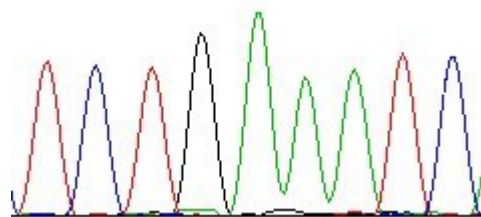


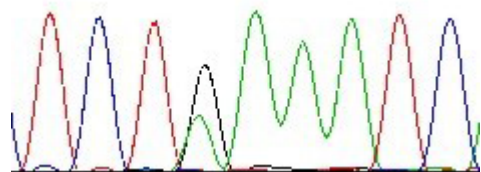
Figure S1

A

Normal

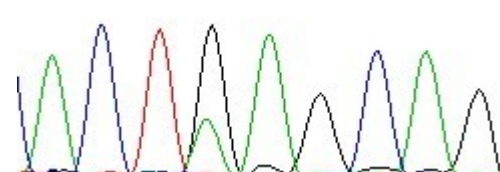
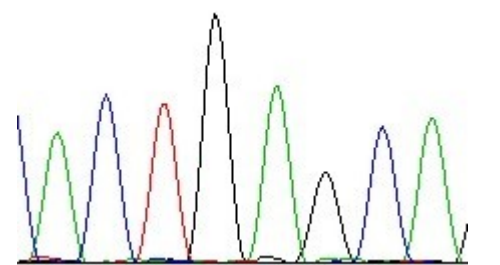


Mutation



T C T G A A A T C

G1624A (E542K)

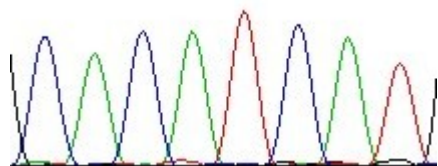


A C T G A G C A

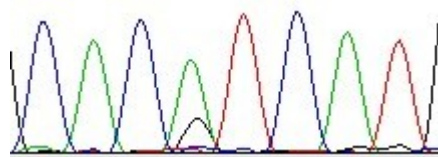
G1633A (E545K)

B

Normal



Mutation



C A C A T C A T

A3140G(H1047R)

C A C A T C A T

A3140L (H1047L)

Figure S2

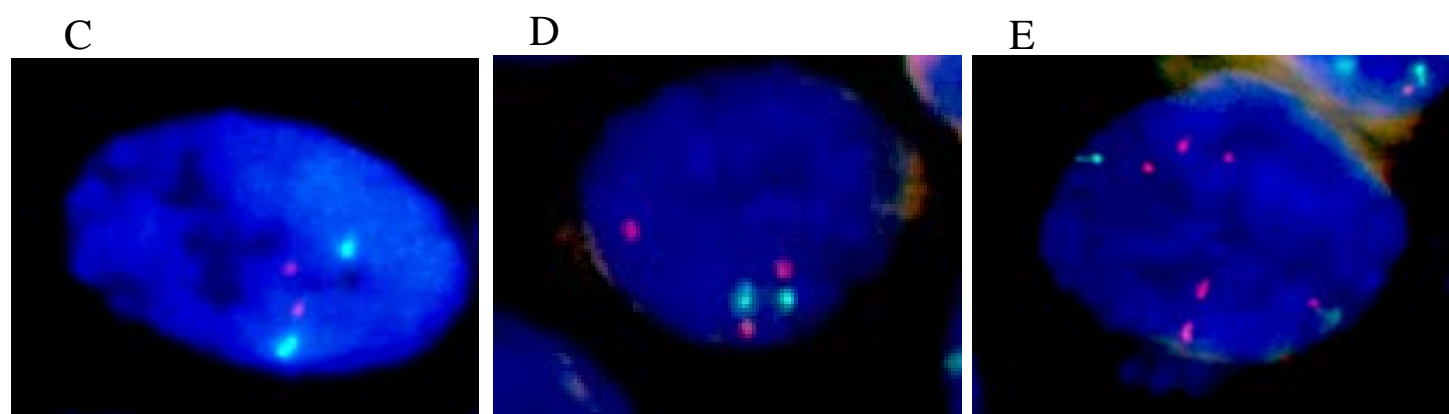
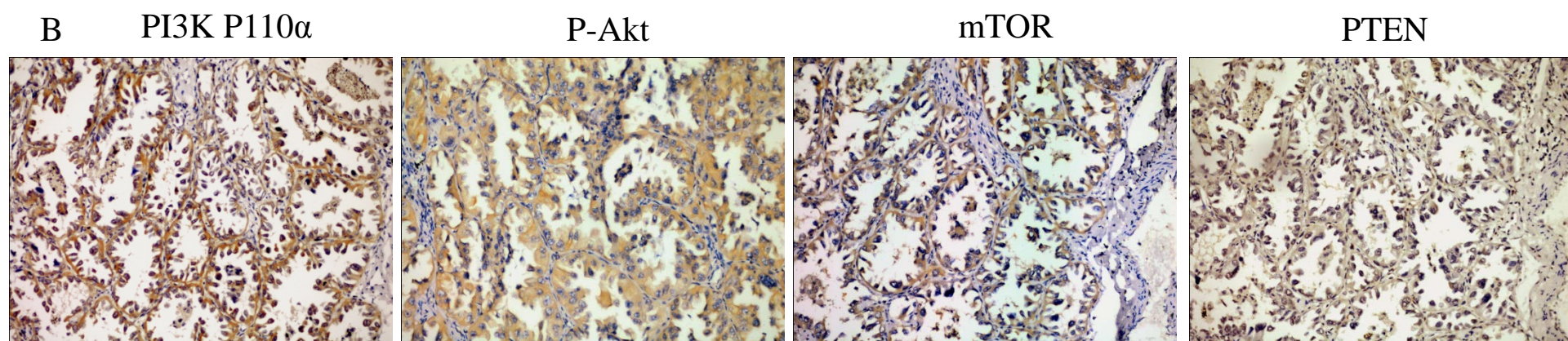
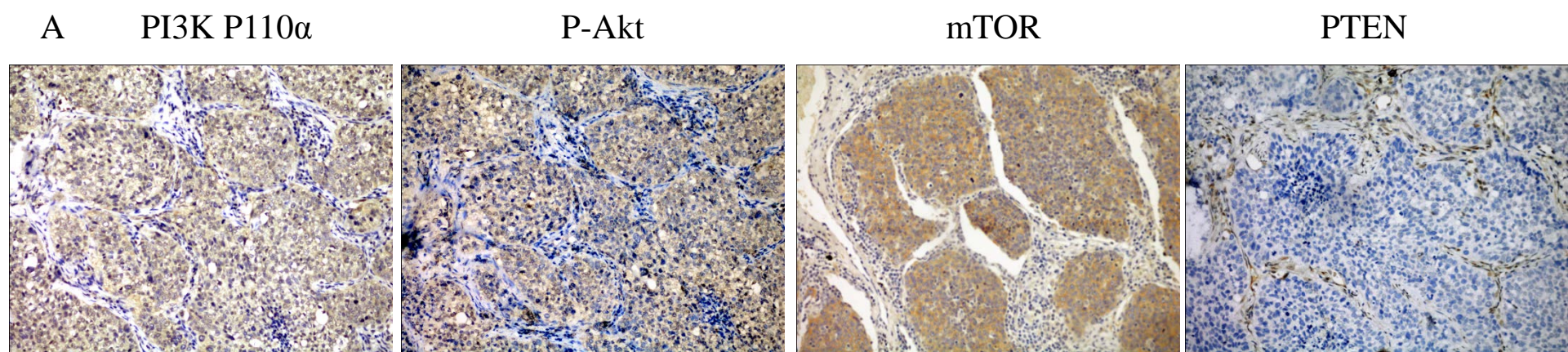
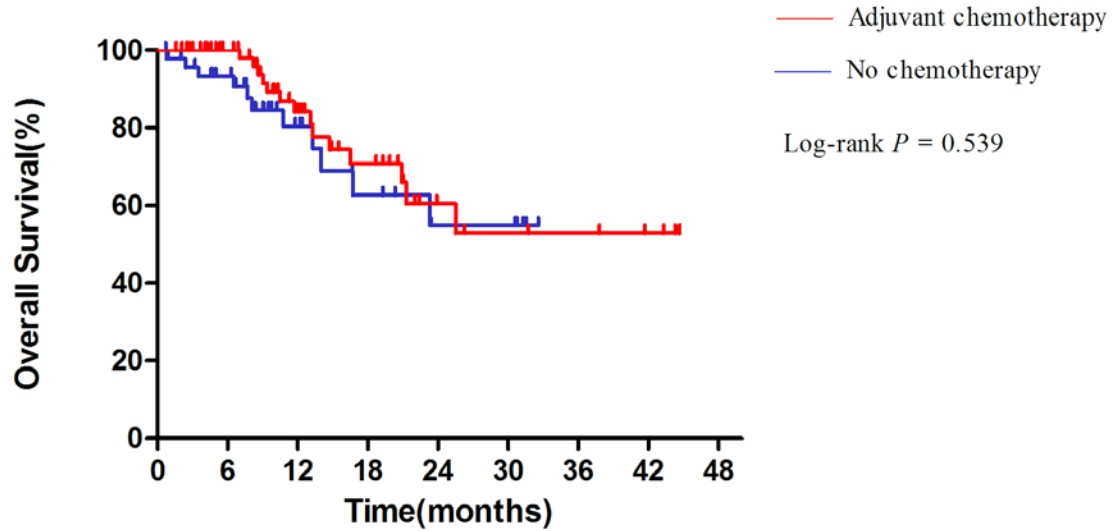


Figure S3

A



B

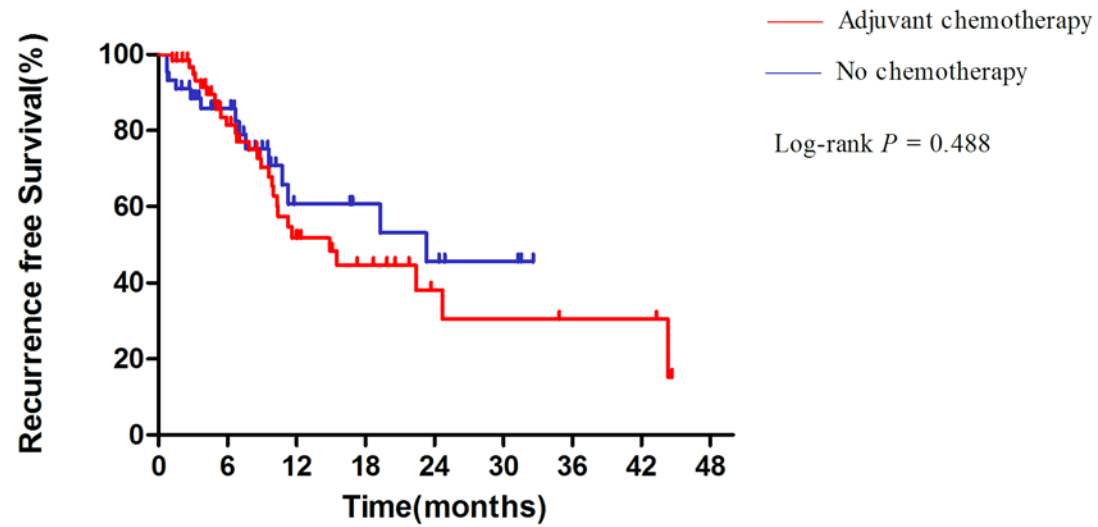
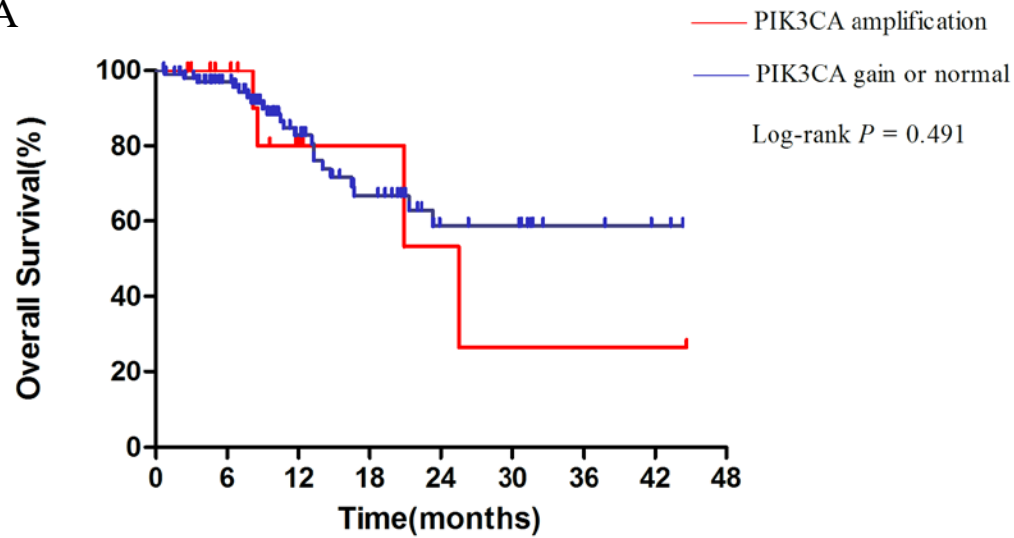


Figure S4

A



B

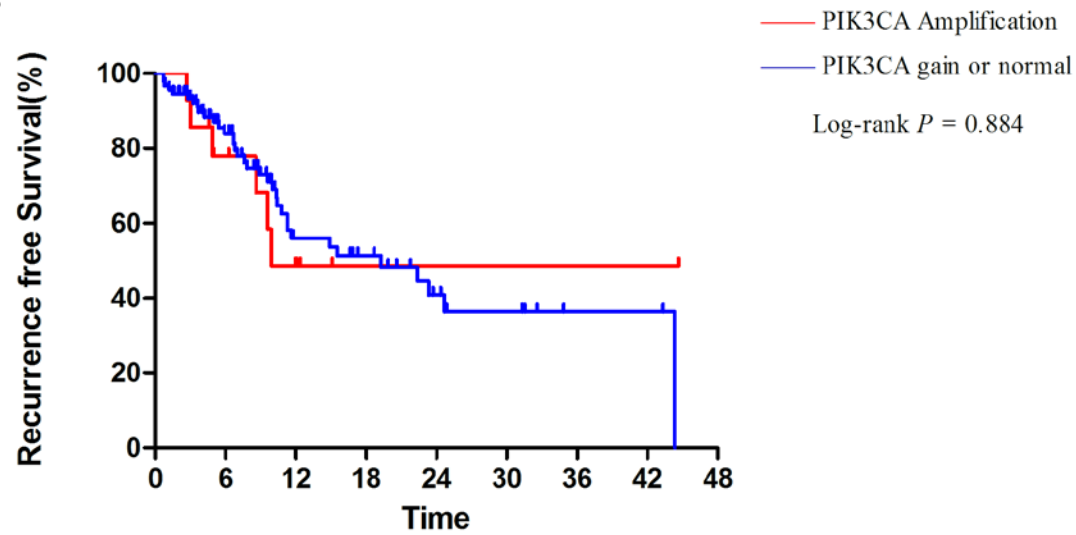


Table S1 Comparison of *PIK3CA* helical(exon9) and kinase(exon20) domain mutation

| Characteristics | Helical N (%) | Kinase N (%) | <i>p</i> -value |
|-------------------------|------------------|-----------------|-----------------|
| Stage | | | |
| I | 6(28.6) | 7(53.8) | |
| II~IV | 15(71.4) | 6(46.2) | 0.141 |
| Lymph node metastasis | | | |
| N0 | 8(38.1) | 7(53.8) | 0.369 |
| N+ | 13(61.9) | 6(46.2) | |
| Smoking history | | | |
| Never | 9(42.9) | 7(53.8) | |
| Former/current | 12(57.1) | 6(46.2) | 0.533 |
| Differentiation | | | |
| Well | 2(9.5) | 2(15.4) | 0.606 |
| Moderately or poorly | 19(90.5) | 11(84.6) | |
| Pathological types | | | |
| AD | 13(61.9) | 9(69.2) | 0.727 |
| SCC | 8(38.1) | 4(30.8) | |
| Age | | | |
| ≤60 | 11(52.4) | 9(69.2) | 0.477 |
| >60 | 10(47.6) | 4(30.8) | |
| Gender | | | |
| Male | 15(71.4) | 6(46.2) | 0.141 |
| Female | 6(28.6) | 7(53.8) | |
| Co-mutation | | | |
| Yes | 13(61.9) | 8(61.5) | |
| No | 8(38.1) | 5(38.5) | 0.983 |

N+: lymph node metastasis positive; AD: adenocarcinoma; SCC:squamous cell carcinoma

Table S2 *ALK* rearrangement in 1117 NSCLC patients

| Patients ID | Pathology | PCR | FISH |
|-------------|-----------|----------------------------|------|
| 245 | AD | E13;A20 | + |
| 324 | AD | E20;A20 | + |
| 347 | AD | E20;A20 | + |
| 399 | AD | E6a/b;A20 | + |
| 460 | AD | E13;A20 | + |
| 490 | AD | E6a/b;A20 | + |
| 578 | AD | E13;A20 | + |
| 584 | AD | E17;A20 | + |
| 591 | AD | E6a/b;A20 | + |
| 636 | AD | E13;A20 | + |
| 667 | AD | E13;A20 | + |
| 732 | AD | E20;A20 | + |
| 737 | AD | E17 ins 65;A20 | + |
| 781 | AD | E6b;A20 | + |
| 782 | AD | E6a/b;A20 | + |
| 788 | AD | E6a/b;A20 | + |
| 834 | AD | E13;A20 | + |
| 877 | AD | E20;A20 | + |
| 964 | AD | E20;A20 | + |
| 966 | AD | E20;A20 | + |
| 974 | AD | E13;A20 | + |
| 981 | AD | E17b ins 39;A20 | + |
| 988 | AD | E10a/b, E13;A20 | + |
| 1003 | AD | E13;A20 | + |
| 1004 | AD | E13;A20 | + |
| 1228 | AD | E13;A20 | + |
| 1335 | AD | E13;A20 | + |
| 1336 | AD | E13;A20 | + |
| 1451 | AD | E13;A20 | + |
| 1459 | AD | E13;A20 | + |
| 1494 | AD | (E6a/b:ALK intron 18bp:A20 | + |
| 1514 | AD | E6a/b;A20 | + |
| B56 | AD | E6a/b;A20 | + |

NOTE: +, positive; AD, adenocarcinoma;

Table S3 Correlations between *PIK3CA* mutations and other gene alterations in lung adenocarcinoma.

| Gene alteration | | <i>PIK3CA</i> mutant N (%) | <i>PIK3CA</i> wildtype N (%) | <i>p</i> -Value |
|-----------------|---------------|-------------------------------|---------------------------------|-----------------|
| <i>EGFR</i> | mutant | 16(72.7) | 506(64.5) | 0.424 |
| | wildtype | 6(27.3) | 279(35.5) | |
| <i>KRAS</i> | mutant | 3(13.6) | 56(7.1) | 0.213 |
| | wildtype | 19(86.4) | 729(92.9) | |
| <i>HER2</i> | mutant | 0(0.0) | 19(2.4) | 1.000 |
| | wildtype | 22(100.0) | 766(97.6) | |
| <i>BRAF</i> | mutant | 0(0.0) | 10(1.3) | 1.000 |
| | wildtype | 22(100.0) | 775(98.7) | |
| <i>AKT1</i> | mutant | 0(0.0) | 1(0.1) | 1.000 |
| | wildtype | 22(100.0) | 784(99.9) | |
| <i>ALK</i> | rearrangement | 0(0.0) | 31(3.9) | 1.000 |
| | wildtype | 22(100.0) | 754(96.1) | |

Table S4 Correlations between *PIK3CA* mutations and other gene alterations in lung squamous cell carcinoma

| Gene alteration | | <i>PIK3CA</i> mutant N (%) | <i>PIK3CA</i> wildtype N (%) | <i>p</i> -Value |
|-----------------|---------------|-------------------------------|---------------------------------|-----------------|
| <i>EGFR</i> | mutant | 1(8.3) | 13(4.4) | 0.432 |
| | wildtype | 11(91.7) | 285(95.6) | |
| <i>KRAS</i> | mutant | 1(8.3) | 7(2.3) | 0.274 |
| | wildtype | 11(91.7) | 291(97.7) | |
| <i>HER2</i> | mutant | 0(0.0) | 1(0.3) | 1.000 |
| | wildtype | 12(100.0) | 297(99.7) | |
| <i>BRAF</i> | mutant | 0(0.0) | 1(0.3) | 1.000 |
| | wildtype | 12(100.0) | 297(97.7) | |
| <i>AKT1</i> | mutant | 0(0.0) | 1(0.3) | 1.000 |
| | wildtype | 12(100.0) | 297(97.7) | |
| <i>ALK</i> | rearrangement | 0(0.0) | 2(0.7) | 1.000 |
| | wildtype | 12(100.0) | 296(99.3) | |

Table S5 Comparison of patients with single *PIK3CA* mutation to those with *PIK3CA* and other oncogene mutation

| Characteristics | Coexistence of <i>PIK3CA</i> and <i>EGFR/KRAS</i> mutations N(%) | Patients with <i>PIK3CA</i> mutation only N(%) | <i>p</i> -value |
|--------------------------|---|---|-------------------|
| Stage | | | |
| I | 8(38.1) | 4(30.8) | 0.727 |
| II~IV | 13(61.9) | 9(69.2) | |
| Smoking history | | | |
| Never smoker | 13(61.9) | 3(23.1) | 0.039 |
| Current or former smoker | 8(38.1) | 10(76.9) | |
| Pathological types | | | |
| AD | 19(90.5) | 3(23.1) | <0.0001 |
| SCC | 2(9.5) | 10(76.9) | |
| Age | | | |
| ≤60 | 15(71.4) | 6(46.2) | 0.168 |
| >60 | 6(28.6) | 7(53.8) | |
| Gender | | | |
| Male | 10(47.6) | 11(84.6) | 0.067 |
| Female | 11(52.4) | 2(15.4) | |
| Domain | | | |
| Helical domain | 13(61.9) | 8(61.5) | 1.000 |
| Kinase domain | 8(38.1) | 5(38.5) | |

AD: adenocarcinoma; SCC: squamous cell carcinoma

Table S6 Histopathological subtype in 785 *PIK3CA* wildtype and 22 *PIK3CA* mutant patients with lung adenocarcinoma

| Histologic subtype | <i>PIK3CA</i> mutations patients N (%) | <i>PIK3CA</i> Wild type patients N (%) | <i>p</i> -Value |
|----------------------------|---|---|-----------------|
| AIS | 1(4.5) | 5(0.6) | |
| MIA | 0(0.0) | 13(1.5) | |
| Lepidic predominant | 2(9.1) | 53(6.8) | |
| Acinar predominant | 11(50) | 412(52.5) | |
| Papillary predominant | 1(4.5) | 121(15.4) | |
| Micropapillary predominant | 0(0.0) | 16(2.0) | |
| Solid predominant | 6(27.3) | 137(17.5) | |
| IMA | 1(4.5) | 25(3.2) | |
| Enteric predominant | 0(0.0) | 3(0.4) | 0.082 |

AIS: adenocarcinoma in situ; MIA: minimally invasive adenocarcinoma;
IMA:invasive mucinous adenocarcinoma

Table S7 Comparison of histopathological subtype between lung adenocarcinoma patients only with *PIK3CA* mutation and those co-exited with *EGFR/KRAS* mutation

| Histologic subtype | Patients with <i>PIK3CA</i> and <i>EGFR/KRAS</i> mutations N(%) | Patients with <i>PIK3CA</i> mutation only N(%) | <i>p</i> -Value |
|-----------------------|---|--|-----------------|
| AIS | 0(0.0) | 1(33.3) | |
| Lepidic predominant | 2(10.5) | 0(0.0) | |
| Acinar predominant | 10(52.6) | 1(33.3) | |
| Papillary predominant | 1(5.3) | 0(0.0) | |
| Solid predominant | 5(26.3) | 1(33.3) | |
| IMA | 1(5.3) | 0(0.0) | 0.121 |

AIS: adenocarcinoma in situ; IMA:invasive mucinous adenocarcinoma

Table S8 Associations of PI3K p110 α , p-Akt, mTOR, PTEN expression and *PIK3CA* amplification with clinicopathologic characteristics of 34 patients in *PIK3CA* mutant group

| Characteristics | PI3K p110 α | | | PTEN loss | | | p-Akt | | | m TOR | | |
|-----------------------|--------------------|---------|----------------|-----------|----------|----------------|----------|----------|-------------------|-----------|---------|-------------------|
| | +(%) | -(%) | <i>P</i> value | +(%) | -(%) | <i>P</i> value | +(%) | -(%) | <i>P</i> value | +(%) | -(%) | <i>P</i> value |
| Stage | | | | | | | | | | | | |
| I | 8(61.5) | 5(38.5) | 0.043 | 2(15.4) | 11(84.6) | 0.444 | 8(61.5) | 5(38.5) | 0.429 | 8(61.5) | 5(38.5) | 0.254 |
| II ~IV | 19(90.5) | 2(9.5) | | 6(28.6) | 15(71.4) | | 10(47.6) | 11(52.4) | | 17(81.0) | 4(19.0) | |
| Lymph node metastasis | | | | | | | | | | | | |
| N0 | 11(73.3) | 4(26.7) | 0.672 | 3(20.0) | 12(80.0) | 1.000 | 10(66.7) | 5(33.3) | 0.154 | 11(73.3) | 4(26.7) | 1.000 |
| N+ | 16(84.2) | 3(15.8) | | 5(26.3) | 14(73.7) | | 8(42.1) | 11(57.9) | | 14(73.7) | 5(26.3) | |
| Smoking history | | | | | | | | | | | | |
| Never smoker | 11(68.8) | 5(31.3) | 0.214 | 2(12.5) | 14(87.5) | 0.233 | 10(62.5) | 6(37.5) | 0.327 | 12(75.0) | 4(25.0) | 1.000 |
| C/F smoker | 16(88.9) | 2(11.1) | | 6(33.3) | 12(66.7) | | 8(44.4) | 10(55.6) | | 13(72.2) | 5(27.8) | |
| Differentiation | | | | | | | | | | | | |
| Well | 3(75.0) | 1(25.0) | 1.000 | 1(25.0) | 3(75.0) | 1.000 | 1(25.0) | 3(75.0) | 0.323 | 3(75.0) | 1(25.0) | 0.610 |
| Moderately or poorly | 24(80.0) | 6(20.0) | | 7(23.3) | 23(76.7) | | 17(56.7) | 13(43.2) | | 22(73.3) | 8(26.7) | |
| Pathological types | | | | | | | | | | | | |
| AD | 17(77.3) | 5(22.7) | 1.000 | 4(18.2) | 18(81.8) | 0.410 | 12(54.5) | 10(15.5) | 0.800 | 15(68.2) | 7(31.8) | 0.439 |
| SCC | 10(83.3) | 2(16.7) | | 4(33.3) | 8(66.7) | | 6(50.0) | 6(50.0) | | 10(83.3) | 2(16.7) | |
| Age | | | | | | | | | | | | |
| ≤60 | 15(71.4) | 6(28.6) | 0.210 | 5(23.8) | 16(76.2) | 0.262 | 12(57.1) | 9(42.9) | 0.533 | 15(71.4) | 6(28.6) | 1.000 |
| >60 | 12(92.3) | 1(7.7) | | 6(46.2) | 7(53.8) | | 6(46.2) | 7(53.8) | | 10(76.9) | 3(23.1) | |
| Gender | | | | | | | | | | | | |
| Male | 18(85.7) | 3(14.3) | 0.387 | 6(28.6) | 15(71.4) | 0.444 | 11(52.4) | 10(47.6) | 0.934 | 16(76.2) | 5(23.8) | 0.704 |
| Female | 9(69.2) | 4(30.8) | | 2(15.4) | 11(84.6) | | 7(53.8) | 6(46.2) | | 9(69.2) | 4(30.8) | |
| PI3K p110 α | | | | | | | | | | | | |
| + | NA | | | 7(25.9) | 20(74.1) | 1.000 | 17(63.0) | 10(37.0) | 0.035 | 23(85.2) | 4(14.8) | 0.007 |
| - | | | | 1(14.3) | 6(85.7) | | 1(14.3) | 6(85.7) | | 2(28.6) | 5(71.4) | |
| PTEN loss | | | | | | | | | | | | |
| + | 7(87.5) | 1(12.5) | 1.000 | NA | | | 4(50.0) | 4(50.0) | 1.000 | 7(87.5) | 1(12.5) | 0.403 |
| - | 20(76.9) | 6(23.1) | | | | | 14(53.8) | 12(46.2) | | 18(69.2) | 8(30.8) | |
| p-Akt | | | | | | | | | | | | |
| + | 17(94.4) | 1(5.6) | 0.035 | 4(22.2) | 14(77.8) | 1.000 | NA | | | 18(100.0) | 0(0.0) | <0.0001 |
| - | 10(62.5) | 6(37.5) | | 4(25.0) | 12(75.0) | | | | | 7(43.8) | 9(56.3) | |
| m TOR | | | | | | | | | | | | |
| + | 23(92.0) | 2(8.0) | 0.007 | 7(28.0) | 18(72.0) | 0.403 | 18(72.0) | 7(28.0) | <0.0001 | NA | | |
| - | 4(44.4) | 5(55.6) | | 1(11.1) | 8(88.9) | | 0(0.0) | 9(100.0) | | | | |

N+: lymph node metastasis positive; C/F: current/former; AD: adenocarcinoma; SCC; squamous cell carcinoma; NA: Not applicable

Table S9 Associations of PI3K p110 α , p-Akt, mTOR, PTEN expression and *PIK3CA* amplification with clinicopathologic characteristics of 108 patients in *PIK3CA* wild-type group

| Characteristics | PI3K p110 α | | | PTEN loss | | | p-Akt | | | m TOR | | |
|-----------------------|--------------------|----------|-------------------|-----------|----------|----------------|----------|----------|-------------------|----------|----------|-------------------|
| | +(%) | -(%) | <i>P</i> value | +(%) | -(%) | <i>P</i> value | +(%) | -(%) | <i>P</i> value | +(%) | -(%) | <i>P</i> value |
| Stage | | | | | | | | | | | | |
| I | 8(29.6) | 19(70.4) | | 5(18.5) | 22(81.5) | | 8(29.6) | 19(70.4) | | 13(48.1) | 14(51.9) | |
| II ~IV | 33(40.7) | 48(59.3) | 0.303 | 23(28.4) | 58(71.6) | 0.310 | 25(30.9) | 56(69.1) | 0.904 | 32(39.5) | 49(60.5) | 0.430 |
| Lymph node metastasis | | | | | | | | | | | | |
| N0 | 23(43.4) | 30(56.6) | 0.253 | 18(34.0) | 35(66.0) | 0.061 | 17(32.1) | 36(67.9) | 0.736 | 25(47.2) | 28(52.8) | 0.255 |
| N+ | 18(32.7) | 37(67.2) | | 10(18.2) | 45(81.8) | | 16(29.1) | 39(70.9) | | 20(36.4) | 35(63.6) | |
| Smoking history | | | | | | | | | | | | |
| Never smoker | 12(40.0) | 18(60.0) | 0.787 | 4(13.3) | 26(86.7) | 0.064 | 8(26.7) | 22(73.3) | 0.586 | 13(43.3) | 17(56.7) | 0.528 |
| C/F smoker | 29(37.2) | 49(62.8) | | 24(30.8) | 54(69.2) | | 25(32.1) | 53(67.9) | | 32(41.0) | 46(59.0) | |
| Differentiation | | | | | | | | | | | | |
| Well | 1(20.0) | 4(80.0) | 0.648 | 2(40.0) | 3(60.0) | 0.603 | 1(20.0) | 4(80.0) | 1.000 | 3(60.0) | 2(40.0) | 0.647 |
| Moderately or poorly | 40(38.8) | 63(61.2) | | 26(25.2) | 77(74.8) | | 32(31.1) | 71(68.9) | | 42(40.8) | 61(59.2) | |
| Pathological types | | | | | | | | | | | | |
| AD | 22(39.3) | 34(60.7) | 0.769 | 13(23.2) | 43(76.8) | 0.505 | 15(26.8) | 41(73.2) | 0.377 | 22(39.3) | 34(60.7) | 0.602 |
| SCC | 19(36.5) | 33(63.5) | | 15(28.8) | 37(71.2) | | 18(34.6) | 34(65.4) | | 23(44.2) | 29(55.8) | |
| Age | | | | | | | | | | | | |
| ≤60 | 21(42.9) | 28(57.1) | 0.340 | 11(22.4) | 38(77.6) | 0.452 | 10(20.4) | 39(79.6) | 0.037 | 19(38.8) | 30(61.2) | 0.579 |
| >60 | 20(33.9) | 39(66.1) | | 17(28.8) | 42(71.2) | | 23(39.0) | 36(61.0) | | 26(44.1) | 33(55.9) | |
| Gender | | | | | | | | | | | | |
| Male | 34(37.8) | 56(62.2) | 0.929 | 24(26.7) | 66(73.3) | 0.694 | 30(33.3) | 60(66.7) | 0.161 | 36(40.0) | 54(60.0) | 0.579 |
| Female | 7(42.2) | 11(61.1) | | 4(22.2) | 14(77.8) | | 3(16.7) | 15(83.3) | | 9(50.0) | 9(50.0) | |
| PI3K p110 α | | | | | | | | | | | | |
| + | NA | | | 7(17.1) | 34(82.9) | 0.101 | 23(56.1) | 18(43.9) | <0.0001 | 32(78.0) | 9(22.0) | <0.0001 |
| - | | | | 21(31.3) | 46(68.7) | | 10(14.9) | 57(85.1) | | 13(19.4) | 54(80.6) | |
| PTEN loss | | | | | | | | | | | | |
| + | 7(25.0) | 21(75.0) | 0.101 | NA | | | 7(25.0) | 21(75.0) | 0.458 | 8(28.6) | 20(71.4) | 0.102 |
| - | 34(42.5) | 46(57.5) | | | | | 26(32.5) | 54(67.5) | | 37(46.3) | 43(53.8) | |
| p-Akt | | | | | | | | | | | | |
| + | 23(69.7) | 10(30.3) | <0.0001 | 7(21.2) | 26(78.8) | 0.458 | NA | | | 21(63.6) | 12(36.4) | 0.002 |
| - | 18(24.0) | 57(76.0) | | 21(28.0) | 54(72.0) | | | | | 24(32.0) | 51(68.0) | |
| m TOR | | | | | | | | | | | | |
| + | 32(71.1) | 13(28.9) | <0.0001 | 8(17.8) | 37(82.2) | 0.102 | 21(46.7) | 24(53.3) | 0.002 | NA | | |
| - | 9(14.3) | 54(85.7) | | 20(31.7) | 43(68.3) | | 12(19.0) | 51(81.0) | | | | |

N+: lymph node metastasis positive; C/F: current/former; AD: adenocarcinoma; SCC; squamous cell carcinoma; NA: Not applicable

Table S10 Associations of PI3K p110 α , p-Akt , mTOR, PTEN expression and *PIK3CA* amplification with clinicopathologic characteristics

| Characteristics | <i>PIK3CA</i> amplification in <i>PIK3CA</i> mutant group | | | <i>PIK3CA</i> amplification in <i>PIK3CA</i> wildtype group | | |
|-----------------------|---|-----------|----------------|---|-----------|-------------------|
| | +(%) | -(%) | <i>P</i> value | +(%) | -(%) | <i>P</i> value |
| Stage | | | | | | |
| I | 2(15.4) | 11(84.6) | 1.000 | 6(22.2) | 21(77.8) | 0.783 |
| II ~IV | 3(14.3) | 18(85.7) | | 16(19.8) | 65(80.2) | |
| Lymph node metastasis | | | | | | |
| N0 | 3(20.0) | 12(80.0) | 0.634 | 12(22.6) | 41(77.4) | 0.565 |
| N+ | 2(10.5) | 17(89.5) | | 10(18.2) | 45(81.8) | |
| Smoking history | | | | | | |
| Never smoker | 2(12.5) | 14(87.5) | 1.000 | 0(0) | 30(100.0) | 0.001 |
| Current/former smoker | 3(16.7) | 15(83.3) | | 22(28.2) | 56(71.8) | |
| Differentiation | | | | | | |
| Well | 1(25.0) | 3(75.0) | 0.488 | 0(0) | 5(100.0) | 0.581 |
| Moderately or poorly | 4(13.3) | 26(86.7) | | 22(21.4) | 81(78.6) | |
| Pathological types | | | | | | |
| AD | 1(4.5) | 21(95.5) | 0.042 | 3(5.4) | 53(94.6) | <0.0001 |
| SCC | 4(33.3) | 8(66.7) | | 19(36.5) | 33(63.5) | |
| Age | | | | | | |
| ≤ 60 | 2(9.5) | 19(90.5) | 0.348 | 8(16.3) | 41(83.7) | 0.342 |
| >60 | 3(23.1) | 10(76.9) | | 14(23.7) | 45(76.3) | |
| Gender | | | | | | |
| Male | 4(19.0) | 17(81.0) | 0.627 | 22(24.4) | 68(75.6) | 0.021 |
| Female | 1(7.7) | 12(92.3) | | 0(0) | 18(100.0) | |
| PI3K p110 α | | | | | | |
| + | 5(18.5) | 22(81.5) | 0.559 | 7(17.1) | 34(82.9) | 0.506 |
| - | 0(0) | 7(100.0) | | 15(22.4) | 52(77.6) | |
| PTEN loss | | | | | | |
| + | 2(25.0) | 6(75.0) | 0.570 | 7(25.0) | 21(75.0) | 0.480 |
| - | 3(11.5) | 23(88.5) | | 15(18.8) | 65(81.3) | |
| p-Akt | | | | | | |
| + | 4(22.2) | 14(77.8) | 0.340 | 6(18.2) | 27(81.8) | 0.708 |
| - | 1(6.3) | 15((93.8) | | 16(21.3) | 59(78.7) | |
| m TOR | | | | | | |
| + | 5(20.0) | 20(80.0) | 0.293 | 10(22.2) | 35(77.8) | 0.686 |
| - | 0(0) | 9(100.0) | | 12(19.0) | 51(81.0) | |

N+: lymph node metastasis positive AD: adenocarcinoma;SCC;squamous cell carcinoma

Supporting information legend:

Figure S1 Representative *PIK3CA* mutations by direct sequencing are shown for exon 9(A) and exon 20(B).

Figure S2 Representative high expression of PI3K P110 α , p-Akt, m TOR and low expression of PTEN protein in lung SCC; original amplification, $\times 200$ (A); Representative high expression of PI3K, p-Akt, m TOR and PTEN protein in lung AD; original amplification, $\times 200$ (B); Representative cell nuclei having normal(C), gain (D), and amplified (E) *PIK3CA* signals (red) and two centromeric signals (green).

Figure S3 Overall survival curves for patients with or without adjuvant chemotherapy (A); Recurrence-free survival curves for patients with or without adjuvant chemotherapy (B).

Figure S4 Overall survival curves for patients with or without *PIK3CA* amplification (A); Recurrence-free survival curves for patients with or without *PIK3CA* amplification (B).

Table S1 Comparison of *PIK3CA* helical(exon9) and kinase(exon20) domain mutation.

Table S2 *ALK* rearrangement in 1117 NSCLC patients

Table S3 Correlations between *PIK3CA* mutations and other gene alterations in lung adenocarcinoma.

Table S4 Correlations between *PIK3CA* mutations and other gene alterations in lung squamous cell carcinoma

Table S5 Comparison of patients with single *PIK3CA* mutation to those with *PIK3CA* and other oncogene mutation

Table S6 Histopathological subtype in 785 *PIK3CA* wildtype and 22 *PIK3CA* mutant patients with lung adenocarcinoma

Table S7 Comparison of histopathological subtype between lung adenocarcinoma patients only with *PIK3CA* mutation and those co-exited with *EGFR/KRAS* mutation

Table S8 Associations of PI3K p110 α , p-Akt, mTOR, PTEN expression and *PIK3CA* amplification with clinicopathologic characteristics of 34 patients in *PIK3CA* mutant group

Table S9 Associations of PI3K p110 α , p-Akt, mTOR, PTEN expression and *PIK3CA* amplification with clinicopathologic characteristics of 108 patients in *PIK3CA* wild-type group

Table S10 Associations of PI3K p110 α , p-Akt, mTOR, PTEN expression and *PIK3CA*

amplification with clinicopathologic characteristics