

Molecular heterogeneity assessment by next-generation sequencing and response to gefitinib of *EGFR* mutant advanced lung adenocarcinoma

Supplementary Material

Supplementary Table 1. Patients' characteristics according to NGS analysis: type of mutation and PMA.

| Patient | Group | Type of Mutation (PMA) | | | | | | |
|---------|--------------|---------------------------|-------------|-------------|---------------|---------------|-------------|--------------|
| | | <i>EGFR</i> | <i>TP53</i> | <i>KRAS</i> | <i>CTNNB1</i> | <i>PIK3CA</i> | <i>MET</i> | <i>SMAD4</i> |
| 1 | Good | L858R (32%) | | | | | | |
| 2 | Good | p.E746_A750del (31%) | | | | | | |
| 3 | Good | L858R (56%) | | | | | | |
| 4 | Good | L858R (86%) | | | | | | |
| 5 | Good | p.E746_A750del (71%) | | | | | | |
| 6 | Good | p.E746_A750del (88%) | | | | | | |
| 7 | Good | p.L747_T751del (64%) | | | S33C (20%) | | | G358E (44%) |
| 8 | Good | p.E746_S752delinsA (28%) | | | S45P (5%) | | | |
| 9 | Intermediate | p.L747QfsTer16 (23%) | R273G (45%) | | | | | |
| 10 | Intermediate | p.E746_A750del (94%) | R248W (48%) | | | | | |
| 11 | Intermediate | p.E745_A750del (30%) | R175H (27%) | | | | | |
| 12 | Poor | L858R (36%) | R273L (47%) | | | | | |
| 13 | Poor | p.E746_T751delinsIA (11%) | | G12C (5%) | | | | |
| 14 | Poor | p.E746_A750del (20%) | | | | | | |
| 15 | Poor | L858R (43%) | | G12C (22%) | | E542K (31%) | | |
| 16 | Poor | p.E746_A750del (31%) | R248L (40%) | | | | | |
| 17 | Poor | E746_A750del (94%) | R175L (37%) | | | | N375S (34%) | |

Legend – Supplementary Table 1. NGS: next generation sequencing; PMA: Proportion of Mutated Alleles,