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errata

Human methylenetetrahydrofolate reductase: isolation of cDNA, mapping and mutation identification

P. Goyette, J. S. Sumner, R. Milos, A. M.V. Duncan, D. S. Rosenblatt, R. G. Matthews & R. Rozen

Nature Genetics 7, 195–200 (1994)

An old version of Fig. 2 was inadvertently printed in this paper. The revised part of Fig. 2 is printed below.

A GenBank accession number has now been assigned — U09806.

```
                                                    300•
QGYHS LRQLV KLSKL EVPQE IKDVI EPIKD NDAAI RN-YGI ELAVS LCQEL LASGL VPGLH FYTLN  mthfr
snfkq akkfa dmtnv riPaw maqmf dgl-D dDAet RklvGa niAmd mvkiL sreG- VkdfH FYTLN  ecometf
snfkq akkfa dmtnv riPsw mslmf Egl-D nDAet RklvGa niAmd mvkiL sreG- VkdfH FYTLN  stymetf

R-EMAT TEVLK RLGMW TEDPR RPLPW ALSAH PKRRE EDVRP IFWAS RPKSY IYRTQ EWDEF PNGRW    mthfr
RaEMsy a-ich tLGvr pgl>                                                         ecometf
RaEMsy a-ich tLGvr pgl>                                                         stymetf

        400•
GNSSS PAFGE LKDYY LFYLK SKSPK E  mthfr
```

The distribution of CpG islands in mammalian chromosomes

Jeffrey M. Craig & Wendy A. Bickmore

Nature Genetics 7, 376–382 (1994)

Figs 3 and 4 were inadvertanly transposed in this paper; the legends were correct, as published.

correction

Heterozygous missense mutation in the rod cGMP phosphodiesterase β-subunit gene in autosomal dominant stationary night blindness

Andreas Gal, Ulrike Orth, Wolfgang Baehr, Eberhard Schwinger & Thomas Rosenberg

Nature Genetics 7, 64–68 (1994)

The authors would like to apologize for two regretful mistakes. The amino acid substitution predicted by the mutation (CAC-258-AAC) is given incorrectly throughout the paper; it should read His258Asn/H258N. Also, residue 259 (codon AAG) in Fig. 2 should read lysine (not leucine). The revised Fig. 2 is shown below.

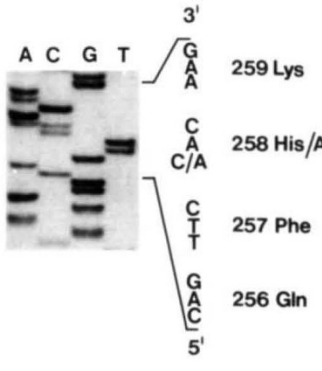

Fig. 2 Detection of the heterozygous His258Asn mutation by direct sequencing of PCR products in exon 4 of the human *βPDE* gene.