Table S7: qPCR additional experimental details

Related to Figure 1A				
Item to check	**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 siNegative for 48 hours	TC32 cells tranfected with siHNRNPH1 for 48 hours	TC32 cells tranfected with siHNRNPH2 for 48 hours	TC32 cells tranfected with siHNRNPH2 for 48 hours
Processing procedure	Cells were harvested by trypsinization 48 hour after treatment			
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 Quantification			
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 Supermix containing oligo(dT) and random primers (Biorad), RNA and water			
Amount of RNA and reaction volume	1000 ng of RNA and 20 uL reaction volume			
Reverse transcriptase and concentration	1X iScript Reverse Transcriptase			
Temperature and time	Priming: 5 min at 25C			
	Reverse transcription: 20 min at 46C			
	Reverse transcription inactivation: 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			

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 replicate group) quality flag
Justification of number and choice of reference genes	Three references genes with minimal standard deviation between replicates and upon treatment were utilized for normalization
Description of normalization method	Comparative CT (ΔΔCT) method
Repeatability (intraassay variation)	see error bars in Figure 1A
Statistical methods for results significance	Multiple comparisons using Bonferroni-Dunn method
Software (source, version)	Applied Biosystems Relative Quantitation Analysis Module and 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 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 each primer			
Polymerase identity and concentration	AmpliTaq Fast DNA Polymerase			
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 system			

Table S7: qPCR additional experimental details

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 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**
Experimental design												
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 each group	n =3	n = 3	n = 3	n = 3	n = 3	n = 3	n = 3	n = 3	n = 3	n = 3	n = 3	n = 3
Sample												
Description	untreated TC32 cells for 48 hours	TC32 cells tranfected with siNegative for 48 hours	TC32 cells tranfected with siHNRNPH1 for 48 hours	TC32 cells tranfected with siFLI1 for 48 hours	TC32 cells tranfected with 20 nM rG1 oligomer for 48 hours	TC32 cells tranfected with 40 nM rG1 oligomer for 48 hours	TC32 cells tranfected with 80 nM rG1 oligomer for 48 hours	TC32 cells tranfected with 160 nM rG1 oligomer for 48 hours	TC32 cells tranfected with 20 nM rG1 mutant 1 oligomer for 48 hours	TC32 cells tranfected with 40 nM rG1 mutant 1 oligomer for 48 hours	TC32 cells tranfected with 80 nM rG1 mutant 1 oligomer for 48 hours	TC32 cells tranfected with 160 nM rG1 mutant 1 oligomer for 48 hours
Processing procedure	Cells were harvested by trypsinization 48 hour after treatment											
If frozen, how and how quickly?	Flash Frozen											
Sample storage conditions and duration	Stored in -80C for 9 days											
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: 556.25 ng/uL	Replicate 1: 329.66 ng/uL	Replicate 1: 126.34 ng/uL	Replicate 1: 109.03 ng/uL	Replicate 1: 256.19 ng/uL	Replicate 1: 103.59 ng/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	Replicate 2: 397.08 ng/uL	Replicate 2: 138.92 ng/uL	Replicate 2: 110.82 ng/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/uL	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/u	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		Nanodrop Nucleic Acid Quantification										
Purity (A260/A280)	Replicate 1: 2.18	Replicate 1: 2.13	Replicate 1: 2.1	Replicate 1: 2.1	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: 2.14	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	1X iScript Reverse Transcription Supermix containing oligo(dT) and random primers (Biorad), RNA and water											
Amount of RNA and reaction volume	1000 ng of RNA and 20 uL reaction volume											
Reverse transcriptase and concentration	1X iScript Reverse Transcriptase											
Temperature and time	Priming: 5 min at 25C											
	Reverse transcription: 20 min at 46C											
	Reverse transcription inactivation: 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											

Item to check	**Sample List**											
	TC32 Untreated	**TC32 siNegative**	**TC32 siHNRNPH1**	**TC32 siFLI1**	**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**
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 reaction volume											
Primer, (probe), Mg2+, and dNTP concentrations	250 nM of each primer											
Polymerase identity and concentration	AmpliTaq Fast DNA Polymerase											
Buffer/kit identity and manufacturer	Fast SYBR Green Master Mix (Applied Biosystems)											
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 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 replicate group) quality flag											
Justification of number and choice of reference gene	One references gene with minimal standard deviation between replicates and upon treatment were utilized for normalization											
Description of normalization method	Comparative CT (ΔΔCT) method											
Repeatability (intraassay variation)	see error bars in Figure 2G											
Statistical methods for results significance	Multiple comparisons by controlling the False Discovery Rate - Two-stage linear set-up procedure of Benjamini, Krieger, and Yekutieli											
Software (source, version)	Applied Biosystems Relative Quantitation Analysis Module and GraphPad Prism 7											

Table S7: qPCR additional experimental details

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								
Description	untreated TC32 cells for 48 hours	TC32 cells tranfected with siNegative for 48 hours	TC32 cells tranfected with siHNRNPH1 for 48 hours	TC32 cells tranfected with siFLI1 for 48 hours	TC32 cells treated with DMSO for 48 hours	TC32 cells treated with 5micromolar of pyridostatin for 48 hours	TC32 cells treated with 10 micromolar of pyridostatin for 48 hours	TC32 cells treated with 15 micromolar of pyridostatin for 48 hours
Processing procedure	Cells were harvested by trypsinization 48 hour after treatment							
If frozen, how and how quickly?	Flash Frozen							
Sample storage conditions and duration	Stored in -80C 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 simplyRNA Purification Kits							
Details of DNase or RNase treatment	Dnase treatment was automated							
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/uL	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/uL	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 Quantification							
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
	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 3: 2.19	Replicate 3: 2.17	Replicate 3: 2.14	Replicate 3: 2.18	Replicate 3: 2.16	Replicate 3: 2.16	Replicate 3: 2.15	Replicate 3: 2.15
RNA integrity: method/instrument	Nanodrop							
Reverse transcription								
Complete reaction conditions	1000 ng of RNA and 20 uL reaction volume							
Amount of RNA and reaction volume	1X iScript Reverse Transcriptase							
Reverse transcriptase and concentration	Priming: 5 min at 25C							
Temperature and time	Reverse transcription: 20 min at 46C							
	Reverse transcription inactivation: 1 min at 95C							
	Reverse transcription inactivation: 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							

Item to check	**Sample List**							
	TC32 Untreated	**TC32 siNegative**	**TC32 siHNRNPH1**	**TC32 siFLI1**	**TC32 DMSO**	**TC32 5uM PDS**	**TC32 10uM PDS**	**TC32 15uM 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 reaction volume							
Primer, (probe), Mg2+, and dNTP concentrations	250 nM of each primer							
Polymerase identity and concentration	AmpliTaq Fast DNA Polymerase							
Buffer/kit identity and manufacturer	Fast SYBR Green Master Mix (Applied Biosystems)							
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 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 replicate group) quality flag							
Justification of number and choice of reference genes	One references gene with							
Description of normalization method	Comparative CT (ΔΔCT) method							
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 Module and GraphPad Prism 7							

Table S7: qPCR additional experimental details

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				
Description	TC32 cells treated with DMSO for 72 hours	TC32 cells treated with 10 micromolar pyridostatin for 72 hours	TC32 cells tranfected with siNegative for 72 hours	TC32 cells tranfected with siHNRNPH1 for 72 hours
Processing procedure	Cells were harvested by trypsinization 72 hours after treatment			
If frozen, how and how quickly?	Flash Frozen			
Sample storage conditions and duration	Stored in -80C for 5 days			
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: 886.76 ng/uL	Replicate 1: 204.88 ng/uL	Replicate 1: 876.96 ng/uL	Replicate 1: 119.11 ng/uL
	Replicate 2: 962.94 ng/uL	Replicate 2: 241.41 ng/uL	Replicate 2: 974.38 ng/uL	Replicate 2: 136.93 ng/uL
	Replicate 3: 1050.86 ng/uL	Replicate 3: 260.64 ng/uL	Replicate 3: 887.18 ng/uL	Replicate 3: 136.09 ng/uL
Instrument and method	Nanodrop Nucleic Acid Quantification			
Purity (A260/A280)	Replicate 1: 2.17	Replicate 1: 2.16	Replicate 1: 2.16	Replicate 1: 2.15
	Replicate 2: 2.17	Replicate 2: 2.17	Replicate 2: 2.18	Replicate 2: 2.17
	Replicate 3: 2.17	Replicate 3: 2.17	Replicate 3: 2.17	Replicate 3: 2.16
RNA integrity: method/instrument	Nanodrop			
Reverse transcription				
Complete reaction conditions	1X iScript Reverse Transcription Supermix containing oligo(dT) and random primers (Biorad), RNA and water			
Amount of RNA and reaction volume	1000 ng of RNA and 20 uL reaction volume			
Reverse transcriptase and concentration	1X iScript Reverse Transcriptase			
Temperature and time	Priming: 5 min at 25C			
	Reverse transcription: 20 min at 46C			
	Reverse transcription inactivation: 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			

	Sample List			
Item to check	**TC32 DMSO**	**TC32 10 uM PDS**	**TC32 siNegative**	**TC32 siHNRNPH1**
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 reaction volume			
Primer, (probe), Mg2+, and dNTP concentrations	250 nM of each primer			
Polymerase identity and concentration	AmpliTaq Fast DNA Polymerase			
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 system			
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 replicate group) quality flag			
Justification of number and choice of reference genes	Two references genes with minimal standard deviation between replicates and upon 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 Rate - Two-stage linear set-up procedure of Benjamini,			
Software (source, version)	Applied Biosystems Relative Quantitation Analysis Module and GraphPad Prism 7			

Table S7: qPCR additional experimental details

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								
Description	HEK-293T transfected with siNegative cells for 48 hours	HEK-293T cells tranfected with siHNRNPH1 for 48 hours	SKNMC transfected with siNegative cells for 48 hours	SKNMC cells tranfected with siHNRNPH1 for 48 hours	TC71 transfected with siNegative cells for 48 hours	TC71 cells tranfected with siHNRNPH1 for 48 hours	RDES transfected with siNegative cells for 48 hours	RDES cells tranfected with siHNRNPH1 for 48 hours
Processing procedure	Cells were harvested by trypsinization 48 hour after treatment							
If frozen, how and how quickly?	Flash Frozen							
Sample storage conditions and duration	Stored in -80C for 1-3 days							
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: 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 Acid 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	Nanodrop							
Reverse transcription								
Complete reaction conditions	1X iScript Reverse Transcription Supermix containing oligo(dT) and random primers (Biorad), RNA and water							
Amount of RNA and reaction volume	1000 ng of RNA and 20 uL reaction volume							
Reverse transcriptase and concentration	1X iScript Reverse Transcriptase							
Temperature and time	Priming: 5 min at 25C							
	Reverse transcription: 20 min at 46C							
	Reverse transcription inactivation: 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							

	Sample 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 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 each primer							
Polymerase identity and concentration	AmpliTaq Fast DNA Polymerase							
Buffer/kit identity and manufacturer	Fast SYBR Green Master Mix (Applied Biosystems)							
Complete thermocycling parameters (all samples)	*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								
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 replicate group) quality flag							
Justification of number and choice of reference genes	One references gene with							
Description of normalization method	Comparative CT (ΔΔCT) method							
Repeatability (intraassay variation)	see error bars in Figure S1A							
Statistical methods for results significance	Multiple comparisons using Bonferroni-Dunn method							
Software (source, version)	Applied Biosystems Relative Quantitation Analysis Module and GraphPad Prism 7							

Table S7: qPCR additional experimental details

Related to Figure S7B				
	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				
Description	TC32 cells treated with DMSO for 48 hours	TC32 cells treated with 10 micromolar pyridostatin for 48 hours	TC32 cells tranfected with siNegative for 48 hours	TC32 cells tranfected with siHNRNPH1 for 48 hours
Processing procedure	Cells were harvested by trypsinization 48 hours after treatment			
If frozen, how and how quickly?	Flash Frozen			
Sample storage conditions and duration	Stored in -80C 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 simplyRNA Purification Kits			
Details of DNase or RNase treatment	Dnase treatment 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 Acid Quantification			
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	Nanodrop			
Reverse transcription				
Complete reaction conditions	1X iScript Reverse Transcription Supermix containing oligo(dT) and random primers (Biorad), RNA and water			
Amount of RNA and reaction volume	1000 ng of RNA and 20 uL reaction volume			
Reverse transcriptase and concentration	1X iScript Reverse Transcriptase			
Temperature and time	Priming: 5 min at 25C			
	Reverse transcription: 20 min at 46C			
	Reverse transcription inactivation: 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			

	Sample List			
Item to check	**TC32 DMSO**	**TC32 10 uM PDS**	**TC32 siNegative**	**TC32 siHNRNPH1**
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 reaction volume			
Primer, (probe), Mg2+, and dNTP concentrations	250 nM of each primer			
Polymerase identity and concentration	AmpliTaq Fast DNA Polymerase			
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 system			
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 replicate group) quality flag			
Justification of number and choice of reference genes	Two references genes with minimal standard deviation between replicates and upon treatment were utilized for			
Description of normalization method	Comparative CT (ΔΔCT) method			
Repeatability (intraassay variation)	see error bars in Figure S7B			
Statistical methods for results significance	Multiple comparisons by controlling the False Discovery Rate - Two-stage linear set-up procedure of Benjamini,			
Software (source, version)	Applied Biosystems Relative Quantitation Analysis Module and GraphPad Prism 7			