

[illegible]

*FBP1* Alu Ya5

[illegible]

[illegible]

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NC000009.12:965286 : GGGCGACAGAGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGTGCCTCATTCTCATTTTACGCCTAAAGAAATATAATGGTTAGCAAATATAGGTCCTTTGGTA
NC000013.11:870234 : GGGCGACAGAGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATTACATGTGACAAGACATAGGATAATAATACTGGTAATGAATAGAAATTAATAAACATTGGAATCAAACCTACAG
NC000005.10:343271 : GGGCGACAGAGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAATTGTTTTTCCTTCCACATTATTATAGAATCGAGGTACATGGCAGCCTTGAAACATG

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**Figure S8.** A-tails of Alu copies closely related to those that induced mutations in the *FGFR2*, *FBP1*, and *PKLR* genes (alignments A-C, respectively). Only the 3'-terminal sequences are given since the upstream ones are identical. The upper sequence corresponds to the Alu copy that caused gene mutations. All copies of the *FGFR2* tribe are given, while randomly selected 49 out of 419 and 59 out of 232 copies are given for the *FBP1* and *PKLR* tribes, respectively. All identified TSDs are underlined. Within A-rich tails, A residues are highlighted yellow; Ts are highlighted purple; while Cs and Gs are highlighted green.