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| **SUPPLEMENTARY TABLE 2.** Summary of selected Diagnostic NSCLC Mutation Profiling Studies. (Studies that Screened for Alterations in at Least 6 genes From at Least 25 Samples are Included. Next Generation Sequencing Reports are Not Included.) |
| No. of samples tested | Histology (% if known) | Type of samples tested if known, stage if known | Method of screening (no. of genes tested) | Mutations identified, % of samples mutated | % of samples with concurrent mutations | Total % cases with mutation identified |
| 275 (20 samples failed testing) | NSCLC | FFPET, mostly biopsies from advanced stage NSCLC | LungCarta, Sequenom | EGFR, 17TP53, 11 STK11, 9.8, MET 7.6 KRAS 6.2 PIK3CA 2.2 BRAF 1.1NRAS 1.1NOTCH1, 0.7DDR2, 0.4EPHA3, 0.4EPHA5, 0.4ERBB2, 0.4MAP2K1, 0.4NRF-2, 0.4PTEN, 0.4  | 10.2 | 48[43](#_ENREF_43) |
| 204  | ADC (100) | FFPET resections, IB | OncoCarta, Sequenom (19)  | KRAS, 37.7EGFR, 14.2BRAF, 0.5PIK3CA, 4.4PDGFRA, 1AKT, 0.5FGFR1, 0.5HRAS, 0.5ALK FISH, 1 | 8.8 | 54[17](#_ENREF_17) |
| 25 | ADC (100) | FFPET resections, 52% I/II48% III/IV | Lung Cancer Mutations Screening Panel, Sequenom (10) | MET, 16*a* EGFR, 4 | 0 | 25[18](#_ENREF_18)\* |
| 61 | ADC (61)SCC (26)NSCLC NOS (12)Other (1) | Fresh-frozen tissue, small biopsies | OncoMap v4, Sequenom (41) | TP53, 39.3EGFR, 31.1MLH1, 9.8KRAS, 4.9PIK3CA, 4.9ERBB2, 3.3ABL1, 1.6HRAS, 1.6 | Unknown | 67[44](#_ENREF_44) |
| 96 | Non-squamous NSCLC (71 )SCC ( 29) | FFPET resections, I | Assay designed with Sequenom MassARRAY V3.1 software (22) | KRAS, 15.6EGFR, 15.6PIK3CA, 7.3TP53, 6.3FGFR3, 1.0CTTNB, 1.0NRAS, 1.0 | 8.3 | 37.5[52](#_ENREF_52) |
| 87 lung tumors(250 mixed tumor types)  | ADC (60)Other lung (40) | FFPET mainly from lung core biopsies | SNaPshot, Applied Biosystems (13) | EGFR, 16.1*b*KRAS, 20.7TP53, 4.6PIK3CA, 1.1NRAS, 1.1CTNNB1, 1.1 | 5.7 | 40 (lung samples only)[38](#_ENREF_38)34 (samples from all sites)  |
| 49 | ADC (100) | FFPET, frozen tissue, cell lines | SNaPshot, Applied Biosystems and PCR-based sizing assay (9) | EGFR, 24.5KRAS, 20.4PIK3CA, 2.0 | 4 | 43 in FFPET[53](#_ENREF_53) |
| 52 | ADC (100) | FFPET | Sanger sequencing (9) and RT-PCR for EML4-ALK | KRAS, 1.9EGFR, 78.8HER2, 3.8PIK3CA, 7.7TP53, 28.8EML4-ALK, 5.8HRAS, 0NRAS, 0LKB1, 0 | 7.7 | 90[45](#_ENREF_45) |
| 349 | ADC (100) | Fresh frozen tissue | Sanger sequencing (4) and RT-PCR for EML4-ALK | KRAS, 2.0EGFR, 76.2HER2, 4.6BRAF, 0.6EML4-ALK, 4.3 | 0 | 88[46](#_ENREF_46) |
| 104 | ADC (100) | FFPET, mixed stage | Sanger sequencing (5) and RT-PCR for EML4-ALK | EGFR, 70.2KRAS, 1.9BRAF, 1.9PIK3CA, 1.9HER2, 0EML4-ALK, 9.6 |  | 83[47](#_ENREF_47) |
| 344  | ADC (87)ASC (3)SCC (2)LCC (1)NSCLC NOS (8) | FFPET not specified, 80% IV / relapsed | Sanger sequencing (5) and ALK FISH | KRAS, 24EGFR, 17BRAF, 5HER2, 4PIK3CA, 2ALK FISH, 5 | <1 | 54[54](#_ENREF_54)  |
| 230 | ADC (100) | Fresh frozen tissue, resections, mixed stage | Sanger sequencing (6) | KRAS, 16.5EGFR, 43.5PI3KCA, 3.5BRAF, 3.0EML4-ALK, 3.0HER2, 0 | Unknown | 69.5[55](#_ENREF_55) |
| 107 | ADC (100) | FFPET resections | Sanger sequencing (8) and multiplex ligation-dependent probe amplification analysis for LKB1 deletion | LKB1, 27.1EGFR, 62.6KRAS, 5.6HER2, 2.8BRAF, 2.8EML4-ALK, 4.7CD74-ROS1, 1.9CCDC6-RET, 0.9 | Unknown | 81[56](#_ENREF_56) |
| *a*Only ALK-rearranged cases were tested*b*Includes 1 deletion in exon 19 of EGFR not detected by SNaPshot genotypingADC, adenocarcinoma; FFPET, formalin-fixed paraffin-embedded tissue; SCC, squamous cell carcinoma; NSCLC NOS, non small cell lung cancer not otherwise specified; ASC, adenosquamous carcinoma; LCC, large cell carcinoma; ALK, anaplastic lymphoma kinase; FISH, fluorescent in situ hybridisation. |