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	θ_{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.