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Short report

Genetic diagnosis of Duchenne and Becker muscular dystrophy through mRNA analysis: new splicing events

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ABSTRACT

Background Up to 7% of patients with Duchenne muscular dystrophy (DMD) or Becker muscular dystrophy (BMD) remain genetically undiagnosed after routine genetic testing. These patients are thought to carry deep intronic variants, structural variants or splicing alterations not detected through multiplex ligation-dependent probe amplification or exome sequencing.

Methods RNA was extracted from seven muscle biopsy samples of patients with genetically undiagnosed DMD/BMD after routine genetic diagnosis. RT-PCR of the *DMD* gene was performed to detect the presence of alternative transcripts. Droplet digital PCR and whole-genome sequencing were also performed in some patients.

Results We identified an alteration in the mRNA level in all the patients. We detected three pseudoexons in *DMD* caused by deep intronic variants, two of them not previously reported. We also identified a chromosomal rearrangement between Xp21.2 and 8p22. Furthermore, we detected three exon skipping events with unclear pathogenicity.

Conclusion These findings indicate that mRNA analysis of the *DMD* gene is a valuable tool to reach a precise genetic diagnosis in patients with a clinical and anatomopathological suspicion of dystrophinopathy that remain genetically undiagnosed after routine genetic testing.

variants usually give place to a partially functional protein and a BMD phenotype.³

Currently, the diagnostic algorithm consists of multiplex ligation-dependent probe amplification (MLPA) followed by exome sequencing (ES) in genomic DNA (gDNA). Exonic deletions and duplications are the most prevalent pathogenic variants (65%–75% of patients), and subsequently, small disease-causing variants are detected in 20%–25% patients.^{4–6} With this diagnostic approach, up to 7% of patients with dystrophinopathy remain without a precise genetic diagnosis.^{7,8} As more than one-third of disease-causing variants in the Human Genome Mutation Database are estimated to perturb pre-mRNA splicing,⁹ patients with undiagnosed DMD/BMD are thought to carry complex structural variants (SVs) or splicing alterations in the *DMD* gene. Nonetheless, pathogenic variants in non-coding regions potentially disrupting canonical splicing of *DMD* are missed in routine diagnosis. Identifying and characterising splicing variants in the *DMD* gene are essential to obtain a precise genetic diagnosis of these patients, to be eligible to mutation-specific therapies, and to offer families appropriate genetic and reproductive counselling.

The aim of this study was to evaluate the utility of mRNA analysis of the *DMD* gene in patients with dystrophinopathy who remained genetically undiagnosed after MLPA and ES. Through *DMD* mRNA analysis in seven patients, we detected three pseudoexons (PEs) in the *DMD* gene, one chromosomal rearrangement between Xp21.2 and 8p22, and three exon skipping events with unclear pathogenicity.

METHODOLOGY

Patients

Patients were recruited from several hospitals in Spain, and they were included when (1) DMD and BMD were suspected in the clinical examination, and it was supported by alterations in dystrophin immunohistochemistry and/or western blot; and (2) MLPA of the *DMD* gene (P034 and P035 Sauce Kit; MRC-Holland, Amsterdam, Netherlands) and ES had negative results. In total, cDNA analysis was performed on seven patients (table 1).

INTRODUCTION

Duchenne muscular dystrophy (DMD, OMIM #310200) and Becker muscular dystrophy (BMD, OMIM #300376) are X-linked recessive disorders caused by pathogenic variants in the *DMD* gene (OMIM *300377), which encodes the dystrophin protein.¹ DMD is the most severe form of the disease and the most common neuromuscular disorder in childhood, affecting 1 in 3500 live male births.² Patients with BMD present a less severe phenotype with a more progressive and variable disease course. Disease severity can be explained by the reading frame rule in 90% of patients: frame-shift variants in the *DMD* gene result in a premature termination codon (PTC) and a non-functional dystrophin leading to DMD. In contrast, in-frame



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Table 1 Relevant clinical and genetic findings of patients

Patient	Phenotype	Onset age*	Relevant clinical findings	Loss of ambulation*	Muscle biopsy findings†	Genomic variant‡	mRNA alteration‡
P1	BMD	Early childhood	Clumsy walking and muscle weakness	No (middle childhood)	Myopathic changes with partial deficiency of DYS-3 staining	g.32584731A>G	PE15
P2	BMD	Early adolescence	Muscle weakness	Yes (adult)	Numerous atrophic and hypertrophic fibres with size variability and internal nuclei Overexpression of utrophin and almost absent expression of DYS3	g.32371864A>C	PE37
P3	BMD	Middle childhood	HyperCKemia	No (early adolescence)	Conserved skeletal muscle architecture, with occasional internalised nuclei Reduction of DYS-2 staining in WB	–	Exon nine skipping
P4	DMD	Early childhood	Difficulties in climbing stairs, difficulties with fine and gross motor skills, mild pseudohypertrophy of gastrocnemius, biceps, triceps and paraspinal muscles	No (early childhood)	Reduction of DYS-1 expression and absence of DYS-2 and DYS-3 expression Reduction of sarcoglycan expression	g.31279418T>C	PE62
P5	BMD	Adult	HyperCKemia, calf hypertrophy, muscle cramps and myalgia after exercise	No (adult)	Mild dystrophic pattern with alterations in dystrophin staining	–	Exon 71 and 78 skipping
P6	BMD/DMD	Early childhood	Down syndrome, with frequent falls and proximal muscle weakness	Yes (early adolescence)	Dystrophic pattern with reduced DYS-2 and DYS-3 staining Partial alteration of dystrophin WB	g.32873008_32873015delins (CCA;chr8:g.16346710_16422443)	Cryptic exon (chr8)
P7	BMD	Middle childhood	HyperCKemia and rhabdomyolysis	No (middle childhood)	Mild dystrophic pattern with reduced DYS-2 and DYS-3 staining Almost absence of DYS-2 in WB	–	Exon 71 skipping

* Early childhood, 2–5 years; middle childhood, 6–11 years; early adolescence, 12–18 years; late adolescence, 19–21 years.
† Monoclonal antibodies detecting the rod domain (DYS1), C-terminal domain (DYS2) and N-terminal (DYS3) domain of dystrophin.
‡ Variant description based on NC_000023.11, NC_000008.10 and NM_004006.2.
BMD, Becker muscular dystrophy; CK, creatine kinase; DMD, Duchenne muscular dystrophy; PE, Pseudoxon; WB, western blot.

Amplification of *DMD* cDNA sequence

RNA was extracted from muscle biopsies using the Animal Tissue RNA Purification Kit (Norgen Biotek, Ontario, Canada). RNA was retrotranscribed using Oligo(dT)20 Primer (Invitrogen, California, USA). The whole mRNA *DMD* was sequenced with overlapping primer pairs (online supplemental table 1). PCR products were sequenced with BigDye Terminator V.1.1 Cycle Sequencing Kit (ThermoFisher) and analysed in an Applied Biosystems 3500 Dx Series Genetic Analyzer (ThermoFisher). Splicing in silico analyses were performed with Alamut Visual software V.2.6.1. Variants have been submitted to the ‘Global Variome shared LOVD’ (<https://databases.lovd.nl/shared/references/DOI:10.1136/jmg-2022-108828>).

gDNA analysis and whole-genome sequencing (WGS)

gDNA was extracted from total peripheral blood using QIAasympy SP (Qiagen). The presence of deep intronic variants (in patient 1 (P1), patient 2 (P2) and patient 4 (P4)) and intronic variants near exon boundaries (in patient 3 (P3), patient 5 (P5) and patient 7 (P7)) was evaluated through Sanger sequencing.

WGS was performed in P6. One microgram of fragmented gDNA was used for library preparation with Truseq DNA PCR-Free (Illumina, California, USA). Sequencing was performed in a NovaSeq 6000 (Illumina). Manta V.1.6.0 was used to detect SVs and junction breakpoints.¹⁰ SVs passing the default filtering were inspected on IGV (Integrative Genomics Viewer). Breakpoints were confirmed by Sanger sequencing.

Droplet digital PCR (ddPCR)

Mini Affinity Plus qPCR probes (Integrated DNA Technologies, Iowa, USA) were designed to quantify exon 9 and 71 skipping (online supplemental table 3). ddPCR reactions were performed with 10 ng of cDNA and ddPCR Supermix for Probes (no dUTP (deoxyuridine Triphosphate)) (Bio-Rad Laboratories, California, USA) following manufacturer protocol. Droplets were generated

with Droplet Generation Oil for Probes (Bio-Rad) in the QX200 Droplet Generator (Bio-Rad). Thermocycling conditions were as follows (ramping rate 2°C/s): 95°C 10 min, 40 cycles of 94°C for 30 s and 58°C for 1 min, and 98°C for 10 min. Droplets were loaded in the QX200 Droplet Reader (Bio-Rad). For each sample, four replicates were performed and a non-template control was included in each assay. The data were analysed with the QX Manager Software Standard Edition V.1.2 (Bio-Rad). Mann-Whitney test was performed. Only wells with more than 10 000 droplet reads were considered.

RESULTS

Deep intronic variants and PE inclusion

We identified the inclusion of PEs in dystrophin mRNA in three patients (P1, P2 and P4) due to deep intronic variants (table 1).

In P1, we detected an inclusion of 214 bp from intron 15 (from c.1813–947 to c.1813–734) into the *DMD* transcript (PE15) (figure 1A). We detected the deep intronic variant g.32584731A>G (c.1813–733A>G) in intron 15, classified as a ‘variant of uncertain significance’ (VUS) following the American College of Medical Genetics guidelines.¹¹ This variant, not present in human genetic variation databases, creates a new donor splice site (SS) in intron 15 near a cryptic acceptor SS (figure 1B and online supplemental table 2). The deep intronic variant c.1813–733A>G results in the disruption of the reading frame of *DMD* transcripts (p.Val605Ilefs*33), probably targeted by nonsense-mediated decay.

In P2, we observed the presence of an in-frame PE between exons 37 and 38 (PE37) that incorporated a PTC (p.Ala-1776Valfs*9) (figure 1C). gDNA analysis revealed the intronic variant g.32371864A>C (c.5326–5219T>G), not previously reported in databases, that results in the retention of 48 bp from intron 37. This variant creates a new cryptic acceptor SS and activates a pre-existing donor SS (figure 1D, (online supplemental table 2)).

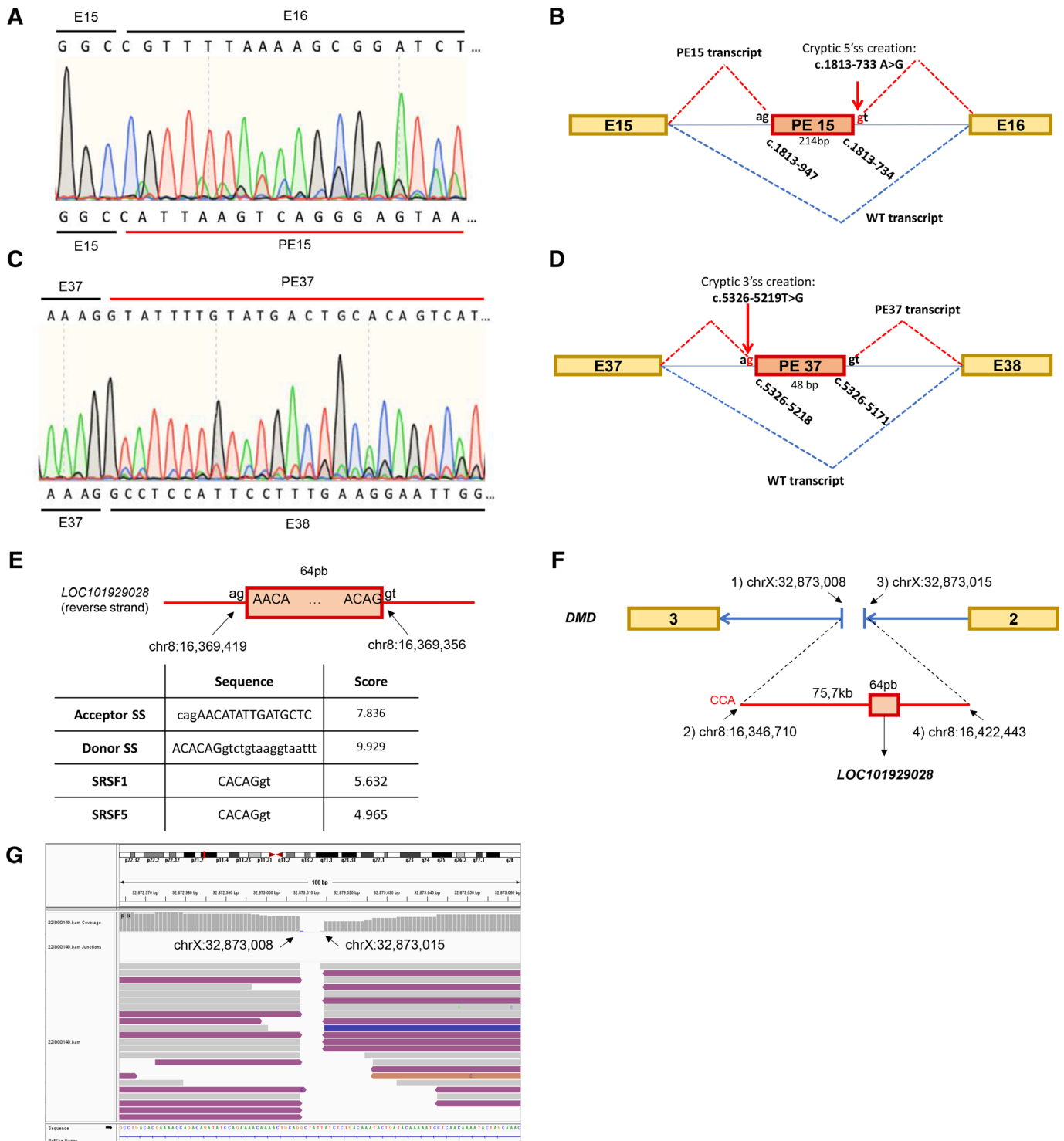


Figure 1 Characterisation of two novel PEs and one chromosomal rearrangement between *DMD* and 8p22. (A) Sanger sequencing in P1 showed two different transcripts: WT transcript and aberrant transcript with PE15 between exons 15 and 16, from c.1813–947 to c.1813–734. (B) Schematic representation of canonical splicing (in blue) and alternative splicing (in red) taking place in P1. At the gDNA level, it was detected that the variant g.32584731A>G (c.1813–733A>G) creates a novel donor SS. (C) mRNA analysis in P2 revealed residual levels of WT transcript and an alternative transcript with an inclusion of 48 bp of intron 37 (PE37). (D) Schematic view of canonical (in blue) and alternative (in red) splicing due to the presence of the hemizygous variant g.32371864A>C (c.5326–5219T>G), which creates a new acceptor SS and results in the inclusion of the in-frame PE37. (E) Splicing predictor scores of the cryptic exon from the *LOC101929028* locus (8p22) detected in the mature *DMD* transcript in p6. Acceptor, donor SSs and binding sites of SR proteins were predicted by ESEfinder V.3.0. (F) Schematic view of the translocation of 75.7 kb from chromosome 8 (chr8: 16 346 710–16 422 443) to intron 2 of the *DMD* gene involving a 6 bp deletion in the breakpoint junctions, and an insertion of three nucleotides ‘CCA’. (G) IGV screenshot of P6 WGS in the junction breakpoint. The upper panel displays the depth coverage, showing the deletion of 6 bp in *DMD* intron 2 (chrX:32,873,008–32,873,015). The bottom panel shows the aligned reads on chromosome X (in grey) and the chimeric reads aligning both chromosome X and chromosome 8 (in purple). PE, pseudoexon; SR, serine-rich; SS, splice site; WT, wild type.

In P4, besides residual levels of full-length dystrophin, we detected a PE of 58 bp between exons 62 and 63 (PE62). The deep intronic variant g.31279418T>C (c.9225–285A>G) was identified, inherited from the patient's mother. PE62 had already been described in patients with BMD.¹² The pathogenic deep intronic variant c.9225–285A>G, located in position+5 from the cryptic donor SS, increases complementarity between the pre-mRNA and U1snRNA, and thus increases the splicing efficiency of the cryptic donor SS.¹²

Chromosomal rearrangement

P6 cDNA sequencing revealed a 64 bp cryptic exon (p.Phe32Asnfs*5) between exons 2 and 5 apart from the wild-type dystrophin transcript. BLAT (BLAST-like alignment tool) analysis of the cryptic exon resulted in 100% identity with *LOC101929028* located in 8p22 (chr8:16 369 356–16 369 419). The flanking region of 64 bp inserted in the mRNA of dystrophin probably confers an exon-like profile with an acceptor, donor SS and exonic splicing enhancers that can be recognised by the spliceosome complex (figure 1E), suggesting the presence of a chromosomal rearrangement between chromosome 8 and *DMD*. WGS was performed in P6 to determine the exact breakpoints of the rearrangement. We detected an insertion of chromosome 8 (chr8: 16 346 710–16 422 443) in intron 2 of the *DMD*, and a 6 bp deletion in *DMD* intron 2 (chrX:32 873 009–32 873 014) (figure 1F). IGV showed the junction breakpoints surrounded by chimeric reads aligning both *DMD* and chromosome 8 (figure 1G). The insertion of 75.7 kb encompassed the *LOC101929028* detected in the mRNA analysis and did not contain any protein-coding gene. In-depth analysis of the flanking sequences of the breakpoint junctions revealed the presence of LINE elements in 5' and 3' junctions.

Alternative exon skipping events with unclear pathogenicity

In three patients with BMD (patient 3 (P3), P5 and P7) (table 1), no other alteration was detected in dystrophin mRNA apart from transcripts with exon skipping events, together with full-length transcript. In P3, a patient with BMD manifesting only hyperCKemia, we detected exon 9 skipping. In P5, who had mild BMD, exon 71 and 78 skipping was revealed. Finally, in P7, we detected exon 71 skipping. No intronic variants were found near canonical SS that could explain the induction of these exon skipping events. Exon 9 and 71 *DMD* skipping isoforms were quantified by ddPCR in P3 and P7. Both exon skipping events were present in slightly higher proportion in patients than in control samples (exon 9 skipping: 0.97%±0.2 in controls and 11.15%±0.3 in P3; exon 71 skipping: 1.34%±0.16 in controls and 16.45%±0.9 in P7) (online supplemental figure 1).

DISCUSSION

Here we show the relevance of performing an mRNA-based analysis of the *DMD* gene to establish a definite genetic diagnosis in patients with undiagnosed dystrophinopathy after MLPA and ES. Up to 7% of the patients remain genetically undiagnosed after routine genetic testing.^{7,8} Nonetheless, having a precise genetic diagnosis is essential for these patients to be eligible for mutation-specific therapies and for their relatives to receive an accurate genetic and reproductive counselling. Here we studied seven patients with clinical suspicion of DMD/BMD but no precise genetic diagnosis after clinical genetic testing (table 1). We detected a transcriptional alteration in the *DMD* in all patients and established a final genetic diagnosis in four of the seven patients. Our

findings indicate that variants that alter *DMD* splicing, such as deep intronic variants and SVs, are an important cause of DMD/BMD in patients with undiagnosed dystrophinopathy.

The implementation of high-throughput technologies in clinical testing has enabled a faster and a more efficient exploration of the human genome. As a result, invasive procedures such as muscle biopsy tend to be avoided. However, this procedure remains an essential tool in the differential diagnosis of several neuromuscular disorders. If in the first approach we had performed WGS instead of mRNA sequencing of *DMD*, we would not have been able to interpret and validate some of the findings responsible for the pathology in our cohort. For instance, through WGS, we would have detected two novel deep intronic variants in P1 and P2 (figure 1A–D), but we would not have been able to assess their pathogenicity. Computational algorithms for predicting alternative splicing are usually less reliable for deep intronic variants than for variants in canonical SSs.¹³ In these cases, performing an RNA-based analysis is essential to assess the impact of deep intronic variants in the canonical splicing of the *DMD* gene and to reclassify intronic variants previously classified as VUS.

The *DMD* is a complex gene for the spliceosome machinery due to its large protein-coding sequence and intronic regions. In muscle tissue, few alternative splicing events are observed in comparison with other tissues, as a tight splicing regulation is needed in the muscle tissue to maintain dystrophin functionality.^{14,15} In our cohort, we detected three exon skipping events with unclear pathogenicity that commonly occur in non-muscle tissues (exon 9 skipping in P3, exon 71 skipping in P5 and P7, and exon 78 skipping in P5).^{16,17} P3, P5 and P7 present mild forms of BMD with hyperCKemia, muscle cramps or rhabdomyolysis (table 1). Similar works have also reported exon skipping events in patients with BMD with no other genomic alteration.^{18,19} However, further analyses in a larger patient cohort will be needed to clarify the role of these exon skipping events.

In summary, after evaluating splicing alterations in the *DMD* gene through cDNA sequencing, we found a transcriptional alteration in all patients who remained undiagnosed after clinical genetic testing and established a precise diagnosis in four of the patients. Recently, RNA sequencing (RNA-seq) is being considered as a promising diagnostic approach in undiagnosed patients after ES. It is estimated that RNA-seq increases the genetic diagnostic rate in Mendelian disorders by up to 35%.²⁰ One of the main advantages of this approach is the ability to evaluate not only alternative splicing events but also transcript isoform abundance, monoallelic expression and differential gene expression in the targeted tissue. However, to detect the presence of SVs, RNA-seq can only detect those that alter canonical splicing, such as the insertion identified in P6 (figure 1E–G). SVs that do not have a direct effect in RNA processing would have been missed through an RNA-based analysis. Hence, an integrated approach with transcriptomics and WGS can help to achieve a precise genetic diagnosis in patients with dystrophinopathy and may allow them the accessibility to mutation-specific therapies and genetic and reproductive counselling.

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Supplementary Table 1. Primers for cDNA sequencing of the protein-coding region of the *DMD* gene.

Primer Pair	Sequence (5' -> 3')	Exons ¹	Amplicon length (bp)
1	GGAGGCAATTACCTTCGGAGA CATTCAAAGCCAGGCCATCA	5'UTR-6	681
2	CTGCGGGTTTTGCAGAACAAAT TAAGCAGCCTGTGTGTAGGC	4-9	677
3	GTTGCCAAGGCCACCTAAAG GAGGCTCTTCCTCCATTTTCCT	8-12	677
4	GGGAAGTAAGCTGATTGGAACA ATGCTTCGGTCTTCTGGGTC	11-16	722
5	CCTTCTCAAATGGCAACGTCT AGCTGATCTGCTGGCATCTT	14-19	682
6	AAGCTGTGTTGCAGAGTCCT CATGGTCTCCTGATAGCGCA	18-22	629
7	AAAATCCAACCCACCACCC TTCTGAATCCCCAAGGGCAG	20-24	687
8	AAGCGCCCTCTGAAATTAGC ACAGGTGGAGCTTGAGCTATG	23-27	667
9	TGCACGAATGGATGACACAAG ATTTGAGCTGCGTCCACCTT	26-30	712
10	ACAGATGGCGGAGTCATGGA TCCTTTCGCATCTTACGGGAC	29-34	746
11	ACAGGAAGTAGTACAGTCACAGC AGTCCACCTTTGGGCGTATG	32-37	716
12	TCACCTCCCGAGCAGAAGAG AGGAGATCATCAGCCTGCCT	35-40	682
13	CAGATGAGAGAAAGCGAGAGG TGCAATGCTGCTGTCTTCTTG	39-43	676
14	CACTCATGTCTCACAAGCCC GCTGCTCTTTCCAGGTTCAAG	42-46	722
15	GGAAGCCTGAATCTGCGGT GGTTTACCGCCTTCCACTCA	45-50	688
16	CCAACCAAACCAAGAAGGACC TTCAACTGTTGCCTCCGGTT	48-53	663
17	CGTCCCAGTTGGAAGAACT GGCTGTTTTTCATCCAGGTTGT	52-56	709
18	TTCCCCCTGGACCTGGAAAA GCGGAGTGCAGGTTCAATTT	55-59	689

19	CTGACAGAGCAGCCTTTGGA GGATGGTCCCAGCAAGTTGT	58-63	641
20	CAGCACTCTGGAAGACCTGA GCTCAATGTTACTGCCCCCA	60-67	740
21	ATGTGTCTGAACTGGCTGCT CCCCCTCTAAGACAGTCTGC	65-70	682
22	GGTGAAGTTGCATCCTTTGG TTCCATTTCTGCTAGCCTGC	67-73	601
23	ATTATGACATCTGCCAAGC GTTCTGTGCTGCTGCTTTA	69-75	600
24	GATGATGAACATTTGTTAATCCAG AAAACCATGCGGGAATCA	74-3'UTR	782
25	ATCACGCAACTGCTGCTTTG TTCTTTTGGGGAGGTGGTGG	15-16	565
26	TACGGTGACCACAAGGGAAC GGGGTGGTGGGTTGGATTTT	18-19	522
27	ATACGCCCAAAGGTGGACTC CCTCAGCTTGCCTACGCACT	39-40	624
28	AGGTCCCATTTGGAAGCCAG AGGCGCAATTTCTCCTCGAA	58-59	573

Reference sequence: NM_004006.2

Supplementary Table 2. Description of the novel deep intronic pathogenic variants detected in the *DMD* gene.

PE	Sequence [*]	Pathogenic variant and protein effect [†]	RNA change	Size (bp)	Acceptor score [^]	Donor score [^]
PE15	tacagATTAAGTCAGGGAGTAATGTTTCAGTACC CAGGAATTGAATTTGTCTGTGTATCAGGCAA AGTTACTGAGTCAAGTAAAAGAAAACTGCC CTGATTTACTGATTTACATAAACCACTTATT CCTTTCAAATCAACCAAAGGGAGTTTGTAC CCTCCACAGCTCACAGGAACTTTGGAAATAT AAATGGTATAAAAATTGCTTCATAAGACAC(a> g)taag	g.32584731A>G p.Val605Ilefs*33	r.1812_1813ins1813-947_1813-734	214	= 91.95	— ⇒ 88.99
PE37	tata(t<g)GTATTTTGTATGACTGCACAGTCATG CTAAAGCTCTTAAATGAAAAGgtaag	g.32371864A>C p.Ala1776Valfs*9	r.5325_5326ins5326-5218_5326-5171	48	— ⇒ 83.02	= 99.04

BMD: Becker muscular dystrophy; PE: pseudoexon; PTC: Premature Termination Codon

^{*}The pseudoexon sequence is represented in uppercase letter and the flanking intronic sequence in lowercase letter.

[†] Variant description based on NM_004006.2 and NC_000023.11.

[^] Splicing scores calculated with Human Splicing Finder (HSF).

Supplementary Table 3. Primers and Custom Mini Affinity Plus qPCR probes (Integrated DNA Technologies) designed for the digital droplet PCR assays of exon 9 and 71 skipping.**Exon 9 skipping assay**

Forward Primer	5'-AAGGCCACCTAAAGTGAATAA
Reverse Primer 1	5'-TCTTCATATCCCTGTGCTAGA
Reverse Primer 2	5'-CACTCTCCATCAATGAACTGC
WT probe	5'-CAACAGATCACGGT
SK probe	5'-TCAACAGCATTGG

Exon 71 skipping assay

Forward Primer	5'-CCCGAATGGGCTACCTG
Reverse Primer 1	5'-TGGCCAGAAGTTGATCAGAG
Reverse Primer 2	5'-GCATAATGTTCAATGCGTGAATG
WT probe	5'-TGGAAACTCCCGTT
SK probe	5'-TGGAAACGCCTGCC

Supplementary Figure 1. Quantification of dystrophin isoforms with droplet digital PCR (ddPCR) in mRNA extracted from muscle biopsies of P3, P7 and healthy adult controls. A) Exon inclusion percentage of exon 9 of the *DMD* gene in P3 (n=4) and controls (C) (n=8). B) Exon inclusion percentage of exon 71 in P7 (n=4) and controls (n=8). Data represents mean \pm SD. Mann-Whitney test (** $P < 0.005$).

