Nucleotide numbering

Since references to WWW-sites are not yet acknowledged as citations, please mention [den Dunnen JT and Antonarakis SE (2000). Hum.Mutat. 15:7-12](#) *when referring to these pages.*

Genomic reference sequences

For genomic reference sequences, nucleotide numbering is simple 1, 2, 3, ...etc. from the first to the last nucleotide of the reference seqence. No "+", "-" or other signs are used (see xxxDiscussion).

Coding DNA reference sequences

In a coding DNA reference sequence nucleotide "1" is the **A of the ATG translation initiation codon**. The main reason why most people prefer a coding DNA reference sequence is that from the description one immediately gets some information regarding the location of the variant;

- **c.78T>C** >   protein coding
  since the nucleotide "c.78" has no signs attached and is not followed by a "+" or "-" and a second number it is located in the protein coding part of the gene. **NOTE:** *this rules does not hold for alternative transcripts where exons might reside 5' of the translation initiation side, in an intron or 3' of the 3'-terminal exon*

- **c.-78G>A**
  since the nucleotide "c.**-**78" has a "**-**" prefix it is located 5' of the ATG translation initiation codon. **NOTE:** *the length of the 5'UTR determines whether this position is still part of the transcript or*

upstream of the transcription initiation site (cap site)

- **c.*78T>A**
  since the nucleotide "c.*78" has a "*" prefix it is located 3' of the translation termination codon.
  NOTE: *the length of the 3'UTR determines whether this position is still part of the transcript or downstream of the polyA-addition site*

- **c.78+45T>G**
  since the nucleotide "c.78" is followed by "+" and a second number ("45") the nucleotide is in an intron, 3' of the splice donor site and before (5') of the middle of the intron

- **c.79-45G>T**
  since the nucleotide "c.79" is followed by "-" and a second number ("45") the nucleotide is in an intron, 5' of the splice acceptor site and after (3') of the middle of the intron

Dividing the nucleotide number by 3 gives the number of the amino acid residue affected, in the example amino acid 26 (*78:3 = 26*).