**Integrated single-cell and bulk RNA sequencing identifies SERPING1 as a biomarker of immune infiltration and prognosis in Triple-negative breast cancer**

**Supplementary Table 1** ESTIMATE analysis of 118 TNBC samples of TCGA database.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Sample | StromalScore | ImmuneScore | ESTIMATEScore | TumorPurity |
| TCGA.A1.A0SP | -41.7021 | 1045.362 | 1003.66 | 0.73011 |
| TCGA.E2.A1LS | -363.387 | -290.056 | -653.443 | 0.873198 |
| TCGA.BH.A0B9 | -693.333 | 1686.402 | 993.0685 | 0.731172 |
| TCGA.E2.A1LL | -510.315 | -177.32 | -687.635 | 0.875634 |
| TCGA.D8.A1XK | -449.715 | 912.6305 | 462.9156 | 0.781994 |
| TCGA.AN.A04D | -1119.74 | -810.015 | -1929.75 | 0.948692 |
| TCGA.AR.A0U4 | 621.1444 | 2140.603 | 2761.748 | 0.531539 |
| TCGA.A2.A04Q | 1004.329 | 2743.085 | 3747.414 | 0.40386 |
| TCGA.E2.A1B6 | 57.16508 | 2776.096 | 2833.261 | 0.522618 |
| TCGA.B6.A0RS | 372.617 | 1089.372 | 1461.989 | 0.682521 |
| TCGA.D8.A1JL | 1013.045 | 1721.335 | 2734.38 | 0.534938 |
| TCGA.E9.A1ND | 660.8997 | 2225.653 | 2886.552 | 0.515933 |
| TCGA.D8.A147 | -82.6621 | 889.0188 | 806.3567 | 0.749592 |
| TCGA.A1.A0SO | -1148.25 | -616.17 | -1764.42 | 0.94074 |
| TCGA.D8.A27M | 1140.073 | 2012.684 | 3152.756 | 0.482075 |
| TCGA.A7.A26G | 1576.192 | 1339.648 | 2915.84 | 0.512246 |
| TCGA.E2.A1LI | -415.71 | 937.3523 | 521.6424 | 0.776592 |
| TCGA.AO.A129 | 266.0361 | 1560 | 1826.036 | 0.642509 |
| TCGA.AR.A0TS | 627.9921 | 2161.411 | 2789.403 | 0.528096 |
| TCGA.BH.A0AV | 1192.944 | 562.5564 | 1755.5 | 0.650408 |
| TCGA.D8.A1XQ | 611.2205 | 1500.423 | 2111.644 | 0.609829 |
| TCGA.BH.A18V | 707.4722 | 1265.698 | 1973.17 | 0.625811 |
| TCGA.B6.A0RT | 939.3976 | 3107.095 | 4046.492 | 0.363322 |
| TCGA.A7.A0CE | -393.035 | -65.3264 | -458.362 | 0.858886 |
| TCGA.AO.A124 | -760.519 | 148.379 | -612.14 | 0.870228 |
| TCGA.A2.A0YM | 159.2985 | 1054.716 | 1214.014 | 0.708666 |
| TCGA.AQ.A04J | 970.989 | 1873.273 | 2844.261 | 0.521241 |
| TCGA.AO.A12F | 483.1978 | -157.79 | 325.408 | 0.794415 |
| TCGA.EW.A1P4 | 140.7053 | 1547.182 | 1687.887 | 0.657915 |
| TCGA.AN.A0AR | -791.749 | -404.304 | -1196.05 | 0.909207 |
| TCGA.BH.A18Q | -36.2346 | 769.4218 | 733.1872 | 0.756658 |
| TCGA.B6.A0WX | 1008.316 | 903.4054 | 1911.722 | 0.632821 |
| TCGA.BH.A0BW | 278.7814 | 1825.094 | 2103.876 | 0.610732 |
| TCGA.E2.A1AZ | 966.3399 | 1483.407 | 2449.747 | 0.569761 |
| TCGA.B6.A0RE | -250.425 | 95.67596 | -154.749 | 0.835215 |
| TCGA.D8.A143 | -391.779 | 543.2382 | 151.4597 | 0.809662 |
| TCGA.BH.A0E0 | -705.204 | 312.5582 | -392.646 | 0.853906 |
| TCGA.AR.A0TU | -703.036 | 1176.556 | 473.5202 | 0.781023 |
| TCGA.AN.A0AL | 844.4022 | 1223.026 | 2067.428 | 0.61496 |
| TCGA.B6.A0RU | 213.9476 | -183.695 | 30.25293 | 0.819976 |
| TCGA.D8.A1JF | 797.4261 | 503.3271 | 1300.753 | 0.699626 |
| TCGA.AN.A0AT | -494.121 | 480.0182 | -14.1028 | 0.823685 |
| TCGA.A7.A0DA | 415.0641 | -59.2235 | 355.8406 | 0.791693 |
| TCGA.E2.A14X | 75.37283 | 1256.26 | 1331.633 | 0.69638 |
| TCGA.AR.A0U0 | 136.1834 | 1783.182 | 1919.366 | 0.631951 |
| TCGA.BH.A18T | -366.221 | 294.7857 | -71.4351 | 0.828428 |
| TCGA.BH.A0E6 | -28.8401 | 846.9601 | 818.12 | 0.748448 |
| TCGA.A2.A04T | -277.533 | 1142.505 | 864.9721 | 0.743869 |
| TCGA.C8.A12V | 825.7562 | 2935.829 | 3761.586 | 0.401956 |
| TCGA.A2.A0T2 | 125.5044 | 495.6385 | 621.1429 | 0.767308 |
| TCGA.D8.A27F | 451.8931 | 153.5944 | 605.4874 | 0.76878 |
| TCGA.E2.A1LK | -1065.02 | 108.0662 | -956.954 | 0.894038 |
| TCGA.A2.A1G6 | 540.4143 | 574.8819 | 1115.296 | 0.718815 |
| TCGA.D8.A142 | 975.8299 | 789.324 | 1765.154 | 0.649331 |
| TCGA.BH.A1FC | -63.6297 | 1538.253 | 1474.623 | 0.681164 |
| TCGA.EW.A1P7 | 1155.935 | 2622.418 | 3778.353 | 0.399701 |
| TCGA.E2.A150 | 473.8113 | 1018.465 | 1492.276 | 0.679265 |
| TCGA.BH.A0BG | 105.0192 | 1569.097 | 1674.116 | 0.659436 |
| TCGA.BH.A0RX | 1230.459 | 2205.235 | 3435.694 | 0.445282 |
| TCGA.A2.A0T0 | 387.1224 | 517.7023 | 904.8247 | 0.739947 |
| TCGA.EW.A1P8 | 249.2265 | 1368.977 | 1618.203 | 0.665584 |
| TCGA.A2.A0ST | 643.5019 | 3007.854 | 3651.356 | 0.416719 |
| TCGA.AN.A0FL | -604.882 | -287.079 | -891.96 | 0.889723 |
| TCGA.A2.A04U | -192.344 | -267.208 | -459.553 | 0.858976 |
| TCGA.C8.A27B | -144.439 | 1563.897 | 1419.458 | 0.68707 |
| TCGA.AO.A0J4 | 200.7079 | 1398.914 | 1599.622 | 0.667617 |
| TCGA.C8.A134 | -76.5023 | 1139.15 | 1062.648 | 0.724166 |
| TCGA.E2.A1LG | -1046.62 | 211.4941 | -835.127 | 0.885884 |
| TCGA.C8.A1HJ | -277.601 | 103.2025 | -174.398 | 0.836798 |
| TCGA.C8.A26X | 1248.046 | 2072.027 | 3320.073 | 0.460413 |
| TCGA.BH.A18G | 173.6528 | 455.1272 | 628.78 | 0.766589 |
| TCGA.A2.A04P | 368.5172 | 1256.983 | 1625.5 | 0.664784 |
| TCGA.A2.A0D2 | 212.956 | 1112.835 | 1325.791 | 0.696995 |
| TCGA.E2.A158 | -1184.46 | -432.23 | -1616.69 | 0.933165 |
| TCGA.E2.A14R | -394.689 | 1366.446 | 971.7569 | 0.733302 |
| TCGA.BH.A0B3 | 614.563 | 1322.977 | 1937.54 | 0.629882 |
| TCGA.AR.A1AQ | 475.2275 | 1962.765 | 2437.993 | 0.571178 |
| TCGA.A8.A07C | 53.3704 | 815.1896 | 868.56 | 0.743517 |
| TCGA.BH.A0WA | 176.3732 | 333.39 | 509.7633 | 0.777689 |
| TCGA.A2.A0D0 | -910.621 | 918.182 | 7.561358 | 0.821878 |
| TCGA.BH.A1EW | 435.1019 | 949.7088 | 1384.811 | 0.690757 |
| TCGA.E2.A14N | -659.255 | 831.5408 | 172.2855 | 0.807864 |
| TCGA.EW.A1P1 | 1640.375 | 1492.103 | 3132.478 | 0.48468 |
| TCGA.C8.A131 | 560.2148 | 732.8769 | 1293.092 | 0.700429 |
| TCGA.AO.A128 | 612.2756 | 3034.574 | 3646.85 | 0.41732 |
| TCGA.A2.A0YE | -39.4958 | -264.949 | -304.444 | 0.847097 |
| TCGA.EW.A1OV | 935.6015 | 2631.768 | 3567.369 | 0.427893 |
| TCGA.A1.A0SK | -1423.89 | -1308.92 | -2732.81 | 0.979296 |
| TCGA.B6.A0IK | -8.78646 | 390.8779 | 382.0915 | 0.789333 |
| TCGA.A2.A0CM | 671.7204 | 1701.292 | 2373.013 | 0.578981 |
| TCGA.C8.A26Y | -684.2 | 487.7662 | -196.434 | 0.838565 |
| TCGA.EW.A1PB | 136.2154 | 2430.66 | 2566.875 | 0.555548 |
| TCGA.A8.A09X | 1105.755 | 1705.196 | 2810.951 | 0.525408 |
| TCGA.E9.A22G | -963.995 | 92.96984 | -871.026 | 0.888316 |
| TCGA.E2.A1LH | 587.7227 | 2202.407 | 2790.13 | 0.528006 |
| TCGA.AO.A0JL | -2.11334 | -44.1596 | -46.2729 | 0.826354 |
| TCGA.A2.A0SX | 846.3225 | 1975.563 | 2821.886 | 0.524041 |
| TCGA.AN.A0XU | -625.033 | 656.0423 | 31.00879 | 0.819912 |
| TCGA.BH.A0BL | 1481.81 | 1728.223 | 3210.032 | 0.474692 |
| TCGA.B6.A0IQ | -663.794 | 386.529 | -277.265 | 0.84497 |
| TCGA.E2.A1L7 | 334.4905 | 1419.063 | 1753.554 | 0.650625 |
| TCGA.AN.A0G0 | -105.965 | 66.91378 | -39.051 | 0.825756 |
| TCGA.AO.A0J6 | -699.496 | 1285.474 | 585.9771 | 0.770608 |
| TCGA.D8.A27H | 631.6631 | 274.9321 | 906.5953 | 0.739772 |
| TCGA.AR.A1AR | 1081.832 | 1854.143 | 2935.975 | 0.509705 |
| TCGA.EW.A1OW | 557.488 | 452.9516 | 1010.44 | 0.72943 |
| TCGA.B6.A0RG | 62.84426 | -385.162 | -322.317 | 0.848488 |
| TCGA.B6.A0IE | 72.10889 | -76.3536 | -4.24467 | 0.822864 |
| TCGA.D8.A13Z | 628.1544 | 1151.67 | 1779.825 | 0.647692 |
| TCGA.AR.A256 | -98.0873 | 361.4913 | 263.404 | 0.79991 |
| TCGA.AR.A1AI | -285.236 | 1775.641 | 1490.404 | 0.679466 |
| TCGA.E2.A159 | 539.2971 | 1811.868 | 2351.165 | 0.581593 |
| TCGA.AN.A0FX | 267.9692 | -210.072 | 57.89725 | 0.817646 |
| TCGA.AO.A0J2 | -215.335 | 1045.601 | 830.2667 | 0.747264 |
| TCGA.A8.A08R | 560.6759 | 1448.699 | 2009.375 | 0.621657 |
| TCGA.A8.A07O | -247.942 | 736.8853 | 488.943 | 0.779607 |
| TCGA.AR.A1AY | -129.848 | -24.2418 | -154.09 | 0.835162 |
| TCGA.B6.A0RN | 682.443 | -207.37 | 475.0735 | 0.78088 |

**Supplementary Table 2** Univariate Cox regression analysis identified 46 genes significantly associated with OS.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| gene | HR | z | pvalue | lower | upper |
| NFE2L3 | 0.632451 | -1.99669 | 0.045859 | 0.403379 | 0.991609 |
| LAMP3 | 0.675468 | -2.15972 | 0.030794 | 0.473118 | 0.964361 |
| SH3BP1 | 0.450143 | -2.5192 | 0.011762 | 0.241909 | 0.837622 |
| COL9A3 | 0.615675 | -2.38577 | 0.017043 | 0.413332 | 0.917073 |
| NUAK2 | 0.442742 | -2.28261 | 0.022453 | 0.219947 | 0.891217 |
| ANKDD1B | 187.2647 | 2.143261 | 0.032092 | 1.564395 | 22416.38 |
| JPT2 | 2.515105 | 2.069427 | 0.038506 | 1.049996 | 6.024548 |
| EFNA3 | 1.572455 | 1.961604 | 0.049809 | 1.000379 | 2.471679 |
| FOXP4 | 0.55303 | -2.15815 | 0.030916 | 0.322939 | 0.947058 |
| GBP1 | 0.694703 | -2.19461 | 0.028192 | 0.501779 | 0.961802 |
| CARMIL2 | 0.467666 | -1.98367 | 0.047293 | 0.220706 | 0.99096 |
| B3GNT4 | 6.461262 | 1.963237 | 0.049619 | 1.003116 | 41.61822 |
| GZMB | 0.676927 | -2.22484 | 0.026092 | 0.480019 | 0.954608 |
| CLEC6A | 0.019306 | -2.05049 | 0.040316 | 0.000444 | 0.840067 |
| ACSS2 | 0.324287 | -2.8414 | 0.004492 | 0.149134 | 0.705155 |
| RASGRP1 | 0.413426 | -2.99416 | 0.002752 | 0.231896 | 0.737059 |
| PARP3 | 0.46246 | -2.06014 | 0.039386 | 0.222042 | 0.963196 |
| HLA-DOB | 0.60003 | -2.06012 | 0.039387 | 0.369088 | 0.975474 |
| SDS | 2.241296 | 2.762172 | 0.005742 | 1.264137 | 3.973784 |
| BATF2 | 0.635449 | -2.12957 | 0.033207 | 0.418644 | 0.964531 |
| CHRM3 | 0.434646 | -2.05953 | 0.039444 | 0.196683 | 0.96052 |
| AFAP1L2 | 0.404585 | -2.21964 | 0.026443 | 0.181968 | 0.899547 |
| CCL25 | 0.030548 | -2.0854 | 0.037033 | 0.001151 | 0.810727 |
| SERPING1 | 0.514127 | -2.55238 | 0.010699 | 0.308463 | 0.856916 |
| ZBED6CL | 0.39751 | -2.57876 | 0.009915 | 0.197168 | 0.801419 |
| GRIA3 | 5.642603 | 2.707225 | 0.006785 | 1.61223 | 19.74841 |
| SEMA4A | 0.41942 | -2.61467 | 0.008931 | 0.218669 | 0.804475 |
| HLA-DQB2 | 0.593189 | -2.77395 | 0.005538 | 0.410148 | 0.857918 |
| PRDM12 | 47.53413 | 2.814194 | 0.00489 | 3.22882 | 699.7893 |
| TNFRSF13C | 0.307839 | -2.15991 | 0.03078 | 0.105685 | 0.896671 |
| ZNF296 | 2.213393 | 2.423007 | 0.015393 | 1.16397 | 4.208966 |
| CD1B | 0.211469 | -1.98933 | 0.046665 | 0.045757 | 0.977326 |
| HLA-DQA2 | 0.712652 | -2.39285 | 0.016718 | 0.539972 | 0.940555 |
| QRFPR | 0.0026 | -2.05071 | 0.040295 | 8.80E-06 | 0.768448 |
| SLC24A4 | 7.313506 | 2.293453 | 0.021822 | 1.335525 | 40.0497 |
| NDRG2 | 0.72781 | -2.00978 | 0.044454 | 0.533895 | 0.992155 |
| TTYH1 | 0.699443 | -2.21725 | 0.026606 | 0.50994 | 0.959368 |
| TMIGD2 | 0.039076 | -2.05681 | 0.039705 | 0.001779 | 0.858419 |
| PRSS12 | 0.577549 | -2.05239 | 0.040132 | 0.341912 | 0.975583 |
| PEG10 | 0.723799 | -2.85121 | 0.004355 | 0.579585 | 0.903897 |
| GPR25 | 0.002918 | -2.16136 | 0.030667 | 1.47E-05 | 0.580493 |
| CDH12 | 3.633387 | 2.393994 | 0.016666 | 1.263526 | 10.44815 |
| CSF2 | 0.00551 | -2.11678 | 0.034278 | 4.46E-05 | 0.680228 |
| SLC6A14 | 0.736768 | -2.00077 | 0.045417 | 0.546219 | 0.993789 |
| SLC18A1 | 7.61E-12 | -2.05056 | 0.04031 | 1.80E-22 | 0.322679 |
| CXCL13 | 0.791412 | -2.00836 | 0.044605 | 0.629874 | 0.994379 |

LASSO, least absolute shrinkage and selection operator; OS, overall survival.

**Supplementary Table 3** LASSO COX regression analysis identified 11 hub genes

|  |  |
| --- | --- |
| Gene | Coef |
| NUAK2 | -0.12229 |
| ANKDD1B | 1.748856 |
| ACSS2 | -0.36058 |
| RASGRP1 | -0.29247 |
| SDS | 0.225077 |
| SERPING1 | -0.14256 |
| ZBED6CL | -0.09106 |
| HLA-DQB2 | -0.07022 |
| PRDM12 | 0.973098 |
| ZNF296 | 0.020675 |
| PEG10 | -0.08698 |

LASSO, least absolute shrinkage and selection operator.