Supplementary

Table S1 DNA-based NGS results. Both subgroups (patients from 2019 and 2020) were compared using Fisher's exact test

	2019	2020	P value
Testing characteristics - no. (% of all cases with NGS)	n=189	n=243	
DNA-based NGS performed	183 (96.8%)	224 (92.2%)	0.06
DNA-based NGS evaluable	183 (96.8%)	224 (92.2%)	0.06
Alteration detected	161 (85.2%)	187 (77%)	0.037
Detected alterations - no (% of all cases with NGS)	n=189	n=243	
TP53 mutation (all)	90 (47.6%)	104 (42.8%)	0.331
KRAS mutation (all)	62 (32.8%)	80 (32.9%)	>0.9999
G12C	27 (14.3%)	35 (14.4%)	
G12D	8 (4.2%)	14 (5.8%)	
G12V	8 (4.2%)	14 (5.8%)	
G12A	5 (2.6%)	3 (1.2%)	
G13C	5 (2.6%)	1 (0.4%)	
Q61H	2 (1.1%)	3 (1.2%)	
G12F	1 (0.5%)	3 (1.2%)	
G12S	2 (1.1%)	1 (0.4%)	
Q61L	0 (0%)	2 (0.8%)	
other	4 (2.1%)	4 (1.6%)	
EGFR mutation (all)	26 (13.8%)	29 (11.9%)	0.663
Exon 19 del	11 (5.8%)	11 (4.5%)	
L858R	9 (4.8%)	12 (4.9%)	
L861Q	2 (1.1%)	2 (0.8%)	
T790M	0 (0%)	1 (0.4%)	
other	6 (3.2%)	6 (2.5%)	
DDR2 mutation (all)	17 (9%)	13 (5.3%)	0.181
M441I	14 (7.4%)	9 (3.7%)	
Non-M441I	4 (2.1%)	4 (1.6%)	
BRAF mutation (all)	13 (6.9%)	10 (4.1%)	0.28
V600E	4 (2.1%)	3 (1.2%)	
Non-V600E	10 (5.3%)	7 (2.9%)	
MET mutation (all)	14 (7.4%)	8 (3.3%)	0.076
T1010I	10 (5.3%)	6 (2.5%)	
Non-T1010I	4 (2.1%)	2 (0.8%)	
STK11 mutation (all)	8 (4.2%)	13 (5.3%)	0.657
PIK3CA mutation (all)	5 (2.6%)	6 (2.5%)	>0.9999
CTNNB1 mutation (all)	5 (2.6%)	4 (1.6%)	0.513

Table S1 *(continued)*

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Table S1 *(continued)*

	2019	2020	P value
SMAD4 mutation (all)	5 (2.6%)	4 (1.6%)	0.513
FGFR3 mutation (all)	2 (1.1%)	6 (2.5%)	0.475
F386L	2 (1.1%)	4 (1.6%)	
Non-F386L	0 (0%)	2 (0.8%)	
FGFR1 mutation (all)	2 (1.1%)	2 (0.8%)	>0.9999
ERBB2 mutation (all)	1 (0.5%)	2 (0.8%)	>0.9999
ERBB4 mutation (all)	2 (1.1%)	1 (0.4%)	0.584
ALK mutation (all)	1 (0.5%)	1 (0.4%)	>0.9999
FGFR2 mutation (all)	2 (1.1%)	0 (0%)	0.191
NRAS mutation (all)	1 (0.5%)	1 (0.4%)	>0.9999
PTEN mutation (all)	0 (0%)	2 (0.8%)	0.507
FBXW7 mutation (all)	0 (0%)	1 (0.4%)	>0.9999
MAP2K1 mutation (all)	0 (0%)	1 (0.4%)	>0.9999
Sample type - no. (% of all cases with DNA-based NGS)	n=183	n=224	
Resection specimen	57 (31.1%)	77 (34.4%)	0.525
Biopsy	112 (61.2%)	135 (60.3%)	0.919
Cytology/Cell block	14 (7.7%)	12 (5.4%)	0.417
Sample origin - no. (% of all cases with DNA-based NGS)	n=183	n=224	
Lung	146 (79.8%)	169 (75.4%)	0.341
Pleura	4 (2.2%)	10 (4.5%)	0.278
Lymph node	22 (12%)	26 (11.6%)	>0.9999
Distant metastasis	11 (6%)	19 (8.5%)	0.446

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Table S2 RNA-based NGS results. Both subgroups (patients from 2019 and 2020) were compared using Fisher's exact test

	2019	2020	P value
Testing characteristics - no. (% of all cases with NGS)	n=189	n=243	
RNA-based NGS performed	38 (20.1%)	231 (95.1%)	<0.0001
RNA-based NGS evaluable	37 (19.6%)	226 (93%)	<0.0001
Alteration detected	5 (2.6%)	20 (8.2%)	0.021
Detected alterations - no. (% of all cases with NGS)	n=189	n=243	
ALK fusion (all)	2 (1.1%)	7 (2.9%)	0.31
EML4-ALK	2 (1.1%)	6 (2.5%)	
KRT6A-ALK	0 (0%)	1 (0.4%)	
RET fusion (all)	0 (0%)	5 (2.1%)	0.071
CCDC6-RET	0 (0%)	3 (1.2%)	
KIF5B-RET	0 (0%)	2 (0.8%)	
METex14 skipping	1 (0.5%)	3 (1.2%)	0.635
NRG1 fusion (all)	0 (0%)	3 (1.2%)	0.26
CD74-NRG1	0 (0%)	2 (0.8%)	
SLC3A2-NRG1	0 (0%)	1 (0.4%)	
ROS1 fusion (all)	2 (1.1%)	0 (0%)	0.191
EZR-ROS1	1 (0.5%)	0 (0%)	
SDC4-ROS1	1 (0.5%)	0 (0%)	
BRAF fusion (all)	0 (0%)	1 (0.4%)	>0.9999
KLHL7-BRAF	0 (0%)	1 (0.4%)	
EGFR fusion (all)	0 (0%)	1 (0.4%)	>0.9999
EGFR-NUP160	0 (0%)	1 (0.4%)	
NTRK fusion (all)	0 (0%)	0 (0%)	>0.9999
Sample type - no. (% of all cases with RNA-based NGS)	n=38	n=231	
Resection specimen	13 (34.2%)	83 (35.9%)	>0.9999
Biopsy	23 (60.5%)	137 (59.3%)	>0.9999
Cytology/Cell block	2 (5.3%)	11 (4.8%)	>0.9999
Sample origin - no. (% of all cases with RNA-based NGS)	n=38	n=231	
Lung	29 (76.3%)	180 (77.9%)	0.835
Pleura	1 (2.6%)	10 (4.3%)	>0.9999
Lymph node	5 (13.2%)	22 (9.5%)	0.558
Distant metastasis	3 (7.9%)	19 (8.2%)	>0.9999

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