

P006 Sequence motifs and human recombination hotspots
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It is now well understood that the majority of human recombination is concentrated into narrow hotspots, of width one to two kilobases. However, the nature of the relationship between the location of such hotspots, and primary DNA sequence, has remained mysterious. We use a new set of more than 25,000 human hotspots, identified using genome-wide population variation data, to examine this relationship. We find overwhelming evidence that certain short, specific sequence motifs are over-represented in hotspots, and active in a variety of genomic contexts. Further, we identify secondary features of the sequence surrounding these motifs that strongly influence whether hotspots result. There are two human hotspots, DNA2 and NID1, where specific mutations have been previously shown via sperm typing to directly influence hotspot recombination activity. In both cases the polymorphism occurs within, and disrupts, a distinct motif we identify, with the disrupted form being less active. This offers powerful experimental evidence that the presence or absence of motifs can influence local hotspot activity. The very large number of human hotspots now available offers researchers the opportunity to continue to extend our understanding of which sequence features cause hotspots, and this could lead on to new biological insights about the recombination process itself.