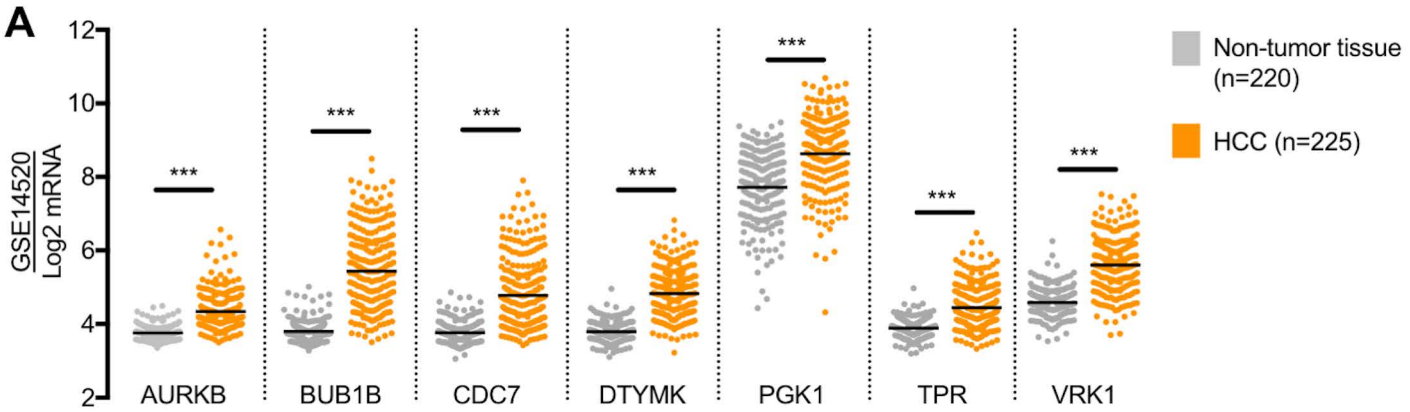
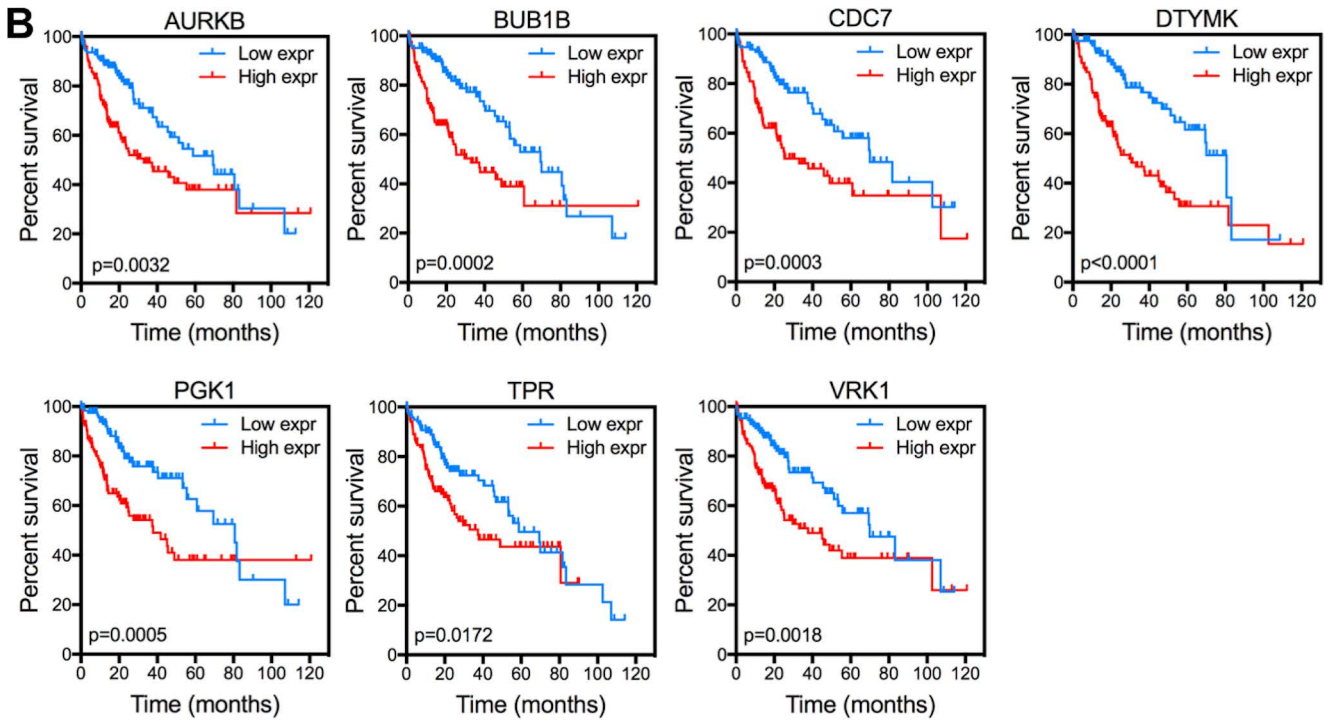
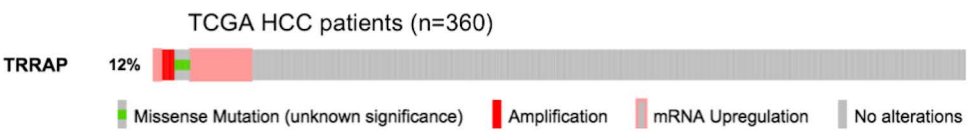
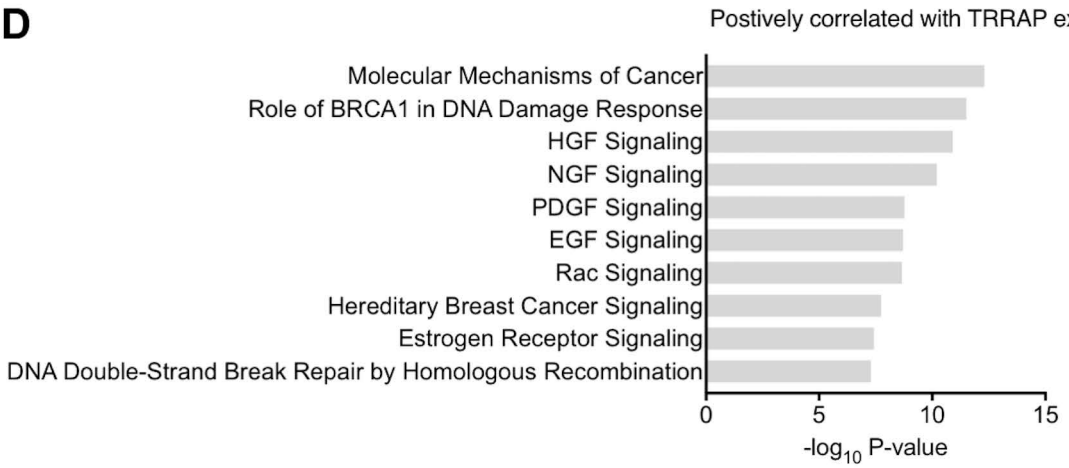
Supplementary fig. 1



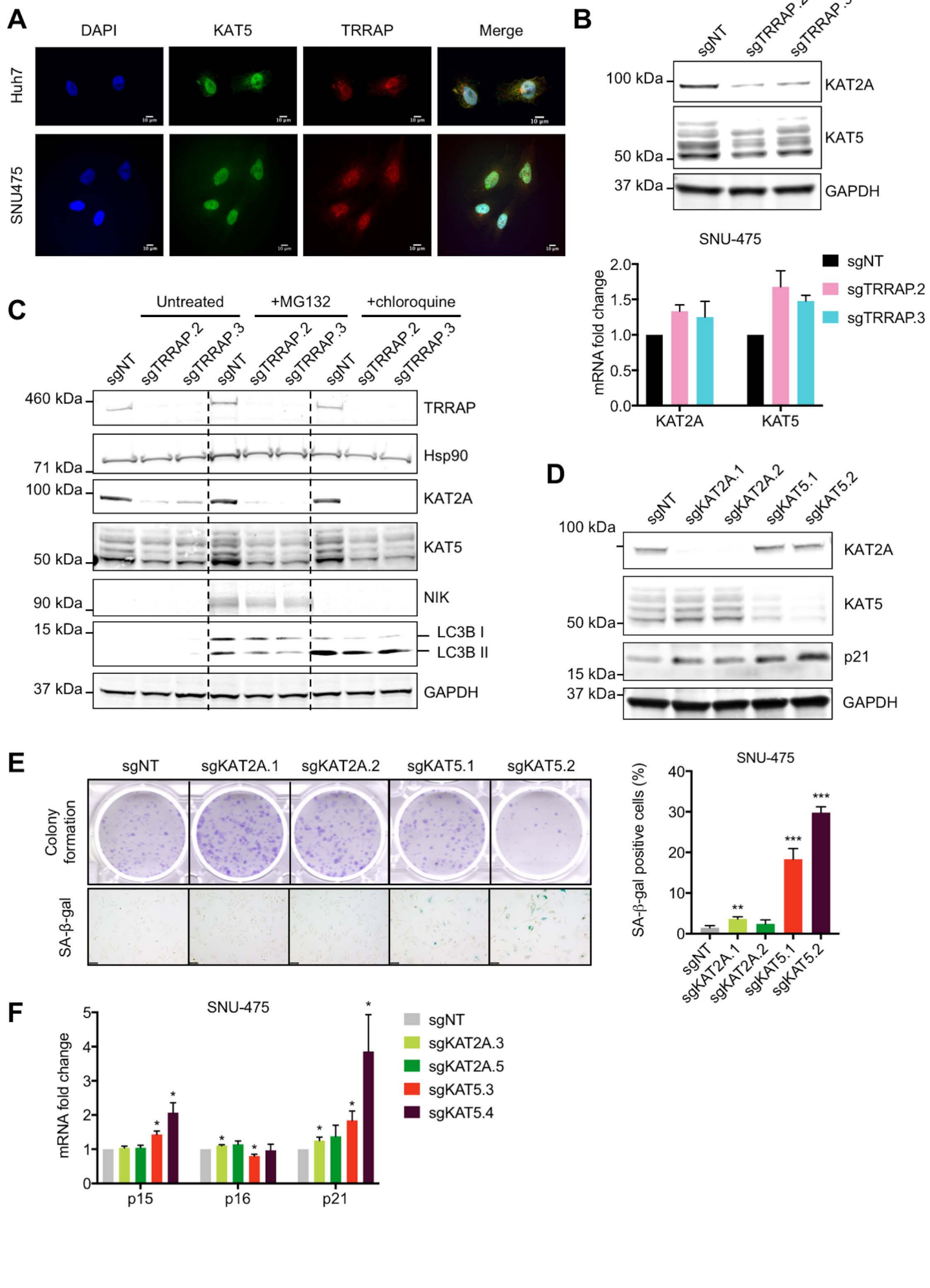




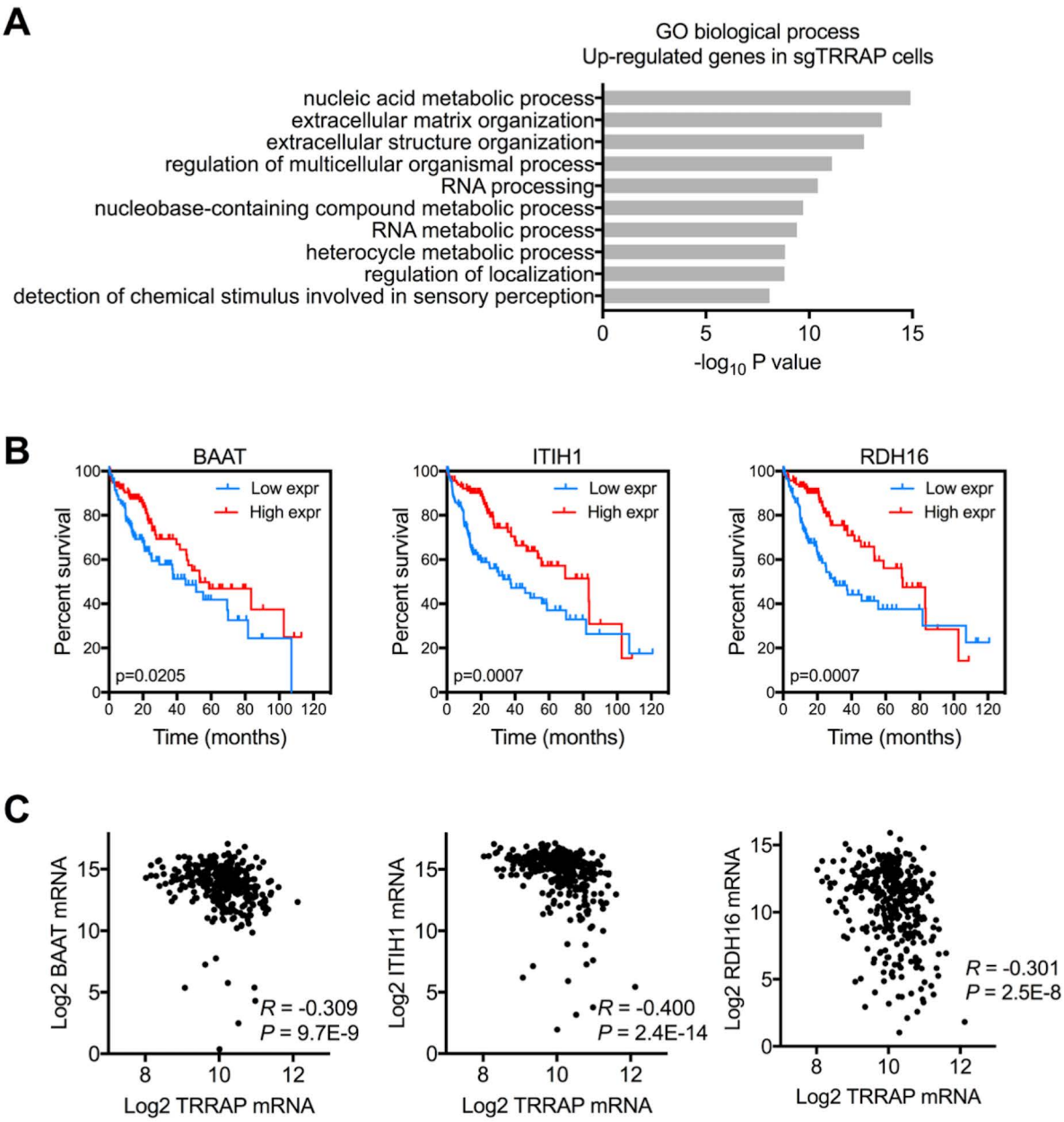
Sample ID	Mutation
TCGA-DD-A4NV-01	V2970M
TCGA-CC-A7IF-01	Q1940L
TCGA-DD-AACC-01	H1262R
TCGA-BC-A10U-01	D408G
TCGA-WQ-A9G7-01	R1144C
TCGA-DD-A39X-01	H634Y
TCGA-DD-A3A0-01	Q2662R
TCGA-DD-A3A0-01	E2803Nfs*29
TCGA-EP-A2KB-01	R1544L



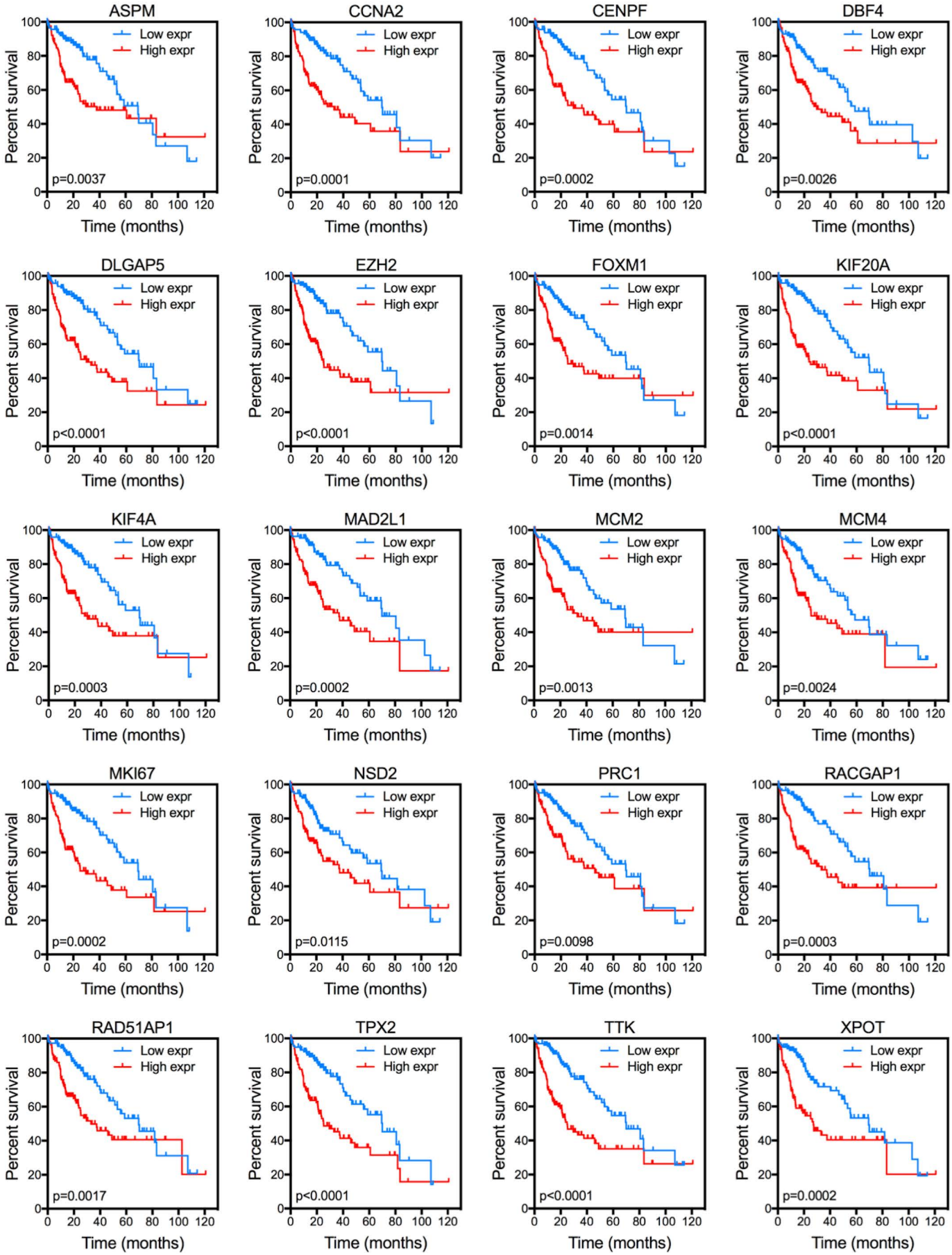
Supplementary fig. 2



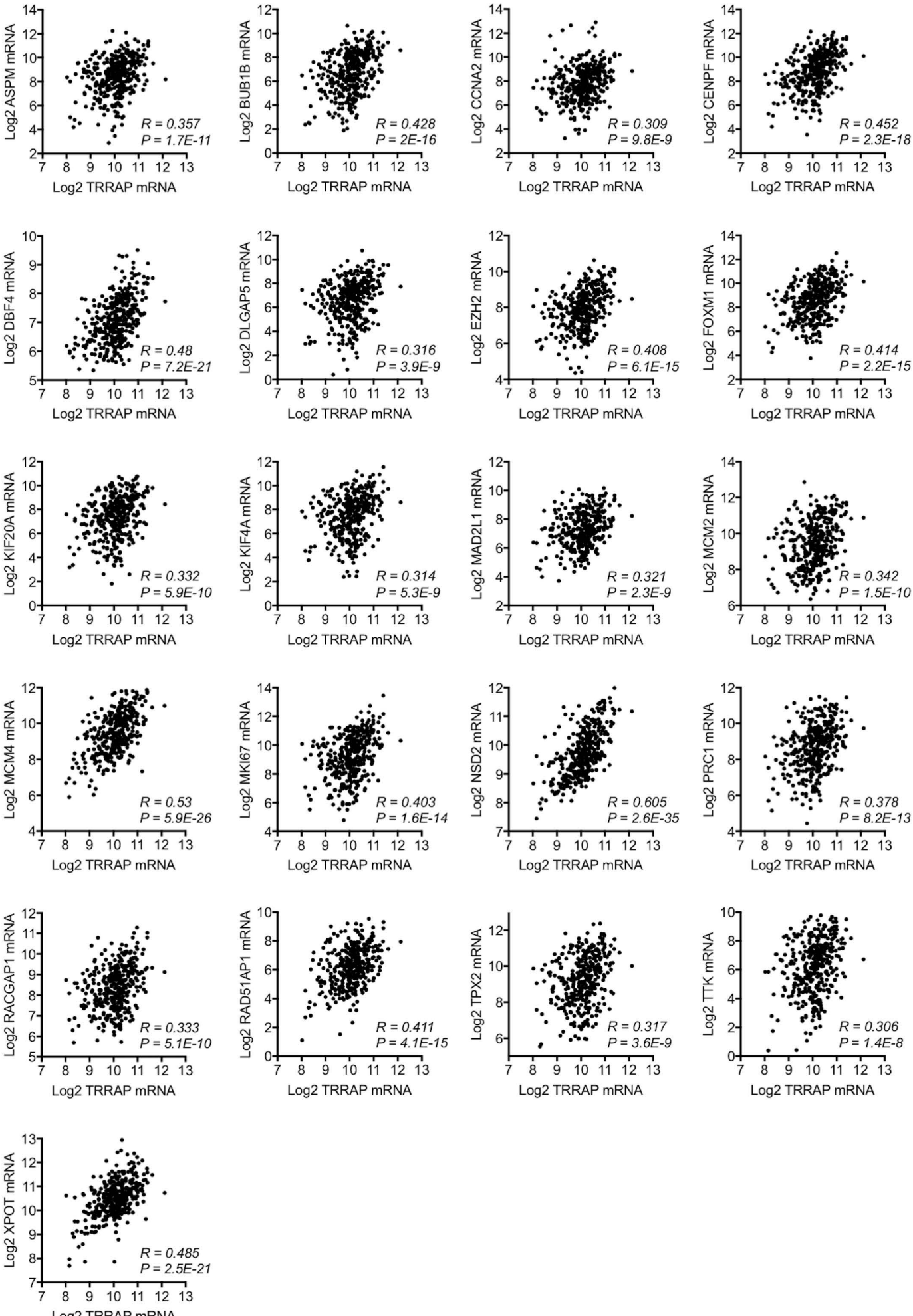
Supplementary fig. 3



Supplemental fig. 4

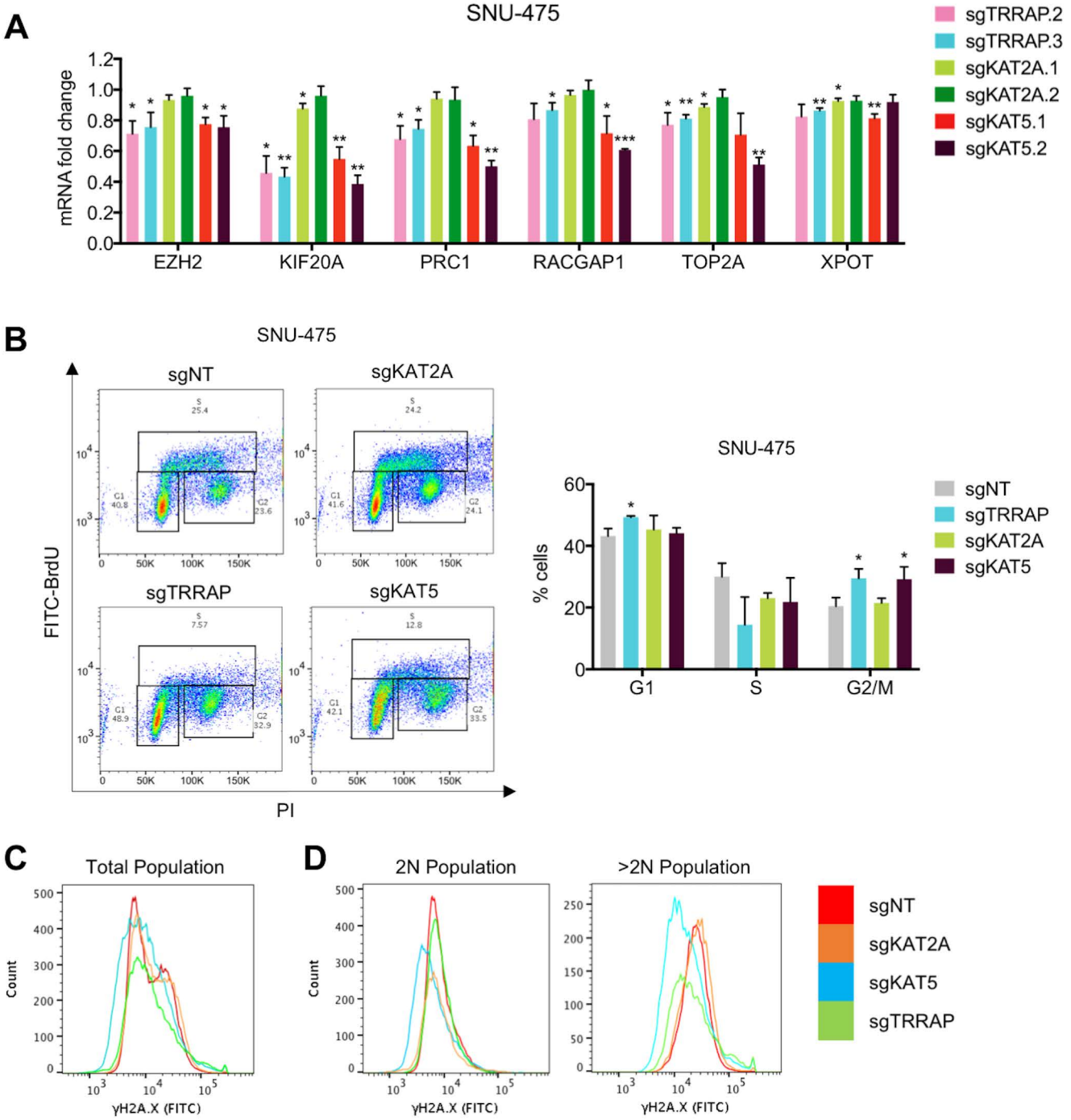


Supplemental fig. 5

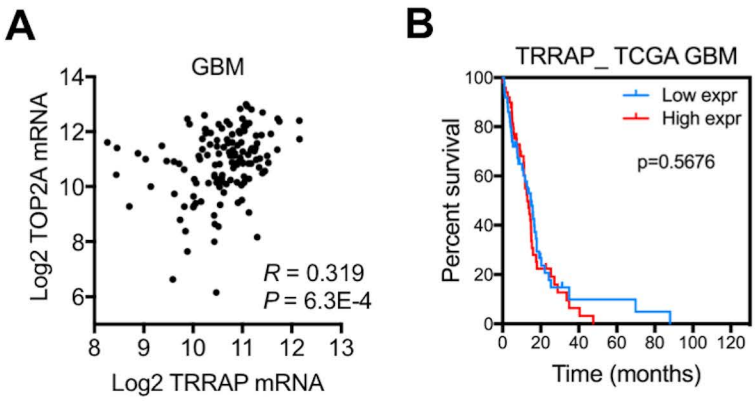


Supplemental fig. 6

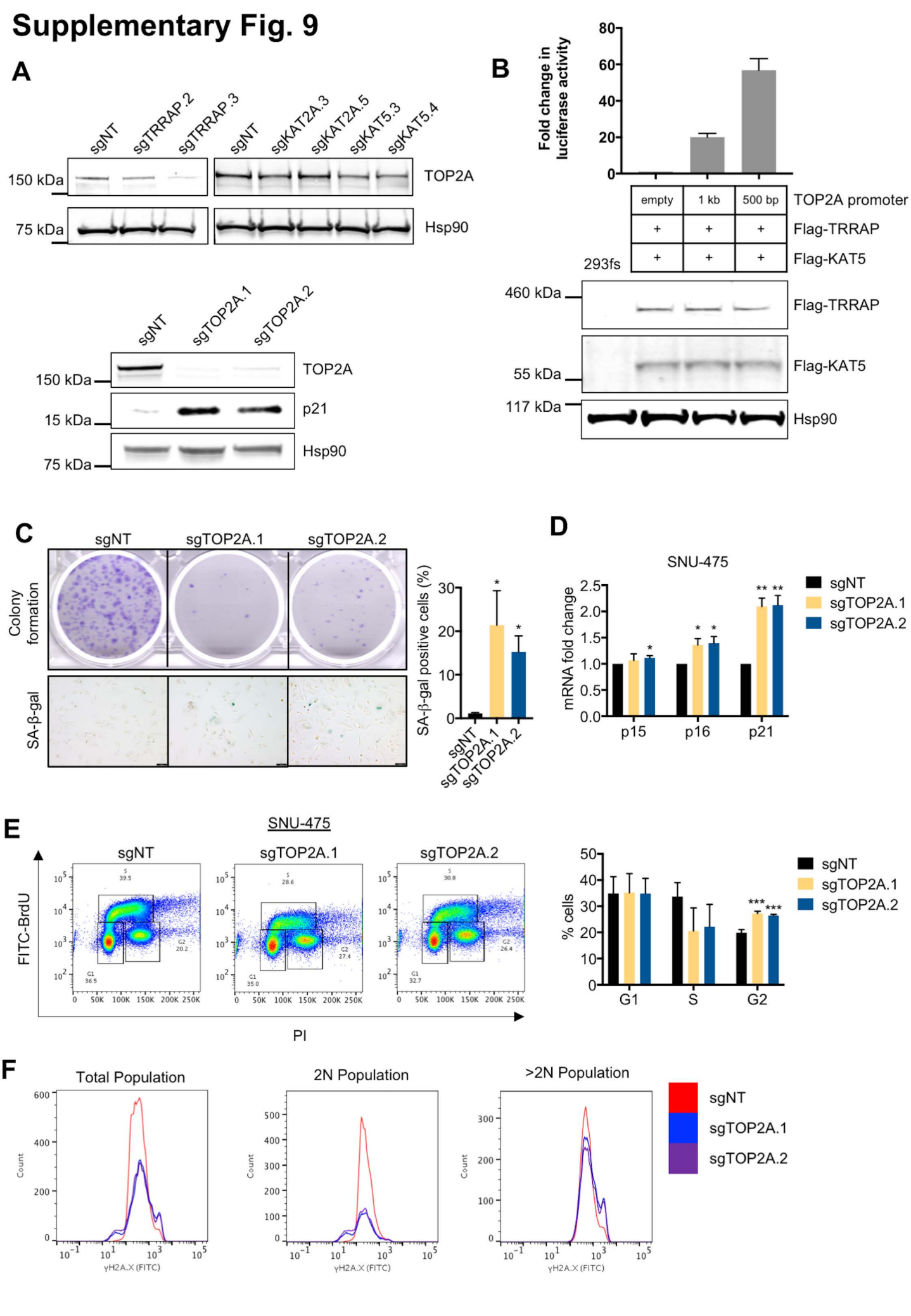
Supplementary Fig. 7



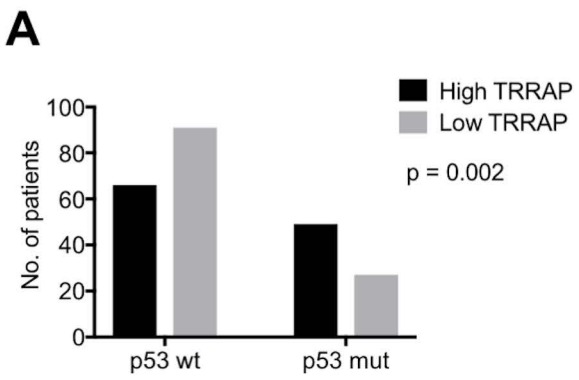
Supplementary Fig. 8



Supplementary Fig. 9



Supplementary Fig. 10



Supplementary Table 1. sgRNA sequences used in this study.

sgRNA name	Sequence (5'-3')
sgTRRAP.1	ACTCCTGATACAAGAGATCG
sgTRRAP.2	CTTGATCCGCCACTATACGA
sgTRRAP.3	CCACTGGGGATCGTTCAGTG
sgKAT2A.1	GCTGCTGGAAAAGTTCCGAG
sgKAT2A.2	TCACCATGCCACCCTCAGAG
sgKAT5.1	GATTGATGGACGTAAGAACA
sgKAT5.2	ACCAGGCTGCCAGTCATGCG
sgp21	GTCACCGAGACACCACTGGA
sgTOP2A.1	TGTACGCTTATCCTGACTGA
sgTOP2A.2	GATGCTGCTATCAGCCTGGT

Supplementary Table 2. Primers used for qRT-PCR in this study.

Primer name	Sequence (5'-3')
p15-F	AAGCTGAGCCCAGGTCTCCTA
p15-R	CCACCGTTGGCCGTAAACT
p16-F	CCCAACGCACCGAATAGTTA
p16-R	ACCAGCGTGTCCAGGAAG
p21-F	CAGCAGAGGAAGACCATGTG
p21-R	GAGGCACAAGGGTACAAGACA
KAT2A-F	CAGGGTGTGCTGAACTTTGTG
KAT2A-R	TCCAGTAGTTAAGGCAGAGCAA
KAT5-F	GGGGAGATAATCGAGGGCTG
KAT5-R	TCCAGACGTTTGTTGAAGTCAAT
EZH2-F	AATCAGAGTACATGCGACTGAGA
EZH2-R	GCTGTATCCTTCGCTGTTTCC
KIF20A-F	GCCAACTTCATCCAACACCT
KIF20A-R	GTGGACAGCTCCTCCTCTTG
PRC1-F	ATCACCTTCGGGAAATATGGGA
PRC1-R	TCTTTCTGACAGACGGATATGCT
RACGAP1-F	CTATGATGCTGAATGTGCGG
RACGAP1-R	AATCCTCAAAGTCCTTCGCC
TOP2A-F	ACCATTGCAGCCTGTAAATGA
TOP2A-R	GGGCGGAGCAAAATATGTTCC

XPOT-F	AGGGAGACGCTCATATCATGG
XPOT-R	TTGGGCGGCTTTATTTCGTAT

Supplementary Table 3. List of genes that are up-regulated in the absence of TRRAP and identified from our bioinformatics analyses.

Gene Symbol	Entrez gene name	RNA-seq sgTRRAP/sgNT		GSE14520 HCC/ non-tumor tissue		TCGA HCC co-expressed with TRRAP	
		Fold change	P-value	Fold change	P-value	Spearman's coefficient	P-value
BAAT	bile acid-CoA:amino acid N-acyltransferase	10.79	4.0E-40	0.41	5.4E-22	-0.309	9.7E-09
ITIH1	inter-alpha-trypsin inhibitor heavy chain 1	2.05	2.9E-03	0.41	1.1E-32	-0.4	2.4E-14
RDH16	retinol dehydrogenase 16	3.54	4.9E-02	0.14	1.3E-73	-0.301	2.5E-08

Supplementary Table 4. TRRAP regulates a similar set of genes in HCC and GBM.

Gene symbol	Spearman's Correlation	p-Value
ASPM	**0.484**	**2.6E-08**
BUB1B	**0.315**	**7.6E-04**
CCNA2	0.117	2.8E-01
CENPF	**0.554**	**5.2E-11**
DBF4	0.139	1.9E-01
DLGAP5	0.211	3.3E-02
EZH2	**0.408**	**5.7E-06**
FOXM1	**0.437**	**8.5E-07**
KIF20A	**0.324**	**5.0E-04**
KIF4A	**0.418**	**2.9E-06**
MAD2L1	-0.084	4.5E-01
MCM2	**0.393**	**1.3E-05**
MCM4	**0.544**	**1.4E-10**
MKI67	**0.590**	**1.3E-12**
NSD2	**0.569**	**1.2E-11**
PRC1	**0.347**	**1.6E-04**
RACGAP1	0.136	2.0E-01
RAD51AP1	-0.036	7.7E-01
TOP2A	**0.319**	**6.3E-04**

TPX2	**0.375**	**3.8E-05**
TTK	0.177	8.2E-02
XPOT	0.205	3.9E-02

Supplementary Table 5. Primers used for cloning the TOP2A promoter.

Primer name	Sequence (5'-3')
TOP2A 500bp F	CTTACGCGTGCTAGCCCTCTCTAGTCCCGC
TOP2A 500bp R	TATATACCCGAATTCTTCACTACTAGCACC
TOP2A 1kb F	CTTACGCGTGCTAGCCATTCCCCTCGCTAA
TOP2A 1kb R	TATATACCCGAATTCCTCAGGAAGGGGGCG