

Supplementary Material V

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PRDX4_WT   GAGTTTCTGCCAGCATTAGCCCATTAAGCCATGTCAGAAATATAAAATAGTTGAGGTAGAAGAGA
DMD_WT     CTCCATCACACTGCTCAAATAACTTTCCCATGGAGCCCTGCTAGATCCCTGCAGTTGGAAGAAATCTGTCTT
BrPT-1     GAGTTTCTGCCAGCATTAGCCCATTAAGCCCTGCTAGATCCCTGCAGTTGGAAGAAATCTGTCTT
BrPT-2     CTCCATCACACTGCTCAAATAACTTACATTAGCCCATGTCAGAAATTCTAACATTAGCCCATGTCAGAAATAAAATAGTTG..
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Alignment of sequences at inversion junctions. Microhomology was found between the wild type sequences in the breakpoint regions (boxed). This microhomology is absent in one of the breakpoints (BrPT-1), and part of a duplicated region (underlined) in the other breakpoint (BrPT-2).