

Erratum: Recurrent ZFX mutations in human sporadic parathyroid adenomas.

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In Figures 1 and 2, the 3-letter amino acid code labels Glu should have been Gln. The corrected Figures 1 and 2 are provided here.

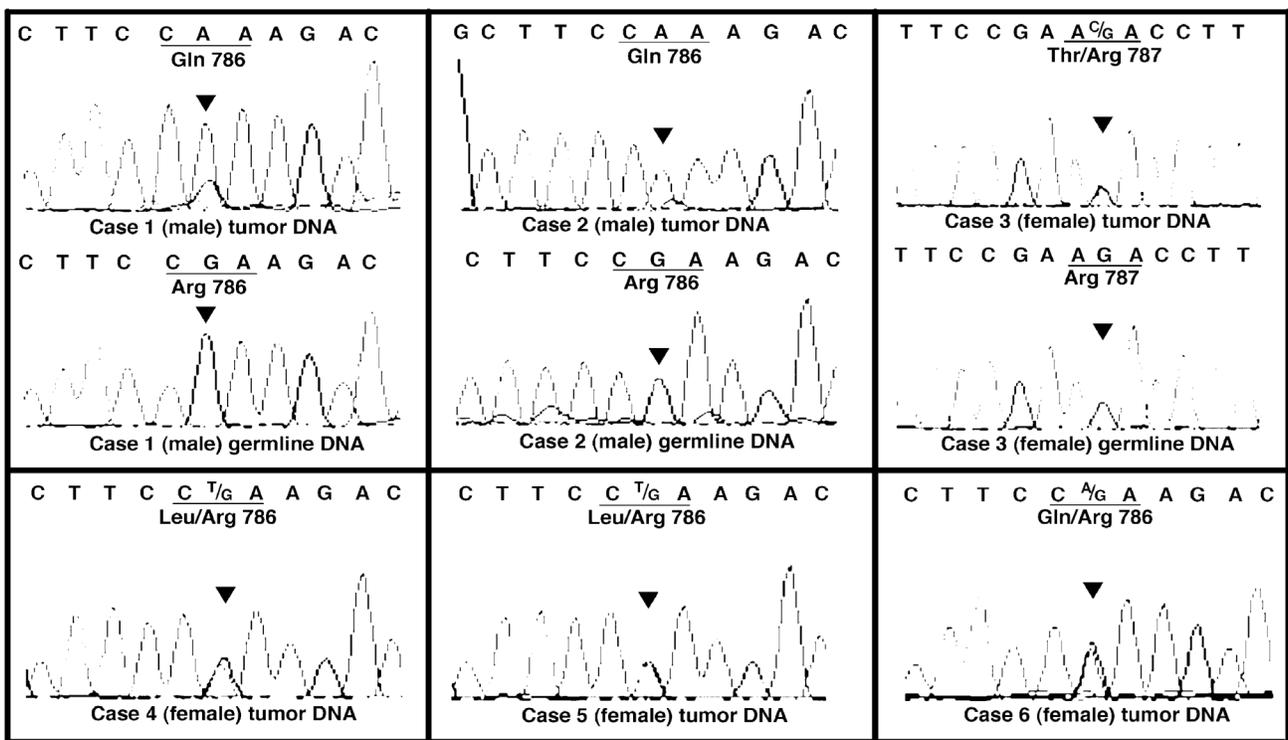


Figure 1: Direct genomic DNA sequencing of ZFX R767/768 mutations. Chromatograms of the ZFX R786/787 mutations in adenoma samples, with matched germline control DNA when available. Germline DNA samples were unavailable for patients 4, 5 and 6. The codons where mutations were identified are underlined for clarity. The red triangle in each chromatogram indicates the location of the mutation.

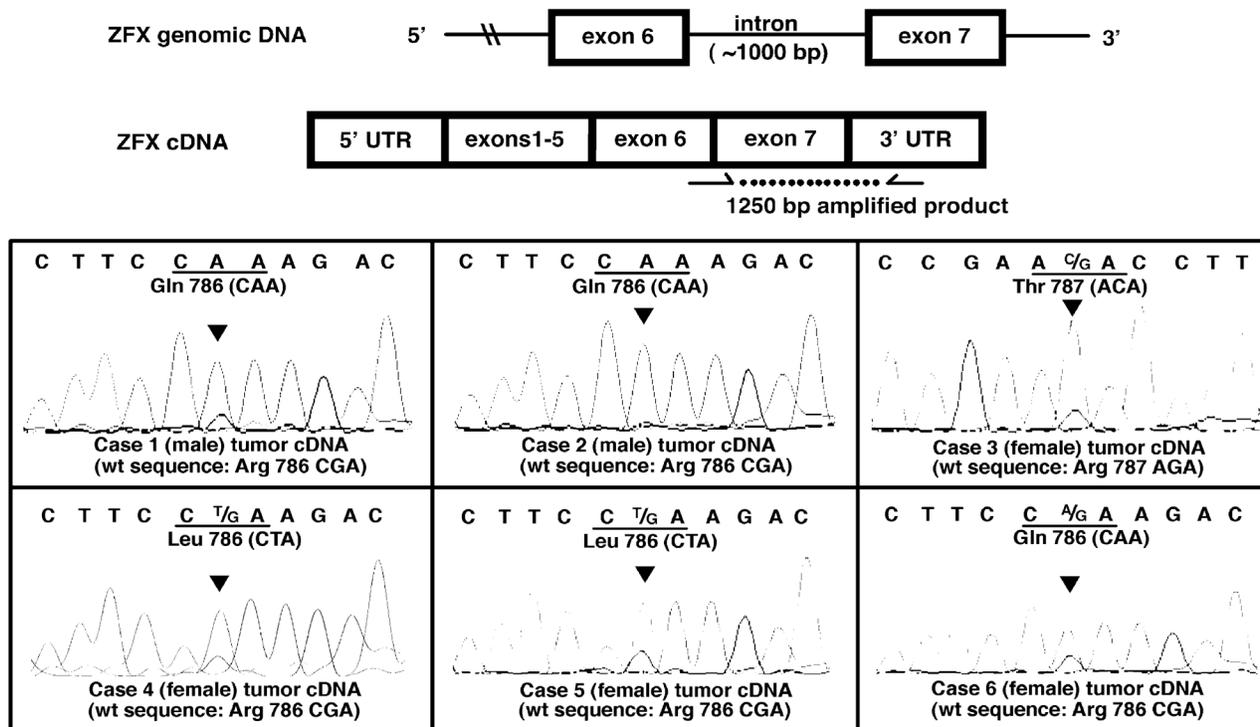


Figure 2: Expression of mutation-bearing ZFX alleles in parathyroid adenomas.

Top: Schema of cDNA amplification to detect mutant transcripts extracted from parathyroid adenomas with ZFX mutations. The red arrows indicate the location of the forward and reverse primers. The forward primer spanned the junction of exon 6 and exon 7, which prevented amplification of genomic DNA.

Bottom: Sequence chromatograms of ZFX cDNA from the parathyroid adenomas with R786/787 mutations. The mutant ZFX transcripts were present in each of the mutation-bearing adenoma samples. For each box, from the top, the first line of nucleotide sequence represents base calls from tumor cDNA. Codon and notation of the mutant/prominent allele is labeled beneath the first line. The red triangle indicates the location of the mutant base in the chromatogram. For convenience, the wild-type (standard reference) ZFX sequences are labeled in parentheses beneath each chromatogram. Nucleotide letters in the chromatogram and codon labels are color coded to match.