Functional analysis of human MLH1 mutations in Saccharomyces cerevisiae

Hideki Shimodaira et al.

Nature Genet. 19, 384–389 (1998).

Due to a typographical error, the genotypes of two yeast strains were reported incorrectly. The corrected genotypes are shown as follows: RKY1732 (*MATα*, *leu2*, *cyh2^r*, *ura3*, *trp1*, *msh2Δ*::*hisG*). A National Institutes of Health grant number was erroneously described as GM50006; it is, in fact, GM44704.

Genomic imprinting is disrupted in interspecific Peromyscus hybrids

Paul Vrana et al.

Nature Genet. 20, 362–365 (1998).

A typographical error occurred on page 362. The sentence should instead read "*P. maniculatus* and *P. polionotus* became evolutionarily separated approximately 100,000 years ago⁹, but it is not known when monogamy became fixed in the latter".

Mutations in the gene encoding gap junction protein $\beta\mbox{-}3$ associated with autosomal dominant hearing impairment

Jia-hi Xia et al.

Nature Genet. 20, 370-373 (1998).

One of the two *GJB3* mutations we described lies at amino acid position 183. The mutation results in the substitution of a lysine residue for a glutamate residue, rather than a glutamine residue, as we originally proposed. We thank Andrew Griffith, of the US National Institutes of Health, for bringing this to our attention.

Options available—from start to finish—for obtaining expression data by microarray

David Bowtell

Nature Genet. 21, 25-32 (1999).

Table 3; High-density microarrays

Details of Affymetrix software are as follows.

GeneChip® EDMT, priced from \$2,500–\$3,250 per seat depending on geography, facilitates the mining of expression data contained in the GATCTM database created by GeneChip LIMS.

GeneChip® LIMS is a client/server software that facilitates the tracking of experimental and expression information in a relational database architecture. The server software is priced from \$70,000–\$98,000 and access licenses are priced from \$2,500–\$3,250 per seat depending on geography.