Related to Figure 1A								
Item to check	Sample List	Sample List						
	TC32 siNegative	TC32 siHNRNPH1	TC32 siHNRNPH2	TC32 siHNRNPF				
Experimental design								
Definition of experimental and control groups	Control group	Experimental group	Experimental group	Experimental group				
Number within each group	n = 3	n = 3	n = 3	n = 3				
Sample								
Description	TC32 cells tranfected with	TC32 cells tranfected with	TC32 cells tranfected with	TC32 cells tranfected with				
	siNegative for 48 hours	siHNRNPH1 for 48 hours	siHNRNPH2 for 48 hours	siHNRNPH2 for 48 hours				
Processing procedure	Cells were harvested by trypsin	ization 48 hour after treatme	nt	-				
If frozen, how and how quickly?	N/A							
Sample storage conditions and duration	Proceeded directly to nucleic acid extraction							
Nucleic acid extraction								
Procedure and/or instrumentation	Promega Maxwell 16 LEV System							
Name of kit and details of any modifications	Maxwell 16 LEV simplyRNA Purification Kits							
Details of DNase or RNase treatment	Dnase treatment was automated							
Nucleic acid quantification	Replicate 1: 617.7 ng/uL	Replicate 1: 308.46 ng/uL	Replicate 1: 562.08 ng/uL	Replicate 1: 418.5 ng/uL				
	Replicate 2: 553.21 ng/uL	Replicate 2: 320.4 ng/uL	Replicate 2: 580.93 ng/uL	Replicate 2: 612.94 ng/uL				
	Replicate 3: 658.76 ng/uL	Replicate 3: 301.57 ng/uL	Replicate 3: 534.33 ng/uL	Replicate 3: 587.55 ng/uL				
Instrument and method	Nanodrop Nucleic Acid Quantif	ication	• • – –	<u> </u>				
Purity (A260/A280)	Replicate 1: 2.14	Replicate 1: 2.15	Replicate 1: 2.13	Replicate 1: 2.14				
	Replicate 2: 2.13	Replicate 2: 2.16	Replicate 2: 2.14	Replicate 2: 2.15				
	Replicate 3: 2.16	Replicate 3: 2.15	Replicate 3: 2.13	Replicate 3: 2.13				
RNA integrity: method/instrument	Nanodrop		· ·	• •				
Reverse transcription	•							
Complete reaction conditions	1X iScript Reverse Transcription	n Supermix containing oligo(d	T) and random primers (Biora	id), RNA and water				
Amount of RNA and reaction volume	1000 ng of RNA and 20 uL reac	tion volume						
Reverse transcriptase and concentration	1X iScript Reverse Transcriptas	e						
Temperature and time	Priming: 5 min at 25C							
	Reverse transcription: 20 min a	it 46C						
	Reverse transcription inactivati	on: 1 min at 95C						
qPCR target information								
Gene symbol	refer to Table S3							
Sequence accession number								
Amplicon length								
In silico specificity screen (BLAST, and so on)	UCSC In-Silico PCR							
What splice variants are targeted?	refer to Table S3							
gPCR validation								
Specificity (gel, sequence, melt, or digest)	Melt							
Data analysis								
gPCR analysis program (source, version)	StepOne Plus Real-time PCR sy	stem						
Method of Cg determination	Applied Biosystems Relative Q	uantitation Analysis Module						
Outlier identification and disposition	OUTLIERRG (Outlier in replicat	e group) quality flag						
Justification of number and choice of reference	Three references genes with m	inimal standard deviation bet	ween replicates and upon tre	atment were utilized for				
genes	normalization							
Description of normalization method	Comparative CT ( $\Delta\Delta$ CT) method	ł						
Repeatability (intraassay variation)	see error bars in Figure 1A	-						
Statistical methods for results significance	Multiple comparisons using Bo	nferroni-Dunn method						
Software (source, version)	Applied Biosystems Relative O	uantitation Analysis Module a	nd GraphPad Prism 7					
Item to check	Sample List							
	TC32 siNegative	TC32 siHNRNPH1	TC32 siHNRNPH2	TC32 siHNRNPF				
qPCR oligonucleotides								
Primer sequences	refer to Table S3							
qPCR protocol								
Complete reaction conditions	1X Fast SYBR Green Master Mi	x (Applied Biosystems), cDNA	, and water					
Reaction volume and amount of cDNA/DNA	100 ng of cDNA and 20 uL reac	tion volume						
Primer, (probe), Mg2+, and dNTP concentrations	250 nM of each primer							
Polymerase identity and concentration	AmpliTaq Fast DNA Polymeras	e						
Buffer/kit identity and manufacturer	Fast SYBR Green Master Mix (	Applied Biosystems)						
Complete thermocycling parameters	Step	Enzyme Activation	PCR					
		Hold	Cycles (40 cycles)					
			Denature	Anneal/Extend				
	Time	20 sec	3 sec	30 sec				
	Temp (°C)	95	95	60				
Manufacturer of qPCR instrument	StepOne Plus Real-time PCR sy	stem						

Related to Figure 2G												
Item to check	Sample List											
	TC32 Untreated	TC32 siNegative	TC32 siHNRNPH1	TC32 siFLI1	TC32 20 nM rG1 oligomer	TC32 40 nM rG1	TC32 80 nM rG1 oligomer	TC32 160 nM rG1	TC32 20 nM rG1 mutant 1	TC32 40 nM rG1 mutant 1	TC32 80 nM rG1 mutant 1	TC32 160 nM rG1 mutant
						oligomer		oligomer	oligomer	oligomer	oligomer	1 oligomer
Experimental desian	1	1					1	1	1 -	1	1	
Definition of experimental and control groups	Control group	Control group	Experimental group	Experimental group	Experimental group	Experimental group	Experimental group	Experimental group	Experimental group	Experimental group	Experimental group	Experimental group
Number within and and control groups		- 2	- 2	- 2	- 2	- 2	- 2		- 2	- 2	- 2	
Number within each group	n =3	n = 3	h = 3	n = 3	n = 3	n = 3	n = 3	n = 3	n = 3	n = 3	n = 3	h = 3
Sample		2000 U.S. C.S. L. M.	T022 11 1 1 1 1	2000 U.S. C.S. I	2000 H . C . I		7000 U.S. 6 . 1	2000 H + C + I H	7000 H . C . I	7000 U.S. 6 . 1	7000 U. C. L. M.	2000 U
Description	untreated TC32 cells for	TC32 cells tranfected with	TC32 cells tranfected	TC32 cells tranfected	TC32 cells tranfected with	TC32 cells tranfected	TC32 cells tranfected with	TC32 cells tranfected with	TC32 cells tranfected with	TC32 cells tranfected with	TC32 cells tranfected with	TC32 cells tranfected
	48 hours	siNegative for 48 hours	with siHNRNPH1 for 48	with siFLI1 for 48 hours	20 nM rG1 oligomer for	with 40 nM rG1	80 nM rG1 oligomer for	160 nM rG1 oligomer for	20 nM rG1 mutant 1	40 nM rG1 mutant 1	80 nM rG1 mutant 1	with 160 nM rG1 mutant
			hours		48 hours	oligomer for 48 hours	48 hours	48 hours	oligomer for 48 hours	oligomer for 48 hours	oligomer for 48 hours	1 oligomer for 48 hours
Processing procedure	Cells were harvested by t	trypsinization 48 hour after t	reatment				1	1	1 -	1	1	
If frozen how and how quickly?	Elash Erozen	.,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,										
Sample storage conditions and duration	Stored in 80C for 0 days											
Sample storage conditions and duration	Stored III-80C for 9 days											
Nucleic acia extraction												
Procedure and/or instrumentation	Promega Maxwell 16 LEV	V System										
Name of kit and details of any modifications	Maxwell 16 LEV simplyR	NA Purification Kits										
Details of DNase or RNase treatment	Dnase treatment was au	tomated										
Nucleic acid quantification	Replicate 1: 556.25 ng/ul	L Replicate 1: 329.66 ng/uL	Replicate 1: 126.34 ng/uL	Replicate 1: 109.03 ng/u	ul Replicate 1: 256.19 ng/uL	Replicate 1: 103.59 ng/i	u Replicate 1: 90.78 ng/uL	Replicate 1: 87.81 ng/uL	Replicate 1: 394.04 ng/uL	Replicate 1: 394.9 ng/uL	Replicate 1: 429.93 ng/uL	Replicate 1: 445.21 ng/uL
	Replicate 2: 234.58 ng/ul	L Replicate 2: 397.08 ng/uL	Replicate 2: 138.92 ng/uL	Replicate 2: 110.82 ng/u	uL Replicate 2: 284.12 ng/uL	Replicate 2: 102.58 ng/	u Replicate 2: 103.23 ng/uL	Replicate 2: 129.63 ng/uL	Replicate 2: 253.56 ng/uL	Replicate 2: 375.7 ng/uL	Replicate 2: 388.36 ng/uL	Replicate 2: 400.66 ng/uL
	Replicate 3: 540.24 ng/u	Replicate 3: 411.7 ng/ul	Replicate 3: 142.52 ng/ul	Replicate 3: 128.3 ng/ul	Replicate 3: 298.16 ng/ul	Replicate 3: 117.69 ng/i	Replicate 3: 116.62 ng/ul	Replicate 3: 124.94 ng/ul	Replicate 3: 408.98 ng/ul	Replicate 3: 215.39 ng/ul	Replicate 3: 347 ng/ul	Replicate 3: 334 ng/ul
Instrument and method	.,	Nanodron Nucleic Acid Qua	intification		.,	.,		.,	.,	.,	,	.,
Purity (A260/A280)	Replicate 1: 2.18	Replicate 1: 2.13	Replicate 1:21	Replicate 1:21	Replicate 1: 2.13	Replicate 1:2.07	Replicate 1: 2.09	Replicate 1: 2.07	Replicate 1: 2.14	Replicate 1:2.12	Replicate 1: 2.13	Replicate 1: 2.12
	Replicate 2: 2.10	Replicate 1.2.15	Replicate 1. 2.1	Replicate 1. 2.1	Replicate 2: 2:13	Replicate 1. 2.07	Replicate 1. 2.05	Replicate 1. 2.07	Replicate 2: 2.14	Doplicate 2: 2.12	Replicate 1. 2.15	Replicate 1: 2:12
	Replicate 2: 2.14	Replicate 2: 2.11	Replicate 2: 2.12	Replicate 2: 2.08	Replicate 2: 2.12	Replicate 2: 2.12	Replicate 2: 2.04	Replicate 2: 2.08	Replicate 2: 2.12	Replicate 2: 2.13	Replicate 2: 2.12	Replicate 2: 2.12
	Replicate 3: 2.23	Replicate 3: 2.12	Replicate 3: 2.08	Replicate 3: 2.08	Replicate 3: 2.14	Replicate 3: 2.1	Replicate 3: 2.11	Replicate 3: 2.09	Replicate 3: 2.12	Replicate 3: 2.1	Replicate 3: 2.12	Replicate 3: 2.13
RNA integrity: method/instrument	Nanodrop											
Reverse transcription												
Complete reaction conditions	1V iScript Reverse Transc	cription Supermix containing	oligo(dT) and random prin	oers (Biorad) RNA and w	ater							
Complete reaction conditions	1000 an of DNA and 20	chiption supermix containing	ongo(ur) and random prin	liers (biorau), KivA aliu w	ater							
Amount of RNA and reaction volume	1000 ng of RNA and 20 u	IL reaction volume										
Reverse transcriptase and concentration	1X iScript Reverse Transo	criptase										
Temperature and time	Priming: 5 min at 25C											
	Reverse transcription: 20	) min at 46C										
	Reverse transcription ina	activation: 1 min at 95C										
aPCR target information												
Gene symbol	refer to Table S3											
Gene symbol	refer to Table S3											
Gene symbol Sequence accession number	refer to Table S3											
Gene symbol Sequence accession number Amplicon length	refer to Table S3											
Gene symbol Sequence accession number Amplicon length In silico specificity screen (BLAST, and so on)	refer to Table S3											
Gene symbol Gene symbol Sequence accession number Amplicon length In silico specificity screen (BLAST, and so on) What splice variants are targeted?	refer to Table S3 UCSC In-Silico PCR refer to Table S3											
Gene symbol Gene symbol Sequence accession number Amplicon length In silico specificity screen (BLAST, and so on) What splice variants are targeted?	refer to Table S3 UCSC In-Silico PCR refer to Table S3											
Gene symbol Sequence accession number Amplicon length In silico specificity screen (BLAST, and so on) What splice variants are targeted? Rem to check	refer to Table S3 UCSC In-Silico PCR refer to Table S3 Sample List	TC23 sillessilus		TC22 -:E115	T2330 #4 +01 alianmar	T(2) 40 M4 (C)	TC23 80 a56 c21 alianmaa	7723 160 -84 -01	TC23 30 +M +C1 ==uto+1 1	T723 40 pM +C1 mutant 1	7723 00 -04 -01	TC23 160 all c1 mutant
Gene symbol Gene symbol Sequence accession number Amplicon length In silico specificity screen (BLAST, and so on) What splice variants are targeted? Item to check	refer to Table S3 UCSC In-Silico PCR refer to Table S3 Sample List TC32 Untreated	TC32 siNegative	TC32 siHNRNPH1	TC32 siFU1	TC32 20 nM rG1 oligomer	TC32 40 nM rG1	TC32 80 nM rG1 oligomer	TC32 160 nM rG1	TC32 20 nM rG1 mutant 1	TC32 40 nM rG1 mutant 1	TC32 80 nM rG1 mutant 1	TC32 160 nM rG1 mutant
Gene symbol Sequence accession number Amplicon length In silico specificity screen (BLAST, and so on) What splice variants are targeted? Rem to check	refer to Table S3 UCSC In-Silico PCR refer to Table S3 Sample List TC32 Untreated	TC32 siNegative	TC32 siHNRNPH1	TC32 siFU1	TC32 20 nM rG1 oligomer	TC32 40 nM rG1 oligomer	TC32 80 nM rG1 oligomer	TC32 160 nM rG1 oligomer	TC32 20 nM rG1 mutant 1 oligomer	TC32 40 nM rG1 mutant 1 oligomer	TC32 80 nM rG1 mutant 1 oligomer	TC32 160 nM rG1 mutant 1 oligomer
Gene symbol Gene symbol Sequence accession number Amplicon length In silico specificity screen (BLAST, and so on) What splice variants are targeted? Item to check gPCR oligonucleotides	refer to Table S3 UCSC In-Silico PCR refer to Table S3 Sample List TC32 Untreated	TC32 siNegative	TC32 siHNRNPH1	TC32 siFU1	TC32 20 nM rG1 oligomer	TC32 40 nM rG1 oligomer	TC32 80 nM rG1 oligomer	TC32 160 nM rG1 oligomer	TC32 20 nM rG1 mutant 1 oligomer	TC32 40 nM rG1 mutant 1 oligomer	TC32 80 nM rG1 mutant 1 oligomer	TC32 160 nM rG1 mutant 1 oligomer
Gene symbol Sequence accession number Amplicon length In silico specificity screen (BLAST, and so on) What splice variants are targeted? Rem to check QPCR oligonucleotides Primer sequences	refer to Table S3 UCSC In-Silico PCR refer to Table S3 Sample List TC32 Untreated refer to Table S3	TC32 siNegative	TC32 siHNRNPH1	TC32 siFU1	TC32 20 nM rG1 oligomer	TC32 40 nM rG1 oligomer	TC32 80 nM rG1 oligomer	TC32 160 nM rG1 oligomer	TC32 20 nM rG1 mutant 1 oligomer	TC32 40 nM rG1 mutant 1 oligomer	TC32 80 nM rG1 mutant 1 oligomer	TC32 160 nM rG1 mutant 1 oligomer
Gene symbol     Gene symbol     Sequence accession number     Amplicon length     In silico specificity screen (BLAST, and so on)     What splice variants are targeted?     Item to check <i>qPCR oligonucleotides</i> Primer sequences <i>qPCR oligonucleotides</i>	refer to Table S3 UCSC In-Silico PCR refer to Table S3 Sample List TC32 Untreated Irefer to Table S3	TC32 siNegative	TC32 siHNRNPH1	TC32 siFU1	TC32 20 nM rG1 oligomer	TC32 40 nM rG1 oligomer	TC32 80 nM rG1 oligomer	TC32 160 nM rG1 oligomer	TC32 20 nM rG1 mutant 1 oligomer	TC32 40 nM rG1 mutant 1 oligomer	TC32 80 nM rG1 mutant 1 oligomer	TC32 160 nM rG1 mutant 1 oligomer
Gene symbol     Gene symbol     Sequence accession number     Amplicon length     In silico specificity screen (BLAST, and so on)     What splice variants are targeted?     Rem to check      qPCR oligonucleotides     Primer sequences     qPCR protocol     Complete reaction conditions	refer to Table S3 UCSC In-Silico PCR refer to Table S3 Sample List TC32 Untreated Irefer to Table S3 IX Fast SYBR Green Mas	TC32 siNegative	TC32 siHNRNPH1 ), cDNA, and water	TC32 siFU1	TC32 20 nM rG1 oligomer	TC32 40 nM rG1 oligomer	TC32 80 nM rG1 oligomer	TC32 160 nM rG1 aligomer	TC32 20 nM rG1 mutant 1 oligomer	TC32 40 nM rG1 mutant 1 oligomer	TC32 80 nM rG1 mutant 1 oligomer	TC32 160 nM rG1 mutant 1 oligomer
Gene symbol     Gene symbol     Sequence accession number     Amplicon length     In silico specificity screen (BLAST, and so on)     What splice variants are targeted?     Item to check <i>qPCR oligonucleotides</i> Primer sequences <i>qPCR processed</i> Complete reaction conditions     Reaction volume and amount of cDNA/DNA	refer to Table S3 UCSC In Silico PCR refer to Table S3 Sample List TC32 Untreated Irefer to Table S3 IX Fast SYBR Green Mas 100 ne of CNR Green Mas	TG2 siNegative	TC32 siHNRNPH1 ), cDNA, and water	TC32 siFU1	TC32 20 nM rG1 oligomer	TC32 40 nM rG1 oligomer	TC32 80 nM rG1 digomer	TC32 160 nM rG1 oligomer	TC32 20 nM rG1 mutant 1 oligomer	TC32 40 nM rG1 mutant 1 oligomer	TC32 80 nM rG1 mutant 1 oligomer	TC32 160 nM rG1 mutant 1 oligomer
Gene symbol     Gene symbol     Sequence accession number     Amplicon length     In silico specificity screen (BLAST, and so on)     What splice variants are targeted?     Rem to check      PCR oligonucleotides     Primer sequences <b>qPCR protocol</b> Complete reaction conditions     Reaction volume and amount of cDNA/DNA     Primer (cmbe). Mo?+ and MDP concentations	refer to Table S3 UCSC In-Silico PCR refer to Table S3 Sample List TC32 Untreated Irefer to Table S3 IX Fast SYBR Green Mas 100 ng of CDNA and 20 u 250 nM of acth nimer	TC32 siNegative iter Mix (Applied Biosystems IL reaction volume	TC32 siHNRNPH1 ), cDNA, and water	TC32 siFU1	TC32 20 nM rG1 oligomer	TC32 40 nM rG1 oligomer	TC32 80 nM rG1 oligomer	TC32 160 nM rG1 aligomer	TC32 20 nM rG1 mutant 1 oligomer	TC32 40 nM rG1 mutant 1 oligomer	TC32 80 nM rG1 mutant 1 oligomer	TC32 160 nM rG1 mutant 1 oligomer
Gene symbol     Gene symbol     Sequence accession number     Amplicon length     In silico specificity screen (BLAST, and so on)     What splice variants are targeted?     Item to check <i>qPCR oligonucleotides</i> Primer sequences <i>qPCR protocol</i> Complete reaction conditions     Reaction volume and amount of cDNA/DNA     Primer, (grobe), Mg2+, and MTP concentrations     Belumerciel (duratitis and necentration	refer to Table S3 UCSC In Silico PCR refer to Table S3 Sample List TG32 Untreated Ix Fast SYBR Green Mas 100 ng of CDNA and 20 u 250 nM of each primer homolity 6 sample DNA Pable	TG32 siNegative	TC32 siHNRNPH1 ), cDNA, and water	TC32 siFU1	TC32 20 nM rG1 oligomer	TC32 40 nM rG1 oligomer	TC32 80 nM rG1 digomer	TC32 160 nM rG1 oligomer	TC32 20 nM rG1 mutant 1 oligomer	TC32 40 nM rG1 mutant 1 oligomer	TC32 80 nM rG1 mutant 1 oligomer	TC32 160 nM rG1 mutant 1 oligomer
Gene symbol     Gene symbol     Sequence accession number     Amplicon length     In silico specificity screen (BLAST, and so on)     What splice variants are targeted?     Rem to check      GPCR oligonucleotides     Primer sequences     GPCR protocol     Complete reaction conditions     Reaction volume and amount of cDNA/DNA     Primer, (probe), Mg2+, and MTP concentrations     Polymerase Identity and concentration	refer to Table S3 UCSC In-Silico PCR refer to Table S3 Sample List TC32 Untreated Iterfer to Table S3 IXF Fast SYBR Green Mas 100 ng of CDNA and 20 u 250 nM of each primer AmpliTag Fast DNA Polyn	TC32 siNegative ster Mix (Applied Biosystems L reaction volume merase	TC32 siHNRNPH1 ), cDNA, and water	TC32 siFU1	TC32 20 nM rG1 oligomer	TC32 40 nM rG1 oligomer	TC32 80 nM rG1 oligomer	TC32 160 nM rG1 aligomer	TC32 20 nM rG1 mutant 1 oligomer	TC32 40 nM rG1 mutant 1 oligomer	TC32 80 nM rG1 mutant 1 oligomer	TC32 160 nM rG1 mutant 1 oligomer
Gene symbol     Gene symbol     Sequence accession number     Amplicon length     In silico specificity screen (BLAST, and so on)     What splice variants are targeted?     Item to check      gPCR oligonucleotides     Primer sequences     gPCR protoco     Complete reaction conditions     Reaction volume and amount of cDNA/DNA     Primer, (probe), Mg2+, and dNTP concentrations     Polyemerase identity and concentrations     Buffer/kit identity and manufacturer	refer to Table S3 UCSC In Silico PCR refer to Table S3 Sample List TG32 Untreated IX Fast SYBR Green Mas LIX Fast SYBR Green Master Fast SYBR ToPA Poly Fast SYBR ToPA Poly Fast SYBR Green Master	TG32 siNegative Iter Mix (Applied Biosystems) Ireaction volume merase Mix (Applied Biosystems)	TC32 siHNRNPH1 ), cDNA, and water	TC32 siFU1	TC32 20 nM rG1 oligomer	TC32 40 nM rG1 oligomer	TC32 80 nM rG1 digomer	TC32 160 nM rG1 oligomer	TC32 20 nM rG1 mutant 1 oligomer	TC32 40 nM rG1 mutant 1 oligomer	TC32 80 nM rG1 mutant 1 oligomer	TC32 160 nM rG1 mutant 1 oligomer
Gene symbol     Gene symbol     Sequence accession number     Amplicon length     In silico specificity screen (BLAST, and so on)     What splice variants are targeted?     Rem to check      GPCR oligonucleotides     Primer sequences     GPCR protocol     Complete reaction conditions     Reaction volume and amount of cDNA/DNA     Primer, (probe), Mg2+, and MTP concentrations     Polymerase identity and concentration     Buffer/kit identity and manufacturer     Complete Immov(ping parameters (all ssamples)	refer to Table S3 UCSC In Silico PCR refer to Table S3 Sample List TC32 Untreated Frefer to Table S3 IXF Fast SYBR Green Mas 100 ng of CDNA and 20 u 250 nM of each primer AmpliTag Fast DNA Polyn Fast SYBR Green Master STep	TC32 siNegative iter Mix (Applied Biosystems) L reaction volume merase Mix (Applied Biosystems) Enzyme Activation	TC32 siHNRNPH1 ), cDNA, and water PCR	TC32 siFU1	TC32 20 nM rG1 oligomer	TC32 40 nM rG1 oligomer	TC32 80 nM rG1 oligomer	TC32 160 nM rG1 oligomer	TC32 20 nM rG1 mutant 1 oligomer	TC32 40 nM rG1 mutant 1 oligomer	TC32 80 nM rG1 mutant 1 oligomer	TC32 160 nM rG1 mutant 1 oligomer
Gene symbol     Gene symbol     Sequence accession number     Amplicon length     In silico specificity screen (BLAST, and so on)     What splice variants are targeted?     Item to check      gPCR oligonucleotides     Primer sequences     gPCR protoco     Complete reaction conditions     Reaction volume and amount of cDNA/DNA     Primer, (probe), Mg2+, and dNTP concentrations     Polymerase identity and concentrations     Buffer/kit identity and manufacturer     Complete thermocycling parameters (all ssamples)	refer to Table S3 UCSC In Silico PCR refer to Table S3 Sample List TC32 Untreated IX Fast SYBR Green Mas LIX Fast SYBR Green Mas LIX on g of CDN and 20 u 250 mM of each primer AmpliTag Fast DNA Polyn Fast SYBR Green Master Step	TG32 siNegative Iter Mix (Applied Biosystems) Lr reaction volume merase Mix (Applied Biosystems) Enzyme Activation Hold	TC32 siHNRNPH1 ), cDNA, and water PCR Cycles (40 cycles)	TC32 siFU1	TC32 20 nM rG1 oligomer	TC32 40 nM rG1 oligomer	TC32 80 nM rG1 digomer	TC32 160 nM rG1 oligomer	TC32 20 nM rG1 mutant 1 oligomer	TG32 40 nM rG1 mutant 1 oligomer	TC32 80 nM rG1 mutant 1 oligomer	TC32 160 nM rG1 mutant 1 oligomer
Gene symbol     Gene symbol     Sequence accession number     Amplicon length     In silico specificity screen (BLAST, and so on)     What splice variants are targeted?     Rem to check      GPCR oligonucleotides     Primer sequences     GPCR protocol     Complete reaction conditions     Reaction volume and amount of cDNA/DNA     Primer, (probe), Mg2+, and MTP concentrations     Polymerase identity and concentration     Buffer/kit identity and manufacturer     Complete thermocycling parameters (all ssamples)	refer to Table S3 UCSC In Silico PCR refer to Table S3 Sample List TC32 Untreated refer to Table S3 IX Fast SYBR Green Mas 100 ng of CDNA and 20 u 250 nM of each primer AmpliTag Fast DNA Poly Fast SYBR Green Master Step	TC32 siNegative ster Mix (Applied Biosystems Li reaction volume merase Mix (Applied Biosystems) Enzyme Activation Hold	TC32 siHNRNPH1 ), cDNA, and water PCR Cycles (40 cycles) Denature	TC32 siFU1	TC32 20 nM rG1 oligomer	TC32 40 nM rG1 oligomer	TC32 80 nM rG1 oligomer	TC32 160 nM rG1 oligomer	TC32 20 nM rG1 mutant 1 oligomer	TC32 40 nM rG1 mutant 1 oligomer	TC32 80 nM rG1 mutant 1 oligomer	TC32 160 nM rG1 mutant 1 oligomer
Gene symbol     Gene symbol     Sequence accession number     Amplicon length     In silico specificity screen (BLAST, and so on)     What splice variants are targeted?     Item to check      gPCR oligonucleotides     Primer sequences     gPCR protoco     Complete reaction conditions     Reaction volume and amount of cDNA/DNA     Primer, (probe), Mg2+, and dNTP concentrations     Polymerase identity and concentrations     Buffer/kit identity and manufacturer     Complete thermocycling parameters (all ssamples)	refer to Table S3 UCSC In Silico PCR refer to Table S3 Sample List TG32 Untreated IX Fast SYBR Green Mas LIX Fast SYBR Green Mas LIX Fast SYBR Green Master Step Time	TG32 siNegative Iter Mix (Applied Biosystems) Ir craction volume merase Mix (Applied Biosystems) Enzyme Activation Hold 20 sec	TC32 siHNRNPH1 ), cDNA, and water PCR Cycles (40 cycles) Denature 3 sec	TC32 siFU1 Anneal/Extend 30 sec	TC32 20 nM rG1 oligomer	TG32 40 nM rG1 oligomer	TC32 80 nM rG1 digomer	TC32 160 nM rG1 oligomer	TC32 20 nM rG1 mutant 1 oligomer	TG32 40 nM rG1 mutant 1 oligomer	TG32 80 nM rG1 mutant 1 oligomer	TC32 160 nM rG1 mutant 1 oligomer
Gene symbol     Gene symbol     Sequence accession number     Amplicon length     In silico specificity screen (BLAST, and so on)     What splice variants are targeted?     Rem to check      GPCR oligonucleotides     Primer sequences     GPCR protocol     Complete reaction conditions     Reaction volume and amount of cDNA/DNA     Primer, (probe), Mg2+, and MTP concentrations     Polymerase identity and concentration     Buffer/kit identity and manufacturer     Complete thermocycling parameters (all ssamples)	refer to Table S3 UCSC In Silico PCR refer to Table S3 Sample List TC32 Untreated refer to Table S3 IX Fast SYBR Green Mas 100 ng of CDNA and 20 u 250 nM of each primer JampliTag Fast DNA Polyn Fast SYBR Green Master Step Time Time Time(Temp(TC))	TC32 siNegative iter Mix (Applied Biosystems traction volume merase Mix (Applied Biosystems) Erayme Activation Hold 20 sec 95	TC32 siHNRNPH1 ), cDNA, and water PCR Cycles (40 cycles) Denature 3 sec 95	TC32 siFU1 Anneal/Extend 30 sec 60	TC32 20 nM rG1 oligomer	TC32 40 nM rG1 oligomer	TC32 80 nM rG1 digomer	TC32 160 nM rG1 oligomer	TC32 20 nM rG1 mutant 1 oligomer	TC32 40 nM rG1 mutant 1 oligomer	TC32 80 nM rG1 mutant 1 oligomer	TC32 160 nM rG1 mutant 1 oligomer
Gene symbol     Gene symbol     Sequence accession number     Amplicon length     In silico specificity screen (BLAST, and so on)     What splice variants are targeted?     Item to check      gPCR oligonucleotides     Primer sequences     gPCR protocol     Complete reaction conditions     Reaction volume and amount of cDNA/DNA     Primer, (probe), Mg2+, and dNTP concentrations     Polymerase identity and concentration     Buffer/kit identity and manufacturer     Complete thermocycling parameters (all ssamples)     Manufacturer of qPCR instrument	refer to Table S3 UCSC In Silico PCR refer to Table S3 Sample List TC32 Untreated IX Fast SYBR Green Mas LIX Fast SYBR Green Master JOOn gol CONA and 20 U 250 nM of each primer AmpliTag Fast DNA Poly Fast SYBR Green Master Step Time Temp (*C)	TG32 siNegative TG32 siNegative Iter Mix (Applied Biosystems) Iteraction volume merase Mix (Applied Biosystems) Enzyme Activation Hold 20 sec 95	TC32 siHNRNPH1 ), cDNA, and water PCR Cycles (40 cycles) Denature 3 sec 95	TC32 siFU1 Anneal/Extend 30 sec 60	TC32 20 nM rG1 oligomer	TG32 40 nM rG1 oligomer	TC32 80 nM rG1 digomer	TC32 160 nM rG1 oligomer	TC32 20 nM rG1 mutant 1 oligomer	TG32 40 nM rG1 mutant 1 oligomer	TG32 80 nM rG1 mutant 1 oligomer	TC32 160 nM rG1 mutant 1 oligomer
Gene symbol     Gene symbol     Sequence accession number     Amplicon length     In silico specificity screen (BLAST, and so on)     What splice variants are targeted?     Rem to check      PCR oligonucleotides     Primer sequences     PCR protocol     Complete reaction conditions     Reaction volume and amount of cDNA/DNA     Primer, (probe), Mg2+, and MTP concentrations     Polymerase identity and concentration     Buffer/kit identity and manufacturer     Complete thermocycling parameters (all ssamples)     Manufacturer of qPCR instrument     DPCR voliderin	refer to Table S3 UCSC In-Silico PCR refer to Table S3 Sample List TC32 Untreated refer to Table S3 IXF Fast SYBR Green Mas 100 ng of CDNA and 20 u 250 nM of each primer AmpliTag Fast DNA Polyn Fast SYBR Green Master Step Time Temp (*C)	TC32 siNegative iter Mix (Applied Biosystems traction volume merase Mix (Applied Biosystems) Erayme Activation Hold 20 sec 95	TC32 siHNRNPH1 ), cDNA, and water PCR Cycles (40 cycles) Denature 3 sec 95	TC32 siFU1 Anneal/Extend 30 sec 60	TC32 20 nM rG1 oligomer	TC32 40 nM rG1 oligomer	TC32 80 nM rG1 oligomer	TC32 160 nM rG1 oligomer	TC32 20 nM rG1 mutant 1 oligomer	TC32 40 nM rG1 mutant 1 oligomer	TC32 80 nM rG1 mutant 1 oligomer	TC32 160 nM rG1 mutant 1 oligomer
Gene symbol     Sequence accession number     Ampticon length     In silico specificity screen (BLAST, and so on)     What splice variants are targeted?      Item to check      PCR oligonucleotides     Primer sequences     qPCR protocol     Complete reaction conditions     Reaction volume and amount of cDNA/DNA     Primer, [prob_M22+, and dNTP concentrations     Polymerase identity and concentration     Buffer/kit lentity and manufacturer     Complete thermocycling parameters (all ssamples)     Manufacturer of qPCR instrument     qPCR volidation     Manufacturer of qPCR instrument     qPCR volidation	refer to Table S3 UCSC In Silico PCR refer to Table S3 Sample List TG32 Untreated IX Fast SYBR Green Mas LX Fast SYBR Green Master Step Time Temp (*C) Motit	TG32 siNegative TG32 siNegative ter Mix (Applied Biosystems) teraction volume merase Mix (Applied Biosystems) Enzyme Activation Hold 20 sec 95	TC32 siHNRNPH1 ), cDNA, and water ), cDNA, and water Cycles (40 cycles) Denature 3 Sec 95	TC32 siFU1 Anneal/Extend 30 sec 60	TC32 20 nM rG1 oligomer	TC32 40 nM rG1 oligomer	TC32 80 nM rG1 digomer	TC32 160 nM rG1 oligomer	TC32 20 nM rG1 mutant 1 oligomer	TG32 40 nM rG1 mutant 1 oligomer	TG32 80 nM rG1 mutant 1 oligomer	TC32 160 nM rG1 mutant 1 oligomer
Gene symbol     Gene symbol     Gene symbol     Sequence accession number     Amplicon length     In silico specificity screen (BLAST, and so on)     What splice variants are targeted?     Rem to check      PCR oligoncleotides     Primer sequences     @PCR protocol     Complete reaction conditions     Reaction volume and amount of cDNA/DNA     Primer, (probe), Mg2+, and MTP concentrations     Polymerase identity and concentration     Buffer/kit identity and manufacturer     Complete thermocycling parameters (all ssamples)     Manufacturer of qPCR instrument     @PCR validation     Specificity (gel, sequence, melt, or digest)	refer to Table S3 UCSC In-Silico PCR refer to Table S3 Sample List TC32 Untreated refer to Table S3 IXF ast SYBR Green Mas 100 ng of cDNA and 20 u Z50 nM of each primer AmpliTag Fast DNA Poly Fast SYBR Green Master Step Time Temp (*C) Melt	TC32 siNegative iter Mix (Applied Biosystems it reaction volume merase Mix (Applied Biosystems) Enzyme Activation Hold 20 sec 95	TC32 siHNRNPH1 ), cDNA, and water PCR Cycles (40 cycles) Denature 3 sec 95	TC32 siFU1 Anneal/Extend 30 sec 60	TC32 20 nM rG1 oligomer	TC32 40 nM rG1 oligomer	TC32 80 nM rG1 oligomer	TC32 160 nM rG1 oligomer	TC32 20 nM rG1 mutant 1 oligomer	TC32 40 nM rG1 mutant 1 oligomer	TC32 80 nM rG1 mutant 1 oligomer	TC32 160 nM rG1 mutant 1 oligomer
Gene symbol     Sequence accession number     Ampticon length     In silico specificity screen (BLAST, and so on)     What splice variants are targeted?     Item to check      PCR oligonucleotides     Primer sequences     qPCR protocol     Complete reaction conditions     Reaction volume and amount of cDNA/DNA     Primer, Ipoveb, Mg2z, and MTP concentrations     Polymerase identity and concentration     Buffer/kit lentity and manufacturer     Complete thermocycling parameters (all ssamples)     Manufacturer of qPCR instrument     qPCR volidation     Specificity (gel, sequence, melt, or digest)     Data analysis	refer to Table S3 UCSC In Silico PCR refer to Table S3 Sample List TC32 Untreated IX Fast SYBR Green Mas LX Fast SYBR Green Master Step Time Temp (*C) Melt	TG32 siNegative TG32 siNegative ter Mix (Applied Biosystems) teraction volume merase Mix (Applied Biosystems) Enzyme Activation Hold 20 sec 95	TC32 siHNRNPH1 ), cDNA, and water ), cDNA, and water Cycles (40 cycles) Denature 3 Sec 95	TC32 siFU1 Anneal/Extend 30 sec 60	TC32 20 nM rG1 oligomer	TG32 40 nM rG1 oligomer	TC32 80 nM rG1 digomer	TC32 160 nM rG1 oligomer	TC32 20 nM rG1 mutant 1 oligomer	TG32 40 nM rG1 mutant 1 oligomer	TG32 80 nM rG1 mutant 1 oligomer	TC32 160 nM rG1 mutant 1 oligomer
Gene symbol     Gene symbol     Sequence accession number     Amplicon length     In silico specificity screen (BLAST, and so on)     What splice variants are targeted?     Rem to check      GPCR oligonucleotides     Primer sequences     GPCR protocol     Complete reaction conditions     Reaction volume and amount of cDNA/DNA     Primer, (probe), Mg2+, and MTP concentrations     Polymerase identity and concentration     Buffer/kit identity and manufacturer     Complete thermocycling parameters (all ssamples)     Manufacturer of qPCR instrument     qPCR validation     Specificity (gel, sequence, melt, or digest)     Data consists     qPCR analysis program (source, version)	refer to Table S3 UCSC In-Silico PCR refer to Table S3 Sample List TC32 Untreated refer to Table S3 IX Fast SYBR Green Mas 100 ng of cDNA and 20 u 250 nM of each primer AmpliTag Fast DNA Poly Fast SYBR Green Master Step Time Temp (*C) Melt StepOne Plus Real-time	TC32 siNegative iter Mix (Applied Biosystems it reaction volume merase Mix (Applied Biosystems) Enzyme Activation Hold 20 sec 195 PCR system	TC32 siHNRNPH1 ), cDNA, and water PCR Cycles (40 cycles) Denature 95	TC32 siFU1 Anneal/Extend 30 sec 60	TC32 20 nM rG1 oligomer	TC32 40 nM rG1 oligomer	TC32 80 nM rG1 oligomer	TC32 160 nM rG1 oligomer	TC32 20 nM rG1 mutant 1 oligomer	TC32 40 nM rG1 mutant 1 oligomer	TC32 80 nM rG1 mutant 1 oligomer	TC32 150 nM rG1 mutant 1 oligomer
Gene symbol     Sequence accession number     Ampticon length     In silico specificity screen (BLAST, and so on)     What splice variants are targeted?     Item to check      PCR oligonucleotides     Primer sequences     qPCR protocol     Complete reaction conditions     Reaction volume and amount of cDNA/DNA     Primer, [probo, Mg2*, and MPT concentrations     Polymerase identity and concentration     Buffer/Ait lentity and amount acturer     Complete thermocycling parameters (all ssamples)     Manufacturer of qPCR instrument     qPCR volidation     Specificity (gel, sequence, melt, or digest)     Data onalysis     pPortare located     parametized     parametized     parametized     primer (accenter between the second	refer to Table S3 UCSC In Silico PCR refer to Table S3 Sample List TC32 Untreated IX Fast SYBR Green Mas LOO ng of CDN and 20 u 250 nM of each primer AmpliTag Fast DNA Poly fast SYBR Green Master Step Time Temp (*C) Melt StepOne Plus Real-time Applied Biosystems Rela	TG32 siNegative TG32 siNegative ter Mix (Applied Biosystems) traction volume merase Mix (Applied Biosystems) Enzyme Activation Hold 20 sec 95 PCR system tive Quantitation Analysis M	TC32 siHNRNPH1 ), cDNA, and water ), cDNA, and water (Crcles (40 cycles) Denature 3 Sec 95 odule	TC32 siFU1 Anneal/Extend 30 sec 60	TC32 20 nM rG1 oligomer	TG32 40 nM rG1 oligomer	TC32 80 nM rG1 digomer	TC32 160 nM rG1 oligomer	TC32 20 nM rG1 mutant 1 oligomer	TG32 40 nM rG1 mutant 1 oligomer	TG32 80 nM rG1 mutant 1 oligomer	TC32 160 nM rG1 mutant 1 oligomer
Gene symbol     Gene symbol     Sequence accession number     Amplicon length     In silico specificity screen (BLAST, and so on)     What splice variants are targeted?     Item to check      PCR oligonucleotides     Primer sequences     PPCR protocol     Complete reaction conditions     Reaction volume and amount of cDNA/DNA     Primer, (probe), Mg2+, and MTP concentration     Buffer/Ait identity and concentration     Dyter administion     QCR validation     Specificity (gel, sequence, melt, or digest)     Data analysis program (source, version)     Method of Cq determination     Outlier identification and disposition	refer to Table S3 UCSC In-Silico PCR refer to Table S3 Sample List TC32 Untreated refer to Table S3 Lix Fast SYBR Green Mas 100 ng of CDNA and 20 u 250 nM of each primer AmpliTag Fast DNA Poly Fast SYBR Green Master Step Time Temp (*C) Melt StepOne Plus Real-time Applied Biosystems Rela	TC32 siNegative iter Mix (Applied Biosystems) I. reaction volume merase Mix (Applied Biosystems) Enzyme Activation Hold 20 sec 95 PCR system tive Quantitation Analysis M	TC32 siHNRNPH1 ), cDNA, and water PCR Cycles (40 cycles) Denature 95 95 odule	TC32 siFU1 Anneal/Extend 30 sec 60	TC32 20 nM rG1 oligomer	TC32 40 nM rG1 oligomer	TC32 80 nM rG1 oligomer	TC32 160 nM rG1 oligomer	TC32 20 nM rG1 mutant 1 oligomer	TC32 40 nM rG1 mutant 1 oligomer	TC32 80 nM rG1 mutant 1 oligomer	TC32 150 nM rG1 mutant 1 oligomer
Gene symbol     Sequence accession number     Ampticon length     In silico specificity screen (BLAST, and so on)     What splice variants are targeted?     Item to check      PCR oligonucleotides     Primer sequences     qPCR protocol     Complete reaction conditions     Reaction volume and amount of cDNA/DNA     Primer, (probe), Mg2+, and PTP concentrations     Polymerase identity and concentration     Buffer/skit entity and amount of cDNA/DNA     Primer, (probe), Mg2+, and Concentration     Polymerase identity and concentration     Buffer/skit entity and manufacturer     Complete thermocycling parameters (all ssamples)     Manufacturer of qPCR instrument     qPCR validation     Specificity (gel, sequence, melt, or digest)     Data analysis program (source, version)     Method of cq determination     Outlier identification and disposition     Justification on fumber and tohice of reference gen	refer to Table S3 UCSC In-Silico PCR refer to Table S3 Sample List TC32 Untreated IZ50 MJ refer to Table S3 IX Fast SYBR Green Mass I200 ng of CNA and 20 u 250 MJ of each primer AmpliTag Fast DNA Poly Fast SYBR Green Master Step Time Temp (*C) Melt StepOne Plus Real-time Raplied Biosystems Rela OUTLIERRG (Dutlier in R Cone references gene with	TG32 siNegative TG32 siNegative Iter Mix (Applied Biosystems) Ireaction volume merase Mix (Applied Biosystems) Erazme Activation Hold 20 sec 95 PCR system tive Quantitation Analysis M plicate group) quality flag plicate group) quality flag	TC32 siHNRNPH1 ), cDNA, and water ), cDNA, and water Cycles (40 cycles) Denature 3 Sec 95 odule n between replicates and	TC32 siFU1 Anneal/Extend 30 sec 60 upon treatment were utili	TC32 20 nM rG1 oligomer	TG32 40 nM rG1 oligomer	TC32 80 nM rG1 digomer	TC32 160 nM rG1 oligomer	TC32 20 nM rG1 mutant 1 oligomer	TG32 40 nM rG1 mutant 1 oligomer	TG32 80 nM rG1 mutant 1 oligomer	TC32 160 nM rG1 mutant 1 oligomer
Gene symbol     Gene symbol     Sequence accession number     Amplicon length     In silico specificity screen (BLAST, and so on)     What splice variants are targeted?     Item to check      PCR oligonucleotides     Primer sequences     QPC protocol     Complete reaction conditions     Reaction volume and amount of cDNA/DNA     Primer, (probe), Mg2r, and MTP Concentrations     Polymerase identity and concentration     Buffer/Att identity and manufacturer     Complete thermocycling parameters (all ssamples)     Manufacturer of qPCR instrument     QPCR volidation     Specificity (gel, sequence, melt, or digest)     Data analysis program (source, version)     Method of Cq determination     Justification of normalization method	refer to Table S3 UCSC In-Silico PCR refer to Table S3 Sample List TC32 Untreated refer to Table S3 LX Fast SYBR Green Mas 100 ng of CDNA and 20 u 250 nM of each primer TampliTag fast DNA Polya Fast SYBR Green Master Step Time Tremp (*C) Melt StepOne Plus Real-time Applied Biosystems Rela OUTLIERR (Outlier in re One references gene with	TC32 siNegative TC32 siNegative Ter Mix (Applied Biosystems) I. reaction volume merase Mix (Applied Biosystems) Enzyme Activation Hold 20 sec 95 PCR system tive Quantitation Analysis M plicate group quality flag th minimal standard deviatio	TC32 siHNRNPH1 ), cDNA, and water //CR Cycles (40 cycles) Denature 95 95 odule n between replicates and u	TC32 siFU1 Anneal/Extend 30 sec 60	TC32 20 nM rG1 oligomer	TC32 40 nM rG1 oligomer	TG32 80 nM rG1 oligomer	TC32 160 nM rG1 oligomer	TC32 20 mM rG1 mutant 1 oligomer	TC32 40 nM rG1 mutant 1 oligomer	TC32 80 nM rG1 mutant 1 oligomer	TC32 150 nM rG1 mutant 1 oligomer
Gene symbol     Sequence accession number     Ampticon length     In silico specificity screen (BLAST, and so on)     What splice variants are targeted?     Item to check      gPCR oligonucleotides     Primer sequences     gPCR protocol     Complete reaction conditions     Reaction volume and amount of CDNA/DNA     Primer, (probe), Mg2+, and MPTP concentrations     Polymerase identity and concentration     Buffer/shit identity and manufacturer     Complete thermocycling parameters (all ssamples)     Manufacturer of qPCR instrument     gPCR validation     Specificity (gel, sequence, melt, or digest)     Data onalysis     pogram (source, version)     Method of Ca determination     Outlier identification and disposition     Justification on number and choice of reference ger     Description of normalization method     method method	refer to Table S3 UCSC In-Silico PCR refer to Table S3 Sample List TC32 Untreated IZSC In-Silico PCR refer to Table S3 IX Fast SYBR Green Mas IXO ng of CNA and 20 ZSO MO f cach primer AmpliTag Fast DNA Polyl Fast SYBR Green Master Step Time Temp (*C) Melt StepOne Plus Real-time Applied Biosystems Rela OUTLIERRG (Outlier in r Comparative CT (AACT) Exe error bars in Fiume 7	TG32 siNegative TG32 siNegative Iter Mix (Applied Biosystems) Ireaction volume merase Mix (Applied Biosystems) Enzyme Activation Hold 20 sec 95 PCR system tive Quantitation Analysis M pplicate group) quality flag pplicate group) quality flag plicate grou	TC32 siHNRNPH1 ), cDNA, and water ), cDNA, and water Cycles (40 cycles) Denature 3 Sec 95 odule n between replicates and u	TC32 siFU1 Anneal/Extend 30 sec 60 upon treatment were utili	TC32 20 nM rG1 oligomer	TG32 40 nM rG1 oligomer	TC32 80 nM rG1 digomer	TC32 160 nM rG1 oligomer	TC32 20 nM rG1 mutant 1 oligomer	TG32 40 nM rG1 mutant 1 oligomer	TG32 80 nM rG1 mutant 1 oligomer	TC32 160 nM rG1 mutant 1 oligomer
Complete teraction conditions     Gene symbol     Sequence accession number     Amplicon length     In silico specificity screen (BLAST, and so on)     What splice variants are targeted?     Item to check      gPCR oligonucleotides     pPimer sequences     gPCR protocol     Complete reaction conditions     Reaction volume and amount of cDNA/DNA     Primer, (probe), Mg2+, and MTP concentration     Buffer/Ait identity and concentration     Buffer/Ait identity and manufacturer     Complete thermocycling parameters (all ssamples)     Manufacturer of qPCR instrument     gPCR oligonucleotides     Specificity (gel, sequence, melt, or digest)     Dato analysis     persony in disposition     Justification of number and choice of reference ger     Description of normalization method     Repeatability (intraassay variation)     Statistical methods for results significance	refer to Table S3 UCSC In-Silico PCR refer to Table S3 Sample List TC32 Untreated refer to Table S3 Lix Fast SYBR Green Mas 100 ng of CDNA and 20 u 250 nM of each primer AmpliTag Fast DNA Poly Fast SYBR Green Master Step Time Temp (*C) Melt StepOne Plus Real-time Applied Biosystems Rela CUTIERR6 (Cutlier in re Con represences cg (advCI) See error bars in Figure 2	TC32 siNegative TC32 siNegative Ter Mix (Applied Biosystems) I. reaction volume merase Mix (Applied Biosystems) Enzyme Activation Hold 20 sec 95 PCR system PCR system tive Quantitation Analysis M plicate group quality flag th minimal standard deviatio acontrolling the False Nierow	TC32 siHNRNPH1  ), cDNA, and water  PCR  Cycles (40 cycles) Denature  3 sec 95  odule  n between replicates and u  ry Rate - Two-stage linear	TC32 siFU1 Anneal/Extend 30 sec 60 upon treatment were utili	TC32 20 nM rG1 oligomer	TC32 40 nM rG1 oligomer	TC32 80 nM rG1 oligomer	TC32 160 nM rG1 oligomer	TC32 20 mM rG1 mutant 1 oligomer	TC32 40 nM rG1 mutant 1 oligomer	TC32 80 nM rG1 mutant 1 oligomer	TC32 150 nM rG1 mutant 1 oligomer
Complete the second secon	refer to Table S3 UCSC In-Silico PCR refer to Table S3 Sample List TC32 Untreated ISS TC32 Untreated ISS TC32 Untreated ISS PS TC32 UNTREATED TS PS TC32 Time Temp ('C) ISS PS TC32 UNTREATED TS PS TC32 Melt StepOne Plus Real-time Applied Biosystems Rela OUTLIERG (Outlier in r Comparative CT (IACT) ISS PS TC32 Meltipe comparisons Dy Multipe comparisons Pails IMMIDIE COMPARISON PAILS ISS PS TC32 IS	TG32 siNegative TG32 siNegative TG32 siNegative Ter Mix (Applied Biosystems) Teaction volume merase Mix (Applied Biosystems) Enzyme Activation Hold 20 sec 95 PCR system Twe Quantitation Analysis M ph inairginus) quality flag thereing and the size Discov Go Go	TC32 siHNRNPH1 ), cDNA, and water ), cDNA, and water (PCR (Cycles (40 cycles)) Denature 3 sec 95 odule odule end replicates and u cyr, Rate - Two-stage lineae	TC32 siFU1 Anneal/Extend 30 sec 60 I upon treatment were utill rset-up procedure of Ben 7	TC32 20 nM rG1 oligomer	TC32 40 nM rG1 oligomer	TC32 80 nM rG1 digomer	TC32 160 nM rG1 oligomer	TC32 20 nM rG1 mutant 1 oligomer	TG32 40 nM rG1 mutant 1 oligomer	TG32 80 nM rG1 mutant 1 oligomer	TC32 160 nM rG1 mutant 1 oligomer

	T	T	T		T			
Related to Figure 7A								
Item to check	Sample List							
	TC32 Untreated	TC32 siNegative	TC32 siHNRNPH1	TC32 siFLI1	TC32 DMSO	TC32 5uM PDS	TC32 10uM PDS	TC32 15uM PDS
Experimental design								
Definition of experimental and control groups	Control group	Control group	Experimental group	Experimental group	Control group	Experimental group	Experimental group	Experimental group
Number within each group	n =3	n = 3	n = 3	n = 3	n = 3	n = 3	n = 3	n = 3
Sample				1 -				
Sumple								
Description	untreated TC22 cells for 48	TC22 cells tranfected	TC22 cells tranfected	TC22 cells tranfacted	TC22 cells treated with	TC22 cells treated with	TC22 cells treated with 10	TC22 cells treated with 15
beschption	untreated resz cens for 40	i CS2 cells trainected	incoz cello cramected	resz cens trainected	DMCO for 40 hours	Factors also of	resz cens treated with 10	resz cens cleated with 15
	nours	with sinegative for 48	with SIHNKNPH1 for 48	With SIFLI1 for 48 hours	DIVISO FOR 48 hours	Smicromolar or	micromolar or	micromolar or pyridostatin
		nours	nours			pyridostatin for 48 hours	pyridostatin for 48 hours	for 48 nours
Processing procedure	Cells were harvested by tryp	sinization 48 hour after tre	atment					
If frozen, how and how quickly?	Flash Frozen							
Sample storage conditions and duration	Stored in -80C for 6 days							
Nucleic acid extraction								
Presedure and /or instrumentation	Dromogo Moveyall 16 LEV St	stom						
Procedure and/or histrumentation	Promega waxwell 16 LEV 3	ystelli Puolfiantian Kita						
Name or kit and details or any modifications	Maxwell 16 LEV SIMPLYRINA	Purification Kits						
Details of DNase or RNase treatment	Dhase treatment was autor	nated		1			1	1
Nucleic acid quantification	Replicate 1: 761.98 ng/uL	Replicate 1: 682.26 ng/ul	Replicate 1: 163 ng/uL	Replicate 1: 149.95 ng/uL	Replicate 1: 731.69 ng/uL	Replicate 1: 336.24 ng/uL	Replicate 1: 201.47 ng/uL	Replicate 1: 149.76 ng/uL
	Replicate 2: 733.85 ng/uL	Replicate 2: 654.15 ng/uL	Replicate 2: 167.39 ng/u	L Replicate 2: 124.67 ng/uL	. Replicate 2: 720.51 ng/uL	Replicate 2: 557.52 ng/uL	Replicate 2: 220.72 ng/uL	Replicate 2: 138.69 ng/uL
	Replicate 3: 697.34 ng/uL	Replicate 3: 714.49 ng/uL	Replicate 3: 168.44 ng/u	L Replicate 3: 125.16 ng/uL	Replicate 3: 726.33 ng/uL	Replicate 3: 568.08 ng/uL	Replicate 3: 246.76 ng/uL	Replicate 3: 147.9 ng/uL
Instrument and method	Nanodrop Nucleic Acid Quar	ntification						
Purity (A260/A280)	Replicate 1: 2.16	Replicate 1: 2.15	Replicate 1: 2.17	Replicate 1: 2.13	Replicate 1: 2.16	Replicate 1: 2.16	Replicate 1: 2.18	Replicate 1: 2.12
runty (h200) h200)	Replicate 2: 2.19	Replicate 2: 2.16	Replicate 2: 2.18	Replicate 2: 2 17	Replicate 2: 2 17	Replicate 2: 2.17	Replicate 2: 2.15	Replicate 2: 2.16
	Replicate 2: 2:10	Replicate 2: 2.10	Replicate 2: 2:10	Replicate 2: 2:17	Replicate 2: 2:17	Replicate 2: 2:17	Replicate 2: 2:15	Replicate 2: 2:10
DNIA laboration another differences and	Replicate 3. 2.19	Replicate 3. 2.17	Replicate 5. 2.14	Replicate 5. 2.18	Replicate 3. 2.10	Replicate 3. 2.10	Replicate 5. 2.15	Replicate 5. 2.15
RNA Integrity: method/instrument	Nanodrop							
Reverse transcription								
Complete reaction conditions	1000 ng of RNA and 20 uL n	eaction volume						
Amount of RNA and reaction volume	1X iScript Reverse Transcrip	tase						
Reverse transcriptase and concentration	Priming: 5 min at 25C							
Temperature and time	Reverse transcription: 20 m	in at 46C						
	Reverse transcription inactiv	vation: 1 min at 95C						
	Reverse transcription inaction	vation: 1 min at 950						
aDCR terract information	neverse d'unsemption maeu							
Gree washel	ft-T-bl-C2							
Gene symbol	refer to Table 53							
Sequence accession number	-							
Amplicon length								
In silico specificity screen (BLAST, and so on)	UCSC In-Silico PCR							
What splice variants are targeted?	refer to Table S3							
Itom to shock	Comple List							
item to check	Sample List							
	IC32 Untreated	IC32 siNegative	IC32 SIHNKNPH1	IC32 SIFLI1	IC32 DMSO	TC32 SuM PDS	1C32 100M PDS	1C32 150M PDS
qPCR oligonucleotides								
Primer sequences	refer to Table S3							
qPCR protocol								
Complete reaction conditions	1X Fast SYBR Green Master	Mix (Applied Biosystems),	cDNA, and water					
Reaction volume and amount of cDNA/DNA	100 ng of cDNA and 20 uL re	eaction volume						
Primer, (probe), Mg2+, and dNTP concentrations	250 nM of each primer							
Polymerase identity and concentration	AmpliTag East DNA Polyme	rase						
Buffer/kit identity and manufacturer	East SYBB Green Master M	(Applied Biosystems)						
Complete the manufactor (all second as)	Char	Carried biosystems)	262	1	1			
complete thermocycling parameters (all ssamples)	step	Enzyme Activation	PCR					
		Hold	Cycles (40 cycles)					
			Denature	Anneal/Extend				
	Time	20 sec	3 sec	30 sec				
	Temp (°C)	95	95	60				
Manufacturer of gPCR instrument								
aPCR validation								
Specificity (gel, sequence, melt, or digest)	Melt							
Data analysis								
aPCP applysis program (source version)	StopOpp Blue Bool time PC	austom						
dPCR analysis program (source, version)	StepOne Plus Real-time PCF	system						
Method of Lq determination	Applied Blosystems Relative	Quantitation Analysis Mo	anie					
Outlier identification and disposition	OUTLIERRG (Outlier in repli	cate group) quality flag						
Justification of number and choice of reference gene	One references gene with							
Description of normalization method	Comparative CT (ΔΔCT) met	hod						
Repeatability (intraassay variation)	see error bars in Figure 7A							
Statistical methods for results significance	Multiple comparisons using	Bonferroni-Dunn method						
Software (source, version)	Applied Biosystems Relative	Quantitation Analysis Mo	dule and GranbPad Prism	7				

Related to Figure 7F								
	Sample List							
Item to check	TC32 DMSO	TC32 10 uM PDS	TC32 siNegative	TC32 siHNRNPH1				
Experimental design								
Definition of experimental and control groups	Control group	Experimental group	Control group	Experimental group				
Number within each group	n = 3	n = 3	n = 3	n = 3				
Sample		•	•	·				
		TC32 cells treated with 10						
	TC32 cells treated with	micromolar pyridostatin for	TC32 cells tranfected with	TC32 cells tranfected with				
Description	DMSO for 72 hours	72 hours	siNegative for 72 hours	siHNRNPH1 for 72 hours				
Processing procedure		Cells were harvested by trypsi	nization 72 hours after treatn	nent				
If frozen, how and how quickly?		Flas	n Frozen					
Sample storage conditions and duration		Stored in -	80C for 5 days					
Nucleic acid extraction		Stored III						
Procedure and/or instrumentation		Promega May	ell 16 LEV System					
Name of kit and details of any modifications		Maxwell 16 LEV sim	nlyRNA Purification Kits					
Details of DNase or RNase treatment			nt was automated					
Nucleic acid quantification	Poplicate 1: 886 76 pg/ul	Peplicate 1: 204 88 ng/ul	Replicate 1: 876.96 pg/ul	Peplicate 1: 119 11 pg/ul				
	Replicate 2: 962 94 pg/ul	Replicate 2: 2/1 /1 ng/ul	Replicate 2: 974 38 ng/ul	Replicate 2: 136.93 pg/ul				
	Replicate 2: 302.34 lig/uL	Replicate 2: 241.41 lig/dL	Replicate 2: 974.38 lig/uL	Replicate 2: 136.09 ng/ul				
Instrument and method		Replicate 3. 150.05 lig/ue						
Purity (A260/A280)	Peplicate 1: 2 17	Replicate 1: 2.16	Peoplicate 1: 2 16	Peplicate 1: 2 15				
Pulity (A260/A280)	Replicate 1. 2.17	Replicate 1. 2.10	Replicate 1. 2.10	Replicate 2: 2.17				
	Replicate 2: 2:17	Replicate 2: 2:17	Replicate 2: 2:18	Replicate 2: 2:17				
PNA integrity method/instrument	Replicate 3. 2.17	Replicate 3. 2.17	nodron	Replicate 3: 2:16				
RNA integrity. methody instrument		Nanourop						
Reverse transcription								
Complete reaction conditions	1X iScript Reverse Tran	scription Supermix containing	oligo(dT) and random prime	rs (Biorad). RNA and water				
Amount of RNA and reaction volume		1000 ng of RNA and	20 uL reaction volume					
Reverse transcriptase and concentration	1X iScrint Reverse Transcrintase							
Temperature and time	Priming: 5 min at 25C							
· - · · · · · · · · · · · · · · · · · ·	Reverse transcription: 20 min at 460							
	Reverse transcription inactivation: 1 min at 950							
aPCR target information								
Gene symbol								
Sequence accession number		refer to Table S3						
Amplicon length								
In silico specificity screen (BLAST, and so on)								
What splice variants are targeted?		refer to	Table S3					
that spile variants are targeted.								
		Com	nlo List					
Itom to chock	TC22 DM60	5dli TC22 10 JM DDS	TC22 ciNogativa					
aPCP aligonucloatidas		1C32 10 UNI PD3	i Coz silvegative					
Primor soquences		rafar t	a Tabla 52					
apcp protocol	<u> </u>	refer t						

qPCR protocol							
Complete reaction conditions	1X Fast SYBR Green Master Mix (Applied Biosystems), cDNA, and water						
Reaction volume and amount of cDNA/DNA	100 ng of cDNA and 20 uL reaction volume						
Primer, (probe), Mg2+, and dNTP concentrations		250 nM of ea	ach primer				
Polymerase identity and concentration	AmpliTaq Fast DNA Polymerase						
Buffer/kit identity and manufacturer	Fast SYBR Green Master Mix (Applied Biosystems)						
Complete thermocycling parameters		Enzyme Activation	I	PCR			
	Step	Hold	Cycles (40 cycles)				
		Hold	Denature	Anneal/Extend			
	Time	20 sec	3 sec	30 sec			
	Temp (°C)	95	95	60			
Manufacturer of qPCR instrument		StepOne Plus Real-	time PCR system				
qPCR validation							
Specificity (gel, sequence, melt, or digest)		Me	lt				
Data analysis							
qPCR analysis program (source, version)	StepOne Plus Real-time PCR system						
Method of Cq determination		Applied Biosystems Relative Q	uantitation Analysis Modu	le			
Outlier identification and disposition		OUTLIERRG (Outlier in rep	licate group) quality flag				
Justification of number and choice of reference genes	Two references genes w	th minimal standard deviation be	etween replicates and upo	n treatment were utilized for			
Description of normalization method		Comparative CT (	ΔΔCT) method				
Repeatability (intraassay variation)		see error bars	in Figure 7F				
Statistical methods for results significance	Multiple comparisons by	controlling the False Discovery F	Rate - Two-stage linear set	-up procedure of Benjamini,			
Software (source, version)	Applied B	iosystems Relative Quantitation	Analysis Module and Grap	hPad Prism 7			

Related to Figure S1A								
	Sample List							
Item to check	HEK-293T siNegative	HEK-293T siHNRNPH1	SKNMC siNegative	SKNMC siHNRNPH1	TC71 siNegative	TC71 siHNRNPH1	RDES siNegative	RDES siHNRNPH1
Experimental design								
Definition of experimental and control groups	Control group	Experimental group	Control group	Experimental group	Control group	Experimental group	Control group	Experimental group
Number within each group	n =3	n = 3	n = 3	n = 3	n = 3	n = 3	n = 3	n = 3
Sample								
		HEK-293T cells tranfected		SKNMC cells tranfected	TC71 transfected with		RDES transfected with	RDES cells tranfected
	HEK-293T transfected with	with siHNRNPH1 for 48	SKNMC transfected with	with siHNRNPH1 for 48	siNegative cells for 48	TC71 cells tranfected with	siNegative cells for 48	with siHNRNPH1 for 48
Description	siNegative cells for 48 hours	hours	siNegative cells for 48 hours	hours	hours	siHNRNPH1 for 48 hours	hours	hours
Processing procedure		·	Cells v	vere harvested by trypsinizati	ion 48 hour after treatment		·	•
If frozen, how and how quickly?				Flash Froz	en			
Sample storage conditions and duration				Stored in -80C for	r 1-3 days			
Nucleic acid extraction								
Procedure and/or instrumentation				Promega Maxwell 16	5 LEV System			
Name of kit and details of any modifications				Maxwell 16 LEV simplyRN	A Purification Kits			
Details of DNase or RNase treatment				Dnase treatment wa	s automated			
Nucleic acid quantification	Replicate 1: 782.11 ng/uL	Replicate 1: 788.14 ng/uL	Replicate 1: 271.18 ng/uL	Replicate 1: 132.25 ng/uL	Replicate 1: 304.84 ng/uL	Replicate 1: 224.66 ng/uL	Replicate 1: 792.1 ng/uL	Replicate 1: 698.13 ng/uL
	Replicate 2: 782.33 ng/uL	Replicate 2: 825.52 ng/uL	Replicate 2: 323.17 ng/uL	Replicate 2: 176.52 ng/uL	Replicate 2: 285.77 ng/uL	Replicate 2: 222.39 ng/uL	Replicate 2: 910.4 ng/uL	Replicate 2: 830.03 ng/uL
	Replicate 3: 701.91 ng/uL	Replicate 3: 826.23 ng/uL	Replicate 3: 262.22 ng/uL	Replicate 3: 196.52 ng/uL	Replicate 3: 301.19 ng/uL	Replicate 3: 200.04 ng/uL	Replicate 3: 893.85 ng/uL	Replicate 3: 907.4 ng/uL
Instrument and method			Nanodrop Nucleic Ac	id Quantification				
Purity (A260/A280)	Replicate 1: 2.15	Replicate 1: 2.17	Replicate 1: 2.11	Replicate 1: 2.04	Replicate 1: 2.13	Replicate 1: 2.15	Replicate 1: 2.17	Replicate 1: 2.16
	Replicate 2: 2.16	Replicate 2: 2.15	Replicate 2: 2.06	Replicate 2: 2.1	Replicate 2: 2.12	Replicate 2: 2.14	Replicate 2: 2.17	Replicate 2: 2.16
	Replicate 3: 2.16	Replicate 3: 2.16	Replicate 3: 2.12	Replicate 3: 2.07	Replicate 3: 2.13	Replicate 3: 2.14	Replicate 3: 2.17	Replicate 3: 2.16
RNA integrity: method/instrument				Nanodroj	р			
Reverse transcription								
Complete reaction conditions			1X iScript Reverse Transcription	on Supermix containing oligo	(dT) and random primers (B	iorad), RNA and water		
Amount of RNA and reaction volume				1000 ng of RNA and 20 ul	L reaction volume			
Reverse transcriptase and concentration				1X iScript Reverse T	ranscriptase			
Temperature and time				Priming: 5 min	at 25C			
				Reverse transcription:	20 min at 46C			
				Reverse transcription inactiv	vation: 1 min at 95C			
qPCR target information								
Gene symbol								
Sequence accession number				refer to Tabl	e \$3			
Amplicon length								
In silico specificity screen (BLAST, and so on)				UCSC In-Silico	o PCR			
What splice variants are targeted?				refer to Tabl	e S3			

	ample List									
Item to check	HEK-293T siNegative	HEK-293T siHNRNPH1	SKNMC siNegative	SKNMC siHNRNPH1	TC71 siNegative	TC71 siHNRNPH1	RDES siNegative	RDES siHNRNPH1		
qPCR oligonucleotides										
Primer sequences	refer to Table S3									
qPCR protocol										
Complete reaction conditions	1X Fast SYBR Green Master M	Fast SYBR Green Master Mix (Applied Biosystems), cDNA, and water								
Reaction volume and amount of cDNA/DNA	100 ng of cDNA and 20 uL rea	ction volume								
Primer, (probe), Mg2+, and dNTP concentrations	250 nM of each primer									
Polymerase identity and concentration	AmpliTaq Fast DNA Polymera	se								
Buffer/kit identity and manufacturer	Fast SYBR Green Master Mix	(Applied Biosystems)								
Complete thermocycling parameters (all samples)	Step	Enzyme Activation	PC	CR						
		Hold	Cycles (4	l0 cycles)						
			Denature	Anneal/Extend						
	Time	20 sec	3 sec	30 sec						
	Temp (°C)	95	95	60						
Manufacturer of qPCR instrument										
qPCR validation										
Specificity (gel, sequence, melt, or digest)	Melt									
Data analysis										
qPCR analysis program (source, version)	StepOne Plus Real-time PCR	system								
Method of Cq determination	Applied Biosystems Relative	Quantitation Analysis Module								
Outlier identification and disposition	OUTLIERRG (Outlier in replica	ate group) quality flag								
Justification of number and choice of reference gene	One references gene with									
Description of normalization method	Comparative CT ( $\Delta\Delta$ CT) meth	od								
Repeatability (intraassay variation)	see error bars in Figure S1A									
Statistical methods for results significance	Multiple comparisons using B	onferroni-Dunn method								
Software (source, version)	Applied Biosystems Relative	Quantitation Analysis Module	and GraphPad Prism 7							

Related to Figure S7B							
		Samp	le List				
Item to check	TC32 DMSO	TC32 10 uM PDS	TC32 siNegative	TC32 siHNRNPH1			
Experimental design	L	1					
Definition of experimental and control groups	Control group	Experimental group	Control group	Experimental group			
Number within each group	n = 3	n = 3	n = 3	n = 3			
Sample							
	T022	1C32 cells treated with 10	TC22	TCDD - III - I - Control - Dil			
Description	DMCO for 48 hours	micromolar pyridostatin for	iC32 cells tranfected with	C32 cells tranfected with			
Description Processing procedure	DIVISO FOR 48 hours	48 nours	sinegative for 48 nours	SINNENPH1 for 48 nours			
If frozen, how and how quickly?	Cei	Flash	Zalion 46 nours after treating	ent			
Sample storage conditions and duration		Stored in -80	C for 6 days				
Nucleic acid extraction							
Procedure and/or instrumentation	Promega Maxwell 16 LEV System						
Name of kit and details of any modifications		Maxwell 16 LEV simpl	yRNA Purification Kits				
Details of DNase or RNase treatment		Dnase treatment	t was automated				
Nucleic acid quantification	Replicate 1: 731.69 ng/uL	Replicate 1: 201.47 ng/uL	Replicate 1: 682.26 ng/uL	Replicate 1: 163 ng/uL			
	Replicate 2: 720.51 ng/uL	Replicate 2: 220.72 ng/uL	Replicate 2: 654.15 ng/uL	Replicate 2: 167.39 ng/uL			
	Replicate 3: 726.33 ng/uL	Replicate 3: 246.76 ng/uL	Replicate 3: 714.49 ng/uL	Replicate 3: 168.44 ng/uL			
Instrument and method		Nanodrop Nucleic A	Acid Quantification	<b>a u</b>			
Purity (A260/A280)	Replicate 1: 2.16	Replicate 1: 2.18	Replicate 1: 2.15	Replicate 1: 2.17			
	Replicate 2: 2.17	Replicate 2: 2.15	Replicate 2: 2.16	Replicate 2: 2.18			
	Replicate 3: 2.16	Replicate 3: 2.15	Replicate 3: 2.17	Replicate 3: 2.14			
RNA Integrity: method/instrument		Nanc	barop				
Reverse transcription							
Complete reaction conditions	1X iScript Reverse Transcr	ription Supermix containing c	oligo(dT) and random primers	(Biorad), RNA and water			
Amount of RNA and reaction volume		1000 ng of RNA and 2	20 uL reaction volume				
Reverse transcriptase and concentration		1X iScript Revers	se Transcriptase				
Temperature and time		Priming: 5	min at 25C				
		Reverse transcript	ion: 20 min at 46C				
		Reverse transcription in	activation: 1 min at 95C				
qPCR target information	1						
Gene symbol							
Sequence accession number	-	refer to	Table S3				
Amplicon length							
What splice variants are targeted?		refer to 1	Table S2				
what spice variants are targeted:							
		Samp	le List	1			
Item to check	TC32 DMSO	TC32 10 uM PDS	TC32 siNegative	TC32 siHNRNPH1			
qPCR oligonucleotides			T.11. C2				
Primer sequences		refer to	lable 53				
Complete reaction conditions	1V Eact	SVPR Groop Master Mix (Ap	plied Piesystems) cDNA and	wator			
Reaction volume and amount of cDNA/DNA	IX Fast	100 ng of cDNA and 2	0 ul reaction volume	i water			
Primer (probe) Mg2+ and dNTP concentrations		250 nM of e	each primer				
Polymerase identity and concentration		AmpliTag Fast [	DNA Polymerase				
Buffer/kit identity and manufacturer		Fast SYBR Green Master	Mix (Applied Biosystems)				
Complete thermocycling parameters		Enzyme Activation	PC	CR			
. , .	Step	, Hold	Cycles (4	0 cycles)			
		HUIU	Denature	Anneal/Extend			
	Time	20 sec	3 sec	30 sec			
	Temp (°C)	95	95	60			
Manufacturer of qPCR instrument		StepOne Plus Real	-time PCR system				
qPCK validation			- 1+				
Specificity (gei, sequence, meit, or digest)	l	M	en				
aPCR analysis program (source version)		StenOne Dluc Pool	-time PCR system				
Method of Ca determination	1	Annlied Biosystems Relative	Quantitation Analysis Module	3			
Outlier identification and disposition	r 	OUTLIERRG (Outlier in re	plicate group) quality flag				
Justification of number and choice of reference genes	Two references genes with	minimal standard deviation b	between replicates and upon	treatment were utilized for			
Description of normalization method	<u> </u>	Comparative CT	$(\Delta\Delta CT)$ method				
Repeatability (intraassay variation)		see error bars	in Figure S7B				
Statistical methods for results significance	Multiple comparisons by co	ntrolling the False Discovery	Rate - Two-stage linear set-u	up procedure of Benjamini,			
Software (source, version)	Applied Biosystems Relative Quantitation Analysis Module and GraphPad Prism 7						