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CORRIGENDA

Expansion of mutation spectrum, determination of mutation cluster regions and predictive structural classification of SPAST mutations in hereditary spastic paraplegia

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Since the publication of the above paper, the authors have identified major errors in Table 1. The amended table is reproduced below.
The authors would like to apologise for this mistake.

Table 1 List of mutations identified in the SPAST gene in our HSP cohort

No.	Exon/ intron	Family no.	Type of mutation	cDNA	Protein	F/S	Onset of phenotype	Pure/complex	Reference/ novel
1	Ex 1	24227	Nonsense	c.373G>T	p.Glu125Term	F	>35	Pure	11
2	Ex 2	25942	Nonsense	c.499C>T	p.Gln167Term	S	>35	Pure	Novel
3	Ex 3	24283	Insertion	c.549_550insT	p.Asn184Term	F	<35	Pure	Novel
4	Ex 5	21987	Deletion	c.692delC	p.Ala231Valfs Term239	?	?	?	Novel
5	Ex 5	19583	Deletion	c.839_840delAG	p.Gln280Argfs Term289	F	<35	Pure	12
6	Ex 5	28146	Splice	c.870 G>A	Unknown	?	?	?	Novel
7	Int 5	25961	Splice	c.870+1G>T	Unknown	?	?	?	Novel
8	Ex 6	24295	Insertion	c.981_982insAT	p.Ile328IlefsTerm329	?	?	?	Novel
9	Ex 7	21937	Missense	c.1067A>G	p.Glu356Gly	?	<10	?	6
10	Ex 7	21935	Missense	c.1081C>T	p.Pro361Ser	F	<35	Complex (cardiomyopathy)	Novel
11	Int 7	21971	Splice/deletion	c.1099-3_1099-1delTAG	Unknown	F	>35	Pure	Novel
12	Ex 8	21977	Deletion	c.1101_1103delGTT	p.Leu367del	F	>35	Pure	Novel
13	Ex 8	25902	Deletion	c.1101_1103delGTT	p.Leu367del	F	<10	Pure	Novel (2)
14	Ex 8	24218	Insertion	c.1115_1116insG	p.Arg372Argfs Term393	?	?	?	Novel
15	Ex 8	25945	Missense	c.1121C>G	p.Pro374Arg	F	<10	?	Novel
16	Ex 8	25946	Missense	c.1154G>A	p.Gly385Glu	S	>35	Pure	Novel
17	Int 8	24292	Splice	c.1174-1G>T	Unknown	F	<35	Pure	Novel
18	Ex 9	21938	Missense	c.1196C>T	p.Ser399Leu	F	?	?	34
19	Ex 9	24224	Missense	c.1196C>T	p.Ser399Leu	?	?	?	34
20	Ex 9	19576	Deletion	c.1202delC	p.Ala401GlufsTerm406	?	?	?	Novel
21	Ex 9	24286	Deletion	c.1215_1219delTATAA	p.Asn405LysfsTerm440	S	>35	Pure	8
22	Ex 9	24268	Missense	c.1216A>G	p.Ile406Val	F	<35	Pure	35
23	Ex 9	21901	Deletion	c.1245delC	p.Tyr415Term	S	>35	Pure	Novel
24	Int 9	24248	Splice	c.1245+1G>T	Unknown	F	<10	Pure	36
25	Ex 10	24231	Missense	c.1250G>A	p.Gly417Glu	F	<35	Complicated (cognitive impairment)	Novel
26	Ex 10	19582	Missense	c.1280T>G	p.Phe427Cys	F	>35	Pure	Novel
27	Ex 10	24233	Deletion	c.1281delT	p.Phe427Leufs Term437	?	?	?	37
28	Ex 10	24212	Nonsense	c.1291C>T	p.Arg431Term	F	>35	Pure	8
29	Ex 11	19593	Missense	c.1339T>G	p.Leu447Val	F	>35	Pure	Novel
30	Ex 11	21214	Missense	c.1378.C>T	p.Arg460Cys	F	>35	Complicated (polyneuropathy)	38
31	Ex 11	24222	Missense	c.1378C>T	p.Arg460Cys	?	<10	?	
32	Ex 11	24285	Missense	c.1378C>T	p.Arg460Cys	F	<35	Pure	38
33	Ex 11	24228	Missense	c.1379G>A	p.Arg460His	F	<35	Pure	Novel

Table 1 (*Continued*)

No.	Exon/ intron	Family no.	Type of mutation	cDNA	Protein	F/S	Onset of phenotype	Pure/complex	Reference/ novel
34	Ex 12	25910	Nonsense	c.1417C>T	p.Gln473Term	F	<10	Autonomic nervous system	Novel
35	Ex 12	24255	Insertion	c.1462_1463insTA	p.Arg488IlefsTerm530	F	>35	Pure	Novel
36	Ex 13	25923	Missense	c.1495C>T	p.Arg499Cys	F	<10	Pure	7
37	Ex 13	21929	Missense	c.1496G>A	p.Arg499His	F	<10	Trunk ataxia	39
38	Ex 13	19598	Missense	c.1507C>T	p.Arg503Trp	?	?	?	14
39	Ex 14	21900	Missense	c.1540A>G	p.Arg514Gly	F	?	?	Novel
40	Ex 14	21985	Missense	c.1540A>G	p.Arg514Gly	F	>35	?	Novel (2)
41	Ex 15	24230	Insertion	c.1649_1650insCCTAAC	p.550_551insLeuThr	F	<35	Pure	Novel
42	Ex 15	19591	Missense	c.1664A>G	p.Asp555Gly	F	<35	Pure	Novel
43	Ex 15	25941	Missense	c.1670C>T	p.Ala557Val	F	<35	Pure	Novel
44	Ex 15	21920	Nonsense	c.1684C>T	p.Arg562Term	?	?	?	8
45	Ex 15	21967	Nonsense	c.1684C>T	p.Arg562Term	?	>35	Pure	8
46	Ex 15	21974	Nonsense	c.1684C>T	p.Arg562Term	F	>35	Pure	8
47	Ex 15	24201	Nonsense	c.1684C>T	p.Arg562Term	F	<35	Pure	8
48	Ex 15	25912	Nonsense	c.1684C>T	p.Arg562Term	F	>35	Pure	8
49	Ex 16	19594	Nonsense	c.1702C>T	p.Gln568Term	?	?	?	Novel
50	Ex 17	19597	Missense	c.1821G>C	p.Trp607Cys	?	?	?	13
51	Ex 17	25936	Missense	c.1821G>C	p.Trp607Cys	F	<35	Pure	13
52	Ex 1-Ex 3	24278	Exon deletion	c.1-?_682+?del	Unknown	?	?	?	19
53	Ex 2-Ex 9	21976	Exon deletion	c.416-?_1493+?del	Unknown	F	<35	Pure	Novel
54	Ex 8	21968	Exon deletion	c.1099-?_1173+?del	Unknown	F	<10	Pure	Novel
55	Ex 9–Ex 17	21940	Exon deletion	c.1174-?_1851+?del	Unknown	F	>35	Pure	Novel
56	Ex 2–Ex16	24270	Exon deletion	c.416-?_1728+?del	Unknown	F	>35	Pure	40
57	Ex 17	24281	Exon deletion	c.1729-?_18511?del	Unknown	?	?	?	19

F, familial; S, sporadic.

Array-CGH fine mapping of minor and cryptic HR-CGH detected genomic imbalances in 80 out of 590 patients with abnormal development

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Since the publication of the above paper, the authors have identified one error regarding Table 1, row No 13: 'dim(5)(q35.1qter)' should be changed to 'enh(5)(q35.1qter)'.

The authors would like to apologise for this mistake.