Figure 3

The figure shows a bar chart depicting the distribution of nucleotide mismatches to the best matching HERV-W loci. The x-axis represents the number of nucleotide mismatches, ranging from 0 to 24. The y-axis indicates the number of sequences, ranging from 0 to 180. The chart is divided into two groups: non-recombined (white bars) and recombined (black bars). The y-axis is labeled as "number of sequences" and the x-axis is labeled as "number of nucleotide mismatches to best matching HERV-W loci."