

Supplementary Data

Table S1. ctDNA studies performed in early-stage tumors

Reference	Cancer type	Samples	Detection approach	Target	Expected mutations in ctDNA	Detected mutations in ctDNA	Range of mutant allelic fraction detected	Clinical outcome
Bettegowda <i>et al</i> , <i>Sci Trans Med</i> 2014	bladder, breast, colorectal, endometrial, head and neck, gastroesophageal, melanoma, non-small cell lung, pancreatic ductal	182	dPCR	panel of genes	variable**	40%-60%	1,1-22000 mutant fragments/5mL	NE
Sausen <i>et al</i> , <i>Nat Commun</i> 2015	pancreatic ductal adenocarcinoma	51	dPCR	<i>KRAS</i>	90%*	43%	0.01%-0.52%	higher risk of relapse in patients with detectable ctDNA at diagnosis
Beaver <i>et al</i> , <i>Clin Can Res</i> 2014	breast cancer	29	dPCR	<i>PIK3CA</i>	52%**	48%	0.01%-2.99%	NE
García-Mutillas <i>et al</i> , <i>Sci Trans Med</i> 2015	breast cancer	55	dPCR	panel of genes	76%**	53%	0.05%-0.8%	ctDNA detection at baseline, not predictive of disease-free survival. ctDNA abundance at baseline not associated with early relapse
Jamal-Hanjani <i>et al</i> , <i>Ann Oncol</i> 2016	lung adenocarcinoma and squamous cell carcinoma	4	multiplex PCR-NGS	panel of SNVs	37 SNVs**	16 SNVs(43%)	0.15-23.25%	NE

* Based on previous studies

** Based on tumor mutations

NE Not evaluated

§ According to concentration of mutations/ml

Table S3. Overview of the *TP53* mutations found in the plasma of 51 Russian SCLC patients with the mutations' allelic fractions (AF, %) detected in the two libraries, in both cfDNA and white-blood cells if applicable (NA, not done). *TP53* mutations are mapped to GenBank reference sequence NM_000546.

Sample	Tumour stage	Detected in cfDNA		Detected in white-blood cells		
		<i>TP53</i> mutation	Smallest AF	Highest AF	Smallest AF	Highest AF
SCLC-1	IB	p.E204*	1.95	4.22		
SCLC-2	IIB	p.R156P	0.67	0.82		
SCLC-3	IIB	P.G154V	0.61	1.13	NA	NA
SCLC-4	IIIA	P.K164E	5.86	7.33		
SCLC-5	IB	p.V272M	0.40	0.54		
SCLC-6	IIB	p.V216M	1.02	1.11		
		e7-2	0.76	1.46		
SCLC-7	IIIA	p.P177R	0.26	0.42		
		p.Q104*	6.88	11.49	NA	NA
SCLC-8	IIIA	p.G245fs	0.42	0.71		
		p.G245V	7.91	13.82		
SCLC-9	IIIA	p.G244C	6.36	8.69		
SCLC-10	IIIA	p.E286*	57.6	60.52	NA	NA
SCLC-11	IIIA	p.V157F	25.04	28.05		
		p.V153fs	57.31	84.08		
SCLC-12	IV	p.L194R	0.12	0.19		
SCLC-13	IIIB	p.H179R	23.89	24.25		
SCLC-14	IV	p.S241fs	0.39	0.57		
		p.S241Y	77.47	84.81		
SCLC-15	IIIA	p.G245V	2.38	2.96		
SCLC-16	IIIA	p.R280*	34.72	37.23	NA	NA
SCLC-17	IV	p.C176Y	6.07	9.64		
SCLC-18	IIIA	p.H179R	1.57	3.20	NA	NA
SCLC-19	IV	p.P72fs	23.94	24.27		
SCLC-20	IIIB	p.P34fs	4.56	4.69		
SCLC-21	IIIB	p.R280G	11.41	11.65		
		p.Y220C	0.90	1.27	0.50	0.70
SCLC-22	IIIB	p.E271V	0.71	0.88		
SCLC-23	IIIB	p.Y163C	0.26	0.27		
SCLC-24	IIIA	p.G244V	15.37	16.86		
SCLC-25	IV	e7-1	61.20	67.18	NA	NA

Table S4. Overview of the *TP53* mutations found in the plasma of 123 non-cancer Russian controls with the mutations' allelic fractions (AF, %) detected in the two libraries, in both cfDNA and white-blood cells if applicable (NA, not done). TA refers to the mutations' functional classification based on the overall transcriptional activity from the IARC *TP53* database. *TP53* mutations are mapped to GenBank reference sequence NM_000546.

Sample	Detected in cfDNA				Detected in white-blood cells		Comments
	<i>TP53</i> mutation	TA	Smallest AF	Highest AF	Smallest AF	Highest AF	
MLT-1	p.K291E	F	0.65	0.96			
MLT-2	p.E258fs		0.23	0.38			
MLT-3	p.H214Y	PF	0.27	4.04	NA	NA	
MLT-4	p.C275W	NF	0.24	0.61			
MLT-5	p.P34L	NF	1.14	1.19			
	p.E346A	F	0.26	0.85			
	p.C238Y	NF	0.50	0.61			
MLT-6	p.R175G	NF	4.09	4.41	4.40	4.50	
	p.R175H	NF	1.31	2.05			
	p.S261T	ST	1.01	1.50			
MLT-7	p.D281E	NF	79.85	84.94			
MLT-8	p.Y205*		0.19	0.49	NA	NA	
MLT-9	p.R273H	NF	1.05	2.50	NA	NA	
MLT-10	p.K382fs		13.68	14.46			
MLT-11	p.R175H	NF	20.92	21.28			
MLT-12	p.G244C	NF	0.33	0.74	NA	NA	
MLT-13	p.144-145del		3.02	5.32			
MLT-14	p.G154S	PF	47.17	50.58	52.10	54.90	likely germline

NF: non-functional

F: functional

PF: partially functional

ST: supertrans

Table S5. Overview of the *TP53* mutations found in the plasma of 9 Greece, 14 Czech Republic (CRE), 40 Italy (ITA), and 39 Argentina (ARG) non-cancer controls with the mutations' allelic fractions (AF, %) detected in the two libraries, in both cfDNA and white-blood cells if applicable (NA, not done). TA refers to the mutations' functional classification based on the overall transcriptional activity from the IARC *TP53* database. *TP53* mutations are mapped to GenBank reference sequence NM_000546.

Sample	Detected in cfDNA			Detected in white-blood cells			Comments
	<i>TP53</i> mutation	TA	Smallest AF	Highest AF	Smallest AF	Highest AF	
ARG-1	p.R273C	NF	5.22	5.58	7.30	10.40	
ARG-2	p.G105S	NF	0.78	1.99			
ARG-3	p.K139R	F	0.47	0.88			
	p.E271V	NF	0.51	0.60			
ARG-4	p.F341C	NF	0.33	0.47			
CRE-5	p.F212fs		0.02	0.05			
	p.S269N	PF	0.18	0.82			
CRE-6	p.I254N	NF	0.07	0.09			
ITA-7	p.S241C	NF	0.06	0.10			
ITA-8	p.V272M	NF	0.78	0.80	0.90	1.40	
ITA-9	p.G302W	F	0.28	0.42			
ITA-10	p.R273L	NF	0.14	0.19			
ITA-11	p.T377I	F	55.84	63.74	NA	NA	likely germline

NF: non-functional

F: functional

PF: partially functional