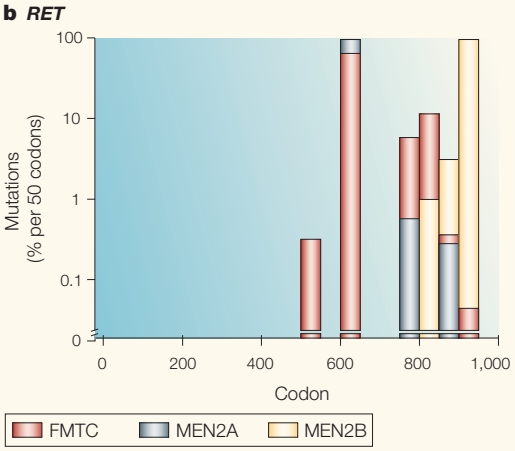
CORRECTION

MOLECULAR GENETICS OF MULTIPLE ENDOCRINE NEOPLASIA TYPES 1 AND 2.

Stephen J. Marx

Nature Rev. Cancer **5**, 367–375 (2005)

The author would like to correct Figure 2b (page 370) of this article. The original figure was produced with an error in the graph and accompanying legend. The corrected figure and legend are shown below.



b | MEN2-related mutations in the *RET* gene. All germline mutations are included, but somatic mutations are omitted because they have a significantly different distribution. Data are plotted by MEN2 variant so that the mutation frequency for each variant totals 100%. The relative prevalence of each variant is approximately 90% for MEN2A, 5% for MEN2B and 5% for FMTC. It should be noted that the data are tabulated from the literature, and therefore there is a bias for relative under-reporting for common mutations for each disease phenotype. Data are pooled across each run of 50 codons. This underemphasizes the asymmetric clustering in codons 634 and 918. Fourteen of the twenty 50-codon runs have no mutations. Where two or three bars are plotted together, the higher bars overlap with the lower ones.