

Pol similarity matrix of endogenous retroviruses (ERVs) and reference sequences

Percent similarity using pairwise deletions and PAM250. The shortest sequence of the two aligned to itself equals 100 % identity.

>80 % Pol similarity is highlighted in **red**

>90 % Pol similarity is highlighted in **red and bold**

ERVs are presented with chromosome positions in respective genomes

hg15: *Homo sapiens* genome version 15

pt01: *Pan troglodytes* genome version 1

gg01: *Gallus gallus* genome version 1

