

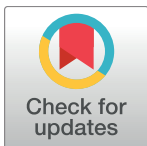
CORRECTION

Correction: Accurate Breakpoint Mapping in Apparently Balanced Translocation Families with Discordant Phenotypes Using Whole Genome Mate-Pair Sequencing

The PLOS ONE Staff

The legend for [Table 1](#) is incorrectly displayed in the third paragraph of the Results section. The publisher apologizes for the error.

The complete [Table 1](#) legend is: Translocation junction and exact breakpoint position as identified by Mate Pair Sequencing (MPS) and Sanger sequencing (SS), respectively, in the affected and non-affected translocation carriers in each family. The number of read-pairs representing each translocation junction, the gene(s) disrupted by each translocation breakpoint as well as insertions/deletions (indels), microhomology and repetitive elements found at the breakpoint sites are indicated. All genomic coordinates are based on the GRCh37/hg19 reference genome assembly. (ID = Intellectual Disability; mat = maternal; bp = base-pair; del. = deletion; dupl. = duplication).



 OPEN ACCESS

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Table 1. Breakpoint mapping and sequencing results for each apparently balanced translocation case included in this study.

Case / phenotype	Translocation junction as estimated by MPS	Junction length	Read-pairs	Translocation breakpoint position as defined by SS	Disrupted gene (s)	Indels (+strand)	Microhomology	Repetitive elements
Family 1 –t(1;7)(p36.1;q22)								
Male with ID, psychomotor delay, epilepsy	chr1:18163342–18163563	222bp	12	chr1:18163344–18163348	—	3bp-AGT del.	T	SINE-MIR-MIRb
	chr7:99019714–99019855	142bp		chr7:99019710–99019714	<i>PTCD1</i> & <i>ATP5J2-PTCD1</i>	3bp-AGA del.	CC	LINE-L1-L1M5
Non-affected mother	chr1:18163366–18163436	71bp	17	chr1:18163344–18163348	—	3bp-AGT del.	T	SINE-MIR-MIRb
	chr7:99019342–99019746	405bp		chr7:99019710–99019714	<i>PTCD1</i> & <i>ATP5J2-PTCD1</i>	3bp-AGA del.	CC	LINE-L1-L1M5
Family 2 –t(7;8)(q32;q24.13)								
Female with ID	chr7:122515289–122515690	402bp	17	chr7:122515671–122515672	<i>CADPS2</i>	—	C	—
	chr8:119865523–119866376	854bp		chr8:119866044–119866050	—	5bp-GTAAA del.	TAA	—
Non-affected sibling	chr7:122514386–122515726	1341bp	20	chr7:122515671–122515672	<i>CADPS2</i>	—	C	—
	chr8:119866031–119866086	56bp		chr8:119866044–119866050	—	5bp-GTAAA del.	TAA	—
Family 3 –t(4;10)(q35;q11.2)								
Female with mild to moderate ID	chr4:189742584–189742790	207bp	15	chr4:189742651–189742656	—	4bp-ATCG del.	T	LINE-L2-L2a
	chr10:43139092–43140045	954bp		chr10:43139266–43139272	—	5bp-CTGGC del.	—	SINE-Alu-AluSc
Non-affected sibling	chr4:189742123–189743225	1103bp	26	chr4:189742651–189742656	—	4bp-ATCG del.	T	LINE-L2-L2a
	chr10:43139186–43139369	184bp		chr10:43139266–43139272	—	5bp-CTGGC del.	—	SINE-Alu-AluSc
Non-affected mother	chr4:189742483–189743387	905bp	25	chr4:189742651–189742656	—	4bp-ATCG del.	T	LINE-L2-L2a
	chr10:43139065–43140359	1295bp		chr10:43139266–43139272	—	5bp-CTGGC del.	—	SINE-Alu-AluSc
Family 4 –t(1;20)(p35.3;q13.3)								
Male with Polysyndactyly, Oral Anomalies	chr1:24738004–24738807	804bp	13	chr1:24738180–24738181	<i>STPG1</i>	—	C	SINE-Alu-AluJr4
	chr20:56177192–56177656	465bp		chr20:56177612–56177613	—	2bp-GA dupl.	—	—
Non-affected mother	chr1:24738108–24738220	113bp	15	chr1:24738180–24738181	<i>STPG1</i>	—	C	SINE-Alu-AluJr4
	chr20:56177454–56178424	971bp		chr20:56177612–56177613	—	2bp-GA dupl.	—	—

Translocation junction and exact breakpoint position as identified by Mate Pair Sequencing (MPS) and Sanger sequencing (SS), respectively, in the affected and non-affected translocation carriers in each family. The number of read-pairs representing each translocation junction, the gene(s) disrupted by each translocation breakpoint as well as insertions/deletions (indels), microhomology and repetitive elements found at the breakpoint sites are indicated. All genomic coordinates are based on the GRCh37/hg19 reference genome assembly. (ID = Intellectual Disability; mat = maternal; bp = base-pair; del. = deletion; dupl. = duplication).

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Reference

1. Aristidou C, Koufaris C, Theodosiou A, Bak M, Mehrjouy MM, Behjati F, et al. (2017) Accurate Break-point Mapping in Apparently Balanced Translocation Families with Discordant Phenotypes Using Whole Genome Mate-Pair Sequencing. PLoS ONE 12(1): e0169935. doi:[10.1371/journal.pone.0169935](https://doi.org/10.1371/journal.pone.0169935) PMID: [28072833](https://pubmed.ncbi.nlm.nih.gov/28072833/)