Computational identification of promoters and first exons in the human genome

R V Davuluri, I Grosse & M Q Zhang

Nature Genet. **29**, 412–417 (2001).

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On page 413, the last line of the caption of Fig. 2 should read "... the CpG window overlapped with the region ranging from –200 bp of the transcription start site to the splice-donor site."
On page 414, the last sentence of the caption of Table 2 should read "Approximately 70% of those 58 promoters are CpG-related."

High-throughput retroviral tagging to identify components of specific signaling pathways in cancer

H Mikkers, J Allen, P Knipscheer, L Romeyn, A Hart, E Vink & A Berns

Nature Genet. **32**, 153–159 (2002).

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The name of the fourth author was misspelled as Lieke Romeyn rather than the correct spelling: Like Romeijn.

The gene mutated in juvenile nephronophthisis type 4 encodes a novel protein that interacts with nephrocystin

G Mollet, R Salomon, O Gribouval, F Silbermann, D Bacq, G Landthaler, D Milford, A Nayir, G Rizzoni, C Antignac & S Saunier

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A sequence analysis error (deletion of two cytosine residues) occurred in the previously named exon –4. This masked a methionine codon located 176 amino acids upstream of the previously reported initiation codon. Correction of this error indicates that NPHP4 contains four additional coding exons, and the protein nephrocystin-4 is composed of 1,426 amino acids instead of 1,250. The exons should be renumbered as follows: exon –5 becomes exon 1, the initiation codon is in exon 2 and the last exon is exon 30. The designations of all the mutations have changed as shown in the following revised version of Table 1.

Table 1 • Mutations detected in *NPHP4*

Type of mutation	Nucleotide change[a]	Amino-acid change	Exon	Individual affected	Mutation Status[b]
nonsense	2044C→T	Arg682X	exon 16	F18[c]	het
	2368G→T	Glu790X	exon 18	F115[d]	hom
	2377C→T	Gln793X	exon 18	F96[d]	hom
frameshift	3272delT[e]	Val1091fsX1121	exon 23	F171[c]	het
missense	2972T→C	Phe991Ser	exon 21	F95[d]	hom
polymorphism	2219G→A[f]	Arg740His	exon 17		
	2542C→T	Arg848Trp	exon 19		
	2818–2A→T	ΔAla940–Gln941	exon 21		

[a]Nucleotides are numbered with respect to the A of the ATG initiation codon according to standard nomenclature[27]. [b]het, heterozygous mutation; hom, homozygous mutation. [c]Only one mutation has been detected in these individuals. [d]These individuals are from a consanguineous family. [e]Only maternal mutation detected. [f]Only found in individuals from the Normandy region of France.