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 inadvertently 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

Locus	Dist (cM)	Recombination fractions (θ)				$\theta_{\max}$	$Z_{\max}$
		0.00	0.05	0.10	0.20		
<i>D7S527*</i>	3.9	—	1.16	1.69	1.77	0.158	1.82
<i>D7S518</i>	3.8	—	2.74	2.94	2.67	0.105	2.94
<i>D7S2453</i>	3.1	—	1.27	1.46	1.19	0.103	1.46
<i>D7S501</i>	0.9	—	4.55	4.36	3.59	0.045	4.55
<i>D7S2420</i>	0.0	—	4.41	4.19	3.37	0.043	4.41
<i>D7S496</i>	0.0	—	3.34	3.44	2.97	0.087	3.45
<i>D7S2459</i>	0.8	—	4.83	4.62	3.79	0.043	4.84
<i>D7S2425</i>	0.0	5.67	5.25	4.81	3.84	0.000	5.67
<i>D7S692</i>	1.9	6.62	6.11	5.57	4.40	0.000	6.62
<i>D7S687</i>	0.0	6.02	5.55	5.06	3.99	0.000	6.02
<i>D7S2418</i>	0.5	5.72	5.30	4.85	3.88	0.000	5.72
<i>D7S523</i>	0.0	6.62	6.11	5.57	4.40	0.000	6.62
<i>D7S2554</i>	1.2	5.72	5.27	4.80	3.78	0.000	5.72
<i>D7S522</i>	0.0	5.41	5.01	4.58	3.66	0.000	5.41
<i>D7S2460</i>	0.1	5.79	5.33	4.85	3.80	0.000	5.79
<i>D7S633</i>	0.1	4.53	4.17	3.79	2.97	0.000	4.53
<i>D7S486*</i>	0.0	6.22	5.71	5.17	4.00	0.000	6.22
<i>CFTR*</i>	1.0	5.46	5.05	4.63	3.70	0.000	5.46
<i>D7S643</i>	0.9	—	4.83	4.62	3.79	0.043	4.83
<i>D7S480</i>	2.2	—	4.62	4.41	3.61	0.044	4.63
<i>D7S2486</i>	0.6	—	4.55	4.36	3.59	0.045	4.55
<i>D7S487</i>	2.6	3.58	3.25	2.90	2.15	0.000	3.58
<i>D7S504</i>	3.8	—	3.45	3.34	2.75	0.054	3.45
<i>D7S530*</i>	—	—	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 Génethon linkage map¹³. Markers indicated with an asterisk were part of the HGMP set¹² 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.