

S1Table. Primer sequences

#	Orient.	Primer sequence
<i>Yeast-Two-Hybrid constructs</i>		
DUX1	F	5' CGGAATTC <u>CGGTTCTGGTTCTGGT</u> TCCCCGTGTCAGTCCGTGAAATTCC 3'
DUX1	R	5' TTCTGCAGCATTGGGGCTGCATTGCAC 3'
DUX1H1	F	5' CGGAATTC <u>CGGTTCTGGTTCTGGT</u> TCCCCGTGTCAGTCCGTGAAATTCC 3'
DUX1H1	R	5' TTCTGCAGACAGGGCCGAGATTGCCGC 3'
DUX1H2	F	5' CGGAATTC <u>CGGTTCTGGTTCTGGT</u> AACCCGCAAAAAGGCAGAC 3'
DUX1H2	R	5' TTCTGCAGCATTGGGGCTGCATTGCAC 3'
DUX4	F	5' CGGAATTC <u>CGGTTCTGGTTCTGGT</u> TCGCGTCCGTCCGTGAAATTCC 3'
DUX4	R	5' TTGGATTCATCACCGGGCCTAGACCTAGAA 3'
DUX4H1	F	5' CGGAATTC <u>CGGTTCTGGTTCTGGT</u> TCGCGTCCGTCCGTGAAATTCC 3'
DUX4H1	R	5' TTCTGCAGGGGCCAGGGCCGAGATTCC 3'
DUX4H2	F	5' CGGAATTC <u>CGGTTCTGGTTCTGGT</u> AGACGCGGCCCGCCAGAAG 3'
DUX4H2	R	5' TTCTGCAGGGCGACCCACGAGGGAGCAG 3'
DUX4t	F	5' CGCAATTC <u>CGGTTCTGGTTCTGGT</u> AGTCACCCTGCTCCCTCGT 3'
DUX4t	R	5' TTGGATTCATCACCGGGCCTAGACCTAGAA 3'
DUX4c	F	5' CGGTT <u>CGGTTCTGGTTCTGGT</u> TCGCGTCCGTCCGTGAAATTCC 3'
DUX4c	R	5' CGGAATTCAGAGCGGGCTCTTCCAC 3'
DUX4ct	F	5' CGGAATTC <u>CGGTTCTGGTTCTGGT</u> AGTCACCCTGCTCCCTCGT 3'
DUX4ct	R	5' CGCGGATCCCAGAGCGGGCTCTTCCAC 3'
<i>pENTR1A-DUX4c construct</i>		
DUX4c	F	5' CACCATGGCCCTCCCGACACCCT 3'
DUX4c	R	5' ATAGTTTAGCGCCGCTGGTGTCTACAGGAGCTCAT 3'
<i>HaloTag constructs</i>		
DUX4c	F	5' ATATGCGATCGCCATGGCCCTCCCGACACCCTCC 3'
DUX4c	R	5' ACGCGTTTAAACCAGGAGCTCATATAACAGGCTGGAGGTG 3'
DUX4	F	5' GGCTGCGATCGCCATGGCCCTCCCGACACCCTC 3'
DUX4	R	5' GTCGGTTTAAACAAGCTCCTCCAGCAGAGCCC 3'
DUX4term	F	5' TAAAGCGATCGCCATGCAAGGCATCCCGGCGCC 3'
DUX4term	R	5' GTCGGTTTAAACAAGCTCCTCCAGCAGAGCCC 3'
EGFP	F	5' AGGAGCGATCGCCATGGTGAGCAAGGGCGAGGAG 3'
EGFP	R	5' ATGGGTTTAAACCTTGACAGCTCGTCCATGCCG 3'

Underlined: a sequence encoding a GSGSG peptide was introduced between the two parts of the hybrid construct to act as a flexible arm; this would allow the construct to avoid steric hindrance and allow optimal protein folding. All constructs were verified by DNA sequencing. t : tail