

Table SI: Baseline characteristics of survival data sets.

| Characteristic | Discovery data ^a | | First replication data ^b | | | Second replication data ^c |
|---------------------------------|-----------------------------|------------|-------------------------------------|------------|-------------|--------------------------------------|
| | GSE31210 | GSE29013 | GSE30219 | GSE37745 | GSE50081 | TCGA |
| Total/event ^d number | 217/60 | 22/6 | 84/45 | 44/28 | 124/49 | 514/187 |
| Age | 59.6±7.4 | 64.8±9.9 | 61.5±9.3 | 63.2±9.2 | 68.6±9.8 | 65.4±9.9 |
| Sex | | | | | | |
| Female | 121 (53.5%) | 9 (40.9%) | 19 (22.6%) | 26 (59.1%) | 61 (49.2%) | 277 (53.9%) |
| Male | 105 (46.5%) | 13 (59.1%) | 65 (77.4%) | 18 (40.9%) | 63 (50.8%) | 237 (46.1%) |
| Pathological stage | | | | | | |
| I | 168 (74.3%) | 16 (72.7%) | 84 (100.0%) | 34 (77.3%) | 90 (72.6%) | 275 (54.3%) |
| II | 58 (25.7%) | 6 (27.3%) | 0 (0.0%) | 10 (22.7%) | 34 (27.4%) | 121 (23.9%) |
| III | 0 (0.0%) | 0 (0.0%) | 0 (0.0%) | 0 (0.0%) | 0 (0.0%) | 84 (16.6%) |
| IV | 0 (0.0%) | 0 (0.0%) | 0 (0.0%) | 0 (0.0%) | 0 (0.0%) | 26 (5.1%) |
| Smoking status | | | | | | |
| Non-smoker | 115 (50.9%) | 2 (9.1%) | 0 (NaN%) | 0 (NaN%) | 23 (20.4 %) | 75 (15.0%) |
| Smoker | 111 (49.1%) | 20 (90.9%) | 0 (NaN%) | 0 (NaN%) | 90 (79.6 %) | 425 (85.0%) |

^aDiscovery dataset was GSE31210. ^bFirst replication was performed using an integrated dataset (GSE29013, GSE30219, GSE37745, GSE50081). ^cSecond replication was performed using TCGA LUAD RNA-Seq V2 RSEM and survival data. TCGA, The Cancer Genome Atlas. ^dEvent indicates relapsed event for discovery data and overall survival event for first and second replication data.

Table SII. Quality control test results for the 246 microarray samples.

| No. | Phenotype | Sample name | 3/5' β -actin <3 | 3/5' GAPDH <1.25 | Hybridization-BioB present | Percent present spread $\leq 10\%$ | Background spread $\leq 20\%$ | Log scale factor-spread ≤ 3 | NUSE median <1.1 | RLE IQR <1 | RNA degradation slope ₁ | Quality test result |
|-----|-----------------|-------------|------------------------|------------------|----------------------------|------------------------------------|-------------------------------|----------------------------------|------------------|-------------|------------------------------------|---------------------|
| 1 | Normal lung | GSM773766 | 1.15 | 1.11 | P | 0.58 | 63 | -1.33 | 0.996527867 | 0.313627628 | 7.519395637 | |
| 2 | Normal lung | GSM773767 | 1.14 | 1.09 | P | 0.59 | 48 | -1.08 | 1.011738139 | 0.365018544 | 7.826264751 | Low |
| 3 | Normal lung | GSM773768 | 1.35 | 1.22 | P | 0.58 | 60 | -1.08 | 1.016197092 | 0.387399442 | 9.478021503 | |
| 4 | Normal lung | GSM773769 | 1.20 | 1.13 | P | 0.58 | 68 | -1.31 | 0.995177953 | 0.304203315 | 7.963236336 | |
| 5 | Normal lung | GSM773770 | 1.13 | 1.11 | P | 0.59 | 71 | -1.61 | 0.991890497 | 0.298019637 | 7.433497265 | |
| 6 | Normal lung | GSM773771 | 1.16 | 1.12 | P | 0.58 | 69 | -1.38 | 0.994289486 | 0.311711897 | 7.80478394 | |
| 7 | Normal lung | GSM773772 | 1.11 | 1.08 | P | 0.59 | 69 | -1.50 | 0.990492947 | 0.2791000 | 7.437928038 | |
| 8 | Normal lung | GSM773773 | 1.11 | 1.09 | P | 0.58 | 72 | -1.56 | 0.9964436 | 0.322900846 | 7.213914809 | |
| 9 | Normal lung | GSM773774 | 1.12 | 1.09 | P | 0.58 | 70 | -1.45 | 0.993418549 | 0.277310908 | 7.437172096 | |
| 10 | Normal lung | GSM773775 | 1.12 | 1.11 | P | 0.57 | 70 | -1.57 | 0.994782647 | 0.28138829 | 7.520751721 | |
| 11 | Normal lung | GSM773776 | 1.14 | 1.11 | P | 0.59 | 64 | -1.55 | 0.990824549 | 0.281042756 | 7.862274592 | |
| 12 | Normal lung | GSM773777 | 1.11 | 1.09 | P | 0.59 | 67 | -1.48 | 0.992100905 | 0.311656643 | 7.621296611 | |
| 13 | Normal lung | GSM773778 | 1.14 | 1.11 | P | 0.59 | 63 | -1.34 | 0.992029353 | 0.291602055 | 7.573814126 | |
| 14 | Normal lung | GSM773779 | 1.14 | 1.09 | P | 0.59 | 65 | -1.44 | 0.996201833 | 0.312625323 | 7.286297335 | |
| 15 | Normal lung | GSM773780 | 1.11 | 1.09 | P | 0.57 | 66 | -1.45 | 1 | 0.328211678 | 7.100774253 | |
| 16 | Normal lung | GSM773781 | 1.14 | 1.08 | P | 0.58 | 69 | -1.38 | 0.995447408 | 0.312951515 | 7.592574961 | |
| 17 | Normal lung | GSM773782 | 1.14 | 1.09 | P | 0.59 | 62 | -1.31 | 0.994663549 | 0.290259714 | 7.455369579 | |
| 18 | Normal lung | GSM773783 | 1.21 | 1.13 | P | 0.57 | 51 | -0.67 | 1.016899682 | 0.370783467 | 8.420301126 | Low |
| 19 | Normal lung | GSM773784 | 1.15 | 1.11 | P | 0.6 | 68 | -1.59 | 1.002571473 | 0.326736002 | 7.799063997 | |
| 20 | Normal lung | GSM773785 | 1.18 | 1.10 | P | 0.6 | 64 | -1.40 | 0.995696479 | 0.323372995 | 8.235219484 | |
| 21 | Triple-negative | GSM773571 | 1.14 | 1.05 | P | 0.58 | 66 | -1.31 | 0.993754329 | 0.304486084 | 7.999278979 | |
| 22 | Triple-negative | GSM773572 | 1.13 | 1.07 | P | 0.58 | 73 | -1.50 | 0.992437274 | 0.284968109 | 7.44517435 | |
| 23 | Triple-negative | GSM773573 | 1.09 | 1.01 | P | 0.55 | 66 | -1.37 | 1.010165041 | 0.410979365 | 6.818789757 | |
| 24 | Triple-negative | GSM773574 | 1.13 | 1.08 | P | 0.57 | 66 | -1.24 | 0.991886388 | 0.28185927 | 7.72521848 | |
| 25 | Triple-negative | GSM773575 | 1.16 | 1.07 | P | 0.57 | 67 | -1.18 | 0.998599788 | 0.365027263 | 7.250516635 | |
| 26 | Triple-negative | GSM773576 | 1.12 | 1.07 | P | 0.54 | 62 | -1.07 | 1.034338971 | 0.403856256 | 6.50203556 | |
| 27 | Triple-negative | GSM773577 | 1.22 | 1.13 | P | 0.58 | 69 | -0.94 | 1.008330141 | 0.336711377 | 9.050695769 | |
| 28 | Triple-negative | GSM773578 | 1.13 | 1.06 | P | 0.58 | 54 | -1.14 | 1.005772786 | 0.379323854 | 7.465809736 | Low |
| 29 | Triple-negative | GSM773579 | 1.12 | 1.06 | P | 0.59 | 73 | -1.60 | 0.989723051 | 0.341740437 | 7.34399186 | |
| 30 | Triple-negative | GSM773580 | 1.16 | 1.08 | P | 0.56 | 69 | -1.15 | 1.000406939 | 0.314409531 | 7.62242706 | |
| 31 | Triple-negative | GSM773581 | 1.08 | 1.04 | P | 0.55 | 77 | -1.48 | 0.998615468 | 0.369620812 | 6.853552641 | |
| 32 | Triple-negative | GSM773582 | 1.10 | 1.02 | P | 0.55 | 65 | -1.55 | 1.008055421 | 0.409311569 | 6.327347601 | |
| 33 | Triple-negative | GSM773583 | 1.15 | 1.05 | P | 0.56 | 65 | -1.56 | 0.998235846 | 0.292579805 | 7.495211832 | |
| 34 | Triple-negative | GSM773584 | 1.23 | 1.11 | P | 0.54 | 65 | -1.18 | 1.003643215 | 0.335398856 | 8.515401088 | |
| 35 | Triple-negative | GSM773585 | 1.15 | 1.08 | P | 0.54 | 64 | -1.12 | 1.003048221 | 0.32987119 | 8.183273775 | |
| 36 | Triple-negative | GSM773586 | 1.07 | 1.02 | P | 0.56 | 73 | -1.72 | 1.005261452 | 0.377278322 | 6.641357797 | |
| 37 | Triple-negative | GSM773587 | 1.14 | 1.07 | P | 0.59 | 68 | -1.62 | 0.993691177 | 0.299393861 | 7.28312451 | |
| 38 | Triple-negative | GSM773588 | 1.13 | 1.07 | P | 0.58 | 60 | -0.99 | 1.00337791 | 0.327375093 | 7.443396001 | |
| 39 | Triple-negative | GSM773589 | 1.13 | 1.05 | P | 0.57 | 69 | -1.27 | 0.996463882 | 0.30157509 | 7.105350648 | |
| 40 | Triple-negative | GSM773590 | 1.16 | 1.08 | P | 0.56 | 65 | -0.99 | 1.000577267 | 0.30237116 | 7.725055921 | |
| 41 | Triple-negative | GSM773591 | 1.11 | 1.05 | P | 0.56 | 70 | -1.57 | 0.992373533 | 0.297089935 | 7.296494666 | |
| 42 | Triple-negative | GSM773592 | 1.15 | 1.12 | P | 0.56 | 65 | -1.32 | 0.998096586 | 0.328748078 | 8.315611137 | |
| 43 | Triple-negative | GSM773593 | 1.21 | 1.06 | P | 0.57 | 62 | -1.19 | 0.994754312 | 0.288928192 | 8.380576044 | |
| 44 | Triple-negative | GSM773594 | 1.16 | 1.08 | P | 0.59 | 62 | -0.97 | 1.007892784 | 0.374908592 | 7.773007003 | |
| 45 | Triple-negative | GSM773595 | 1.13 | 1.09 | P | 0.6 | 68 | -1.51 | 0.996179356 | 0.34065846 | 7.319375854 | |
| 46 | Triple-negative | GSM773596 | 1.14 | 1.09 | P | 0.58 | 66 | -1.43 | 0.988883062 | 0.295030641 | 7.377065973 | |
| 47 | Triple-negative | GSM773597 | 1.14 | 1.08 | P | 0.56 | 75 | -1.50 | 0.995225518 | 0.307798278 | 7.000140724 | |
| 48 | Triple-negative | GSM773598 | 1.14 | 1.03 | P | 0.56 | 68 | -1.21 | 1.007903363 | 0.400811599 | 7.090121203 | |
| 49 | Triple-negative | GSM773599 | 1.20 | 1.09 | P | 0.56 | 63 | -0.97 | 1.02536243 | 0.429248221 | 7.704051858 | |
| 50 | Triple-negative | GSM773600 | 1.12 | 1.10 | P | 0.57 | 74 | -1.38 | 0.998261191 | 0.289403216 | 7.555400366 | |
| 51 | Triple-negative | GSM773601 | 1.14 | 1.04 | P | 0.52 | 69 | -1.34 | 1.020387328 | 0.46817435 | 6.632919286 | |
| 52 | Triple-negative | GSM773602 | 1.16 | 1.09 | P | 0.59 | 67 | -1.30 | 0.996245635 | 0.330763134 | 7.634218709 | |
| 53 | Triple-negative | GSM773603 | 1.12 | 1.07 | P | 0.55 | 64 | -1.19 | 1.001990585 | 0.367018047 | 7.1753192 | |
| 54 | Triple-negative | GSM773604 | 1.12 | 1.05 | P | 0.55 | 77 | -1.54 | 0.995714153 | 0.352184221 | 7.027747224 | |
| 55 | Triple-negative | GSM773605 | 1.18 | 1.10 | P | 0.58 | 66 | -1.04 | 1.005036766 | 0.344662511 | 8.216421706 | |
| 56 | Triple-negative | GSM773606 | 1.12 | 1.07 | P | 0.58 | 72 | -1.56 | 1.000027439 | 0.377391978 | 7.143627344 | |
| 57 | Triple-negative | GSM773607 | 1.14 | 1.09 | P | 0.58 | 71 | -1.42 | 0.997399581 | 0.349042846 | 7.678180251 | |
| 58 | Triple-negative | GSM773608 | 1.19 | 1.12 | P | 0.57 | 47 | -0.74 | 1.014234797 | 0.409991928 | 8.623387003 | Low |
| 59 | Triple-negative | GSM773609 | 1.18 | 1.10 | P | 0.58 | 64 | -1.31 | 0.99515281 | 0.332107248 | 8.077174179 | |
| 60 | Triple-negative | GSM773610 | 1.14 | 1.07 | P | 0.57 | 70 | -1.30 | 0.996894606 | 0.260660412 | 7.378486665 | |
| 61 | Triple-negative | GSM773611 | 1.23 | 1.15 | P | 0.56 | 63 | -1.23 | 1.006577849 | 0.337397447 | 9.122563715 | |

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|-----|------------------------|-----------|------|------|---|------|----|-------|-------------|-------------|-------------|-----|
| 62 | Triple-negative | GSM773612 | 1.17 | 1.10 | P | 0.58 | 67 | -1.31 | 0.997680927 | 0.340242786 | 7.913230778 | |
| 63 | Triple-negative | GSM773613 | 1.18 | 1.08 | P | 0.57 | 70 | -1.50 | 0.996862481 | 0.347531906 | 8.044399443 | |
| 64 | Triple-negative | GSM773614 | 1.15 | 1.08 | P | 0.57 | 65 | -1.32 | 0.992297816 | 0.310420108 | 7.747447405 | |
| 65 | Triple-negative | GSM773615 | 1.13 | 1.06 | P | 0.55 | 64 | -1.55 | 1.006441003 | 0.398355584 | 6.649453276 | |
| 66 | Triple-negative | GSM773616 | 1.10 | 1.02 | P | 0.53 | 76 | -1.49 | 1.017733349 | 0.479201227 | 6.344580754 | |
| 67 | Triple-negative | GSM773617 | 1.10 | 1.06 | P | 0.54 | 80 | -1.61 | 1.016200336 | 0.372357085 | 6.808597444 | |
| 68 | Triple-negative | GSM773618 | 1.15 | 1.10 | P | 0.57 | 66 | -1.77 | 1.002516138 | 0.353802987 | 7.465476426 | |
| 69 | Triple-negative | GSM773619 | 1.20 | 1.11 | P | 0.57 | 70 | -1.44 | 0.99939075 | 0.28127183 | 8.140504462 | |
| 70 | Triple-negative | GSM773620 | 1.14 | 1.09 | P | 0.59 | 61 | -1.57 | 0.990846279 | 0.314278212 | 7.858155663 | |
| 71 | Triple-negative | GSM773621 | 1.06 | 1.04 | P | 0.55 | 70 | -1.61 | 0.998551493 | 0.347327224 | 6.934850236 | |
| 72 | Triple-negative | GSM773622 | 1.13 | 1.10 | P | 0.58 | 65 | -1.55 | 0.995571224 | 0.348984827 | 7.248715866 | |
| 73 | Triple-negative | GSM773623 | 1.32 | 1.17 | P | 0.57 | 62 | -1.02 | 1.006473836 | 0.367229525 | 8.632884501 | |
| 74 | Triple-negative | GSM773624 | 1.28 | 1.13 | P | 0.57 | 62 | -1.05 | 1.005831394 | 0.394325906 | 8.710774235 | |
| 75 | Triple-negative | GSM773625 | 1.12 | 1.08 | P | 0.59 | 69 | -1.82 | 0.987868404 | 0.304733095 | 7.367337285 | |
| 76 | Triple-negative | GSM773626 | 1.17 | 1.11 | P | 0.58 | 68 | -1.30 | 0.992042507 | 0.282131537 | 7.839488806 | |
| 77 | Triple-negative | GSM773627 | 1.12 | 1.07 | P | 0.59 | 69 | -1.76 | 0.992734375 | 0.329857786 | 7.337486461 | |
| 78 | Triple-negative | GSM773628 | 1.20 | 1.12 | P | 0.56 | 66 | -1.16 | 1.001544268 | 0.346516628 | 8.308354402 | |
| 79 | Triple-negative | GSM773629 | 1.18 | 1.12 | P | 0.58 | 65 | -1.48 | 0.991340247 | 0.297917113 | 8.075602083 | |
| 80 | Triple-negative | GSM773630 | 1.14 | 1.09 | P | 0.57 | 70 | -1.59 | 1.001874101 | 0.448745933 | 7.261119478 | |
| 81 | Triple-negative | GSM773631 | 1.18 | 1.12 | P | 0.58 | 67 | -1.23 | 0.998746228 | 0.376059043 | 8.437333557 | |
| 82 | Triple-negative | GSM773632 | 1.16 | 1.09 | P | 0.58 | 69 | -1.54 | 1.003809248 | 0.367309802 | 7.352721483 | |
| 83 | Triple-negative | GSM773633 | 1.21 | 1.12 | P | 0.56 | 74 | -1.42 | 1.011367482 | 0.374941781 | 8.332426315 | |
| 84 | Triple-negative | GSM773634 | 1.16 | 1.11 | P | 0.56 | 80 | -1.39 | 0.999732701 | 0.319810331 | 7.576435772 | |
| 85 | Triple-negative | GSM773635 | 1.11 | 1.08 | P | 0.58 | 79 | -1.39 | 1.011033593 | 0.328513986 | 7.279826049 | |
| 86 | Triple-negative | GSM773636 | 1.14 | 1.04 | P | 0.55 | 72 | -1.45 | 0.997348973 | 0.358350333 | 7.073341248 | |
| 87 | Triple-negative | GSM773637 | 1.10 | 1.08 | P | 0.56 | 73 | -1.47 | 0.988810326 | 0.25761382 | 7.257760695 | |
| 88 | Triple-negative | GSM773638 | 1.15 | 1.14 | P | 0.6 | 71 | -1.54 | 1.004579626 | 0.417215446 | 8.107184725 | |
| 89 | EGFR mutation-positive | GSM773639 | 1.13 | 1.06 | P | 0.57 | 72 | -1.60 | 0.995086099 | 0.322787623 | 7.052336502 | |
| 90 | EGFR mutation-positive | GSM773640 | 1.12 | 1.07 | P | 0.58 | 64 | -1.37 | 0.996262715 | 0.314689638 | 7.179580509 | |
| 91 | EGFR mutation-positive | GSM773641 | 1.13 | 1.05 | P | 0.54 | 61 | -0.98 | 1.011915435 | 0.390444777 | 6.657220216 | |
| 92 | EGFR mutation-positive | GSM773642 | 1.18 | 1.08 | P | 0.55 | 67 | -1.10 | 1.003978615 | 0.392933002 | 7.497798951 | |
| 93 | EGFR mutation-positive | GSM773643 | 1.14 | 1.09 | P | 0.57 | 68 | -1.33 | 0.995967287 | 0.278039038 | 7.49266406 | |
| 94 | EGFR mutation-positive | GSM773644 | 1.10 | 1.07 | P | 0.58 | 66 | -1.35 | 0.998703554 | 0.314575756 | 6.828699919 | |
| 95 | EGFR mutation-positive | GSM773645 | 1.22 | 1.10 | P | 0.57 | 64 | -0.97 | 1.011748957 | 0.394171142 | 8.523235176 | |
| 96 | EGFR mutation-positive | GSM773646 | 1.12 | 1.06 | P | 0.58 | 68 | -1.31 | 0.996681851 | 0.308049761 | 7.06908548 | |
| 97 | EGFR mutation-positive | GSM773647 | 1.16 | 1.09 | P | 0.58 | 74 | -1.34 | 0.99489802 | 0.288954671 | 7.664486461 | |
| 98 | EGFR mutation-positive | GSM773648 | 1.18 | 1.10 | P | 0.58 | 69 | -1.18 | 0.998323754 | 0.365105331 | 8.205917193 | |
| 99 | EGFR mutation-positive | GSM773649 | 1.11 | 1.06 | P | 0.58 | 63 | -1.34 | 0.996065149 | 0.32080777 | 7.201733703 | |
| 100 | EGFR mutation-positive | GSM773650 | 1.17 | 1.08 | P | 0.59 | 67 | -1.54 | 0.995825063 | 0.412650401 | 7.372364679 | |
| 101 | EGFR mutation-positive | GSM773651 | 1.08 | 1.03 | P | 0.56 | 68 | -1.49 | 1.004801151 | 0.417918461 | 6.56760187 | |
| 102 | EGFR mutation-positive | GSM773652 | 1.10 | 1.06 | P | 0.55 | 65 | -1.19 | 1.002862299 | 0.316556863 | 6.744208405 | |
| 103 | EGFR mutation-positive | GSM773653 | 1.14 | 1.11 | P | 0.59 | 71 | -1.25 | 0.994696771 | 0.302525141 | 7.631831989 | |
| 104 | EGFR mutation-positive | GSM773654 | 1.12 | 1.07 | P | 0.57 | 70 | -1.56 | 0.991732053 | 0.311059179 | 7.378739225 | |
| 105 | EGFR mutation-positive | GSM773655 | 1.19 | 1.11 | P | 0.58 | 67 | -1.11 | 1.00200322 | 0.360218078 | 8.20929991 | |
| 106 | EGFR mutation-positive | GSM773656 | 1.12 | 1.08 | P | 0.58 | 64 | -1.19 | 1.000050303 | 0.296790789 | 7.205062459 | |
| 107 | EGFR mutation-positive | GSM773657 | 1.15 | 1.09 | P | 0.58 | 59 | -1.20 | 0.994519795 | 0.297888221 | 7.509038715 | Low |
| 108 | EGFR mutation-positive | GSM773658 | 1.13 | 1.03 | P | 0.55 | 69 | -1.58 | 1.001400984 | 0.396594389 | 6.847174086 | |
| 109 | EGFR mutation-positive | GSM773659 | 1.13 | 1.05 | P | 0.56 | 65 | -1.32 | 1.003168545 | 0.373610927 | 7.451138392 | |
| 110 | EGFR mutation-positive | GSM773660 | 1.12 | 1.06 | P | 0.58 | 67 | -1.56 | 0.994248998 | 0.330706236 | 7.304304767 | |
| 111 | EGFR mutation-positive | GSM773661 | 1.16 | 1.08 | P | 0.55 | 70 | -1.31 | 1.000786054 | 0.334221392 | 7.694264726 | |
| 112 | EGFR mutation-positive | GSM773662 | 1.16 | 1.10 | P | 0.55 | 69 | -1.38 | 0.999070365 | 0.331154976 | 7.469914684 | |
| 113 | EGFR mutation-positive | GSM773663 | 1.11 | 1.07 | P | 0.57 | 57 | -1.14 | 1.014747308 | 0.371532654 | 6.812109779 | Low |
| 114 | EGFR mutation-positive | GSM773664 | 1.24 | 1.16 | P | 0.57 | 65 | -0.99 | 1.010304076 | 0.337392416 | 8.207062581 | |
| 115 | EGFR mutation-positive | GSM773665 | 1.11 | 1.04 | P | 0.56 | 69 | -1.41 | 1.011570025 | 0.393869103 | 7.016797184 | |
| 116 | EGFR mutation-positive | GSM773666 | 1.10 | 1.06 | P | 0.58 | 66 | -1.30 | 1.009320125 | 0.312219094 | 7.104906768 | |

| | | | | | | | | | | | | |
|-----|------------------------|-----------|------|------|---|------|----|-------|-------------|-------------|-------------|-----|
| 117 | EGFR mutation-positive | GSM773667 | 1.22 | 1.08 | P | 0.57 | 68 | -1.12 | 1.012419548 | 0.386772144 | 7.926958552 | |
| 118 | EGFR mutation-positive | GSM773668 | 1.19 | 1.15 | P | 0.56 | 63 | -1.10 | 1.009566871 | 0.348993364 | 7.663933594 | |
| 119 | EGFR mutation-positive | GSM773669 | 1.15 | 1.08 | P | 0.58 | 69 | -1.07 | 1.008845393 | 0.31790733 | 7.600925402 | |
| 120 | EGFR mutation-positive | GSM773670 | 1.13 | 1.10 | P | 0.57 | 70 | -1.27 | 0.994376398 | 0.256455042 | 7.693265705 | |
| 121 | EGFR mutation-positive | GSM773671 | 1.22 | 1.13 | P | 0.60 | 69 | -1.35 | 1.00374019 | 0.323784031 | 8.35068397 | |
| 122 | EGFR mutation-positive | GSM773672 | 1.24 | 1.11 | P | 0.58 | 53 | -0.64 | 1.022516978 | 0.386432146 | 8.734274981 | Low |
| 123 | EGFR mutation-positive | GSM773673 | 1.10 | 1.05 | P | 0.57 | 75 | -1.68 | 1.007943469 | 0.44127298 | 6.90021172 | |
| 124 | EGFR mutation-positive | GSM773674 | 1.10 | 1.06 | P | 0.56 | 65 | -1.34 | 1.014937655 | 0.414006885 | 7.071617079 | |
| 125 | EGFR mutation-positive | GSM773675 | 1.15 | 1.09 | P | 0.58 | 66 | -1.34 | 0.9984498 | 0.316473202 | 7.699437597 | |
| 126 | EGFR mutation-positive | GSM773676 | 1.09 | 1.05 | P | 0.59 | 67 | -1.52 | 1.004192437 | 0.324080564 | 7.177091893 | |
| 127 | EGFR mutation-positive | GSM773677 | 1.10 | 1.06 | P | 0.57 | 69 | -1.54 | 1.000389185 | 0.311402949 | 7.1523647 | |
| 128 | EGFR mutation-positive | GSM773678 | 1.13 | 1.07 | P | 0.61 | 67 | -1.41 | 0.996077186 | 0.294266495 | 7.965597758 | |
| 129 | EGFR mutation-positive | GSM773679 | 1.17 | 1.08 | P | 0.59 | 69 | -1.30 | 1.003147807 | 0.311431208 | 7.890632373 | |
| 130 | EGFR mutation-positive | GSM773680 | 1.12 | 1.06 | P | 0.56 | 74 | -1.36 | 1.007478835 | 0.362727644 | 6.897534191 | |
| 131 | EGFR mutation-positive | GSM773681 | 1.18 | 1.12 | P | 0.59 | 67 | -1.24 | 0.991526722 | 0.288589563 | 8.14276698 | |
| 132 | EGFR mutation-positive | GSM773682 | 1.14 | 1.08 | P | 0.57 | 70 | -1.38 | 1.000795938 | 0.303681196 | 7.796788869 | |
| 133 | EGFR mutation-positive | GSM773683 | 1.08 | 1.03 | P | 0.56 | 65 | -1.58 | 1.006085538 | 0.422456877 | 6.76854067 | |
| 134 | EGFR mutation-positive | GSM773684 | 1.13 | 1.10 | P | 0.57 | 64 | -1.06 | 1.003431631 | 0.274877026 | 7.44646749 | |
| 135 | EGFR mutation-positive | GSM773685 | 1.13 | 1.11 | P | 0.56 | 65 | -1.19 | 1.001281758 | 0.315339152 | 6.900432357 | |
| 136 | EGFR mutation-positive | GSM773686 | 1.22 | 1.15 | P | 0.59 | 69 | -1.40 | 0.99193888 | 0.275255133 | 8.530566688 | |
| 137 | EGFR mutation-positive | GSM773687 | 1.10 | 1.10 | P | 0.58 | 69 | -1.40 | 0.994795206 | 0.287668301 | 7.285914104 | |
| 138 | EGFR mutation-positive | GSM773688 | 1.09 | 1.07 | P | 0.57 | 68 | -1.64 | 0.998056583 | 0.32942666 | 6.977069266 | |
| 139 | EGFR mutation-positive | GSM773689 | 1.25 | 1.13 | P | 0.59 | 60 | -1.22 | 0.995771777 | 0.297654836 | 8.744112559 | |
| 140 | EGFR mutation-positive | GSM773690 | 1.13 | 1.08 | P | 0.56 | 65 | -1.42 | 0.998003947 | 0.302403687 | 7.14487503 | |
| 141 | EGFR mutation-positive | GSM773691 | 1.19 | 1.13 | P | 0.59 | 61 | -1.31 | 0.990138527 | 0.298534082 | 7.825390935 | |
| 142 | EGFR mutation-positive | GSM773692 | 1.14 | 1.08 | P | 0.59 | 67 | -1.32 | 0.989953139 | 0.256211121 | 7.643781872 | |
| 143 | EGFR mutation-positive | GSM773693 | 1.16 | 1.12 | P | 0.56 | 78 | -1.53 | 1.002241989 | 0.302544202 | 7.368979789 | |
| 144 | EGFR mutation-positive | GSM773694 | 1.13 | 1.09 | P | 0.58 | 67 | -1.40 | 0.994774484 | 0.292346554 | 7.292282389 | |
| 145 | EGFR mutation-positive | GSM773695 | 1.14 | 1.10 | P | 0.60 | 65 | -1.44 | 0.994031639 | 0.313660696 | 7.722152481 | |
| 146 | EGFR mutation-positive | GSM773696 | 1.16 | 1.15 | P | 0.57 | 72 | -1.43 | 0.993190513 | 0.306240167 | 7.678911558 | |
| 147 | EGFR mutation-positive | GSM773697 | 1.15 | 1.09 | P | 0.58 | 65 | -1.26 | 1.008387062 | 0.436405259 | 7.88710972 | |
| 148 | EGFR mutation-positive | GSM773698 | 1.15 | 1.10 | P | 0.54 | 69 | -1.15 | 1.008647609 | 0.39807201 | 7.610801287 | |
| 149 | EGFR mutation-positive | GSM773699 | 1.09 | 1.10 | P | 0.56 | 66 | -1.12 | 1.007836264 | 0.301273922 | 6.993092929 | |
| 150 | EGFR mutation-positive | GSM773700 | 1.22 | 1.10 | P | 0.56 | 69 | -1.01 | 1.00037679 | 0.327825929 | 8.093812763 | |
| 151 | EGFR mutation-positive | GSM773701 | 1.16 | 1.10 | P | 0.57 | 66 | -1.04 | 1.004574957 | 0.276106594 | 7.961647789 | |
| 152 | EGFR mutation-positive | GSM773702 | 1.15 | 1.08 | P | 0.56 | 60 | -0.97 | 1.017727456 | 0.362902616 | 6.969773452 | |
| 153 | EGFR mutation-positive | GSM773703 | 1.32 | 1.19 | P | 0.55 | 69 | -0.90 | 1.030479817 | 0.48727298 | 9.392996258 | |
| 154 | EGFR mutation-positive | GSM773704 | 1.24 | 1.17 | P | 0.58 | 67 | -1.09 | 1.003844246 | 0.336103191 | 8.902086506 | |
| 155 | EGFR mutation-positive | GSM773705 | 1.12 | 1.08 | P | 0.57 | 71 | -1.32 | 1.009204651 | 0.273258814 | 7.215698571 | |
| 156 | EGFR mutation-positive | GSM773706 | 1.21 | 1.15 | P | 0.58 | 75 | -1.36 | 0.994545831 | 0.295958369 | 8.186038388 | |
| 157 | EGFR mutation-positive | GSM773707 | 1.09 | 1.05 | P | 0.56 | 72 | -1.49 | 1.005526802 | 0.307480262 | 6.7215775 | |
| 158 | EGFR mutation-positive | GSM773708 | 1.24 | 1.10 | P | 0.55 | 65 | -1.20 | 1.003373038 | 0.384276006 | 7.650707024 | |
| 159 | EGFR mutation-positive | GSM773709 | 1.21 | 1.15 | P | 0.59 | 67 | -1.23 | 1 | 0.312734115 | 8.812973895 | |
| 160 | EGFR mutation-positive | GSM773710 | 1.18 | 1.11 | P | 0.59 | 66 | -1.25 | 0.992831839 | 0.28975689 | 7.728394017 | |
| 161 | EGFR mutation-positive | GSM773711 | 1.13 | 1.12 | P | 0.58 | 67 | -1.39 | 0.992263415 | 0.252938679 | 7.520036972 | |
| 162 | EGFR mutation-positive | GSM773712 | 1.31 | 1.17 | P | 0.56 | 66 | -0.75 | 1.033283069 | 0.448524852 | 8.636168406 | |
| 163 | EGFR mutation-positive | GSM773713 | 1.15 | 1.09 | P | 0.56 | 69 | -1.53 | 1 | 0.318266657 | 7.757481639 | |

| | | | | | | | | | | | | |
|-----|------------------------|-----------|------|------|---|------|----|-------|-------------|-------------|-------------|-----|
| 164 | EGFR mutation-positive | GSM773714 | 1.15 | 1.08 | P | 0.55 | 67 | -1.46 | 1.016775252 | 0.416507966 | 7.17444769 | |
| 165 | EGFR mutation-positive | GSM773715 | 1.15 | 1.12 | P | 0.55 | 75 | -1.40 | 1.000629181 | 0.381329165 | 7.307403357 | |
| 166 | EGFR mutation-positive | GSM773716 | 1.10 | 1.05 | P | 0.58 | 74 | -1.65 | 0.999848732 | 0.348077586 | 7.025491344 | |
| 167 | EGFR mutation-positive | GSM773717 | 1.30 | 1.16 | P | 0.56 | 67 | -1.03 | 1.011378587 | 0.396162577 | 8.778075046 | |
| 168 | EGFR mutation-positive | GSM773718 | 1.15 | 1.09 | P | 0.59 | 63 | -1.44 | 0.991452218 | 0.280147261 | 7.989074331 | |
| 169 | EGFR mutation-positive | GSM773719 | 1.14 | 1.10 | P | 0.58 | 65 | -1.29 | 0.989488115 | 0.254786629 | 7.551399515 | |
| 170 | EGFR mutation-positive | GSM773720 | 1.16 | 1.09 | P | 0.56 | 67 | -1.29 | 0.993425019 | 0.288218265 | 7.466422958 | |
| 171 | EGFR mutation-positive | GSM773721 | 1.12 | 1.09 | P | 0.58 | 74 | -1.50 | 0.996098874 | 0.273846488 | 7.414571047 | |
| 172 | EGFR mutation-positive | GSM773722 | 1.14 | 1.10 | P | 0.59 | 63 | -1.31 | 0.990191882 | 0.273742294 | 7.589725417 | |
| 173 | EGFR mutation-positive | GSM773723 | 1.16 | 1.10 | P | 0.56 | 66 | -1.21 | 1.005677752 | 0.348054931 | 8.270455734 | |
| 174 | EGFR mutation-positive | GSM773724 | 1.15 | 1.09 | P | 0.56 | 67 | -1.36 | 0.99720028 | 0.28814609 | 7.657687676 | |
| 175 | EGFR mutation-positive | GSM773725 | 1.15 | 1.09 | P | 0.59 | 68 | -1.52 | 0.988568858 | 0.284964456 | 7.649930544 | |
| 176 | EGFR mutation-positive | GSM773726 | 1.14 | 1.08 | P | 0.58 | 65 | -1.29 | 0.993030979 | 0.276132357 | 7.57463584 | |
| 177 | EGFR mutation-positive | GSM773727 | 1.13 | 1.06 | P | 0.57 | 68 | -1.50 | 0.995918982 | 0.332669641 | 6.890475271 | |
| 178 | EGFR mutation-positive | GSM773728 | 1.12 | 1.09 | P | 0.57 | 67 | -1.37 | 0.998105048 | 0.286578956 | 7.605007102 | |
| 179 | EGFR mutation-positive | GSM773729 | 1.11 | 1.08 | P | 0.57 | 58 | -1.32 | 1.013804603 | 0.3692428 | 6.898116626 | Low |
| 180 | EGFR mutation-positive | GSM773730 | 1.18 | 1.08 | P | 0.58 | 69 | -1.42 | 0.9967583 | 0.333421649 | 7.857943048 | |
| 181 | EGFR mutation-positive | GSM773731 | 1.21 | 1.10 | P | 0.58 | 61 | -1.12 | 0.995913709 | 0.296261784 | 8.19307244 | |
| 182 | EGFR mutation-positive | GSM773732 | 1.20 | 1.15 | P | 0.58 | 65 | -1.41 | 0.994167622 | 0.311874651 | 7.853547138 | |
| 183 | EGFR mutation-positive | GSM773733 | 1.19 | 1.15 | P | 0.58 | 61 | -1.24 | 0.99876147 | 0.311576364 | 8.061551236 | |
| 184 | EGFR mutation-positive | GSM773734 | 1.24 | 1.12 | P | 0.59 | 66 | -1.21 | 0.998040788 | 0.327495336 | 8.375542351 | |
| 185 | EGFR mutation-positive | GSM773735 | 1.26 | 1.14 | P | 0.56 | 65 | -1.09 | 1.00065265 | 0.32938458 | 7.995140549 | |
| 186 | EGFR mutation-positive | GSM773736 | 1.16 | 1.11 | P | 0.56 | 71 | -0.83 | 1.014196824 | 0.305692088 | 7.705450507 | |
| 187 | EGFR mutation-positive | GSM773737 | 1.26 | 1.14 | P | 0.57 | 66 | -0.92 | 1.00736534 | 0.339153891 | 9.074496305 | |
| 188 | EGFR mutation-positive | GSM773738 | 1.24 | 1.13 | P | 0.56 | 65 | -0.94 | 1.010099749 | 0.39794288 | 8.150331713 | |
| 189 | EGFR mutation-positive | GSM773739 | 1.28 | 1.10 | P | 0.57 | 62 | -0.75 | 1.015210209 | 0.378133731 | 8.332889278 | |
| 190 | EGFR mutation-positive | GSM773740 | 1.21 | 1.10 | P | 0.59 | 52 | -1.00 | 1.007647172 | 0.38177252 | 8.605470893 | Low |
| 191 | EGFR mutation-positive | GSM773741 | 1.15 | 1.11 | P | 0.56 | 74 | -1.34 | 1.010459365 | 0.34122242 | 7.371594386 | |
| 192 | EGFR mutation-positive | GSM773742 | 1.22 | 1.13 | P | 0.59 | 78 | -1.48 | 1.001584608 | 0.392264796 | 8.555325635 | |
| 193 | EGFR mutation-positive | GSM773743 | 1.21 | 1.10 | P | 0.59 | 66 | -1.21 | 1.000087667 | 0.326275082 | 8.176346128 | |
| 194 | EGFR mutation-positive | GSM773744 | 1.20 | 1.15 | P | 0.56 | 63 | -0.98 | 1.005106517 | 0.340245679 | 8.051567845 | |
| 195 | EGFR mutation-positive | GSM773745 | 1.16 | 1.11 | P | 0.60 | 67 | -1.43 | 0.994622105 | 0.337265657 | 8.002494673 | |
| 196 | EGFR mutation-positive | GSM773746 | 1.11 | 1.07 | P | 0.56 | 69 | -1.37 | 0.995927669 | 0.279344283 | 6.968632359 | |
| 197 | EGFR mutation-positive | GSM773747 | 1.20 | 1.09 | P | 0.55 | 69 | -1.15 | 1.008969014 | 0.379592502 | 7.283051119 | |
| 198 | EGFR mutation-positive | GSM773748 | 1.17 | 1.11 | P | 0.58 | 51 | -1.12 | 1.004039122 | 0.341790092 | 7.946468736 | Low |
| 199 | EGFR mutation-positive | GSM773749 | 1.14 | 1.09 | P | 0.57 | 70 | -1.59 | 1.003876518 | 0.307714343 | 7.832744923 | |
| 200 | EGFR mutation-positive | GSM773750 | 1.16 | 1.13 | P | 0.59 | 76 | -1.51 | 0.986742254 | 0.22697064 | 7.885205011 | |
| 201 | EGFR mutation-positive | GSM773751 | 1.19 | 1.07 | P | 0.56 | 73 | -1.34 | 1.000186649 | 0.344155411 | 7.73227289 | |
| 202 | EGFR mutation-positive | GSM773752 | 1.19 | 1.11 | P | 0.55 | 77 | -1.29 | 1.002124777 | 0.345854218 | 7.565184436 | |
| 203 | EGFR mutation-positive | GSM773753 | 1.14 | 1.09 | P | 0.58 | 78 | -1.54 | 0.989364741 | 0.284362463 | 7.515768372 | |
| 204 | EGFR mutation-positive | GSM773754 | 1.17 | 1.10 | P | 0.58 | 79 | -1.53 | 0.993267133 | 0.301274509 | 7.773132524 | |
| 205 | EGFR mutation-positive | GSM773755 | 1.15 | 1.12 | P | 0.57 | 79 | -1.44 | 0.998266586 | 0.366190222 | 7.389025276 | |
| 206 | EGFR mutation-positive | GSM773756 | 1.14 | 1.06 | P | 0.58 | 73 | -1.41 | 1.001595392 | 0.312295838 | 7.455922919 | |
| 207 | EGFR mutation-positive | GSM773757 | 1.14 | 1.09 | P | 0.58 | 73 | -1.40 | 0.995394229 | 0.28701234 | 7.777010009 | |
| 208 | EGFR mutation-positive | GSM773758 | 1.15 | 1.10 | P | 0.56 | 79 | -1.38 | 0.996303708 | 0.302358913 | 7.524592201 | |
| 209 | EGFR mutation-positive | GSM773759 | 1.16 | 1.13 | P | 0.57 | 75 | -1.40 | 0.999354463 | 0.342486012 | 7.387192328 | |
| 210 | EGFR mutation-positive | GSM773760 | 1.20 | 1.13 | P | 0.57 | 71 | -1.16 | 0.99657912 | 0.303101337 | 8.298017174 | |

| | | | | | | | | | | | | |
|-----|------------------------|-----------|------|------|---|------|----|-------|-------------|-------------|-------------|-----|
| 211 | EGFR mutation-positive | GSM773761 | 1.16 | 1.08 | P | 0.58 | 74 | -1.34 | 0.989213652 | 0.241738187 | 7.725050771 | |
| 212 | EGFR mutation-positive | GSM773762 | 1.14 | 1.11 | P | 0.55 | 78 | -1.41 | 1.009368502 | 0.37850077 | 7.118074405 | |
| 213 | EGFR mutation-positive | GSM773763 | 1.12 | 1.10 | P | 0.58 | 76 | -1.48 | 0.992179133 | 0.264444738 | 7.533115597 | |
| 214 | EGFR mutation-positive | GSM773764 | 1.16 | 1.10 | P | 0.56 | 70 | -1.26 | 0.999116178 | 0.331558282 | 7.598280534 | |
| 215 | EGFR mutation-positive | GSM773765 | 1.15 | 1.12 | P | 0.58 | 70 | -1.32 | 0.993226312 | 0.277817236 | 7.546887725 | |
| 216 | KRAS mutation-positive | GSM773551 | 1.14 | 1.09 | P | 0.58 | 64 | -1.24 | 0.993959619 | 0.300803385 | 7.58941251 | |
| 217 | KRAS mutation-positive | GSM773552 | 1.09 | 1.02 | P | 0.56 | 68 | -1.39 | 0.999672878 | 0.365883395 | 7.011678014 | |
| 218 | KRAS mutation-positive | GSM773553 | 1.11 | 1.08 | P | 0.53 | 68 | -1.28 | 1.015663509 | 0.416943367 | 6.477434455 | |
| 219 | KRAS mutation-positive | GSM773554 | 1.17 | 1.10 | P | 0.54 | 74 | -1.48 | 1.004393639 | 0.399915872 | 7.27438172 | |
| 220 | KRAS mutation-positive | GSM773555 | 1.20 | 1.08 | P | 0.55 | 59 | -0.96 | 1.012779992 | 0.392306431 | 7.781919205 | Low |
| 221 | KRAS mutation-positive | GSM773556 | 1.19 | 1.09 | P | 0.56 | 67 | -1.11 | 1.003235029 | 0.388685017 | 7.719667736 | |
| 222 | KRAS mutation-positive | GSM773557 | 1.13 | 1.08 | P | 0.57 | 73 | -1.33 | 1.001061839 | 0.322047761 | 7.264808658 | |
| 223 | KRAS mutation-positive | GSM773558 | 1.15 | 1.04 | P | 0.55 | 65 | -1.23 | 1.00645765 | 0.398395148 | 7.755604778 | |
| 224 | KRAS mutation-positive | GSM773559 | 1.09 | 1.02 | P | 0.54 | 68 | -1.38 | 1.014491342 | 0.449753098 | 6.432989157 | |
| 225 | KRAS mutation-positive | GSM773560 | 1.10 | 1.05 | P | 0.57 | 70 | -1.32 | 1.000671818 | 0.338856492 | 7.047272655 | |
| 226 | KRAS mutation-positive | GSM773561 | 1.23 | 1.12 | P | 0.59 | 67 | -1.14 | 1.000658965 | 0.354791297 | 8.938824962 | |
| 227 | KRAS mutation-positive | GSM773562 | 1.28 | 1.10 | P | 0.56 | 68 | -0.86 | 1.019416964 | 0.369072591 | 8.69701025 | |
| 228 | KRAS mutation-positive | GSM773563 | 1.13 | 1.06 | P | 0.57 | 66 | -1.61 | 0.998242676 | 0.33669175 | 7.562502067 | |
| 229 | KRAS mutation-positive | GSM773564 | 1.10 | 1.06 | P | 0.56 | 76 | -1.60 | 1.005777493 | 0.343976879 | 6.653306987 | |
| 230 | KRAS mutation-positive | GSM773565 | 1.12 | 1.04 | P | 0.55 | 64 | -1.25 | 0.994963015 | 0.335396833 | 7.099317478 | |
| 231 | KRAS mutation-positive | GSM773566 | 1.09 | 1.04 | P | 0.59 | 67 | -1.55 | 0.99063263 | 0.286288092 | 6.898903999 | |
| 232 | KRAS mutation-positive | GSM773567 | 1.18 | 1.10 | P | 0.56 | 63 | -1.37 | 0.996979658 | 0.291628808 | 7.817219748 | |
| 233 | KRAS mutation-positive | GSM773568 | 1.08 | 1.06 | P | 0.57 | 66 | -1.45 | 0.992524075 | 0.293775206 | 7.013583291 | |
| 234 | KRAS mutation-positive | GSM773569 | 1.16 | 1.11 | P | 0.57 | 68 | -1.44 | 0.993895678 | 0.321578175 | 7.316448988 | |
| 235 | KRAS mutation-positive | GSM773570 | 1.20 | 1.09 | P | 0.57 | 63 | -1.20 | 1.002115197 | 0.347631495 | 7.946752329 | |
| 236 | EML4-ALK-positive | GSM773540 | 1.28 | 1.10 | P | 0.54 | 67 | -0.86 | 1.015908493 | 0.430555676 | 8.373654518 | |
| 237 | EML4-ALK-positive | GSM773541 | 1.11 | 1.04 | P | 0.56 | 69 | -1.45 | 0.998924818 | 0.333571584 | 6.848848344 | |
| 238 | EML4-ALK-positive | GSM773542 | 1.12 | 1.05 | P | 0.55 | 69 | -1.36 | 1.002452438 | 0.341191504 | 6.933878605 | |
| 239 | EML4-ALK-positive | GSM773543 | 1.11 | 1.05 | P | 0.56 | 73 | -1.64 | 1.000206331 | 0.408515874 | 6.670260549 | |
| 240 | EML4-ALK-positive | GSM773544 | 1.18 | 1.08 | P | 0.57 | 71 | -1.39 | 0.996488273 | 0.337672437 | 7.66433712 | |
| 241 | EML4-ALK-positive | GSM773545 | 1.15 | 1.08 | P | 0.58 | 71 | -1.33 | 0.988670553 | 0.250902255 | 7.53368303 | |
| 242 | EML4-ALK-positive | GSM773546 | 1.13 | 1.05 | P | 0.56 | 73 | -1.46 | 0.995931572 | 0.309823676 | 7.168587149 | |
| 243 | EML4-ALK-positive | GSM773547 | 1.12 | 1.05 | P | 0.58 | 70 | -1.39 | 0.998596331 | 0.307753833 | 7.206199832 | |
| 244 | EML4-ALK-positive | GSM773548 | 1.21 | 1.10 | P | 0.56 | 70 | -1.27 | 1.009358733 | 0.36891516 | 8.765199457 | |
| 245 | EML4-ALK-positive | GSM773549 | 1.11 | 1.06 | P | 0.56 | 67 | -1.56 | 0.997558332 | 0.301391288 | 6.736712084 | |
| 246 | EML4-ALK-positive | GSM773550 | 1.18 | 1.08 | P | 0.56 | 73 | -1.45 | 0.997056428 | 0.320575775 | 7.872221132 | |

The RNA degradation plot proposes to plot the average intensity of each probes across all probe-sets, ordered from the 5' to the 3' end. Probe intensities are expected to be globally lowered at that end of a probe set when compared to the 3' end. The RNA degradation plot aims at visualizing this trend.

Table SIII. Experimental conditions used in western blot analysis.

| Target protein | Loading amount, μg | Gel % | Primary antibody | | | | Secondary antibody | | | |
|---------------------|-------------------------------|-------|---------------------------------|----------|----------|------------|---------------------------|-----------|----------|------------|
| | | | Supplier | Cat. no. | Dilution | Conditions | Supplier | Cat. No | Dilution | Conditions |
| SMAD3 | 30 | 10 | Cell Signaling Technology, Inc. | 9523 | 1:1,000 | 4°C, O/N | Bethyl Laboratories, Inc. | A120-101P | 1:5,000 | RT, 1 h |
| pSMAD3 (Ser423/425) | 30 | 10 | Cell Signaling Technology, Inc. | 9520 | 1:1,000 | 4°C, O/N | Bethyl Laboratories, Inc. | A120-101P | 1:5000 | RT, 1 h |
| SMAD2 | 40 | 10 | Cell Signaling Technology, Inc. | 3122 | 1:1,000 | 4°C, O/N | Bethyl Laboratories, Inc. | A120-101P | 1:5000 | RT, 1 h |
| pSMAD2 (Ser423/425) | 40 | 10 | Cell Signaling Technology, Inc. | 3101 | 1:1,000 | 4°C, O/N | Bethyl Laboratories, Inc. | A120-101P | 1:5000 | RT, 1 h |
| Vimentin | 10 | 10 | Santa Cruz Biotechnology, Inc. | sc-5565 | 1:500 | 4°C, O/N | Bethyl Laboratories, Inc. | A120-101P | 1:5000 | RT, 1 h |
| Fibronectin | 10 | 6 | Santa Cruz Biotechnology, Inc. | sc-8422 | 1:500 | 4°C, O/N | Bethyl Laboratories, Inc. | A90-116P | 1:5000 | RT, 1 h |
| N-cadherin | 20 | 6 | Santa Cruz Biotechnology, Inc. | sc-7939 | 1:500 | 4°C, O/N | Bethyl Laboratories, Inc. | A120-101P | 1:5000 | RT, 1 h |
| E-cadherin | 10 | 6 | Cell Signaling Technology, Inc. | 3195 | 1:1,000 | 4°C, O/N | Bethyl Laboratories, Inc. | A120-101P | 1:5000 | RT, 1 h |
| β -tubulin | 10 | 10 | Sigma-Aldrich; Merck KGaA | T4026 | 1:5,000 | 4°C, O/N | Sigma-Aldrich; Merck KGaA | A90-116P | 1:5000 | RT, 1 h |

O/N, overnight; RT, room temperature; p, phosphorylated

Table SIV. Relative expression ratios of fucosylation pathway genes in each molecular subtype of NSCLC.

| Gene | Triple-negative | | EGFR mutation-positive | | KRAS mutation-positive | | EML4-ALK-positive | |
|---------|-------------------|---------------------|------------------------|---------------------|------------------------|---------------------|-------------------|---------------------|
| | Fold change (SEM) | P-value | Fold change (SEM) | P-value | Fold change (SEM) | P-value | Fold change (SEM) | P-value |
| FUT1 | 0.385 (±0.030) | <0.001 ^c | 0.355 (±0.017) | <0.001 ^c | 0.379 (±0.051) | <0.001 ^c | 0.261 (±0.032) | <0.001 ^c |
| FUT2 | 3.786 (±0.285) | <0.001 ^c | 3.451 (±0.156) | <0.001 ^c | 4.419 (±0.807) | 0.001 ^c | 6.277 (±0.726) | <0.001 ^c |
| FUT3 | 3.168 (±0.349) | <0.001 ^c | 2.890 (±0.179) | <0.001 ^c | 4.971 (±1.029) | 0.001 ^c | 6.387 (±0.576) | <0.001 ^c |
| FUT4 | 1.154 (±0.120) | 0.509 | 0.887 (±0.029) | 0.157 | 1.630 (±0.303) | 0.055 | 0.720 (±0.095) | 0.012 |
| FUT5 | 1.032 (±0.075) | 0.841 | 1.162 (±0.055) | 0.284 | 1.139 (±0.159) | 0.487 | 0.861 (±0.129) | 0.448 |
| FUT6 | 2.163 (±0.208) | <0.001 ^c | 1.813 (±0.086) | <0.001 ^c | 2.754 (±0.326) | <0.001 ^c | 3.563 (±0.709) | 0.005 ^b |
| FUT7 | 0.853 (±0.065) | 0.297 | 0.874 (±0.046) | 0.322 | 0.958 (±0.122) | 0.806 | 0.835 (±0.242) | 0.500 |
| FUT8 | 2.671 (±0.191) | <0.001 ^c | 2.672 (±0.149) | <0.001 ^c | 2.816 (±0.340) | <0.001 ^c | 4.911 (±0.726) | <0.001 ^c |
| FUT9 | 1.743 (±0.263) | 0.151 | 1.329 (±0.096) | 0.201 | 1.288 (±0.264) | 0.360 | 1.655 (±0.270) | 0.032 |
| FUT10 | 1.164 (±0.042) | 0.010 ^a | 1.048 (±0.031) | 0.563 | 1.245 (±0.074) | 0.008 ^a | 1.043 (±0.100) | 0.655 |
| FUT11 | 1.158 (±0.059) | 0.033 | 1.004 (±0.032) | 0.945 | 1.070 (±0.074) | 0.418 | 0.880 (±0.087) | 0.179 |
| POFUT1 | 1.052 (±0.036) | 0.477 | 1.012 (±0.030) | 0.817 | 0.879 (±0.082) | 0.204 | 0.955 (±0.080) | 0.602 |
| POFUT2 | 1.058 (±0.030) | 0.359 | 1.145 (±0.025) | 0.034 | 1.004 (±0.050) | 0.955 | 1.028 (±0.070) | 0.737 |
| GMDS | 2.519 (±0.324) | <0.001 ^c | 1.800 (±0.083) | <0.001 ^c | 3.860 (±1.187) | 0.027 | 3.246 (±0.501) | 0.001 ^c |
| TSTA3 | 2.058 (±0.143) | <0.001 ^c | 2.123 (±0.153) | 0.006 | 3.095 (±0.474) | <0.001 ^c | 2.536 (±0.301) | <0.001 ^c |
| FUK | 1.290 (±0.047) | <0.001 ^c | 1.574 (±0.047) | <0.001 ^c | 1.319 (±0.091) | 0.003 ^b | 1.569 (±0.138) | 0.002 ^b |
| FPGT | 1.099 (±0.034) | 0.041 | 1.243 (±0.034) | <0.001 ^c | 1.051 (±0.076) | 0.544 | 1.137 (±0.092) | 0.185 |
| SLC35C1 | 1.181 (±0.047) | 0.054 | 1.124 (±0.024) | 0.005 ^b | 1.824 (±0.424) | 0.069 | 2.230 (±0.240) | <0.001 ^c |

^aP<0.05. ^bP<0.01. ^cP<0.005. EGFR, epidermal growth factor receptor; EML4-ALK, echinoderm microtubule-associated protein-like 4 - anaplastic lymphoma kinase fusion.

Table SV. Replication of survival analysis using different datasets.

| Genes | Discovery data ^a | | First replication data ^b | | Second replication data ^c | |
|-------|-----------------------------------|---------|-------------------------------------|---------|--------------------------------------|---------|
| | HR (95% CI) | P-value | HR (95% CI) | P-value | HR (95% CI) | P-value |
| FUT1 | 4.469 (1.657-12.051) ^d | 0.003 | 2.237 (1.159-4.315) ^d | 0.016 | 1.963 (1.251-3.081) ^d | 0.003 |
| FUT2 | 2.527 (1.228-5.203) | 0.012 | 1.072 (0.624-1.840) | 0.802 | 0.730 (0.465-1.146) | 0.171 |
| FUT3 | 2.190 (1.073-4.470) | 0.031 | 0.820 (0.459-1.466) | 0.504 | 1.197 (0.768-1.866) | 0.428 |
| FUT5 | 2.619 (1.286-5.332) ^d | 0.008 | 1.367 (0.771-2.423) ^d | 0.285 | 0.574 (0.3892-0.861) ^d | 0.007 |
| FUT6 | 1.962 (1.018-3.780) | 0.044 | 1.491 (0.863-2.575) | 0.152 | 1.117 (0.727-1.717) | 0.613 |
| FUT8 | 2.530 (1.112-5.760) | 0.027 | 0.415 (0.222-0.778) | 0.006 | 1.765 (1.121-2.780) | 0.014 |
| TSTA3 | 2.464 (1.118-5.431) | 0.025 | 0.995 (0.568-1.742) | 0.985 | 1.069 (0.687-1.663) | 0.768 |

^aDiscovery dataset was GSE31210. ^bFirst replication was performed using an integrated dataset (GSE29013, GSE30219, GSE37745, GSE50081).

^cSecond replication was performed using TCGA LUAD RNA-Seq V2 RSEM and survival data. ^dHR for low expression (bottom 25% expression value). TCGA, The Cancer Genome Atlas. HR, hazard ratio; CI, confidence interval.