|  |
| --- |
| **Supplementary Table S1** Genotyping of *NAT2* variants |
| **S.No.** | **NAT2 variants** | **Primers** | **Annealing temperature** | **Restriction enzyme** | **Cutting pattern after digestion** |
| 1. | 481C>T | FP: 5’-GCTGGGTCTGGAAGCTCCTC-3’RP: 5’-TTGGGTGATACATACACAAGGG-3’ | 63˚C | *KpnI* | CC: 433, 114 bpTT: 547 bpCT: 547, 433, 114 bp |
| 2. | 590G>A | *TaqI* | GG: 222, 170, 155 bpAA: 392, 155 bpGA: 392, 222, 170, 155 bp |
| 3. | 803A>G | *DdeI* | AA: 345, 137, 65 bpGG: 345, 114, 65 bpAG: 345, 137, 114, 65 bp |
| 4. | 857G>A | *BamHI* | GG: 490, 57 bpAA: 547 bpGA: 547, 490, 57 bp |
| Note: FP- forward primer, RP- reverse primer |

|  |
| --- |
| **Supplementary Table S2**Genotypic and allelic distribution of the *NAT* genetic variant and its association with risk of lung cancer overall and according to tumor histology |
|  **Genotype OVERALL Genotype** |
| **rs1799930****590G>A**  | **Controls (550) N(%)** | **Cases (550) N(%)** | **AOR** **(95% CI) a** | ***p*b** | **rs1208****803A>G**  | **Controls (550) N(%)** | **Cases** **(550) N(%)** | **AOR** **(95% CI)a** | ***p*b** |
| **Codominant model** |  |
| GG | 221 (40.18) | 226 (41.09) | 1.00 (Reference) |  | AA | 267 (48.55) | 281 (51.09) | 1.00 (Reference) |  |
| GA | 245 (44.55) | 257 (46.73) | 1.04 (0.81-1.35) | 0.74 | AG | 219 (39.82) | 196 (35.64) | 0.84 (0.65-1.08) | 0.18 |
| AA | 84 (15.27) | 67 (12.18) | 0.78 (0.54-1.14) | 0.20 | GG | 64 (11.63) | 73 (13.27) | 1.04 (0.86-1.25) | 0.71 |
| **Dominant model** |  |
| GG | 221 (40.18) | 226 (41.09) | 1.00 (Reference) |  | AA | 267 (48.55) | 281 (51.09) | 1.00 (Reference) |  |
| GA+AA | 329 (59.82) | 324 (58.91) | 0.98 (0.77-1.25) | 0.86 | AG+GG | 283 (51.45) | 269 (48.91) | 0.89 (0.70-1.13) | 0.34 |
| **Recessive model** |  |
| GG+GA | 466 (84.73) | 483 (87.82) | 1.00 (Reference) |  | AA+AG | 486 (88.36) | 477 (88.73) | 1.00 (Reference) |  |
| AA | 84 (15.27) | 67 (12.18) | 0.78 (0.55-1.10) | 0.16 | GG | 64 (11.64) | 73 (13.27) | 1.16 (0.81-1.66) | 0.41 |
| **ADCC** |
| **rs1799930****590G>A**  | **Controls (550) N(%)** | **Cases (200) N(%)** | **AOR** **(95% CI) a** | ***p*b** | **rs1799929****481C>T**  | **Controls (550) N(%)** | **Cases (200) N(%)** | **AOR** **(95% CI) a** | ***p*b** |
| **Codominant model** | **Codominant model** |
| GG | 221 (40.18) | 83 (41.50) | 1.00 (Reference) |  | CC | 184 (33.45) | 81 (40.50) | 1.00 (Reference) |  |
| GA | 245 (44.55) | 90 (45.00) | 0.92 (0.65-1.32) | 0.67 | CT | 272 (49.45) |  93 (46.50) | 0.81 (0.57-1.17) | 0.26 |
| AA | 84 (15.27) | 27 (13.50) | 0.82 (0.49-1.37) | 0.44 | TT | 94 (17.10) |  26 (13.00) | 0.67 (0.40-1.12) | 0.13 |
| **Dominant model** |  | **Dominant model** |
| GG | 221 (40.18) | 83 (41.50) | 1.00 (Reference) |  | CC | 184 (33.45) | 81 (40.50) | 1.00 (Reference) |  |
| GA+AA | 329 (59.82) | 117 (58.50) | 0.91 (0.65-1.27) | 0.57 | CT+TT | 366 (66.45) |  119(59.50) | 0.79 (0.56-1.11) | 0.17 |
| **Recessive model** | **Recessive model** |
| GG+GA | 466 (84.73) | 173 (86.50) | 1.00 (Reference) |  | CC+CT | 456 (82.91) |  174(87.00) | 1.00 (Reference) |  |
| AA | 84 (15.27) | 27 (13.50) | 0.87 (0.54-1.40) | 0.56 | TT | 94 (17.10) |  26 (13.00) | 0.78 (0.48-1.25) | 0.30 |
| **ADCC** | **SQCC** |
| **rs1208****803A>G**  | **Controls (550) N(%)** | **Cases** **(200) N(%)** | **AOR** **(95% CI)a** | ***p*b** | **rs1799930****590G>A**  | **Controls (550) N(%)** | **Cases (216) N(%)** | **AOR** **(95% CI) a** | ***p*b** |
| **Codominant model** |  |
| AA | 267 (48.55) | 98 (49.00) | 1.00 (Reference) |  | GG | 221 (40.18) | 89 (41.20) | 1.00 (Reference) |  |
| AG | 219 (39.82) | 71 (35.50) | 0.90 (0.63-1.30) | 0.59 | GA | 245 (44.55) | 106 (49.08) | 1.15 (0.81-1.62) | 0.43 |
| GG | 64 (11.63) | 31 (15.50) | 1.16 (0.90-1.48) | 0.25 | AA | 84 (15.27) | 21 (9.72) | 0.64 (0.37-1.11) | 0.11 |
| **Dominant model** |  |
| AA | 267 (48.55) | 98 (49.00) | 1.00 (Reference) |  | GG | 221 (40.18) | 89 (41.20) |  |  |
| AG+GG | 283 (51.45) | 102 (51.00) | 1.002(0.72-1.39) | 0.99 | GA+AA | 329 (59.82) | 127 (58.80) | 1.02 (0.73-1.41) | 0.92 |
| **Recessive model** |  |
| AA+GA | 486 (88.36) | 169 (84.50) | 1.00 (Reference) |  | GG+GA | 466 (84.73) |  195(90.28) | 1.00 (Reference) |  |
| GG | 64 (11.64) | 31 (15.50) | 1.40 (0.87-2.25) | 0.16 | AA | 84 (15.27) | 21 (9.72) | 0.60 (0.36-1.01) | 0.05 |
| **SQCC** | **SCLC** |
| **rs1208****803A>G**  | **Controls (550) N(%)** | **Cases** **(216) N(%)** | **AOR** **(95% CI)a** | ***p*b** | **rs1799930****590G>A**  | **Controls (550) N(%)** | **Cases (127) N(%)** | **AOR** **(95% CI) a** | ***p*b** |
| **Codominant model** |  |
| AA | 267 (48.55) |  115(53.24) | 1.00 (Reference) |  | GG | 221 (40.18) | 50 (39.37) | 1.00 (Reference) |  |
| AG | 219 (39.82) |  80 (37.04) | 0.80 (0.57-1.13) | 0.21 | GA | 245 (44.55) | 59 (46.46) | 1.15 (0.74-1.79) | 0.53 |
| GG | 64 (11.63) |  21 (9.72) | 0.84 (0.64-1.10) | 0.21 | AA | 84 (15.27) | 18 (14.17) | 1.12 (0.60-2.08) | 0.71 |
| **Dominant model** |  |
| AA | 267 (48.55) | 115 (53.24) | 1.00 (Reference) |  | GG | 221 (40.18) | 50 (39.37) | 1.00 (Reference) |  |
| AG+GG | 283 (51.45) | 101 (46.76) | 0.78 (0.56-1.07) | 0.13 | GA+AA | 329 (59.82) | 77 (60.63) | 1.13 (0.75-1.72) | 0.55 |
| **Recessive model** |  |  |  |  | **Recessive model** |  |  |  |  |
| AA+AG | 486 (88.36) | 195 (90.28) | 1.00 (Reference) |  | GG+GA | 466 (84.73) |  109(85.83) | 1.00 (Reference) |  |
| GG | 64 (11.64) | 21 (9.72) | 0.77 (0.45-1.32) | 0.35 | AA | 84 (15.27) | 18 (14.17) | 1.01 (0.57-1.77) | 0.97 |
| **SCLC** |
| **rs1799931****857G>A**  | **Controls (550) N(%)** | **Cases** **(127) N(%)** | **AOR** **(95% CI)a** |  | **rs1208****803A>G**  | **Controls (550) N(%)** | **Cases** **(127) N(%)** | **AOR** **(95% CI)a** | ***p*b** |
| **Codominant model** | **Codominant model** |
| GG | 264 (48.00) | 59 (46.46) | 1.00 (Reference) |  | AA | 267 (48.55) | 64 (50.39) | 1.00 (Reference) |  |
| GA | 223 (40.55) |  53 (41.73) | 0.97 (0.63-1.51) | 0.91 | AG | 219 (39.82) | 44 (34.65) | 0.79 (0.51-1.24) | 0.30 |
| AA | 63 (11.45) | 15 (11.81) | 1.004(0.52-1.95) | 0.67 | GG | 64 (11.63) | 19 (14.96) | 1.12 (0.83-1.52) | 0.46 |
| **Dominant model** | **Dominant model** |
| GG | 264 (48.00) | 59 (46.46) | 1.00 (Reference) |  | AA | 267 (48.55) | 64 (50.39) | 1.00 (Reference) |  |
| GA+AA | 286 (52.00) | 68 (53.54) | 0.99 (0.66-1.50) | 0.99 | AG+GG | 283 (51.45) | 63 (49.61) | 0.89 (0.59-1.33) | 0.56 |
| **Recessive model** | **Recessive model** |
| GG+GA | 487 (88.55) | 112 (88.19) | 1.00 (Reference) |  | AA+AG | 486 (88.36) | 108 (85.04) | 1.00 (Reference) |  |
| AA | 63 (11.45) | 15 (11.81) | 1.04 (0.56-1.94) | 0.89 | GG | 64 (11.64) | 19 (14.96) | 1.38 (0.77-2.46) | 0.28 |
| a)-Adjusted Odds ratios, 95% confidence intervals and their corresponding *p*-values were calculated by logistic regression analysis after adjusting for age, gender and smoking status. (b)-Two-sided χ2 test for either genotype distribution or allelic frequencies between the cases and controls. The number in bold indicates the significant values in the table. |

|  |
| --- |
| **Supplementary Table S3** Relationship of different *NAT2* genotypes with the smoking status of cases and controls |
| **SMOKER** |
| **Genotype****rs1799930****590G>A**  | **Controls (425) N(%)** | **Cases (444) N(%)** | **AOR** **(95% CI) a** | ***p*b** | **Genotype****rs1799931****857G>A**  | **Controls (425) N(%)** | **Cases** **(444) N(%)** | **AOR** **(95% CI)a** |  |
| **Codominant model** |  |
| GG | 177 (41.65) | 188 (42.34) | 1.00 (Reference) |  | GG | 195 (45.88) | 182 (40.99) | 1.00 (Reference) |  |
| GA | 184 (43.29) | 203 (45.72) | 1.05 (0.78-1.40) | 0.75 | GA | 177 (41.65) |  216(48.65) | 1.32 (0.99-1.75) | 0.06 |
| AA | 64 (15.06) | 53 (11.94) | 0.81 (0.53-1.24) | 0.33 | AA | 53 (12.47) | 46 (10.36) | 0.91 (0.58-1.44) | 0.69 |
| **Dominant model** |  |
| GG | 177 (41.65) | 188 (42.34) | 1.00 (Reference) |  | GG | 195 (45.88) | 182 (40.99) | 1.00 (Reference) |  |
| GA+AA | 248 (58.35) | 256 (57.66) | 0.98 (0.75-1.29) | 0.91 | GA+AA | 230 (54.12) | 262 (59.01) | 1.23 (0.94-1.62) | 0.14 |
| **Recessive model** |  |
| GG+GA | 361 (84.94) | 391 (88.06) | 1.00 (Reference) |  | GG+GA | 372 (87.53) | 398 (89.64) | 1.00 (Reference) |  |
| AA | 64 (15.06) | 53 (11.94) | 0.79 (0.53-1.18) | 0.25 | AA | 53 (12.47) | 46 (10.36) | 0.82 (0.53-1.25) | 0.35 |
| **SMOKER** | **NON-SMOKER** |
| **Genotype****rs1208****803A>G**  | **Controls (425) N(%)** | **Cases** **(444) N(%)** | **AOR** **(95% CI)a** | ***p*b** | **Genotype****rs1799930****590G>A**  | **Controls (125) N(%)** | **Cases (106) N(%)** | **AOR** **(95% CI) a** | ***p*b** |
| **Codominant model** |  |
| AA | 200 (47.06) | 230 (51.80) | 1.00 (Reference) |  | GG | 44 (35.20) | 38 (35.85) | 1.00 (Reference) |  |
| AG | 173 (40.70) | 159 (35.81) | 0.79 (0.59-1.06) | 0.12 | GA |  61 (48.80) |  54 (50.94) | 1.07 (0.60-1.92) | 0.81 |
| GG | 52 (12.24) | 55 (12.39) | 0.95 (0.76-1.18) | 0.63 | AA |  20 (16.00) |  14 (13.21) | 0.79 (0.33-1.89) | 0.60 |
| **Dominant model** |  |
| AA | 200 (47.06) | 230 (51.80) | 1.00 (Reference) |  | GG | 44 (35.20) | 38 (35.85) | 1.00 (Reference) |  |
| AG+GG | 225 (52.94) | 214 (48.20) | 0.81 (0.62-1.07) | 0.14 | GA+AA | 81(64.80) | 68 (64.15) | 1.03 (0.59-1.80) | 0.91 |
| **Recessive model** |  |
| AA+AG | 373 (87.76) | 389 (87.61) | 1.00 (Reference) |  | GG+GA | 105 (84.00) | 92 (86.79) | 1.00 (Reference) |  |
| GG | 52 (12.24) | 55 (12.39) | 0.99 (0.66-1.50) | 0.97 | AA | 20 (16.00) | 14 (13.21) | 0.87 (0.41-1.87) | 0.73 |
| **NON-SMOKER** |
| **Genotype****rs1799929****481C>T**  | **Controls (125) N(%)** | **Cases (106) N(%)** | **AOR** **(95% CI) a** | ***p*b** | **Genotype****rs1208****803A>G**  | **Controls (125) N(%)** | **Cases** **(106) N(%)** | **AOR** **(95% CI)a** | ***p*b** |
| **Codominant model** |  |
| CC | 58 (46.40) | 44 (41.51) | 1.00 (Reference) |  | AA | 67 (53.60) | 51 (48.11) | 1.00 (Reference) |  |
| CT |  53 (42.40) | 48 (45.28) | 1.12 (0.64-1.98) | 0.68 | AG | 46 (36.80) | 37 (34.91) | 1.27 (0.70-2.31) | 0.42 |
| TT | 14 (11.20) | 14 (13.21) | 1.22 (0.51-2.89) | 0.65 | GG | 12 (9.60) | 18 (16.98) | 1.41 (0.92-2.15) | 0.11 |
| **Dominant model** |  |
| CC | 58 (46.40) | 44 (41.51) | 1.00 (Reference) |  | AA | 67 (53.60) | 51 (48.11) | 1.00 (Reference) |  |
| CT+TT | 67 (53.60) | 62 (58.49) | 1.14 (0.67-1.95) | 0.63 | AG+GG | 58 (46.40) | 55 (51.89) | 1.42 (0.83-2.43) | 0.20 |
| **Recessive model** |  |
| CC+CT | 111 (88.80) | 92 (86.79) | 1.00 (Reference) |  | AA+AG | 113 (90.40) | 88 (83.02) | 1.00 (Reference) |  |
| TT | 14 (11.20) | 14 (13.21) | 1.16 (0.51-2.61) | 0.72 | GG | 12 (9.60) | 18 (16.98) | 1.81 (0.81-4.05) | 0.14 |
| **LIGHT-SMOKER** |
| **Genotype****rs1799930****590G>A**  | **Controls (300) N(%)** | **Cases (248) N(%)** | **AOR** **(95% CI) a** | ***p*b** | **Genotype****rs1799931****857G>A**  | **Controls (300) N(%)** | **Cases** **(248) N(%)** | **AOR** **(95% CI)a** |  |
| **Codominant model** |  |
| GG | 124 (41.33) | 102 (41.13) | 1.00 (Reference) |  | GG | 143 (47.67) | 105 (42.34) | 1.00 (Reference) |  |
| GA | 127 (42.33) | 118 (47.58) | 1.13 (0.78-1.64) | 0.51 | GA | 123 (41.00) |  116 (46.77) | 1.28 (0.89-1.85) | 0.18 |
| AA | 49 (16.34) | 28 (11.29) | 0.71 (0.41-1.23) | 0.23 | AA | 34 (11.33) | 27 (10.89) | 0.99 (0.55-1.80) | 0.98 |
| **Dominant model** |  |
| GG | 124 (41.33) | 102 (41.13) | 1.00 (Reference) |  | GG | 143 (47.67) | 105 (42.34) | 1.00 (Reference) |  |
| GA+AA | 176 (58.67) | 146 (58.87) | 1.02 (0.71-1.44) | 0.93 | GA+AA | 157 (52.33) | 143 (57.66) | 1.23 (0.87-1.75) | 0.24 |
| **Recessive model** |  |
| G+GA | 251 (83.66) | 220 (88.71) | 1.00 (Reference) |  | GG+GA | 266 (88.67) | 221 (89.11) | 1.00 (Reference) |  |
| AA | 49 (16.34) | 28 (11.29) | 0.67 (0.39-1.09) | 0.10 | AA | 34 (11.33) | 27 (10.89) | 0.93 (0.53-1.61) | 0.78 |
| **LIGHT-SMOKER** | **HEAVY-SMOKER** |
| **Genotype****rs1208****803A>G**  | **Controls (300) N(%)** | **Cases** **(248) N(%)** | **AOR** **(95% CI)a** | ***p*b** | **Genotype****rs1799930****590G>A**  | **Controls (125) N(%)** | **Cases (196) N(%)** | **AOR** **(95% CI) a** | ***p*b** |
| **Codominant model** |  |
| AA | 144 (48.00) | 129 (52.01) | 1.00 (Reference) |  | GG | 53 (42.40) | 86 (43.88) | 1.00 (Reference) |  |
| AG | 119 (39.67) | 89 (35.89) | 0.82 (0.57-1.20) | 0.31 | GA |  57 (45.60) |  85 (43.37) | 0.94 (0.58-1.52) | 0.79 |
| GG | 37 (12.33) | 30 (12.10) | 0.95 (0.72-1.25) | 0.70 | AA |  15 (12.00) |  25 (12.75) | 1.15 (0.55-2.40) | 0.71 |
| **Dominant model** |  |
| AA | 144 (48.00) | 129 (52.02) | 1.00 (Reference) |  | GG | 53 (42.40) | 86 (43.88) | 1.00 (Reference) |  |
| AG+GG | 156 (52.00) | 119 (47.98) | 0.84 (0.59-1.18) | 0.32 | GA+AA | 72 (57.60) | 110 (56.12) | 0.97 (0.61-1.53) | 0.89 |
| **Recessive model** |  |
| AA+AG | 263 (87.67) | 218 (87.90) | 1.00 (Reference) |  | GG+GA | 110 (88.00) | 171 (87.25) | 1.00 (Reference) |  |
| GG | 37 (12.33) | 30 (12.10) | 0.96 (0.56-1.64) | 0.88 | AA | 15 (12.00) | 25 (12.75) | 1.13 (0.57-2.24) | 0.73 |
| **HEAVY-SMOKER** |
| **Genotype****rs1799931****857G>A**  | **Controls (125) N(%)** | **Cases** **(196) N(%)** | **AOR** **(95% CI)a** |  | **Genotype****rs1208****803A>G**  | **Controls (125) N(%)** | **Cases** **(196) N(%)** | **AOR** **(95% CI)a** | ***p*b** |
| **Codominant model** | **Codominant model** |
| GG | 52 (41.60) | 77 (39.29) | 1.00 (Reference) |  | AA | 56 (44.80) | 101 (51.53) | 1.00 (Reference) |  |
| GA | 54 (43.20) | 100 (51.02) | 1.24 (0.76-2.01) | 0.39 | AG | 54 (43.20) | 70 (35.71) | 0.68 (0.42-1.12) | 0.13 |
| AA | 19 (15.20) | 19 (9.69) | 0.70 (0.34-1.45) | 0.34 | GG | 15 (12.00) | 25 (12.76) | 0.83 (0.40-1.74) | 0.63 |
| **Dominant model** |  |  |  |  | **Dominant model** |
| GG | 52 (41.60) | 77 (39.29) | 1.00 (Reference) |  | AA | 56 (44.80) | 101 (51.53) | 1.00 (Reference) |  |
| GA+AA | 73 (58.40) | 119 (60.71) | 1.09 (0.69-1.73) | 0.70 | AG+GG | 69 (55.20) | 95 (48.47) | 0.72 (0.45-1.13) | 0.15 |
| **Recessive model** | **Recessive model** |
| GG+GA | 106 (84.80) | 177 (90.31) | 1.00 (Reference) |  | AA+AG | 110 (88.00) | 171 (87.24) | 1.00 (Reference) |  |
| AA | 19 (15.20) | 19 (9.69) | 0.62 (0.31-1.22) | 0.17 | GG | 15 (12.00) | 25 (12.76) | 1.06 (0.53-2.11) | 0.87 |
| a)-Adjusted Odds ratios, 95% confidence intervals and their corresponding *p*-values were calculated by logistic regression analysis after adjusting for age, gender. (b)-Two-sided χ2 test for either genotype distribution or allelic frequencies between the cases and controls. The number in bold indicates the significant values in the table. |

|  |
| --- |
| **Supplementary Table S4**Relationship of different *NAT2* polymorphisms on the basis of gender |
| **MALE** |
| **Genotype****rs1799931****857G>A**  | **Controls (459) N(%)** | **Cases** **(458) N(%)** | **AOR** **(95% CI)a** |  | **Genotype****rs1208****803A>G**  | **Controls (459) N(%)** | **Cases** **(458) N(%)** | **AOR** **(95% CI)a** | ***p*b** |
| **Codominant model** | **Codominant model** |
| GG | 212 (46.19) | 189 (41.27) | 1.00 (Reference) |  | AA | 221 (48.15) | 241 (52.62) | 1.00 (Reference) |  |
| GA | 190 (41.39) | 221 (48.25) | 1.32 (1.00-1.74) | **0.048** | AG | 181 (39.43) | 160 (34.93) | 0.81 (0.61-1.07) | 0.14 |
| AA | 57 (12.42) | 48 (10.48) | 0.93 (0.60-1.44) | 0.75 | GG | 57 (12.42) | 57 (12.45) | 0.89 (0.59-1.35) | 0.59 |
| **Dominant model** | **Dominant model** |
| GG | 212 (46.19) | 189 (41.27) | 1.00 (Reference) |  | AA | 221 (48.15) | 241 (52.62) | 1.00 (Reference) |  |
| GA+AA | 247 (53.81) | 269 (58.73) | 1.24 (0.95-1.61) | 0.11 | AG+GG | 238 (51.85) | 217 (47.38) | 0.83 (0.64-1.07) | 0.15 |
| **Recessive model** | **Recessive model** |
| GG+GA | 402 (87.58) | 410 (89.52) | 1.00 (Reference) |  | AA+AG | 402 (87.58) | 401 (87.55) | 1.00 (Reference) |  |
| AA | 57 (12.42) | 48 (10.48) | 0.83 (0.55-1.25) | 0.38 | GG | 57 (12.42) | 57 (12.45) | 0.98 (0.66-1.45) | 0.92 |
| **FEMALE** |
| **Genotype****rs1799929****481C>T**  | **Controls (91) N(%)** | **Cases (92) N(%)** | **AOR** **(95% CI) a** | ***p*b** |  |  |  |  |  |
| **Codominant model** |  |
| CC | 44 (48.35) | 39 (42.39) | 1.00 (Reference) |  |  |  |  |  |  |
| CT | 37 (40.66) | 39 (42.39) | 1.19 (0.61-2.35) | 0.61 |  |  |  |  |  |
| TT | 10 (10.99) | 14 (15.22) | 1.37 (0.49-3.80) | 0.54 |  |  |  |  |  |
| **Dominant model** |  |
| CC | 44 (48.35) | 39 (42.39) | 1.00 (Reference) |  |  |  |  |  |  |
| CT+TT | 47 (51.65) | 53 (57.61) | 1.37 (0.49-3.80) | 0.54 |  |  |  |  |  |
| **Recessive model** |  |
| CC+CT | 81 (89.01) | 78 (84.78) | 1.00 (Reference) |  |  |  |  |  |  |
| TT | 10 (10.99) | 14 (15.22) | 1.27 (0.48-3.31) | 0.63 |  |  |  |  |  |
| a)-Adjusted Odds ratios, 95% confidence intervals and their corresponding *p*-values were calculated by logistic regression analysis after adjusting for age, gender. (b)-Two-sided χ2 test for either genotype distribution or allelic frequencies between the cases and controls. The number in bold indicates the significant values in the table. |

|  |
| --- |
| **SupplementaryTable S5** Relationship of different *NAT2* genotypes with the clinical-pathological parameters |
| **CLINICAL STAGE** |
| **Genotype****rs1799930****590G>A**  | **III** **N= 229(%)** | **IV** **N= 247(%)** | **AOR** **(95% CI) a** | ***p*b** | **Genotype****rs1799929****481C>T**  | **III** **N= 229(%)** | **IV** **N= 247(%)** | **AOR** **(95% CI) a** | ***p*b** |
| **Codominant model** | **Codominant model** |
| GG | 102 (44.54) | 95 (38.46) | 1.00 (Reference) |  | CC | 100 (43.67) | 101 (40.89) | 1.00 (Reference) |  |
| GA | 99 (43.23) | 119 (48.18) | 1.24 (0.83-1.85) | 0.30 | CT | 103 (44.98) | 116 (46.96) | 1.10 (0.74-1.64) | 0.64 |
| AA | 28 (12.23) | 33 (13.36) | 1.20 (0.65-2.21) | 0.56 | TT | 26 (11.35) | 30 (12.15) | 1.10 (0.58-2.04) | 0.79 |
| **Dominant model** | **Dominant model** |
| GG | 102 (44.54) | 95 (38.46) | 1.00 (Reference) |  | CC | 100 (43.67) | 101 (40.89) | 1.00 (Reference) |  |
| GA+AA | 127 (55.46) | 152 (61.54) | 1.23 (0.84-1.80) | 0.29 | CT+TT | 129 (56.33) | 146 (59.11) | 1.10 (0.75-1.62) | 0.61 |
| **Recessive model** | **Recessive model** |
| GG+GA | 201 (87.77) | 214 (86.64) | 1.00 (Reference) |  | CC+CT | 203 (88.65) | 217 (87.85) | 1.00 (Reference) |  |
| AA | 28 (12.23) | 33 (13.36) | 1.10 (0.62-1.93) | 0.74 | TT | 26 (11.35) | 30 (12.15) | 1.06 (0.59-1.90) | 0.85 |
| **Genotype****rs1799931****857G>A**  | **III** **N= 229(%)** | **IV** **N= 247(%)** | **AOR** **(95% CI)a** |  | **Genotype****rs1208****803A>G**  | **III** **N= 229(%)** | **IV** **N= 247(%)** | **AOR** **(95% CI)a** | ***p*b** |
| **Codominant model** | **Codominant model** |
| GG | 94 (41.05) | 96 (38.87) | 1.00 (Reference) |  | AA | 116 (50.65) | 121 (48.99) | 1.00 (Reference) |  |
| GA | 112 (48.91) | 126 (51.01) | 1.07 (0.72-1.59) | 0.75 | AG | 82 (35.81) | 92 (37.24) | 1.05 (0.70-1.59) | 0.80 |
| AA | 23 (10.04) | 25 (10.12) | 0.98 (0.50-1.91) | 0.96 | GG | 31 (13.54) | 34 (13.77) | 1.00 (0.56-1.77) | 0.99 |
| **Dominant model** | **Dominant model** |
| GG | 94 (41.05) | 96 (38.87) | 1.00 (Reference) |  | AA | 116 (50.65) | 121 (48.99) | 1.00 (Reference) |  |
| GA+AA | 135 () | 151 () | 1.05 (0.71-1.54) | 0.81 | AG+GG | 113 (49.34) | 126 (51.01) | 1.03 (0.71-1.50) | 0.87 |
| **Recessive model** | **Recessive model** |
| GG+GA | 206 (89.96) | 222 (89.88) | 1.00 (Reference) |  | AA+AG | 198 (86.46) | 213 (86.23) | 1.00 (Reference) |  |
| AA | 23 (10.04) | 25 (10.12) | 0.96 (0.52-1.79) | 0.90 | GG | 31 (13.54) | 34 (13.77) | 0.96 (0.55-1.66) | 0.88 |
| **PRIMARY TUMOR EXTENSION** |
| **Genotype****rs1799930****590G>A**  | **T3** **N= 115(%)** | **T4** **N= 299(%)** | **AOR** **(95% CI) a** | ***p*b** | **Genotype****rs1799929****481C>T**  | **T3** **N= 115(%)** | **T4** **N= 299(%)** | **AOR** **(95% CI) a** | ***p*b** |
| **Codominant model** | **Codominant model** |
| GG | 43 (37.39) | 125 (41.81) | 1.00 (Reference) |  |  | 48 (41.74) | 132 (44.15) | 1.00 (Reference) |  |
| GA | 56 (48.70) | 140 (46.82) | 0.83 (0.52-1.33) | 0.44 |  | 52 (45.22) | 136 (45.48) | 0.98 (0.61-1.55) | 0.92 |
| AA | 16 (13.91) | 34 (11.37) | 0.74 (0.36-1.50) | 0.40 |  | 15 (13.04) | 31 (10.37) | 0.70 (0.34-1.44) | 0.33 |
| **Dominant model** | **Dominant model** |
| GG | 43 (37.39) | 125 (41.81) | 1.00 (Reference) |  |  | 48 (41.74) | 132 (44.15) | 1.00 (Reference) |  |
| GA+AA | 72 (62.61) | 174 (58.19) | 0.81 (0.52-1.26) | 0.35 |  | 67 (58.26) | 167 (55.85) | 0.93 (0.60-1.45) | 0.76 |
| **Recessive model** | **Recessive model** |
|  | 99 (86.09) | 265 (88.63) | 1.00 (Reference) |  |  | 100 (86.96) | 268 (89.63) | 1.00 (Reference) |  |
|  | 16 (13.91) | 34 (11.37) | 1.10 (0.63-1.93) | 0.74 |  | 15 (13.04) | 31 (10.37) | 0.79 (0.41-1.54) | 0.49 |
| **Genotype****rs1799931****857G>A**  | **T3** **N= 115(%)** | **T4** **N= 299(%)** | **AOR** **(95% CI)a** |  | **Genotype****rs1208****803A>G**  | **T3** **N= 115(%)** | **T4** **N= 299(%)** | **AOR** **(95% CI)a** | ***p*b** |
| **Codominant model** | **Codominant model** |
| GG | 52 (45.22) | 108 (36.12) | 1.00 (Reference) |  | AA | 58 (50.43) | 154 (51.51) | 1.00 (Reference) |  |
| GA | 57 (49.56) | 160 (53.51) | 1.38 (0.88-2.17) | 0.16 | AG | 39 (33.91) | 106 (35.45) | 1.01 (0.62-1.63) | 0.97 |
| AA | 6 (5.22) | 31 (10.37) | 2.41 (0.94-6.19) | 0.06 | GG | 18 (15.65) | 39 (13.04) | 0.81 (0.43-1.54) | 0.52 |
| **Dominant model** | **Dominant model** |  |
| GG | 52 (45.22) | 108 (36.12) | 1.00 (Reference) |  | AA | 58 (50.43) | 154 (51.51) | 1.00 (Reference) |  |
| GA+AA | 63 (54.78) | 191 (63.88) | 1.49 (0.96-2.32) | 0.07 | AG+GG | 57 (49.57) | 145 (48.49) | 0.96 (0.62-1.47) | 0.84 |
| **Recessive model** | **Recessive model** |
| GG+GA | 109 (94.78) | 268 (89.63) | 1.00 (Reference) |  | AA+AG | 97 (84.35) | 260 (86.96) | 1.00 (Reference) |  |
| AA | 6 (5.22) | 31 (10.37) | 2.05 (0.83-5.07) | 0.12 | GG | 18 (15.65) | 39 (13.04) | 0.82 (0.44-1.51) | 0.52 |
| **LYMPH NODE INVASION** |
| **Genotype****rs1799930****590G>A**  | **Nx+N0+N1** **N= 110(%)** | **N2+N3+N4** **N= 390(%)** | **AOR** **(95% CI) a** | ***p*b** | **Genotype****rs1799929****481C>T**  | **Nx+N0+N1** **N= 110(%)** | **N2+N3+N4** **N= 390(%)** | **AOR** **(95% CI) a** | ***p*b** |
| **Codominant model** | **Codominant model** |
| GG | 33 (30.00) | 171 (43.85) | 1.00 (Reference) |  | CC | 48 (43.64) | 165 (42.31) | 1.00 (Reference) |  |
| GA | 62 (56.36) | 173 (44.36) | 0.53 (0.33-0.85) | **0.009** | CT | 48 (43.64) | 179 (45.90) | 1.10 (0.69-1.73) | 0.69 |
| AA | 15 (13.64) | 46 (11.79) | 0.56 (0.28-1.15) | 0.11 | TT | 14 (12.72) | 46 (11.79) | 0.94 (0.47-1.88) | 0.87 |
| **Dominant model** | **Dominant model** |
| GG | 33 (30.00) | 171 (43.85) | 1.00 (Reference) |  | CC | 48 (43.64) | 165 (42.31) | 1.00 (Reference) |  |
| GA+AA | 77 (70.00) | 219 (56.15) | 0.54 (0.34-0.85) | **0.008** | CT+TT | 62 (56.36) | 225 (57.69) | 1.07 (0.69-1.64) | 0.76 |
| **Recessive model** | **Recessive model** |
| GG+GA | 95 (86.36) | 344 (88.21) | 1.00 (Reference) |  | CC+CT | 96 (87.27) | 344 (88.21) | 1.00 (Reference) |  |
| AA | 15 (13.64) | 46 (11.79) | 0.83 (0.44-1.56) | 0.57 | TT | 14 (12.72) | 46 (11.79) | 0.93 (0.49-1.77) | 0.82 |
| **Genotype****rs1799931****857G>A**  | **Nx+N0+N1** **N= 110(%)** | **N2+N3+N4** **N= 390(%)** | **AOR** **(95% CI)a** |  | **Genotype****rs1208****803A>G**  | **Nx+N0+N1** **N= 110(%)** | **N2+N3+N4** **N= 390(%)** | **AOR** **(95% CI)a** | ***p*b** |
| **Codominant model** | **Codominant model** |
| GG | 47 (42.73) | 148 (37.95) | 1.00 (Reference) |  | AA | 67 (60.91) | 183 (46.92) | 1.00 (Reference) |  |
| GA | 55 (50.00) | 199 (51.03) | 1.16 (0.74-1.81) | 0.52 | AG | 36 (32.73) | 146 (37.44) | 1.49 (0.94-2.36) | 0.09 |
| AA | 8 (7.27) | 43 (11.02) | 1.70 (0.74-3.88) | 0.21 | GG | 7 (6.36) | 61 (15.64) | 3.22 (1.39-7.42) | **0.006** |
| **Dominant model** | **Dominant model** |
| GG | 47 (42.73) | 148 (37.95) | 1.00 (Reference) |  | AA | 67 (60.91) | 183 (46.92) | 1.00 (Reference) |  |
| GA+GG | 63 (57.27) | 242 (62.05) | 1.23 (0.79-1.89) | 0.35 | AG+GG | 43 (39.09) | 207 (53.08) | 1.78 (1.15-2.75) | **0.0091** |
| **Recessive model** | **Recessive model** |
| GG+GA | 102 (92.73) | 347 (88.98) | 1.00 (Reference) |  | AA+AG | 103 (93.64) | 329 (84.36) | 1.00 (Reference) |  |
| AA | 8 (7.27) | 43 (11.02) | 1.58 (0.72-3.46) | 0.26 | GG | 7 (6.36) | 61 (15.64) | 2.78 (1.23-6.29) | **0.014** |
| **METASTASIS** |
| **Genotype****rs1799930****590G>A**  | **No (M0)** **N= 256(%)** | **Yes (M1)****N= 246(%)** | **AOR** **(95% CI) a** | ***p*b** | **Genotype****rs1799929****481C>T**  | **No (M0)** **N= 256(%)** | **Yes (M1)****N= 246(%)** | **AOR** **(95% CI) a** | ***p*b** |
| **Codominant model** | **Codominant model** |
| GG | 110 (42.97) | 95 (38.62) | 1.00 (Reference) |  | CC | 115 (44.92) | 100 (40.65) | 1.00 (Reference) |  |
| GA | 117 (45.70) | 119 (48.37) | 0.86 (0.58-1.28) | 0.47 | CT | 110 (42.97) | 117 (47.56) | 1.25 (0.85-1.85) | 0.25 |
| AA | 29 (11.33) | 32 (13.01) | 0.80 (0.44-1.48) | 0.49 | TT | 31 (12.11) | 29 (11.79) | 1.05 (0.58-1.91) | 0.87 |
| **Dominant model** | **Dominant model** |
| GG | 110 (42.97) | 95 (38.62) | 1.00 (Reference) |  | CC | 115 (44.92) | 100 (40.65) | 1.00 (Reference) |  |
| GA+AA | 146 (62.14) | 151 (57.03) | 0.86 (0.59-1.24) | 0.41 | CT+TT | 141 (55.08) | 146 (59.35) | 1.22 (0.84-1.77) | 0.29 |
| **Recessive model** | **Recessive model** |
| GG+GA | 227 (88.67) | 214 (86.99) | 1.00 (Reference) |  | CC+CT | 225 (87.89) | 217 (88.21) | 1.00 (Reference) |  |
| AA | 29 (11.33) | 32 (13.01) | 0.88 (0.50-1.54) | 0.65 | TT | 31 (12.11) | 29 (11.79) | 0.97 (0.55-1.70) | 0.92 |
| **Genotype****rs1799931****857G>A**  | **No (M0)** **N= 256(%)** | **Yes (M1)****N= 246(%)** | **AOR** **(95% CI)a** |  | **Genotype****rs1208****803A>G**  | **No (M0)** **N= 256(%)** | **Yes (M1)****N= 246(%)** | **AOR** **(95% CI)a** | ***p*b** |
| **Codominant model** | **Codominant model** |
| GG | 103 (40.23) | 94 (38.21) | 1.00 (Reference) |  | AA | 134 (52.34) | 118 (47.97) | 1.00 (Reference) |  |
| GA | 128 (50.00) | 126 (51.22) | 1.05 (0.72-1.55) | 0.79 | AG | 86 (33.60) | 96 (39.02) | 0.78 (0.53-1.16) | 0.23 |
| AA | 25 (9.77) | 26 (10.57) | 1.10 (0.58-2.09) | 0.77 | GG | 36 (14.06) | 32 (13.01) | 1.04 (0.60-1.83) | 0.88 |
| **Dominant model** |  |  |  |  | **Dominant model** |
| GG | 103 (40.23) | 94 (38.21) | 1.00 (Reference) |  | AA | 134 (52.34) | 118 (47.97) | 1.00 (Reference) |  |
| GA+AA | 153 (59.77) | 152 (61.79) | 1.06 (0.73-1.54) | 0.76 | AG+GG | 122 (47.66) | 128 (52.03) | 0.85 (0.59-1.22) | 0.38 |
| **Recessive model** | **Recessive model** |
| GG+GA | 231 (90.23) | 220 (89.43) | 1.00 (Reference) |  | AA+AG | 220 (85.94) | 214 (86.99) | 1.00 (Reference) |  |
| AA | 25 (9.77) | 26 (10.57) | 1.08 (0.59-1.97) | 0.80 | GG | 36 (14.06) | 32 (13.01) | 1.17 (0.68-2.01) | 0.56 |
| a)-Adjusted Odds ratios, 95% confidence intervals and their corresponding *p*-values were calculated by logistic regression analysis after adjusting for age, gender. (b)-Two-sided χ2 test for either genotype distribution or allelic frequencies between the cases and controls. The number in bold indicates the significant values in the table. |

|  |
| --- |
| **Supplementary Table S6** Relationship of genotypic distribution with clinic-pathological parameter on the basis of response to chemotherapy |
| **Genotype****rs1799930****590G>A**  | **CR+PR****(118), n (%)** | **SD+PD****(148), n (%)** | **AOR (95% CI) a** | ***p*b** | **Genotype****rs1799929****481C>T**  | **CR+PR****(118), n (%)** | **SD+PD****(148), n (%)** | **AOR (95% CI) a** | ***p*b** |
| **Codominant model** | **Codominant model** |
| GG | 41 (34.75) | 60 (40.54) | 1.00 (Reference) |  | CC | 54 (45.76) | 63 (42.57) | 1.00 (Reference) |  |
| GA | 62 (52.54) | 75 (50.68) | 1.22 (0.72-2.07) | 0.47 | CT | 49 (41.53) | 65 (43.92) | 0.88 (0.52-1.48) | 0.63 |
| AA | 15 (12.71) | 13 (8.78) | 1.90 (0.79-4.58) | 0.15 | TT | 15 (12.71) | 20 (13.51) | 0.83 (0.38-1.81) | 0.65 |
| **Dominant model** | **Dominant model** |
| GG | 41 (34.75) | 60 (40.54) | 1.00 (Reference) |  | CC | 54 (45.76) | 63 (42.57) | 1.00 (Reference) |  |
| GA+AA | 77 (65.25) | 88 (59.46) | 1.31 (0.79-2.17) | 0.30 | CT+TT | 64 (54.24) | 85 (57.43) | 0.87 (0.53-1.42) | 0.58 |
| **Recessive model** | **Recessive model** |
| GG+GA | 103 (87.29) | 135 (91.22) | 1.00 (Reference) |  | CC+CT | 103 (87.29) | 128 (86.49) | 1.00 (Reference) |  |
| AA | 15 (12.71) | 13 (8.78) | 1.61 (0.72-3.59) | 0.24 | TT | 15 (12.71) | 20 (13.51) | 0.89 (0.43-1.84) | 0.76 |
| **Genotype****rs1799931****857G>A**  | **CR+PR****(118), n (%)** | **SD+PD****(148), n (%)** | **AOR (95% CI) a** | ***p*b** | **Genotype****rs1208****803A>G**  | **CR+PR****(118), n (%)** | **SD+PD****(148), n (%)** | **AOR (95% CI) a** | ***p*b** |
| **Codominant model** | **Codominant model** |
| GG | 45 (38.14) | 55 (37.16) | 1.00 (Reference) |  | AA | 63 (53.39) | 66 (44.60) | 1.00 (Reference) |  |
| GA | 66 (55.93) | 77 (52.03) | 1.03 (0.61-1.73) | 0.91 | AG | 39 (33.05) | 64 (43.24) | 0.63 (0.37-1.08) | 0.09 |
| AA | 7 (5.93) | 16 (10.81) | 0.52 (0.19-1.40) | 0.20 | GG | 16 (13.56) | 18 (12.16) | 0.94 (0.43-2.02) | 0.87 |
| **Dominant model** | **Dominant model** |
| GG | 45 (38.14) | 55 (37.16) | 1.00 (Reference) |  | AA | 63 (53.39) | 66 (44.60) | 1.00 (Reference) |  |
| GA+AA | 73 (61.86) | 93 (62.84) | 0.94 (0.57-1.56) | 0.81 | AG+GG | 55 (46.61) | 82 (55.40) | 0.70 (0.42-1.14) | 0.15 |
| **Recessive model** | **Recessive model** |
| GG+GA | 111 (94.07) | 132 (89.19) | 1.00 (Reference) |  | AA+AG | 102 (86.44) | 130 (87.84) | 1.00 (Reference) |  |
| AA | 7 (5.93) | 16 (10.81) | 0.52 (0.20-1.31) | 0.16 | GG | 16 (13.56) | 18 (12.16) | 1.13 (0.54-2.33) | 0.75 |
| a)-Adjusted Odds ratios, 95% confidence intervals and their corresponding *p*-values were calculated by logistic regression analysis after adjusting for age, gender. (b)-Two-sided χ2 test for either genotype distribution or allelic frequencies between the cases and controls. The number in bold indicates the significant values in the table |

|  |
| --- |
| **Supplementary Table S7** Association of *NAT2* on overall survival in lung cancer cases and on basis of histology |
| **OVERALL** |
| **Genotype****rs1799930****590G>A**  | **CASES****n(%), N=473** | **DEAD****n(%), N=362** | **ALIVE****n(%), N=111** | **Univariate analysis** | **Multivariate analysis** |
| **MST (months)** | **Log rank *p*** | **Unadjusted HRa** | **Adjusted HRb (95% CI)** | ***p*** |
| GG | 192 (40.59) | 147 (40.61) | 45 (40.54) | 7.53 |  |  |  |  |
| GA | 222 (46.93) | 174 (48.07) | 48 (43.24) | 9.20 | 0.79 | 0.97 (0.78-1.21) | 1.02 (0.81-1.29) | 0.86 |
| AA | 59 (12.48) | 41 (11.32) | 18 (16.22) | 7.57 | 0.57 | 0.90 (0.64-1.27) | 1.01 (0.69-1.46) | 0.98 |
| GA+AA | 281 (59.41) | 215 (59.39) | 66 (59.46) | 8.63 | 0.69 | 0.96 (0.78-1.18) | 1.01 (0.81-1.26) | 0.95 |
| **Genotype****rs1799931****857G>A**  | **CASES****n(%), N=473** | **DEAD****n(%), N=362** | **ALIVE****n(%), N=111** | **Univariate analysis** | **Multivariate analysis** |
| **MST (months)** | **Log rank *p*** | **Unadjusted HRa** | **Adjusted HRb (95% CI)** | ***P*** |
| GG | 171 (36.15) | 139 (38.40) | 32 (28.83) | 8.40 |  |  |  |  |
| GA | 249 (52.64) | 187 (51.66) | 62 (55.86) | 7.57 | 0.80 | 1.03 (0.82-1.28) | 1.06 (0.84-1.34) | 0.59 |
| AA | 53 (11.21) | 36 (9.94) | 17 (15.31) | 8.23 | 0.43 | 0.86 (0.61-1.23) | 0.99 (0.66-1.47) | 0.95 |
| GA+AA | 302 (63.85) | 223 (61.60) | 79 (71.17) | 7.60 | 0.95 | 0.99 (0.80-1.23) | 1.04 (0.83-1.30) | 0.72 |
| **Genotype****rs1799929****481C>T**  | **CASES****n(%), N=473** | **DEAD****n(%), N=362** | **ALIVE****n(%), N=111** | **Univariate analysis** | **Multivariate analysis** |
| **MST (months)** | **Log rank *p*** | **Unadjusted HRa** | **Adjusted HRb (95% CI)** | ***P*** |
| CC | 196 (41.44) | 159 (43.92) | 37 (33.33) | 8.13 |  |  |  |  |
| CT | 221 (46.72) | 161 (44.48) | 60 (54.05) | 7.60 | 0.39 | 0.91 (0.73-1.13) | 0.89 (0.71-1.13) | 0.35 |
| TT | 56 (11.84) | 42 (11.60) | 14 (12.61) | 9.13 | 0.29 | 0.83 (0.60-1.15) | 0.75 (0.52-1.08) | 0.13 |
| CT+TT | 277 (58.56) | 203 (56.08) | 74 (66.67) | 8.40 | 0.28 | 0.89 (0.72-1.10) | 0.87 (0.70-1.08) | 0.21 |
| **Genotype****rs1208****803A>G**  | **CASES****n(%), N=473** | **DEAD****n(%), N=362** | **ALIVE****n(%), N=111** | **Univariate analysis** | **Multivariate analysis** |
| **MST (months)** | **Log rank *p*** | **Unadjusted HRa** | **Adjusted HRb (95% CI)** | ***P*** |
| AA | 236 (49.89) | 185 (51.10) | 51 (45.95) | 9.13 |  |  |  |  |
| AG | 175 (37.00) | 131 (36.19) | 44 (39.64) | 6.90 | 0.34 | 1.11 (0.89-1.39) | 1.15 (0.91-1.46) | 0.23 |
| GG | 62 (13.11) | 46 (12.71) | 16 (14.41) | 7.57 | 0.93 | 1.01 (0.73-1.40) | 1.05 (0.74-1.48) | 0.78 |
| AG+GG | 237 (50.11) | 177 (48.90) | 60 (54.05) | 7.27 | 0.41 | 1.09 (0.89-1.34) | 1.12 (0.90-1.39) | 0.29 |
| **ADCC** |
| **Genotype****rs1799930****590G>A**  | **CASES****n(%), N=178** | **DEAD****n(%), N=127** | **ALIVE****n(%), N=51** | **Univariate analysis** | **Multivariate analysis** |
| **MST (months)** | **Log rank *p*** | **Unadjusted HRa** | **Adjusted HRb (95% CI)** | ***P*** |
| GG | 75 (42.13) | 54 (42.52) | 21 (41.18) | 7.70 |  |  |  |  |
| GA | 79 (44.38) | 56 (44.09) | 23 (45.10) | 9.77 | 0.50  | 0.88 (0.60-1.28) | 0.98 (0.65-1.46) | 0.92 |
| AA | 24 (13.48) | 17 (13.39) | 7 (13.72) | 5.80 | 0.64 | 1.14 (0.65-2.00) | 1.66 (0.92-3.02) | 0.09 |
| GA+AA | 103 (57.87) | 73 (57.48) | 30 (58.82) | 9.43 | 0.71 | 0.93 (0.66-1.33) | 1.09 (0.75-1.59) | 0.64 |
| **Genotype****rs1799931****857G>A**  | **CASES****n(%), N=178** | **DEAD****n(%), N=127** | **ALIVE****n(%), N=51** | **Univariate analysis** | **Multivariate analysis** |
| **MST (months)** | **Log rank *p*** | **Unadjusted HRa** | **Adjusted HRb (95% CI)** | ***P*** |
| GG | 59 (33.15) | 42 (33.07) | 17 (33.33) | 9.70 |  |  |  |  |
| GA | 98 (55.05) | 71 (55.91) | 27 (52.94) | 7.60 | 0.45 | 1.15 (0.79-1.68) | 1.30 (0.85-1.98) | 0.23 |
| AA | 21 (11.80) | 14 (11.02) | 7 (13.73) | 7.80 | 0.79 | 1.08 (0.58-2.01) | 0.90 (0.43-1.88) | 0.79 |
| GA+AA | 119 (66.85) | 85 (66.93) | 34 (66.67) | 7.80 | 0.48 | 1.14 (0.79-1.64) | 1.20 (0.80-1.81) | 0.38 |
| **Genotype****rs1799929****481C>T**  | **CASES****n(%), N=178** | **DEAD****n(%), N=127** | **ALIVE****n(%), N=51** | **Univariate analysis** | **Multivariate analysis** |
| **MST (months)** | **Log rank *p*** | **Unadjusted HRa** | **Adjusted HRb (95% CI)** | ***P*** |
| CC | 69 (38.76) | 56 (44.09) | 13 (25.49) | 7.80 |  |  |  |  |
| CT | 84 (47.19) | 55 (43.31) | 29 (56.86) | 9.20 | 0.36 | 0.84 (0.58-1.22) | 0.82 (0.55-1.23) | 0.35 |
| TT | 25 (14.05) | 16 (12.60) | 9 (17.65) | 9.43 | 0.52 | 0.83 (0.49-1.42) | 0.71 (0.38-1.35) | 0.30 |
| CT+TT | 109 (61.24) | 71 (55.91) | 38 (74.51) | 9.43 | 0.32 | 0.84 (0.59-1.19) | 0.80 (0.55-1.18) | 0.26 |
| **Genotype****rs1208****803A>G**  | **CASES****n(%), N=178** | **DEAD****n(%), N=127** | **ALIVE****n(%), N=51** | **Univariate analysis** | **Multivariate analysis** |
| **MST (months)** | **Log rank *p*** | **Unadjusted HRa** | **Adjusted HRb (95% CI)** | ***P*** |
| AA | 83 (46.63) | 63 (49.61) | 20 (39.22) | 9.13 |  |  |  |  |
| AG | 68 (38.20) | 44 (34.64) | 24 (47.06) | 8.23 | 0.74 | 0.94 (0.64-1.37) | 0.91 (0.60-1.37) | 0.66 |
| GG | 27 (15.17) | 20 (15.75) | 7 (13.72) | 7.57 | 0.93 | 1.02 (0.61-1.69) | 1.05 (0.62-1.79) | 0.86 |
| AG+GG | 95 (53.37) | 64 (50.39) | 31 (60.78) | 8.23 | 0.85 | 0.97 (0.68-1.37) | 0.96 (0.66-1.39) | 0.81 |
| **SQCC** |
| **Genotype****rs1799930****590G>A**  | **CASES****n(%), N=192** | **DEAD****n(%), N=148** | **ALIVE****n(%), N=44** | **Univariate analysis** | **Multivariate analysis** |
| **MST (months)** | **Log rank *p*** | **Unadjusted HRa** | **Adjusted HRb (95% CI)** | ***P*** |
| GG | 82 (42.71) | 64 (43.24) | 18 (40.91) | 6.47 |  |  |  |  |
| GA | 91 (47.40) | 71 (47.98) | 20 (45.45) | 8.40 | 0.76 | 0.95 (0.68-1.33) | 0.86 (0.60-1.22) | 0.40 |
| AA | 19 (9.89) | 13 (8.78) | 6 (13.64) | 7.80 | 0.65 | 0.87 (0.49-1.54) | 0.83 (0.44-1.56) | 0.56 |
| GA+AA | 110 (57.29) | 84 (56.76) | 26 (59.09) | 8.20 | 0.70 | 0.94 (0.68-1.30) | 0.85 (0.60-1.19) | 0.34 |
| **Genotype****rs1799931****857G>A**  | **CASES****n(%), N=192** | **DEAD****n(%), N=148** | **ALIVE****n(%), N=44** | **Univariate analysis** | **Multivariate analysis** |
| **MST (months)** | **Log rank *p*** | **Unadjusted HRa** | **Adjusted HRb (95% CI)** | ***P*** |
| GG | 69 (35.94) | 58 (39.19) | 11 (25.00) | 8.07 |  |  |  |  |
| GA | 104 (54.17) | 78 (52.70) | 26 (59.09) | 7.17 | 0.98 | 1.005(0.71-1.41) | 1.14 (0.78-1.66) | 0.51 |
| AA | 19 (9.89) | 12 (8.11) | 7 (15.91) | 9.53 | 0.17 | 0.65 (0.37-1.12) | 1.16 (0.59-2.26) | 0.67 |
| GA+AA | 123 (64.06) | 90 (60.81) | 33 (75.00) | 7.57 | 0.65 | 0.93 (0.66-1.29) | 1.15 (0.80-1.66) | 0.45 |
| **Genotype****rs1799929****481C>T**  | **CASES****n(%), N=192** | **DEAD****n(%), N=148** | **ALIVE****n(%), N=44** | **Univariate analysis** | **Multivariate analysis** |
| **MST (months)** | **Log rank *p*** | **Unadjusted HRa** | **Adjusted HRb (95% CI)** | ***P*** |
| CC | 79 (41.14) | 63 (42.57) | 16 (36.36) | 7.93 |  |  |  |  |
| CT | 93 (48.44) | 69 (46.62) | 24 (54.54) | 7.17 | 0.53 | 0.90 (0.64-1.26) | 0.91 (0.64-1.31) | 0.63 |
| TT | 20 (10.42) | 16 (10.81) | 4 (9.10) | 8.83 | 0.28 | 0.74 (0.45-1.23) | 0.73 (0.39-1.36) | 0.32 |
| CT+TT | 113 (58.86) | 85 (57.43) | 28 (63.64) | 7.60 | 0.38 | 0.86 (0.62-1.20) | 0.87 (0.61-1.23) | 0.44 |
| **Genotype****rs1208****803A>G**  | **CASES****n(%), N=192** | **DEAD****n(%), N=148** | **ALIVE****n(%), N=44** | **Univariate analysis** | **Multivariate analysis** |
| **MST (months)** | **Log rank *p*** | **Unadjusted HRa** | **Adjusted HRb (95% CI)** | ***P*** |
| AA | 101 (52.60) | 77 (52.03) | 24 (54.55) | 8.60 |  |  |  |  |
| AG | 70 (36.46) | 57 (38.51) | 13 (29.55) | 5.27 | 0.20 | 1.25 (0.88-1.78) | 1.34 (0.94-1.91) | 0.10 |
| GG | 21 (10.94) | 14 (9.46) | 7 (15.90) | 8.50 | 0.66 | 0.88 (0.51-1.52) | 1.09 (0.57-2.09) | 0.78 |
| AG+GG | 91 (47.40) | 71 (47.97) | 20 (45.45) | 6.73 | 0.36 | 1.16 (0.84-1.60) | 1.25 (0.90-1.75) | 0.18 |
| **SCLC** |
| **Genotype****rs1799930****590G>A**  | **CASES****n(%), N=98** | **DEAD****n(%), N=84** | **ALIVE****n(%), N=14** | **Univariate analysis** | **Multivariate analysis** |  |
| **MST (months)** | **Log rank *p*** | **Unadjusted HRa** | **Adjusted HRb (95% CI)** | ***P*** |
| GG | 31 (31.63) | 26 (30.95) | 5 (35.71) | 7.53 |  |  |  |  |
| GA | 51 (52.04) | 47 (55.95) | 4 (28.57) | 8.27 | 0.74 | 1.08 (0.67-1.74) | 1.21 (0.70-2.08) | 0.50 |
| AA | 16 (16.33) | 11 (13.10) | 5 (35.71) | 7.53 | 0.29 | 0.68 (0.35-1.33) | 0.63 (0.26-1.54) | 0.32 |
| GA+AA | 67 (68.37) | 58 (69.05) | 9 (64.29) | 8.40 | 0.84 | 0.95 (0.60-1.52) | 0.99 (0.59-1.67) | 0.98 |
| **Genotype****rs1799931****857G>A**  | **CASES****n(%), N=98** | **DEAD****n(%), N=84** | **ALIVE****n(%), N=14** | **Univariate analysis** | **Multivariate analysis** |
| **MST (months)** | **Log rank *p*** | **Unadjusted HRa** | **Adjusted HRb (95% CI)** | ***P*** |
| GG | 42 (42.86) | 38 (45.24) | 4 (28.57) | 9.10 |  |  |  |  |
| GA | 44 (44.90) | 36 (42.86) | 8 (57.14) | 7.47 | 0.89 | 1.03 (0.65-1.63) | 1.02 (0.62-1.67) | 0.95 |
| AA | 12 (12.24) | 10 (11.90) | 2 (14.29) | 2.53 | 0.39 | 1.35 (0.63-2.90) | 1.99 (0.84-4.75) | 0.12 |
| GA+AA | 56 (57.14) | 46 (54.76) | 10 (71.43) | 7.23 | 0.71 | 1.08 (0.71-1.66) | 1.12 (0.70-1.79) | 0.63 |
| **Genotype****rs1799929****481C>T**  | **CASES****n(%), N=98** | **DEAD****n(%), N=84** | **ALIVE****n(%), N=14** | **Univariate analysis** | **Multivariate analysis** |
| **MST (months)** | **Log rank *p*** | **Unadjusted HRa** | **Adjusted HRb (95% CI)** | ***P*** |
| CC | 46 (46.94) | 39 (46.43) | 7 (50.00) | 9.10 |  |  |  |  |
| CT | 42 (42.86) | 36 (42.86) | 6 (42.86) | 6.07 | 0.97 | 1.01 (0.64-1.59) | 0.86 (0.50-1.45) | 0.57 |
| TT | 10 (10.20) | 9 (10.71) | 1 (7.14) | 8.40 | 0.95 | 1.02 (0.49-2.12) | 0.72 (0.31-1.65) | 0.44 |
| CT+TT | 52 (53.06) | 45 (53.57) | 7 (50.00) | 6.87 | 0.95 | 1.01 (0.66-1.55) | 0.85 (0.52-1.40) | 0.53 |
| **Genotype****rs1208****803A>G**  | **CASES****n(%), N=98** | **DEAD****n(%), N=84** | **ALIVE****n(%), N=14** | **Univariate analysis** | **Multivariate analysis** |
| **MST (months)** | **Log rank *p*** | **Unadjusted HRa** | **Adjusted HRb (95% CI)** | ***P*** |
| AA | 50 (51.02) | 43 (51.19) | 7 (50.00) | 9.40 |  |  |  |  |
| AG | 36 (36.73) | 30 (35.71) | 6 (42.86) | 5.20 | 0.17 | 1.37 (0.84-2.23) | 1.33 (0.81-2.19) | 0.26 |
| GG | 12 (12.25) | 11 (13.10) | 1 (7.14) | 5.00 | 0.31 | 1.40 (0.67-2.93) | 1.41 (0.70-2.84) | 0.34 |
| AG+GG | 48 (48.98) | 41 (48.81) | 7 (50.00) | 5.20 | 0.13 | 1.38 (0.90-2.14) | 1.36 (0.86-2.14) | 0.19 |
| aUnadjustedHazards ratio for Kaplan meier analysis, bhazards ratio for age, sex, smoking, histology, stage, KPS, ECOG |

|  |
| --- |
| **Supplementary Table S8** Association of *NAT2* genotype on survival in lung cancer cases on basis of chemotherapeutic regimen |
| **Docetaxel** |
| **Genotype****rs1799930****590G>A**  | **CASES****n(%), N=70** | **DEAD****n(%), N=57** | **ALIVE****n(%), N=13** | **Univariate analysis** | **Multivariate analysis** |
| **MST (months)** | **Log rank *p*** | **Unadjusted HRa** | **Adjusted HRb (95% CI)** | ***P*** |
| GG | 32 (45.71) | 24 (42.11) | 8 (61.54) | 9.83 |  |  |  |  |
| GA | 33 (47.14) | 29 (50.88) | 4 (30.77) | 8.63 | 0.22 | 1.39 (0.81-2.39) | 1.34 (0.72-2.53) | 0.36 |
| AA | 5 (7.14) | 4 (7.01) | 1 (7.69) | 4.67 | 0.29  | 1.75 (0.47-6.52) | 4.56 (0.82-25.15) | 0.08 |
| GA+AA | 38 (54.29) | 33 (57.89) | 5 (38.46) | 8.40 | 0.17 | 1.44 (0.85-2.41) | 1.38 (0.74-2.57) | 0.31 |
| **Genotype****rs1799931****857G>A**  | **CASES****n(%), N=70** | **DEAD****n(%), N=57** | **ALIVE****n(%), N=13** | **Univariate analysis** | **Multivariate analysis** |
| **MST (months)** | **Log rank *p*** | **Unadjusted HRa** | **Adjusted HRb (95% CI)** | ***P*** |
| GG | 30 (42.86) | 27 (47.37) | 3 (23.08) | 8.43 |  |  |  |  |
| GA | 33 (47.14) | 27 (47.37) | 6 (46.15) | 8.37 | 0.57 | 1.16 (0.68-1.98) | 1.14 (0.59-2.23) | 0.69 |
| AA | 7 (10.00) | 3 (5.26) | 4 (30.77) | - | 0.037 | 0.31 (0.14-0.69) | 0.41 (0.12-1.49) | 0.18 |
| GA+AA | 40 (57.14) | 30 (52.63) | 10 (76.92) | 8.63 | 0.66 | 0.89 (0.53-1.50) | 1.01 (0.54-1.91) | 0.97 |
| **Genotype****rs1799929****481C>T**  | **CASES****n(%), N=70** | **DEAD****n(%), N=57** | **ALIVE****n(%), N=13** | **Univariate analysis** | **Multivariate analysis** |
| **MST (months)** | **Log rank *p*** | **Unadjusted HRa** | **Adjusted HRb (95% CI)** | ***P*** |
| CC | 28 (40.00) | 22 (38.60) | 6 (46.15) | 8.43 |  |  |  |  |
| CT | 31 (44.29) | 27 (47.37) | 4 (30.77) | 8.63 | 0.45 | 1.24 (0.71-2.17) | 1.44 (0.77-2.69) | 0.25 |
| TT | 11 (15.71) | 8 (14.03) | 3 (23.08) | 10.13 | 0.57 | 0.79 (0.37-1.71) | 0.46 (0.16-1.29) | 0.14 |
| CT+TT | 42 (60.00) | 35 (61.40) | 7 (53.85) | 8.63 | 0.72 | 1.10 (0.65-1.87) | 0.98 (0.54-1.78) | 0.96 |
| **Genotype****rs1208****803A>G**  | **CASES****n(%), N=70** | **DEAD****n(%), N=57** | **ALIVE****n(%), N=13** | **Univariate analysis** | **Multivariate analysis** |
| **MST (months)** | **Log rank *p*** | **Unadjusted HRa** | **Adjusted HRb (95% CI)** | ***P*** |
| AA | 35 (50.00) | 29 (50.88) | 6 (46.15) | 8.43 |  |  |  |  |
| AG | 24 (34.29) | 20 (35.09) | 4 (30.77) | 8.63 | 0.87 | 1.05 (0.59-1.86) | 1.29 (0.66-2.52) | 0.46 |
| GG | 11 (15.71) | 8 (14.03) | 3 (23.08) | 10.30 | 0.87 | 0.94 (0.43-2.02) | 0.53 (0.19-1.49) | 0.23 |
| AG+GG | 35 (50.00) | 28 (49.12) | 7 (53.85) | 9.13 | 0.94 | 1.02 (0.61-1.71) | 0.96 (0.51-1.82) | 0.91 |
| **Paclitaxel** |
| **Genotype****rs1799930****590G>A**  | **CASES****n(%), N=57** | **DEAD****n(%), N=39** | **ALIVE****n(%), N=18** | **Univariate analysis** | **Multivariate analysis** |
| **MST (months)** | **Log rank *p*** | **Unadjusted HRa** | **Adjusted HRb (95% CI)** | ***P*** |
| GG | 21 (36.84) | 15 (38.46) | 6 (33.33) | 5.37 |  |  |  |  |
| GA | 27 (47.37) | 19 (48.72) | 8 (44.45) | 11.47 | 0.48 | 0.78 (0.39-1.57) | 0.49 (0.22-1.09) | 0.08 |
| AA | 9 (15.79) | 5 (12.82) | 4 (22.22) | 9.27 | 0.43 | 0.66 (0.26-1.69) | 0.32 (0.07-1.42) | 0.14 |
| GA+AA | 36 (63.16) | 24 (61.54) | 12 (66.67) | 9.27 | 0.41 | 0.76 (0.39-1.49) | 0.50 (0.23-1.10) | 0.09 |
| **Genotype****rs1799929****481C>T**  | **CASES****n(%), N=57** | **DEAD****n(%), N=39** | **ALIVE****n(%), N=18** | **Univariate analysis** | **Multivariate analysis** |
| **MST (months)** | **Log rank *p*** | **Unadjusted HRa** | **Adjusted HRb (95% CI)** | ***P*** |
| CC | 21 (36.84) | 14 (35.90) | 7 (38.89) | 8.60 |  |  |  |  |
| CT | 30 (52.63) | 20 (51.28) | 10 (55.56) | 8.40 | 0.80 | 0.92 (0.46-1.83) | 0.82 (0.41-1.66) | 0.59 |
| TT | 6 (10.53) | 5 (12.82) | 1 (5.55) | 3.27 | 0.52 | 1.39 (0.45-4.24) | 0.93 (0.26-3.26) | 0.91 |
| CT+TT | 36 (63.16) | 25 (64.10) | 11 (61.11) | 8.07 | 0.99 | 0.99 (0.52-1.91) | 0.85 (0.44-1.66) | 0.64 |
| **Irinotecan** |
| **Genotype****rs1799929****481C>T**  | **CASES****n(%), N=61** | **DEAD****n(%), N=51** | **ALIVE****n(%), N=10** | **Univariate analysis** | **Multivariate analysis** |
| **MST (months)** | **Log rank *p*** | **Unadjusted HRa** | **Adjusted HRb (95% CI)** | ***P*** |
| CC | 32 (52.46) | 27 (52.94) | 5 (50.00) | 9.10 |  |  |  |  |
| CT | 25 (40.98) | 20 (39.22) | 5 (50.00) | 9.80 | 0.78 | 0.92 (0.52-1.64) | 0.70 (0.35-1.40) | 0.31 |
| TT | 4 (6.56) | 4 (7.84) | 0 (0.00) | 4.43 | 0.06 | 2.57 (0.54-12.13) | 3.01 (0.65-13.94) | 0.16 |
| CT+TT | 29 (47.54) | 24 (47.06) | 5 (50.00) | 6.73 | 0.91 | 1.03 (0.59-1.79) | 0.78 (0.40-1.51) | 0.46 |
| **Genotype****rs1208****803A>G**  | **CASES****n(%), N=61** | **DEAD****n(%), N=51** | **ALIVE****n(%), N=10** | **Univariate analysis** | **Multivariate analysis** |
| **MST (months)** | **Log rank *p*** | **Unadjusted HRa** | **Adjusted HRb (95% CI)** | ***P*** |
| AA | 34 (55.74) | 28 (54.90) | 6 (60.00) | 10.57 |  |  |  |  |
| AG | 19 (31.15) | 16 (31.37) | 3 (30.00) | 6.07 | 0.23 | 1.45 (0.75-2.79) | 1.73 (0.85-3.52) | 0.13 |
| GG | 8 (13.11) | 7 (13.73) | 1 (10.00) | 5.00 | 0.19 | 1.71 (0.63-4.62) | 2.12 (0.73-6.19) | 0.17 |
| AG+GG | 27 (65.76) | 23 (45.10) | 4 (40.00) | 6.07 | 0.13 | 1.51 (0.85-2.68) | 1.72 (0.91-3.26) | 0.10 |
| **Pemetrexed** |
| **Genotype****rs1799930****590G>A**  | **CASES****n(%), N=108** | **DEAD****n(%), N=79** | **ALIVE****n(%), N=29** | **Univariate analysis** | **Multivariate analysis** |
| **MST (months)** | **Log rank *p*** | **Unadjusted HRa** | **Adjusted HRb (95% CI)** | ***P*** |
| GG | 48 (44.44) | 38 (48.10) | 10 (34.48) | 7.60 |  |  |  |  |
| GA | 47 (43.52) | 33 (41.77) | 14 (48.28) | 12.23 | 0.13 | 0.70 (0.44-1.12) | 0.86 (0.52-1.42) | 0.56 |
| AA | 13 (12.04) | 8 (10.13) | 5 (17.24) | 7.57 | 0.76 | 0.89 (0.43-1.86) | 0.94 (0.40-2.21) | 0.88 |
| GA+AA | 60 (55.56) | 41 (51.90) | 19 (65.52) | 12.07 | 0.17 | 0.74 (0.47-1.15) | 0.88 (0.55-1.40) | 0.59 |
| **Genotype****rs1799931****857G>A**  | **CASES****n(%), N=108** | **DEAD****n(%), N=79** | **ALIVE****n(%), N=29** | **Univariate analysis** | **Multivariate analysis** |
| **MST (months)** | **Log rank *p*** | **Unadjusted HRa** | **Adjusted HRb (95% CI)** | ***P*** |
| GG | 34 (31.48) | 27 (34.18) | 7 (24.14) | 9.43 |  |  |  |  |
| GA | 62 (57.41) | 43 (54.43) | 19 (65.52) | 11.63 | 0.87 | 0.96 (0.59-1.56) | 1.06 (0.63-1.79) | 0.82 |
| AA | 12 (11.11) | 9 (11.39) | 3 (10.34) | 7.10 | 0.59 | 1.23 (0.55-2.72) | 1.45 (0.60-3.53) | 0.41 |
| GA+AA | 74 (68.52) | 52 (65.82) | 22 (75.86) | 8.23 | 0.97 | 0.99 (0.62-1.58) | 1.07 (0.65-1.77) | 0.77 |
| **Genotype****rs1799929****481C>T**  | **CASES****n(%), N=108** | **DEAD****n(%), N=79** | **ALIVE****n(%), N=29** | **Univariate analysis** | **Multivariate analysis** |
| **MST (months)** | **Log rank *p*** | **Unadjusted HRa** | **Adjusted HRb (95% CI)** | ***P*** |
| CC | 47 (43.52) | 38 (48.10) | 9 (31.03) | 7.90 |  |  |  |  |
| CT | 45 (41.67) | 29 (36.71) | 16 (55.17) | 12.07 | 0.18  | 0.72 (0.45-1.17) | 0.74 (0.44-1.25) | 0.27 |
| TT | 16 (14.81) | 12 (15.19) | 4 (13.80) | 6.97 | 0.84 | 1.07 (0.55-2.06) | 1.35 (0.64-2.88) | 0.43 |
| CT+TT | 61 (56.48) | 41 (51.90) | 20 (68.97) | 10.30 | 0.32  | 0.80 (0.51-1.25) | 0.78 (0.49-1.23) | 0.28 |
| **Genotype****rs1208****803A>G**  | **CASES****n(%), N=108** | **DEAD****n(%), N=79** | **ALIVE****n(%), N=29** | **Univariate analysis** | **Multivariate analysis** |
| **MST (months)** | **Log rank *p*** | **Unadjusted HRa** | **Adjusted HRb (95% CI)** | ***P*** |
| AA | 50 (46.30) | 39 (49.37) | 11 (37.93) | 7.90 |  |  |  |  |
| AG | 42 (38.89) | 28 (35.44) | 14 (48.28) | 9.77 | 0.39 | 0.81 (0.50-1.31) | 0.81 (0.48-1.34) | 0.41 |
| GG | 16 (14.81) | 12 (15.19) | 4 (13.79) | 7.57 | 0.79 | 0.91 (0.49-1.72) | 0.86 (0.43-1.71) | 0.67 |
| AG+GG | 58 (53.70) | 40 (50.63) | 18 (62.07) | 9.77 | 0.44 | 0.84 (0.54-1.31) | 0.83 (0.52-1.32) | 0.43 |
| aUnadjustedHazards ratio for Kaplan meier analysis, bhazards ratio for age, sex, smoking, histology, stage, KPS, ECOG |