

Supplemental Figure legends

Figure S1. (a) Expression of hnRNP E1 transcript levels in NMuMG cells treated with TGF β . β Actin was used as a loading control. **(b)** Polysome profiling of NMuMG cells either untreated or treated with TGF β for 7 days. hnRNP E1 is actively translated under both conditions, whereas, the positive control inhibin β A shifts to heavier polysome fractions following TGF β treatment. **(c)** Immunoblot of hnRNP E1 and Hsp90 (loading control) following treatment of NMuMG cells with cycloheximide for 12h and co-treatment with either the ER-Golgi trafficking inhibitor Brefeldin A, the lysosome inhibitor chloroquine or the proteasome inhibitor MG132. **(d)** Interaction between hnRNP E1 and ARIH1 in yeast 2 hybrid assay. Growth observed on Leu-/Trp-/Ade- plates indicating interaction between hnRNP E1 and ARIH1. **(e)** Immunoblot of hnRNP E1, ARIH1 and Hsp90 (loading control) following ARIH1 siRNA in NMuMG cells. **(f)** hnRNP E1 protein levels following treatment with the neddylation inhibitor MLN4924. **(g)** Immunoprecipitation of exogenous V5 tagged hnRNP E1 followed by K63 ubiquitin immunoblot. **(h)** Protein stability, assessed by cycloheximide chase assay, of WT and K314R or K351R mutant V5-tagged hnRNP E1 with or without MG132 treatment.

Figure S2. (a) Transcript levels of the epithelial marker, E-cadherin, in NMuMG cells treated with TGF β , as determined by semi-quantitative PCR. β Actin was used as a loading control. **(b)** Rhodamine phalloidin staining of actin in NMuMG control and ARIH1 KD cells following 2 d of TGF β treatment. **(c)** 3D invasion assay of NMuMG control and ARIH1 KD cells; representative images of invasion in Matrigel, invasive areas are delineated. **(d)** Immunoblot of ARIH1 expression levels in SUM159 control and ARIH1 ORF cells and SUM159 scrambled control and ARIH1 KD clones (sh5 and sh11). Hsp90 was used as a loading control. **(e)** Protein levels of hnRNP E1 in cycloheximide-treated SUM159 scrambled control and ARIH1 KD cells. Hsp90 is used as a loading control. **(f)** Proliferation of SUM159 WT, scrambled control and ARIH1 KD cells, as assessed by MTT assay. **(g)** Immunoblot of ARIH1 expression levels in LM2 scrambled control

(scram) and ARIH1 sh8 KD cells. Hsp90 was used as a loading control. **(h)** Proliferation rates of LM2 scrambled control and ARIH1 KD cells.

Figure S3. (a) Protein levels of hnRNP E1 and the mesenchymal markers N-Cadherin and Vimentin in TGF β -treated SUM159 control and ARIH1 ORF cells. **(b)** 2D invasion assay of SUM159 control and ARIH1 ORF cells; representative images of invasive cells (left panel) and quantitation (Mean \pm SD, unpaired t-test compared to control; * = $P < 0.05$). **(c)** 3D invasion assay of SUM159 control and ARIH1 ORF cells; representative images of invasion in Matrigel. **(d)** Mammosphere assay of SUM159 control and ARIH1 ORF cells; representative images of spheres and quantitation of sphere number (Mean \pm SEM, paired t-test compared to control was not significant). **(e)** Image of excised tumors from mice injected with SUM159 cells stably expressing scrambled control. **(f)** Image of excised tumors from mice injected with SUM159 control and ARIH1 ORF cells. **(g)** Tumor volumes in NOD-SCID mice mammary fat pad injected with SUM159 control and ARIH1 ORF cells (mean \pm SEM). **(h)** Quantitation of tumor weight following xenograft of SUM159 control and ARIH1 ORF cells (n = 9 control xenografts, n = 7 ORF xenografts; mean + SEM, unpaired t-test; n.s = not significant).

Figure S4. (a) Protein levels of Vimentin and CD44 in LM2 scrambled control, ARIH1 Sh8 KD cells and ARIH1 sh8 KD with hnRNP E1 silencing (CRISPR 50 and 52). **(b)** Proliferation rates of LM2 scrambled control cells, ARIH1 sh8 KD cells and ARIH1 sh8 KD cells with hnRNP E1 silencing. **(c)** Representative image of excised tumors and **(d)** tumor weights from mice injected with LM2 ARIH1 sh8 E1 CRISPR 50 and 52. **(e)** Quantitation of 2D invasion, following crystal violet stain extraction, using LM2 ARIH1 KD cells and ARIH1 KD with hnRNP E1 silencing (mean +SD). **(f)** Representative images of 3D invasion assay with LM2 scrambled control cells and ARIH1 KD cells with hnRNP E1 silencing. **(g)** Protein levels of hnRNP E1 in SUM159 ARIH1 KD cells with hnRNP E1 CRISPR. **(h)** Proliferation rates of parental SUM159 ARIH1 KD cells and ARIH1 KD cells with hnRNP E1 CRISPR. **(i)** Representative

images of 3D invasion assay with SUM159 scrambled control cells, ARIH1 KD cells and ARIH1 KD cells with hnRNP E1 silencing. **(j)** Mammosphere formation in SUM159 scrambled control cells, ARIH1 KD cells and ARIH1 KD cells with hnRNP E1 silencing. V5 hnRNP E1 protein levels in **(k)** SUM159 ARIH1 ORF cells 3 d post transient nucleofection, and **(l)** stably selected SUM159 cells. V5 hnRNP E1 protein levels in stably selected SUM159 cells treated with cycloheximide for **(m)** 0, 4 and 8 h and for **(n)** 0 and 17 h. Hsp90 is used as a loading control. **(o)** V5 hnRNP E1 protein levels in stably selected SUM159 cells transiently transfected with control or ARIH1 siRNA for 72 h. **(p)** Proliferation of SUM159 cells stably expressing WT, K314R and K351R V5 hnRNP E1, as assessed by cell count. **(q)** Representative images and quantitation of mammosphere number (Mean \pm SEM, paired t-test compared to control; ** = $P < 0.01$, *** = $P < 0.001$). **(r)** Representative images of 2D invasion assay using SUM159 cells stably expressing WT, K314R and K351R V5 hnRNP E1.

Figure S5. (a) Kaplan-Meier analysis of survival in TCGA breast cancer patient data. (n = 1194, TCGA dataset; $P=0.05$, log-rank test). **(b)** Kaplan-Meier analysis of relapse-free survival in breast cancer patients. (n = 3951, KM-plotter; $P<0.001$, log-rank test). Correlation between ARIH1 protein levels and the epithelial markers **(c)** E-cadherin and **(d)** Occuldin in breast cancer patient samples analyzed using cBioPortal. **(e)** Protein expression of ARIH1 in normal lung and lung adenocarcinoma tissue. **(f)** Protein expression of ARIH1 across lung cancer grade.

Figure S6. (a) Protein levels of hnRNP E1 and ARIH1 across a panel of colorectal cancer cell lines. Hsp90 was used as a loading control (top panel). hnRNP E1 transcript levels are not altered across these lines, as assessed by semi-quantitative PCR. GAPDH was used as a loading control (bottom panel). **(b)** Representative images of HCT116 scrambled control and ARIH1 KD cell morphology. **(c)** Proliferation of HCT116 scrambled control and ARIH1 KD cells, as assessed by cell count across 4 days. **(d)** 3D invasion assay of HCT116 WT, scrambled control and ARIH1 KD cells; representative images of invasion in Cultrex. **(e)** Correlation between ARIH1 protein

levels and the mesenchymal marker Vimentin (left panel) and the epithelial marker E-Cadherin (right panel) in colorectal cancer patient samples analyzed using cBioPortal.

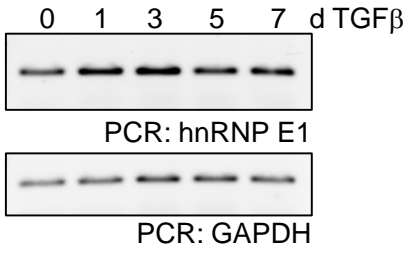
Table S1. Sequences and expected product size of primers used for PCR.

Table S2. List of proteins identified from ARIH1-miniTurboID experiment.

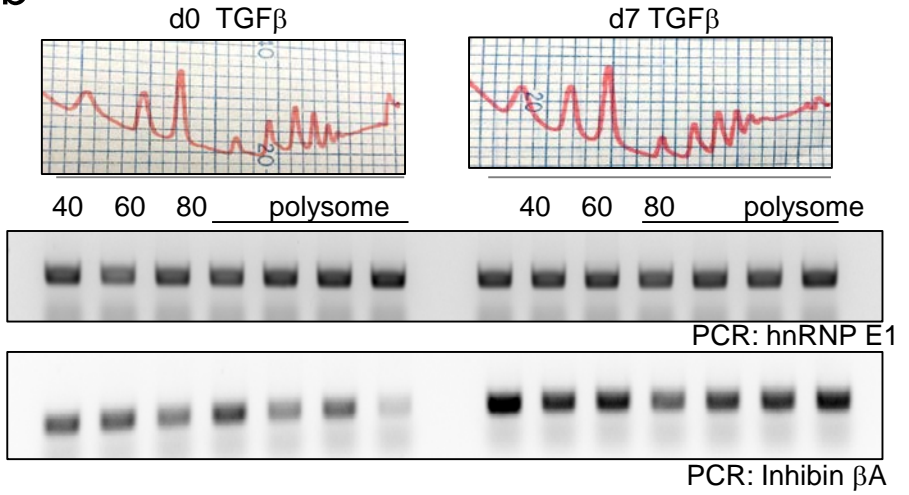
Table S3. Sanger sequencing results for hnRNP E1 CRISPR clones.

Supplemental Figure 1

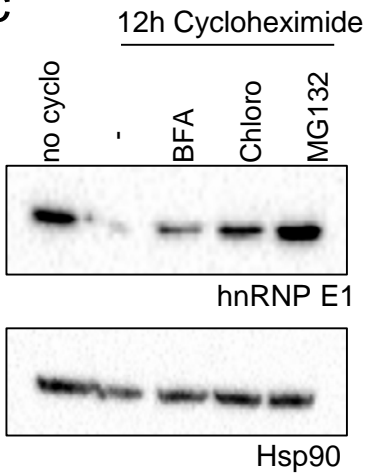
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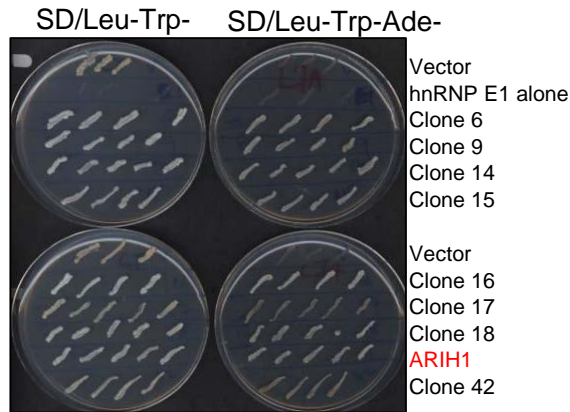
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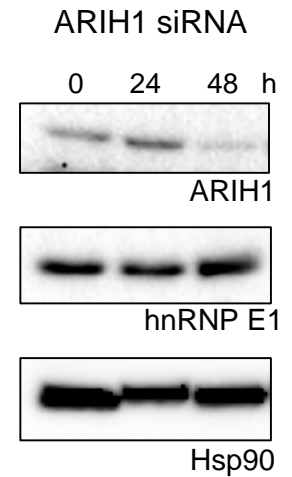
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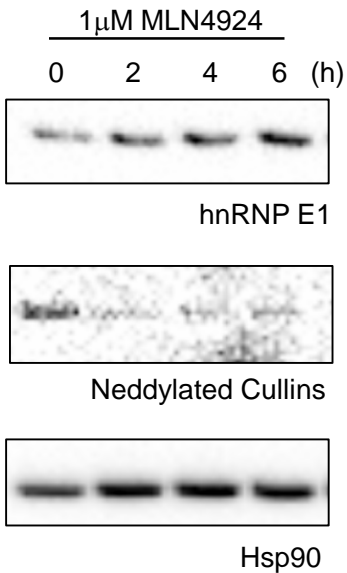
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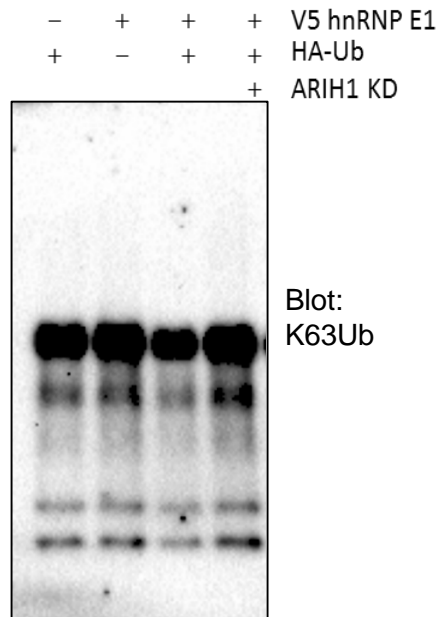
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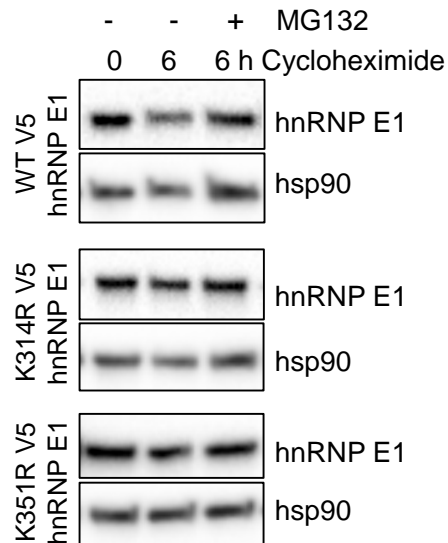
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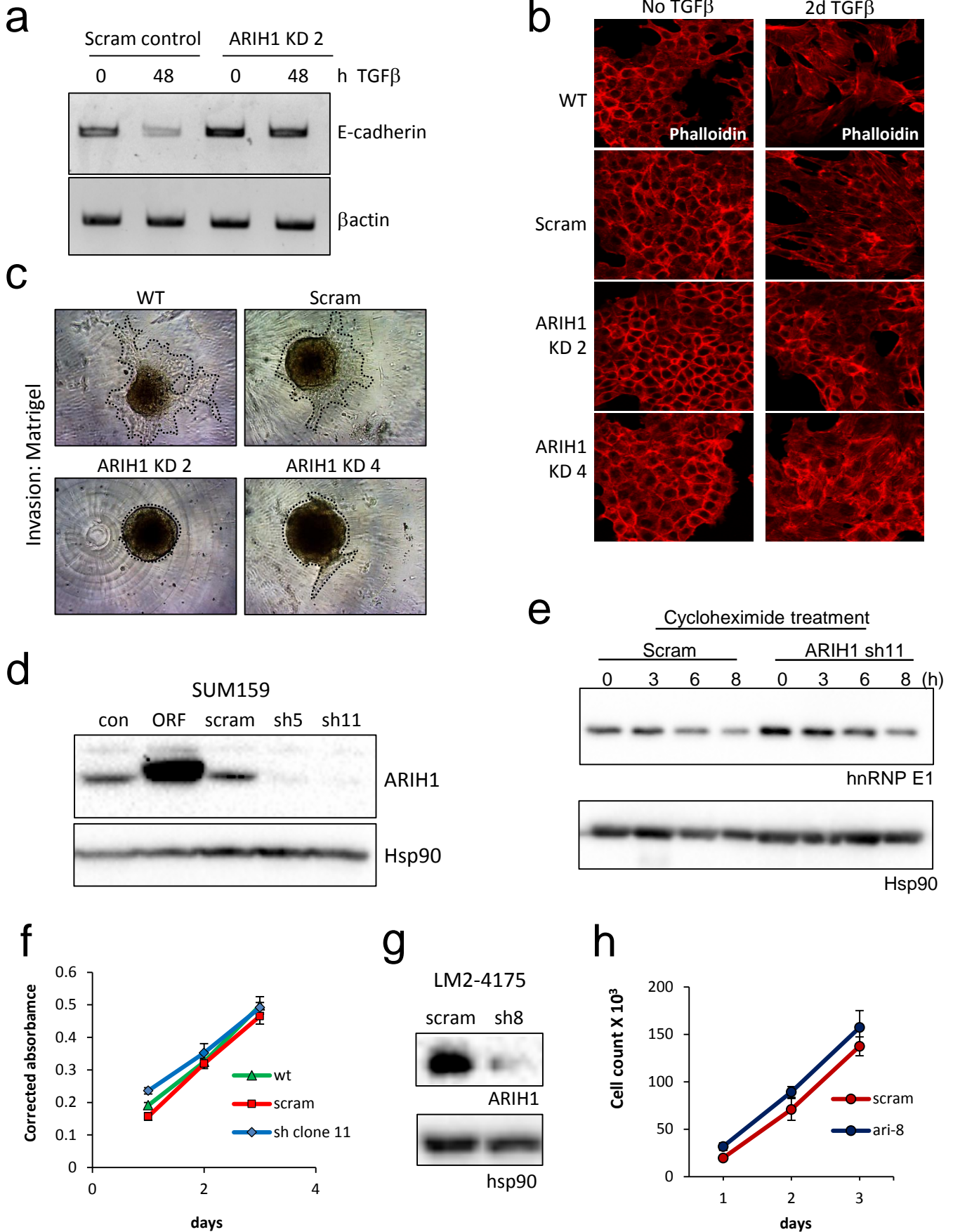
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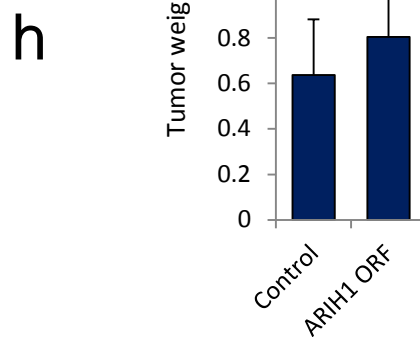
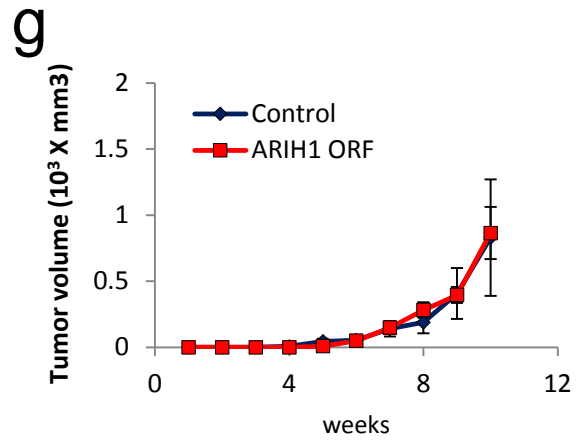
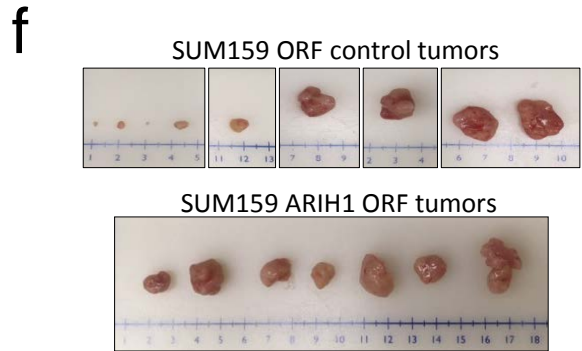
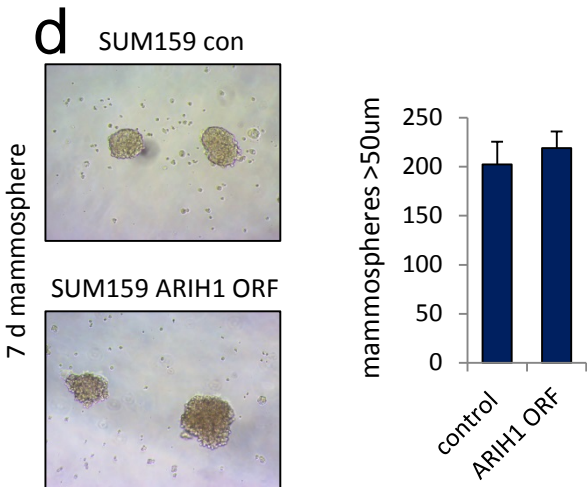
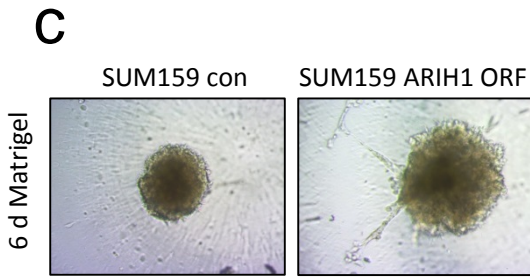
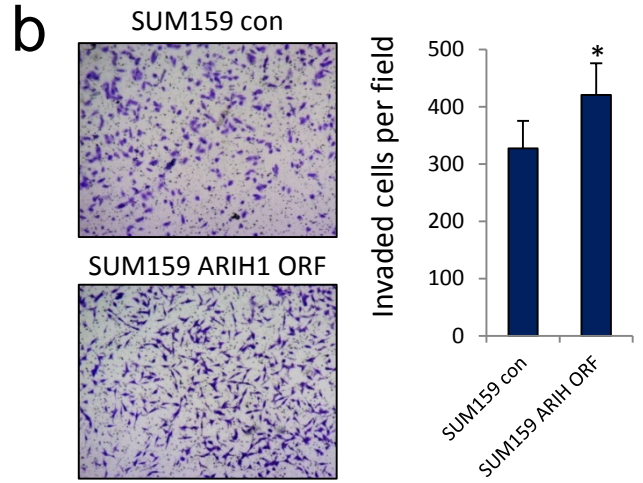
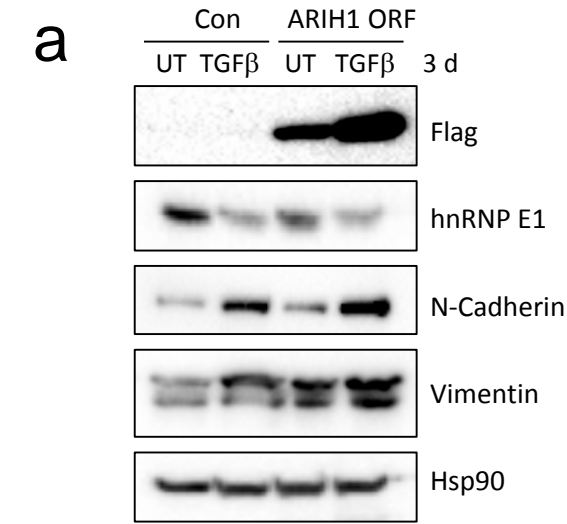
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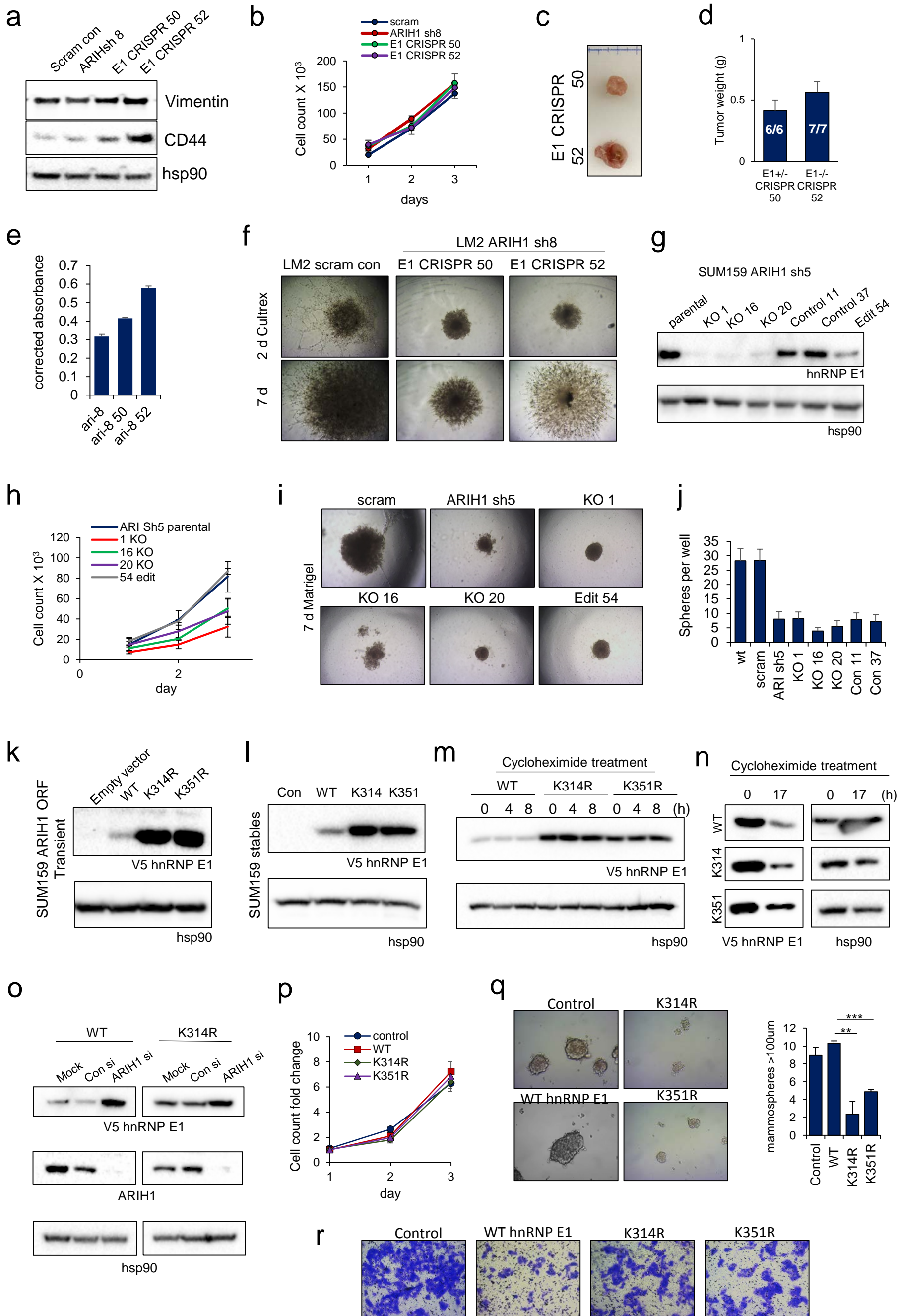


Supplemental Figure 2



Supplemental Figure 3





Supplemental Figure 6

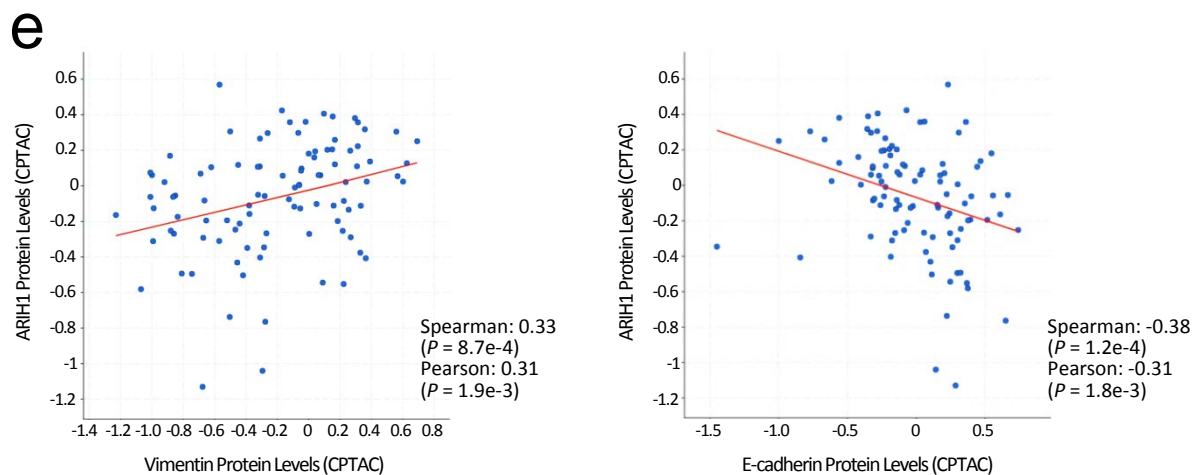
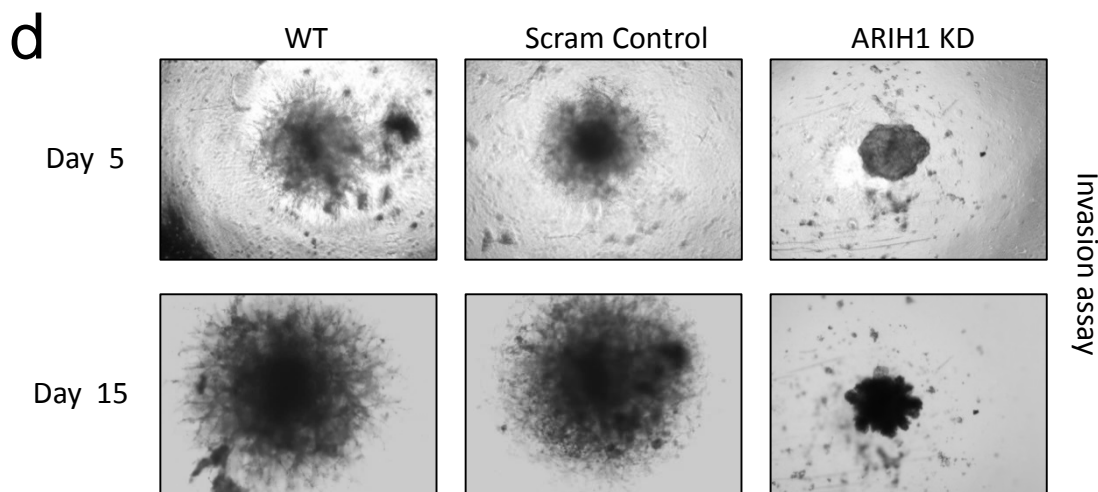
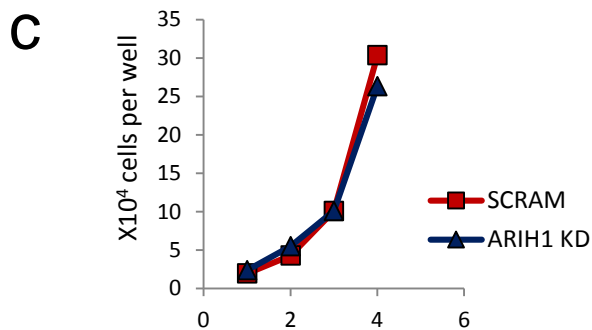
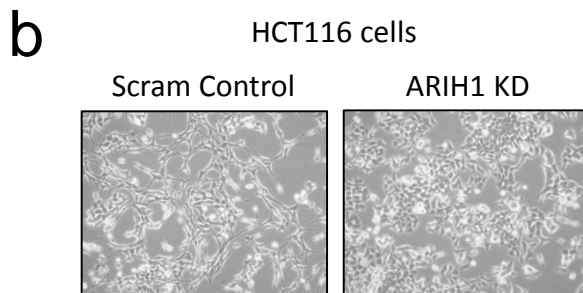
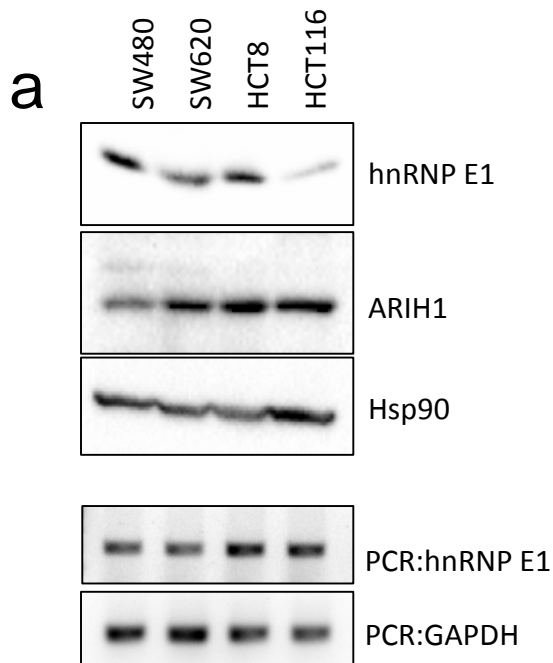


Table S1. Primers used for PCR

Target	Sequence	Product size
Mouse hnRNP E1	Forward: AAGGCGCCAACATCAATGAG; Reverse: GGGTTACGAGCGAACCTACG	204 bp
Mouse ARIH1	Forward:GAGGTCATCCAGAATCCAGCA ; Reverse:TGCGCAGGACACGAAATAGT	338 bp
Mouse E-Cadherin	Forward: GAAGGCTTGAGCACAAACAGC; Reverse: AGATGGGGGCTTCATTACCG	400 bp
Mouse Inhibin β A	Forward: TCCCCACCCAGGATCCGA; Reverse: ACCGGCTGGGTGACATCGGG	173 bp
Mouse GAPDH	Forward: GGTTGTCTCCTGCGACTTCA; Reverse: TAGGGCTCTCTTGCTCAGT	220 bp
Human hnRNP E1	Forward: CCACGTAACGAGCCCAACT; Reverse: CCCTCCGAGATGTTGATCCG	200 bp
Human ARIH1	Forward: AGAGAATGCCACAGAGGTGC; Reverse: CCCTTCGTCGACTCTCACAG	119 bp
Human Aldh1a1	Forward: ATCAAAGAAGCTGCCGGGAA; Reverse: GCATTGTCCAAGTCGGCATC	101 bp
Human Klf4	Forward: ATGCTCACCCACCTTCTTC; Reverse: GGTGGTCCGACCTGGAAAAT	340 bp
Human Oct4	Forward: CTCACCCTGGGGGTTCTATT; Reverse: CTGGTTCGCTTTCTCTTTTCG	203 bp
Human Sox2	Forward: AACCAGCGCATGGACAGTTA; Reverse: GACTTGACCACCGAACCCAT	278 bp
Human Nanog	Forward: AAAGGCAACAACCCACTTC; Reverse: CATTGCTATTCTTCGGCCAG	274 bp
Human GAPDH	Forward: TGATGACATCAAGAAGGTGGTGAAG; Reverse: TCCTTGAGGCCATGTGGGCCAT	240 bp
β -Actin	Forward: TCATGAAGTGTGACGTTGACATCCGT; Reverse: CCTAGAAGCATTTCGGGTGCACGATG	285 bp
miniturboid ARIH1	Forward: GGTGGTAAGCTTATGGACTCGGACGAGGGCTACA; Reverse: TGCTTAGCGGCCCGCTCCTCAATGTACTCCCACA	1.6 kb
hnRNP E1 CRISPR primer set A	Forward: ACTTGACCACGTAACGAGCC; Reverse: TCCAGCATGACCAGGCAAAT	554 bp
hnRNP E1 CRISPR primer set B	Forward: TCGGCTTCTTATGCACGGAA; Reverse: CTTCTCCAGCTTGTCGATGA	197 bp
K351 site directed mut. primers	Forward: CCCCATGCCCTCTCAGAGGAAAGCCTGGC; Reverse: GCCAGGCTTCTCTGAGAGGGGCATGGGG	n/a
K314 site directed mut. primers	Forward: CTGGGTTGGCAATTCTGATCTGGGCCCCG; Reverse: CGGGGCCAGATCAGAATTGCCAACCCAG	n/a

Table S2. Proteins identified from ARIH1-miniTurboID experiment

reference	Gene Symbol	Annotation	Unique hits: Hek_ARIH1 mTbioID_Con	Total hits: Hek_ARIH1 mTbioID_Con	Unique hits: Hek_ARIH1 mTbioID_Biotin	Total hits: Hek_ARIH1 mTbioID_Biotin
sp P21333 FLNA_HUMAN	FLNA	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	0	0	51	56
sp P49327 FASN_HUMAN	FASN	Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3	0	0	21	21
sp P50990 TCPQ_HUMAN	CCT8	T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4	0	0	16	16
sp Q04637 IF4G1_HUMAN	EIF4G1	Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=4	0	0	9	10
sp P11388 TOP2A_HUMAN	TOP2A	DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3	0	0	7	7
sp Q99613 EIF3C_HUMAN	EIF3C	Eukaryotic translation initiation factor 3 subunit C OS=Homo sapiens GN=EIF3C PE=1 SV=1	0	0	7	7
sp Q6WCQ1 MPRIP_HUMAN	MPRIP	Myosin phosphatase Rho-interacting protein OS=Homo sapiens GN=MPRIP PE=1 SV=3	0	0	7	7
sp P46060 RAGP1_HUMAN	RANGAP1	Ran GTPase-activating protein 1 OS=Homo sapiens GN=RANGAP1 PE=1 SV=1	0	0	7	7
sp Q09666 AHNAK_HUMAN	AHNAK	Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	0	0	7	7
sp P27816 MAP4_HUMAN	MAP4	Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3	0	0	7	7
sp P37802 TAGLN2_HUMAN	TAGLN2	Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3	0	0	6	7
sp P52907 CAZA1_HUMAN	CAPZA1	F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3	0	0	5	6
sp Q9UM54 MYO6_HUMAN	MYO6	Unconventional myosin-VI OS=Homo sapiens GN=MYO6 PE=1 SV=4	0	0	5	5
sp Q86VP6 CAND1_HUMAN	CAND1	Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2	0	0	5	5
sp Q9Y4X5 ARI1_HUMAN	ARIH1	E3 ubiquitin-protein ligase ARIH1 OS=Homo sapiens GN=ARIH1 PE=1 SV=2	0	0	4	4
sp Q14152 EIF3A_HUMAN	EIF3A	Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=EIF3A PE=1 SV=1	0	0	4	4
sp Q6Y7W6 GGYF2_HUMAN	GIGYF2	GRB10-interacting GYF protein 2 OS=Homo sapiens GN=GIGYF2 PE=1 SV=1	0	0	4	4
sp P40227 TCPZ_HUMAN	CCT6A	T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3	0	0	4	4
sp Q9Y5K6 CD2AP_HUMAN	CD2AP	CD2-associated protein OS=Homo sapiens GN=CD2AP PE=1 SV=1	0	0	4	4
sp O75367 H2AFY_HUMAN	H2AFY	Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4	0	0	4	4
sp P49368 TCPG_HUMAN	CCT3	T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4	0	0	4	4
sp Q00341 VIGLN_HUMAN	HDLBP	Vigilin OS=Homo sapiens GN=HDLBP PE=1 SV=2	0	0	3	3
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sp Q9P0K7 RAI14_HUMAN	RAI14	Ankycorbin OS=Homo sapiens GN=RAI14 PE=1 SV=2	0	0	3	3
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sp P49411 EFTU_HUMAN	TUFM	Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2	0	0	3	3
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sp Q16512 PKN1_HUMAN	PKN1	Serine/threonine-protein kinase N1 OS=Homo sapiens GN=PKN1 PE=1 SV=2	0	0	3	3
sp P49959 MRE11_HUMAN	MRE11	Double-strand break repair protein MRE11 OS=Homo sapiens GN=MRE11 PE=1 SV=3	0	0	3	3
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sp P52597 HNRPF_HUMAN	HNRNPF	Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3	0	0	2	3
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sp P50914 RL14_HUMAN	RPL14	60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4	0	0	2	2
sp O00303 EIF3F_HUMAN	EIF3F	Eukaryotic translation initiation factor 3 subunit F OS=Homo sapiens GN=EIF3F PE=1 SV=1	0	0	2	2
sp P07814 SYEP_HUMAN	EPRS	Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5	0	0	2	2
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sp P17661 DESM_HUMAN	DES	Desmin OS=Homo sapiens GN=DES PE=1 SV=3	0	0	2	2
sp P78527 PRKDC_HUMAN	PRKDC	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3	0	0	2	2
sp P14868 SYDC_HUMAN	DARS	Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2	0	0	2	2
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sp P06576 ATPB_HUMAN	ATP5B	ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3	1	1	3	3
sp P26373 RL13_HUMAN	RPL13	60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4	2	2	6	6
sp P17844 DDX5_HUMAN	DDX5	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1	2	2	4	5
sp P34931 HS71L_HUMAN	HSPA1L	Heat shock 70 kDa protein 1-like OS=Homo sapiens GN=HSPA1L PE=1 SV=2	3	3	9	10
sp P0DMV9 HS71B_HUMAN	HSPA1B	Heat shock 70 kDa protein 1B OS=Homo sapiens GN=HSPA1B PE=1 SV=1	3	3	8	8
sp P19338 NUCL_HUMAN	NCL	Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3	3	3	7	7
sp P09874 PARP1_HUMAN	PARP1	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4	4	4	13	13
sp P52272 HNRPM_HUMAN	HNRNPM	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3	4	4	10	10

Table S3. Sanger sequencing of hnRNP E1 CRISPR clones

Legend: Guide RNA, Ref = ARIH1 KD parental sequencing results.	
LM2-4175 ARIH1 sh8 hnRNP E1 CRISPR clone 50 product (550 bp)	
Ref	TCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCCTGCTGGCCG
Seq 1	TCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCCTGCTGGCCG
Seq 2	TCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCCTGCTGGCCG
Ref	CGGTACTGTTGGTCATGGAGCTGTTGATATCTTCCCTCCAGCTTGTGATGATCATAGCGAAAGCCTTAAAGATGGCATTGGTGGGGCCGGTCAGAGTGAT
Seq 1	CGGTACTGTTGGTCATGGAGCTGTTGATATCTTCCCTCCAGCTTGTGATGATCATAGCGAAAGCCTTAAAGATGGCATTGGTGGGGCCGGTCAGAGTGAT
Seq 2	CGGTACTGTTGGTCATGGAGCTGTTGATATCTTCCCTCCAGCTTGTGATGATCATAGCGAAAGCCTTAAAGATGGCATTGGTGGGGCCGGTCAGAGTGAT
Ref	GATTCTCTCCGGACAATCCCCCTCCGAGATGTTGATCCGCGGCCACTCTCCTCGGGATCCTCTTAACCGACTCCCCTTTCTTCCCAATGATGCTTCTC
Seq 1	GATTCTCTCCGGACAATCCCCCTCCGAGATGTTGATCCGCGGCCACTCTCCTCGGGATCCTCTTAACCGACTCCCCTTTCTTCCCAATGATGCTTCTC
Seq 2	GATTCTCTCCGGACAATCCCCCTCCGAGATGTTGATCCGCGGCCACTCTCCTCGGGATCCTCTTAACCGACTCCCCTTTCTTCCCAATGATGCTTCTC
Ref	ACTTCCTTTCCGTGCATAAGAAGCCGAATGGTGAGAGTCACATTTAGTCCAC-TTTCAGTCACACCGGCATCCATGGCGAGCGGGCGGGCGCTTCGGGG
Seq 1	ACTTCCTTTCCGTGCATAAGAAGCCGAATGGTGAGAGTCACATTTAGTCCAC-TTTCAGTCACACCGGCATCCATGGCGAGCGGGCGGGCGCTTCGGGG
Seq 2	ACTTCCTTTCCGTGCATAAGAAGCCGAATGGTGAGAGTCACATTTAGTCCAC-TTTCAGTCACACCGGCATCCATGGCGAGCGGGCGGGCGCTTCGGGG
LM2-4175 ARIH1 sh8 hnRNP E1 CRISPR clone 52 product A (550 bp)	
Ref	TCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCCTGCTGGCCG
Seq 1	TCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCCTGCTGGCCG
Seq 2	TCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCCTGCTGGCCG
Seq 3	TCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCCTGCTGGCCG
Ref	CGGTACTGTTGGTCATGGAGCTGTTGATATCTTCC-----TC---CAGCTTGTGATGATC-----ATAGCGAAAGCCTTAAAGATGG---CA
Seq 1	CGGTGAAGTGGTGATAGAAC-----CTTCCGA---T-----TTGTCCATCATC-----TTTGCGAATGACTTAAAGAAAG---CC
Seq 2	CGGTGGCGGTGGTCAT-----TGA-ATCCTGCGAATTTGCCCTCATCTTGGCGAA-----AGACCTAA---CGAAAGCCTTG---AAGGGGACCG
Seq 3	CGGTGCTTCTGGGTATG-----TG-----TGCG---GTCA-TCATCTTGTGCGAGCTCGCCGAGAT-TAATAGCAAAACACTAGAAAATGGAA---
Ref	TTGGTGGGGC-CGGTCA---GAGTGATG---ATTCTCTCC--GGACAATCCCCCTCCG--AGATGTTGATCCGCGCCCACTCTCCTCGGGATCCTCT
Seq 1	TTGAAGGGGA-CGGTTG---GAGGGCG---GTTCTAACC--GAAAATTTCCCG--CGAAAATGCCATCCGAAAGGTACTCCCTCCCGATCCTCT
Seq 2	TTGGAGGGG--CGGT---TCTAAGGGTG--ATTTCC--CCCTGGAAAATTTCCCTCCGAAAGCTT-----ATCCCTCCCGATCCTCT
Seq 3	-TGGGGGGATCAGTCACTTA-----TGCAATCTCTCGCC---AAATCTGTTC--ACGCTTCGGATTTCCCGCAACTCTCTCGCAATTTCTC
Ref	TAACCGACTCCCCTTTCTTCCCAATGATGCTTCC--TACTTCTTTCCGTGCAT-----AAGAGCCGAATG---GTGAGA-----G---T---
Seq 1	TAACGGACCCCTTATCTTCCCGCCCTTGTCTCC--TACTGACGTTCCCTACTT-----CCTAACCCGAATG---AAGAGA--CCAACGG---TTAA
Seq 2	TACCGGACCCCTTAAACACCCCTTTGCTTCCA--ATTCTTTCTTGTCTC-----TTAACCCGAATG---AAGAGACCCATTG---TTAA
Seq 3	TTCCGGA-----TT-----CCCAGTCTCCAATGATGC-----CTTCGACTATAATTACCCGATTGTAAAGTGA---AATGGGGATTAA
Ref	-----CACATTTAGTCCACTTTCAGTCACACCGGCATCCATGGCGAGCGGGCGG
Seq 1	AA-CACTCTTTACTCCACTT-----CATCCCGCGCACCAGCGGG
Seq 2	AAGCCCTTTTAA-TCCACTTCT--CCA-----C-----GGCTCCAGCGGG
Seq 3	AAC-----A-TCGACA-CCTGTGACATTGGTA----GGCGT-----GGG
LM2-4175 ARIH1 sh8 hnRNP E1 CRISPR clone 52 product B (~300 bp)	
Ref	TCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCCTGCTGGCCG
Seq1	TCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCCTGCTGGCCG
Ref	CGGTACTGTTGGTCATGGAGCTGTTGATATCTTCCCTCCAGCTTGTGATGATCATAGCGAAAGCCTTAAAGATGGCATTGGTGGGGCCGGTCAGAGTGAT
Seq1	CGGT-----
Ref	GATTCTCTCCGGACAATCCCCCTCCGAGATGTTGATCCGCGGCCACTCTCCTCGGGATCCTCTTAACCGACTCCCCTTTCTTCCCAATGATGCTTCTC
Seq1	-----
Ref	ACTTCCTTTCCGTGCATAAGAAGCCGAATGGTGAGAGTCACATTTAGTCCACTTTCAGTCACACCGGCATCCATGGCGAGC
Seq1	-----CAGTCACACCGGCATCCATGGCGAGC
SUM159 ARIH1 sh5 hnRNP E1 CRISPR clone 1 product A (550 bp)	
Ref	TCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCCTGCTGGCCG
Seq1	TCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCCTGCTGGCCG
Seq2	TCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCCTGCTGGCCG
Ref	CGGTACTGTTGGTCATGGAGCTGTTGATATCTTCCCTCCAGCTTGTGATGATCATAG-CGAAAGCCTTAAAGATGGCATTGGTGGGGCCGGTCAGAGTGA
Seq1	CGGTACTGTTGGTCATGGAGCTGTTGATATCTTCCCTCCAGCTTGTGATGATCATAG-CGAAAGCCTTAAAGATGGCATTGGTGGGGCCGGTCAGAGTGA
Seq2	CGGCCTTGTGGCCAGCGTCCGGCGAAATGGTGGGGCGGCTTGTGGGTACTCATAGCCGTAA-CCTGAAAGATGACATTGGTGGGGCCGGTCAGAGTGA
Ref	TGATTCTCTCCGGACAATCCCCCTCCGAGATGTTGATCCGCGGCCACTCTCCTCGGGATCCTCTTAACCGACTCCCCTTTCTTCCCAATGATGCTTCC
Seq1	TGATTCTCTCCGGACAATCCCCCTCCGAGATGTTGATCCGCGGCCACTCTCCTCGGGATCCTCTTAACCGACTCCCCTTTCTTCCCAATGATGCTTCC
Seq2	TGATTCTCTCCGGACAATCCCCCTCCGAGATGTTGATCCGCGGCCACTCTCCTCGGGATCCTCTTAACCGACTCCCCTTTCTTCCCAATGATGCTTCC

Ref TACTTCCTTTCCGTGCATAAGAAGCCGAATGGTGAGAGTACATTTAGTC-CAC**TTTCAGTCAACCCGGCATC**CATGGCGAGCGGGCGGC-GG
Seq1 TACTTCCTTTCCGTGCATAAGAAGCCGAATGGTGAGAGTACATTTAGTC-CACTT-----GGCATCCCTGCCGCGCGGGCGGG
Seq2 TACTTCCTTTCCGTGCATAAGAAGCCGAATGGTGAGAGTACATTTAGTACACC---GTCACACAGGGATACATGGCGAGCGCTTGCGGG

SUM159 ARIH1 sh5 hnRNP E1 CRISPR clone 1 product B (~300 bp)

Ref **CGGTACTGTTGGTCATGGAG**CTGTTGATATCTTCTCCAGCTTGTGCGATGATCATAGCGAAAGCCTTAAAGATGGCATTGGTGGGGCCGGTCCAGAGTGAT
Seq1 CGGTA-----AGT---
Seq2 CTG-----CCTCCA-----

Ref GATTCCTCCGGACAATCCCTCCGAGATGTTGATCCGCGGCCACTCTCCTCGCGGATCCTCTTAACCGACTCCCTTTCTTCCCAATGATGCTTCCT
Seq1 -----CTCGC-----
Seq2 -----

Ref ACTTCCTTTCCGTGCATAAGAAGCCGAATGGTGAGAGTACATTTAGTCCAC**TTTCAGTCAACCCGGCATC**CATGGCGAGCGGGCGGGCGGCTTCGGGGG
Ref -----CAGCGGC---CATGG-----GCGGTCCGCGGG
Seq2 -----ACACGGGCATCGATGGCGATCGGGGGGAGCGGGCGGGG

Ref AGTTGGGCTCGTTA
Seq1 CGTGTCTTCGTTA
Seq2 ACGTGGGCTCGTTA

SUM159 ARIH1 sh5 hnRNP E1 CRISPR clone 16 product A (550 bp)

Ref TCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCTGCTGGCCG
Seq1 TCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCTGCTGGCCG
Seq2 TCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCTGCTGGCCG

Ref **CGGTACTGTTGGTCATGGAG**CTGTTGATATCTTCTCCAGCTTGTGCGATGATCATAGCGAAAGCCTTAAAGATGGCATTGGTGGGGCC---GGTCAGAGT
Seq1 CGGTACTGTTGGTCATGGAGCTGTTGATATCTTCTCCAGCTTGTGCGATGATCATAGCGAAAGCCTTAAAGATGGCATTGGTGGGGCC---GGTCAGAGT
Seq2 CGGT-----GGAGCTGGTGTATTTGTCCAAATGTCGACGACTCTGGCGAAAATCTTAAAGAAGGCATTGGAGAGGACATTGGT---AGG

Ref GATGATTCTCTCCGGACA--ATTCCCCTCCGAGATGTTGATCCGCGGCCACTCTCCTCGCGGATCCTCTTAACCGACTCCCTTTCT--TCCCAATGAT
Seq1 GATGATTCTCTCCGGACA--ATTCCCCTCCGAGATGTTGATCCGCGGCCACTCTCCTCGCGGATCCTCTTAACCGACTCCCTTTCT--TCCCAATGAT
Seq2 GATGATTCTATC--GATAATATTCTCTGACAAATGCTGATCCACACGCGGATCTCCTCGCGGATCCTCTTAACGAACCTCCCTTTCTACTCCCT--AT

Ref GCTTCCTACTTCTTTCCGTGCATAAGAAGCCGAATGGTGAGAGTACATTTAGTC-CAC**TTTCAGTCAACCCGGCATC**CATGGCGAGCGGGCGGGCGGG
Seq1 GCTTCCTACTTCTTTCCGTGCATAAGAAGCCGAATGGTGAGAGTACATTTAGTC-CAC-----CGGCATCCATGGCGAGCGGGCGGGCGGG
Seq2 CTTTCCTACTATGTTTCTTAGTATCTTAAACCGAATGGTAAGACTAACGTTGAGACTCATTTTACTC-CACCGCATCCATGGCAAGCGGGCGGGCGGG

SUM159 ARIH1 sh5 hnRNP E1 CRISPR clone 16 product B (~300 bp)

Ref GTACTCTCGC-GGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCTG
Seq1 GTACTCTCGCGGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCTG
Seq2 GTACAGTCGCGTCATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGTCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCTG

Ref CTGGCCG**CGGTACTGTTGGTCATGGAG**CTGTTGATATCTTCTCCAGCTTGTGCGATGATCATAGCGAAAGCCTTAAAGATGGCATTGGTGGGGCCGGTCA
Seq1 ATGGCCGG-----ACCTGT-----
Seq2 CTGGTCGCTGT-----

Ref GAGTGATGATTCTCTCCGGACAATCCCTCCGAGATGTTGATCCGCGGCCACTCTCCTCGCGGATCCTCTTAACCGACTCCCTTTCTTCCCAATGAT
Seq1 -----
Seq2 -----

Ref GCTTCCTACTTCTTTCCGTGCATAAGAAGCCGAATGGTGAGAGTACATTTAGTCCAC**TTTCAGTCAACCCGGCATC**CATGGCGAGCGGGCGGGCGGCT
Seq1 -----CACACCAGCATCCATGGCGAGCGGGCGGGCGGCT
Seq2 -----CAGGCACACCAGCATCCATGGCGAGCGGGCGGGCGGCT

Ref TCGGGGGAGTTGGGCTCGTTACGGG
Seq1 TCGGGGGAGTTGGGCTCGTTACGTGG
Seq2 TCGGGGGAGTTGGGCTCGTTACGTGG

SUM159 ARIH1 sh5 hnRNP E1 CRISPR clone 20 product A (550 bp)

Ref **CGGT-ACTGTTGGTCATG**---GAGCTGTTGATATCTTCTCCAGCTTGTGCGATGATCATAGCGAAAGCCTTAAAGATGGCATTGGTGGGGCCGGTCCAGAGT
Seq1 CGGT-ACTGTTGGTCATG---GAGCTGTTGATATCTTCTCCAGCTTGTGCGATGATCATAGCGAAAGCCTTAAAGATGGCATTGGTGGGGCCGGTCCAGAGT
Seq2 GTGTGACCGGCATCCATGGCGAGCGGAGGG---CGGCTTACGCTTGTCTATGATCATAGCGAAAGCCTTAAAGATGGCATTGGTGGGGCCGGTCCAGAGT

Ref GATGATTCTCTCCGGACAATCCCTCCGAGATGTTGATCCGCGGCCACTCTCCTCGCGGATCCTCTTAACCGACTCCCTTTCTTCCCAATGATGCTT
Seq1 GATGATTCTCTCCGGACAATCCCTCCGAGATGTTGATCCGCGGCCACTCTCCTCGCGGATCCTCTTAACCGACTCCCTTTCTTCCCAATGATGCTT
Seq2 GATGATTCTCTCCGGACAATCCCTCCGAGATGTTGATCCGCGGCCACTCTCCTCGCGGATCCTCTTAACCGACTCCCTTTCTTCCCAATGATGCTT

Ref CCTACTTCTTTCCGTGCATAAGAAGCCGAATGGTGAGAGTACATTTAGTCCAC**TTTCAGTCAACCCGGCATC**CATGGCG
Seq1 CCTACTTCTTTCCGTGCATAAGAAGCCGAATGGTGAGAGTACATTTAGTCCACTTTCAGTCAACCCGGCATCCATGGCG

Seq2 CCTACTTCCTTTCCGTGCATAAGAAGCCGAATGGTGAGAGTCACATT-----CAGTCACACCGGCATCCATGGCG

SUM159 ARIH1 sh5 hnRNP E1 CRISPR clone 20 product B (~300 bp)

Ref TCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCTGCTGGCCG
Seq1 TCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCTGCTGGCCG
Seq2 TCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCTGATGGTGC

Ref CGGTACTGTTGGTCATGGAGCTGTTGATATCTTCCCTCCAGCTTGTGCGATGATCATAGCGAAAGCCTTAAAGATGGCATTGGTGGGGCCGGTCAGAGTGAT
Seq1 -----GTGTGA-
Seq2 -----

Ref GATTCTCTCCGGACAATTCCCTCCGAGATGTTGATCCGCGGCCACTCTCCTCGCGGATCCTCTTAACCGACTCCCCTTCTTCCCAATGATGCTTCCT
Seq1 -----
Seq2 -----

Ref ACTTCCTTTCCGTGCATAAGAAGCCGAATGGTGAGAGTCACATTTAGTCCA**CTTTCAGTCACACCGGCAT**CCATGGCGAGCGCGGGCGCGCTTCGGGGG
Seq1 -----CCGGCATCCATGGCGAGCGCGGGCGCGCTTCGGGGG
Seq2 -----GTGCGA-----CCGGAATTAATGGCGAGCGCGGGCGCGCTTCGGGGG

SUM159 ARIH1 sh5 hnRNP E1 CRISPR clone 54 product (550 bp)

Ref TCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCTGCTGGCCG
Seq1 TCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCTGCTGGCCG
Seq2 TCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCTGCTGATTGGCAAGCACTTCCAGACTGAAGGTGAGGGGGGGCCGAGGGAT

Ref CGGTACTGT-TGGTCATGGAGCTGTTGATATCTT-----CCTCCA-GCTTGTGCGATGATCATAGCGAAAGCCTTAA-AGA-TGGCATTGGTGGGGCCG
Seq1 CGGTACTGT-TGGTCATGGAGCTGTTGATATCTT-----CCTCCA-GCTTGTGCGATTATCATAGCGAAAGCCTTAA-AGA-TGGCATTGGTGGGGCCG
Seq2 CAGT-CTCTCCGGACAATTACCTGCTGATATGTTGATCCGCGCTCCACTCTCCTCTCAGATCCT-----CTTAACCGACTCCCCTTCTTCGGCCG

Ref GTCAGAGTGATGATTCTCTCCGGACAATTCCCTCCGAGATGTTGA--TCCGCGGCCACTCTCCTCGCGGATCCTCTTAACCGACTCCCCTTCTTCC
Seq1 GTCAGAGTGATGATTCTCTCCGGACAATTCCCTCCGAGATGTTGA--TCCGCGGCCACTCTCCTCGCGGATCCTCTTAACCGACTCCCCTTCTTCC
Seq2 G-CAGAATGATGATTCTCTTCCGACCAATTCCCTCCAAAAGT-GAGAGTCCCGC--CACTCCCCTTCCGATCCTCTTAACCGACTCCCCTTCTTCGTCG

Ref CAAT-GATGCTTCTACTTCCCTTCCGTGCATAAGAAGCCGAATGGTGAGAGTCACATTTAGTCCA**C-TTTCAGTCACACCGGCAT**CCATGGCGAGCGGC
Seq1 CAAT-GATGCTTCTACTTCCCTTCCGTGCATAAGAAGCCGAATGGTGAGAGTCACATTTAGTCCAC-TTTCAGTCACACCGGCATCCATGGCGAGCGGC
Seq2 GAATGGATGCT-CCGACTTCTTTCGTGGATTAGAAAGCAAAGGTGAGAAGCACATTTAATCCACTTTTCATTCGCCCGTTTCATTGGAAGGGGG

SUM159 ARIH1 sh5 hnRNP E1 CRISPR clone 11 product (550 bp)

Ref TCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCTGCTGGCCG
Seq1 TCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCTGCTGGCCG
Seq2 TCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCTGCTGGCCG

Ref CGGTACTGTTGGTCATGGAGCTGTTGATATCTTCCCTCCAGCTTGTGCGATGATCATAGCGAAAGCCTTAAAGATGGCATTGGTGGGGCCGGTCAGAGTGAT
Seq1 CGGTACTGTTGGTCATGGAGCTGTTGATATCTTCCCTCCAGCTTGTGCGATGATCATAGCGAAAGCCTTAAAGATGGCATTGGTGGGGCCGGTCAGAGTGAT
Seq2 CGGTACTGGTGGGCATGGAGCTGTTGATATCTTCCCTCCAGCTTGGCGATGATCATACGAAAGCCTTAAAGATGGGATTGGTGGGGCCGGCAGAATGAT

Ref GATTCTCTCCGGACAATTCCCTCCGAGATGTTGATCCGCGGCCACTCTCCTCGCGGATCCTCTTAACCGACTCCCCTTCTTCCCAATGATGCTTCCT
Seq1 GATTCTCTCCGGACAATTCCCTCCGAGATGTTGATCCGCGGCCACTCTCCTCGCGGATCCTCTTAACCGACTCCCCTTCTTCCCAATGATGCTTCCT
Seq2 GAATCTCTCCGGACAATTCCCTCCGAGATGTTGATCCGCGGCCACTCTCCTCGCGGATCCTCTTAACCGACTCCCCTTCTTCCCAATGATGCTTCCT

Ref ACTTCCTTTCCGTGCATAAGAAGCCGAATGGTGAGAGTCACATTTAGTCCA**CTTTCAGTCACACCGGCAT**CCATGGCG
Seq1 ACTTCCTTTCCGTGCATAAGAAGCCGAATGGTGAGAGTCACATTTAGTCCA**CTTTCAGTCACACCGGCAT**CCATGGCG
Seq2 ACTTCCTTTCCGTGCATAAGAAGCCGAATGGTGAGAGTCACATTTAATCCACTT-CAGTCACACCGGCATCCATGGCG

SUM159 ARIH1 sh5 hnRNP E1 CRISPR clone 37 product (550 bp)

Ref TCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCTGCTGGCCG
Seq1 TCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCTGCTGGCCG
Seq2 TCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCTGCTGGCCG

Ref CGGTACTGTTGGTCATGGAGCTGTTGATATCTTCCCTCCAGCTTGTGCGATGATCATAGCGAAAGCCTTAAAGATGGCATTGGTGGGGCCGGTCAGAGTGAT
Seq1 CGGTACTGTTGGTCATGGAGCTGTTGATATCTTCCCTCCAGCTTGTGCGATGATCATAGCGAAAGCCTTAAAGATGGCATTGGTGGGGCCGGTCAGAGTGAT
Seq2 CGGTACTGTTGGTCATGGAGCTGTTGATATCTTCCCTCCAGCTTGTGCGATGATCATAGCGAAAGCCTTAAAGATGGCATTGGTGGGGCCGGTCAGAGTGAT

Ref GATTCTCTCCGGACAATTCCCTCCGAGATGTTGATCCGCGGCCACTCTCCTCGCGGATCCTCTTAACCGACTCCCCTTCTTCCCAATGATGCTTCCT
Seq1 GATTCTCTCCGGACAATTCCCTCCGAGATGTTGATCCGCGGCCACTCTCCTCGCGGATCCTCTTAACCGACTCCCCTTCTTCCCAATGATGCTTCCT
Seq2 GATTCTCTCCGGACAATTCCCTCCGAGATGTTGATCCGCGGCCACTCTCCTCGCGGATCCTCTTAACCGACTCCCCTTCTTCCCAATGATGCTTCCT

Ref ACTTCCTTTCCGTGCATAAGAAGCCGAATGGTGAGAGTCACATTTAGTCCA**CTTTCAGTCACACCGGCAT**CCATGGCG
Seq1 ACTTCCTTTCCGTGCATAAGAAGCCGAATGGTGAGAGTCACATTTAGTCCA**CTTTCAGTCACACCGGCAT**CCATGGCG
Seq2 ACTTCCTTTCCGTGCATAAGAAGCCGAATGGTGAGAGTCACATTTAGTCCA**CTTTCAGTCACACCGGCAT**CCATGGCG