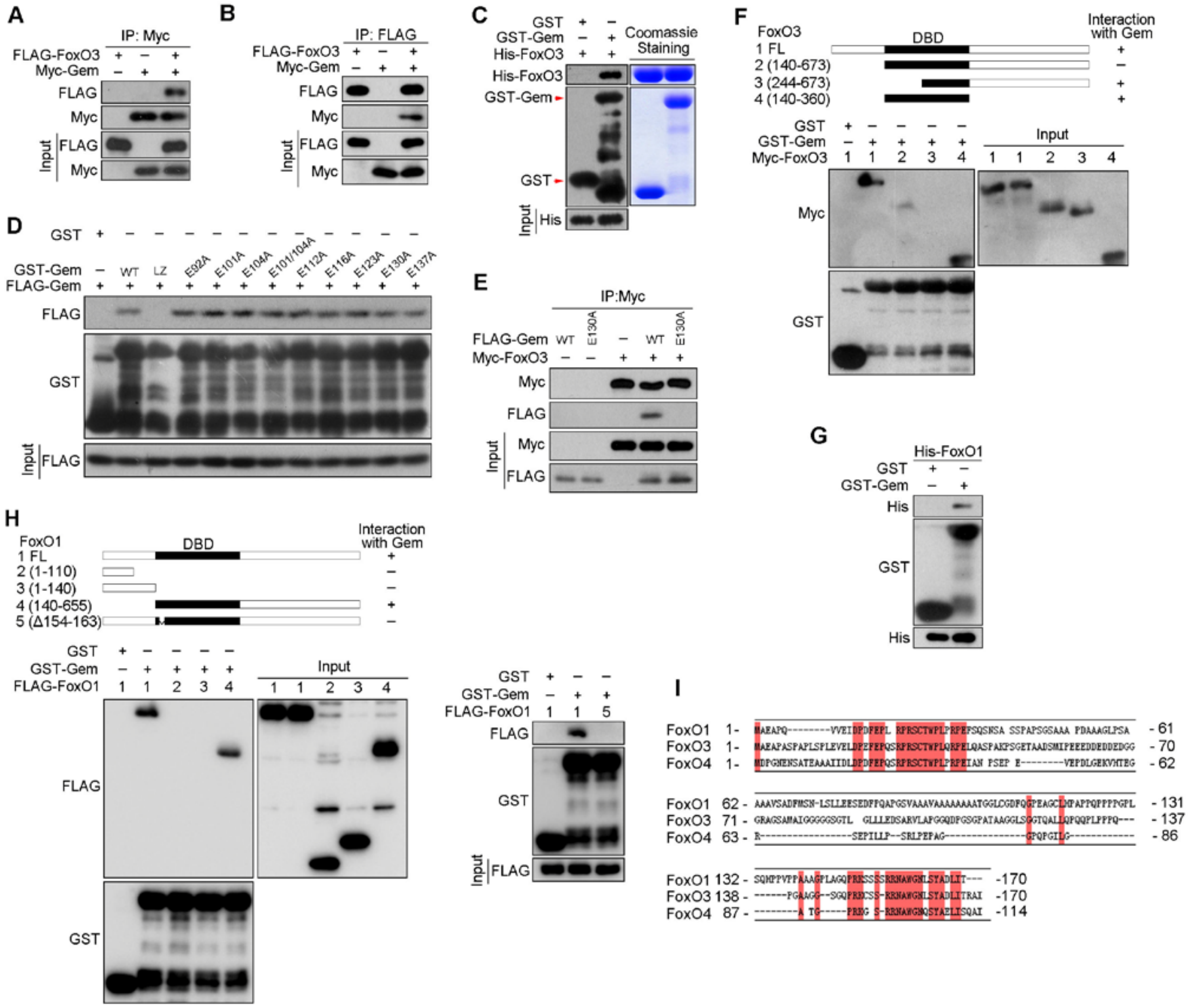
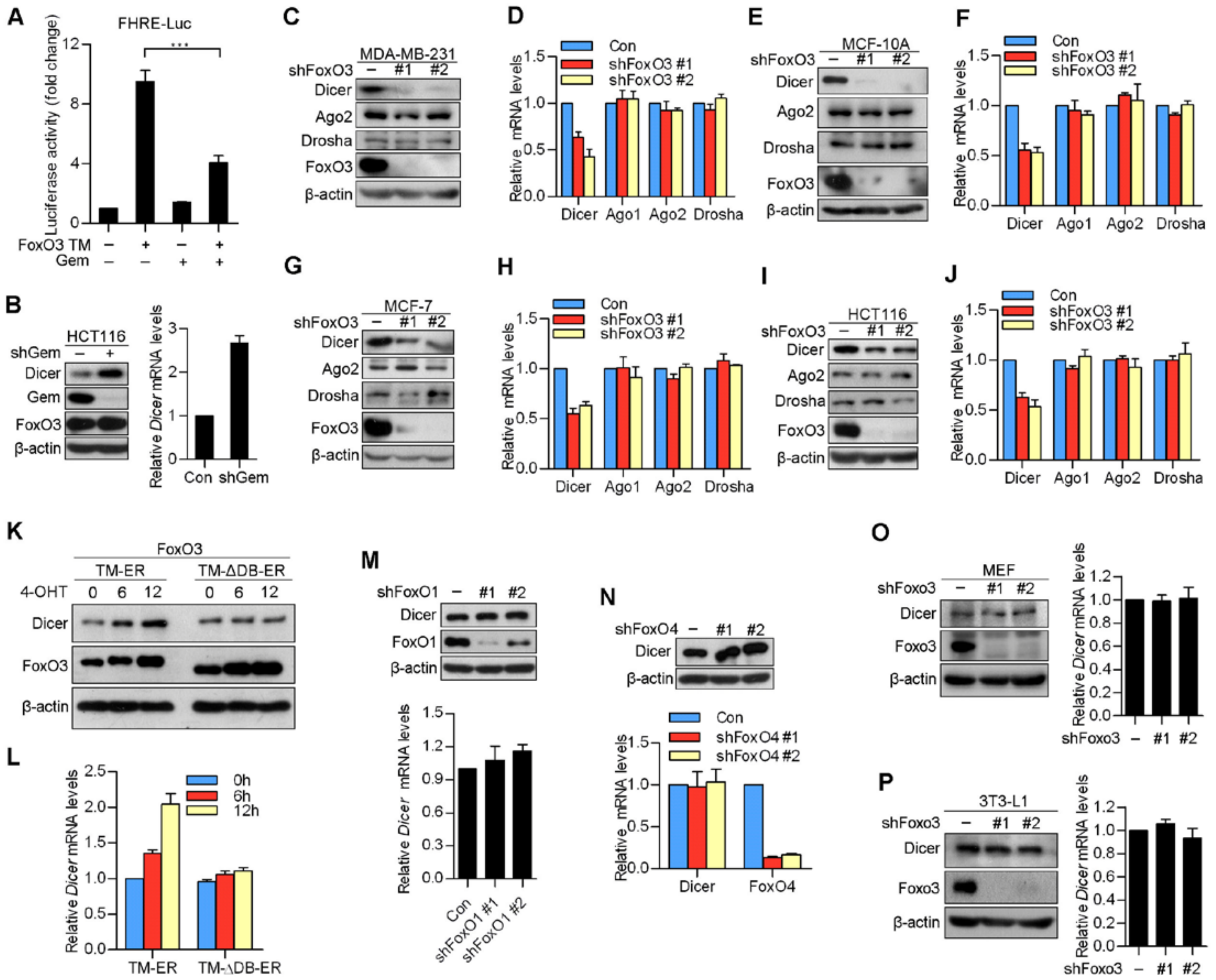
Zhang et al., Supplemental figures, Methods, References and Tables

Supplemental figures



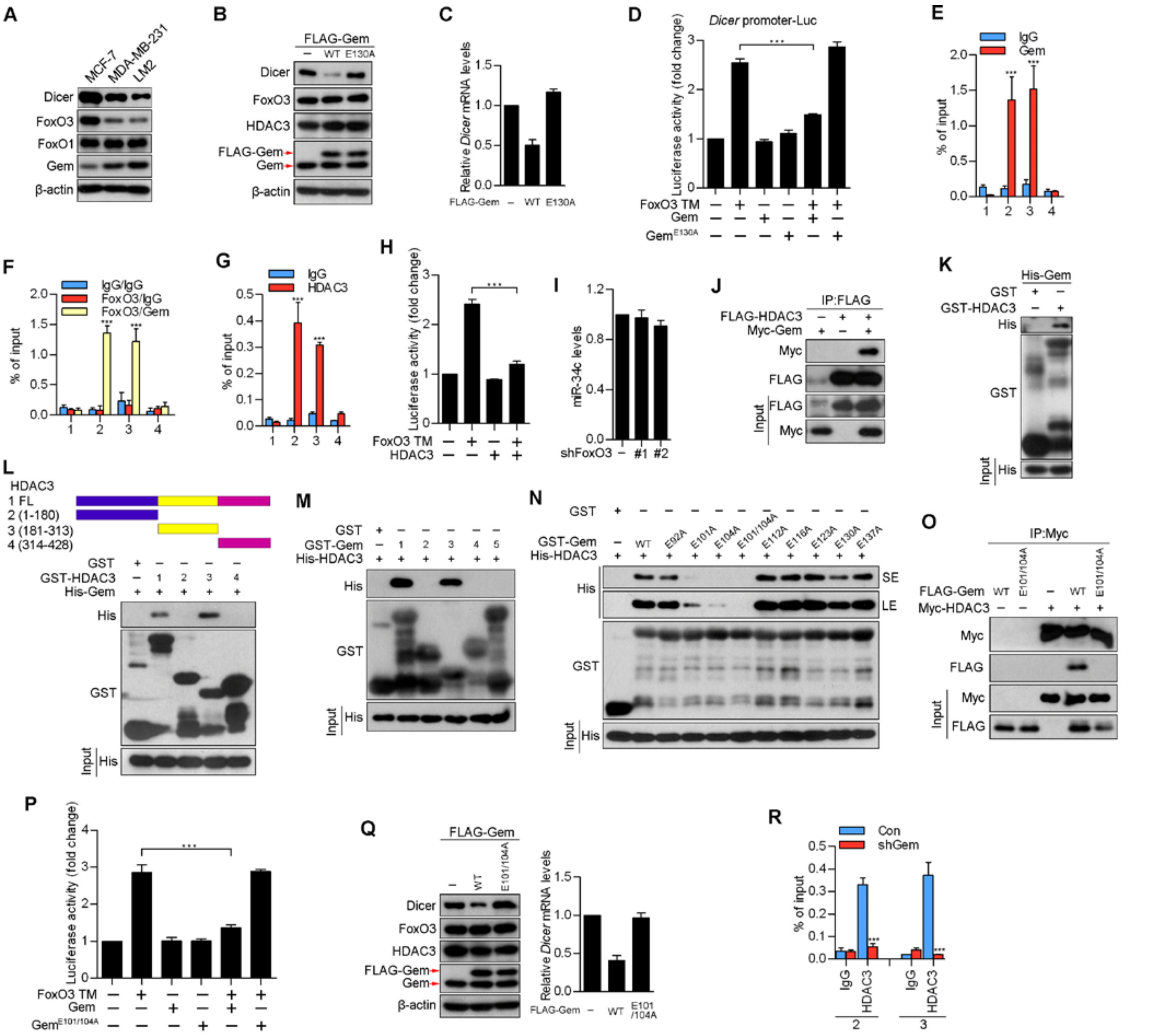
Supplemental Figure 1. Geminin interacts with FoxO3

(A and B) Cell lysates from HEK-293T cells transfected with the indicated constructs were subjected to immunoprecipitation with anti-Myc (A) or anti-FLAG (B). The immunoprecipitates were then blotted with the indicated antibodies. **(C)** Purified His-FoxO3 was incubated with GST or GST-Geminin coupled to GSH-Sepharose. Proteins retained on sepharose were then blotted with anti-GST and anti-His antibodies. **(D)** Cell lysates from HEK-293T cells transfected with FLAG-Geminin were incubated with the indicated GST recombinant proteins. Proteins retained on sepharose were then blotted with anti-FLAG and anti-GST antibodies. **(E)** Cell lysates from HEK-293T cells transfected with the indicated constructs were subjected to immunoprecipitation with anti-Myc antibody. The immunoprecipitates were then blotted with the indicated antibodies. **(F)** HEK-293T cells transfected with the indicated Myc-FoxO3 constructs were lysed and lysates were incubated with GST or GST-Geminin coupled to GSH-Sepharose. Proteins retained on sepharose were then blotted with the indicated antibodies. **(G)** Purified His-FoxO1 was incubated with GST or GST-Geminin coupled to GSH-Sepharose. Proteins retained on sepharose were then blotted with the indicated antibodies. **(H)** HEK-293T cells transfected with the indicated FLAG-FoxO1 constructs were lysed and lysates were incubated with GST or GST-Geminin coupled to GSH-Sepharose. Proteins retained on sepharose were then blotted with the indicated antibodies. (**I**) Sequence alignment of the N-terminal and partial DNA-binding domain from FoxO1, FoxO3 and FoxO4 are shown with reference to the residue numbers. Residues that are identical among family members are shaded in red.



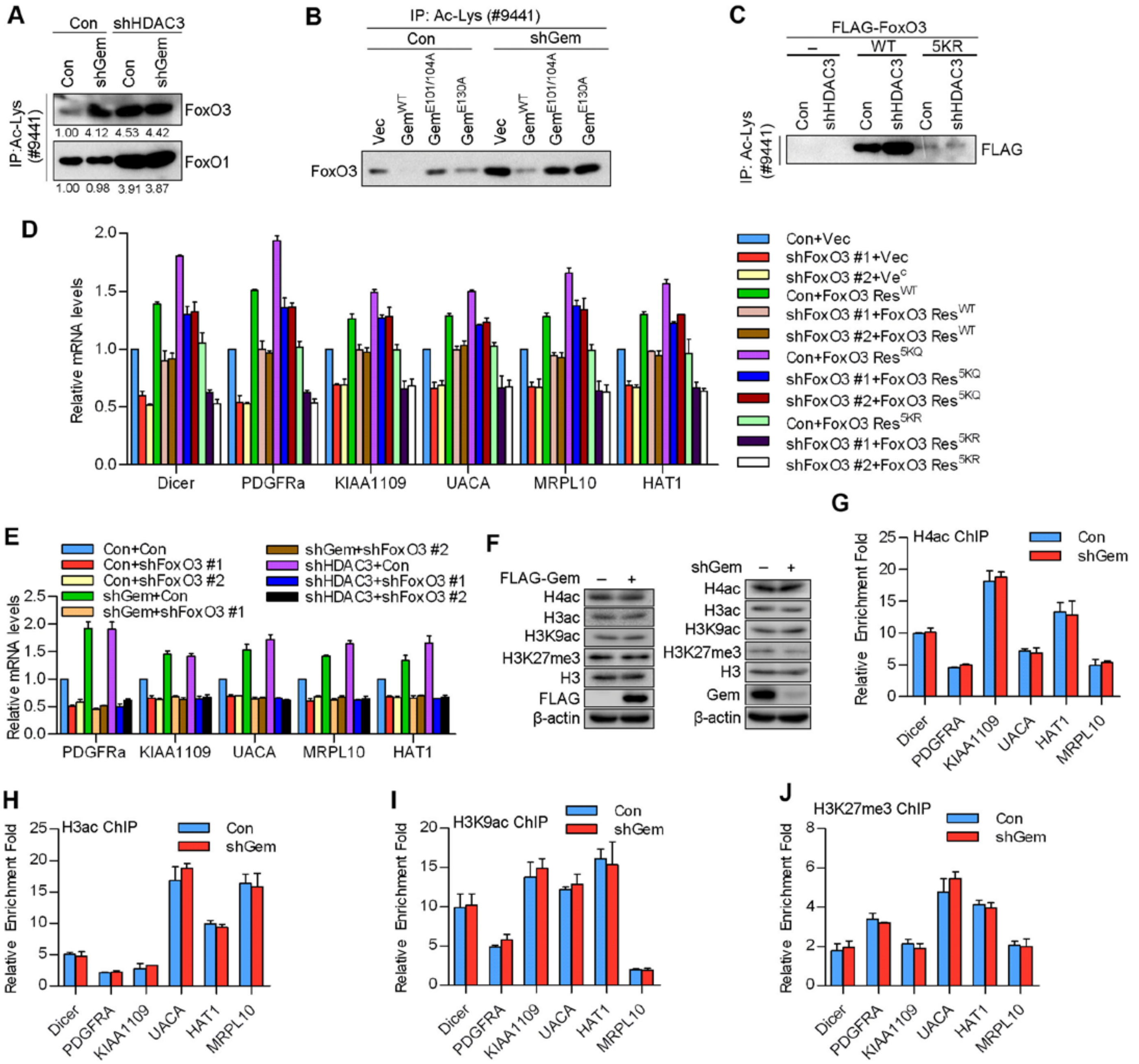
Supplemental Figure 2. FoxO3 regulates Dicer expression

(A) Luciferase assay of HEK-293T cells co-transfected with the FHRE luciferase reporter and FoxO3-TM and/or Geminin. Luciferase reporter activity results are depicted as bar graph with mean±s.d. n=3 independent experiments. ***, P<0.001, Student's t-test. **(B)** HCT116 cells infected with Geminin shRNA lentivirus were harvested and subjected to Western blotting analysis with the indicated antibodies (left panel). qRT-PCR analysis of Dicer mRNA level (right panel). For right panel, results are shown as mean±s.d. n=3 independent experiments. **(C-J)** MDA-MB231 (C and D), MCF-10A (E and F), MCF-7 (G and H) and HCT116 (I and J) cells were infected with lentivirus encoding FoxO3 shRNAs. Cell lysates and RNA were extracted and subjected to Western blotting (C, E, G and I) or qRT-PCR (D, F, H and J) analysis. Bar graphs (D, F, H and J) are shown as mean±s.d. n=3 independent experiments. **(K and L)** HCT116 cells expressing HA-FoxO3-TMER or TM□ DBER were exposed to 4-OHT (1μM) for the indicated times. Protein lysates and RNA were extracted and subjected to Western blotting (K) or qRT-PCR (L). Bar graphs (L) are shown as mean±s.d. n=3 independent experiments. **(M and N)** MDA-MB-231 cells were infected with lentivirus encoding FoxO1 (M) or FoxO4 (N) shRNAs. Cell lysates and RNA were extracted and subjected to Western blotting (upper panel) or qRT-PCR (lower panel). For lower panel, results are shown as mean±s.d. n=3 independent experiments. **(O and P)** MEF (O) and 3T3-L1 (P) cells were infected with lentivirus encoding Control or Foxo3 shRNAs. Cell lysates and RNA were extracted and subjected to Western blotting (left panel) or qRT-PCR (right panel) analysis. Bar graphs (right panel) are shown as mean±s.d. n=3 independent experiments.



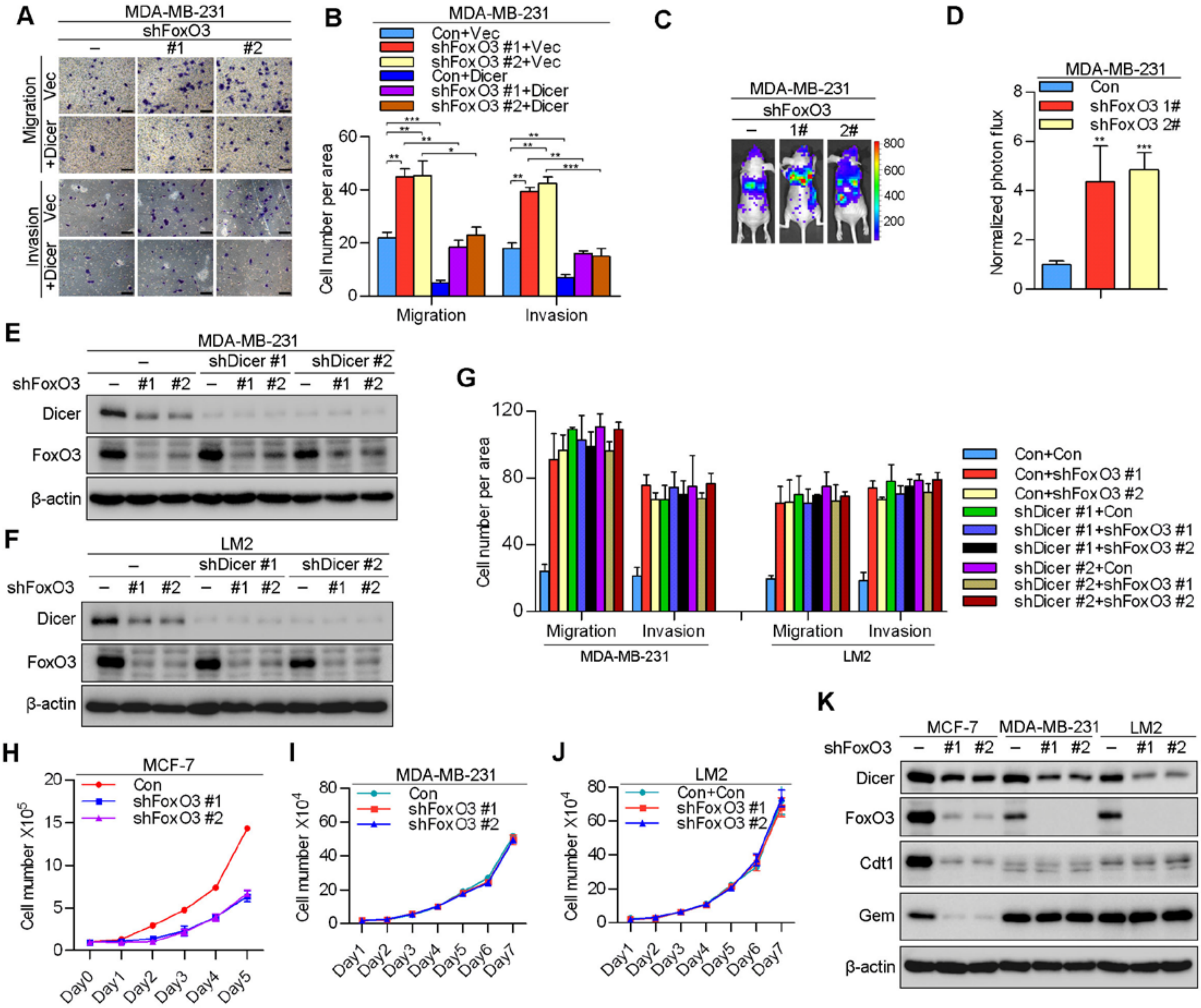
Supplemental Figure 3. Geminin suppresses Dicer expression via coupling HDAC3 to FoxO3

(A) Protein lysates from MCF-7, MDA-MB-231 and LM2 cells were extracted and subjected to Western blotting. **(B and C)** LM2 cells were infected with indicated lentivirus. Protein lysates and RNA were extracted and subjected to Western blotting (B) or qRT-PCR (C). Bar graphs (C) are shown as mean±s.d. n=3 independent experiments. **(D)** Luciferase assay of HEK-293T cells co-transfected with the *Dicer* promoter luciferase reporter and the indicated constructs. Luciferase reporter activity results are depicted as bar graph with mean±s.d. n=3 independent experiments. ***, *P*<0.001, Student's *t*-test. **(E)** ChIP assay to analyze the occupancy of Geminin on *Dicer* promoter. Results are shown as mean±s.d. n=3 independent experiments.***, *P*<0.001, Student's *t*-test. **(F)** ChIP-reChIP was conducted in LM2 cells. Results are shown as mean±s.d. n=3 independent experiments. ***, *P*<0.001, Student's *t*-test. **(G)** ChIP assay to analyze the occupancy of HDAC3 on *Dicer* promoter. Results are shown as mean±s.d. n=3 independent experiments. ***, *P*<0.001, Student's *t*-test. **(H)** Luciferase assay of HEK-293T cells co-transfected with the *Dicer* promoter luciferase reporter and the indicated plasmids. Luciferase reporter activity results are depicted as bar graph with mean±s.d. n=3 independent experiments. ***, *P*<0.001, Student's *t*-test. **(I)** LM2 cells were infected with lentivirus encoding FoxO3 shRNAs. RNA was extracted and subjected to qRT-PCR. Results are shown as mean±s.d. n=3 independent experiments. **(J)** Cell lysates from HEK-293T cells transfected with the indicated constructs were subjected to immunoprecipitation with anti-FLAG antibody. The immunoprecipitates were then blotted with anti-Myc and anti-FLAG antibodies. **(K)** Purified His-Geminin was incubated with GST or GST-HDAC3 coupled to GSH-Sepharose. Proteins retained on sepharose were then blotted with the indicated antibodies. **(L-N)** Purified His-Geminin (L) or His-HDAC3 (M and N) was incubated with the indicated GST recombinant proteins. Proteins retained on sepharose were then blotted with the indicated antibodies. **(O)** Cell lysates from HEK-293T cells transfected with the indicated constructs were subjected to immunoprecipitation with anti-Myc antibody. The immunoprecipitates were then blotted with the indicated antibodies. **(P)** Luciferase assay of HEK-293T cells co-transfected with the *Dicer* promoter luciferase reporter and the indicated plasmids. Luciferase reporter activity results are depicted as bar graph with mean±s.d. n=3 independent experiments. ***, *P*<0.001, Student's *t*-test. **(Q)** LM2 cells were infected with the indicated lentiviral constructs. Protein lysates and RNA were extracted and subjected to Western blotting (left panel) or qRT-PCR (right panel) analysis. Bar graphs (right panel) are shown as mean±s.d. n=3 independent experiments. **(R)** ChIP assay to analyze the occupancy of HDAC3 on *Dicer* promoter in LM2 cells with control versus Geminin depletion. n=3 independent experiments. **, *P*<0.01, Student's *t*-test.



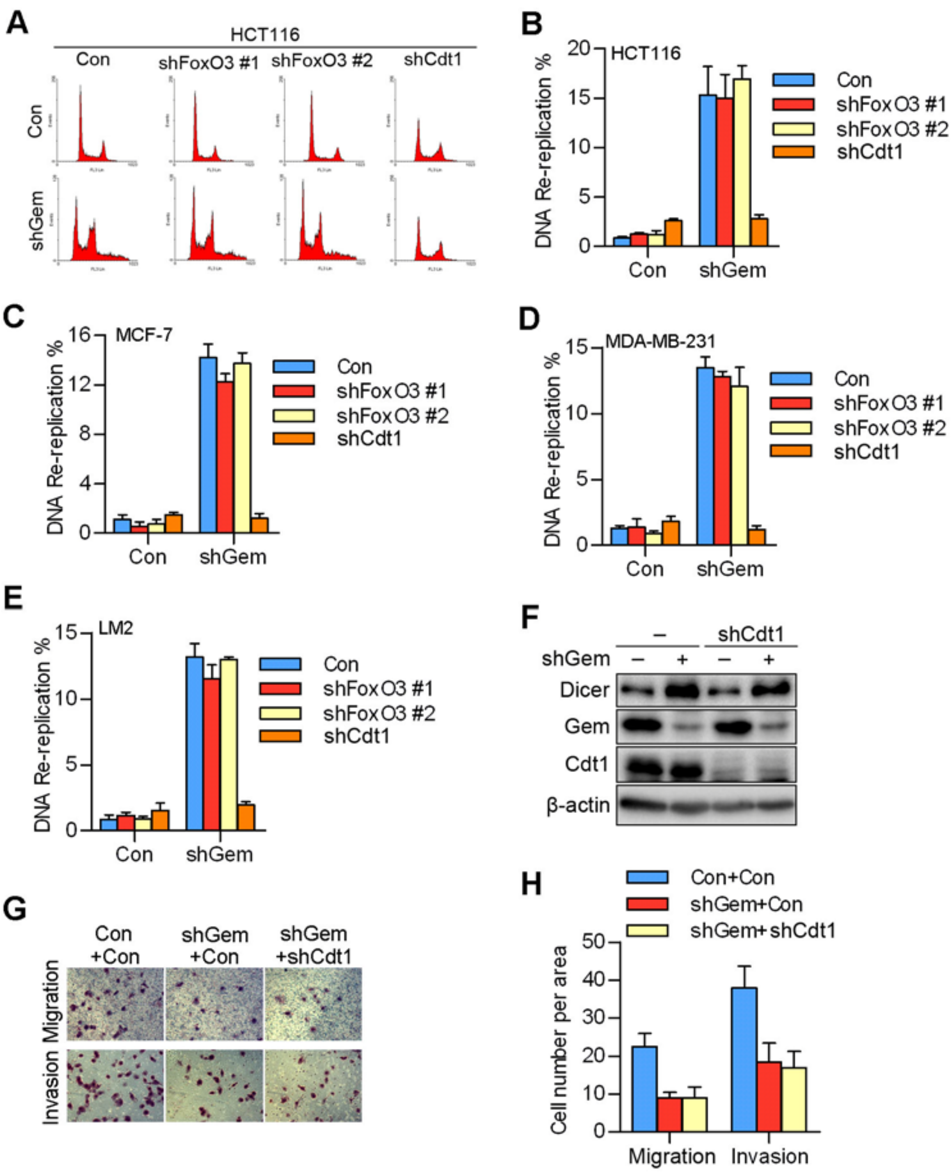
Supplemental Figure 4. Geminin inhibits FoxO3 via recruiting HDAC3 to deacetylate FoxO3

(A) LM2 cells infected with the indicated lentivirus were lysed and subjected to immunoprecipitation with anti-Ac-Lys antibody. The immunoprecipitates were then blotted with the indicated antibodies. **(B)** Geminin-depleted LM2 cells were reconstituted with the indicated Geminin constructs. Cell lysates were then subjected to immunoprecipitation with anti-Ac-Lys antibody. The immunoprecipitates were blotted with anti-FoxO3 antibody. **(C)** FoxO3-depleted LM2 cells were first reconstituted with the indicated FoxO3 constructs and then infected with lentivirus encoding the indicated shRNAs. Cells were lysed and lysates were subjected to immunoprecipitation with anti-Ac-Lys antibody. The immunoprecipitates were then blotted with anti-FLAG antibody. **(D and E)** LM2 cells were infected with lentivirus encoding the indicated shRNAs. RNA was extracted and subjected to qRT-PCR analysis of the indicated mRNA levels. Results are shown as mean±s.d. n=3 independent experiments. **(F)** LM2 cells were infected with lentivirus encoding the indicated shRNAs. Cell lysates were extracted and subjected to Western blotting. **(G-J)** ChIP analysis of the indicated histone modifications at the indicated FoxO3 target promoters in Geminin-depleted LM2 cells. Results are shown as mean±s.d. n=3 independent experiments.

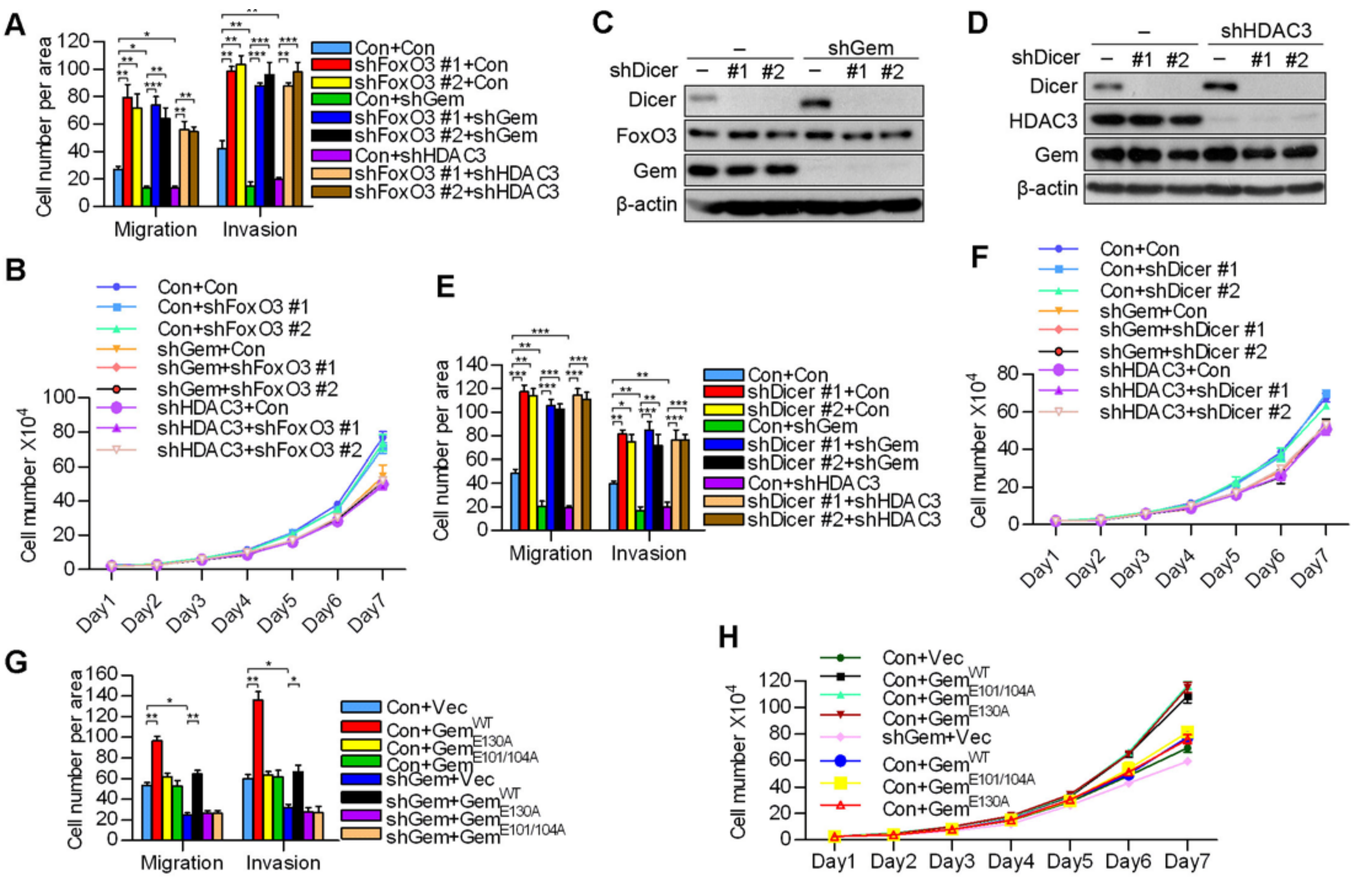


Supplemental Figure 5. FoxO3 regulates metastasis through Dicer

(A and B) MDA-MB-231 cells infected with the indicated lentivirus were subjected to migration and invasion assay. Bar graphs (B) are shown as mean±s.d. n=3 independent experiments. Scale bar, 50μm. ****P*<0.001, ***P* <0.01, **P*<0.05 by ANOVA Bonferroni post hoc test. **(C and D)** Luciferase-labeled MDA-MB-231 cells infected with lentivirus encoding FoxO3 shRNA were injected into fat pad of nude mice. Representative BLI images of mice with spontaneous metastasis (C) and quantification of the bioluminescence signal (D) were shown. Bar graphs (D) are shown as mean±s.d. n=8 mice/group. ****P*<0.001, ***P*<0.01 by Student's *t* test. **(E and F)** MDA-MB-231 (E) or LM2 (F) cells were infected with lentivirus encoding FoxO3 and/or Dicer shRNAs. Cell lysates were extracted and subjected to Western blotting. **(G)** Cells from (E) and (F) were subjected to transwell migration and invasion assays. Results were shown as mean±s.d. n=3 independent experiments. **(H-J)** MCF-7 (H), MDA-MB-231 (I) and LM2 (J) Cells infected with lentivirus encoding FoxO3 shRNAs were subjected to cell proliferation assay. Results are shown as mean±s.d. n=3 independent experiments. **(K)** MCF-7, MDA-MB-231 and LM2 Cells infected with lentivirus encoding FoxO3 shRNAs were subjected to Western blotting analysis with the indicated antibodies.



Supplemental Figure 6. Geminin's dual roles in DNA-replication and in metastasis are separate from each other. (A-E) Flow cytometric profiles of HCT116 (A and B), MCF-7 (C), MDA-MB-231 (D) and LM2 (E) cells infected with indicated shRNAs. Results are depicted as bar graph with mean±s.d. n=3 independent experiments. **(F)** LM2 cells were infected with lentivirus encoding Gem and/or Cdt1 shRNAs. Cell lysates were extracted and subjected to Western blotting. **(G and H)** Cells from (F) were subjected to transwell migration and invasion assays. Results were shown as mean±s.d. n=3 independent experiments.



Supplemental Figure 7. Geminin/HDAC3 complex regulates metastasis through FoxO3-Dicer axis

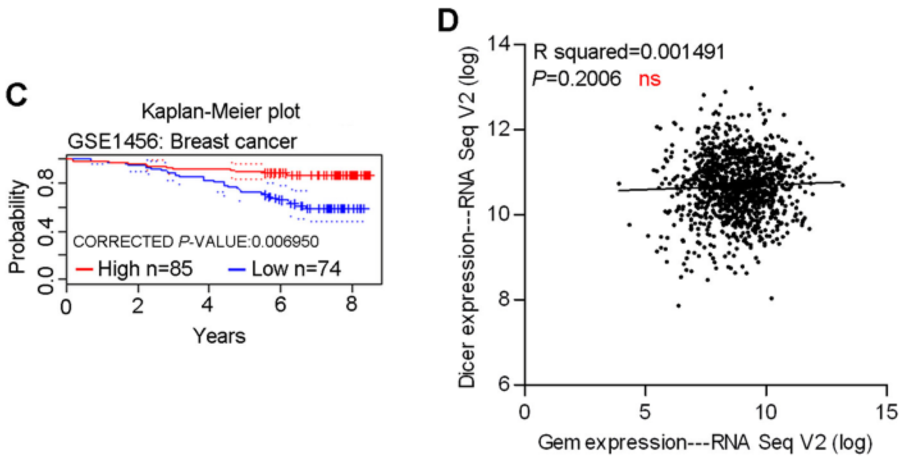
(A and B) LM2 cells infected with lentivirus encoding FoxO3 shRNA and/or Geminin or HDAC3 shRNA were subjected to migration/invasion (A) and proliferation assay (B). Bar graphs are shown as mean±s.d. n=3 independent experiments. ***P<0.001, **P <0.01, *P<0.05 by ANOVA Bonferroni post hoc test. **(C and D)** LM2 cells were infected with lentivirus encoding the indicated shRNAs. Proteins were extracted and subjected to Western blotting analysis with the indicated antibodies. **(E and F)** LM2 cells infected with lentivirus encoding Dicer shRNAs and/or shRNAs targeting Geminin or HDAC3 were subjected to migration/invasion (E) and proliferation assay (F). Bar graphs are shown as mean±s.d. n=3 independent experiments. ***P<0.001, **P <0.01, *P<0.05 by ANOVA Bonferroni post hoc test. **(G and H)** LM2 cells infected with lentivirus encoding Geminin shRNAs and/or Geminin expression constructs were subjected to migration/invasion (G) and proliferation assay (H). Bar graphs are shown as mean±s.d. n=3 independent experiments. **P <0.01, *P<0.05 by ANOVA Bonferroni post hoc test.

A

	Case	Gem staining%	*P* value	Dicer staining%	*P* value
ER positive	64	35.95±3.489	NS	29.41±3.645	NS
ER negative	119	35.36±2.394		28.82±2.053	
Her2 positive	84	35.98±3.153	NS	28.23±3.106	NS
Her2 negative	99	35.37±2.493		27.34±2.194	
Triple negative	91	34.97±2.624	NS	29.65±2.175	NS
Non-triple negative	92	36.16±2.956		28.21±3.106	
Grade I/II	109	33.88±2.216	0.0114	31.66±2.439	0.0235
Grade III	74	43.76±3.372		23.27±2.636	

B

	Case	FoxO3 staining%	*P* value	HDAC3 staining%	*P* value
ER positive	64	25.95±2.345	NS	32.33±3.574	NS
ER negative	119	24.44±2.494		31.75±3.112	
Her2 positive	84	25.36±3.254	NS	31.33±2.548	NS
Her2 negative	99	25.46±3.186		32.25±2.825	
Triple negative	91	25.875±3.587	NS	31.75±2.475	NS
Non-triple negative	92	25.16±3.256		31.57±2.306	
Grade I/II	109	28.568±2.356	0.0328	30.75±2.587	0.0075
Grade III	74	21.36±2.268		43.84±2.636	



Supplemental Figure 8. Negative correlation between Geminin/HDAC3 and acetyl-FoxO3-Dicer in clinical breast cancer samples

(A and B) Summary and statistical analysis of Immunohistochemical staining data in Figure 7A. **(C)** Kaplan-Meier analysis of overall survival in breast cancer patients with high versus low *Dicer* expression. The data were obtained from PrognoScan and the GSE number is shown in the panel. (D) Correlation analysis between Geminin and Dicer expression using breast cancer samples from TCGA database.

Supplemental methods

Western Blotting

Cultured cells were lysed with RIPA lysis buffer (50mM Tris-HCl, 150mM NaCl, 1% Triton X-100, 1% Sodium deoxycholate, 0.1% SDS). Protein concentration of each sample was determined using the BCA kit (Pierce, 23235) as manufacturer's instructions. Equal amounts of protein extracts were separated by electrophoresis on appropriate Tris-Glycine gel, and then transferred to a nitrocellulose membrane (Roche, 03010040001). The membrane was probed with different primary antibodies, followed by secondary antibodies conjugated to horseradish peroxidase. Quantitative densitometry analysis was performed with image analysis software (Quantity one, Bio-Rad).

RNA Interference

Lentiviral based vector pLV-H1-EF1α (Biosettia) was used for RNA interference experiment. shRNA sequences for target genes as follows:

Control: 5'-GCAAAGAAGGCCACTACTATA-3';

shFoxO3 #1: 5'-GCACAACCTGTCACTGCATAG-3';

shFoxO3 #2: 5'-GCTCACTTCGGACTCACTTAG-3';

shGeminin: 5'-TGCCAACTCTGGAATCAAA-3';

shHDAC3: 5'-GCTTCACCAAGAGTCTTAATG-3';

shDicer #1: 5'-GCAGCTCTGGATCATAATACC-3;

shDicer #2: 5'-GGAAGAATCAGCCTCGCAACA-3;

shCdt1: 5'- GCGCAATGTTGGCCAGATCAA-3'. Lentiviruses were generated according to the manufacturer's protocol. The viruses were used to infected cells in the presence of protamine sulfate (8μg/ml).

Quantitative RT-PCR

Total RNA was isolated from samples with Trizol reagents following the manufacturer's instructions (Invitrogen). cDNA was prepared with the MMLV Reverse Transcriptase (Fermentas). Quantitative PCR was performed using the StepOne-Plus real-time PCR system (Applied Biosystems Inc., Foster City, CA) that measures real-time SYBR green fluorescence and then calculated by means of the comparative Ct method ($2^{-\Delta\Delta Ct}$) with the expression of TBP as an internal control. The primer sequences used for the real-time PCR experiments are listed in Table S4.

Plasmids and Antibodies.

FoxO3, Geminin, HDAC3 and Dicer were cloned into expression vectors and deletion mutants were generated by a PCR-based approach. All constructs were sequenced prior to use. The following antibodies were used: anti-FoxO3 (Cell Signaling, #2497), anti-FKHRL1 (Santa Cruz, #11351), anti-FoxO1 (Cell Signaling, #2880), anti-Geminin (Santa Cruz, #8448), anti-HDAC3 (Cell Signaling, #3949), anti-Dicer (Cell Signaling, #3363), anti-Acetyl Lysine (Cell Signaling, #9441), anti-Ac-FKHR (Santa Cruz, #49437), anti-FLAG (Sigma, F7425), anti-FLAG (Sigma, F3165), anti-FLAG (Abcam, ab1257), anti-Myc (Cell Signaling, #2276), anti-Myc (Cell Signaling, #2278), anti-c-Myc (Abcam, ab32072), anti-HA (Roche, #11867423001), anti-β-actin (Sigma, A1978), anti-His (Santa Cruz, #803), anti-GST (Cell Signaling, #2622), anti-Ago2(Proteintech, 10686-1-AP), anti-Drosha(Proteintech, 55001-1-AP), anti-Histone H3(Cell Signaling, #4499), anti-acetyl-Histone H3(Millipore, #06-599), anti-acetyl-Histone H4(Millipore, #06-866), anti-Histone H3 (acetyl K9) (Abcam, ab10812), anti-Tri-Methyl-Histone H3 (Lys27) (Cell Signaling, #9733).

Immunoprecipitation (IP) and Two-step co-immunoprecipitation.

Cells were lysed in IP buffer containing 50mM Tris-HCl, 100mM NaCl, 40mM β-glycerol phosphate, 1mM Na_4VO_3, 10mM NaF, supplemented with phosphatase inhibitor and protease inhibitor (Roche). Cell lysates were incubated with antibody overnight at 4°C. ProteinA/G beads were added and 2hr later washed 3 times with IP buffer and analyzed by SDS-PAGE and immunoblotting.

Two-step co-immunoprecipitation was performed essentially according to the procedures described previously (Harada et al., 2003). Briefly, LM2 cells were lysed with LSLD buffer, sonicated and centrifuged. The supernatant was subjected to immunoprecipitation by incubating with an anti-Geminin antibody overnight at 4°C. ProteinA/G beads were added and 2hr later the beads were washed with lysis buffer containing NaCl (150 mM) three times, and the Geminin-based protein complexes were eluted with lysis buffer (300 µl) containing NaCl (250 mM) and Geminin antigen for 2 h at 4°C. The second immunoprecipitation was performed using elute (150 µl) from the first immunoprecipitates and lysis buffer (350 µl) containing NaCl (150 mM) and an HDAC3 antibody or a control IgG. The immunoprecipitates were then blotted with indicated antibodies.

Supplemental references.

Harada, J., Kokura, K., Kanei-Ishii, C., Nomura, T., Khan, M.M., Kim, Y., and Ishii, S. (2003). Requirement of the co-repressor homeodomain-interacting protein kinase 2 for ski-mediated inhibition of bone morphogenetic protein-induced transcriptional activation. J Biol Chem *278*, 38998-39005.

Supplemental Table 1: RNA Sequencing Data

Symbol	RawIntensity-control	RawIntensity-shFoxO3	TPM-control	TPM-shFoxO3	log2 Ratio (f3/control)	*P*-Value	FDR	transcriptID
IFI27	7	245	2.08	71.46	5.10248	8.76E-06	9.26E-05	NM_001130080
IFIT1	18	515	5.34	150.22	4.814093	9.80E-09	1.76E-07	NM_001548
IFIT3	2	47	0.59	13.71	4.53837	0.000114	0.00091	NM_001031683
OASL	6	108	1.78	31.5	4.145403	1.54E-05	0.000154	NM_198213
PSMB9	17	59	5.04	17.21	1.771751	1.29E-06	1.63E-05	NM_002800
C19orf66	26	87	7.71	25.38	1.718889	7.72E-09	1.40E-07	NM_018381
RARA	18	60	5.34	17.5	1.712443	1.82E-06	2.24E-05	NM_001145302
FBXW7	13	43	3.85	12.54	1.703607	6.13E-05	0.000524	NM_033632
TNFAIP1	20	66	5.93	19.25	1.698754	6.39E-07	8.56E-06	NM_021137
FSTL3	24	79	7.12	23.04	1.694192	5.14E-08	8.40E-07	NM_005860
TAP1	38	124	11.27	36.17	1.682306	1.03E-11	2.73E-10	NM_000593
CST3	305	982	90.44	286.44	1.6632	7.83E-13	2.74E-11	NM_000099
CFDP1	14	45	4.15	13.13	1.661684	5.53E-05	0.000477	NM_006324
ABLIM3	17	54	5.04	15.75	1.643856	1.12E-05	0.000116	NM_014945
ICA1L	14	44	4.15	12.83	1.628338	8.48E-05	0.000703	NM_138468
LOC400027	15	46	4.45	13.42	1.592507	7.56E-05	0.000633	NR_028408
VGF	23	70	6.82	20.42	1.582139	1.08E-06	1.39E-05	NM_003378
UBASH3B	42	126	12.45	36.75	1.561599	8.04E-11	1.92E-09	NM_032873
DUOX1	15	45	4.45	13.13	1.56099	0.000115	0.000918	NM_017434
CILP2	37	110	10.97	32.09	1.54856	1.61E-09	3.24E-08	NM_153221
GLIPR2	54	159	16.01	46.38	1.53453	6.01E-13	2.16E-11	NM_022343
NGFR	17	50	5.04	14.58	1.532495	5.92E-	0.0005	NM_002507

						05	07	
OAS3	26	76	7.71	22.17	1.523806	7.56E-07	9.97E-06	NM_006187
HOXB9	22	64	6.52	18.67	1.517778	6.22E-06	6.80E-05	NM_024017
LOXL2	56	163	16.61	47.54	1.51709	4.71E-13	1.74E-11	NM_002318
JAG1	40	116	11.86	33.84	1.512626	1.12E-09	2.31E-08	NM_000214
C8ORFK29	25	72	7.41	21	1.502844	1.91E-06	2.33E-05	NR_015428
PBX2	97	279	28.76	81.38	1.500611	1.16E-13	4.94E-12	NM_002586
WRB	24	69	7.12	20.13	1.499398	3.23E-06	3.76E-05	NM_001146218
STAT1	254	730	75.32	212.93	1.499274	4.89E-13	1.80E-11	NM_007315
RRM2B	169	460	50.11	134.18	1.420999	2.62E-14	1.27E-12	NM_001172478
NDRG1	88	239	26.09	69.71	1.417869	5.48E-14	2.52E-12	NM_001135242
SAMD4A	43	116	12.75	33.84	1.408232	7.73E-09	1.40E-07	NM_001161576
CRIM1	69	186	20.46	54.25	1.406817	2.32E-13	9.21E-12	NM_016441
PPM1A	62	167	18.38	48.71	1.406081	4.13E-12	1.18E-10	NM_021003
ARID3B	29	78	8.6	22.75	1.403458	2.42E-06	2.90E-05	NM_006465
C5orf28	32	86	9.49	25.09	1.402632	7.41E-07	9.81E-06	NM_022483
ANKRD5	38	102	11.27	29.75	1.400402	7.02E-08	1.11E-06	NM_198798
NR1D1	68	182	20.16	53.09	1.396945	5.86E-13	2.12E-11	NM_021724
SH2D5	37	99	10.97	28.88	1.396507	1.18E-07	1.78E-06	NM_001103161
TRIM14	52	137	15.42	39.96	1.373754	7.13E-10	1.49E-08	NM_014788
FGF2	30	78	8.9	22.75	1.353989	4.45E-06	5.02E-05	NM_002006
ARTN	47	122	13.94	35.59	1.352241	9.23E-09	1.66E-07	NM_057091
OGFR	54	140	16.01	40.84	1.35101	7.73E-10	1.62E-08	NM_007346
ZBTB22	27	70	8.01	20.42	1.350109	1.46E-05	0.000146	NM_001145338
UBE2L6	175	451	51.89	131.55	1.342083	4.03E-	1.53E-	NM_198183

						13	11	
PSMB5	143	366	42.4	106.76	1.332235	0	0	NM_001130725
INPP5K	54	138	16.01	40.25	1.330015	1.60E-09	3.22E-08	NM_016532
SERF2	80	204	23.72	59.5	1.326786	1.80E-13	7.26E-12	NM_001018108
MTERFD1	40	102	11.86	29.75	1.326786	2.32E-07	3.38E-06	NM_015942
KIFC3	38	96	11.27	28	1.312939	6.46E-07	8.65E-06	NM_005550
COTL1	682	1435	202.23	418.57	1.049472	1.48E-12	4.75E-11	NM_021149
HAUS6	39	82	11.56	23.92	1.049076	0.000122	0.000965	NM_017645
FADS3	59	124	17.49	36.17	1.048263	2.23E-06	2.70E-05	NM_021727
PAQR3	90	18	26.69	5.25	-2.34591	3.47E-13	1.33E-11	NM_001040202
NFATC2IP	140	28	41.51	8.17	-2.34505	9.58E-20	6.56E-18	NM_032815
TMEM180	70	23	20.76	6.71	-1.62942	4.84E-07	6.64E-06	NM_024789
FABP5	628	207	186.22	60.38	-1.62487	1.00E-51	1.61E-49	NM_001444
SLBP	443	147	131.36	42.88	-1.61515	1.11E-36	1.32E-34	NM_006527
C5orf62	42	14	12.45	4.08	-1.6095	0.00012	0.000954	NM_032947
SLCO4A1	42	14	12.45	4.08	-1.6095	0.00012	0.000953	NM_016354
SRPR	96	32	28.47	9.33	-1.60949	4.92E-09	9.24E-08	NM_001177842
AMH	93	31	27.58	9.04	-1.60923	8.57E-09	1.55E-07	NM_000479
DICER1	72	24	21.35	7	-1.60881	4.24E-07	5.93E-06	NM_030621
DPY30	144	48	42.7	14	-1.60881	7.18E-13	2.54E-11	NM_032574
MRPS2	126	42	37.36	12.25	-1.60871	1.95E-11	5.02E-10	NM_016034
FIS1	582	194	172.58	56.59	-1.60865	2.13E-47	3.31E-45	NM_016068
SUN2	54	18	16.01	5.25	-1.60858	1.24E-05	0.000126	NM_001199579
ZNF544	69	23	20.46	6.71	-1.60842	7.41E-07	9.82E-06	NM_014480
SDSL	53	19	15.72	5.54	-1.50464	3.76E-	0.0003	NM_138432

						05	34	
ADAM19	153	55	45.37	16.04	-1.50006	2.10E-12	6.48E-11	NM_033274
PGLS	111	40	32.91	11.67	-1.49572	2.39E-09	4.69E-08	NM_012088
LMNB1	158	57	46.85	16.63	-1.49426	1.05E-12	3.50E-11	NM_001198557
HR	80	29	23.72	8.46	-1.48737	4.70E-07	6.48E-06	NM_018411
IFT80	55	20	16.31	5.83	-1.48419	3.22E-05	0.000295	NM_001190241
SKI	55	20	16.31	5.83	-1.48419	3.22E-05	0.000295	NM_003036
BCL9	55	20	16.31	5.83	-1.48419	3.22E-05	0.000294	NM_004326
AAMP	355	129	105.27	37.63	-1.48414	1.94E-26	1.70E-24	NM_001087
SLC37A3	118	43	34.99	12.54	-1.48041	1.02E-09	2.10E-08	NM_207113
PSENEN	74	27	21.94	7.88	-1.4773	1.43E-06	1.79E-05	NM_172341
RANGRF	74	27	21.94	7.88	-1.4773	1.43E-06	1.79E-05	NM_001177801
CCND3	63	23	18.68	6.71	-1.47711	8.93E-06	9.41E-05	NM_001760
RPS9	1340	492	397.34	143.51	-1.46922	1.04E-93	2.35E-91	NM_001013
SMAD1	49	18	14.53	5.25	-1.46865	9.95E-05	0.00081	NM_001003688
C9orf167	149	55	44.18	16.04	-1.46172	1.03E-11	2.73E-10	NM_017723
MED6	233	86	69.09	25.09	-1.46136	1.64E-17	9.70E-16	NM_005466
HDGFRP2	233	86	69.09	25.09	-1.46136	1.64E-17	9.65E-16	NM_032631
TRMT5	138	51	40.92	14.88	-1.45943	6.16E-11	1.49E-09	NM_020810
WDHD1	73	27	21.65	7.88	-1.4581	2.13E-06	2.59E-05	NM_007086
CS	627	232	185.92	67.67	-1.45809	2.67E-44	3.81E-42	NM_004077
SH3PXD2A	54	20	16.01	5.83	-1.45741	4.82E-05	0.00042	NM_014631
NUP93	224	83	66.42	24.21	-1.45601	8.37E-17	4.72E-15	NM_014669
MAP3K11	70	26	20.76	7.58	-1.45354	3.73E-06	4.28E-05	NM_002419
HSD11B2	51	19	15.12	5.54	-1.4485	8.47E-	0.0007	NM_000196

						05	03	
SF3B2	778	290	230.7	84.59	-1.44746	5.58E-54	9.21E-52	NM_006842
PHGDH	126	47	37.36	13.71	-1.44627	5.50E-10	1.18E-08	NM_006623
C1QBP	2898	1082	859.33	315.6	-1.44512	########	########	NM_001212
FBL	632	236	187.4	68.84	-1.4448	4.65E-44	6.58E-42	NM_001436
ZNF507	192	72	56.93	21	-1.4388	2.22E-14	1.10E-12	NM_001136156
IRGQ	56	21	16.61	6.13	-1.43809	4.10E-05	0.000362	NM_001007561
HSBP1L1	72	27	21.35	7.88	-1.43797	3.18E-06	3.71E-05	NM_001136180
KCTD9	213	80	63.16	23.33	-1.43682	9.27E-16	4.99E-14	NM_017634
WWP2	85	32	25.2	9.33	-1.43347	4.37E-07	6.08E-06	NM_007014
KIF22	170	64	50.41	18.67	-1.43299	7.90E-13	2.76E-11	NM_007317
SKA1	69	26	20.46	7.58	-1.43254	5.54E-06	6.16E-05	NM_001039535
CSRP1	154	58	45.66	16.92	-1.4322	9.52E-12	2.56E-10	NM_001193571
PSMG3	218	83	64.64	24.21	-1.41682	8.53E-16	4.61E-14	NM_032302
ANAPC13	186	71	55.15	20.71	-1.41303	1.22E-13	5.15E-12	NM_001242375
PRIM2	94	36	27.87	10.5	-1.40832	1.55E-07	2.31E-06	NM_000947
ZFP36L2	99	38	29.36	11.08	-1.40589	7.63E-08	1.20E-06	NM_006887
HIF1A	168	65	49.82	18.96	-1.39377	3.13E-12	9.16E-11	NM_181054
AFMID	459	178	136.1	51.92	-1.3903	1.03E-30	1.03E-28	NM_001145526
SAT1	1405	545	416.62	158.97	-1.38998	1.94E-90	4.30E-88	NR_027783
MAP7D1	157	61	46.55	17.79	-1.38771	1.87E-11	4.83E-10	NM_018067
KDM2B	108	42	32.02	12.25	-1.38619	2.71E-08	4.62E-07	NM_032590
RAB21	72	28	21.35	8.17	-1.38583	5.89E-06	6.52E-05	NM_014999

263

264

Supplemental Table 2: Exiqon microRNA array results

Probe ID	Name	Normalized Intensity		
		FoxO3 knockdown	Control	Fold change
17888	hsa-let-7a-3p	5.248694699	13.581526	0.386458392
147165	hsa-let-7b-5p	1.393728401	5.134844	0.271425656
42668	hsa-let-7c-3p	1.072371173	2.858405	0.375164182
145820	hsa-let-7c-5p	0.020371135	3.890275	0.005236425
145968	hsa-let-7d-5p	0.248673531	3.4373431	0.072344693
145846	hsa-let-7e-5p	2.193184425	2.8843405	0.760376393
145840	hsa-let-7f-1-3p	2.361203602	5.6085796	0.420998501
148250	hsa-let-7f-2-3p	1.879232278	5.6085796	0.335063851
17752	hsa-let-7f-5p	4.288340709	5.6085796	0.764603699
42778	hsa-let-7g-3p	1.330147081	2.5085323	0.530249134
46438	hsa-let-7g-5p	0.023544986	4.3534894	0.005408302
10916	hsa-miR-1	11.12521259	5.3931494	2.062841536
145694	hsa-miR-100-3p	0.817996488	3.6611314	0.223427241
145943	hsa-miR-100-5p	1.613821116	4.459224	0.361906268
31026	hsa-miR-101-3p	0.259402541	2.5085323	0.103408093
17935	hsa-miR-101-5p	0.769554235	4.2524843	0.180965803
42562	hsa-miR-105-3p	1.739766765	4.2524843	0.40911774
5250	hsa-miR-105-5p	0.907855451	2.5085323	0.361907021
42508	hsa-miR-106a-3p	1.327608029	3.8210106	0.347449449
46801	hsa-miR-106a-5p	13.70071534	5.378524	2.547300215
17854	hsa-miR-106b-3p	3.715316457	8.177286	0.454345911
19582	hsa-miR-106b-5p	3.676286236	8.177286	0.449572907
10923	hsa-miR-107	0.848934714	2.5085323	0.338418889
28019	hsa-miR-10a-3p	2.415358215	5.702542	0.423558163
13485	hsa-miR-10a-5p	1.782637322	5.844227	0.305025339
42969	hsa-miR-10b-3p	1.041773406	2.5085323	0.415292004
10925	hsa-miR-10b-5p	1.000310935	2.5085323	0.398763426
46822	hsa-miR-1178-3p	1.140026622	2.5085323	0.454459614
46735	hsa-miR-1179	0.958943354	5.0050015	0.191597016
168601	hsa-miR-146b-3p	6.794175411	3.3126929	2.050952387
10306	hsa-miR-146b-5p	1.213726619	2.876522	0.421942408
146121	hsa-miR-1470	1.346539456	2.876522	0.468113735
146052	hsa-miR-1471	2.577381617	5.9797707	0.431016798
10954	hsa-miR-147a	1.366458257	3.4255304	0.39890414
168968	hsa-miR-147b	33.17614835	13.3389435	2.487164621
42736	hsa-miR-148b-5p	0.484398995	2.8999696	0.167035887
169087	hsa-miR-149-3p	1.911348731	4.5270305	0.422208053
42810	hsa-miR-149-5p	0.963919291	2.8540592	0.337736264
42850	hsa-miR-150-3p	1.051361099	2.8540592	0.368373963
145678	hsa-miR-150-5p	0.734199567	4.5405283	0.16169915
17463	hsa-miR-151a-3p	0.848354551	3.386517	0.250509462
11260	hsa-miR-151a-5p	0.876525343	2.791005	0.314053663
42902	hsa-miR-185-5p	10.35286601	4.7865305	2.162916544

148057	hsa-miR-186-3p	3.292113573	9.802156	0.335856068
10990	hsa-miR-196a-5p	4.352965599	10.639929	0.409116038
145995	hsa-miR-196b-3p	0.519426136	2.5085323	0.207063763
145889	hsa-miR-196b-5p	2.054920861	6.290021	0.32669539
146142	hsa-miR-1972	28.07307428	13.345192	2.103609621
146165	hsa-miR-1973	5.669616516	13.345192	0.424843383
42783	hsa-miR-197-3p	2.897952919	13.345192	0.217153333
169017	hsa-miR-197-5p	6.146849476	13.345192	0.460604049
146140	hsa-miR-1976	1.78702914	5.4082212	0.330428264
148637	hsa-miR-198	0.221204173	3.8729517	0.057115139
10995	hsa-miR-199a-3p	0.862674446	7.548056	0.114290944
29562	hsa-miR-199a-5p	0.682629717	7.548056	0.090437818
19591	hsa-miR-199b-5p	3.482948465	7.548056	0.46143649
10997	hsa-miR-19a-3p	1.365983566	7.548056	0.180971573
42549	hsa-miR-19a-5p	15.20423292	7.548056	2.01432434
17883	hsa-miR-19b-1-5p	2.273699454	5.2354283	0.434291012
42918	hsa-miR-19b-2-5p	28.10511019	5.2354283	5.368254244
10998	hsa-miR-19b-3p	1.906669204	5.2354283	0.364185907
168819	hsa-miR-200a-3p	2.06463473	5.2354283	0.394358324
145827	hsa-miR-200a-5p	2.431601032	5.096446	0.477117001
147186	hsa-miR-200b-3p	1.129297435	2.5085323	0.450182537
145974	hsa-miR-200b-5p	5.333329547	8.063998	0.661375356
17427	hsa-miR-200c-3p	2.317557737	8.063998	0.287395624
17851	hsa-miR-200c-5p	4.749087539	8.063998	0.588924692
148685	hsa-miR-202-3p	6.468290683	2.5085323	2.578516004
42507	hsa-miR-202-5p	1.90307472	6.1345997	0.31021987
146116	hsa-miR-2116-3p	5.214689456	6.1345997	0.850045596
148386	hsa-miR-219b-5p	6.321536651	6.1345997	1.030472559
11022	hsa-miR-221-3p	21.09298263	6.1345997	3.438363326
42475	hsa-miR-221-5p	1.670674709	4.2147202	0.39639042
11023	hsa-miR-222-3p	0.932984905	3.6949162	0.252505024
17918	hsa-miR-222-5p	1.519754102	4.4571605	0.340969122
11024	hsa-miR-223-3p	1.742115061	4.4571605	0.390857601
42460	hsa-miR-223-5p	1.414167157	3.3971329	0.416282553
11020	hsa-miR-22-3p	1.462069057	4.868551	0.300308872
146163	hsa-miR-224-3p	0.742826153	2.5085323	0.296119828
168772	hsa-miR-224-5p	1.824051998	3.7477036	0.486711916
42532	hsa-miR-22-5p	1.012059584	3.7285514	0.271435063
145638	hsa-miR-29a-5p	3.878036612	3.7285514	1.040092035
17810	hsa-miR-29b-1-5p	1.343340412	3.4296086	0.391689131
42792	hsa-miR-29b-2-5p	0.771106149	3.6692657	0.210152715
11040	hsa-miR-29b-3p	1.360680879	6.104528	0.222896984
11041	hsa-miR-29c-3p	0.940086404	4.0280128	0.233387144
14300	hsa-miR-29c-5p	1.135246322	3.5151527	0.322957896
169419	hsa-miR-300	1.469291467	4.4623127	0.32926681
13143	hsa-miR-301a-3p	2.368768409	5.5179453	0.429284504
28191	hsa-miR-30e-5p	0.911368565	2.5085323	0.363307486

11063	hsa-miR-330-3p	1.251415184	2.5085323	0.498863493
145843	hsa-miR-330-5p	1.095851079	3.6788268	0.297880585
42887	hsa-miR-331-3p	0.829848288	2.5085323	0.330810286
17866	hsa-miR-331-5p	1.187468467	3.5432253	0.335137725
145745	hsa-miR-335-3p	1.133132143	4.5223107	0.250564859
11065	hsa-miR-335-5p	0.970971481	4.1359015	0.234766587
42673	hsa-miR-337-3p	12.99466245	3.9894013	3.257296389
17944	hsa-miR-337-5p	1.056655462	3.0183666	0.350075256
42592	hsa-miR-338-3p	1.463007906	4.179124	0.350075256
17825	hsa-miR-338-5p	6.447832461	4.179124	1.542866989
42912	hsa-miR-339-3p	1.23376837	4.179124	0.295221767
42739	hsa-miR-339-5p	1.233771791	4.179124	0.295222585
42934	hsa-miR-345-5p	1.176331406	4.179124	0.281477986
145732	hsa-miR-346	0.283442611	4.179124	0.067823451
148595	hsa-miR-34a-3p	11.79783773	4.179124	2.82304084
168586	hsa-miR-34a-5p	1.973892698	4.179124	0.472322118
148640	hsa-miR-34b-3p	1.66158554	4.179124	0.397591825
11073	hsa-miR-34b-5p	0.390991094	4.5012717	0.086862362
148601	hsa-miR-3617-5p	0.605258573	2.5085323	0.24127996
168786	hsa-miR-3618	0.441689828	2.5085323	0.176075001
168665	hsa-miR-3619-3p	7.258465788	3.2472324	2.235277582
42476	hsa-miR-374b-3p	5.229298825	2.5085323	2.08460494
148098	hsa-miR-374b-5p	0.796518908	2.5085323	0.31752388
148052	hsa-miR-374c-3p	0.94552828	2.5085323	0.376924898
148430	hsa-miR-374c-5p	3.110432823	10.157288	0.306226704
46918	hsa-miR-375	0.293298686	2.5085323	0.116920434
146009	hsa-miR-376a-3p	0.925247678	2.5085323	0.368840249
42885	hsa-miR-376a-5p	0.247608632	2.5085323	0.098706575
169406	hsa-miR-376b-3p	0.123738685	2.5085323	0.049327125
168947	hsa-miR-3975	1.493316343	5.5119386	0.27092398
169316	hsa-miR-3976	1.698024784	6.724288	0.252521127
169069	hsa-miR-3977	5.879126724	3.4803019	1.689257683
168894	hsa-miR-3978	0.653788751	3.4803019	0.187854034
11240	hsa-miR-409-3p	0.779736437	3.4803019	0.224042758
42925	hsa-miR-409-5p	11.87583837	3.4803019	3.412301206
11102	hsa-miR-410-3p	0.920275168	4.803857	0.191570059
148187	hsa-miR-410-5p	10.32630886	4.690214	2.201671152
148559	hsa-miR-411-3p	1.413859744	3.5666237	0.39641405
17482	hsa-miR-411-5p	0.046902341	6.107152	0.007679904
42764	hsa-miR-412-3p	0.680847933	2.5085323	0.271412863
147957	hsa-miR-412-5p	5.160491628	2.5085323	2.057175675
148192	hsa-miR-421	0.510592593	2.5085323	0.203542363
168676	hsa-miR-499b-5p	0.504339635	2.5085323	0.201049688
42669	hsa-miR-505-3p	0.907779941	2.5085323	0.361876919
42490	hsa-miR-505-5p	11.81271031	3.5095258	3.365899265
11138	hsa-miR-506-3p	0.022228902	2.5085323	0.008861318
168704	hsa-miR-506-5p	0.640881493	2.5085323	0.255480662

11139	hsa-miR-507	0.5342903	3.0139923	0.177269962
11140	hsa-miR-508-3p	0.961321906	2.5085323	0.38322086
42812	hsa-miR-508-5p	0.732937294	2.7002382	0.27143431
168629	hsa-miR-5087	0.68611717	4.63487	0.148033746
11149	hsa-miR-515-5p	1.819235632	4.607603	0.394833416
145717	hsa-miR-516a-3p	1.92407284	4.607603	0.417586507
148650	hsa-miR-516a-5p	1.184796609	4.607603	0.257139473
11151	hsa-miR-516b-5p	1.904126619	4.607603	0.413257526
13130	hsa-miR-517-5p	1.235208355	4.607603	0.268080465
145999	hsa-miR-517a-3p	0.743521594	3.6730704	0.202425087
11154	hsa-miR-517c-3p	0.634430815	4.3409047	0.146151749
169090	hsa-miR-5186	0.941455414	7.456826	0.126254175
169185	hsa-miR-5187-3p	1.365039476	3.7719111	0.361895983
168897	hsa-miR-5187-5p	1.080582738	4.0262494	0.268384452
168632	hsa-miR-5188	0.030848411	4.0167704	0.007679904
169218	hsa-miR-5189-5p	1.100538645	3.6202512	0.303995105
11155	hsa-miR-518a-3p	0.02736889	3.0885801	0.008861318
145905	hsa-miR-518a-5p	0.605065672	3.503089	0.172723466
148641	hsa-miR-518b	1.541039287	3.503089	0.439908688
169387	hsa-miR-5703	10.43976001	3.503089	2.980158371
17814	hsa-miR-570-3p	0.018832044	3.105969	0.006063178
169211	hsa-miR-5704	0.713010268	3.4364495	0.207484576
169196	hsa-miR-5705	2.461947194	6.478985	0.379989642
168579	hsa-miR-5706	3.215057925	7.0612164	0.455312193
169000	hsa-miR-5707	0.013390929	3.0837464	0.004342422
169084	hsa-miR-5708	10.84532244	3.7565415	2.887049813
17490	hsa-miR-571	0.01760916	3.7565415	0.004687599
42837	hsa-miR-577	0.942228224	2.8926654	0.325730112
17302	hsa-miR-578	1.007697249	3.141336	0.320786203
42622	hsa-miR-579-3p	2.248586256	4.619998	0.486707193
17459	hsa-miR-580-3p	1.78109964	4.619998	0.385519569
14962	hsa-miR-581	1.666910017	4.619998	0.36080319
42478	hsa-miR-593-5p	1.854016508	5.7979307	0.319772106
17349	hsa-miR-595	3.697829153	11.4941635	0.321713638
145833	hsa-miR-596	0.947374348	2.5085323	0.377660813
42818	hsa-miR-597-5p	76.52367703	6.264686	12.21508581
145648	hsa-miR-598-3p	0.209396251	2.5085323	0.083473611
30592	hsa-miR-599	2.165499681	4.5589733	0.474997228
17377	hsa-miR-600	1.220465549	5.0209403	0.243075097
148677	hsa-miR-637	0.872634479	5.091284	0.171397722
42832	hsa-miR-638	0.117604143	5.091284	0.023099113
145962	hsa-miR-639	5.567497877	6.3862724	0.871791481
169225	hsa-miR-640	5.97620013	3.6286883	1.646931242
17530	hsa-miR-641	3.006085731	8.998323	0.334071774
169059	hsa-miR-642a-3p	1.0767897	2.5085323	0.429250881
29190	hsa-miR-708-5p	2.002963792	4.72044	0.424317181
146196	hsa-miR-711	1.234934491	2.5085323	0.492293638

11277	hsa-miR-7-1-3p	0.483855347	7.134042	0.067823451
146064	hsa-miR-718	1.915029402	5.1071153	0.374972815
42964	hsa-miR-7-2-3p	1.082144018	2.5085323	0.431385324
42970	hsa-miR-744-3p	1.089178856	3.3438077	0.325730112
27568	hsa-miR-744-5p	0.599019412	4.505517	0.132952425
32891	hsa-miR-769-5p	1.430235445	4.505517	0.317440916
28251	hsa-miR-770-5p	0.790750083	4.732048	0.167105254
30442	hsa-miR-802	2.938606066	2.5085323	1.171444381
168991	hsa-miR-873-3p	1.273850302	4.479733	0.284358533
42493	hsa-miR-892b	1.975939463	4.479733	0.441084204
42932	hsa-miR-920	2.102019055	4.479733	0.469228647
46507	hsa-miR-921	5.322350729	13.147345	0.404823235
42683	hsa-miR-922	2.066019622	7.611733	0.271425656
42788	hsa-miR-924	1.179508265	4.4784594	0.263373665
42926	hsa-miR-92a-1-5p	1.581071406	6.048903	0.261381511
42801	hsa-miR-92a-2-5p	1.268635355	4.4190598	0.28708264
145693	hsa-miR-92a-3p	1.117943956	3.755281	0.297699148
145897	hsa-miR-92b-3p	5.441760598	3.755281	1.449095447
146115	hsa-miR-940	2.461332221	6.9323063	0.355052433
148625	hsa-miR-941	2.22926235	5.226414	0.426537651
11182	hsa-miR-98-5p	1.366904374	4.280859	0.319306096
42708	hsa-miR-99a-5p	1.327971622	4.280859	0.310211484
11184	hsa-miR-99b-5p	2.023897628	4.280859	0.47277839

Supplemental Table 3. RNA Sequencing Data

Gene_ID	readcount_shGem+shFoxO3	readcount_Con+Con	log2.Fold_change.	pvalue	qvalue	Associated Gene Name
ENSG00000054654	67.4078	136.1346	-1.014	1.94E-06	0.00025608	SYNE2
ENSG00000066279	79.74898	176.9055	-1.1494	1.71E-09	6.22E-07	ASPM
ENSG00000075539	69.98539	142.7329	-1.0282	8.18E-07	0.00012131	FRYL
ENSG00000080345	46.709	110.783	-1.246	3.61E-07	6.15E-05	RIF1
ENSG00000100697	66.70483	138.8434	-1.0576	6.36E-07	9.96E-05	DICER1
ENSG00000100852	145.2822	294.2868	-1.0184	2.16E-12	1.74E-09	ARHGAP5
ENSG00000102189	33.58674	85.08411	-1.341	2.28E-06	0.00028869	EEA1
ENSG00000117724	161.0601	375.0647	-1.2195	3.46E-20	7.41E-17	CENPF
ENSG00000118193	40.77274	89.73769	-1.1381	2.09E-05	0.0017516	KIF14
ENSG00000118482	72.48487	171.2795	-1.2406	2.87E-10	1.35E-07	PHF3
ENSG00000125676	50.22389	118.9094	-1.2434	1.42E-07	2.84E-05	THOC2
ENSG00000131747	374.375	788.886	-1.0753	2.21E-33	1.06E-29	TOP2A
ENSG00000134318	66.00185	154.7489	-1.2294	2.69E-09	8.78E-07	ROCK2
ENSG00000135837	44.8344	111.616	-1.3159	9.59E-08	2.03E-05	CEP350
ENSG00000137831	90.29365	196.0755	-1.1187	5.60E-10	2.37E-07	UACA
ENSG00000137962	261.6641	541.6906	-1.0498	1.42E-22	5.47E-19	ARHGAP29
ENSG00000138246	40.3822	89.18204	-1.143	2.07E-05	0.0017516	DNAJC13
ENSG00000138688	56.47259	117.937	-1.0624	4.08E-06	0.00045476	KIAA1109
ENSG00000139793	41.2414	87.8624	-1.0912	4.78E-05	0.0034798	MBNL2
ENSG00000145725	34.9927	80.43053	-1.2007	2.57E-05	0.0020494	PPIP5K2
ENSG00000148516	33.5086	77.305	-1.206	3.47E-05	0.0026498	ZEB1
ENSG00000164023	43.74087	95.57203	-1.1276	1.31E-05	0.0012353	SGMS2
ENSG00000164327	35.22702	82.2364	-1.2231	1.57E-05	0.0014094	RICTOR
ENSG00000173230	45.14683	96.12768	-1.0903	2.13E-05	0.0017648	GOLGB1
ENSG00000134853	58.26909	121.2709	-1.0574	3.26E-06	0.00036774	PDGFRA
ENSG00000189057	24.2918	61.95512	-1.3508	4.98E-05	0.0035974	FAM111B
ENSG00000198677	39.36678	93.97453	-1.2553	2.42E-06	0.00030292	TTC37
ENSG00000159111	9.008495	34.02252	-1.9171	3.88E-05	0.0012804	MRPL10
ENSG00000128708	29.5172	69.78293	-1.2413	1.12E-05	0.00042804	HAT1

Supplemental Table 4. Primers for quantitative real time PCR

Name	Sequence(5’→3’)
Dicer-ChIP-F1	AGGAACACAAAGGGCATATCTTG
Dicer-ChIP-R1	TCACACCTGTCCTAGTGTCACAAA
Dicer-ChIP-F2	GGGCGGAAGTGGGTGTTTGTTAT
Dicer-ChIP-R2	ACCTTCCCACTCGCCTGCGTTTCC
Dicer-ChIP-F3	GCTAAGCTCTCCGGGAAACA
Dicer-ChIP-F3	TCCTTCTGGCACCCACAGA
Dicer-ChIP-F4	CCAACTCAAACTGTCCTCATTAACA
Dicer-ChIP-F4	AGTGACAGGAAGTAGAATGGTGGTT
Dicer-qRT-F	CATGGATAGTGGGATGTCAC
Dicer-qRT-R	CTACTTCCACAGTGACTCTG
mDicer-qRT-F	CTTGAGGCTGCTTCGGTTCT
mDicer-qRT-R	CAGGCCCCACGAGCAA
Ago1-qRT-F	GAGCCTATGTTCCGGCATCTC
Ago1-qRT-R	GAGTGTATCTCCGACACGTTTCAC
Ago2-qRT-F	CCAGCTACA CTCAGACCAACAGA
Ago2-qRT-R	GAAAACGGAGAATCTAATAAAATCA
Drosha-qRT-F	TAGGCTGTGGGAAAGGACCAAG
Drosha-qRT-R	GTTCGATGAACCGCTTCTGATG
PDGFRA-qRT-F	GAGCATCTTTGACAACCTCTACAC
PDGFRA-qRT-R	CCGGTACCCACTCTTGATCTTATTG
TBP-qRT-F	GCACAGGAGCCAAGAGTGAA
TBP-qRT-R	TCACAGCTCCCCACCATATT
HAT1-qRT-F	CGAGACTTTGTGCTTGTGAAGCT
HAT1-qRT-R	CCATATCTTCATTGAATCCTTGCA
KIAA1109-qRT-F	AAAGATGGGTGCAATTCGAG
KIAA1109-qRT-R	TCCGTAGCACTGCAGGCT
UACA-qRT-F	GGCAGATTGTCCTTCTAGCATACA
UACA-qRT-R	GTGGTGTCCGCCCGTCTAC
MRPL10-qRT-F	CTGTCCGCTATGGCTCCAA
MRPL10-qRT-R	TCTGCCGCTGAAAGTGCAT
KIAA1109-ChIP-F	GGTTGTTAGGGTAGCAAAGTGATTTT
KIAA1109-ChIP-R	CGCCCTGTTTCCTCCTCTCT
UACA-ChIP-F	CAGACGGAAGGGAAGGAACTT
UACA-ChIP-R	GCCTTTGCCACCTCTCATCTT
PDGFRA -ChIP-F	TTGAGCCCATTACTGTTGGA
PDGFRA -ChIP-R	ACGGCCTCCAATGATCTCTT
HAT -ChIP-F	GGGAAAGCAGTTCCTACAGCTACT
HAT-ChIP-R	TCTTGCATGCCACATGTCCTA
MRPL10-ChIP-F	CCTTACCCCGCTGTTTTCC
MRPL10-ChIP-R	TATTTTAGATCATGTCTGGAGGTGAGTAG