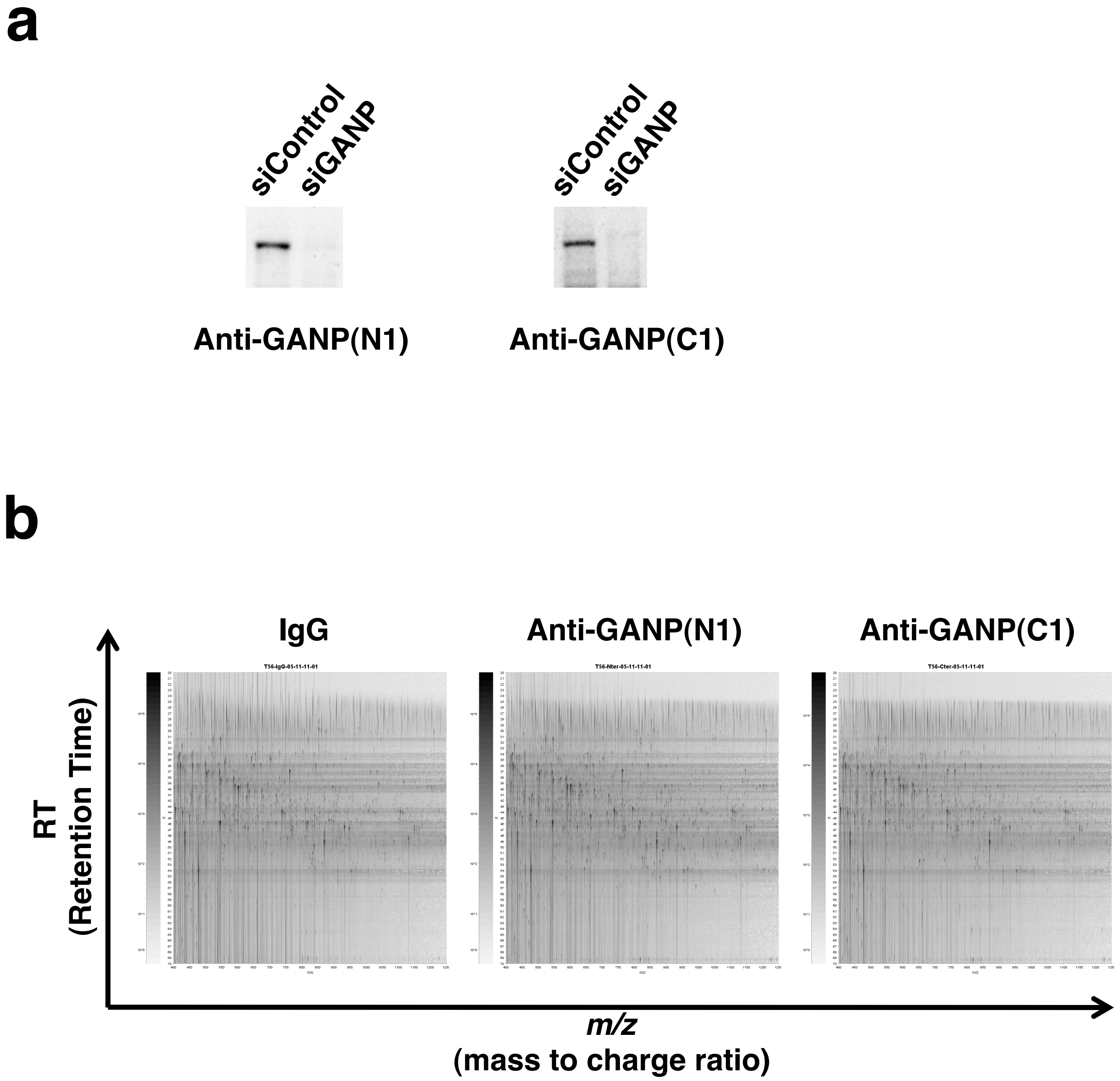
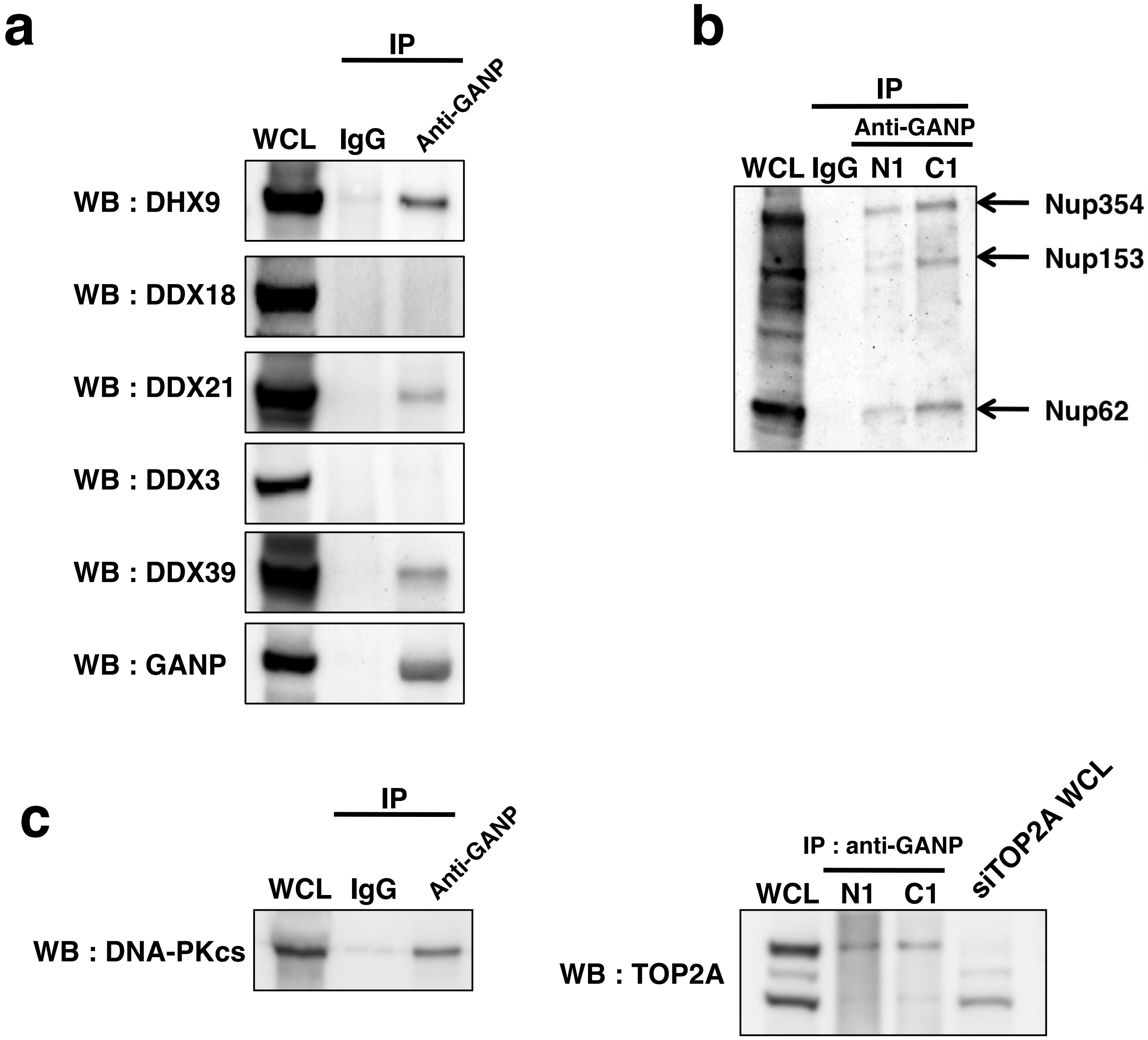
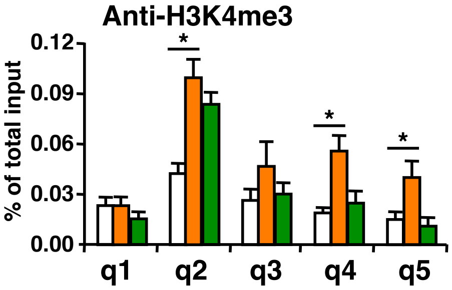


Supplementary Figure S1. 2DICAL analysis of GANP complex from Ramos nuclei. (a) Specificity of the Abs was confirmed by using GANP siRNA-treated cell extract. (b) Two-dimensional display of the entire set (>110,000) of MS peaks detected by 2DICAL with m/z values along the X-axis and retention time along the Y-axis. The images from IgG (left), anti-GANP(N1) Ab (middle), and anti-GANP(C1) Ab (right) were shown.



Supplementary Figure S2. GANP interacts with helicases, Nups, DNA-PKcs, and TOP2A in B-cell. Whole cell lysates (WCLs) from Ramos cells were IP using anti-GANP Ab. WB was carried out with indicated Abs. IgG was used as a negative control. WCL is shown in the left. Mab414 Ab recognized several Nup proteins. For the TOP2A analysis, siTOP2A-treated 293T cell extract was used as a control.



Supplementary Figure S3. ChIP-qPCR analysis of GFP-positive cells from GFP-alone (white columns), GFP-GANP (orange columns), and GFP-ΔHAT_G (green columns) transfectants by anti-H3K4me3 Abs.

a

AID-bound IgV

AID-bound IgV	GFP-alone	GFP-GANP
Sequence	47	54
Mutation	32	70
Total sequenced nt	17,390	19,980
Mutation frequency (X10^{-3})	1.8	3.5
G/A C/T mutated (%)	47	63

GFP-alone

To

From

	A	C	G	T
A		1	1	0
C	0		4	2
G	13	10		1
T	0	0	0	

GFP-GANP

To

From

	A	C	G	T
A		2	3	0
C	3		3	19
G	25	9		2
T	2	1	1	

b

H3K9ac-bound IgV

H3K9ac-bound IgV	GFP-alone	GFP-GANP
Sequence	22	25
Mutation	7	3
Total sequenced nt	8,140	9,250
Mutation frequency (X10^{-3})	0.9	0.3

GFP-alone

To

From

	A	C	G	T
A		0	1	0
C	0		1	2
G	3	0		0
T	0	0	0	

GFP-GANP

To

From

	A	C	G	T
A		0	0	0
C	0		0	1
G	1	0		0
T	0	1	0	

c

CTCF-bound IgV

CTCF-bound IgV	GFP-alone	GFP-GANP
Sequence	29	24
Mutation	8	5
Total sequenced nt	8,100	9,250
Mutation frequency (X10^{-3})	1.0	0.5

GFP-alone

To

From

	A	C	G	T
A		0	0	0
C	0		2	1
G	1	1		0
T	0	0	0	

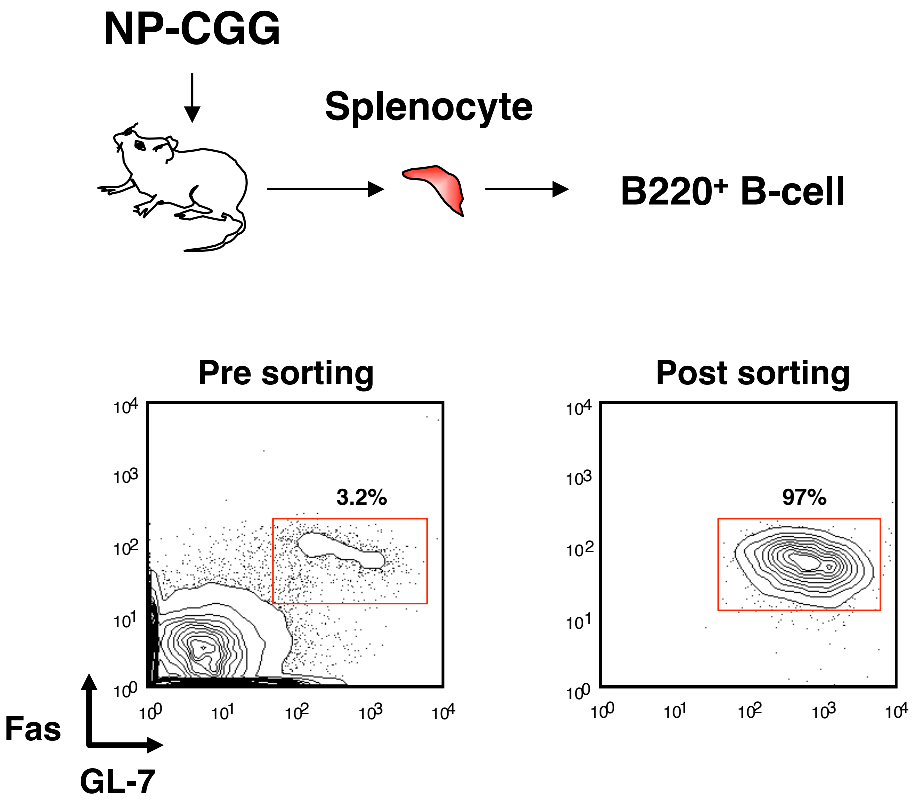
GFP-GANP

To

From

	A	C	G	T
A		0	0	0
C	0		1	0
G	3	1		2
T	1	0	0	

Supplementary Figure S4 Sequencing of the ChIP-bound IgV-region in GANP overexpressed Ramos cells.



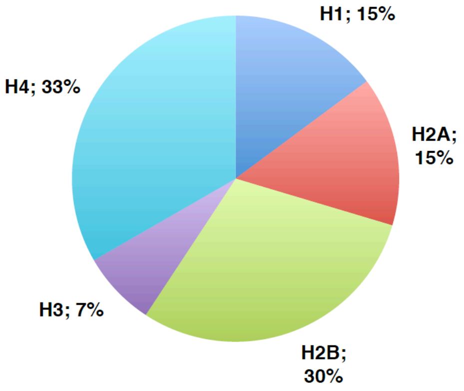
Supplementary Figure S5. Isolation of GC B-cells.
The AID accession to the *IgV_H-region* gene was examined in B-cells from *ganp* mutant mice. Mice were immunized by the peritoneal injection of NP-CGG (100 µg/mouse) in alum. After 14 days, splenic B220$^+$ cells were obtained by MACS-beads separation and the B220$^+$GL-7$^+$Fas$^+$ GC B-cells were purified (>95%). ChIP was examined by DNA-ChIP assay with the primers described in Supplementary Table S3.

Supplementary Table S1 | Potential GANP-interacting proteins in Ramos nuclei

Gene symbol	Description	Expect value	Sequence
RNA processing & splicing			
ARL6IP4	ADP–ribosylation factor–like protein 6–interacting protein 4	0.0000056	SAGEEEDGPVLTDEQK
		0.0000130	GDGEVLEEIVTK
HNRNPA2B1	Heterogeneous nuclear ribonucleoproteins A2/B1	0.0002800	IDTIEIITDR
HNRNPC	Heterogeneous nuclear ribonucleoproteins C1/C2	0.0004400	VPPPPPIAR
HNRNPU	Heterogeneous nuclear ribonucleoprotein U	0.0430000	NFILDQTNVSAAAQR
PNN	Pinin	0.0002200	VELAQLQEEWNEHNAK
PRPF19	Pre–mRNA–processing factor 19	0.0000460	TLQLDNNFEVK
RBM8A	RNA–binding protein 8A	0.0026000	GYTLVEYETYK
SNRPE	Small nuclear ribonucleoprotein E	0.0250000	VMVQPINLIFR
SFRS2B	Splicing factor, arginine/serine–rich 2B	0.0003000	VGDVYIPR
SFRS7/9G8	Splicing factor, arginine/serine–rich 7	0.0004300	AFSYYGPLR
		0.0000006	VYVGNLGTGAGK
SF3B3	Splicing factor 3B subunit 3	0.0000009	TVLDPVTGDLSDTR
SFRS10	Splicing factor, arginine/serine–rich 10	0.0002200	YGPIADVSIVYDQQSR
DKC1	H/ACA ribonucleoprotein complex subunit 4	0.0036000	LDTSQWPLLLK
FBL	rRNA 2' –O–methyltransferase fibrillarin	0.0000640	VSISEGDDKIEYR
		0.0037000	TNIIPVIEDAR
SRRM2	Serine/arginine repetitive matrix protein 2	0.0330000	TAAALAPASLTSAR
		0.0006100	TPQAPASANLVGPR
		0.0058000	ENSFGSPLEFR
		0.0073000	SSTGPEPPAPTPLLAER
Nuclear envelope			
AHCTF1/ELYS	AT–hook–containing transcription factor 1	0.0000540	VAIAENLLDVIK
LMNB1	Lamin–B1	0.0005500	AGGPTTPLSPTR
		0.0000092	ALYETELADAR
		0.0001600	SMYEEEINETR
		0.0055000	LSSEMNTSTVNSAR
		0.0004700	LREYEAALNSK
		0.0002100	LALDMEINAYR
NUP160	Nucleoporin Nup160	0.0340000	TAPLLLSYYLIK
NUP107	Nucleoporin Nup107	0.0061000	SGFGEISSPVIR
NUP85	Nucleoporin Nup85	0.0000640	IMLGDEAALLEQK
RNA helicase			
DDX9	DEAH box protein 9	0.0380000	DFVNYLVR
		0.0005200	ISAVSVAER
DDX18	DEAD (Asp–Glu–Ala–Asp) box protein 18	0.0490000	LGNGINIIVATPGR
DDX21	DEAD (Asp–Glu–Ala–Asp) box protein 21	0.0000400	VSVFFGGLSIK
Chromatin regulation			
NSD	Nuclear receptor binding SET domain protein	0.0390000	DRIIDAGPK
CIR	CBF1–interacting corepressor	0.0050000	DQPFGIQVR
NPM1	Nucleophosmin	0.0000003	MSVQPTVSLGGFEITPPVVLR

Supplementary Table S2 | GANP-interacting histones in Ramos nuclei

Gene symbol	Expect value	Sequence
Histones		
Histone H1.2	0.000063	SGVSLAALK
Histone H1.5	0.000110	ATGPPVSELITK
Histone H1.5	0.008700	ALAAGGYDVEK
Histone H1t	0.000100	ALAAAGYDVEK
Histone H2A	0.000001	AGLQFPVGR
Histone H2A	0.000000	VTIAQGGVLPNIQAVLLPK
Histone H2A	0.000000	VTIAQGGVLPNIQAVLLPK
Histone H2A	0.000930	GDEELDSLIK
Histone H2B	0.000150	ESYSIYVYK
Histone H2B	0.000000	AMGIMNSFVNDIFER
Histone H2B	0.000008	AMGIMNSFVNDIFER
Histone H2B	0.000000	AMGIMNSFVNDIFER
Histone H2B	0.000000	AMGIMNSFVNDIFER
Histone H2B	0.000000	AMGIMNSFVNDIFER
Histone H2B	0.000220	LLLPGELAK
Histone H2B	0.035000	KESYSVYVYK
Histone H3	0.001800	STELLIR
Histone H3	0.006700	YRPGTVALR
Histone H4	0.000001	DNIQGITKPAIR
Histone H4	0.000001	ISGLIYEETR
Histone H4	0.000000	TVTAMDVVYALK
Histone H4	0.002100	TVTAMDVVYALK
Histone H4	0.000009	TVTAMDVVYALK
Histone H4	0.000000	TVTAMDVVYALK
Histone H4	0.000082	KTVTAMDVVYALK
Histone H4	0.000005	DNIQGITKPAIR
Histone H4	0.001000	VFLENVIR



Supplementary Table S3 | Primers, probes, and siRNA

	sense	antisense
q1	GGCACAGCCAGCATACACCT	AGGATTTGCATGTGGGTGGT
q2	CATGCAAATCCTCACTTAGGCA	AGGTCCATGACTCTCAGAAAGCA
q3	GCTTTCTGAGAGTCATGGACCTC	CGCATTCCTGAGACACTCACAT
q4	CAGCAACTACAACCCGTCCC	TGTCCGCGGCGTTC
q5	GACACGTCCAAGAAACAGC	GCCCTAGTAATAACTCTCGC
DP63-01	ATGAAACACCTGTGGTTCTTCCTCCTCCTG	TGGGATCAGAGGCAGCATCTCATATCTTCA
DP63-02	GTGGCAGCTCCCAGATGTGAGTGTCTCAGG	CCTGTGAACAGAAAAACCCACAGTGAGCCC
DP63-03	AATGCGGATATGAAGATATGAGATGCTGCC	CACTGCTGTAGCTGCACCTGGGACAGGACC
DP63-04	TCTGATCCCAGGGCTCACTGTGGGTTTTTC	GTCTCCGAAGGCTTCAACAGTCCTGCGCCC
DP63-05	TGTTCACAGGGGTCCTGTCCCAGGTGCAGC	CCACCATAAACACCGCAGGTGAGGGACAGG
DP63-06	TACAGCAGTGGGGCGCAGGACTGTTGAAGC	ATCCAGCTCCAGTAGTAACCACTGAAGGAC
DP63-07	CTTCGGAGACCCTGTCCCTCACCTGCGGTG	CACTCCAGCCCCTTCCCTGGGGGCTGGCGG
DP63-08	TTTATGGTGGGTCCTTCAGTGGTTACTACT	CTGCTTCCACTATGATTGATTTCCCCAATC
DP63-09	GGAGCTGGATCCGCCAGCCCCCAGGGAAGG	ACTCGACTCTTGAGGGACGGGTTGTAGTTG
DP63-10	GGCTGGAGTGGATTGGGGAAATCAATCATA	TGTTTCTTGGACGTGTCTACTGATATGGTG
DP63-11	GTGGAAGCAGCAACTACAACCCGTCCCTCA	GCGTTCACAGAGCTCAACTTCAGGGAGAGC
DP63-12	AGAGTCGAGTCACCATATCAGTAGACACGT	CTCGCACAGTAATACACAGCCGTGTCCGCG
DP63-13	CCAAGAAACAGCTCTCCCTGAAGTTGAGCT	TCTGTGCCAGGACTCGCCCTAGTAATAACT
DP63-14	CTGTGAACGCCGCGGACACGGCTGTGTATT	TGGCCCCAGACGTCCATACCGTACCTCCCG
DP63-15	ACTGTGCGAGAGTTATTACTAGGGCGAGTC	CTGAGGAGACGGTGACCGTGGTCCCT
VH186.2	CTGCAAGGCTTCTGGCTACAC	TCAATCCTTCCAATCCACTC
p53	ACAGCGTGGTGGTACCTTAT	TATACTCAGAGCCGGCCT

	TaqMan probe
mAICDA	Mm00507774_m1
mGANP	Mm00490242_m1
mGAPDH	Mm99999915_g1

	MISSION siRNA
GANP	SASI_Hs01_00195876
TOP2A	SASI_Hs02_00311873
control	SIC-001