

Fig. S1. Readthrough is reduced in OIS. **A.** SA- β -gal of proliferating (Vector) and senescent IMR90 (H-RasV12 oncogene) cells, fixed at day 12 post-infection. Data were quantified from many fields within one experiment to represent the entire petri dish. Three independent cell counts up to a total of at least 100 cells are presented as the mean and SD of positive cells. **B.** RT-qPCRs for senescent marker mRNAs were performed in IMR-90 cells at day 12 post-infection for cells as in **(A)**. Data are normalized over TBP and HMBS, and presented as means relative to vector infected cells. Error bars indicate SD of technical triplicates. ** = $p < 0.01$, *** = $p < 0.001$ are significantly different, using two-tailed Student's t-test. **C.** Luciferase activities from non-readthrough control (CGA-Positive control) in proliferating (Vector) and H-RasV12 senescent cells measured at days 5 (D5), 12 (D12) and 20 (D20) post-infection. Assays are representative of 2 independent experiments with similar results with technical triplicates for each experiment. One-way ANOVA with post-hoc Tukey HSD were performed. Error bars indicate SD of technical triplicates. **D.** Normalized Fluc/Rluc ratios indicate that readthrough level does not change in non-senescent cells (Vector) at day 5 (D5), 12 (D12) or 20 (D20) post-infection. Error bars indicate SD of biological triplicates. **E.** Luciferase activities from AQP4 reporter were measured at day 12 post-infection. Normalized Fluc/Rluc ratios from non-senescent (Vector) and senescent cells (H-RasV12), starved (Starv) or supplied with fetal bovine serum (FBS) are represented. Starvation was performed for a week to induce quiescence. Data are presented as means relative to empty vector-infected cells, which are representative of 2 independent experiments with similar results with technical triplicates for each experiment. One-way ANOVA with post-hoc Tukey HSD were performed. Error bars indicate SD of technical triplicates. Tukey HSD p-values indicate that * = $p < 0.05$, ** = $p < 0.01$, *** = $p < 0.001$ are significantly different.

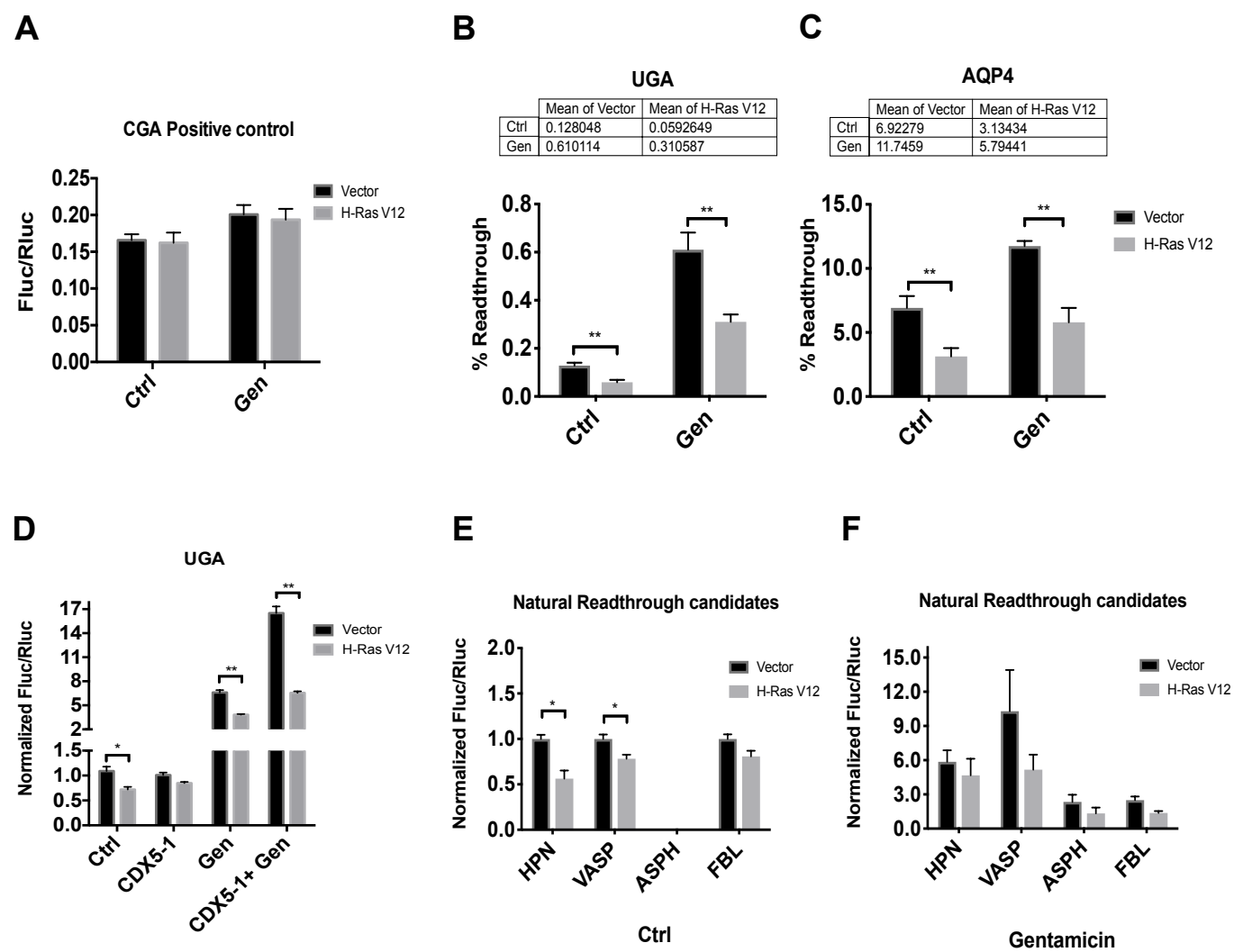


Fig. S2. Senescent cells are resistant to gentamicin-induced readthrough. **A.** IMR-90 cells were transduced with an empty vector

(Vector) or H-RasV12 oncogene to induce OIS and with indicated non-readthrough control luciferase reporter. Cells were treated with vehicle (Ctrl) or with 900 $\mu\text{g/ml}$ of gentamicin sulfate (Gen) 24 hours before measuring luciferase activities at day 12 post-infection. Error bars indicate SD of biological triplicates. **B-C.** The percent of readthrough was determined by dividing Fluc/Rluc ratio from UGA or AQP4 luciferase reporters by Fluc/Rluc ratio from non-readthrough controls multiplied by 100. Error bars indicate SD of biological triplicates. ** = $p < 0.01$ is significantly different, using two-tailed Student's t-test. **D.** IMR-90 cells were transduced with an empty vector (Vector) or H-RasV12 oncogene to induce OIS and with a UGA luciferase reporter. Cells were treated with vehicle (Ctrl) and/or 600 $\mu\text{g/ml}$ of gentamicin sulfate (Gen) and/or 25 μM of CDX5-1 72 hours before measuring luciferase activities at day 12 post-infection. Error bars indicate SD of biological triplicates. * = $p < 0.05$, ** = $p < 0.01$ are significantly different, using two-tailed Student's t-test. **E.** A stop codon within natural contexts from VASP, ASPH, HPN and FBL, was inserted in the intercistronic region of Rluc-Fluc luciferase reporter. IMR-90 cells were transduced with an empty vector (Vector) or H-RasV12 oncogene to induce OIS and with luciferase reporters. Luciferase activities were measured in non-senescent and senescent cells at day 12 post-infection. Error bars indicate SD of biological triplicates. * = $p < 0.05$ is significantly different, using two-tailed Student's t-test. **F.** Cells as in (**E**) were treated with 900 $\mu\text{g/ml}$ of gentamicin sulfate (Gen) 24 hours before measuring luciferase activities at day 12 post-infection. Normalized Fluc/Rluc ratios indicate the efficiency of readthrough. Normalizations are presented as means relative to vector-infected cells from three independent experiments with technical triplicates for each experiment. Unpaired Student's t-test with equal SD were performed. Error bars indicate SD of biological triplicates.

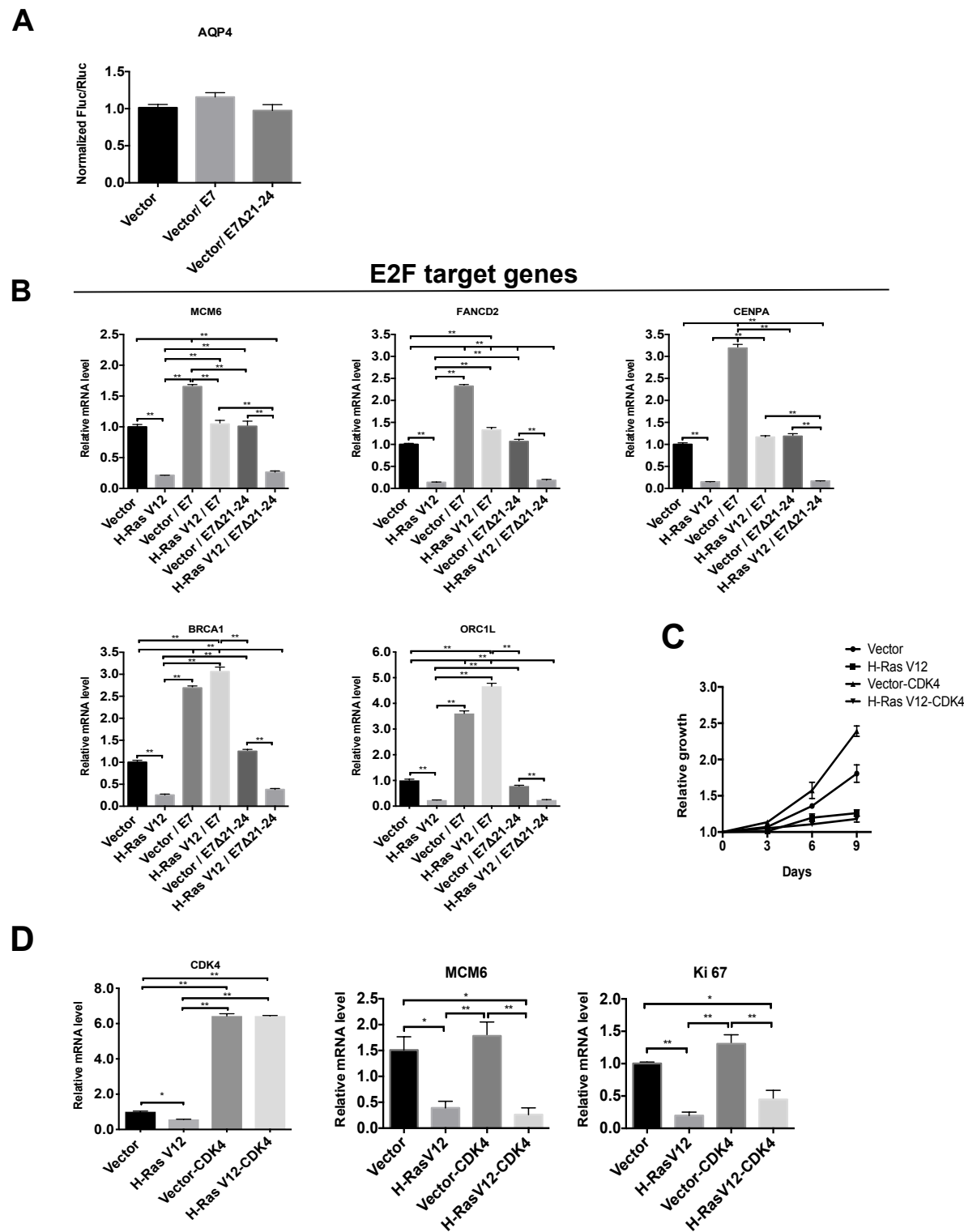


Fig. S3. RB pathway disruption affects the efficiency of readthrough. **A.** IMR-90 cells were transduced with luciferase reporter AQP4 and an empty vector (Vector), wild-type E7 or E7 Δ 21-24 mutant oncogene. Luciferase activities were measured at day 12 post-infection. Normalized Fluc/Rluc ratios indicate the efficiency of readthrough. Normalizations are presented as means relative to vector-infected cells from three independent experiments with technical triplicates for each experiment. Error bars indicate SD of biological triplicates. **B.** Representative RT-qPCR from E2Fs' target mRNAs were performed in IMR-90 cells transduced with an empty control vector (pLXSN), wild-type E7 or E7 Δ 21-24 mutant oncogene, and with an empty vector (Vector) or with H-RasV12 oncogene to induce OIS at day 12 post-infection. Data are normalized over TBP and HMBS, and presented as means relative to vector infected cells. Experiments were done three times with technical triplicates for each experiment. Error bars indicate SD of technical triplicates. Tukey HSD p-values indicate that ** = $p < 0.01$ is significantly different. **C.** Growth curves of non-senescent (Vector) and H-RasV12 senescent IMR-90s overexpressing or not CDK4. Data are presented as means normalized to day 0 of each condition. Assays are representative of 2 independent experiments with similar results with technical triplicates for each experiment. Error bars indicate SD of technical triplicates. **D.** RT-qPCRs for CDK4, MCM6 and Ki67 mRNAs were performed in IMR-90 cells as in (C) and at day 12 post-infection. Data are normalized over TBP and HMBS, and presented as means relative to vector infected cells from three independent experiments with technical triplicates for each experiment. One-way ANOVA with post-hoc Tukey HSD were performed in (A, B, D) and Unpaired Student's t-test with equal SD was performed in (C). Error bars indicate SD of biological triplicates. Tukey HSD p-values indicate that * = $p < 0.05$, ** = $p < 0.01$ are significantly different.

A E2F target genes

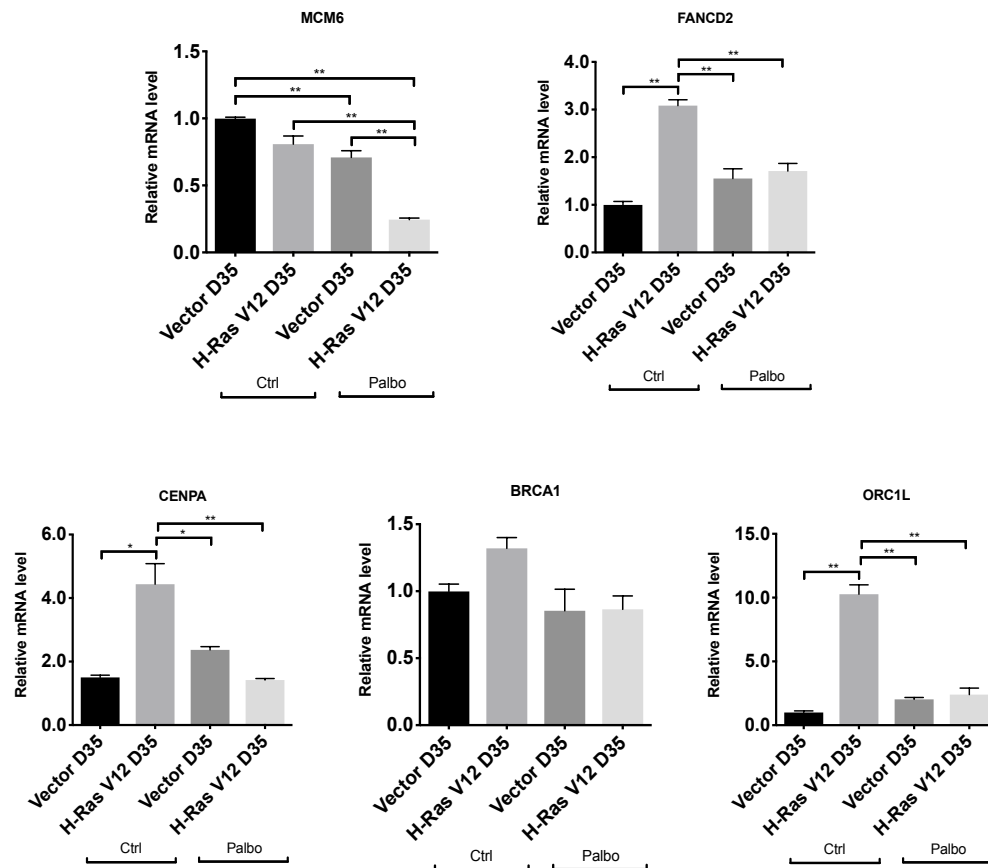


Fig. S4. E2Fs target genes.A. RT-qPCR for E2Fs' target mRNAs were performed in IMR-90 at day 35 post-infection with an empty vector (Vector D35) or with the oncogene H-RasV12 (H-RasV12 D35) and treated with vehicle (Ctrl) or with 1 μ M of palbociclib (Palbo) for 5 days before cell lysis. Data are normalized over TBP and HMBS, and presented as means relative to vector infected cells from three independent experiments with technical triplicates for each experiment. One-way ANOVA with post-hoc Tukey HSD were performed. Error bars indicate SD of technical triplicates. Tukey HSD p-values indicate that * = $p < 0.05$, ** = $p < 0.01$ are significantly different.

Table S1. PCR cloning primers

Name	5' forward primer (5'-3')	3' reverse primer (5'-3')
pMSCV-RLUC-FLUC UGA STOP CODON	GGAAGAAAGCGGCCGCTTCAGATCCGCTAGAGCC CCAAGCTTGCACCAGTGACCAGCAAGGTGTACG	TGGATGCATGAATTTTCGTCATCGCTGAATAC CGTACACCTTGTGGTCACTGGTGCAAGCTTGG

Table S2. Readthrough region

Gene name	Readthrough context
AQP4 Aquaporin 4 NM_001650.4	ATCTGGAGAGGTATTGCTTTCAGTATGACTAGAAAGATCGCACTGAAAGCAGACAAGACTCCTTAGAA
ASPH Aspartate beta hydroxylase NM_004318.3	AGAACAGCAGGAAGTACCACAGATACTTAAGCTTCAAAAAGACTGCCCTACCACCGGGCC
FBL Fibrillarin NM_001436.3	GTACAGGCCACCCCAAGGTGAAGAAGTGAAGTTTCAGCGCTGTGAGGATTGCGAGAGATGGG
HPN Hepsin NM_182983.2	TCGAGGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGCTTCTGCTGCGCAGCCTCCAGGG
MMuLV Moloney Murine Leukemia Virus	CTAGGGAGGTGAGGGTCTGAGGACCCCTGAAACCCAGGATAACCTCAAAGTCGGGGGGCC
VASP Vasodilator-stimulated phosphoprotein NM_003370.3	GGAGCTGAGGAAGCGGGTTCTCCCTGACCCAGGGACCCAGAAGACCCGCTTCTGGGCCCCA

Table S3. Readthrough candidates

Readthrough code	Gene name	peptides used by MS analysis	peptides + confintop-DNA 3'UTR	RTP (readthrough propensity) (Ref 22)	RTP Linfs3 (Ref 22)	
RT_012331.1	FAM134S family with sequence similarity 19 (chemokine [C-C motif])	AFPSDGLRLR	NP_001074346	3608	0.309	0.646
RT_00885.1	Zn2 finger protein 182	YGKSLSLSHLNPK	NP_001171570.1, NP_001	3732	0.143	0.215
RT_00208.1	ACADS acyl-CoA dehydrogenase, C-2 to C-3 short chain	LGQMGAPVQGMQSLVPPR	NP_000088.1, NP_000088.1	817	-0.077	0.066
RT_017649.1	ACSL5 acyl-CoA synthetase long-chain family member 5	VLYLPAHCLLVR	NP_076313.1, NP_076314	690	-0.08	-0.226
RT_009441.1	ADCK2 aar domain containing kinase 2	AGHSQEPFLVQLGR	NP_443085.2, NP_01151	464	0.237	0.065
RT_013024.1	ADCY7 adenylylase cyclase 7	GILLDSEK	NP_001050.1, NP_01152	9511	-0.029	0.028
RT_02165.1	ADGRE3 adhesion G protein-coupled receptor E5	MVLDGPAAPVATALYTK	NP_510966.1, NP_01151	6737	0.084	0.112
RT_004627.1	AES amino-terminal enhancer of split	LGSGTGEGRQ	NP_945320.1, NP_00672	1	0.232	0.107
RT_004601.1	AGAP2 AGAP with GTPase domain, ankyrin repeat and PH domain	IEGLVHR	NP_005085.1, NP_00526	6583	0.059	0.072
RT_008047.1	AHL adenylate kinase 1	QKNGVDFSEPRFTFS	NP_000467.1, NP_01151	5773	0.054	0.424
RT_002208.1	AKAP8L A kinase (PKA) anchor protein 8-like	PELAGAGAR	NP_00129407, NP_00525	524	0.42	0.432
RT_017612.1	alpha-1,3-L-fucosyltransferase 9	NFSLAHNLMNR	NP_005072.2, NP_01151	652	-0.081	-0.089
RT_022128.1	AMOT1 angiomotin	SRADYVQK	NP_573072.1, NP_01152	3141	0.051	-0.111
RT_017376.1	ANKLE2 ankyrin repeat and LIM domain containing 2	EGRIVLNLCKD	NP_005929.1, NP_00526	2085	-0.028	-0.215
RT_00581.1	ANKRD35 ankyrin repeat domain 13 family, member D	AIAGGLALRPFAR	NP_097217.2, NP_01154	10572	0.041	0.066
RT_001281.1	ANO10 anoctamin 10	GLICLITFCGAGGGTNGSVPFNP	NP_00193762, NP_01151	7239	0.236	0.259
RT_005813.1	AP1 amyloid beta (A4) precursor-like protein 1	ACTPLPFAPEQLPA	NP_00109978.1, NP_001	2785	0.271	0.432
RT_015810.1	APPL2 adaptor protein, phosphotyrosine interaction, PH domain and LTRCAG	NP_006412.1, NP_00671	20075	0.027	0.147	
RT_023876.1	AQP2B aquaporin 2B	ALSKSAAARSVPAR	NP_0010150	9555	0.214	0.066
RT_00975.1	ARHGAP17 Rho GTPase activating protein 17	RTWRPRLK	NP_006254.4, NP_01154	3300	0.319	0.437
RT_018159.1	ARHGAP18 Rho guanine nucleotide exchange factor 1	IGLFLFNLYLR	NP_005025	8079	0.186	0.382
RT_023804.1	ARPP21 cAMP-regulated phosphoprotein 21kDa	KLQMGFNK	NP_00125455, NP_00671	4165	0.28	0.373
RT_009721.1	ASB14 ankyrin repeat and SOCS box containing 14, predicted transmembrane protein	ISSAWLAEGLLHGRSR	NP_00626	2144	0.161	0.151
RT_011768.1	ASPH aspartate beta-hydroxylase	KTAPITGGPA	NP_001152227.1, NP_001	5997	0.123	0.033
RT_01317.1	ASTN2 astrotactin 2	GRVLPVSTETLNGR	NP_054729.3, NP_01151	235	0.001	0.028
RT_013285.1	AT9A9 autophagy related 9A	DSLIPR	NP_070990.4, NP_00307	1836	0.105	0.162
RT_006571.1	ATP10B ATPase, class V, type 10C	DREYKQDAR	NP_061586.3, NP_00624	2160	0.203	0.444
RT_003127.1	ATP11C ATPase, class VI, type 11C	QMPNLELMLVYK	NP_079562.2, NP_01152	3117	0.129	0.152
RT_007887.1	ATP13A1 ATPase type 13A1	CPEMAHNVPTAFGRG	NP_01151	666	-0.032	0.056
RT_007205.1	ATP16B ATPase, H+ transporting, lysosomal 21kDa, V0 subunit b	LVGVGPPCTFLLR	NP_004038.1, NP_00304	2970	0.123	0.127
RT_035167.1	BCOR1 BC16 corepressor-like 1	LQNEAIR	NP_068705.3, NP_00526	1	0.176	0.341
RT_003899.1	C10orf105 chromosome 10 open reading frame 105	WGVHQAFTSP	NP_001161862, NP_01151	9533	0.056	-0.113
RT_023546.1	C10orf111 core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta	KVMNMQGR	NP_064541.1, NP_00524	1008	0.112	0.056
RT_024012.1	C10orf138 chromosome 10 open reading frame 138	IPNFQKQVSMDSYI	NP_001007445, NP_00527	1009	0.127	0.382
RT_014922.1	C15 complement component 1, s subcomponent	YIPASPR	NP_058850.1, NP_00525	4939	0.001	-0.075
RT_007816.1	C22orf23 chromosome 22 open reading frame 23	GQGLTFRVA	NP_072226.2, NP_00526	8506	0.116	-0.15
RT_019748.1	C22orf23 chromosome 22 open reading frame 23	LTPASAC; CSPSPTFCV	NP_00193991, NP_00526	1593	0.131	-0.134
RT_013060.1	C5orf60 chromosome 5 open reading frame 60	VITIGLGLGR	NP_01151	7069	0.364	0.122
RT_014551.1	CACNA1C calcium channel, voltage-dependent, P/Q type, alpha 1A	THFRFGKAGHR	NP_001120694.1, NP_01151	2949	-0.086	-0.112
RT_018787.1	CAPN1 capain 1, (mu) large subunit	QPRPVPSPSHR	NP_001185797, NP_00671	4819	0.169	0.119
RT_005409.1	CAK calcium/calmodulin-dependent serine protein kinase (MAGUK) 1	IASLSALQZQVMVPR	NP_001119527, NP_00672	1200	-0.161	-0.156
RT_010840.1	CDC58 coiled-coil domain containing serine protein kinase	REILFFFFRLLRTGSSHK	NP_001017928, NP_00524	3768	-0.285	0.259
RT_004671.1	CCL3 chemokine (C-C motif) ligand 3	GVOKR	NP_002974.1, NP_01151	287	0.291	0.028
RT_012415.1	CCLN cyclin H	PFVDFSMLTNEX	NP_0012930.1, NP_00188	7561	0.402	0.48
RT_004395.1	CD72 molecule	NWVTPGK	NP_00671	1058	0.231	0.147
RT_016795.1	CD82 molecule	TLLPLTSLRSLGSA	NP_002222.1, NP_00671	4030	0.065	0.119
RT_006924.1	CDH23 cadherin-related 23	FILGEGK	NP_001165402, NP_01151	7762	0.136	0.035
RT_019066.1	CDK2AP2 cyclin-dependent kinase 2 associated protein 2	LDLSDHCAPAPSPSR	NP_008421.1, NP_01151	4819	0.153	0.152
RT_00865.1	CEK1A4 carcinoembryonic antigen-related cell adhesion molecule 4	KEGALVPLFHIG	NP_00107004, NP_00526	3977	0.015	-0.122
RT_022767.1	CEP350 centrosomal protein 350kDa-like 1	QNKYVFLMNPVSETLNCLWF	NP_00107004, NP_00526	8129	0.29	0.468
RT_002951.1	CFAP4 cilia and flagella associated 4	INTRODKTR	NP_01151	1470	0.333	0.666
RT_023936.1	CHRF3 complement factor H-related 3	GSVTLVNCVSTPFLRLMVGSK	NP_066303.3, NP_001166	9546	0.059	-0.059
RT_003463.1	CHRN1 cholinergic receptor, nicotinic, alpha 1	AEMELSLPFWNFCQRAGEEELSM	NP_000070.1, NP_01151	1587	0.219	0.292
RT_011669.1	CLEC12A C-type lectin domain family 12, member A	SVGGGDSRL	NP_001193939, NP_01151	2968	0.238	0.119
RT_010570.1	COG3 component of oligomeric golgi complex 3	SLAVKTRP	NP_113619.2, NP_01151	3531	0.213	0.114
RT_014946.1	COL1A1 collagen, type I, alpha 1	TFPHTLFPQTFPFR	NP_000079.2, NP_01151	3380	0.046	-0.078
RT_004138.1	COL4A4 collagen, type IV, alpha 4	RMRNFPTR	NP_000083.3, NP_00524	180	0.2	0.215
RT_014934.1	CORO2A coronin, actin binding protein, 2A	AETSLTLR	NP_438171.1, NP_01151	20475	0.259	0.292
RT_004782.1	CPS1 carbonyl phosphate synthase 1, mitochondrial	HPSHR	NP_001116205, NP_01150	5966	0.222	0.215
RT_011692.1	CREB3L4 cAMP responsive element binding protein 3-like 4	AGDLPGLPQHK	NP_570968.1, NP_00671	671	0.075	0.008
RT_012161.1	CLX1 cut-like homeobox 1	GAALGRAAR	NP_001189472, NP_01151	2074	0.237	0.028
RT_013211.1	CYB5B1 cytochrome b5-like	RLQDQRLA	NP_001006.3, NP_00525	12362	0.292	0.156
RT_019392.1	CYB5D cytochrome b5 domain containing 2	AVASVNTQRALPST	NP_001241685, NP_01152	4132	0.057	-0.112
RT_011989.1	CY8 cytochrome 8	APVNDKHMAYQHAARPAFLP	NP_001151	1296	0.399	0.658
RT_016292.1	DAAH2 dishevelled associated activator of morphogenesis 2	PGLATQAGRQGLVR	NP_001188356, NP_00671	12479	0.226	0.373
RT_013823.1	DACH1 dachshund family transcription factor 1	VLELRPEFCVLMFKR	NP_004383.4, NP_01151	5689	0.121	0.44
RT_013666.1	DENND2A DENN/MADD domain containing 2A	LGSSLDEHGAWEVSPKGR	NP_005040.3, NP_00526	6495	0.12	0.536
RT_013006.1	DGDO decylglyoxylase, delta 130kDa	RLSHWALWPS	NP_006018.2, NP_01151	2801	0.227	0.151
RT_02327.1	DHODH dihydroorotate dehydrogenase (quinone)	LSVWPWDHK	NP_001352.2, NP_00525	1317	0.035	0.345
RT_00739.1	DOCK11 dedicator of cytokinesis 11	GNADYVNDLQSLYELCK	NP_613209.3, NP_00526	4740	0.306	0.345
RT_012489.1	DOCK4 dedicator of cytokinesis 4	TVQVCLITLQAPMNGK	NP_005200.3, NP_01151	796	0.054	0.17
RT_011312.1	DOCK8 dedicator of cytokinesis 8	EPKPSFVETLQVPR	NP_002272.2, NP_01151	2611	0.054	0.103
RT_017352.1	DOHH decylhydroxylase/hydroxylase/monooxygenase	SRPAELWR	NP_001138637, NP_01151	1607	0.047	0.103
RT_009501.1	DRP4 developmental protein associated 4	ATSMVINGRK	NP_006069.3, NP_01151	23756	0.046	-0.134
RT_014102.1	DRAM1 DNA-damage regulated autophagy modulator 1	NSVLSDECR	NP_006840.2, NP_00526	626	0.267	0.437
RT_014648.1	DUSP12 dual specificity phosphatase 18	AFHPALESEVQYIC	NP_689724.3, NP_00672	1	0.309	0.066
RT_024715.1	DUSP22 dual specificity phosphatase 22	LGQAVVVAEDER	NP_001273484, NP_01151	1	0.23	0.307
RT_006951.1	EDN3 endothelin 3	FPVLYRQVLPQAEHPK	NP_960917.1, NP_01152	1113	0.153	-0.258

Table S4.

Relative Fluc fold change

Condition	N1	N2	N3
Norm Fluc/Ruc	SD	Norm Fluc/Ruc	SD
Vector	1.0000	1.0000	1.0000
H-Ras V12-D5	0.9593	0.9209	0.9202
H-Ras V12-D12	0.9563	0.9336	0.9347
H-Ras V12-D28	0.9453	0.9241	0.9283

Condition	N1	N2	N3
Norm Fluc/Ruc	SD	Norm Fluc/Ruc	SD
Vector	1.0000	1.0000	1.0000
H-Ras V12-D5	1.7850	0.6203	0.8558
H-Ras V12-D12	0.7813	0.0213	0.2300
H-Ras V12-D28	0.9394	0.0507	0.2036

Condition	N1	N2	N3
Norm Fluc/Ruc	SD	Norm Fluc/Ruc	SD
Vector	1.0000	1.0000	1.0000
H-Ras V12	0.4507	0.1307	0.2343
Vector Gen	1.9220	0.0264	11.3030
H-Ras V12 Gen	1.1860	0.1066	1.7875

Condition	N1	N2	N3
Norm Fluc/Ruc	SD	Norm Fluc/Ruc	SD
Vector	1.0000	0.9584	1.0000
H-Ras V12	0.3274	0.1348	0.5268
Vector Gen	2.4203	0.4244	1.8830
H-Ras V12 Gen	0.9056	0.0759	1.4380

Condition	N1	N2	N3
Norm Fluc/Ruc	SD	Norm Fluc/Ruc	SD
Vector	0.7927	0.2747	1.0000
H-Ras V12	1.0000	0.0011	1.2630
Vector Gen	0.7581	0.0735	1.0250
H-Ras V12 Gen	1.646	0.1354	1.3480

Condition	N1	N2	N3
Norm Fluc/Ruc	SD	Norm Fluc/Ruc	SD
Vector	1.1310	0.1031	0.8210
PML-ER	1.0800	0.2771	1.0000
Vector 4OHT	1.1430	0.1341	0.8441
PML-ER 4OHT	0.9587	0.1138	0.9200

Condition	N1	N2	N3
Norm Fluc/Ruc	SD	Norm Fluc/Ruc	SD
Vector	1.0000	0.0554	1.0000
PML-ER	0.8623	0.0563	0.9104
Vector 4OHT	1.1640	0.2160	1.0570
PML-ER 4OHT	0.6873	0.0927	0.7387

Condition	N1	N2	N3
Norm Fluc/Ruc	SD	Norm Fluc/Ruc	SD
Vector	1.0000	0.0107	1.0000
PML-ER	0.8476	0.0784	0.9101
Vector 4OHT	1.0130	0.1778	1.1320
PML-ER 4OHT	0.8051	0.1133	0.8146

Relative Fluc fold change

Condition	N1	N2	N3
Norm Fluc/Ruc	SD	Norm Fluc/Ruc	SD
Vector D12	1.0000	0.2130	1.0000
H-Ras V12 D12	0.8578	0.1954	0.7436
Vector D35	1.0000	0.0378	1.0000
H-Ras V12 D35	0.9529	0.0330	1.0336

Condition	N1	N2	N3
Norm Fluc/Ruc	SD	Norm Fluc/Ruc	SD
Vector D12	1.0000	0.2054	1.0000
H-Ras V12 D12	0.3274	0.1348	0.5268
Vector D35	1.0000	0.0378	1.0000
H-Ras V12 D35	1.5119	0.3544	1.8362

Condition	N1	N2	N3
Norm Fluc/Ruc	SD	Norm Fluc/Ruc	SD
Vector D12	1.0000	0.2050	1.0000
H-Ras V12 D12	0.7189	0.0187	1.0000
Vector D35	1.0000	0.2036	1.0000
H-Ras V12 D35	2.3362	0.3314	2.2841

Condition	N1	N2	N3
Norm Fluc/Ruc	SD	Norm Fluc/Ruc	SD
Vector D12	1.0000	0.2050	1.0000
H-Ras V12 D12	0.5396	0.1724	0.4845
Vector D35	1.0000	0.2036	1.0000
H-Ras V12 D35	3.3752	0.3530	1.6540

Condition	N1	N2	N3
Norm Fluc/Ruc	SD	Norm Fluc/Ruc	SD
Vector	1.0000	0.1731	1.0000
H-Ras V12	0.3856	0.2237	0.6659
H-Ras V12E6	0.4181	0.0877	0.8446
H-Ras V12E67	2.3976	0.4076	3.8336

Condition	N1	N2	N3
Norm Fluc/Ruc	SD	Norm Fluc/Ruc	SD
Vector	1.0000	0.2050	1.0000
H-Ras V12	0.2937	0.078	0.8011
H-Ras V12E6	0.3333	0.0778	0.9688
H-Ras V12E67	0.9557	0.3248	1.374

Condition	N1	N2	N3
Norm Fluc/Ruc	SD	Norm Fluc/Ruc	SD
Vector	1	0.2191	1
H-Ras V12	0.4874	0.02819	0.4709
H-Ras V12E6	0.8765	0.01425	0.4316
H-Ras V12E67	1.844	0.3842	0.9383

Condition	N1	N2	N3
Norm Fluc/Ruc	SD	Norm Fluc/Ruc	SD
Vector	1	0.1713	1
H-Ras V12	0.3133	0.0854	0.5884
H-Ras V12 E7	0.9597	0.1668	0.8384
H-Ras V12 E7A21-24	0.2852	0.0311	0.3682

Condition	N1	N2	N3
Norm Fluc/Ruc	SD	Norm Fluc/Ruc	SD
Vector	1	0.0912	1
H-Ras V12	0.8729	0.07417	0.7811
Vector CDK4	0.9616	0.2399	1.127
H-Ras V12E6CDK4	0.8721	0.08102	1.397

Relative Fluc fold change

Condition	N1	N2	N3
Norm Fluc/Ruc	SD	Norm Fluc/Ruc	SD
Vector	1.0000	1.0000	1.0000
H-Ras V12	1.372	0.1402	0.8938
Vector Palbo	20.4	3.266	10.59
Vector Palbo + Gen	11.23	1.73	1.708

Condition	N1	N2	N3
Norm Fluc/Ruc	SD	Norm Fluc/Ruc	SD
Vector	1.0000	1.0000	1.0000
H-Ras V12	0.7022	0.0302	0.9950
Vector D35	1.0000	0.2612	4.8140
Vector Palbo + Gen	1.3210	0.1188	5.2490

Condition	N1	N2	N3
Norm Fluc/Ruc	SD	Norm Fluc/Ruc	SD
Vector D35	1	1.42	1
H-Ras V12 D35	1.466	0.1202	1.25
Vector D35 Palbo	0.873	0.2202	0.7346
H-Ras V12 D35 Palbo	0.8395	0.0812	0.7551

Condition	N1	N2	N3
Norm Fluc/Ruc	SD	Norm Fluc/Ruc	SD
Vector D5	1.0000	0.2050	1.0000
H-Ras V12 D5	0.8620	0.3315	0.9551
Vector D28	1.0000	0.1937	0.8956

Condition	N1	N2	N3
Norm Fluc/Ruc	SD	Norm Fluc/Ruc	SD
Vector D12	0.9991	0.2321	0.931
Vector D12	0.7887	0.1582	1.004
Vector D35	0.7829	0.1658	1.056

Condition	N1	N2	N3
Norm Fluc/Ruc	SD	Norm Fluc/Ruc	SD
VectorStar	1	0.2623	1
H-Ras V12Star	0.4751	0.0574	0.5905
Vector FBS	0.928	0.2028	0.8961
H-Ras V12E67	0.8000	0.1223	0.889

Condition	N1	N2	N3
Norm Fluc/Ruc	SD	Norm Fluc/Ruc	SD
HPN-Vector	0.07324	0.99999	0.00011
HPN-H-Ras V12	0.388893	0.384338	0.728758
VASP-Vector	0.999999	0.00484	0.999999
VASP-H-Ras V12	0.748287	0.05055	0.876331
ASPH-Vector	0	0	0
ASPH-H-Ras V12	0	0	0
FBL-Vector	0.178778	0.999999	0.187891
FBL-H-Ras V12	0.641643	0.16488	0.830588

Condition	N1	N2	N3
Norm Fluc/Ruc	SD	Norm Fluc/Ruc	SD
HPN-Vector	0.0240	0.9702	0.0087
HPN-H-Ras V12	0.7846	0.2833	2.4933
VASP-Vector	19.0749	1.8238	4.4482
VASP-H-Ras V12	0.2412	1.1154	3.1288
ASPH-Vector	3.6887	0.4123	1.0000
ASPH-H-Ras V12	2.4933	1.4170	0.1653
FBL-Vector	3.1437	0.4300	1.8573
FBL-H-Ras V12	1.7089	0.1028	1.0205

Condition	N1	N2	N3
Norm Fluc/Ruc	SD	Norm Fluc/Ruc	SD
Vector	1	0.1713	1
Vector E7	1.206	0.2172	1.121
Vector E7A21-24	0.8017	0.1072	1.321

Fluc/Ruc

Condition	N1	N2	N3
Fluc/Ruc	SD	Fluc/Ruc	SD
Vector D5	0.1813	0.01333	0.1832
H-Ras V12-D5	0.1915	0.03221	0.1917
Vector D12	0.1777	0.02328	0.2036
H-Ras V12-D12	0.1877	0.05967	0.1853
Vector D28	0.1976	0.0184	0.187
H-Ras V12-D28	0.2116	0.02771	0.2083

Condition	N1	N2	N3
Fluc/Ruc	SD	Fluc/Ruc	SD
Vector	0.1568	0.03292	0.1633
H-Ras V12	0.1553	0.007874	0.1812
Vector CDK4-1	0.973	0.098	1.545
H-Ras V12 CDK4-1	0.837	0.178	0.860
Vector Gen	7.038	0.741	5.910
H-Ras V12 Gen	3.702	0.460	3.876
Vector CDK4-1 + Gen	16.828	3.804	14.750
H-Ras V12 CDK4-1 + Gen	4.898	0.400	4.784

Condition	N1	N2	N3
Fluc/Ruc	SD	Fluc/Ruc	SD
Vector	1.000	0.000	1.124
H-Ras V12	0.625	0.162	0.748
Vector CDK4-1	0.973	0.098	1.545
H-Ras V12 CDK4-1	0.837	0.178	0.860
Vector Gen	7.038	0.741	5.910
H-Ras V12 Gen	3.702	0.460	3.876
Vector CDK4-1 + Gen	16.828	3.804	14.750
H-Ras V12 CDK4-1 + Gen	4.898	0.400	4.784

Table S5. Real time PCR primers

Gene Name	5' forward primer (5'-3')	3' reverse primer (5'-3')
BRCA1	GGTTGTTGATGTGGAGGGGCAA	CCAGATTCCAGGTAAGGGGTTTC
CDKN1A/p21	ACCCTTGTGCCTCGCTCAGG	GCGTTTGGAGTGGTAGAAATCTGT
CDK4	CAGTGCAGTCGGTGGTACCTGA	GGCAGAGATTTCGCTTGTGTGG
CENPA	AATGGATTCTGCGATGCTGTCTGG	TTTTTCAGGCCTTTGGAACGGTGTT
FANCD2	CCTTAGTAGCCGACTGAAACAGG	TGCAAGTAATGGACGCTCTG
GADD45A	TTGCAATATGACTTTGGAGGAA	CATCCCCACCTTATCCAT
HMBS	GGCAATGCGGCTGCAA	GGGTACCCACGCGAATCAC
H-RAS	TTGCCATCAACAACACCAAGTC	ATCCGAGTCCTTCACCCGTTTG
KI67	AGAAGACAGTACCGCAGATGA	CGGCTCACTAATTTAACGCTGG
MCM6	ATCCCTCTTGCCAAGGATTT	GAAAAGTTCCGCTCACAAGC
ORC1L	CCCGGCTCAAGCATCYAAAGG	TCGTGCATCTCCAGACAGTCT
TBP	GCTGGCCCATAGTGATCTTTGC	CTTACACGCCAAGAAACAGTGA
MCM6	ATCCCTCTTGCCAAGGATTT	GAAAAGTTCCGCTCACAAGC
IL-6	CCAGGAGCCCAGCTATGAACTC	AAGGCAGCAGGCAACACCAG
CXCL8/IL-8	GGCACAAACTTTCAGAGACAGCA	GGCAAAACTGCACCTTCACACA