

Supplementary Table 1**Shortened 3'UTRs**

APA site	gene ID	lost PUM sites	log fold change	-value diff. exp	gene symbol
p.1301.6	1301	1	3.34604	1.20E-05	COL11A1
p.81611.1	81611	1	1.84336	0.000678749	ANP32E
p.10097.1	10097	1	1.76786	3.37E-05	ACTR2
p.51026.1	51026	1	1.74004	9.13E-06	GOLT1B
p.51659.1	51659	1	1.59379	6.14E-05	GIN52
p.79572.1	79572	1	1.59155	0.00035399	ATP13A3
p.5062.1	5062	2	1.49865	8.96E-05	PAK2
p.4893.2	4893	1	1.48177	0.002016624	NRAS
p.8507.1	8507	1	1.37817	0.007869441	ENC1
p.10276.2	10276	2	1.37096	0.00099952	NET1
p.9877.1	9877	2	1.33103	4.95E-06	ZC3H11A
p.80155.1	80155	1	1.31275	4.48E-07	NAA15
p.55706.1	55706	1	1.31015	0.000572818	TMEM48
p.92140.2	92140	3	1.30391	4.98E-06	MTDH
p.25932.1	25932	2	1.30381	0.00644907	CLIC4
p.528.3	528	1	1.29909	0.000144482	ATP6V1C1
p.84955.2	84955	2	1.27068	4.94E-05	NUDCD1
p.8543.1	8543	1	1.26135	0.019855937	LMO4
p.55284.1	55284	1	1.24239	6.14E-07	UBE2W
p.117178.3	117178	1	1.23431	9.53E-05	SSX2IP
p.51018.4	51018	1	1.22593	2.35E-06	RRP15
p.57532.6	57532	3	1.22504	1.72E-05	NUFIP2
p.112858.2	112858	1	1.18547	7.93E-05	TP53RK
p.8669.2	8669	1	1.1763	5.05E-06	EIF3J
p.10890.4	10890	1	1.09651	9.14E-08	RAB10
p.3267.1	3267	1	1.09645	4.22E-06	AGFG1
p.6745.2	6745	1	1.0902	0.000747828	SSR1
p.79677.2	79677	2	1.08962	3.66E-05	SMC6
p.23527.2	23527	2	1.07493	0.000213667	ACAP2
p.5203.1	5203	1	1.07094	0.00070456	PFDN4
p.79888.2	79888	1	1.05371	0.001510546	LPCAT1
p.26046.2	26046	1	1.05281	0.000231483	LTN1
p.153339.1	153339	1	1.04776	0.000311249	TMEM167A
p.55110.1	55110	2	1.03488	0.001739127	MAGOHB
p.5469.1	5469	2	1.02688	0.050409219	MED1
p.54800.1	54800	2	1.0235	0.002063174	KLHL24
p.11320.3	11320	4	1.00629	0.028935489	MGAT4A
p.54149.1	54149	1	0.997606	0.006795977	C21orf91
p.55971.1	55971	1	0.989322	0.001160397	BAIAP2L1
p.22797.2	22797	1	0.986222	0.007900227	TFEC
p.7994.2	7994	1	0.966617	0.02085234	MYST3
p.10059.2	10059	1	0.957199	0.000454561	DNM1L
p.25917.2	25917	1	0.93798	0.000124526	THUMPD3
p.2786.2	2786	1	0.932943	0.03126166	GNG4

p.133619.2	133619	2	0.932475	6.05E-05	PRRC1
p.56852.2	56852	2	0.928459	0.0137244	RAD18
p.6731.7	6731	1	0.917953	2.07E-05	SRP72
p.57720.3	57720	1	0.911116	5.37E-05	GPR107
p.8634.2	8634	1	0.891051	0.001914598	RTCD1
p.25836.1	25836	4	0.876987	0.005399843	NIPBL
p.135228.3	135228	2	0.875933	0.001249262	CD109
p.157680.4	157680	2	0.872486	0.005159905	VPS13B
p.9097.2	9097	1	0.871557	0.0013773	USP14
p.2885.2	2885	2	0.865555	0.000138914	GRB2
p.8030.1	8030	1	0.863186	0.011890665	CCDC6
p.125228.3	125228	1	0.858339	0.011574755	C18orf19
p.7175.1	7175	1	0.857776	0.000151936	TPR
p.57089.1	57089	1	0.848759	1.12E-06	ENTPD7
p.90806.2	90806	1	0.837183	0.001403134	ANGEL2
p.55207.1	55207	1	0.820868	0.022784284	ARL8B
p.10203.1	10203	2	0.807331	0.003429625	CALCRL
p.55153.2	55153	3	0.80623	0.002703631	SDAD1
p.7227.1	7227	3	0.80539	0.049064692	TRPS1
p.283209.1	283209	1	0.802976	0.013351419	PGM2L1
p.8065.2	8065	1	0.802513	0.000151257	CUL5
p.79828.1	79828	1	0.797501	0.000505914	METTL8
p.56943.1	56943	1	0.797174	0.000932962	ENY2
p.84901.2	84901	1	0.793092	2.86E-06	NFATC2IP
p.255520.1	255520	1	0.792406	0.006672674	ELMOD2
p.5087.1	5087	1	0.790327	0.081207269	PBX1
p.84259.1	84259	1	0.788728	0.00425738	DCUN1D5
p.286148.5	286148	1	0.779111	0.003963532	DPY19L4
p.134430.1	134430	4	0.777661	0.000135153	WDR36
p.1737.3	1737	1	0.776573	0.004454858	DLAT
p.56474.1	56474	1	0.765375	0.003952036	CTPS2
p.6198.1	6198	1	0.765057	0.020871033	RPS6KB1
p.116150.1	116150	1	0.750093	0.0322726	NUS1
p.5048.2	5048	3	0.746829	0.002203512	PAFAH1B1
p.9969.5	9969	1	0.742792	0.011596419	MED13
p.56888.2	56888	2	0.741086	0.000265759	KCMF1
p.9126.2	9126	1	0.738587	0.002221341	SMC3
p.51122.3	51122	1	0.732167	0.026314018	COMMD2
p.6272.2	6272	2	0.722032	0.019363657	SORT1
p.9166.1	9166	1	0.71989	0.022713572	EBAG9
p.9868.1	9868	1	0.715714	0.003029771	TOMM70A
p.93663.2	93663	1	0.714849	0.018461196	ARHGAP18
p.808.1	808	1	0.70889	0.00084125	CALM3
p.2932.1	2932	4	0.706221	0.00148557	GSK3B
p.5873.1	5873	1	0.687671	0.009466502	RAB27A
p.55775.2	55775	1	0.684457	0.000295737	TDP1
p.55342.1	55342	1	0.6826	0.000318993	STRBP

p.3093.1	3093	2	0.661935	0.000702017	UBE2K
p.6924.1	6924	1	0.661442	0.000129949	TCEB3
p.6249.4	6249	2	0.659843	0.01775643	CLIP1
p.94104.2	94104	1	0.658328	0.000385359	GCFC1
p.64225.1	64225	2	0.65562	0.04834206	ATL2
p.55109.3	55109	2	0.644681	0.00450987	AGGF1
p.1362.1	1362	1	0.644267	0.164735867	CPD
p.127018.1	127018	1	0.640176	0.013850442	LYPLAL1
p.54726.2	54726	2	0.634034	0.000739965	OTUD4
p.7803.3	7803	4	0.632354	0.024478859	PTP4A1
p.4287.2	4287	4	0.625629	0.008551638	ATXN3
p.4026.4	4026	1	0.623232	0.037022049	LPP
p.9140.4	9140	1	0.622513	0.007886147	ATG12
p.25978.1	25978	1	0.61774	0.039418085	CHMP2B
p.58528.1	58528	1	0.614936	0.096105373	RRAGD
p.22936.1	22936	2	0.610072	0.049572333	ELL2
p.79939.1	79939	2	0.609574	0.006803917	SLC35E1
p.8545.1	8545	1	0.601315	0.016649492	CGGBP1
p.23161.1	23161	1	0.596947	0.000534007	SNX13
p.11052.2	11052	2	0.57751	0.001072231	CPSF6
p.163590.2	163590	1	0.575751	0.000151844	TOR1AIP2
p.11163.1	11163	2	0.574426	0.06813305	NUDT4
p.4205.2	4205	2	0.571992	0.058540682	MEF2A
p.9958.6	9958	1	0.571921	0.018085617	USP15
p.9373.2	9373	1	0.557663	0.039796087	PLAA
p.1432.1	1432	2	0.546392	0.060952202	MAPK14
p.143384.2	143384	1	0.541097	0.018544243	C10orf46
p.8774.1	8774	1	0.537813	0.009392055	NAPG
p.57456.1	57456	1	0.531792	0.005923904	KIAA1143
p.10892.1	10892	4	0.520433	0.084999374	MALT1
p.5586.1	5586	1	0.518789	0.039169085	PKN2
p.23704.1	23704	1	0.516073	0.201070101	KCNE4
p.518.1	518	1	0.514817	0.007245646	ATP5G3
p.57168.1	57168	1	0.514457	0.00304206	ASPHD2
p.9262.2	9262	1	0.514405	0.044452468	STK17B
p.26984.2	26984	1	0.493885	0.023470657	SEC22A
p.1629.1	1629	1	0.492596	0.016998642	DBT
p.55471.1	55471	1	0.490821	0.025843519	C2orf56
p.55320.1	55320	1	0.483879	0.003715179	MIS18BP1
p.5527.5	5527	1	0.477724	0.035496227	PPP2R5C
p.163.2	163	1	0.472397	0.118516768	AP2B1
p.54994.2	54994	1	0.470611	0.015759	C20orf11
p.51762.2	51762	1	0.454929	0.019597276	RAB8B
p.9306.3	9306	1	0.451307	0.08547743	SOCS6
p.377.1	377	1	0.449607	0.02246586	ARF3
p.1540.1	1540	4	0.444419	0.104850773	CYLD
p.11169.2	11169	1	0.44378	4.21E-05	WDHD1

p.23142.1	23142	1	0.430607	0.044486472	DCUN1D4
p.10100.3	10100	3	0.426983	0.106741319	TSPAN2
p.9180.4	9180	1	0.42312	0.300312912	OSMR
p.286205.2	286205	2	0.409166	0.000401905	SCAI
p.11127.2	11127	1	0.398149	0.044541766	KIF3A
p.4780.2	4780	1	0.390668	0.035514343	NFE2L2
p.285282.2	285282	1	0.390133	0.068636111	RABL3
p.1027.2	1027	1	0.38651	0.345813534	CDKN1B
p.23057.2	23057	1	0.377734	0.128271244	NMNAT2
p.7182.1	7182	4	0.377357	0.001919509	NR2C2
p.55973.2	55973	1	0.37611	0.003439249	BCAP29
p.23621.1	23621	1	0.375918	0.088379782	BACE1
p.488.3	488	2	0.364977	0.036378751	ATP2A2
p.285672.1	285672	1	0.36385	0.035363477	SREK1IP1
p.961.1	961	2	0.361648	0.360347354	CD47
p.81550.2	81550	1	0.360271	0.01056503	TDRD3
p.4097.1	4097	1	0.351628	0.062194883	MAFG
p.148808.1	148808	2	0.338065	0.279902064	MFSD4
p.91775.2	91775	1	0.337272	0.024718201	FAM55C
p.5786.1	5786	1	0.334142	0.046893298	PTPRA
p.55031.1	55031	1	0.334125	0.057210628	USP47
p.23362.4	23362	2	0.333083	0.503671369	PSD3
p.57539.1	57539	1	0.332467	0.076105229	WDR35
p.57148.2	57148	2	0.332243	0.009685689	RALGAPB
p.89796.2	89796	1	0.331881	0.284561598	NAV1
p.361.1	361	1	0.320445	0.326873028	AQP4
p.55796.2	55796	5	0.317619	0.006151172	MBNL3
p.4763.4	4763	3	0.313912	0.084647177	NF1
p.4238.1	4238	1	0.311914	0.12584843	MFAP3
p.55186.2	55186	1	0.305336	0.177787916	SLC25A36
p.9962.1	9962	1	0.303373	0.084565323	SLC23A2
p.92126.2	92126	1	0.301246	0.056845437	DSEL
p.64093.1	64093	1	0.295977	0.121331237	SMOC1
p.93.1	93	4	0.290566	0.170491525	ACVR2B
p.2137.1	2137	1	0.287783	0.073052301	EXTL3
p.10413.1	10413	1	0.286149	0.449788783	YAP1
p.5737.1	5737	2	0.28555	0.351363717	PTGFR
p.4848.2	4848	1	0.28483	0.196843522	CNOT2
p.10725.1	10725	2	0.277295	0.28728263	NFAT5
p.137492.2	137492	1	0.276748	0.265356893	VPS37A
p.128637.1	128637	2	0.271548	0.054531759	TBC1D20
p.79685.1	79685	1	0.27136	0.087746336	SAP30L
p.8763.1	8763	1	0.270601	0.544178404	CD164
p.29974.1	29974	3	0.268273	0.031311624	A1CF
p.51552.1	51552	2	0.268008	0.13921524	RAB14
p.3572.1	3572	1	0.264442	0.420538133	IL6ST
p.9139.2	9139	1	0.259734	0.064771407	CBFA2T2

p.208.1	208	1	0.257889	0.139680389	AKT2
p.23064.1	23064	1	0.254912	0.049366953	SETX
p.161742.1	161742	5	0.250255	0.281846114	SPRED1
p.64398.3	64398	1	0.249777	0.386893254	MPP5
p.5578.2	5578	3	0.243364	0.04786041	PRKCA
p.6400.3	6400	1	0.242434	0.240415741	SEL1L
p.91404.1	91404	3	0.23832	0.348952623	SESTD1
p.83548.3	83548	1	0.237782	0.129399801	COG3
p.54545.1	54545	2	0.235296	0.284736973	MTMR12
p.23493.1	23493	1	0.227029	0.61623904	HEY2
p.6641.2	6641	1	0.224681	0.295617098	SNTB1
p.80014.1	80014	1	0.22367	0.244246628	WWC2
p.1374.1	1374	1	0.217355	0.04804195	CPT1A
p.5728.2	5728	1	0.210932	0.357658116	PTEN
p.26092.2	26092	1	0.206119	0.446531071	TOR1AIP1
p.3709.1	3709	1	0.205776	0.432292013	ITPR2
p.387338.1	387338	1	0.205606	0.253652804	NSUN4
p.8492.2	8492	2	0.200164	0.101984163	PRSS12
p.84333.2	84333	1	0.195877	0.297644452	PCGF5
p.6452.2	6452	1	0.193542	0.17595779	SH3BP2
p.26268.1	26268	1	0.191478	0.231516911	FBXO9
p.81573.4	81573	2	0.188175	0.137506831	ANKRD13C
p.9469.1	9469	1	0.184347	0.102089212	CHST3
p.84236.1	84236	1	0.178655	0.29395844	RHBDD1
p.115.1	115	1	0.178495	0.332623239	ADCY9
p.23001.1	23001	1	0.177003	0.43282014	WDFY3
p.7799.4	7799	1	0.174549	0.077378442	PRDM2
p.152137.1	152137	2	0.173612	0.491083372	CCDC50
p.9218.1	9218	2	0.170494	0.556554949	VAPA
p.3423.5	3423	2	0.166722	0.312045127	IDS
p.6886.1	6886	2	0.164429	0.136548178	TAL1
p.10657.1	10657	1	0.152746	0.318756281	KHDRBS1
p.143684.1	143684	2	0.152616	0.396998309	FAM76B
p.56243.4	56243	2	0.152163	0.414429553	KIAA1217
p.1983.6	1983	1	0.151745	0.493572749	EIF5
p.7520.2	7520	1	0.149639	0.309652006	XRCC5
p.148932.1	148932	1	0.149625	0.266023362	MOBK2C
p.56990.1	56990	1	0.141538	0.589484246	CDC42SE2
p.84056.1	84056	2	0.138149	0.176426541	KATNAL1
p.23390.1	23390	1	0.136651	0.315837341	ZDHHC17
p.2800.1	2800	1	0.129072	0.380388077	GOLGA1
p.56889.1	56889	1	0.128404	0.684977517	TM9SF3
p.27230.2	27230	1	0.125736	0.45835779	SERP1
p.83876.1	83876	1	0.125323	0.132301439	MRO
p.51343.1	51343	1	0.119375	0.50695366	FZR1
p.57496.3	57496	5	0.119347	0.120758719	MKL2
p.79817.2	79817	1	0.114455	0.494455151	MOBK2B

p.801.3	801	2	0.109818	0.553505488	CALM1
p.51100.1	51100	2	0.108578	0.698189614	SH3GLB1
p.133746.1	133746	2	0.106794	0.474647079	JMY
p.4204.1	4204	1	0.105201	0.454633022	MECP2
p.154810.1	154810	2	0.100534	0.325051574	AMOTL1
p.11276.2	11276	1	0.0988962	0.581457768	SYNRG
p.26065.3	26065	3	0.0979143	0.585140705	LSM14A
p.79776.1	79776	1	0.0975801	0.167849972	ZFHX4
p.4093.1	4093	2	0.0962148	0.330471158	SMAD9
p.102.2	102	3	0.0960521	0.763043747	ADAM10
p.55719.3	55719	1	0.0946039	0.547054847	FAM178A
p.2674.2	2674	1	0.085502	0.883468476	GFRA1
p.143098.2	143098	2	0.0838597	0.567212111	MPP7
p.7057.2	7057	4	0.08262	0.788089149	THBS1
p.2889.1	2889	1	0.0762866	0.672692496	RAPGEF1
p.9236.2	9236	1	0.0577848	0.80076936	CCPG1
p.1106.3	1106	1	0.0564997	0.672185612	CHD2
p.2729.4	2729	1	0.0407808	0.88883392	GCLC
p.83999.1	83999	1	0.0403445	0.73255589	KREMEN1
p.4660.2	4660	1	0.0372442	0.544487442	PPP1R12B
p.7204.3	7204	1	0.0286435	0.878192293	TRIO
p.4208.1	4208	2	0.0280783	0.851422555	MEF2C
p.10026.5	10026	2	0.0178547	0.94038073	PIGK
p.10424.4	10424	2	0.0134776	0.93881968	PGRMC2
p.3340.3	3340	1	0.0121369	0.9089681	NDST1
p.50808.2	50808	1	0.0118442	0.950998769	AK3
p.51621.1	51621	2	0.0094747	0.956808803	KLF13
p.54855.2	54855	1	0.00896938	0.977763612	FAM46C
p.81488.1	81488	1	0.00768531	0.963160408	GRINL1A
p.56605.4	56605	1	0.00643096	0.974446673	ERO1LB
p.10735.1	10735	1	0.00393394	0.98576474	STAG2
p.4851.1	4851	1	-0.00162789	0.989875918	NOTCH1
p.5494.1	5494	4	-0.0122894	0.946107026	PPM1A
p.8897.2	8897	1	-0.0139983	0.906803551	MTMR3
p.160518.2	160518	2	-0.0152684	0.7962659	DENND5B
p.894.1	894	1	-0.0197799	0.913461919	CCND2
p.7020.2	7020	2	-0.0274538	0.956229834	TFAP2A
p.79819.6	79819	1	-0.0322384	0.737824555	WDR78
p.9839.2	9839	2	-0.0383425	0.827712284	ZEB2
p.5337.3	5337	1	-0.0410481	0.766926242	PLD1
p.8313.1	8313	1	-0.0445589	0.619988739	AXIN2
p.22822.2	22822	6	-0.0457664	0.90306617	PHLDA1
p.8649.2	8649	2	-0.0532616	0.796255436	LAMTOR3
p.83464.1	83464	1	-0.0568737	0.719683748	APH1B
p.84668.1	84668	1	-0.0607184	0.639382996	FAM126A
p.23140.3	23140	1	-0.0662972	0.469960771	ZZEF1
p.140885.2	140885	1	-0.0689954	0.743861141	SIRPA

p.153396.1	153396	1	-0.0710312	0.67834599	TMEM161B
p.7058.5	7058	1	-0.0856479	0.815942131	THBS2
p.1902.1	1902	1	-0.104382	0.52560646	LPAR1
p.130574.2	130574	4	-0.107264	0.365770639	LYPD6
p.79745.3	79745	2	-0.107655	0.616144501	CLIP4
p.89795.1	89795	1	-0.131101	0.119900809	NAV3
p.54756.1	54756	2	-0.131135	0.271271129	IL17RD
p.54665.3	54665	1	-0.135868	0.392906769	RSBN1
p.10015.2	10015	1	-0.144086	0.493182855	PDCD6IP
p.51201.1	51201	1	-0.145307	0.430826575	ZDHHC2
p.66008.4	66008	1	-0.150806	0.524273993	TRAK2
p.55715.3	55715	1	-0.163888	0.13452526	DOK4
p.23405.2	23405	2	-0.172374	0.486693047	DICER1
p.23387.3	23387	2	-0.174896	0.392031886	SIK3
p.538.1	538	1	-0.178314	0.402682107	ATP7A
p.11099.1	11099	1	-0.185514	0.013349693	PTPN21
p.11334.2	11334	1	-0.201129	0.228502379	TUSC2
p.1602.1	1602	2	-0.202125	0.460408697	DACH1
p.29123.7	29123	1	-0.202347	0.410008021	ANKRD11
p.7556.1	7556	1	-0.20608	0.204396309	ZNF10
p.2060.3	2060	2	-0.211391	0.244547165	EPS15
p.29068.1	29068	2	-0.227284	0.296079005	ZBTB44
p.3915.3	3915	1	-0.265352	0.353620201	LAMC1
p.10217.3	10217	2	-0.274235	0.130316239	CTDSPL
p.6500.6	6500	1	-0.280407	0.151985502	SKP1
p.153222.3	153222	3	-0.298181	0.093405869	C5orf41
p.6777.1	6777	1	-0.316894	0.030150255	STAT5B
p.83700.2	83700	2	-0.318731	8.57E-05	JAM3
p.5412.4	5412	1	-0.326029	0.13943951	UBL3
p.23768.1	23768	1	-0.359359	0.000294524	FLRT2
p.5937.1	5937	1	-0.366876	0.110424796	RBMS1
p.2119.2	2119	1	-0.37498	0.111021787	ETV5
p.6867.1	6867	1	-0.380351	0.306685828	TACC1
p.26053.2	26053	2	-0.382417	0.031395058	AUTS2
p.57616.1	57616	1	-0.406895	0.024206049	TSHZ3
p.79875.3	79875	1	-0.412747	0.106648899	THSD4
p.6926.1	6926	3	-0.429427	0.17521498	TBX3
p.92.1	92	1	-0.475598	0.011835869	ACVR2A
p.10929.1	10929	1	-0.509401	0.013936609	SRSF8
p.1500.2	1500	1	-0.521875	0.040376858	CTNND1
p.7905.2	7905	2	-0.546689	0.074385262	REEP5
p.6558.1	6558	2	-0.563669	0.186800463	SLC12A2
p.89797.1	89797	1	-0.565451	0.003070541	NAV2
p.55450.1	55450	1	-0.709479	0.210456846	CAMK2N1
p.4211.1	4211	1	-0.777265	8.24E-06	MEIS1
p.80310.1	80310	1	-0.80233	4.40E-06	PDGFD
p.116496.2	116496	1	-0.884717	0.034323472	FAM129A

p.36.1	36	1	-0.918384	0.047647336	ACADSB
p.23452.1	23452	1	-0.976362	1.14E-07	ANGPTL2
p.10350.3	10350	1	-1.20567	6.29E-16	ABCA9
p.3725.2	3725	2	-1.21448	0.000139363	JUN
p.120.1	120	1	-1.40224	0.000412452	ADD3
p.7021.1	7021	2	-1.46108	0.022040325	TFAP2B
p.1846.3	1846	1	-1.55448	0.005487796	DUSP4
p.3479.1	3479	1	-1.6844	2.18E-09	IGF1
p.8614.2	8614	1	-2.77791	8.24E-11	STC2

Lengthened 3'UTRs

APA site	gene ID	Gain PUM sites	log fold change	P-value diff. expr.	gene symbol
p.2308.2	2308	1	-1.6295	1.64E-08	FOXO1
p.6309.2	6309	1	-1.62248	2.12E-06	SC5DL
p.9252.2	9252	1	-1.54632	0.00011932	RPS6KA5
p.3667.2	3667	8	-1.4955	0.001657433	IRS1
p.57125.1	57125	1	-1.30928	0.000306387	PLXDC1
p.56898.1	56898	1	-1.2938	8.58E-05	BDH2
p.6925.1	6925	3	-1.25683	0.000600007	TCF4
p.3176.2	3176	2	-1.19904	0.00027889	HNMT
p.81563.5	81563	1	-1.16602	0.001680965	C1orf21
p.55603.1	55603	1	-1.12472	0.007161292	FAM46A
p.11170.1	11170	1	-1.09491	0.006247135	FAM107A
p.81539.1	81539	3	-0.828634	0.019664202	SLC38A1
p.10491.3	10491	1	-0.790634	0.000170561	CRTAP
p.51312.2	51312	1	-0.782017	0.058080082	SLC25A37
p.26469.2	26469	1	-0.70474	0.011680346	PTPN18
p.131566.7	131566	1	-0.690306	0.00437571	DCBLD2
p.9218.6	9218	2	-0.671798	0.001230882	VAPA
p.79365.1	79365	1	-0.668554	0.112433371	BHLHE41
p.573.2	573	1	-0.631085	0.025300848	BAG1
p.6622.1	6622	1	-0.600955	4.63E-06	SNCA
p.64778.2	64778	1	-0.578246	0.038028609	FNDC3B
p.200958.1	200958	2	-0.553899	0.135360905	MUC20
p.64388.1	64388	1	-0.534599	0.002645254	GREM2
p.171425.3	171425	1	-0.516825	0.015380678	CLYBL
p.23038.1	23038	2	-0.509143	0.000334	WDTC1
p.175.1	175	2	-0.429467	0.154322571	AGA
p.84897.2	84897	1	-0.406707	0.018423573	TBRG1
p.8874.2	8874	1	-0.399612	0.043162955	ARHGEF7
p.55333.3	55333	1	-0.396708	0.114101202	SYNJ2BP
p.54491.1	54491	1	-0.289698	0.053320848	FAM105A
p.23607.2	23607	2	-0.225057	0.1281634	CD2AP
p.51249.1	51249	1	-0.167554	0.508842086	TMEM69
p.80306.1	80306	1	-0.145682	0.567196653	MED28
p.79752.2	79752	1	-0.144008	0.677482834	ZFAND1
p.9562.1	9562	1	0.00641579	0.970841107	MINPP1
p.115350.1	115350	2	0.0147064	0.899185368	FCRL1
p.1977.1	1977	3	0.0440604	0.654658669	EIF4E
p.6672.5	6672	1	0.0604781	0.78030873	SP100
p.6651.1	6651	1	0.0629671	0.755235526	SON
p.65108.1	65108	1	0.0936532	0.697927499	MARCKSL1
p.149371.1	149371	1	0.180538	0.358534392	EXOC8
p.6738.1	6738	1	0.211184	0.241726643	TROVE2
p.4883.1	4883	1	0.226194	0.201443	NPR3
p.90268.2	90268	1	0.29415	0.063667699	FAM105B

p.3225.2	3225	1	0.306857	0.395120885	HOXC9
p.3842.3	3842	1	0.307704	0.107106004	TNPO1
p.23213.2	23213	1	1.05363	0.020403615	SULF1
p.259266.1	259266	1	1.25827	4.23E-05	ASPM
p.51514.1	51514	1	1.87144	1.63E-06	DTL

Miles Supplementary Table 2: Primers and siRNAs

Primers

3'RACE RT-PCR Primer	Sequence
P7-t25-vn oligo-dT primer	CAAGCAGAAGACGGCATAACGAGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
CSTF2 forward	ATCCTTGCCTGCGAATGTCC
CSTF2 reverse	GGGTGGTCCTCGGCTCTC
CSTF3 forward	TGAAGTGGATAGAAAACCAGAATACCC
CSTF3 reverse	TGAAACAGATAGGAGGAGGGAGA
CPSF2 forward	CTTTGGAACCCCTTGCCACCT
CPSF2 reverse	TGCGGACTGCTACTTGATTGTTG
TMEM119 proximal forward	CCCTGGCAACATTGTGAGACC
TMEM119 distal forward	TCTCCCCATCCCTCCATCT
FAM100B proximal forward	CAGGAGTTTTTCAGGCAAGTTTTTC
FAM100B distal forward	AGTGGAGAGCCTGCCTTTGG
P7 forward	CAAGCAGAAGACGGCATAACGAGA
NRAS distal forward	GGATGTCCGTGGAAGTTGTAA
NRAS proximal forward	TTTGTTCCTAGCTTACTGA
JUN distal forward	GGTGCTTATTCTCAAAGCAGGA
JUN proximal forward	GCTTCTGTACTCCTTAAGAACACA
actin forward distal	CAGCCAGGGCTTACCTGT

Tumor RT-PCR Primers	Sequence
FOXA1 TUMOR RT FOR	CTCCTACTGGACGCTGCAC
FOXA1 TUMOR RT REV	GCAAGTAGCAGCCGTTCTC
SMG1 TUMOR RT FOR	GACGTGCTTAATGAAAGTAGCAA
SMG1 TUMOR RT REV	AAGGCCAAGACAGCAAGC
CCND1 TUMOR RT FOR	AGATCATCCGCAAACACG
CCND1 TUMOR RT REV	TGAACTTCACATCTGTGGCA
STAT5B UTR 2 TUMOR FOR	CATGTGGCTGTTTGAATAAGAGA
STAT5B UTR 2 TUMOR REV	GACGAAGACTCACTGGAGCA
STAT5B CDS TUMOR FOR	GCTAAAGCTGTTGATGGATACG
STAT5B CDS TUMOR REV	GATGCGTTCACAAACTCAGG
PTEN UTR2 TUMOR FOR	GTCATGCATGCAGATGGAA
PTEN UTR2 TUMOR REV	CTGCCAAATACTACAGTTAAAGCC
PTEN CDS TUMOR FOR	ACACGACGGGAAGACAAGTT
PTEN CDS TUMOR REV	CTTTGATATCACCACACACAGG
FOXO1 UTR1 TUMOR FOR	AGACTTGGCAGCAAAGACATT
FOXO1 UTR1 TUMOR REV	GCAGCACATAACCTGCACA
FOXO1 UTR2 TUMOR FOR	TGAATCCTTGGTAGCTCTCTGA
FOXO1 UTR1 TUMOR REV	TTGCTTTCCAGACAGACCAG
RHOF UTR2 TUMOR FOR	CGTCAGCTAAACCTGAGCTTC
RHOF UTR2 TUMOR REV	GGGAGGGTCTCAGAAGGC
RHOF UTR1 TUMOR FOR	CTGCGGCTAGACTCTTGGA
RHOF UTR1 TUMOR REV	GGGAGTTTGTGGTCAGAGC
IRS1 UTR1 TUMOR FOR	GCACTCTGTAGGTTAGTCCATCA
IRS1 UTR1 TUMOR REV	CCGCCAAGGTCTTAATTCAC
IRS1 UTR2 TUMOR FOR	GCCATGGGTCCTTTCTGA
IRS1 UTR2 TUMOR REV	ACAGACTTACAGAACTACGGAAGG
c-JUN RT-PCR for tumor CDNA1	aacgtgacagatgagcagga
c-JUN RT-PCR rev tumor CDNA1	gtttctggctgtgcagttc
c-JUN RT-PCR for tumor CDNA2	gaaggaggagcctcagacag
c-JUN RT-PCR rev tumor CDNA2	ctgggactccatgtcagtg
c-JUN RT-PCR for tumor 3utr1	aagttgcgacggagagaaaa
c-JUN RT-PCR rev tumor 3utr1	acgcaaccagtcctcaactt
c-JUN RT-PCR for tumor 3utr2	tcaataaacagcttcagccttt
c-JUN RT-PCR rev tumor 3utr2	acaactctggcaggatacc

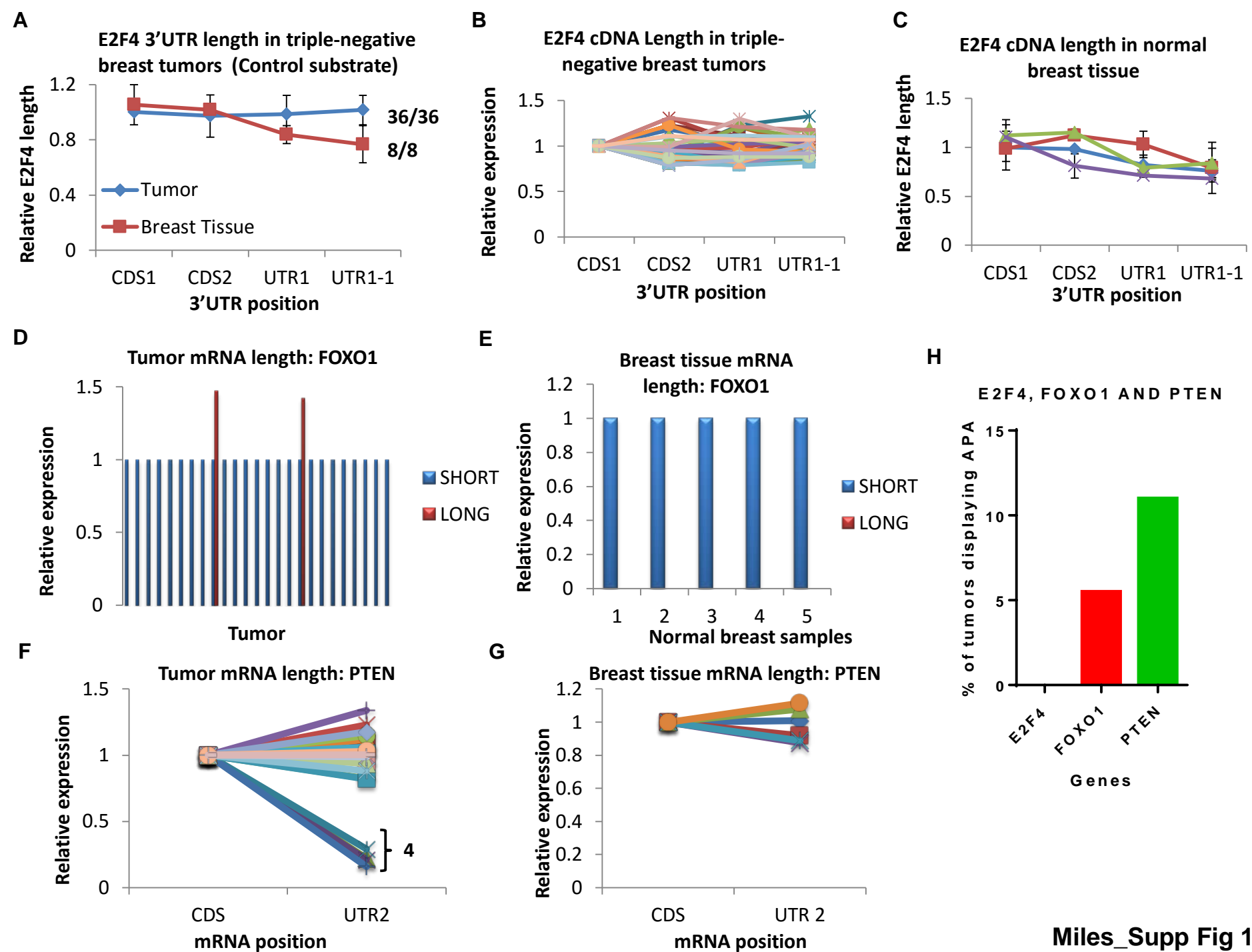
c-JUN RT-PCR for tumor 3utr2-1	ggatagtgcgatgttcagga
c-JUN RT-PCR rev tumor 3utr2-1	gacttctcagtggtgtcc
NRAS RT-PCR FOR TUMOR1 CDS 1	tggtgaaacctgtttgttg
NRAS RT-PCR REV TUMOR1 CDS 1	tcgcctgtcctcatgtattg
NRAS RT-PCR FOR TUMOR1 CDS 2	acaaaacaagcccacgaact
NRAS RT-PCR REV TUMOR1 CDS 2	aacaccctgtctggcttgg
NRAS RT-PCR FOR TUMOR1 3UTR1	cacccagggttttcatctg
NRAS RT-PCR REV TUMOR1 3'UTR1	gaattcacgtttgcggtt
NRAS RT-PCR FOR TUMOR1 3UTR1-1	ttgagagcagatgccattt
NRAS RT-PCR REV TUMOR1 3'UTR1-1	ctgggaaagcccaaac
NRAS RT-PCR FOR TUMOR1 3UTR2	ctctacagctccccacag
NRAS RT-PCR REV TUMOR1 3'UTR2	ggtccattagcaccatgctt
NRAS RT-PCR FOR TUMOR1 3UTR2-1	agcctgggtgacaagagaga
NRAS RT-PCR REV TUMOR1 3'UTR2-1	cctttgtccaaattcaca
E2F4 RT-PCR FOR TUMORS CDS1	tcacagaggacgtgcagaac
E2F4 RT-PCR REV TUMORS CDS1	agggtatctccagcaagca
E2F4 RT-PCR FOR TUMORS CDS1-1	ggaccaacccttctacctc
E2F4 RT-PCR REV TUMORS CDS1-1	tgacagctctttggggagtt
E2F4 RT-PCR FOR TUMORS 3UTR1	accgaggagctgccattac
E2F4 RT-PCR REV TUMORS 3UTR1	ctggcagaagcaagacactg
E2F4 RT-PCR FOR TUMORS 3UTR1-1	cacttctgctgggcctttag
E2F4 RT-PCR REV TUMORS 3UTR1-1	ccccagagacctctgttct
CSTF2 TUMOR Forward	TAGTCTCTGGAGGAGGAATG
CSTF2 TUMOR Reverse	CGTTCCATGGACACTGGTC
CPSF2 TUMOR Forward	GCAGCTTCTGACAAATGTCCT
CPSF2 TUMOR Reverse	CCTGCTGTGTCCACTGCTAT
E2F1 TUMOR Forward	TGCAGAGCAGATGGTTATGG
E2F1 TUMOR Reverse	GAAAGTTCTCCGAAGAGTCCA
E2F4 TUMOR Forward	GAGATACCCTCTTGGCCATC
E2F4 TUMOR Reverse	CCCATTGAGACCCTCTGG
CFIM25 TUMOR FOR	ATACTGGGTCGTCAGGATGG
CFIM25 TUMOR REV	TCTCCACCAGTTACCAATGC
KRT7 For tumor	AGGTGGATGCCCTGAATG
KRT7 rev tumor	GCTCTGTCAACTCCGTCTCA
KRT19 for tumor	TTGTCCTGCAGATCGACAAAT
KRT 19 rev tumor	GTCTCAAACCTTGTTCCGAAG
TIMP1 for tumor	AGTGTCTGCGGATACTTCCA
TIMP1 rev tumor	TTCCAGCAATGAGAACTCCT
PUM1 tumor forward	ACTTGCTCTGGAGGGAAGAG
PUM1 tumor reverse	TGGATTCATCTGTTTCCCAA
PUM2 tumor forward	TGGAAGTGTAACCTTTGGG
PUM2 tumor reverse	TGCCAACTGATGAACCAAAT

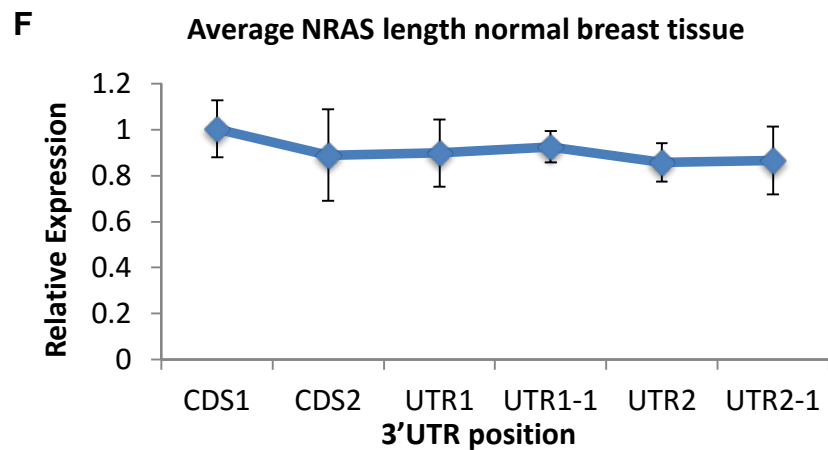
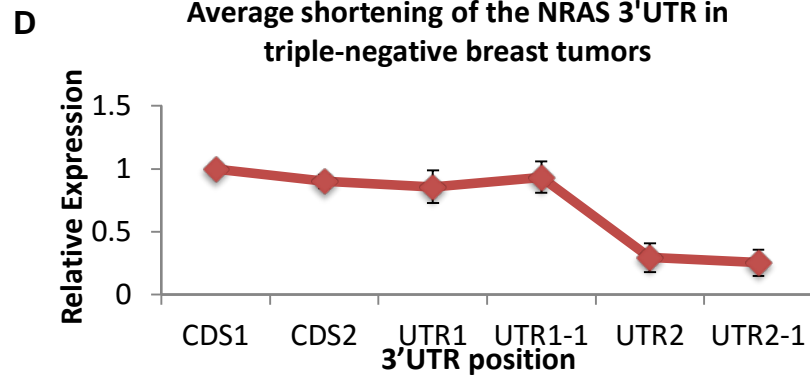
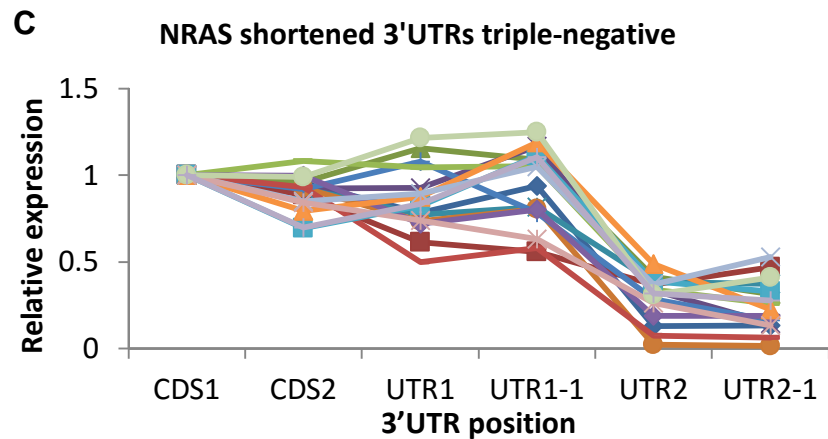
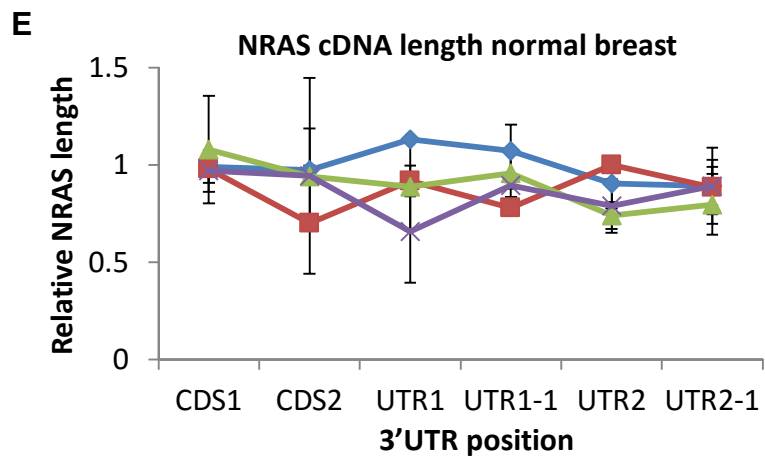
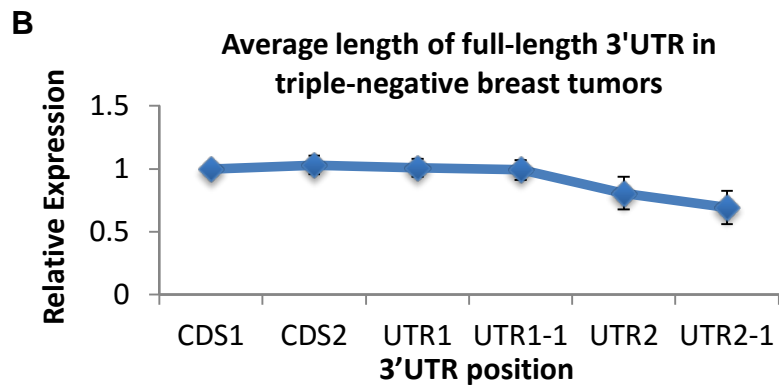
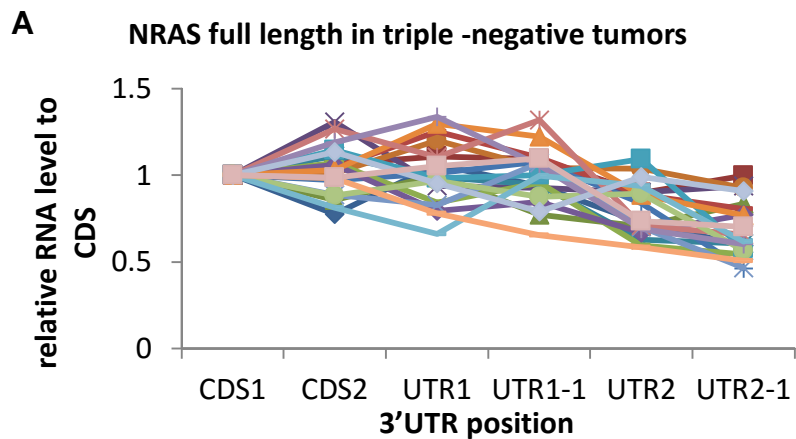
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cycd1 Reverse	ATGGCCAGCGGAAGAC
bim Forward	TGGCAAAGCAACCTTCTGATG
bim Reverse	GCAGGCTGCAATTGTCTACCT
trail Forward	GCTCTGGGCCGCAAAAT
trail Reverse	TGCAAGTTGCTCAGGAATGAA
DR5 Forward	GGGCCACAGGGACACCTT
DR5 Reverse	GCATCTCGCCCGGTTTT

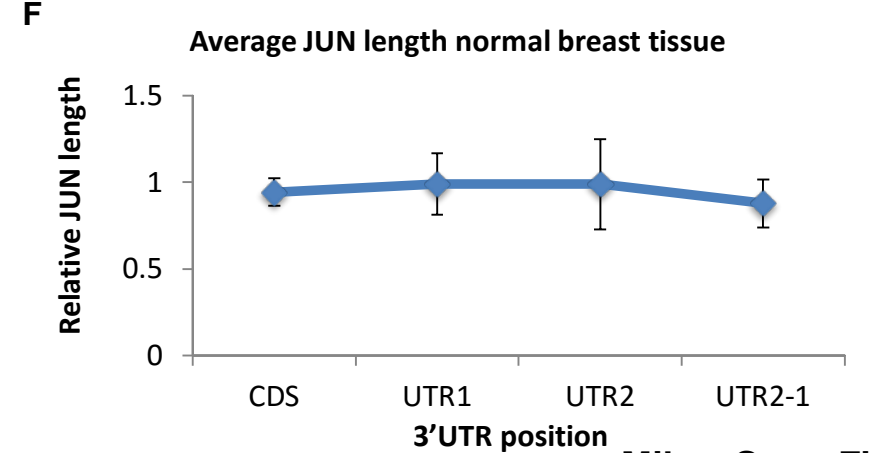
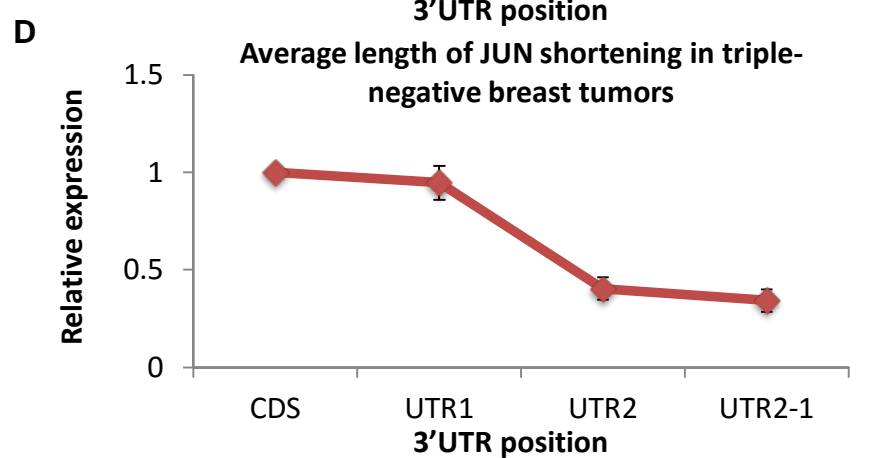
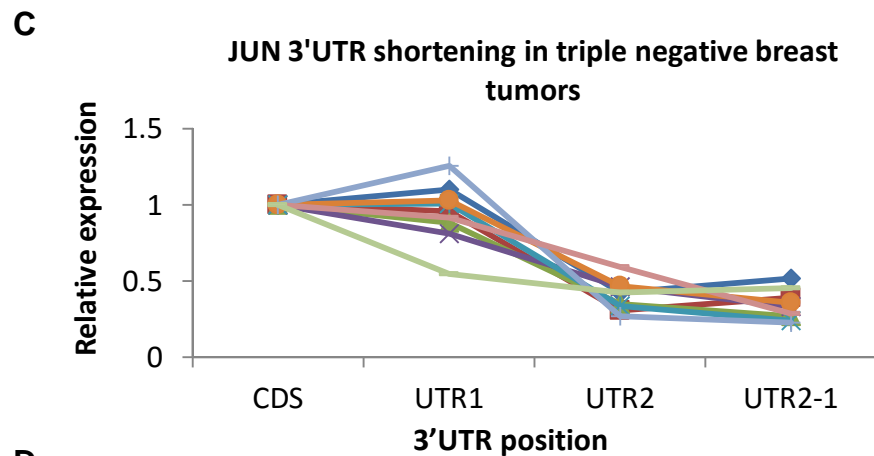
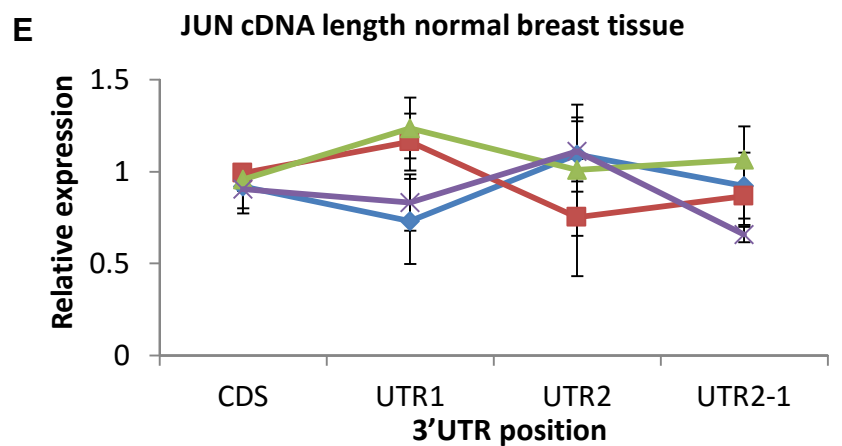
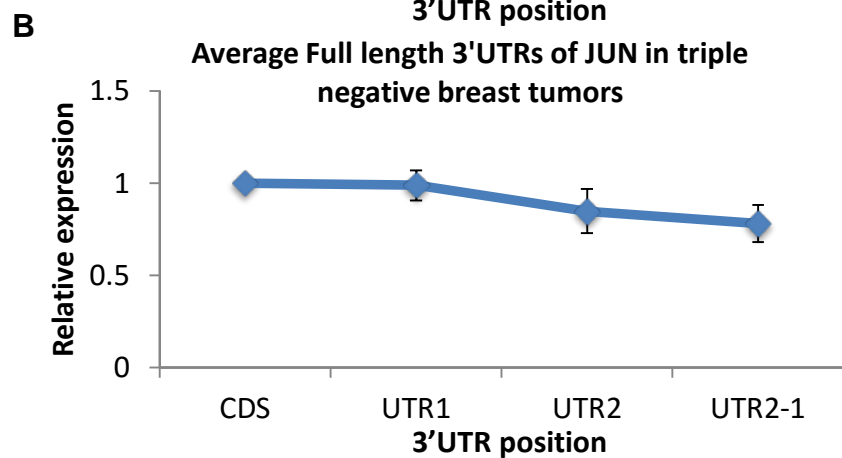
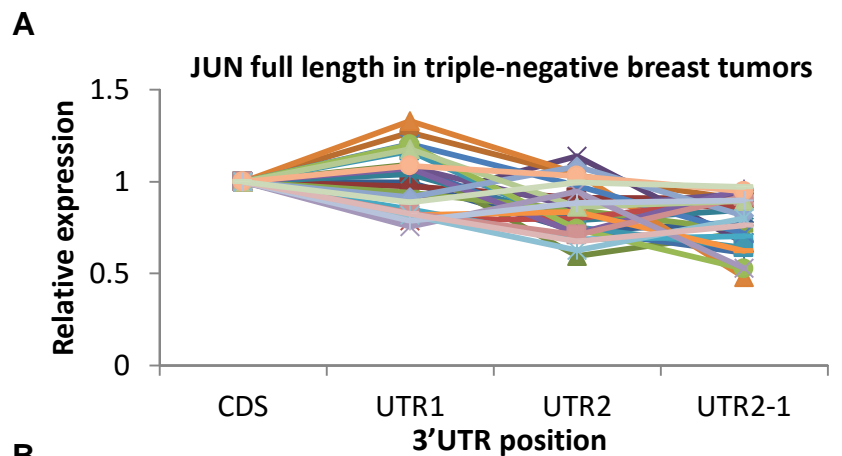
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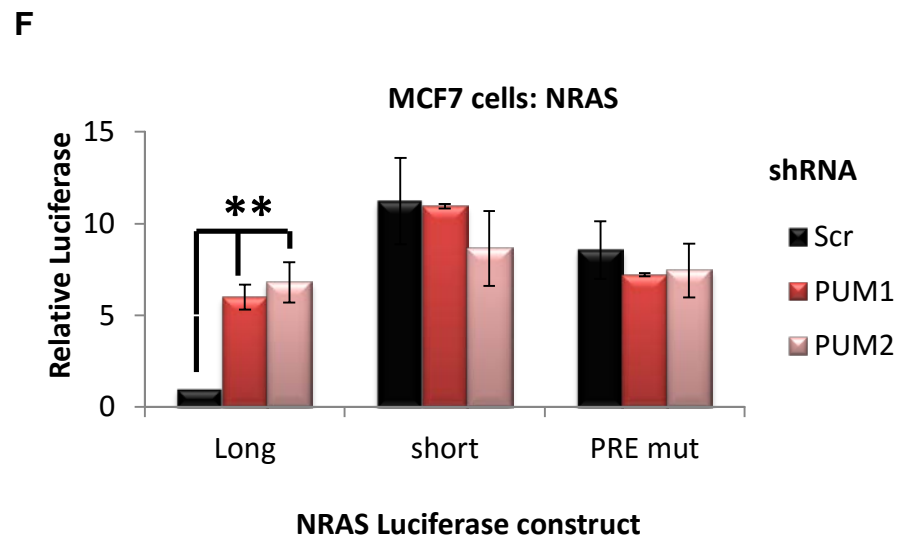
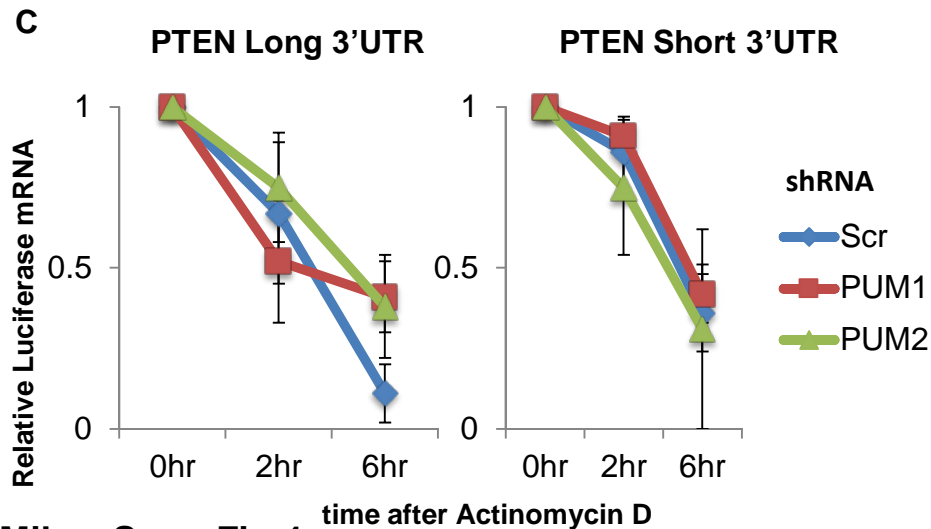
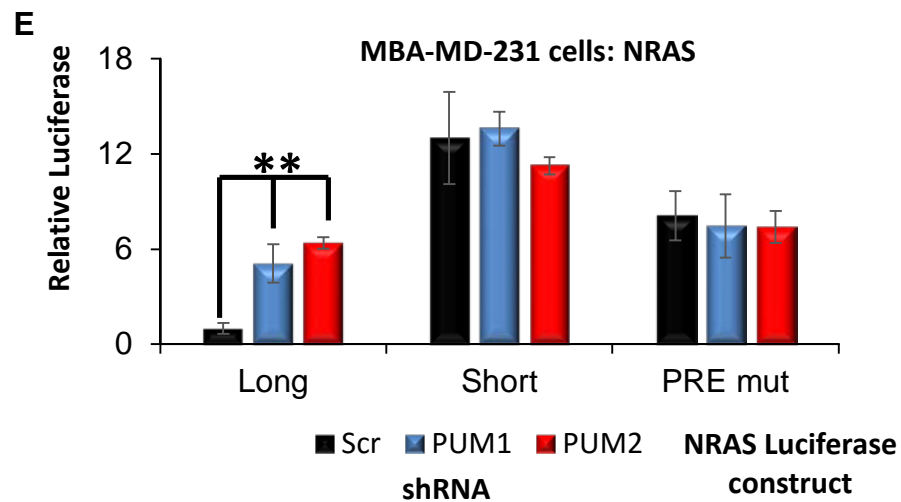
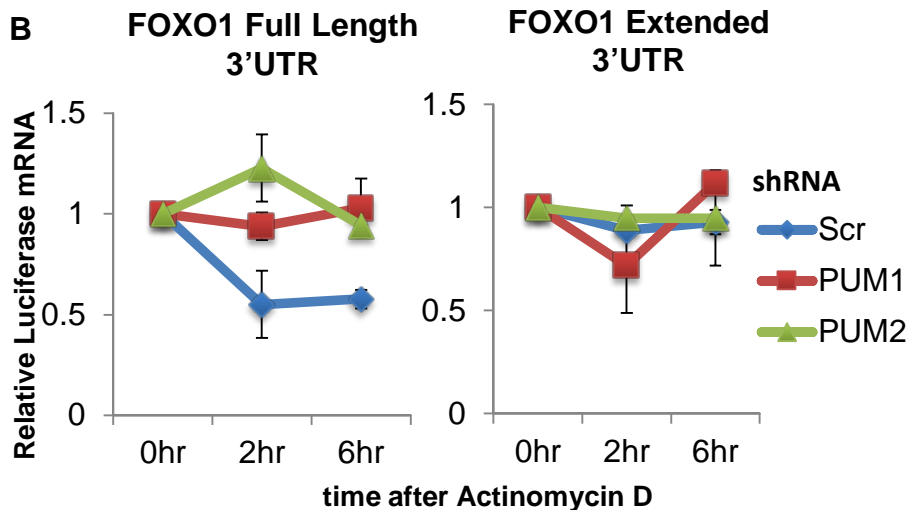
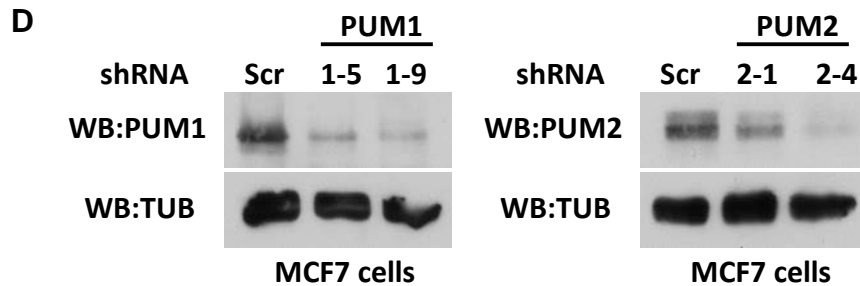
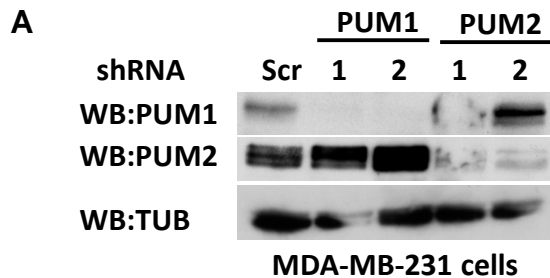
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CSTF77-145771	GCAUUCUCAUUCGAGAGGC
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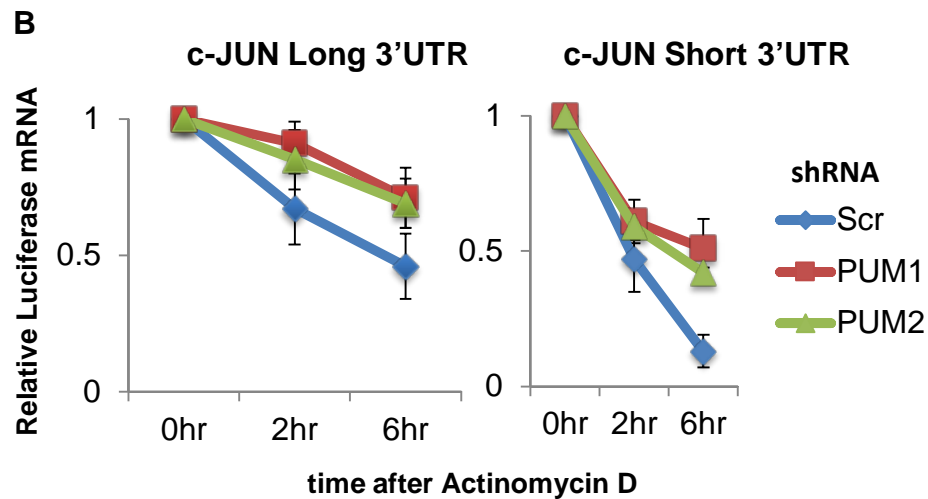
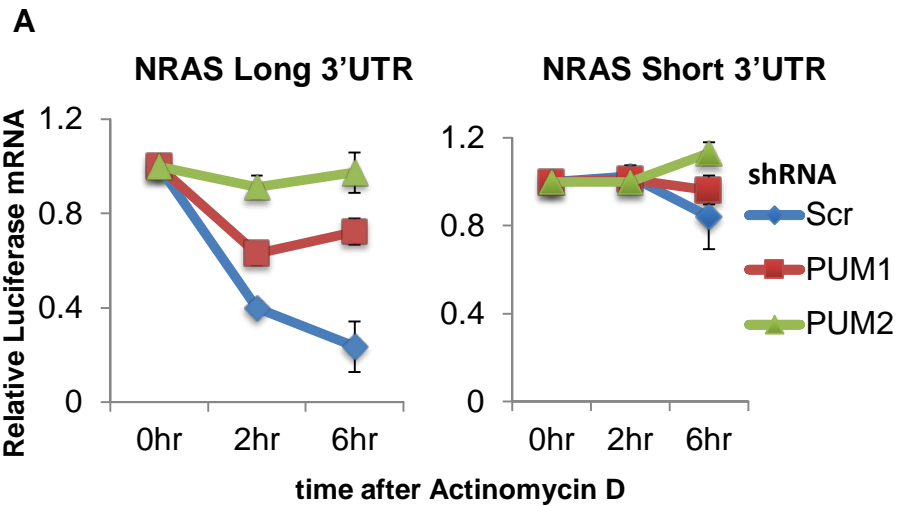
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PABPN1-J-011803-06	AGUCAACCGUGUUACCAUA
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PABPN1-J-011803-08	UAUCAAGCUCGAGUCAGG

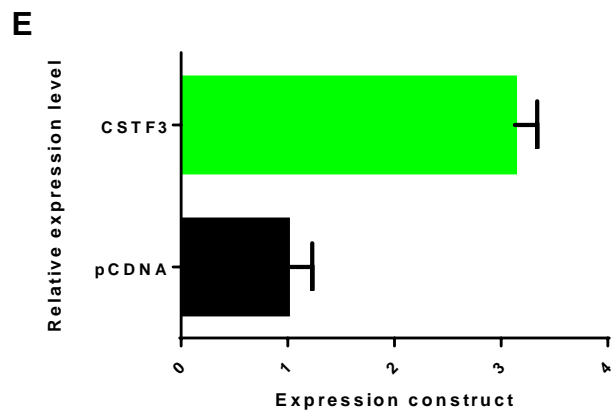
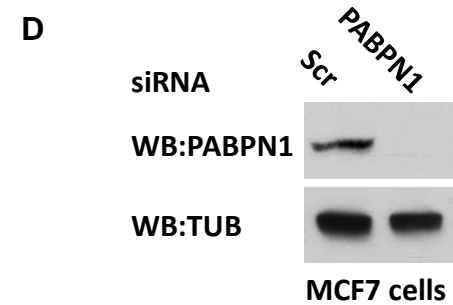
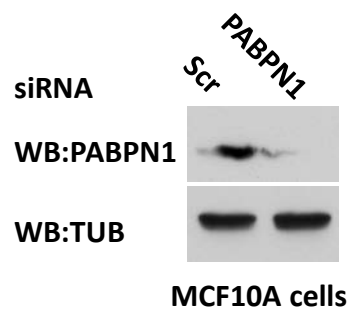
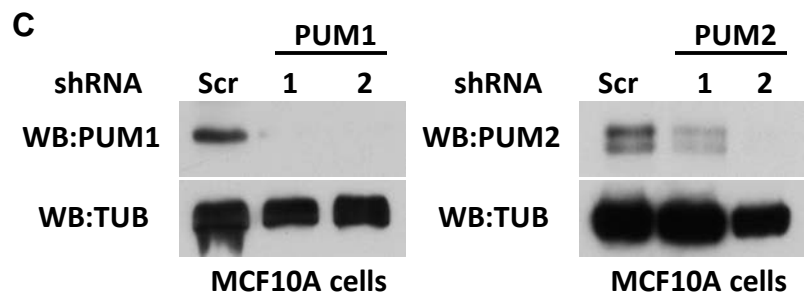
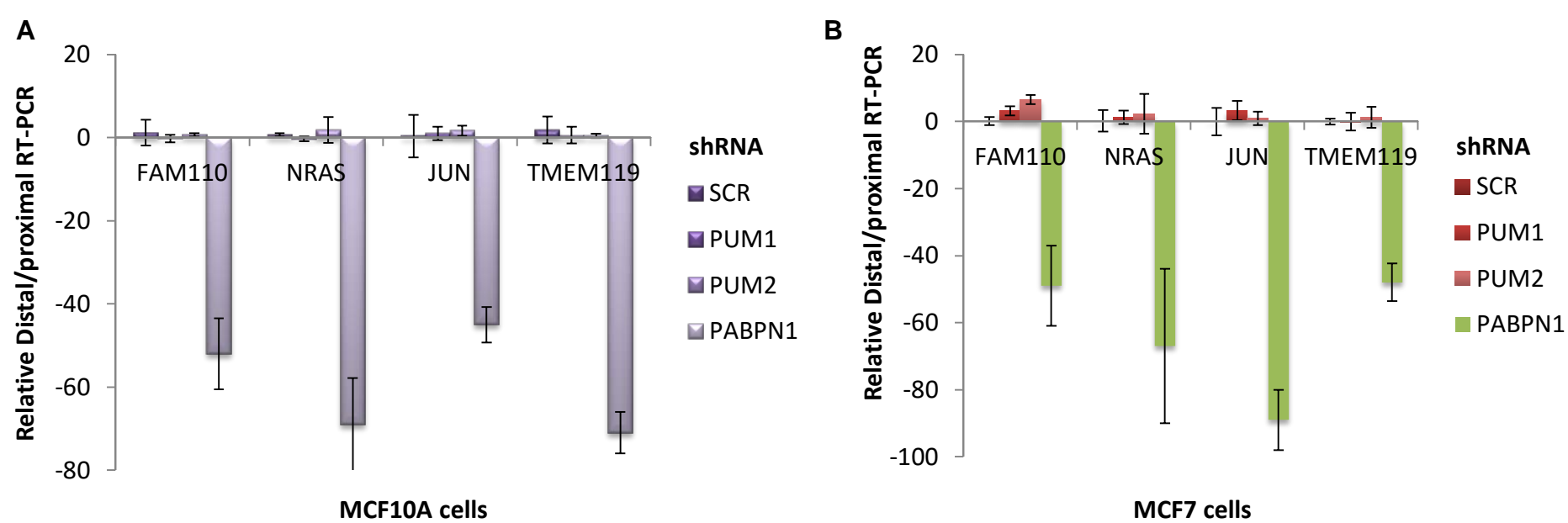












Supplementary Figure Legends

Supp Table 1: APA shortened transcripts in Basal-like and Triple-negative breast tumors

(A) List of shortened mRNAs from Basal-like breast tumors. (B) List of shortened mRNAs from Triple-negative breast tumors.

Supp Table 2: List of primers and siRNAs used in this study

Supp Fig 1: 3'UTR length variations in an independent cohort of triple-negative breast tumors

(A) Mean and standard deviation of the E2F4 transcript from normal breast tissue and triple-negative breast tumors. (B) RT-PCR results from triple-negative breast tumors of the E2F4 3'UTR (negative control). Expression of the E2F4 coding sequence set to 1. (C) RT-PCR results from normal breast tissue mapping the length of the E2F4 3'UTR. (D) RT-PCR of the FOXO1 mRNA and 3'UTR from triple-negative breast tumors. (E) RT-PCR of the FOXO1 mRNA and 3'UTR from normal breast tissue. (F) RT-PCR of the PTEN mRNA and 3'UTR from triple-negative breast tumors. (G) RT-PCR of the PTEN mRNA and 3'UTR from normal breast tissue. (H) Percentage of triple-negative tumors displaying APA of E2F4, FOXO1 and PTEN.

Supp Fig 2: Alternative poly-adenylation of the NRAS in Triple-negative breast tumors

(A) RT-PCR results from triple-negative breast tumors which retain a full length NRAS 3'UTR. Expression of the NRAS coding sequence set to 1, only tumors which have more than 50% of UTR region 2 in this collection. (B) Mean and standard deviation of NRAS expression from all of the tumors included in A. (C) RT-PCR results from triple-negative breast tumors which have shortened the NRAS 3'UTR. Expression of the NRAS coding sequence set to 1, only tumors which have less than 50% of UTR region 2 in this collection. (D) Mean and standard deviation of NRAS expression from all of the tumors included in C. (E) RT-PCR results from normal breast tissue mapping the length of the NRAS 3'UTR. (F) Mean and standard deviation of NRAS expression from the normal breast tissue included in E.

Supp Fig 3: Alternative poly-adenylation of the c-JUN in Triple-negative breast tumors

(A) RT-PCR results from triple-negative breast tumors which retain a full length c-JUN 3'UTR. Expression of the c-JUN coding sequence set to 1, only tumors which have more than 50% of UTR region 2 in this collection. (B) Mean and standard deviation of c-JUN expression from all of the tumors included in A. (C) RT-PCR results from triple-negative breast tumors which have shortened the c-JUN 3'UTR. Expression of the c-JUN coding sequence set to 1, only tumors which have less than 50% of UTR region 2 in this collection. (D) Mean and standard deviation of c-JUN expression from all of the tumors included in C. (E) RT-PCR results from normal breast tissue mapping the length of the c-JUN 3'UTR. (F) Mean and standard deviation of c-JUN expression from the normal breast tissue included in E.

Supp Fig 4: APA of FOXO1, PTEN and NRAS change their sensitivity to PUM activity.

(A) Western blots of PUM1, PUM2, and TUB from MDA-MB-231 cells infected with two independent shRNAs targeting PUM1, PUM2 or Scrambled control sequences. **(B)** mRNA stability assays of the FOXO1 short and long 3'UTR isoforms from MDA-MB-231 cells depleted of PUM1, PUM2 or Scrambled controls sequences. **(C)** mRNA stability assays of the PTEN short and long 3'UTR isoforms from MDA-MB-231 cells depleted of PUM1, PUM2 or Scrambled controls sequences. **(D)** Western blots of PUM1, PUM2, and TUB from MCF7 cells infected with two independent shRNAs targeting PUM1, PUM2 or Scrambled control sequences. **(E)** Luciferase expression levels from MDA-MB-231 cells depleted of PUM1, PUM2 and Scrambled sequences and then transfected with Luciferase constructs containing either the short, long or PRE-mutant 3'UTR isoforms of NRAS. Long isoform in Scramble depleted cells set to 1. (**p=0.01). **(F)** Luciferase expression levels from MCF7 cells depleted of PUM1, PUM2 and Scrambled sequences and then transfected with Luciferase constructs containing either the short, long or PRE-mutant 3'UTR isoforms of NRAS. Long isoform in Scramble depleted cells set to 1. (**p=0.01).

Supp Fig 5: APA of FOXO1, PTEN and NRAS change their sensitivity to PUM activity.

(A) mRNA stability assays of the NRAS short and long 3'UTR isoforms from MDA-MB-231 cells depleted of PUM1, PUM2 or Scrambled controls sequences. **(B)** mRNA stability assays of the c-JUN short and long 3'UTR isoforms from MDA-MB-231 cells depleted of PUM1, PUM2 or Scrambled controls sequences.

Supp Figure 6: Pumilio does not affect alternative poly-adenylation status of candidate substrates.

(A) 3'RACE RT-PCR of FAM110, NRAS, c-JUN and TMEM119 from MCF10a cells depleted of PUM1, PUM2, PABPN1 or Scrambled control sequences by shRNA. Distal APA site divided by proximal site from Scrambled treated cells set to 0. **(B)** 3'RACE RT-PCR of FAM110, NRAS, c-JUN and TMEM119 from MCF7 cells depleted of PUM1, PUM2, PABPN1 or Scrambled control sequences by shRNA. Distal APA site divided by proximal site from Scrambled treated cells set to 0. **(C)** Western blots of PUM1, PUM2, PABPN1 and TUB from MCF10a cells treated with shRNAs or siRNAs targeting PUM, PABPN1 or Scrambled control sequences. **(D)** Western blots of PABPN1 and TUB from MCF7 cells treated with siRNAs targeting PABPN1 or Scrambled control sequences. **(E)** RT-qPCR results from RPE cells transfected an empty control vector (pCDNA) or one containing CSTF3.