

Supplementary figures and figure legends

**NheI** ↓ **mCherry**

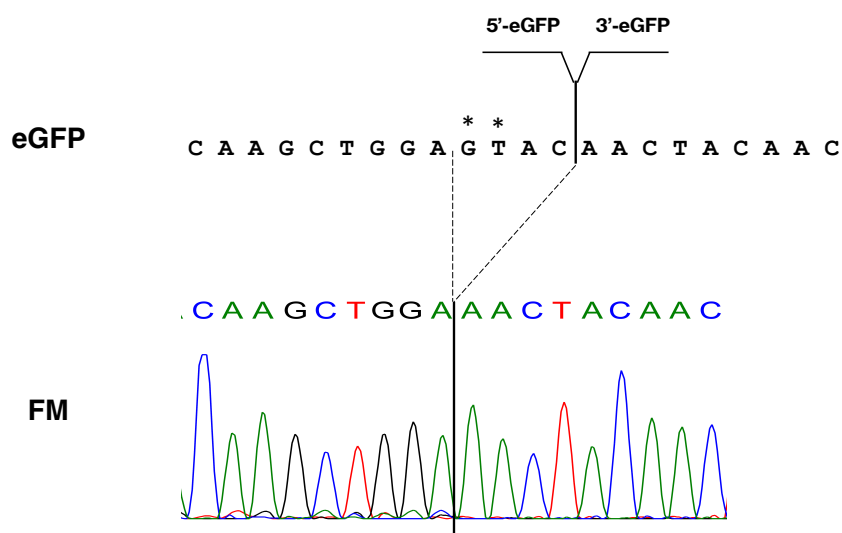
FM  
FMv2

GCTAGCGCCACCATGGTGAGCAAGGGCGAGGAGGATAACATGGCCATCATCAAGGAGTTC 60  
-----  
ATGCGCTTCAAGGTGCACATGGAGGGCTCCGTGAACGGCCACGAGTTCGAGATCGAGGGC 120  
-----  
GAGGGCGAGGGCCGCCCTACGAGGGCACCCAGACCGCCAAGCTGAAGTGACCAAGGGT 180  
-----  
GGCCCCCTGCCCTTCGCCTGGGACATCCTGTCCCTCAGTTCATGTACGGCTCCAAGGCC 240  
-----  
TACGTGAAGCACCCCGCCGACATCCCCGACTACTTGAAGCTGTCTTCCCCGAGGGCTTC 300  
-----  
AAGTGGGAGCGCGTGATGAACTTCGAGGACGGCGCGTGGTGACCGTGACCCAGGACTCC 360  
-----  
TCCCTGCAGGACGGCGAGTTCATCTACAAGGTGAAGCTGCGCGGCACCAACTTCCCTCC 420  
-----  
GACGGCCCCGTAATGCAAGAAGACCATGGGCTGGGAGGCCCTCCGAGCGGATGTAC 480  
-----  
CCCAGGACGGCGCCCTGAAGGGCGAGATCAAGCAGAGGCTGAAGCTGAAGSACGGCGGC 540  
-----  
CACTACGACGCTGAGGTCAAGACCACCTACAAGGCCAAGAAGCCGTGCAGCTGCCCGGC 600  
-----  
GCCTACAACGTCAACATCAAGTTGGACATCACCTCCCACAACGAGGACTACACCATCGTG 660  
-----  
GAACAGTACGAACGGCCGAGGGCCGCCACTCCACGGCGGCATGGACGAGCTGTACAAG 720  
-----  
↓ **5'-eGFP**  
GTTAGCAAAGCGCAAGAAGTGTACCGAGTTGTCCCATTTCTGGTTCGAGCTTGTATGGC 780  
-----  
GACGTGAATGACACAAAGTTTACGCTCTCAGGAGAAGGAGAAGGAGATGCCAATATGGG 840  
-----  
AAACTGACCTGAAGTTCATCTGCACAACCTGGGAAATGCTGTGCCTTGGCCGACTCTA 900  
-----  
GTGACAACCTCACTTATGGCGTGCAGTGTCTCCCGATACCCCGATCACATGAAACAG 960  
-----  
CATGACTTCTTAAAGTCTGCCATGCCAGAAGGATATGTACAGGAACGTACCATCTTCTC 1020  
-----  
AAAGATGACGGCAACTACAAGACGAGGGCTGAAGTGAAGTTTGAGGGCCGACACACTCGTC 1080  
-----  
AATCGGATTGAGCTGAAAGGCATCGACTTTAAGGAGGATGGGAACATACTTGGTCAACAAG 1140  
-----  
↓ **5'-end of DMD intron 18**  
CTGGAATACGTAGGTTATGCATTAATTTTATATCTGTACTCATTTTGTGCTGCTTGTAA 1200  
-----  
↓ **MCS**  
ACTCCGTGCTTTGTTAAAGCTTGGTACCAGCTCGGATCCACTAGTCCAGTGTGGTGAA 1260  
-----  
↓ **3'-end of DMD intron 19**  
TTCTGCAGATATCTGGTTTGAATCATTCTATGGTGAATACCTTTATAATTAGGATGTG 1320  
-----  
TTGGCTTTCAGATCATTCTTTCAGTCTGTGGGTTGAGGGATATATTTAATTATTTTTT 1380  
-----  
↓ **3'-eGFP**  
TCTTTCTAGAACTACAACTCCCATACGCTGTATATCATGGCTGACAAGCAGAAGTGGC 1440  
-----  
ATAAAAGTGAAGTCAAAATCCGCCATAATATCGAGGATGGTTCAGTCCAACTCGCAGAC 1500  
-----  
CATTACCAGCAGAACACTCCAATTGGCGATGGACCTGTGTGCTTCCGGACAATCACTAC 1560  
-----  
CTGTCAACCAANTCTGCGCTGAGCAAGACCCCAATGAGAAACGAGATCACATGTTCTG 1620  
-----  
CTGGAGTTTGTGACAGCAGCCGGGATTACCTCGGCATGGACGAAGTGTATAAGTAACTC 1680  
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↓ **XhoI**

GAG 1683  
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Supplementary Figure 1 Nucleotide sequences of FM and FMv2 minigenes

Nucleotide sequences of FM and FMv2 minigenes are described. Upper and lower lines indicate FM and FMv2, respectively. Dashes represent identical sequences between FM and FMv2. Arrows indicate borders of segments consisting of *NheI* and *XhoI* restriction enzyme recognition sequences, and mCherry, 5'-eGFP, MCS and 3'-eGFP sequences.



Supplementary Figure 2 Nucleotide sequences at the junction of the 5'-eGFP and the 3'-eGFP

Nucleotide sequences at the junction of the 5'-eGFP and the 3'-eGFP of FM product are shown (FM, lower). The normal eGFP cDNA sequences are described (eGFP, upper). Four nucleotides of GTAC were deleted in the FM product. GT dinucleotides (asterisks) were activated as a splice donor site, producing non-functional minigene transcript. Vertical bars indicate the junction.


  
AAGCTTCTAGGTGGTCTTGGATGACGATTCTGTTTATTGTCATATTCACCTTTGTGAAGAA 60

AAAAAGACTAAAGGGGGGAAGAGGGCTATTTTAAAAGTCCCTTTGGTTGGTAAGGGGA 120

GGGGATAAAATGGTGCCTGAGCCAGCACACTTTGTCTTTTCTCCATGTGTCAGATTGCAT 180

GTTTCTATAAAAAGGCAATGTTTCTGTCTCTGCAAGATTGGGTGTTCCATCATGCA 240

CTCATGTGGAGTCTTCCAGACTCAGCAAAAACAAACACACAGCATAGCTTTCATATAAC 300

TCGGCCCTTCAAGGAAAGCCAGTTACTTGTGTGGTGTCTTTGATGAAACAATAAATCTA 360

TCTCAGTTCGGGAGATATAGTCAGTATGTGCTTCTTTCCTCTTGGCCAGATGTGAATAT 420

TTAAAAAATCAGCTGTAGACCATAAGCCACCTTCAGGTAGTGGTTTGGGAAATCAAGCA 480

▼ **Exon v8**

ATAACACTAATATTGATTCCTTCAGATATGGACTCCAGTCATAGTACAACGCTTCAGCCT 540

ACTGCAAAATCCAAACACAGGTTTGGTGGAGATTGGACAGGACAGGACCTCTTCAATG 600

▼

ACAACGCGTAAGAATAACGATGCTCAGCCACTTTATTGACTTGTATTCTGCTTCATCTC 660

TTACTCGCTATTGGCCAAGATGCAGAGCTTTGGTGGTGGAAATGGTGTATGTGGCTTACT 720

TCAGCCAGAGTGTGAAACTGTCTTCATTGTCTGTATTTCTTGTGGAGGTCTCTCAACCT 780


GATTTTCCTTCATTTCTTTGTGCCTTCCAGATTAAATGACTTTGTGTTTTAAGAAAAG 840

TAGGACTCTATTCAACTCCATTTTCATTCTCTAAGTAGTTATGTCAGTGAAACACATGCC 900

CACTTCCAGGATAGTGATTTCTCTATGTTTTAACTGACCATTTCTTTCAATGTCCATCT 960

TTCTCCAGCCAGTGCAGAAGAGGGTAGGATTGCTTGCATGGTTGTA AAAAGACATTTT 1020

TGGGGCCAGATAATCCTAGAGATCACATCAGTTCAGAGGAGAGGCAAGGCATGTTATT 1080

GACAATCAACAAAGGTGGCGGGATCGGATCC 1111
  


Supplementary Figure 3 Nucleotide sequences of *CD44* exon v8 and flanking introns

Nucleotide sequences of the PCR amplified fragment of *CD44* exon v8 and flanking introns

are described. Sequences of *CD44* exon v8 are present between inverted triangles. Arrows indicate primer location and direction.