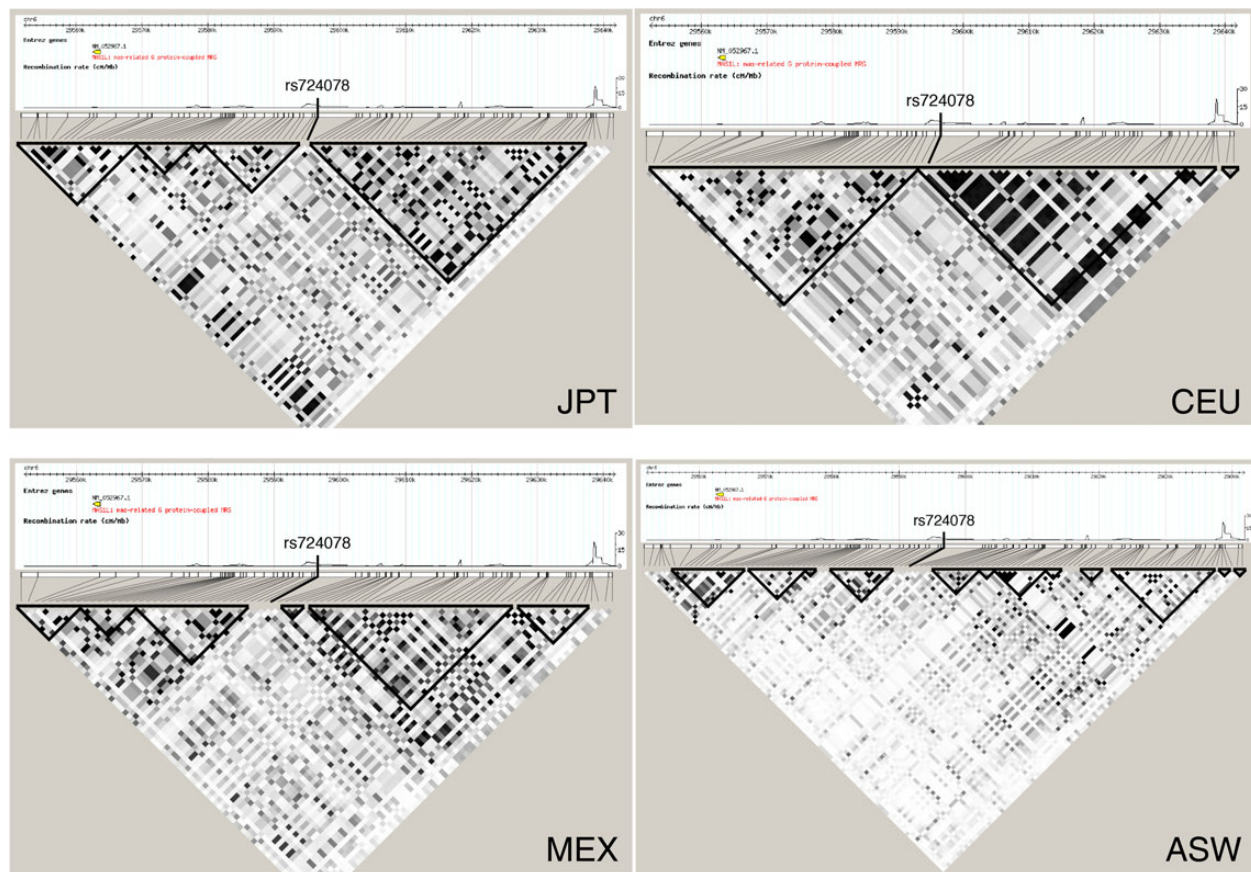


**Supplementary Figure S2** Comparisons of linkage disequilibrium (LD) patterns of rs12870438 for male fertility traits among human populations. See legend to [Supplementary Fig. S1](#) for description of symbols.



**Supplementary Figure S3** Comparisons of linkage disequilibrium (LD) patterns of rs7174015 for male fertility traits among human populations. See legend to [Supplementary Fig. S1](#) for description of symbols.





**Supplementary Figure S4** Comparisons of linkage disequilibrium (LD) patterns of rs724078 for male fertility traits among human populations. See legend to [Supplementary Fig. S1](#) for description of symbols.