

**Suppl. Table 1:** miRNAs differentially regulated upon TACC3 depletion in MCF7 cells thereby undergoing premature senescence.

miRNA	Regulation	Fold increase / decrease	P value
hsa-miR-146b-5p	up	3,82	0,0094
hsa-miR-1977	up	2,34	0,0345
hsa-miR-181a*	up	2,20	0,0174
hsa-miR-193b*	up	2,14	0,0243
hsa-miR-141	up	1,98	0,0046
hsa-miR-1973	up	1,92	0,0229
hsa-miR-29b-1*	up	1,77	0,0033
hsa-miR-125b	up	1,72	0,0322
hsa-miR-21*	up	1,71	0,0213
hsa-miR-491-3p	up	1,69	0,0001
hsa-miR-30c	up	1,68	0,0203
hsa-miR-200a*	up	1,64	0,0189
hsa-miR-30e	up	1,54	0,0450
hsa-miR-200c*	up	1,53	0,0424
hsa-miR-1275	up	1,53	0,0002
hsa-miR-183*	down	3,34	0,0037
hsa-miR-501-3p	down	2,65	0,0046
hsa-miR-345	down	2,63	0,0140
hsa-miR-18a	down	2,27	0,0071
hsa-miR-194	down	2,07	0,0429
hsa-miR-33a	down	2,06	0,0005
hsa-miR-218	down	1,99	0,0341
hsa-miR-32	down	1,94	0,0046
hsa-miR-17	down	1,93	0,0205
hsa-miR-18b	down	1,84	0,0169
hsa-miR-19a	down	1,83	0,0115
hsa-miR-19b	down	1,83	0,0109
hsa-miR-7	down	1,82	0,0388
hsa-miR-192	down	1,77	0,0072
hsa-miR-19b-1*	down	1,75	0,0011
hsa-miR-101	down	1,70	0,0301
hsa-miR-362-3p	down	1,70	0,0051
hsa-miR-769-5p	down	1,64	0,0164
hsa-miR-20a	down	1,62	0,0339
hsa-miR-15b	down	1,61	0,0207
hsa-miR-590-5p	down	1,57	0,0243
hsa-miR-503	down	1,54	0,0283
hsa-miR-219-5p	down	1,52	0,0284

Analysis of differentially expressed miRNAs using the Genespring software (ver11) (expression changes  $\geq 1.5$ -fold were determined four days after DOX-induced TACC3 shRNA expression that triggers premature senescence;  $p \leq 0.05$ ; student's t-test).

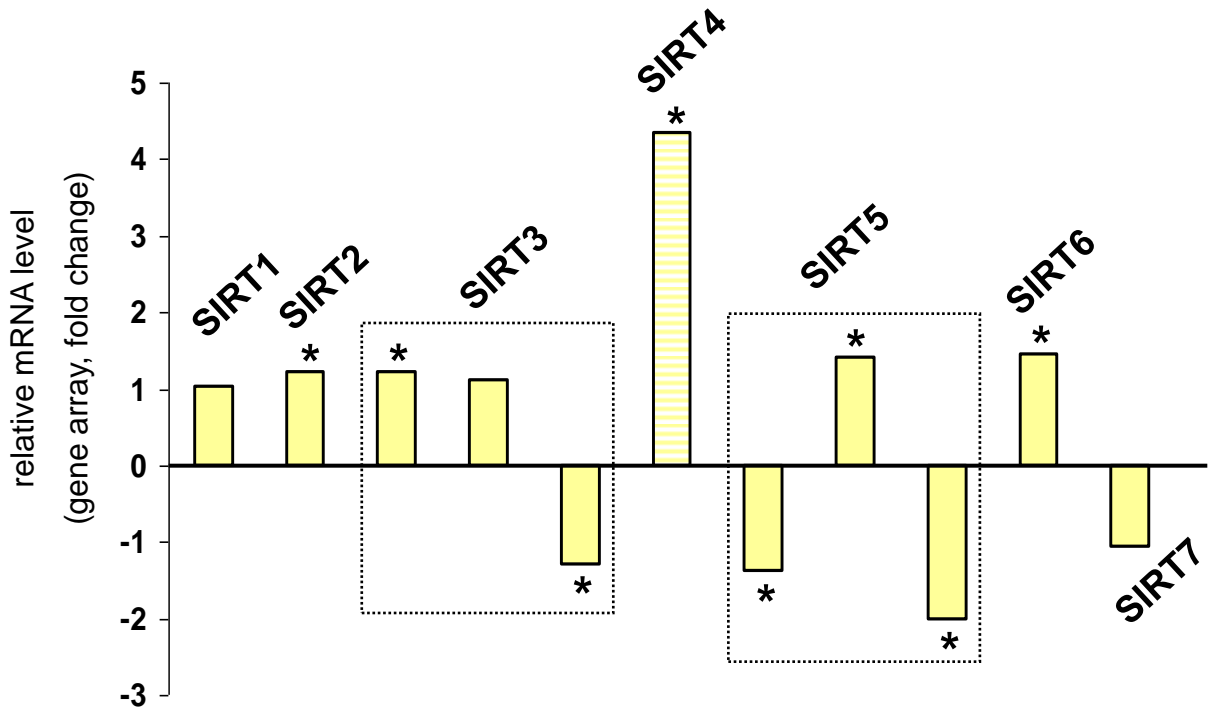
**Suppl. Table 2:** Overview of the number of differentially regulated, putative miRNA target genes vs. the total number of candidate miRNA target genes.

	miRNA	Differentially regulated putative target genes	Candidate target genes (total)	P value
<b>1</b>	<b>hsa-miR-17</b>	<b>138</b>	<b>1601</b>	<b>0,000011</b>
<b>2</b>	<b>hsa-miR-20a</b>	<b>138</b>	<b>1594</b>	<b>0,000008</b>
<b>3</b>	<b>hsa-miR-30e</b>	<b>129</b>	<b>1445</b>	<b>0,000004</b>
<b>4</b>	<b>hsa-miR-30c</b>	<b>124</b>	<b>1440</b>	<b>0,000031</b>
<b>5</b>	<b>hsa-miR-19a</b>	<b>124</b>	<b>1385</b>	<b>0,000004</b>
<b>6</b>	<b>hsa-miR-19b</b>	<b>124</b>	<b>1383</b>	<b>0,000004</b>
<b>7</b>	<b><i>hsa-miR-15b</i></b>	<b>108</b>	<b>1359</b>	<b>0,001533</b>
8	hsa-miR-21*	99	1345	0,021258
<b>9</b>	<b>hsa-miR-32</b>	<b>96</b>	<b>992</b>	<b>0,000002</b>
10	hsa-miR-218	75	928	0,005707
11	hsa-miR-101	65	855	0,032452
12	hsa-miR-125b	61	845	0,088203
<b>13</b>	<b>hsa-miR-7</b>	<b>53</b>	<b>473</b>	<b>0,000007</b>
14	hsa-miR-503	35	355	0,002857
15	hsa-miR-18a	32	320	0,003698
16	hsa-miR-18b	32	320	0,003698
17	hsa-miR-590-5p	30	307	0,006633
18	hsa-miR-219-5p	29	417	0,342896
19	hsa-miR-491-3p	25	278	0,028984
20	hsa-miR-194	23	363	0,651865
21	hsa-miR-362-3p	21	327	0,634296
22	hsa-miR-146b-5p	20	168	0,002443
23	hsa-miR-33a	15	376	0,148934
24	hsa-miR-192	13	125	0,051686
25	hsa-miR-345	11	140	0,277760
26	hsa-miR-501-3p	9	241	0,211704
27	hsa-miR-769-5p	7	126	1,000000
28	hsa-miR-1275	3	90	0,493812

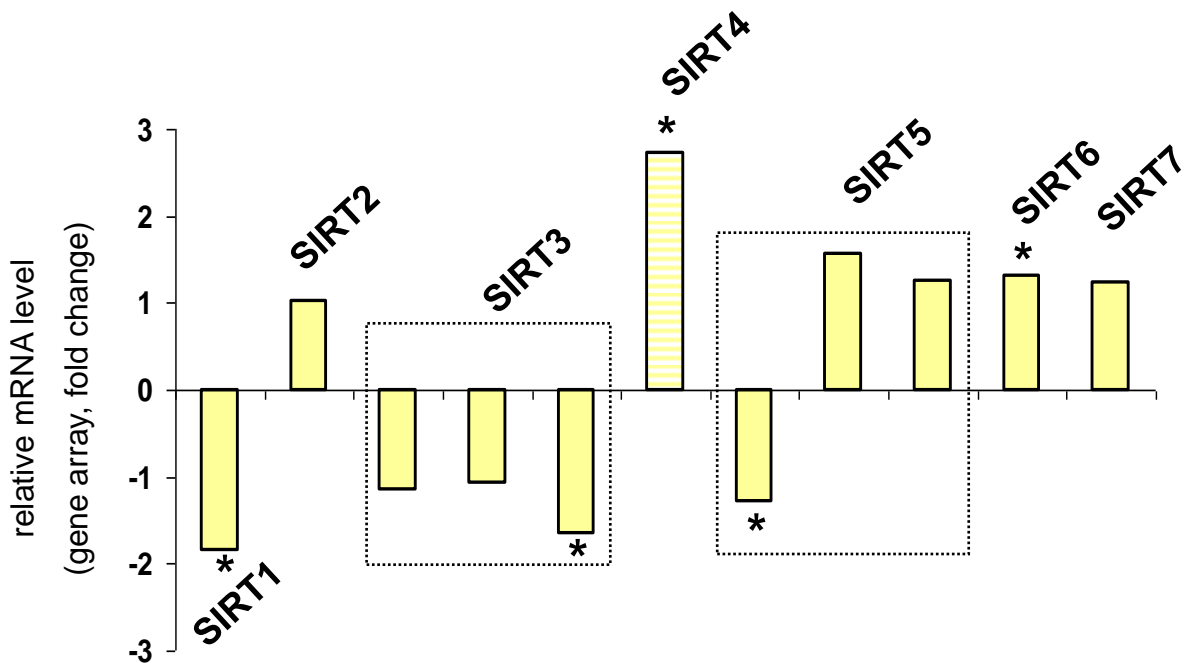
Analysis of putative target mRNAs differentially regulated by miRNAs was performed using the Genespring software (ver11). Expression changes  $\geq 1.75$  were determined four days after DOX-induced TACC3 shRNA expression and senescence induction ( $p \leq 0.05$ ; student's t-test). As indicated in the last column, significant correlations between the total number of putative target mRNAs vs. the number of differentially expressed candidate target mRNAs were determined using Fisher's exact test ( $p \leq 0.05$ ) and a Bonferroni correction (highly significant miRNA-mRNA correlations with  $p \leq 0.0018$  are indicated in bold).

**A**

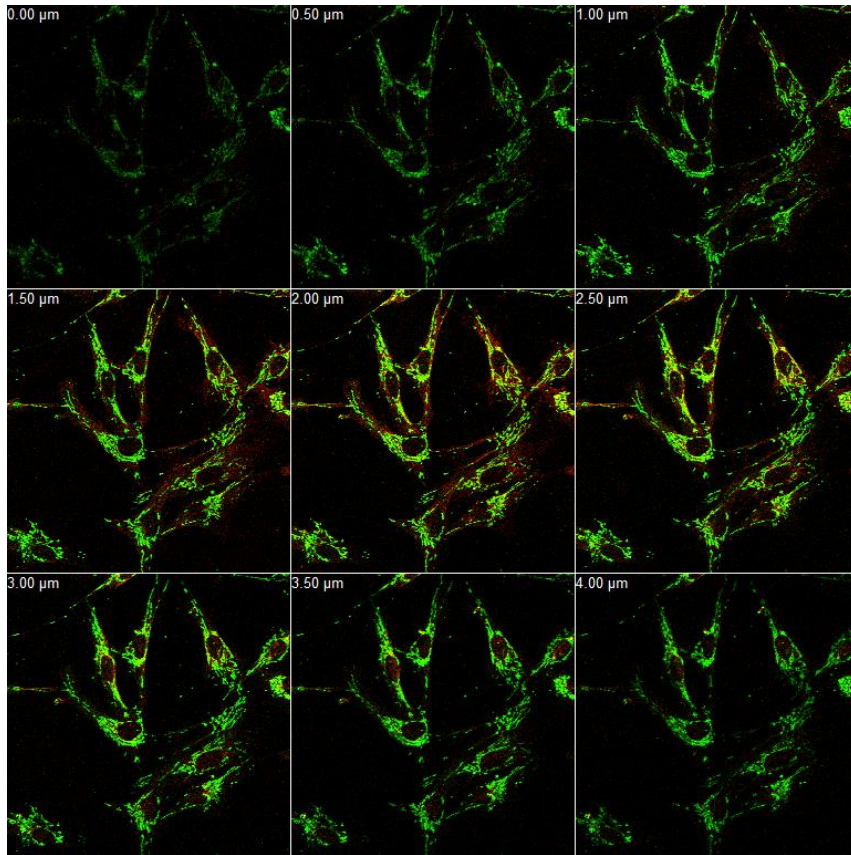
TACC3 depletion  
(TACC3 shRNA vs. control shRNA, day 4 of DOX treatment)

**B**

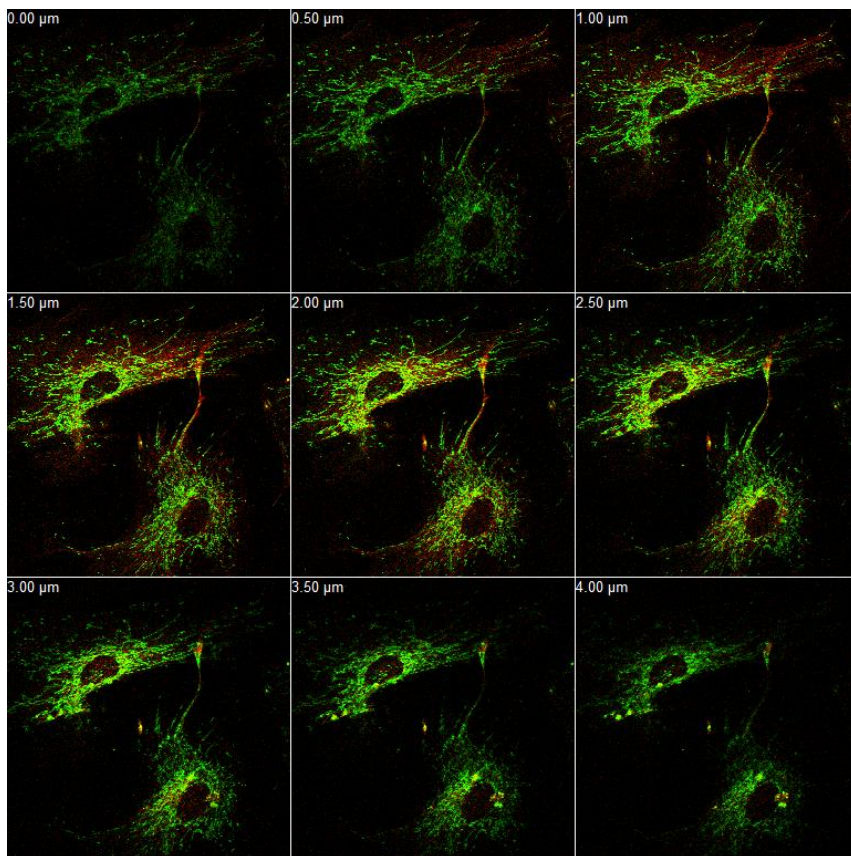
$\gamma$ IR (20 Gy) vs. control (day 4)



# Merge (MTCO2 / SIRT4)

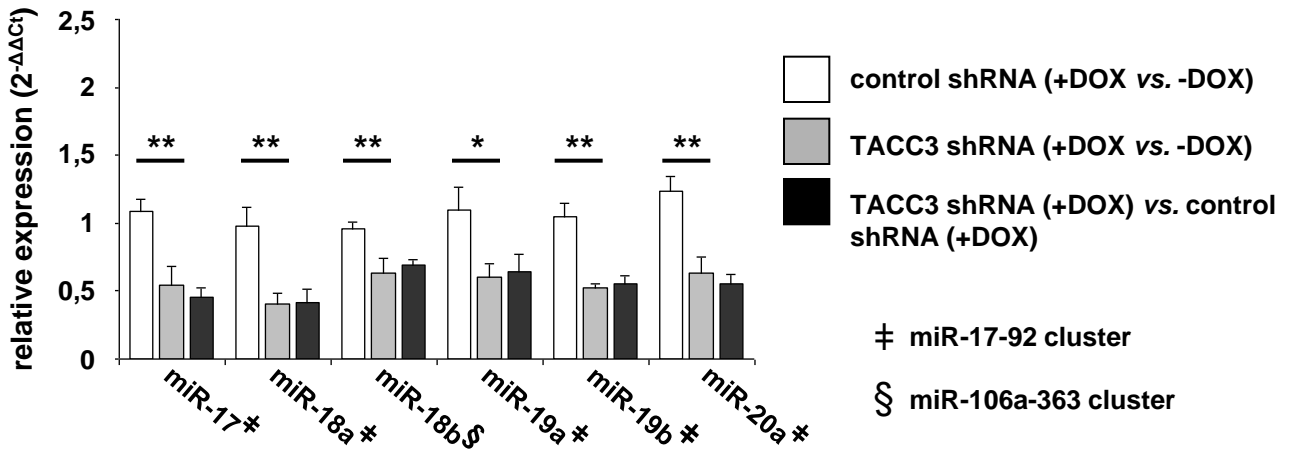
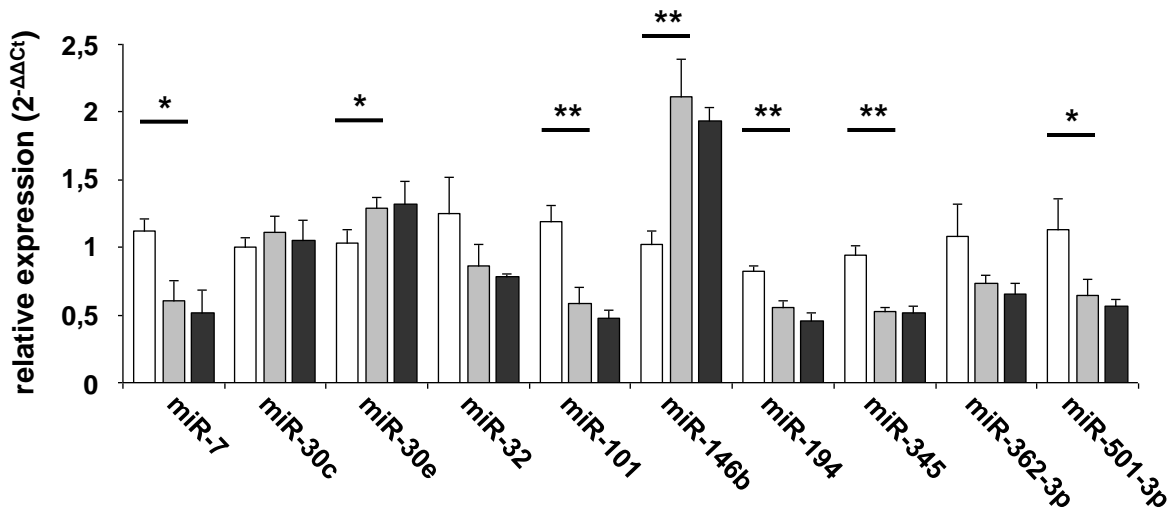


sham

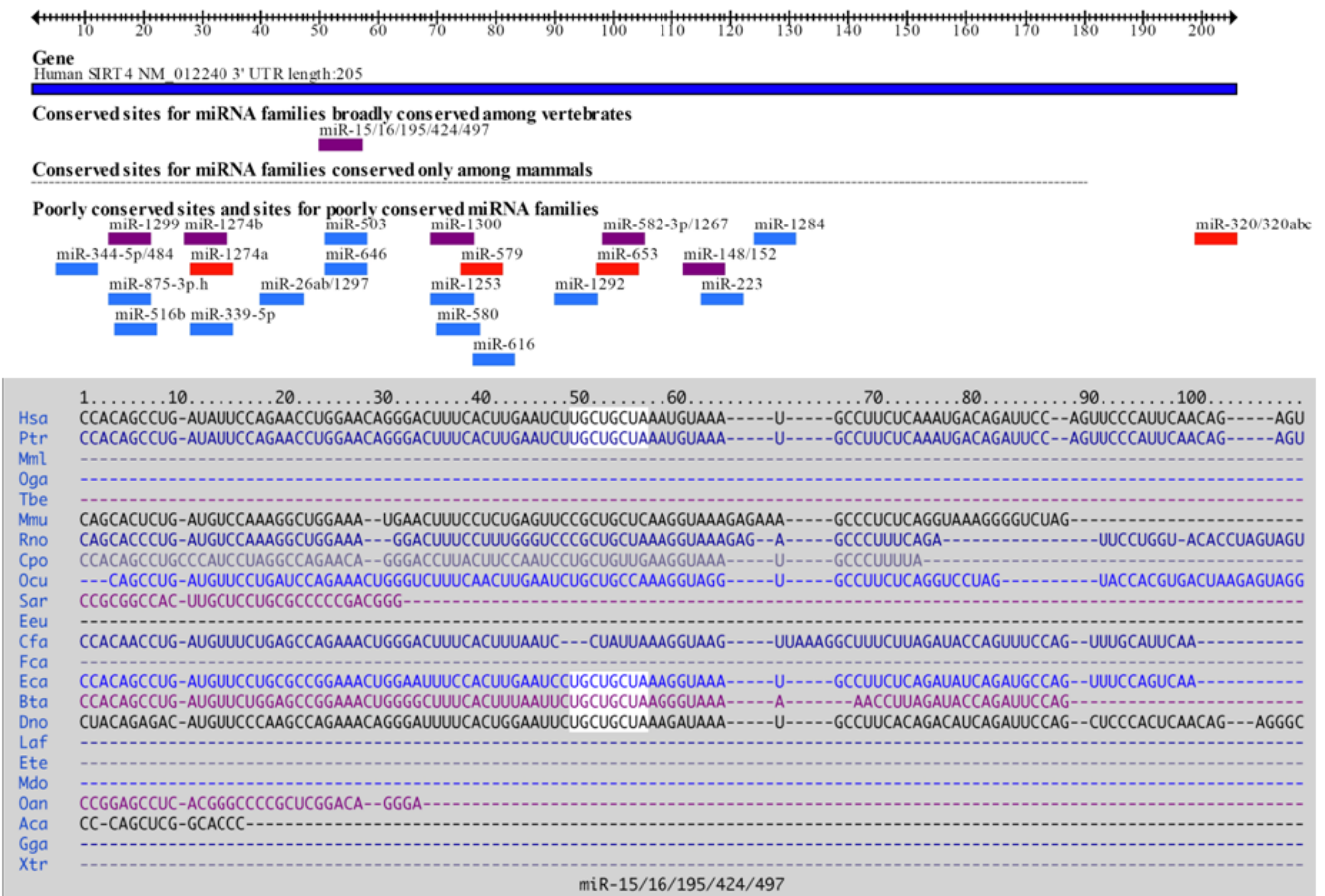


$\gamma$ IR

suppl. Figure 2

**A****B**

**A**



[http://www.targetscan.org/cgi-bin/vert\\_50/view\\_gene.cgi?gs=SIRT4&taxid=9606&members=&showcnc=1&shownc=1](http://www.targetscan.org/cgi-bin/vert_50/view_gene.cgi?gs=SIRT4&taxid=9606&members=&showcnc=1&shownc=1)

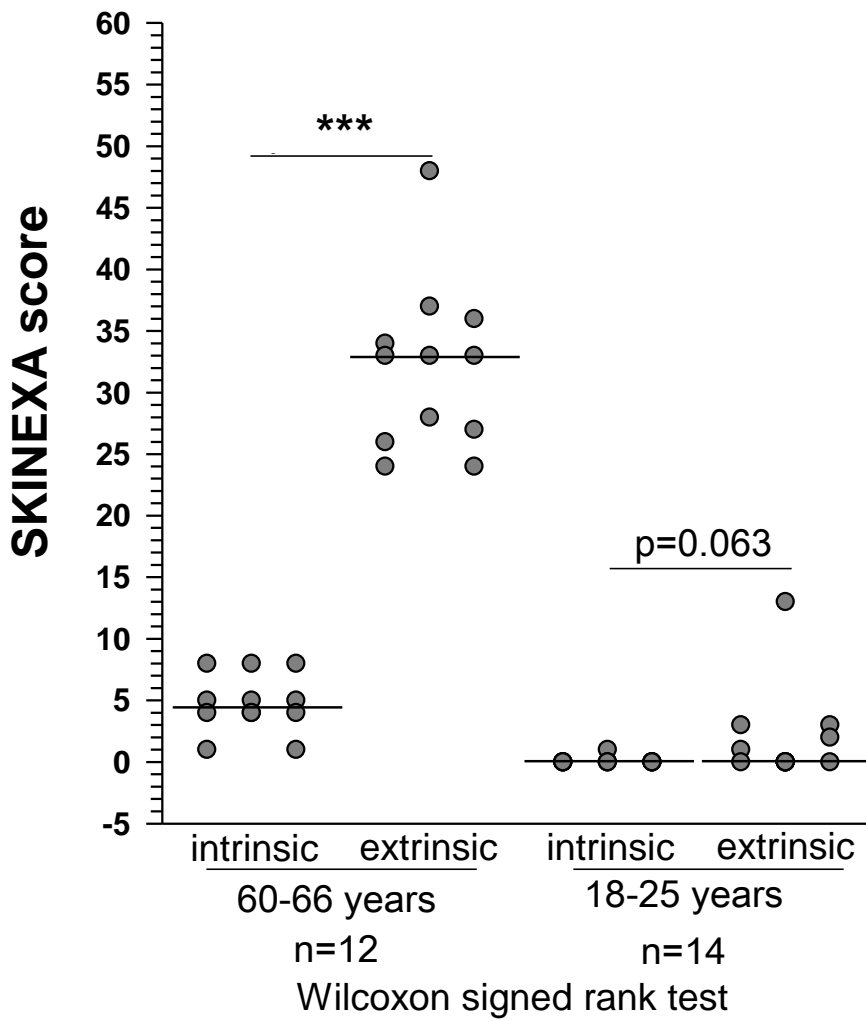
**B**

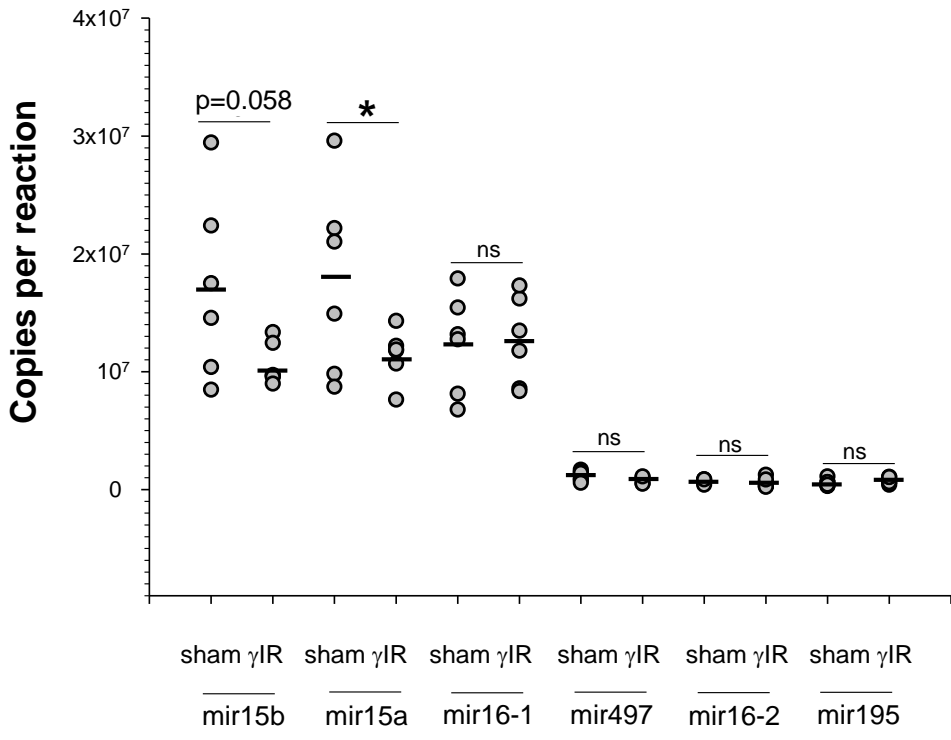
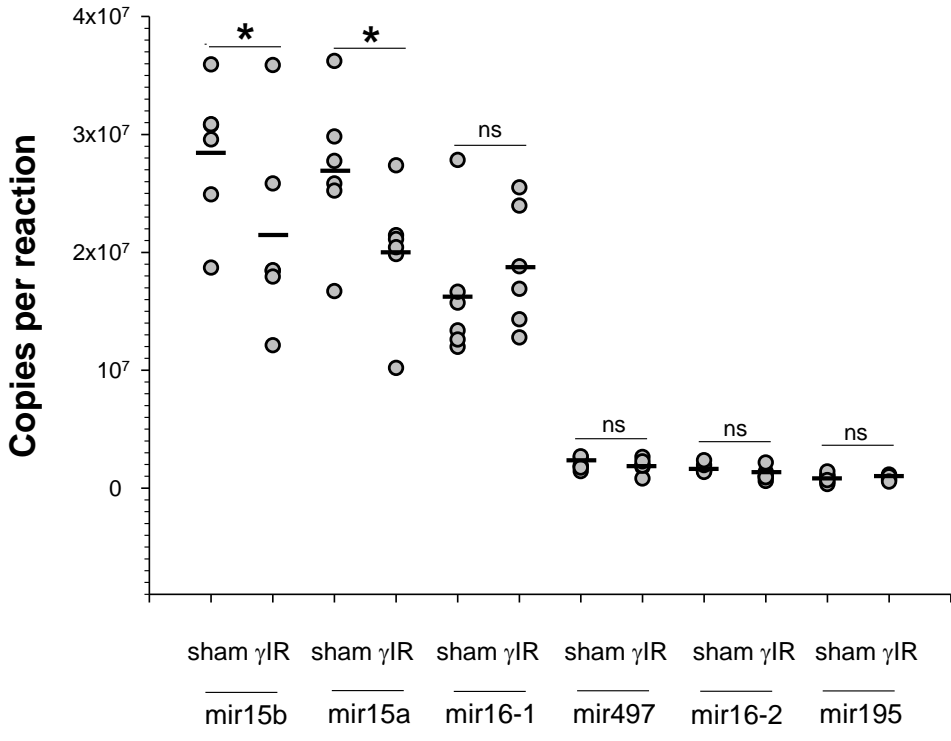
**Human SIRT4 3' UTR miRNA Table** [Sort table by aggregate  $P_{CT}$ ]  
 Table sorted by total context score

miRNA families broadly conserved among vertebrates

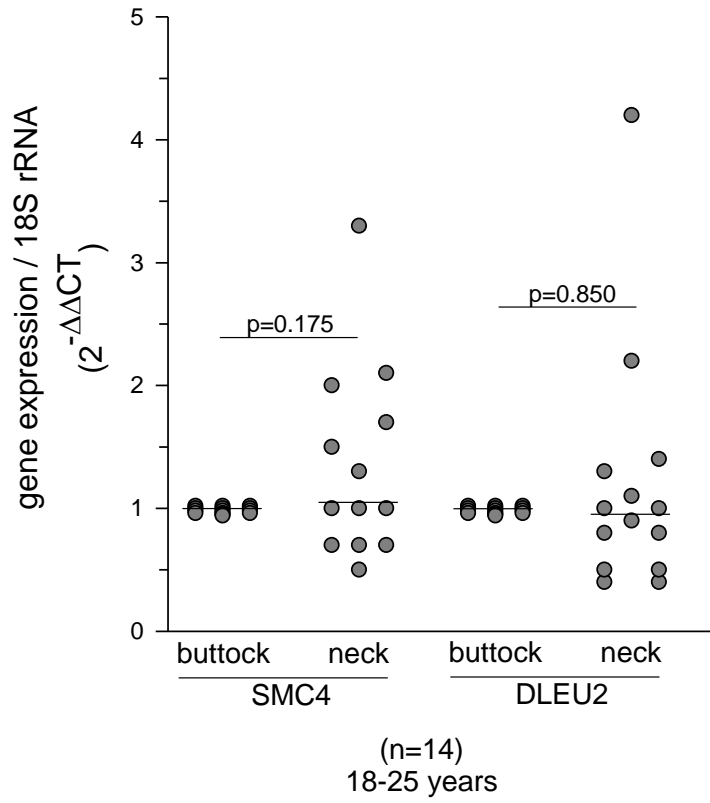
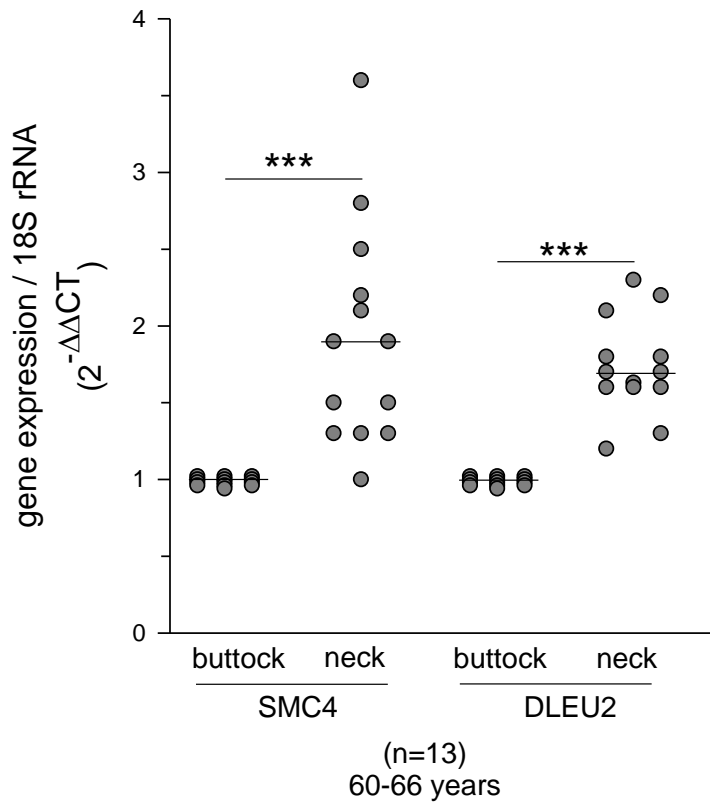
miRNA	conserved sites				poorly conserved sites				Total Context score	Aggregate $P_{CT}$
	Total	8mer	7mer-m8	7mer-1A	Total	8mer	7mer-m8	7mer-1A		
miR-15/16/195/424/497	1	1	0	0	0	0	0	0	-0.47	< 0.1
miR-148/152	0	0	0	0	1	1	0	0	-0.32	0.22
miR-503	0	0	0	0	1	0	0	1	-0.20	< 0.1
miR-26ab/1297	0	0	0	0	1	0	0	1	-0.16	< 0.1
miR-223	0	0	0	0	1	0	0	1	-0.13	0.20

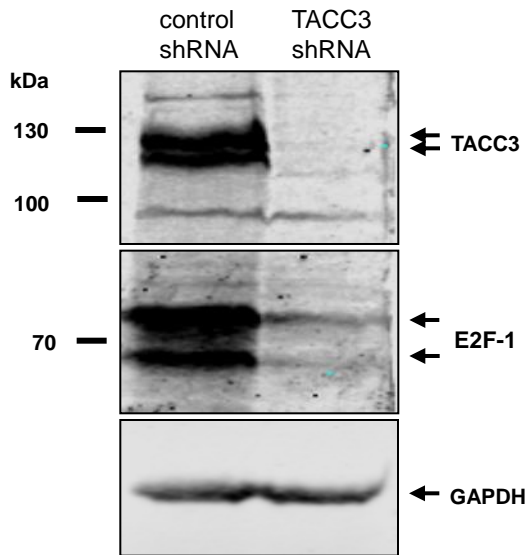
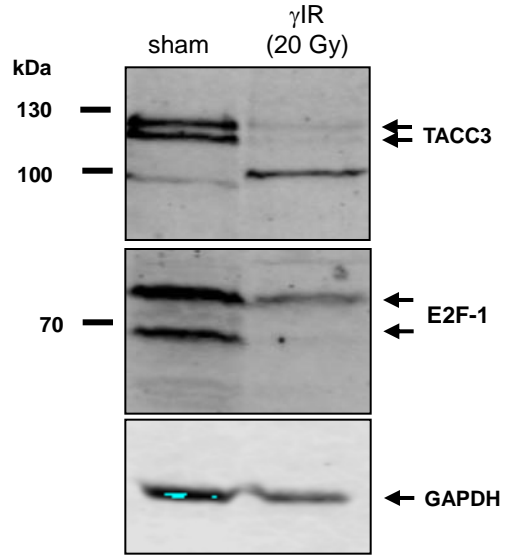
[http://www.targetscan.org/cgi-bin/vert\\_50/view\\_genetable.cgi?gs=SIRT4&taxid=9606&members=&showcnc=1&shownc=1&sortText=cs](http://www.targetscan.org/cgi-bin/vert_50/view_genetable.cgi?gs=SIRT4&taxid=9606&members=&showcnc=1&shownc=1&sortText=cs)

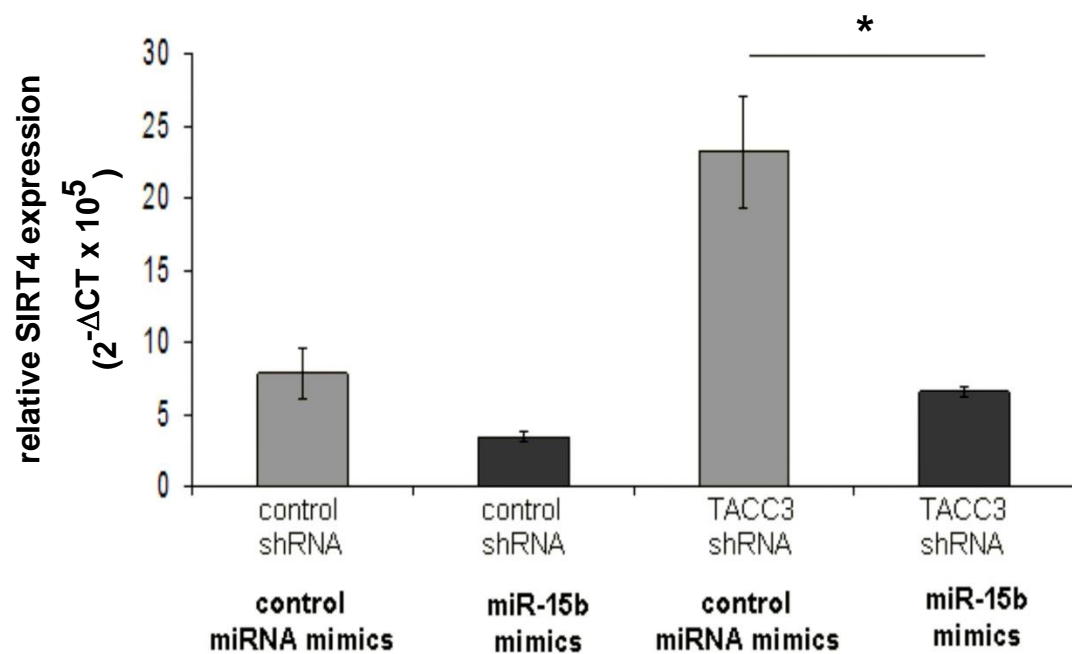


**A****B**



**A****B**

**A****B**

**A****B**