# errata

## Mutations in *GLUT2*, the gene for the liver-type glucose transporter, in patients with Fanconi-Bickel syndrome

René Santer, Reinhard Schneppenheim, Anja Dombrowski, Hermann Götze, Beat Steinmann & Jürgen Schaub

*Nature Genet.* **17**, 324–326 (1997).

Due to an error, the designation of the *GLUT2* mutation of patient 0301 is wrong. C1251T has to be replaced by C1213T. As the amino-acid code (R301X) was correctly stated, this does not affect the discussion of the results and the conclusions of the paper. We regret this error.

## Atm selectively regulates distinct p53-dependent cell-cycle checkpoint and apoptotic pathways

Carrolee Barlow, Kevin D. Brown , Chu-Xia Deng, Danilo A. Tagle & Anthony Wynshaw-Boris

*Nature Genet.* **17**, 453–456 (1997).

We inadvertantly failed to acknowledge Stacie Anderson for her assistance and advice in performing the flow cytometry experiments. We regret this omission.

# corrections

## Genomic DNA transfer with a high-capacity adenovirus vector results in improved *in vivo* gene expression and decreased toxicity

Gudrun Schiedner, Núria Morral, Robin J. Parks, Ying Wu, Suzanne C. Koopmans, Claire Langston, Frank L. Graham, Arthur L. Beaudet & Stefan Kochanek

*Nature Genet.* **18**, 180–183 (1998).

The corresponding author's e-mail address was printed incorrectly. Dr. Stefan Kochanek's e-mail address is stefan.kochanek@medizin.uni-koeln.de. We regret this error.

## Localisation of a gene implicated in a severe speech and language disorder

Simon Fischer, Faraneh Vargha-Khadem, Kate E. Watkins, Anthony P. Monaco & Marcus E. Pembry

*Nature Genet.* **18**, 168–170 (1998).

Due to a printing error, the text on Table 1, printed here in full, was obscured. We regret this error.

**Table 1• Pairwise lod scores for linkage of *SPCH1* to 7q markers**

| | | Recombination fractions (θ) | | | | | |
|---|---|---|---|---|---|---|---|
| Locus | Dist (cM) | 0.00 | 0.05 | 0.10 | 0.20 | $\theta_{max}$ | $Z_{max}$ |
| *D7S527** | 3.9 | −∞ | 1.16 | 1.69 | 1.77 | 0.158 | 1.82 |
| *D7S518* | 3.8 | −∞ | 2.74 | 2.94 | 2.67 | 0.105 | 2.94 |
| *D7S2453* | 3.1 | −∞ | 1.27 | 1.46 | 1.19 | 0.103 | 1.46 |
| *D7S501* | 0.9 | −∞ | 4.55 | 4.36 | 3.59 | 0.045 | 4.55 |
| *D7S2420* | 0.0 | −∞ | 4.41 | 4.19 | 3.37 | 0.043 | 4.41 |
| *D7S496* | 0.0 | −∞ | 3.34 | 3.44 | 2.97 | 0.087 | 3.45 |
| *D7S2459* | 0.8 | −∞ | 4.83 | 4.62 | 3.79 | 0.043 | 4.84 |
| *D7S2425* | 0.0 | 5.67 | 5.25 | 4.81 | 3.84 | 0.000 | 5.67 |
| *D7S692* | 1.9 | 6.62 | 6.11 | 5.57 | 4.40 | 0.000 | 6.62 |
| *D7S687* | 0.0 | 6.02 | 5.55 | 5.06 | 3.99 | 0.000 | 6.02 |
| *D7S2418* | 0.5 | 5.72 | 5.30 | 4.85 | 3.88 | 0.000 | 5.72 |
| *D7S523* | 0.0 | 6.62 | 6.11 | 5.57 | 4.40 | 0.000 | 6.62 |
| *D7S2554* | 1.2 | 5.72 | 5.27 | 4.80 | 3.78 | 0.000 | 5.72 |
| *D7S522* | 0.0 | 5.41 | 5.01 | 4.58 | 3.66 | 0.000 | 5.41 |
| *D7S2460* | 0.1 | 5.79 | 5.33 | 4.85 | 3.80 | 0.000 | 5.79 |
| *D7S633* | 0.1 | 4.53 | 4.17 | 3.79 | 2.97 | 0.000 | 4.53 |
| *D7S486** | 0.0 | 6.22 | 5.71 | 5.17 | 4.00 | 0.000 | 6.22 |
| *CFTR** | 1.0 | 5.46 | 5.05 | 4.63 | 3.70 | 0.000 | 5.46 |
| *D7S643* | 0.9 | −∞ | 4.83 | 4.62 | 3.79 | 0.043 | 4.83 |
| *D7S480* | 2.2 | −∞ | 4.62 | 4.41 | 3.61 | 0.044 | 4.63 |
| *D7S2486* | 0.6 | −∞ | 4.55 | 4.36 | 3.59 | 0.045 | 4.55 |
| *D7S487* | 2.6 | 3.58 | 3.25 | 2.90 | 2.15 | 0.000 | 3.58 |
| *D7S504* | 3.8 | −∞ | 3.45 | 3.34 | 2.75 | 0.054 | 3.45 |
| *D7S530** | | −∞ | 2.27 | 2.71 | 2.59 | 0.131 | 2.76 |

Markers are listed in the order proximal-distal. Distances between neighbouring markers are from the latest Généthon linkage map[13]. Markers indicated with an asterisk were part of the HGMP set[12] used in the genome-wide linkage search; the remaining markers were used for fine mapping of the implicated region. Shading indicates the 3.8–5.6 cM region that co-segregates perfectly with the disorder.