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ERRATUM: Novel candidate genes and regions for childhood apraxia of speech identified by array comparative genomic hybridization

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In the published version of this article, the participant numbers in **Table 3** are incorrect. The corrected **Table 3** is reprinted below:

In addition, a number of related portions of the text are incorrect. The corrections are listed below:

Page 930, left column, last line: "participant 5" should be "participant 8".

Page 930, right column, Results section, first line: "participant 5" should be "participant 8".

Page 933, left column, line 8: "participant 2" should be "participant 12".

Page 933, left column, line 9: "participant 12" should be "participant 11".

Page 933, left column, *2p14* section, line 2: "participant 7" should be "participant 10".

Page 933, left column, *2p14* section, line 6: "participant 7" should be "participant 10".

Page 933, left column, *2q24.1* section, line 1: "participant 5" should be "participant 4".

Page 933, left column, *2q24.1* section, line 3: This sentence should have been deleted: "This participant was also found to have a heterozygous, likely pathogenic, *FOXP2* mutation."

Page 933, left column, *2q24.1* section, line 13: This sentence should have been deleted: "Additional phenotype evaluation will be necessary to determine the contributory significance of the CNV, if any, to the *FOXP2*-associated phenotype."

Page 933, right column, *2q31.2* section, line 1: "participant 3" should be "participant 8".

Page 933, right column, Chromosome 6 section, line 1: "participant 11" should be "participant 2".

Page 933, right column, Chromosome 6 section, line 9: "participant 11" should be "participant 2".

Page 934, left column, line 8: This sentence should have been deleted: "As reported next, this participant also had a deletion on chromosome 8 detected by array."

Page 934, left column, Chromosome 8 section, line 2: "Participants 8 and 10" should be "Participants 7 and 1".

Page 934, left column, Chromosome 8 section, line 6: "participant 8" should be "participant 7".

Page 934, left column, Chromosome 9 section, line 1: "participant 9" should be "participant 5".

Page 934, left column, Chromosome 16 section, line 2: "Participant 4" should be "Participant 9".

Page 934, right column, lines 1-2: "participant 2. Participant 2" should be "participant 12. Participant 12"

Page 934, right column, line 6: "participant 2" should be "participant 12".

Table 3 Array comparative genomic hybridization findings for 12 participants with childhood apraxia of speech

Array comparative genomic hybridization (aCGH) findings						Participant number
Chromosome	**Location**	**Size (bp)**	**aCGH finding**	**Genes and loci**	**Reported gene functions and phenotypic associations**	
2	2q31	1,853,226	arr 2q31.1(172,500,884–174,354,110)×1	*DLX1, DLX2*	Transcription factor; craniofacial patterning; forebrain development	3
				ITGA6	Cell surface–mediated signaling	
				RAPGEF HAT, MAP1D, PDK1, AL157450, CGEF2, ZAK, CDCA7, MLK7-AS1	Memory retrieval[21] and spiny synapse remodeling[22]	
2	2q31	182,463	arr 2q31.2(178,467,013–178,649,476)×1	*PDE11A*	Expression restricted to brain; role in regulating brain function; intragenic[45]	8
2	2q24	667,426	arr 2q24.1(158,644,817–159,312,243)×1	*UPP2, CCDC148, PK4P, AK126351*		4
2	2p14	66,812	arr 2p14(65,428,705–65,495,517)×1	*SPRED2*		10
4	4p15.1	91,228	arr 4p15.1(33,734,758–33,825,986)×3	None		11
6	6p12.1	714,847	arr 6p12.1(56,611,129–57,325,976)×3	*DST, BEND6, ZNF451, BAG2, RAB23 PRIM2*	Carpenter syndrome	2
7	7q35	35,598	arr 7q35(146,991,585–147,027,183)×1	*CNTNAP2*	Human *CNTNAP2* expression was enriched in circuits involved in higher cortical functions, including language.[30] The transcription factor FOXP2 (605317) directly regulates expression of *CNTNAP2* by binding to a regulatory sequence in intron 1.	6
8	8q11.23	223,801	arr 8q11.23(54,459,425–54,683,226)×3	*AK056897*		7
8	8q21.13	127,880	arr 8q21.13(83,142,138–83,270,018)×1	None		1
9	9q32	70,554	arr 9q32(114,786,772–114,857,326)×1	*LOC169834, ZFP37*	Brain development	5
13	13q13.3	310,656	arr 13q13.3(36,204,182–36,514,838)×3	*RFXAP, SMAD9, ALG5, EXOSC8, FAM48* (partial involvement)		12
14	14q23.2	119,849	arr 14q23.2(62,065,906–62,185,755)×1	None		12
16	16p11.2	568,305	arr 16p11.2(29,531,556–30,099,861)×1	Known microdeletion syndrome region		12
16	16p13.2	127,866	arr 16p13.2(8,690,828–8,818,694)×1	*ABAT, TMEM186, PMM2*	The ABAT deficiency phenotype includes psychomotor retardation, hypotonia, hyperreflexia, lethargy, refractory seizures, and electroencephalograph abnormalities; 4-aminobutyrate aminotransferase (ABAT) is responsible for catabolism of gamma-aminobutyric acid, an important, mostly inhibitory neurotransmitter in the central nervous system, into succinic semialdehyde.[27]	9
16	16p13.2	237,467	arr 16p13.2(8,725,553–8,963,020)×1	*ABAT, TMEM186, PPM2, CARSHP1, USP7*		6
17	17q23.2	53,144	arr 17q23.2(52,748,147–52,801,291)×1	*MSI2*	Strongly expressed in neuronal precursor cells[46]	11