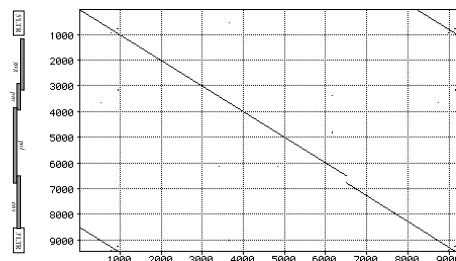
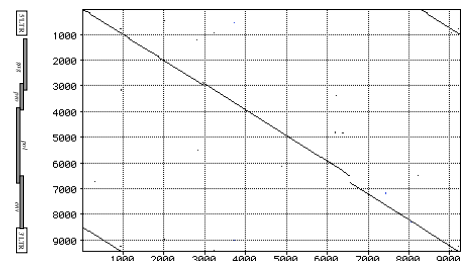


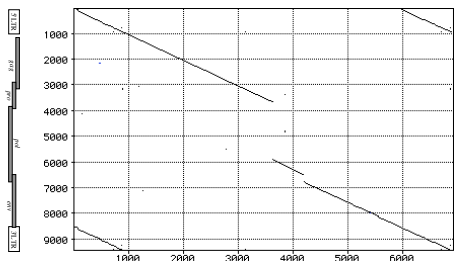
c1_A



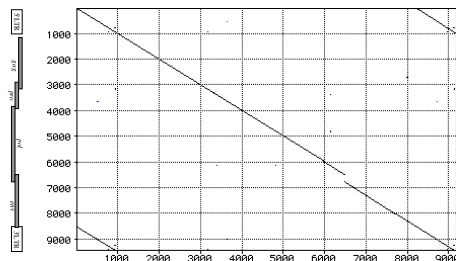
c1_B



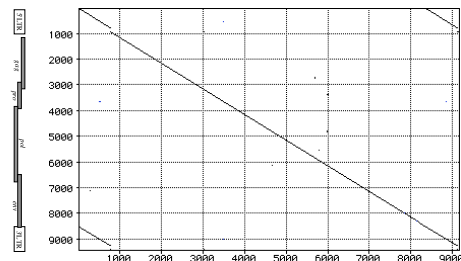
c1_C



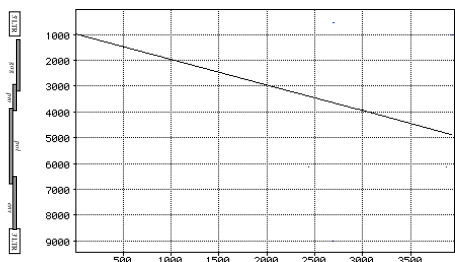
c3_A



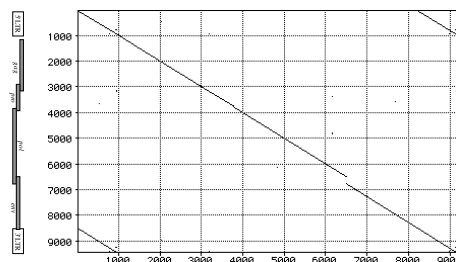
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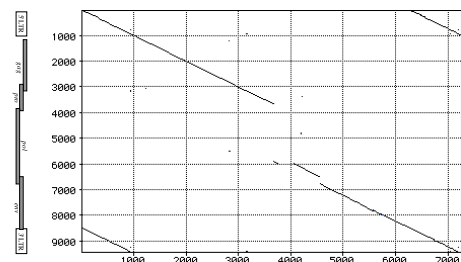
c3_C



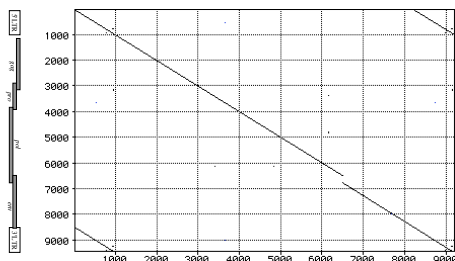
c3_D



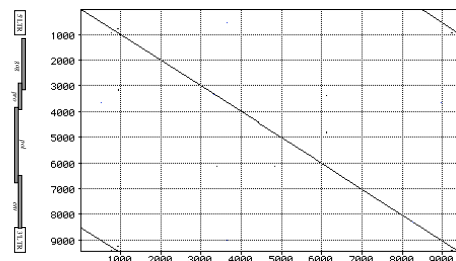
c3_E



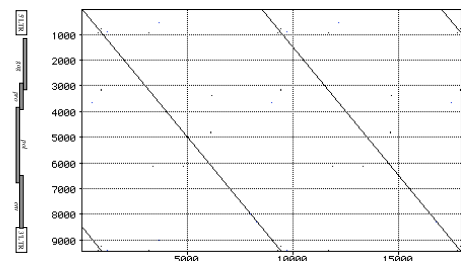
c4_A



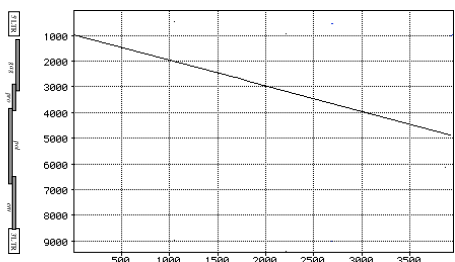
c5_A



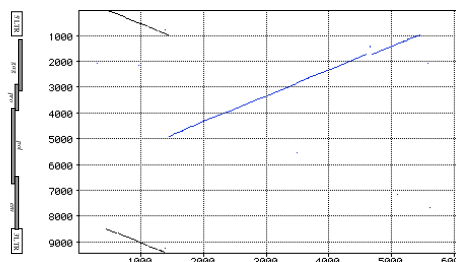
c6_A



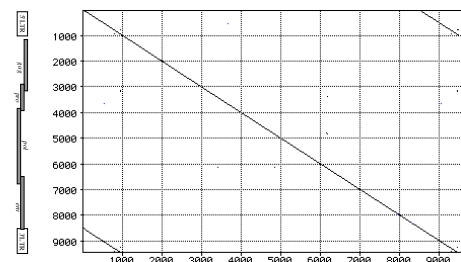
c7_A



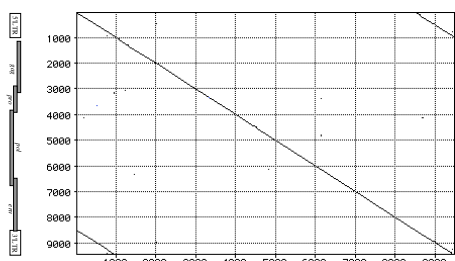
c7_B



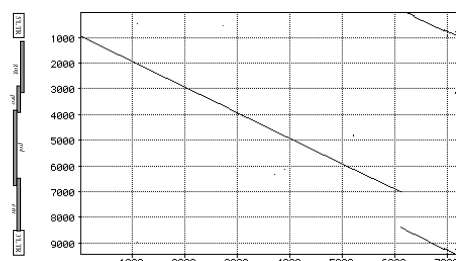
c7_C



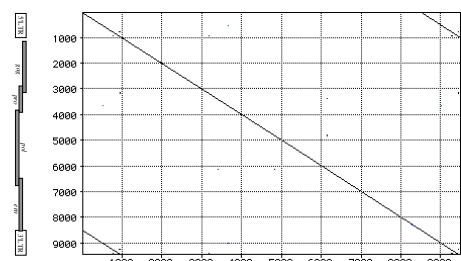
c8_A



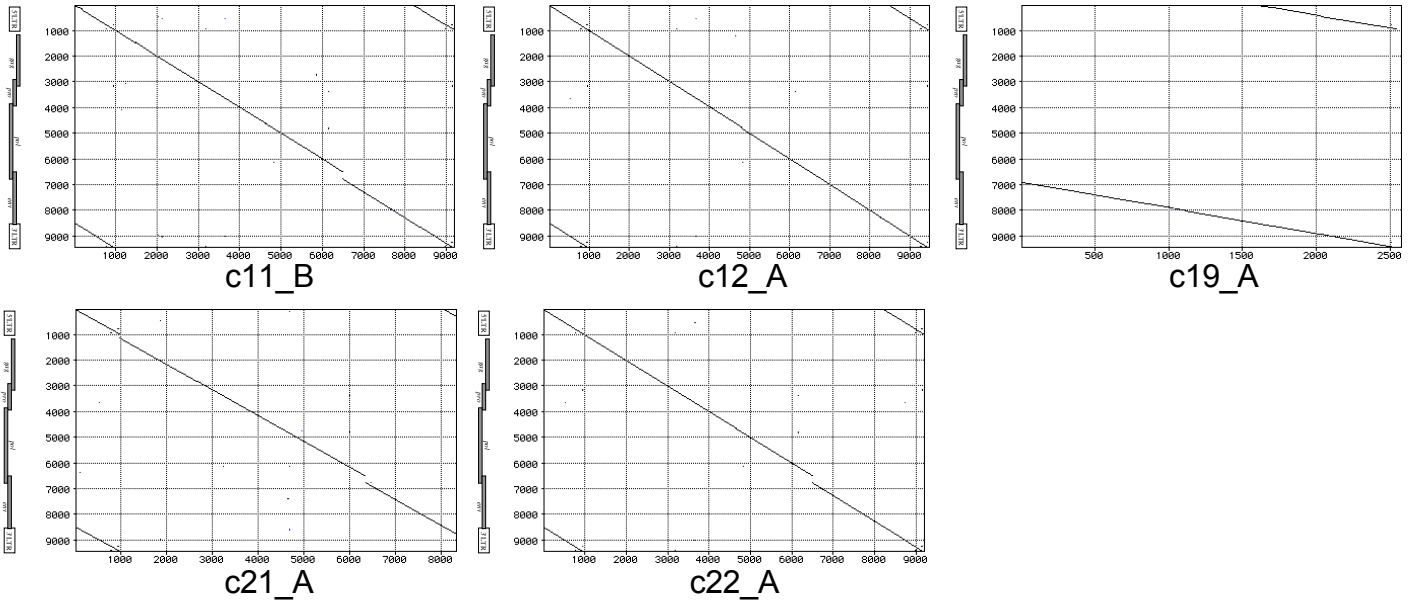
c10_A



c10_B



c11_A



Flockerzi et al. [Additional Figure 1](#): Pustell matrix comparisons of HERV-K(HML-2) proviruses identified as transcriptionally active in this study. Proviral sequences were compared to the previously published HERV-K(HML-2.HOM) sequence. Location of LTR and proviral *gag*, *pro*, *pol* and *env* genes within the latter sequence is indicated. The following parameters were applied for comparisons: Window size = 30 nt; Min. % Score = 55; Hash Value = 6; Jump = 1; Strands = both. Note that provirus *c7_A*—the actual HERV-K(HML-2.HOM) provirus—is represented in tandem structure in the human genome reference sequence. HERV-K(HML-2) type 1 loci display a gap at nt 6500 with respect to the HERV-K(HML-2.HOM) sequence, as opposed to type 2 loci. Provirus sequences were reverse complemented prior to comparison if located in antisense on the respective human chromosome. The following parameters were applied for comparisons: Window size = 30 nt; Min. % Score = 55; Hash Value = 6; Jump = 1; Strands = both. Thus, each position in one sequence that shares on the DNA level at least 55% similarity in a 30 nt window to the other sequence is marked by a dot, and producing a line for longer stretches of DNA.