

CORRIGENDUM

Micro-exons of the cardiac myosin binding protein C gene: flanking introns contain a disproportionately large number of hypertrophic cardiomyopathy mutations

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Since the above publication, the authors have noticed wrong numbers in column 'ASSP' of Table 2. The correct table is shown below.

The authors would like to apologise for this mistake.

Table 2 Splice site predictions for exons 10, 11 and 14 and flanking aberrant splice sites

Location	Mutation	Splice site	Sequence ^a	S&S score	ASSP	NetGene2
Exon 10		Authentic 3'ss	ctgctgtggcccag AGA gtaaga	78.7	2.166	NI
		Authentic 5'ss	ctgctgtggcccag AGA gtaaga	74.1	8.532	0.45
	c.906-1G>C	Mutated 3'ss	ctgctgtggcccac AGA gtaaga	62.6	NI	NI
		Cryptic 3'ss	ctgctgtggcccacag A gtaaga	81	5.095	NI
	c.906-36G>A	Mutated 5'ss	ctgctgtggcccac AGA gtaaga	74.1	9.172	0.46
		De Novo 3'ss	tccctctccccag CCCCTCC	86	9.923	0.95
Exon 11		Authentic 3'ss	cccctggagcag CAGTTT	70.6	0.241	NI
		Authentic 5'ss	TCCGGACCCCGAG gtgagt	96.7	15.196	0.82
Exon 14		Authentic 3'ss	cttctgttctacag CAA gtaagt	89.6	9.936	NI
		Authentic 5'ss	cttctgttctacag CAA gtaagt	87.6	13.567	0.86
	c.1224-2A>G	Mutated 3'ss	cttctgttctacgg CAA gtaagt	54.8	-1.026	NI
		Mutated 5'ss	cttctgttctacgg CAA gtaagt	87.6	13.136	0.93
	c.1224-19G>A	De Novo 3'ss	gaacctcaacag CCCCTTC	70.8	-1.438	NI

^aMutated nucleotide positions are underlined in sequence, calculated values are for splice sites in bold.

ASSP values in italics are below default cutoff values, 3'-ss = 2.2 and 5'-ss = 4.5. NI: Not identified.

Scores are given for the authentic splice site (ss) and the effect the mutation has on the particular site (mutated splice site). The value is also given for the cryptic splice site that can then be activated. The *de novo* splice site scores are given for comparison to the competing authentic splice site.