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CORRIGENDUM

Therapeutic exon skipping for dysferlinopathies?

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Correction to: *European Journal of Human Genetics* advance online publication, 10 February 2010; doi:10.1038/ejhg.2010.4

The authors of this paper apologise for having to report an error in Figure 3 and Table 2. The corrected figure and table are presented below.

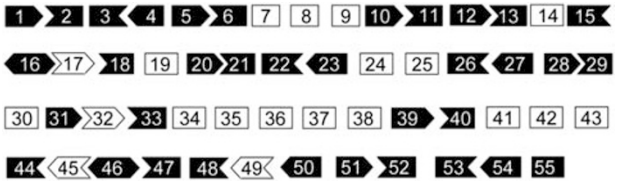

Figure 3

Moreover, due to a regrettable mix-up in the ordering procedures, the sequences of h32DYSF1 and h34DYSF2 have been swapped (Table 2) – h32DYSF1 targets exon 34 and h34DYSF2 targets exon 32. We refer to our correspondence with Levy *et al* in this issue.

Table 2 Properties of dysferlin exons

Exon	Domain	In frame	Combination[a]	Remarks	Applicability[b]	Priority[c]
1	C2-1	no	no		0%	NA
2	C2-1	no	2, 3, 4 and 5		1.8%	9
3	C2-1	no	3 and 4		2.1%	8
4	C2-1	no	3 and 4		1.3%	8
5	C2-1	no	5 and 6		4.2%	8
6	None	no	5 and 6		6.1%	8
7	C2-2	yes			1.6%	7
8	C2-2	yes			2.9%	7
9	C2-2	yes			1.8%	7
10	C2-2 & FerL	no	10 and 11		1.6%	8
11	C2-2 & FerL	no	10 and 11		0.5%	8
12	C2-3	no	12 and 13		16.6%	8
13	C2-3	no	12 and 13		4.5%	8
14	C2-3	yes	14		0.3%	7
15	C2-3	no	15, 16, 17 and 18		2.6%	9
16	C2-3	no	15, 16, 17 and 18		1.1%	9
				No mutations reported		1
17	C2-3	yes		Alternatively spliced	0%	
18	none	no	18, 19 and 20		4.0%	3
19	none	yes		Skip pathogenic	5.8%	NA
20	none	no	20 and 21		5.3%	2
21	none	no	20 and 21		1.8%	2
22	FerA	no	22 and 23		0.8%	6
23	FerA & FerB	no	22 and 23		3.2%	6
24	FerB	yes		Skip possibly pathogenic	4.5%	5
25	FerB	yes		Skip pathogenic	3.7%	NA
26	Dysf-N-1	no	26 and 27		1.8%	6
27	Dysf-N-2	no	26 and 27		6.6%	6
28	Dysf-N-2	no	28 and 29		5.3%	6
29	Dysf-C-1	no	28 and 29		6.6%	6
30	Dysf-C-2	yes		Skip possibly pathogenic	8.4%	5
31	None	31, 32, 33	no		3.7%	3
32	C2-4	yes		Skip does not disturb function	4.0%	1
33	C2-4	31, 32, 33	no		2.4%	3
34	C2-4	yes		Skip possibly pathogenic	4.5%	4
35	None	yes		No mutations reported	0%	1
36	None	yes			0.8%	1
37	C2-5	yes		Skip possibly pathogenic	3.7%	7
38	C2-5	yes			3.7%	7
39	C2-5	no	39 and 40		3.2%	8
40	none	no	39 and 40		0.3%	8
41	none	yes		Skip possibly pathogenic	3.4%	4
42	none	yes			0.8%	1
43	C2-6	yes			4.2%	7
44	C2-6	no	44, 45, 46 and 47		11.9%	9
45	C2-6	yes		Skip pathogenic in mouse	5.3%	NA
46	none	no	46, 47 and 48		2.4%	9
47	none	no	46, 47 and 48		2.1%	9
48	C2-7	no	46, 47 and 48		1.1%	9
49	C2-7	yes		Skip pathogenic	4.7%	NA
50	C2-7	no	50, 51, 52 and 53		3.7%	9
51	C2-7	no	51 and 52		5.8%	8
52	C2-7	no	51 and 52		3.7%	8
53	none	no	53 and 54		5.0%	8
54	TMB	no	53 and 54		3.4%	8
55	TMB	no	not applicable		1.6%	NA

[a]Indicates which combination of exons would be in-frame.
[b]The applicability is based on the mutations reported in the DYSF database (http://www.dmd.nl). As most patients have heterozygous mutations, the total applicability is >100%.
[c]Indicates which exons make good targets on a scale of 1–9, where 1 is optimal and 9 is least optimal; NA stands for unsuitable exons.