

Figure S1

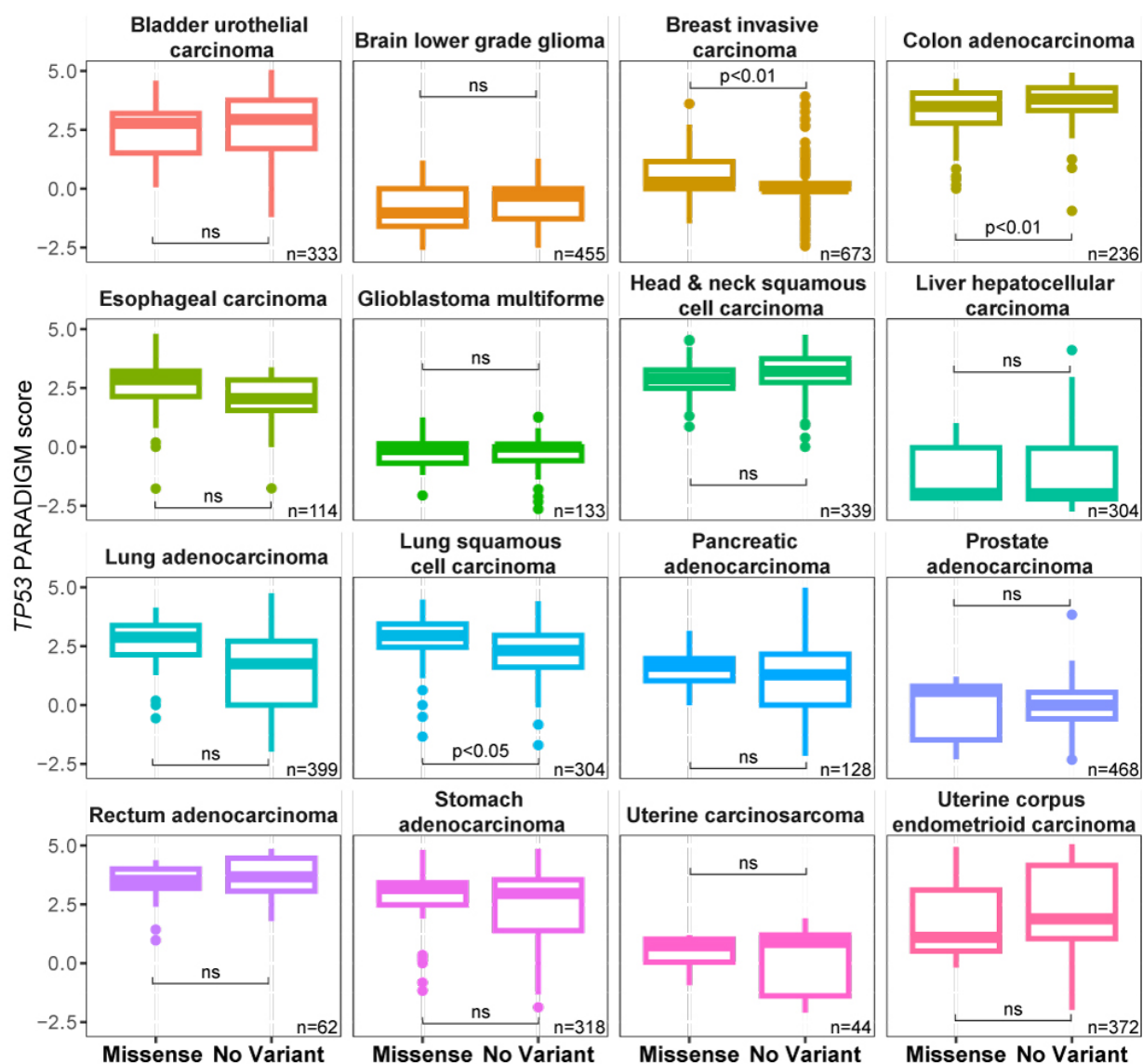


Figure S1. TP53 PARADIGM score in selected tumors comparing two subgroups: p53 missense mutations versus no variant.

Figure S2

Breast invasive carcinoma: 1067 patients

Genes correlated	Pearson's rho (r)	P-value
TMUB1-BAX	0,67	5,56e ⁻¹⁴¹
TMUB1-BBC3	0,59	1,69e ⁻¹⁰⁰
TMUB1-NOXA1	0,57	5,28e ⁻⁹¹

Heatmap correlation index

	BAX	BBC3	NOXA1
2-1	*** p <0.001	*** p <0.001	*** p <0.001
3-1	*** p <0.001	*** p <0.001	*** p <0.001
4-1	*** p <0.001	*** p <0.001	*** p <0.001
3-2	*** p <0.001	*** p <0.001	*** p <0.001
4-2	*** p <0.001	*** p <0.001	*** p <0.001
4-3	*** p <0.001	*** p <0.001	*** p <0.001

Quartiles comparison

Lung adenocarcinoma: 475 patients

Genes correlated	Pearson's rho (r)	P-value
TMUB1-BAX	0,41	5,23e ⁻²¹
TMUB1-BBC3	0,46	4,98e ⁻²⁶
TMUB1-NOXA1	0,43	9,88e ⁻²³

Heatmap correlation index

	BAX	BBC3	NOXA1
2-1	*** p <0.001	*** p <0.001	** p =0,008
3-1	*** p <0.001	*** p <0.001	*** p <0.001
4-1	*** p <0.001	*** p <0.001	*** p <0.001
3-2	ns p =0,945	ns p =0,473	ns p =0,101
4-2	* p =0,032	* p =0,014	*** p <0.001
4-3	ns p =0,130	ns p =0,394	ns p =0,187

Quartiles comparison

Pancreatic adenocarcinoma: 164 patients

Genes correlated	Pearson's rho (r)	P-value
TMUB1-BAX	0,51	2,49e ⁻¹²
TMUB1-BBC3	0,72	2,47e ⁻²²
TMUB1-NOXA1	0,75	8,25e ⁻³²

Heatmap correlation index

	BAX	BBC3	NOXA1
2-1	ns p =0,104	*** p <0.001	*** p <0.001
3-1	*** p <0.001	*** p <0.001	*** p <0.001
4-1	*** p <0.001	*** p <0.001	*** p <0.001
3-2	ns p =0,422	ns p =0,316	ns p =0,999
4-2	*** p <0.001	*** p <0.001	* p =0,034
4-3	* p =0,019	* p =0,014	* p =0,037

Quartiles comparison

Figure S2. Correlation values related to heatmap showed in Figure 6 into selected tumors data. The tables on the left display the p-value of comparison in HOPS/TMUB1 quartiles among the apoptotic genes BAX, BBC3 and NOXA1.

Table 1. Primer sequences used in the RT-qPCR assays.

Target	Primer name	Sequence (5'→3')
<i>β-actin</i>	β-actin H F	CACTCTTCCAGCCTTCCT
	β-actin H R	CAGGTCTTTGCGGATGTC
<i>Myc</i>	Myc H F	CACACATCAGCACAACTACG
	Myc H R	CTGTCCAACCTTGACCCTCTT
<i>Tp63</i>	TP63 H F	CGTGTCCTTCCAGCAGTC
	TP63 H R	GGCAGTAGAGTTTCTTCAGTTCA

Figure S3

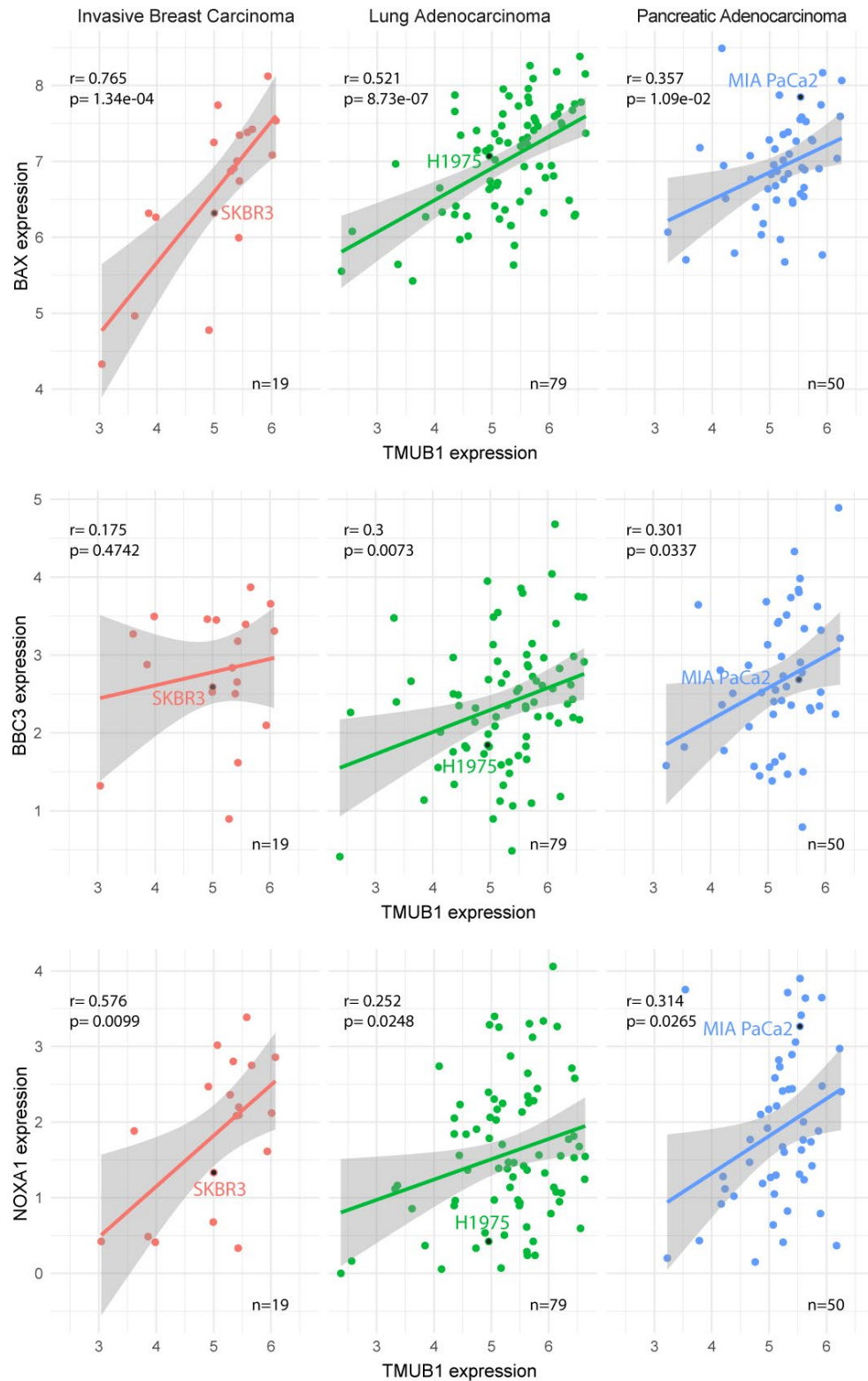


Figure S3. Correlation analysis in selected cell lines type (Invasive Breast Carcinoma, n=19; Lung Adenocarcinoma, n=79; Pancreatic Adenocarcinoma, n=50) between *TMUB1* expression and the apoptotic genes analysed (*BAX*, *BBC3* and *NOXA1*). Correlation score is reported in each scatter plot. Regression line is shown to estimate the linear relationship between the genes.

FACS analysis raw data

Samples identification:

SAMPLE 1) Control

SAMPLE 2) Dead cells (FVD)

SAMPLE 3) FVD control

SAMPLE 4) Cy7 control

SAMPLE 5) GFP control

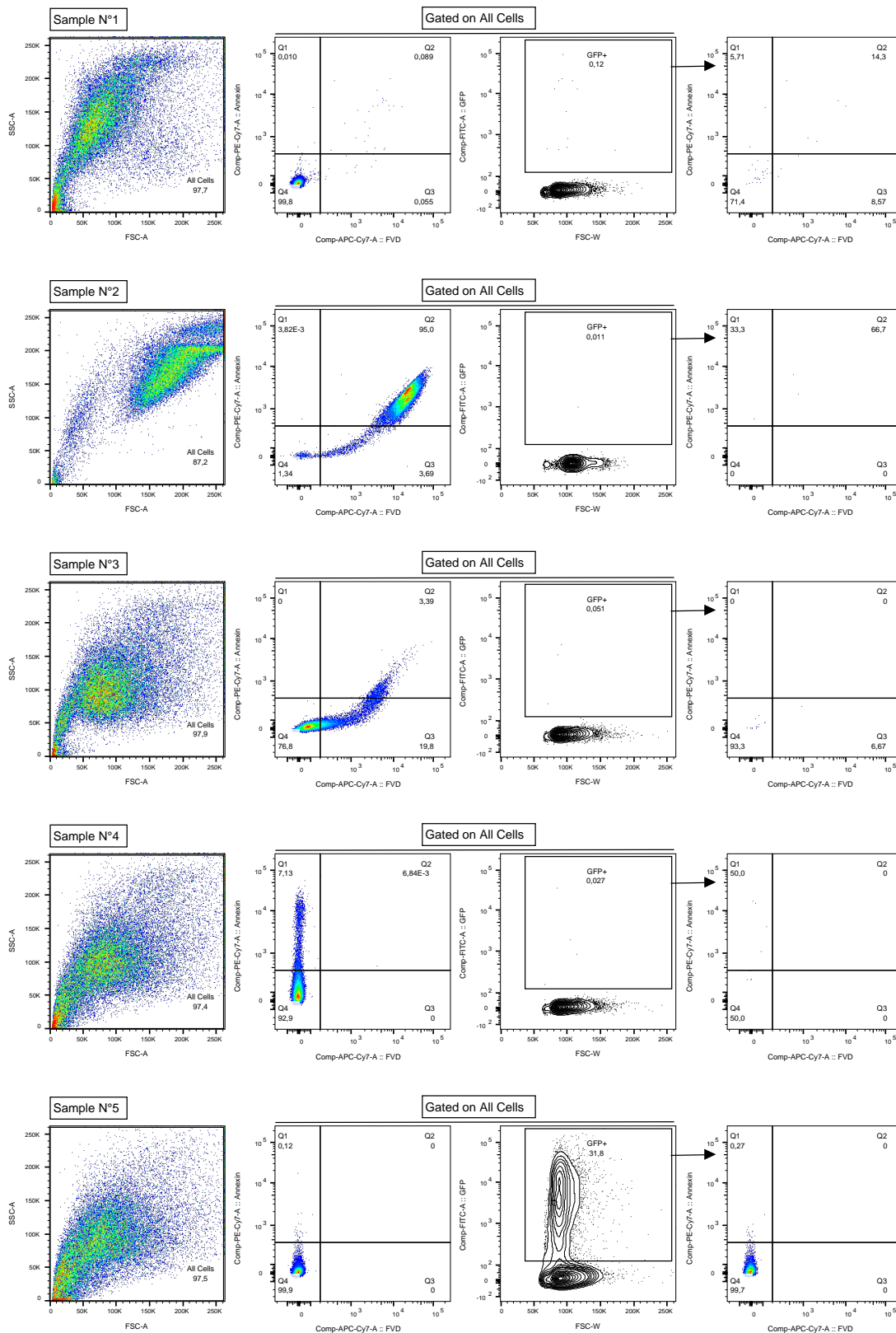
SAMPLE 6) GFP + FVD control

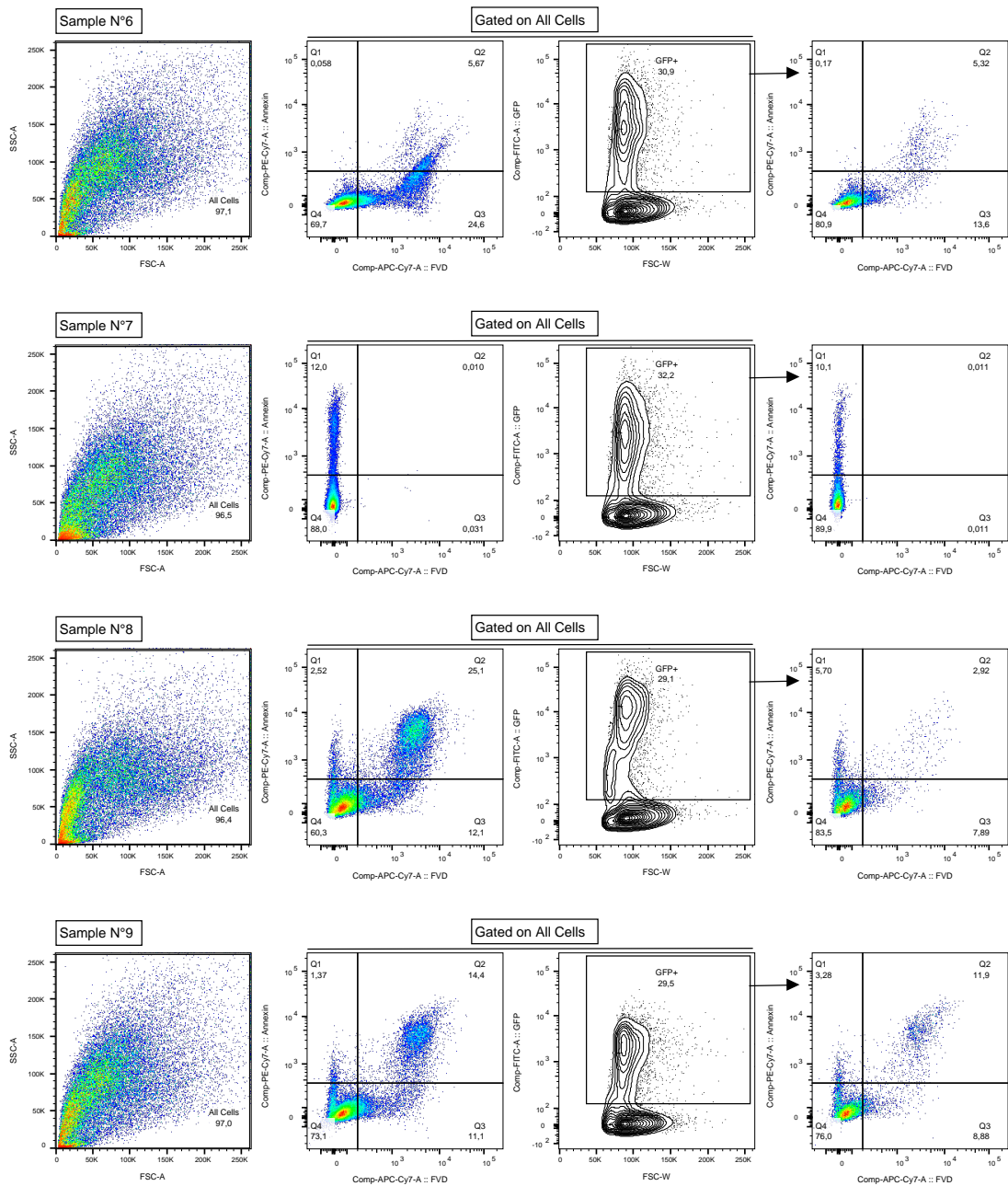
SAMPLE 7) GFP + Cy7 control

SAMPLE 8) pEGFP-N1 (+GFP)

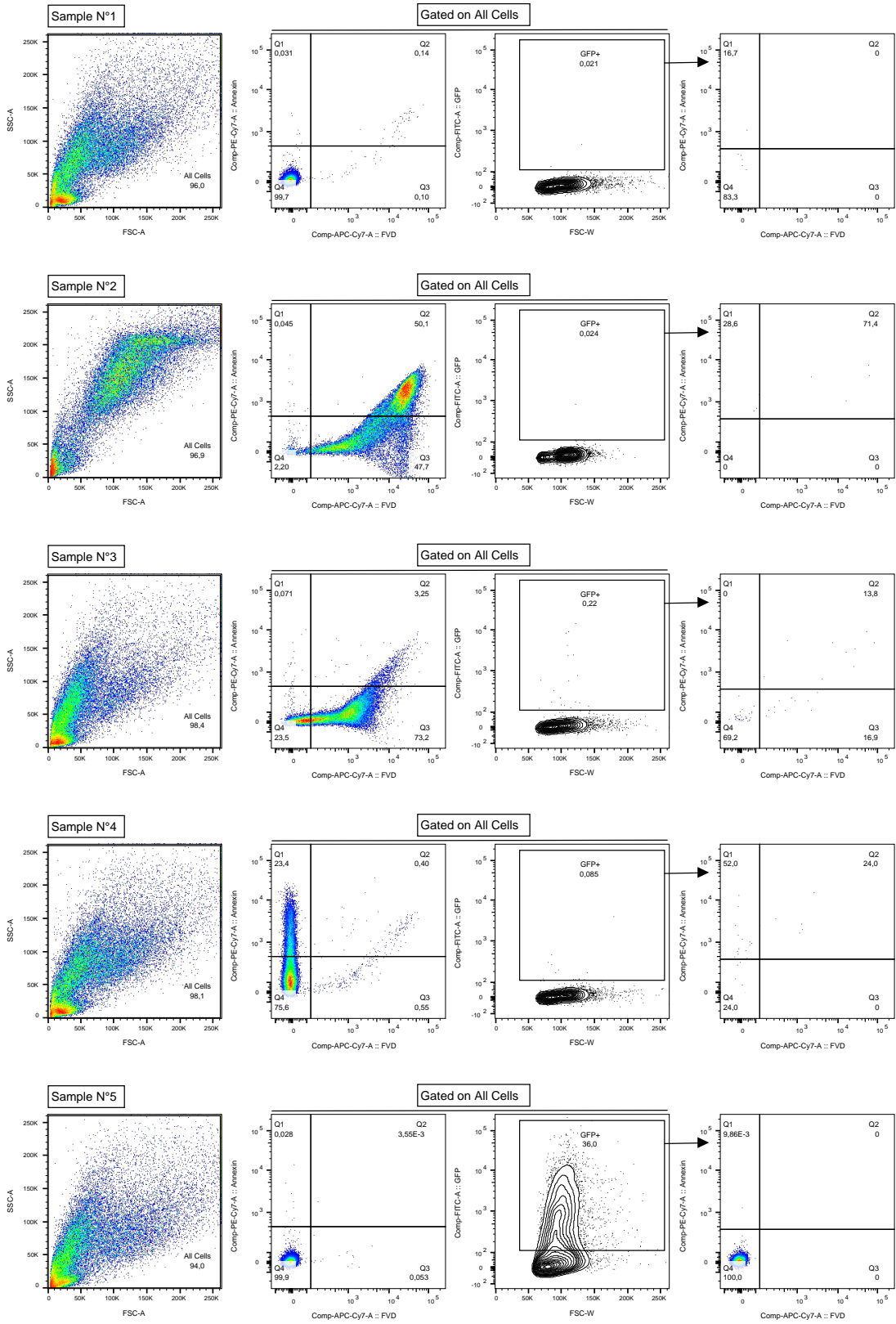
SAMPLE 9) pEGFP-N1-HOPS (+HOPS-GFP)

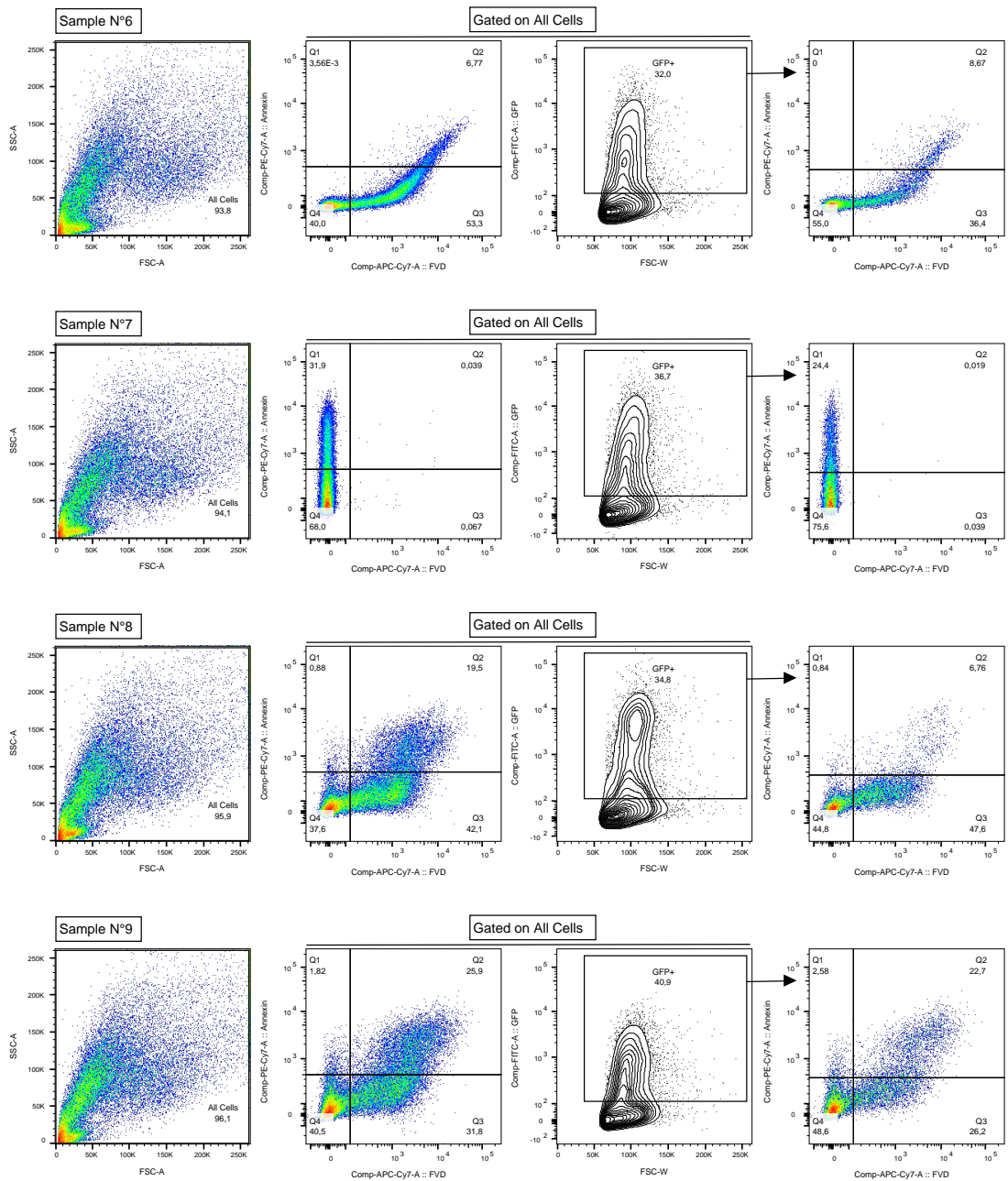
SKBR3



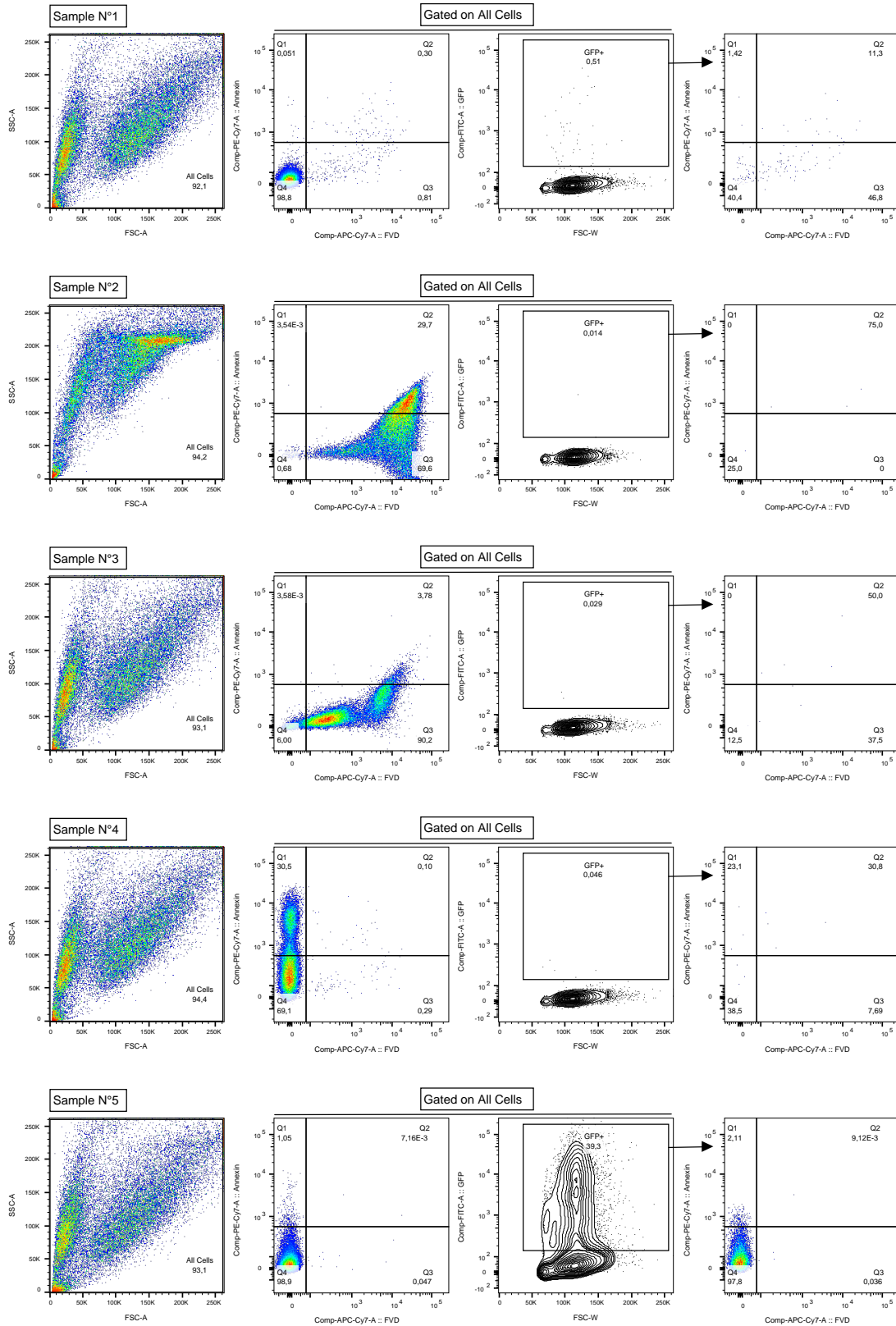


MIA PaCa 2





H1975



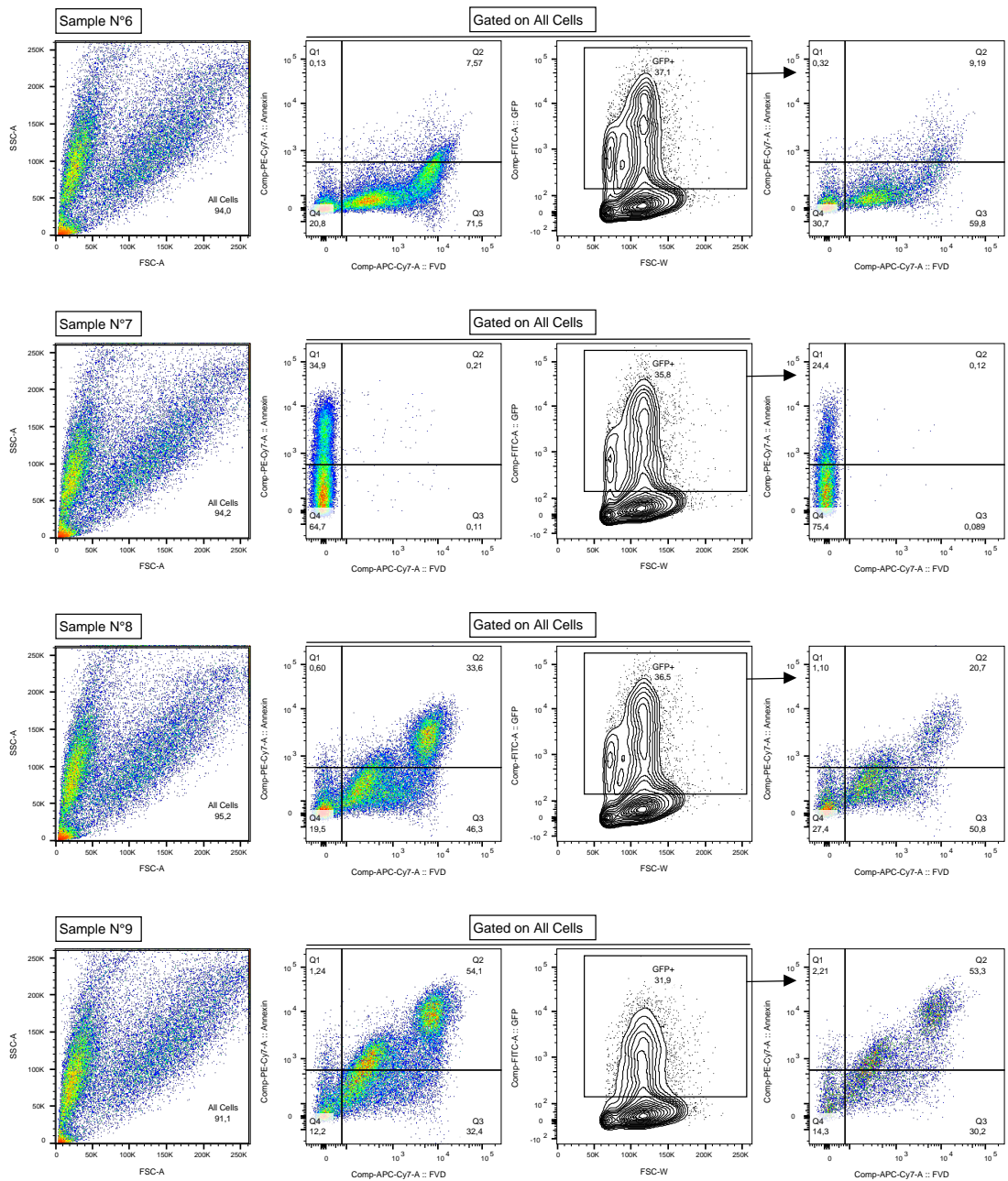


Table S2. Tumors selection workflow

	Mutations count in <i>TP53</i> DBD					Selected tumors Mutation counts per tumor type	
	R175	R213	R248	R273	R282		
Adrenocortical cancer	0	0	0	1	0		1
Bladder urothelial carcinoma	3	1	20	7	2	X	33
Brain lower grade glioma	8	1	11	66	6	X	92
Breast invasive carcinoma	15	0	7	17	3	X	42
Cholangiocarcinoma	0	0	1	0	0		1
Colon adenocarcinoma	17	2	19	16	10	X	64
Diffuse large B-cell lymphoma	0	0	1	1	0		2
Esophageal carcinoma	9	0	13	10	6	X	38
Glioblastoma multiforme	3	0	4	4	1	X	12
Head & neck squamous cell carcinoma	6	1	16	14	10	X	47
Kidney chromophobe	0	0	0	0	1		1
Kidney clear cell carcinoma	0	1	1	0	0		2
Liver hepatocellular carcinoma	1	2	3	2	0	X	8
Lung adenocarcinoma	1	0	5	9	2	X	17
Lung squamous cell carcinoma	8	2	10	15	5	X	40
Mesothelioma	0	0	0	2	0		2
Pancreatic adenocarcinoma	4	0	8	5	3	X	20
Prostate adenocarcinoma	2	0	5	1	2	X	10
Rectum adenocarcinoma	7	1	7	7	8	X	30
Sarcoma	5	1	4	1	0		11
Stomach adenocarcinoma	12	0	7	17	6	X	42
Thymoma	0	0	1	1	0		2
Uterine carcinosarcoma	2	0	7	4	0	X	13
Uterine corpus endometrioid carcinoma	9	0	10	14	6	X	39
Total counts	112	12	160	214	71		569

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Target	Primer name	Sequence (5'→3')
<i>β-actin</i>	β-actin H F	CACTCTTCCAGCCTTCCT
	β-actin H R	CAGGTCTTTGCGGATGTC
<i>Myc</i>	Myc H F	CACACATCAGCACAACTACG
	Myc H R	CTGTCCAACCTTGACCCTCTT
<i>Tp63</i>	TP63 H F	CGTGTCCTTCCAGCAGTC
	TP63 H R	GGCAGTAGAGTTTCTTCAGTTCA