

Supplementary File 1A

Gene	Disorder
AARS2	mitochondrial cardiomyopathy
ABCC9	DCM
ACTA1	research candidate
ACTC1	DCM,HCM,LVNC
ACTN2	DCM
AGK	mitochondrial cardiomyopathy
AKAP1	research candidate
AKAP1	research candidate
AKAP10	research candidate
AKAP12	research candidate
AKAP13	research candidate
AKAP5	research candidate
AKAP6	research candidate
AKAP7	research candidate
AKAP9	LQT
ANK2	LQT
ANKRD1	DCM,HCM
ASPH	research candidate
BAG3	DCM
CACNA1C	LQT,Brugada
CACNA2D1	Brugada
CACNA2D2	research candidate
CACNA2D3	research candidate
CACNB2	Brugada
CALM1	CPVT
CASQ2	CPVT
CAV3	HCM, LQT
CMYA5	research candidate
COX15	mitochondrial cardiomyopathy

CRYAB	DCM,HCM
CSRP3	DCM,HCM
CTF1	DCM
CTNNA3	ARVC
DES	DCM,RCM
DMD	DCM
DNAJC19	DCM
DPP6	VF
DSC2	ARVC
DSG2	ARVC
DSP	DCM,ARVC
DTNA	LVNC
EMD	DCM
EYA4	DCM
FHL1	HCM
FHL2	DCM
FKTN	DCM
FLNC	research candidate
FOXD4	DCM
GAA	Pompe
GJA1	research candidate
GJA5	SCD
GLA	Fabry
GPD1L	Brugada
HCN4	Brugada
HRC	research candidate
HSPB2	research candidate
HSPB6	research candidate
HSPB7	research candidate
HSPB8	research candidate
ILK	DCM
JPH2	HCM

JUP	DCM,ARVC
KCNA5	research candidate
KCND3	research candidate
KCNE1	LQT
KCNE1L	research candidate
KCNE2	LQT
KCNE3	Brugada
KCNE4	research candidate
KCNH2	LQT
KCNIP2	research candidate
KCNJ11	research candidate
KCNJ2	LQT
KCNJ4	research candidate
KCNJ8	research candidate
KCNK1	research candidate
KCNN2	research candidate
KCNN3	research candidate
KCNQ1	LQT
KLF10	HCM
LAMA4	DCM
LAMP2	Danon
LDB3	DCM, LVNC
LMNA	DCM
LMOD2	research candidate
MIB1	LVNC
MRPL3	mitochondrial cardiomyopathy
MURC	HCM
MYBPC3	DCM,HCM
MYH6	HCM
MYH7	DCM,HCM,RCM, LVNC
MYL2	HCM
MYL3	HCM

MYLK2	research candidate
MYOM1	research candidate
MYOT	research candidate
MYOZ2	HCM
MYPN	DCM
NDUFAF1	mitochondrial cardiomyopathy
NDUFS2	mitochondrial cardiomyopathy
NEBL	DCM
NEXN	DCM,HCM
NOS1AP	research candidate
NPPA	AF
OBSCN	HCM
PDE3A	research candidate
PDE4A	research candidate
PDE4B	research candidate
PDE4D	research candidate
PDE4DIP	research candidate
PDLIM3	DCM
PKP2	ARVC
PLN	DCM
PRKAG2	HCM
PSEN1	DCM
PSEN2	DCM
RANGRF	Brugada
RBM20	DCM
RBM24	research candidate
RYR2	ARVC,CPVT
SCN10A	research candidate
SCN1B	Brugada
SCN2B	research candidate
SCN3B	Brugada
SCN4B	LQT

SCN5A	DCM,Brugada,LQT
SCN7A	research candidate
SCO2	mitochondrial cardiomyopathy
SDHA	DCM
SGCD	DCM
SLC25A3	mitochondrial cardiomyopathy
SLC25A4	mitochondrial cardiomyopathy
SLMAP	Brugada
SNTA1	LQT
SVIL	research candidate
SYNE1	DCM
SYNE2	DCM
SYNM	research candidate
TAZ	DCM,LVNC, mitochondrial cardiomyopathy
TCAP	DCM,HCM
TGFB3	ARVC
TLN1	research candidate
TMEM43	ARVC
TMEM70	mitochondrial cardiomyopathy
TMOD1	research candidate
TMPO	DCM
TNNC1	DCM,HCM
TNNI3	DCM,HCM,RCM
TNNT2	DCM,HCM,RCM
TPM1	DCM,HCM
TRDN	CPVT
TRIM63	research candidate
TTN	DCM,HCM
TTR	HCM
USP13	research candidate
UTRN	research candidate
VCL	DCM,HCM

VIM	research candidate
XIRP1	research candidate
ZYX	research candidate

Supplementary File 1B

Primer	Application	Function	Sequence
Univ_UMI_RACE	5'RACE	template switching oligonucleotide	CTCAAGCTATGCAT CCAACGCGNNNN/ ideoxyU/NNNN/ ideoxyU/NNNN/ ideoxyU/CTTrGrG+G
dr_e116_rt	5'RACE	reverse transcription (zebrafish)	TTGGTTCCAGCTTT GTACCC
mm_e224_rt	5'RACE	reverse transcription (mouse)	TGGCCTGAGTTTTG AAATCC
univ_f	5'RACE	PCR (mouse, zebrafish)	CTCAAGCTATGCAT CCAACGCG
mm_exon224_nest	5'RACE	PCR (mouse)	AGGGTGAGCGTGT GAACTCT
dr_exon116_nest	5'RACE	PCR (zebrafish)	ATTCCACAGGTATG CCCTCA
hs_mm_exon222/239_f	Alternative Promoter Analysis	PCR (human, mouse)	TCTAGTGCCACCT CCGAGTTAA
mm_altprom_f	Alternative Promoter Analysis	PCR (mouse)	GAGACAGATGCAG CGCAGATTTCT
mm_hs_e225/242_r	Alternative Promoter Analysis	PCR (human, mouse)	GACCCTGCCATCAG CAACAATTTTC
hs_altprom_f_1	Alternative Promoter Analysis	PCR (human)	GAGACAGATGCAG CACAGATTTCTCG
dr_e115_f	Alternative Promoter Analysis	PCR (zebrafish)	GCTAAATCCAAAGC TCAGCTCAGAGTT
dr_altprom_f	Alternative Promoter Analysis	PCR (zebrafish)	TCCTGGAACCTGGAGGTGA CTAAC
dr_exon118_r	Alternative Promoter Analysis	PCR (zebrafish)	AAACCACCTGACCT CTGCTT
gRNA-n1	CRISPR/Cas9	gRNA-n1	GGTCAGGAGCAGT GGGAAGA

gRNA-n2	CRISPR/ Cas9	gRNA-n2	GGAGACTACAAATT TGTGGC
gRNA-n3	CRISPR/ Cas9	gRNA-n3	GGTGATGGTGCCG CCTGTGC
gRNA-c1	CRISPR/ Cas9	gRNA-c1	GGCAAACCACTGA CTTCTGC
gRNA-c2	CRISPR/ Cas9	gRNA-c2	GGCCAGCACCTAAA GTTACT
gRNA-c3	CRISPR/ Cas9	gRNA-c3	GGTACTGGGGAATT CAGTGA
gRNA-e113	CRISPR/ Cas9	gRNA-e113	GGACTACACCGCA GTCGAGA
gRNA-e114	CRISPR/ Cas9	gRNA-e114	GGTCCGTCCACTGT ACAGTG
gRNA-e115	CRISPR/ Cas9	gRNA-e115	GGCTGTGAAATTAA GGAGGA
gRNA-e116	CRISPR/ Cas9	gRNA-e116	GGCTGCGAACTGT CTTATGA
gRNA-e122	CRISPR/ Cas9	gRNA-e122	GGAGGCTTTGTAGT CCTCAT
n1_geno_f	genotyping (PCR,Cel1), <i>in situ</i>	mut-n1	TGCAATAGCCAAAC TCATTGAT
n1_geno_r	genotyping (PCR,Cel1), <i>in situ</i>	mut-n1	AGGGACAGGCACA TTTTCAG
n2_geno_f	genotyping (PCR,Cel1)	mut-n2	GCTCAGAGAGTTCG CATTCA
n2_geno_r	genotyping (PCR,Cel1)	mut-n2	CCTTCTCTTCCAGC TGTGCT
n3_geno_f	genotyping (PCR,Cel1)	mut-n3	GAATGGGATCACCA CCAAC
n3_geno_r	genotyping (PCR,Cel1)	mut-n3	CAAGCCTTCGCTTC CTTACA
c1_geno_f	genotyping (PCR,Cel1)	mut-c1	TCATAACTTACCCAA CACTTCCA
c1_geno_r	genotyping (PCR,Cel1)	mut-c1	TGAGCCTTCAATAA CCATGACT
c2_geno_f	genotyping (PCR,Cel1)	mut-c2	TGAAGATTACCTAA GACTTTGACACG
c2_geno_r	genotyping (PCR,Cel1)	mut-c2	CGTGTGTCTGCTCA AAACCA
c3_geno_f	genotyping (PCR,Cel1)	mut-c3	CCAGCTCTGATGCA AACAGT

c3_geno_r	genotyping (PCR,Cel1)	mut-c3	AGCACCACCATCAG TTCCTC
n1_as_wt_f	genotyping (allele-specific)	mut-n1	TAAAGTGTGGCTTC TGTTGCGGTTCTTT GTCATAGAGGTCAC CCT CTC
n1_as_mu_t_f	genotyping (allele-specific)	mut-n1	TTTTCTTTGTCATAG AGGTCACCCTGCTC
n1_as_r	genotyping (allele-specific)	mut-n1	TAAGGATGTTGCAC CACCAGAGATTG
n2_as_wt_f	genotyping (allele-specific)	mut-n2	GTTTCAGCAGATCC AGCCACA
n2_as_mu_t_f	genotyping (allele-specific)	mut-n2	TTCAGCAGATCCAG CCAA
n2_as_r	genotyping (allele-specific)	mut-n2	CCTTCTCTCCAGC TGTGCT
n3_as_wt_f	genotyping (allele-specific)	mut-n3	TTGTCAAATTTCTTA ACTTCGAGTGGTGG TGATGGTGCCGCCA GTG
n3_as_mu_t_f	genotyping (allele-specific)	mut-n3	TTGTGGTGGTGATG GTGCCGCCTACT
n3_as_r	genotyping (allele-specific)	mut-n3	ATGGTTTAGCCCTG GATTTGGAT
c1_as_wt_f	genotyping (allele-specific)	mut-c1	CATCCTTCAGCCAT TCAATCAGTGGCAT TGGCAAACCACTGA CTTCTG
c1_as_mu_t_f	genotyping (allele-specific)	mut-c1	TTTGGCATTGGCAA ACCACTGACTGGC
c1_as_r	genotyping (allele-specific)	mut-c1	CGGCTCCAAGTTTG CGTATGCTG
c2_as_wt_f	genotyping (allele-specific)	mut-c2	ACGTGACCCCTCCT TATGACTATGTCAAC ACCAATGCGCTTCC AAGTA
c2_as_mu_t_f	genotyping (allele-specific)	mut-c2	ATTGTCAACACCAA TGCGCTTCCACCT

c2_as_r	genotyping (allele-specific)	mut-c2	GGGTCTTAGTGTCA GAGCAGGATGT
c3_as_wt_f	genotyping (allele-specific)	mut-c3	ACTTACCAACTCTTT CAGAACATGCAGTT TCCATACTGCCTTC ACTGA
c3_as_mut_f	genotyping (allele-specific)	mut-c3	GGTGCAGTTTCCAT ACTGCCTTCACTAG
c3_as_r	genotyping (allele-specific)	mut-c3	TTTAGAGTGGCTGC TGTCATGCT
dr_e115/ e116_qpcr_f	qPCR - Cronos to FL ratio	e115/e116	TCAGCTCAGAGTTAAAGCA CGA
dr_e116_q pcr_r	qPCR - Cronos to FL ratio	e116	CCCTAGGAACCATTCACAG
dr_cronos _qpcr_f	qPCR - Cronos to FL ratio	cronos	CAATGTCTTCTCCTGAATCC AA
dr_cronos _e117_qpcr_r	qPCR - Cronos to FL ratio	e117	GTGTGAGATCTGCCTTCAG C
mm_e222 _qpcr_f	qPCR - Cronos to FL ratio	e222	TTACACAACCTGCCGCCTAG A
mm_e223/ e224_qpcr_r	qPCR - Cronos to FL ratio	e223	CAGACCAATTACCCGTGGT T
mm_cronos_qpcr_f	qPCR - Cronos to FL ratio	cronos	AGGCATTTTGTTTCTCTCG
mm_e224 _qpcr_r	qPCR - Cronos to FL ratio	e224	CTTCCTTCTGAACGTGTCA CC
n1_outer_f	NMD estimate	mut-n1	AGGAAGTCTGGTTGAGTTG GCAG
n1_outer_r	NMD estimate	mut-n1	GACACCACTATCTCTGGAAT AAGCAACT
n1_nest_f	NMD estimate	mut-n1	GCATCTTCGCTATGGTCAG GAGC

n1_nest_r	NMD estimate	mut-n1	CAGGTCCAAACCGCTTCAT CCG
n2_outer_f	NMD estimate	mut-n2	TGTTCACTTTGGGGATGTT GGAGACT
n2_outer_r	NMD estimate	mut-n2	GATGTGCTTGGTGA ACTCAATGACTC
n3_outer_f	NMD estimate	mut-n3	GCAAAGCTACCAATGAGGC TGGT
n3_outer_r	NMD estimate	mut-n3	TCTTTGGCACCTCAATGAA GAACAAG
c1_outer_f	NMD estimate	mut-c1	GCTACAATAAGAGGAAGGC CAGCA
c1_outer_r	NMD estimate	mut-c1	TCGGGAATGACGAGGAAG GTC
c1_nest_f	NMD estimate	mut-c1	GCGTATGCTGAAACACTTC AAGGG
c1_nest_r	NMD estimate	mut-c1	CATCATCCTTCAGCCATTCA ATCTTTGG
c2_outer_f	NMD estimate	mut-c2	AAGGGTCTTAGTGTCAGAG CAGGA
c2_outer_r	NMD estimate	mut-c2	CAGTTGCGTCCAGTCCACC A
c2_nest_f	NMD estimate	mut-c2	GCTACAATAAGAGGAAGGC CAGCA
c2_nest_r	NMD estimate	mut-c2	TCGGGAATGACGAGGAAG GTC
c3_outer_f	NMD estimate	mut-c3	GCTTTAGAGTGGCTGCTGT CAATG
c3_outer_r	NMD estimate	mut-c3	ATCAGGTAGCTCAATATCAG GGATTTCAA
zCronos_probe_F	in situ	cronos	GAAAGCGCTATGTGGATTT GTAG

zCronos_ probe_T7 R	in situ	cronos	GCGTAATACGACTCACTATA GCTTTGGATTTCAGGAGAAG ACATTG
ttna_e4_q pcr_f	ttna morpholino efficacy	qPCR	TGAGGAAGAAGCCGTACCT G
ttna_e4_e 5_qpcr_r	ttna morpholino efficacy	qPCR	CGAGCTTCCACTCTCTT CTCC