Table S1: sgRNAs targeting the FSHD locus

sgRNA	target	*19-nt sequence + PAM (**NGG**)	score**	Enrich^	OT(12)#	OT(19)##
1	p13-E11	TACCACAGACAGCCAACTG**GGG**	0.61	6.9	18	0
2	p13-E11	TTCACCCAGAACAGTAACT**GGG**	0.60	1.6	27	0
3	*DUX4* E1	CACCCGGGCAAAAGCCGGG**AGG**	0.61	2.5	8	1 (Y)
4	*DUX4* E1	CTGGAAGCACCCCTCAGCG**AGG**	0.85	2.4	9	3 (14/18/Y)
5	*DUX4* E1	CTGGAGGAGCTTTAGGACG**CGG**	0.65	2.2	14	6 (14/18/20/22/Y)
6	*DUX4* prom	CTCGCTCTGGTCTTCTACG**TGG**	0.72	2.0	4	0
7	*DUX4* prom	CCGTCCGTGAAATTCCGGC**CGG**	0.76	1.7	10	1 (20)
8	*DUX4* prom	TCGGACAGCACCCTCCCCG**CGG**	0.79	2.6	19	3 (3/14/Y)
9	*DUX4* E3	CTCCCTTGCACGTCAGCCG**GGG**	0.84	3.4	7	2 (14/18)
10	*DUX4* E3	GAATTTCACGGAAGAACAA**GGG**	0.76	1.8	5	0
11	*DUX4* E3	ATCTTCTATAGGATCCACA**GGG**	0.88	2.0	9	0

*CpGs are underlined

**sgRNA Designer score (http://www.broadinstitute.org/rnai/public/analysis-tools/sgrna-design).

^Relative enrichment of dCas9-VP64-HA (Addgene plasmid #50918) at each target region measured by chromatin immunoprecipitation (ChIP) using HA antibodies normalized to mouse IgG.

#Number of off-target (non-Ch 4/10) matches to 12-nt seed sequence + NGG in human genomic database (https://blast.ncbi.nlm.nih.gov).

##Number of off-target (non-Ch 4/10) matches to 19-nt sequence + NGG in human genomic database (https://blast.ncbi.nlm.nih.gov) (chromosomes in parentheses). All off-target matches except those underlined are in D4Z4 homologous repeat sequences [1, 2].

Table S2: Sequences of oligonucleotide primers (5' to 3')

qRT-PCR primers (human):

DUX4-fl-F: GCTCTGCTGGAGGAGCTTTAGGA [3]
DUX4-fl-R: GCAGGTCTGCWGGTACCTGG [3]
MyHC1-F: TGGAGGCCAGGGTTCGTGAA [3]
MyHC1-R: ATTGTTCCTCCGCTTCTTCAGC [3]
FRG1-F: TCTACAGAGACGTAGGCTGTCA [4]
FRG1-R: CTTGAGCACGAGCTTGGTAG [4]
FRG2-F: GGGAAAACTGCAGGAAAA [5]
FRG2-R: CTGGACAGTTCCCTGCTGTGT [5]
TRIM43-F: ACCCATCACTGGACTGGTGT [6]
TRIM43-R: CACATCCTCAAAGAGCCTGA [6]
ZSCAN4-F: TGGAAATCAAGTGGCAAAAA [6]
ZSCAN4-R: CTGCATGTGGACGTGGAC [6]
MBD3L2-F: GCGTTCACCTCTTTTCCAAG [6]
MBD3L2-R: GCCATGTGGATTTCTCGTTT [6]
Jumonji-F: AAGAAAAAGCCTCGAAAGTG
Jumonji-R: AGAGCACACTCCAGACAGAA
KLF14-F: TGCAACGTGTATATCATCCT
KLF14-R: ACACCAGAGTCCTTTGAGAC
UBR4-F: GGAGTCTGTGGCAACTGTGGAGAGAATG[7]
UBR4-R: CCGGTCTTCTTCATTCTCAATGGGATCCACT[7]

ChIP primers:

OT-F: GAATGTGGACACGGTAAAGA (intergenic region on Ch. 8, ref NC_018919.2)
OT-R: TAGGTTTGACTGCCAATGAC (intergenic region on Ch. 8, ref NC_018919.2)
p13-E11-F: TGGGCATTTTCTCATTAGCC
p13-E11-R: CTGGAGCAGAGATGACCACA
DUX4-exon1-F: GACACCCTCGGACAGCAC
DUX4-exon1-R: GTACGGGTTCCGCTCAAAG
DUX4-intron1-F: CTCAGCGAGGAAGAATACCG
DUX4-intron1-R: AGTCTCTCACCGGGCCTAGA
DUX4-exon3-F: CTGACGTGCAAGGGAGCT
DUX4-exon3-R: CAGGTTTGCCTAGACAGCG

Supplementary References

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