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Human endogenous retroviruses

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Our genomes are scattered with large numbers of [human endogenous retroviruses \(HERVs\)](#), presumed left-overs from early retroviral infections. In the Advanced Online Publication of [Nature Genetics](#), Jennifer Hughes and John Coffin, from the [Tufts University School of Medicine](#) in Boston, describe 23 new members of the HERV-K (HML-2) group of sequences and examine their rearrangement during evolution (DOI: 10.1038/ng775). They analysed the 5' and 3' LTR sequences of 35 provirus HERV-K elements and found evidence for inter-element recombination events in six elements (16%). HERV recombination may have influenced genomic rearrangements and the evolution of the human genome, for example via insertion/deletion events in the [class I major histocompatibility region](#).

References

1. Many human endogenous retrovirus K (HERV-K) proviruses are unique to humans.
2. *Nature Genetics*, [<http://genetics.nature.com>]
3. Tufts University School of Medicine , [<http://www.tufts.edu/med/>]
4. Coevolution of PERB11 (MIC) and HLA class I genes with HERV-16 and retroelements by extended genomic duplication.