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Structure and variability of recently inserted alu family members

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Addendum

Factor IX_{Basel}: a Swiss family with severe haemophilia B having a point mutation in EGF type B domain

by M.Alkan, M.Rodriguez Ponte, N.T.Malik, S.Hofmann, N.Bösch-Al Jadooa, Hj.Müller and E.M.Bühler

Nucleic Acids Research, **19**, p. 409 (1991)

D.D.Koeberl *et al.* recently reported $FIX_{Toronto\ 2}$ mutation which Cys 56 within the EGF type B domain is substituted by thyrosine resulting also in severe haemophilia B (*Am.J.Hum.Genet.*, **47**, 202–217, 1990).

Corrigendum

Optimization of the annealing temperature for DNA amplification *in vitro*

by W.Rychlik, W.J.Spencer and R.E.Rhoads

Nucleic Acids Research, **18**, pp. 6409–6412 (1990)

Equation (iii) from the above article is published below in complete form

$$T_m^{product} = 81.5 + 0.41\ (\%G + \%C) + 16.6\ \log[K+] - 675/l$$

Erratum

Structure and variability of recently inserted Alu family members

by M.A.Batzer, G.E.Kilroy, P.E.Richard, T.H.Shaikh, T.D.Desselle, C.L.Hoppens and P.L.Deininger

Nucleic Acids Research, **18**, pp. 6793–6798 (1990)

The publishers wish to apologize for an error which occurred during printing of the above article. Figure 1 appeared with an incorrect figure legend. The correct figure and legend are published below.

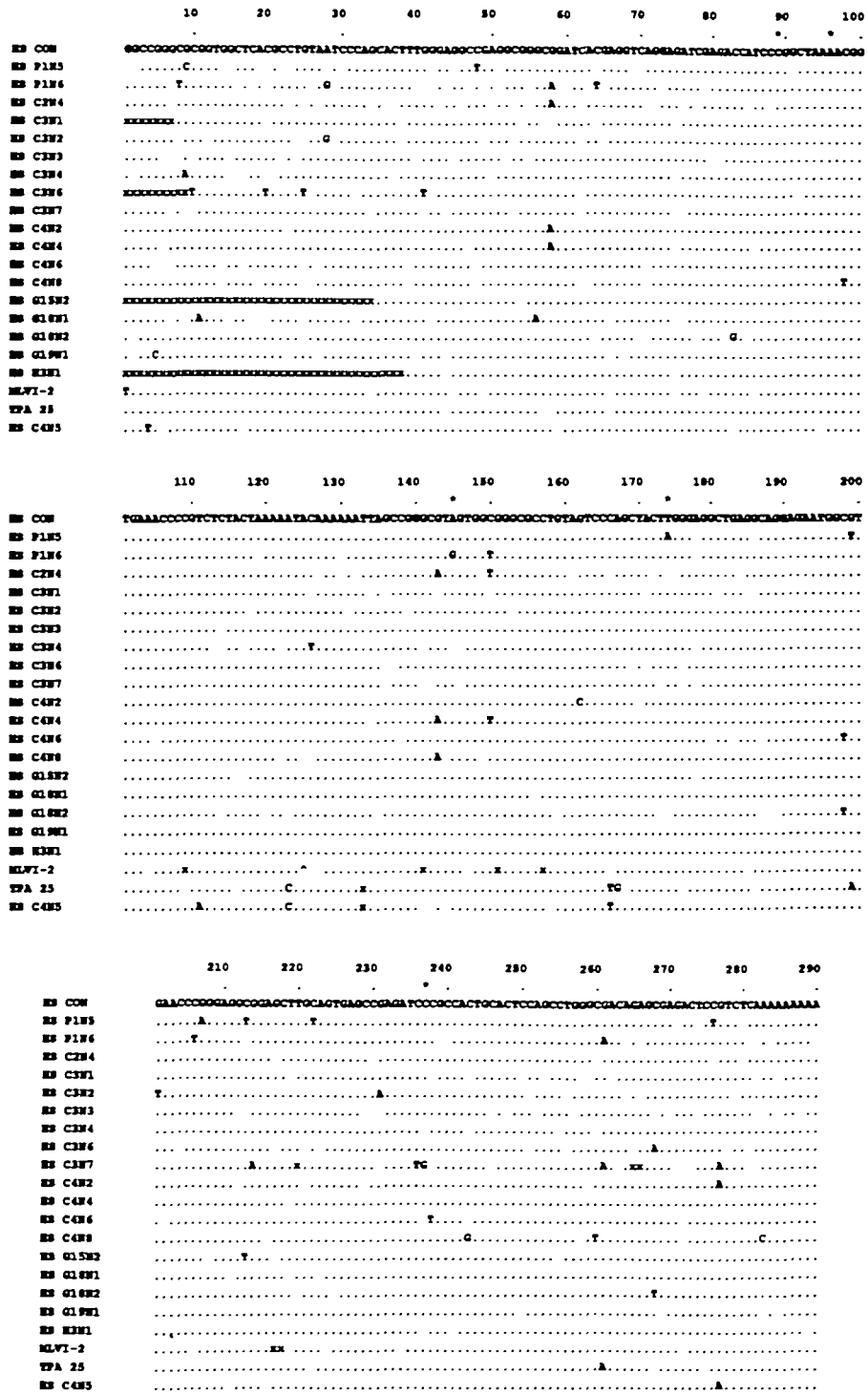

Figure 1. Alignment of HS subfamily members. Alignment of TPA 25 (19), MLVI-2 (20), HS C2N4, C3N1, C4N4, C4N5, C4N6, and C4N8 (18), as well as several other sequences reported here. The HS-1 subfamily consensus (con) is derived from the most common nucleotide found at each position within the subfamily members. The HS-1 consensus differs from the consensus for older Alu sequences at five positions (shown as a star above the consensus) as previously reported (18). Nucleotide substitutions at each position are indicated with the appropriate nucleotide. Insertions are indicated with an ^. Deletions are marked by an X.