**Supplementary Table 4** Assessment of Immune, Stromal, and Estimate Scores and Overall Tumor Purity Using the Estimation of STromal and Immune cells in MAlignant Tumours using Expression data (ESTIMATE) Algorithm

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Samples** | **StromalScore** | **ImmuneScore** | **ESTIMATEScore** | **TumorPurity** |
| TCGA-DD-A4NG-01A | -815.9115986 | 482.9726438 | -332.9389548 | 0.84931204 |
| TCGA-G3-AAV4-01A | -894.9827433 | -81.52979724 | -976.5125405 | 0.895320328 |
| TCGA-2Y-A9H1-01A | -829.3157692 | 1131.280355 | 301.964586 | 0.796499918 |
| TCGA-BC-A10Y-01A | -804.5338282 | 454.0598472 | -350.473981 | 0.850667985 |
| TCGA-K7-AAU7-01A | -257.2354619 | 664.3279865 | 407.0925245 | 0.787074935 |
| TCGA-BC-A10W-01A | -599.0825781 | 487.1750233 | -111.9075549 | 0.831740716 |
| TCGA-DD-AACV-01A | -1364.272979 | -700.9398871 | -2065.212866 | 0.954791737 |
| TCGA-DD-AAD3-01A | 35.62348107 | 716.6057642 | 752.2292453 | 0.754827176 |
| TCGA-DD-A1EI-01A | 20.45950675 | 529.8720238 | 550.3315306 | 0.773931984 |
| TCGA-DD-AAC9-01A | 180.8107605 | 1130.608118 | 1311.418878 | 0.698506307 |
| TCGA-DD-AACT-01A | -334.7782407 | 962.2720936 | 627.4938529 | 0.766709755 |
| TCGA-GJ-A6C0-01A | -521.7252978 | 1106.564616 | 584.8393178 | 0.770714346 |
| TCGA-CC-5258-01A | -541.6158395 | 627.2592818 | 85.64344227 | 0.815294531 |
| TCGA-DD-AADP-01A | -504.3117403 | 386.6747803 | -117.6369599 | 0.83220732 |
| TCGA-DD-AACW-01A | -1076.201677 | 181.7953722 | -894.4063049 | 0.889887089 |
| TCGA-ZS-A9CD-01A | -242.1441581 | 671.0804522 | 428.9362942 | 0.785092993 |
| TCGA-UB-A7MF-01A | -583.4491842 | 1807.429996 | 1223.980812 | 0.707633222 |
| TCGA-WX-AA46-01A | -262.2004372 | 443.3732802 | 181.1728431 | 0.807094899 |
| TCGA-CC-A8HV-01A | -1217.038566 | -397.2179544 | -1614.256521 | 0.933036814 |
| TCGA-DD-AADQ-01A | -1128.933794 | 549.8337844 | -579.1000091 | 0.867828104 |
| TCGA-DD-AADB-01A | -853.1922127 | 1225.207979 | 372.0157663 | 0.790240601 |
| TCGA-DD-A1EA-01A | -873.7455993 | 719.0058039 | -154.7397954 | 0.835214725 |
| TCGA-5R-AA1C-01A | -827.4496694 | 356.3566065 | -471.093063 | 0.859841997 |
| TCGA-DD-A113-01A | -696.2788325 | 512.0224706 | -184.2563619 | 0.837589528 |
| TCGA-2Y-A9H9-01A | -651.9705626 | 342.2291697 | -309.7413929 | 0.84750958 |
| TCGA-CC-A7IE-01A | -635.4080697 | 1249.91024 | 614.5021701 | 0.76793266 |
| TCGA-XR-A8TD-01A | 410.7700618 | 1899.292321 | 2310.062382 | 0.586490262 |
| TCGA-DD-AAD2-01A | 294.8788096 | 1014.641152 | 1309.519961 | 0.698705747 |
| TCGA-DD-AACY-01A | -720.640647 | 334.4733162 | -386.1673308 | 0.85341065 |
| TCGA-CC-A7IF-01A | -1068.179759 | -327.6584031 | -1395.838162 | 0.921024248 |
| TCGA-DD-AACD-01A | -359.5678836 | 1062.112188 | 702.5443039 | 0.759590824 |
| TCGA-ED-A4XI-01A | 208.5841426 | 1149.983112 | 1358.567255 | 0.693537042 |
| TCGA-CC-A9FW-01A | -1304.04907 | 174.7442668 | -1129.304804 | 0.90508432 |
| TCGA-G3-A5SJ-01A | -568.7952642 | 1244.481383 | 675.686119 | 0.762149102 |
| TCGA-DD-AAE2-01A | -214.072666 | 929.4279425 | 715.3552765 | 0.758366401 |
| TCGA-G3-A7M9-01A | -1325.555145 | -329.7101463 | -1655.265291 | 0.935185638 |
| TCGA-EP-A2KC-01A | -775.5011281 | 149.1816777 | -626.3194504 | 0.871251131 |
| TCGA-2Y-A9GS-01A | -501.5384906 | 634.0874875 | 132.5489969 | 0.811288392 |
| TCGA-ED-A7PX-01A | 52.1094127 | 401.5171183 | 453.626531 | 0.782843068 |
| TCGA-DD-AADC-01A | -1068.627764 | -94.12014768 | -1162.747912 | 0.907160896 |
| TCGA-DD-AAVZ-01A | -762.7599977 | 110.2731833 | -652.4868144 | 0.873130038 |
| TCGA-CC-A3MA-01A | -465.9554842 | -74.95867956 | -540.9141638 | 0.865029441 |
| TCGA-2Y-A9GY-01A | -920.7037153 | 1748.60331 | 827.8995947 | 0.74749507 |
| TCGA-ED-A627-01A | 737.7766116 | 1908.7268 | 2646.503412 | 0.545791248 |
| TCGA-2Y-A9GW-01A | 50.00160871 | 1477.156943 | 1527.158552 | 0.675498067 |
| TCGA-DD-AADO-01A | -753.44964 | 1455.699485 | 702.2498449 | 0.759618936 |
| TCGA-DD-AADK-01A | -178.930302 | 807.8975686 | 628.9672666 | 0.766570886 |
| TCGA-DD-A1EH-01A | -460.9538863 | -83.28941572 | -544.243302 | 0.865274519 |
| TCGA-G3-AAV7-01A | -642.5223299 | 830.0490584 | 187.5267285 | 0.806543876 |
| TCGA-DD-AACA-01A | -1009.464881 | -213.0035744 | -1222.468455 | 0.910814703 |
| TCGA-FV-A3R3-01A | 444.2436842 | 820.1038323 | 1264.347516 | 0.70343408 |
| TCGA-KR-A7K0-01A | -507.8113598 | 314.3613453 | -193.4500145 | 0.838326008 |
| TCGA-DD-AACC-01A | 154.6199926 | 2597.067129 | 2751.687121 | 0.532789417 |
| TCGA-BC-A3KG-01A | -1251.049332 | -83.48569339 | -1334.535025 | 0.917482008 |
| TCGA-G3-AAV2-01A | -757.3953462 | 99.59646347 | -657.7988827 | 0.873509891 |
| TCGA-CC-A7IK-01A | -1273.830469 | -544.6532716 | -1818.483741 | 0.943401553 |
| TCGA-G3-A25S-01A | -991.6122915 | 658.4671002 | -333.1451913 | 0.849328021 |
| TCGA-DD-AADR-01A | -786.5974153 | 563.2725242 | -223.324891 | 0.840708663 |
| TCGA-UB-A7MD-01A | -233.7429359 | 939.2076054 | 705.4646696 | 0.759311943 |
| TCGA-DD-A4NS-01A | 588.2201086 | 1236.359089 | 1824.579197 | 0.642672974 |
| TCGA-CC-A9FU-01A | -1543.071773 | -65.21466611 | -1608.28644 | 0.932721166 |
| TCGA-DD-AAE3-01A | -170.1917163 | 423.8911072 | 253.699391 | 0.800763618 |
| TCGA-DD-AACP-01A | -1590.922929 | -278.7301818 | -1869.653111 | 0.945865985 |
| TCGA-2Y-A9H8-01A | -893.4921555 | 927.3075305 | 33.81537495 | 0.819676141 |
| TCGA-FV-A3I1-01A | -323.9679121 | 887.8956531 | 563.927741 | 0.772666588 |
| TCGA-2Y-A9H7-01A | -1143.965359 | 338.5891749 | -805.3761838 | 0.883849628 |
| TCGA-DD-AAVU-01A | -1153.557528 | 30.10750386 | -1123.450024 | 0.904718535 |
| TCGA-BC-A110-01A | 669.8402255 | 1577.616696 | 2247.456922 | 0.593908693 |
| TCGA-ZP-A9CZ-01A | -212.5975894 | 1152.695515 | 940.0979261 | 0.736454097 |
| TCGA-DD-AAE1-01A | -1107.742257 | 350.8819656 | -756.8602916 | 0.880495979 |
| TCGA-GJ-A3OU-01A | 934.2827136 | 2589.911151 | 3524.193865 | 0.433612884 |
| TCGA-RC-A7SB-01A | -1035.402552 | 49.13234412 | -986.2702083 | 0.895957394 |
| TCGA-DD-AAVS-01A | -657.0797335 | 225.6757186 | -431.4040148 | 0.856852953 |
| TCGA-CC-A8HS-01A | -1133.521242 | -381.6826321 | -1515.203874 | 0.92770724 |
| TCGA-FV-A3I0-01A | -443.3286065 | 368.197636 | -75.13097046 | 0.828731625 |
| TCGA-2Y-A9GT-01A | -144.4984495 | 1506.461182 | 1361.962732 | 0.693177886 |
| TCGA-2Y-A9HA-01A | -978.477447 | -30.98177328 | -1009.45922 | 0.897463999 |
| TCGA-FV-A2QQ-01A | -426.396646 | 871.7967915 | 445.4001455 | 0.78359385 |
| TCGA-DD-AAEH-01A | -165.2364576 | 1475.698221 | 1310.461764 | 0.698606838 |
| TCGA-DD-AADM-01A | -550.9060367 | 534.1106791 | -16.79535759 | 0.823909055 |
| TCGA-G3-A3CK-01A | -677.5126405 | 719.8304225 | 42.31778198 | 0.818960583 |
| TCGA-EP-A26S-01A | -873.1276401 | -283.0344732 | -1156.162113 | 0.906753692 |
| TCGA-DD-A11A-01A | -1028.601645 | -186.8427655 | -1215.444411 | 0.910388586 |
| TCGA-DD-AAE6-01A | -1575.337813 | -849.277603 | -2424.615416 | 0.969139183 |
| TCGA-XR-A8TE-01A | -505.5228582 | 23.10452565 | -482.4183326 | 0.860689573 |
| TCGA-DD-A73B-01A | -1123.283445 | -338.7630712 | -1462.046517 | 0.924766145 |
| TCGA-EP-A3JL-01A | 22.26833732 | 1353.429201 | 1375.697538 | 0.691723333 |
| TCGA-CC-A3MB-01A | -942.5954851 | 44.58445155 | -898.0110336 | 0.890128344 |
| TCGA-DD-AAD0-01A | -1388.769801 | -228.0662953 | -1616.836096 | 0.933172979 |
| TCGA-MI-A75I-01A | -1122.475239 | 220.3233949 | -902.1518444 | 0.890405171 |
| TCGA-DD-AACZ-01A | -427.6529131 | 2044.550278 | 1616.897365 | 0.665726759 |
| TCGA-CC-A8HU-01A | -1165.992631 | -214.2377746 | -1380.230406 | 0.92012946 |
| TCGA-RC-A6M5-01A | 348.7987776 | 236.6130233 | 585.4118009 | 0.770660799 |
| TCGA-2Y-A9GZ-01A | -969.736148 | -375.7758238 | -1345.511972 | 0.91812175 |
| TCGA-DD-AACO-01A | -456.4895743 | 929.1733672 | 472.6837929 | 0.78109942 |
| TCGA-LG-A6GG-01A | -1058.681189 | -67.76440158 | -1126.44559 | 0.90490577 |
| TCGA-BC-4073-01B | -1.057565766 | 1912.563359 | 1911.505793 | 0.632845109 |
| TCGA-ED-A7PZ-01A | -1450.064494 | -498.6262866 | -1948.69078 | 0.949567698 |
| TCGA-DD-A4NV-01A | -201.9875833 | 260.750242 | 58.76265869 | 0.817572972 |
| TCGA-DD-A73G-01A | -680.8414832 | 621.0615605 | -59.77992267 | 0.82746844 |
| TCGA-G3-AAV3-01A | -295.5879003 | 1368.704686 | 1073.116786 | 0.723105712 |
| TCGA-G3-A25U-01A | -1053.663638 | -204.1523277 | -1257.815966 | 0.912944369 |
| TCGA-BC-A5W4-01A | -1422.313213 | -619.8908376 | -2042.204051 | 0.953782266 |
| TCGA-UB-AA0U-01A | 58.14405715 | 763.1396247 | 821.2836819 | 0.748139813 |
| TCGA-EP-A12J-01A | -828.9930142 | 57.5365979 | -771.4564163 | 0.881509637 |
| TCGA-G3-A5SI-01A | -1013.435008 | -470.3951035 | -1483.830111 | 0.925978209 |
| TCGA-DD-AACA-02B | -1349.998414 | -605.0840012 | -1955.082415 | 0.94986147 |
| TCGA-FV-A4ZQ-01A | -939.4652633 | 1747.445141 | 807.9798778 | 0.749434178 |
| TCGA-DD-A4ND-01A | 630.6024408 | 1153.709773 | 1784.312214 | 0.647190169 |
| TCGA-ED-A8O5-01A | -686.0176647 | -171.3190762 | -857.3367408 | 0.887391673 |
| TCGA-UB-A7ME-01A | -394.6440063 | 1194.396085 | 799.7520785 | 0.750233254 |
| TCGA-CC-5264-01A | -967.1432507 | 86.21851475 | -880.924736 | 0.888982593 |
| TCGA-DD-AADA-01A | -267.0770283 | 1048.238558 | 781.16153 | 0.752034719 |
| TCGA-2Y-A9HB-01A | -214.7358596 | 958.4423431 | 743.7064835 | 0.755647174 |
| TCGA-DD-AACS-01A | -1197.904706 | -335.6626281 | -1533.567334 | 0.928710138 |
| TCGA-DD-AAE0-01A | -634.5550136 | 72.21841736 | -562.3365962 | 0.866602856 |
| TCGA-G3-A5SK-01A | -282.7516052 | 1006.045178 | 723.2935732 | 0.757606343 |
| TCGA-BC-A69I-01A | -239.1964482 | 491.3335009 | 252.1370527 | 0.800900963 |
| TCGA-BC-A10R-01A | -81.95910579 | 22.95215463 | -59.00695116 | 0.827404724 |
| TCGA-BC-A10X-01A | 367.2327193 | 866.8221082 | 1234.054827 | 0.706587594 |
| TCGA-BC-A10S-01A | 50.24597787 | 1160.119157 | 1210.365135 | 0.709043995 |
| TCGA-DD-AAVX-01A | -456.9361162 | 972.4804119 | 515.5442958 | 0.77715558 |
| TCGA-DD-AAVQ-01A | -277.8774658 | 2007.317987 | 1729.440522 | 0.653309306 |
| TCGA-RC-A7SH-01A | -1217.222416 | -380.3454054 | -1597.567822 | 0.932152657 |
| TCGA-G3-A3CJ-01A | -780.5162489 | 260.3156797 | -520.2005693 | 0.863499955 |
| TCGA-DD-A115-01A | -313.6646027 | 466.0724031 | 152.4078004 | 0.809580679 |
| TCGA-BC-A10Q-01A | -664.7899453 | 226.2177154 | -438.5722299 | 0.857394958 |
| TCGA-DD-A1EE-01A | -1012.58325 | -216.0966183 | -1228.679868 | 0.911190714 |
| TCGA-ZP-A9CY-01A | -63.58436157 | 636.8511878 | 573.2668263 | 0.771795618 |
| TCGA-FV-A23B-01A | -637.9119497 | 498.4353994 | -139.4765503 | 0.833980543 |
| TCGA-HP-A5MZ-01A | 630.2730833 | 1544.589959 | 2174.863043 | 0.602447861 |
| TCGA-DD-AACK-01A | -1032.374991 | 155.9223524 | -876.4526384 | 0.888681785 |
| TCGA-CC-A1HT-01A | 183.4644675 | 2093.742659 | 2277.207126 | 0.59038966 |
| TCGA-DD-A11B-01A | -844.380374 | -288.3419009 | -1132.722275 | 0.905297521 |
| TCGA-ZP-A9D4-01A | -938.1007517 | -202.6636498 | -1140.764402 | 0.905798337 |
| TCGA-DD-AACA-02A | -917.1970175 | -695.0103091 | -1612.207327 | 0.93292855 |
| TCGA-HP-A5N0-01A | 194.35382 | 574.64482 | 768.9986401 | 0.7532103 |
| TCGA-EP-A2KB-01A | -1092.119649 | -4.659707495 | -1096.779357 | 0.903043801 |
| TCGA-DD-A4NN-01A | -817.051304 | -392.8060579 | -1209.857362 | 0.910048955 |
| TCGA-ES-A2HS-01A | -469.0928022 | 14.49622144 | -454.5965808 | 0.85860316 |
| TCGA-G3-A3CG-01A | -401.5156458 | 461.8626894 | 60.34704363 | 0.817439031 |
| TCGA-DD-AAVR-01A | 407.0540604 | 1704.380276 | 2111.434337 | 0.609852972 |
| TCGA-DD-AAD1-01A | 280.5893193 | 1359.444257 | 1640.033576 | 0.663188749 |
| TCGA-DD-A73D-01A | -1489.227188 | -637.1872199 | -2126.414408 | 0.957423799 |
| TCGA-DD-AAVW-01A | 243.0347802 | 819.8920026 | 1062.926783 | 0.72413809 |
| TCGA-DD-A4NF-01A | -819.5330436 | -399.5369177 | -1219.069961 | 0.910608653 |
| TCGA-DD-AACN-01A | -284.2231944 | 365.7655398 | 81.54234538 | 0.815642965 |
| TCGA-DD-A3A2-01A | -538.3893209 | 184.8064646 | -353.5828563 | 0.850907799 |
| TCGA-K7-A5RF-01A | 317.1331184 | 1347.729555 | 1664.862673 | 0.660456524 |
| TCGA-DD-A116-01A | -630.9453397 | 459.6140631 | -171.3312767 | 0.836551551 |
| TCGA-DD-A4NI-01A | -107.1621389 | 1027.461853 | 920.2997136 | 0.738416957 |
| TCGA-BC-A10T-01A | 149.3166891 | 217.532453 | 366.8491421 | 0.790705119 |
| TCGA-DD-AADJ-01A | -978.1734173 | 472.4019149 | -505.7715024 | 0.862429798 |
| TCGA-DD-AACE-01A | -692.5749921 | -50.58070234 | -743.1556944 | 0.879540555 |
| TCGA-FV-A3R2-01A | -1054.865349 | 146.2789554 | -908.5863936 | 0.890834688 |
| TCGA-DD-AAE7-01A | -201.1692879 | 884.0882482 | 682.9189603 | 0.761461328 |
| TCGA-DD-AADD-01A | -1444.76261 | -82.54131613 | -1527.303926 | 0.928368828 |
| TCGA-4R-AA8I-01A | -709.1577053 | 193.0280781 | -516.1296272 | 0.863198418 |
| TCGA-FV-A496-01A | -1274.570848 | -547.054597 | -1821.625445 | 0.9435544 |
| TCGA-DD-A39X-01A | -411.1510713 | 570.9602317 | 159.8091604 | 0.808942456 |
| TCGA-DD-AADS-01A | -667.5537717 | 1423.275852 | 755.7220808 | 0.75449078 |
| TCGA-DD-AAE9-01A | -1343.723024 | 32.39452731 | -1311.328497 | 0.916121679 |
| TCGA-ZS-A9CF-02A | -837.9655748 | 151.9797406 | -685.9858341 | 0.875516579 |
| TCGA-G3-AAUZ-01A | -353.2867775 | 1039.605515 | 686.3187376 | 0.761137745 |
| TCGA-WX-AA47-01A | -1347.469729 | -391.5608516 | -1739.030581 | 0.939469481 |
| TCGA-NI-A4U2-01A | -448.83836 | 207.6701895 | -241.1681705 | 0.842124035 |
| TCGA-DD-AACI-01A | -132.8111479 | 1856.424958 | 1723.61381 | 0.653956602 |
| TCGA-ZP-A9D1-01A | -184.2106203 | 655.9549797 | 471.7443594 | 0.781185517 |
| TCGA-UB-A7MB-01A | -1223.835798 | -450.9457932 | -1674.781591 | 0.936196379 |
| TCGA-DD-AAVP-01A | -596.1788067 | 115.189214 | -480.9895927 | 0.860582778 |
| TCGA-DD-A4NR-01A | 182.2456398 | 2288.796114 | 2471.041754 | 0.567189122 |
| TCGA-RG-A7D4-01A | -1064.243706 | 1528.294562 | 464.0508564 | 0.78189005 |
| TCGA-5R-AAAM-01A | 535.6727091 | 1107.36178 | 1643.034489 | 0.662858993 |
| TCGA-DD-A3A4-01A | -843.3795398 | -430.0641672 | -1273.443707 | 0.913878099 |
| TCGA-BC-A217-01A | -1085.046043 | 704.6371607 | -380.4088822 | 0.852969756 |
| TCGA-RC-A6M3-01A | -1362.901113 | 267.2931829 | -1095.60793 | 0.902969926 |
| TCGA-DD-A4NQ-01A | -931.2454842 | 634.3271801 | -296.918304 | 0.846509002 |
| TCGA-CC-A9FV-01A | 1099.464053 | 2242.73094 | 3342.194994 | 0.457528451 |
| TCGA-UB-A7MC-01A | -1298.637862 | -460.1795606 | -1758.817422 | 0.940460686 |
| TCGA-MR-A8JO-01A | 775.9150933 | 1458.832859 | 2234.747952 | 0.595408537 |
| TCGA-DD-AAEG-01A | -968.9207861 | -212.5855213 | -1181.506307 | 0.90831609 |
| TCGA-DD-A39W-01A | -958.1016784 | -36.27488138 | -994.3765597 | 0.89648525 |
| TCGA-DD-A39Z-01A | -1337.04057 | -186.0303197 | -1523.070889 | 0.928137713 |
| TCGA-BC-A10Z-01A | -1445.948825 | -713.7758234 | -2159.724649 | 0.958823896 |
| TCGA-WQ-AB4B-01A | -240.5333294 | 634.9033898 | 394.3700604 | 0.788225549 |
| TCGA-CC-A123-01A | -820.193825 | 381.2362583 | -438.9575667 | 0.857424067 |
| TCGA-YA-A8S7-01A | 112.0761983 | 1782.66656 | 1894.742758 | 0.634748396 |
| TCGA-2Y-A9H2-01A | -958.6975138 | 588.5292333 | -370.1682805 | 0.852184181 |
| TCGA-5C-A9VG-01A | -400.9088786 | -282.5970309 | -683.5059095 | 0.875340629 |
| TCGA-CC-A3M9-01A | 902.6157844 | 2811.02253 | 3713.638315 | 0.408390477 |
| TCGA-EP-A2KA-01A | -748.1893022 | 1452.937192 | 704.7478901 | 0.759380405 |
| TCGA-DD-AADW-01A | -516.67461 | -345.9872759 | -862.661886 | 0.887751764 |
| TCGA-DD-AAED-01A | -1495.872141 | 184.1928451 | -1311.679296 | 0.916142322 |
| TCGA-LG-A9QD-01A | -744.2298286 | 508.1604196 | -236.069409 | 0.841720178 |
| TCGA-DD-AADV-01A | -406.0429786 | 185.7727127 | -220.2702659 | 0.840465784 |
| TCGA-G3-A3CH-01A | -401.9324534 | 602.040365 | 200.1079117 | 0.805450737 |
| TCGA-G3-AAV1-01A | -744.6024497 | -27.511677 | -772.1141267 | 0.881555217 |
| TCGA-ZS-A9CG-01A | -710.040101 | 112.3944453 | -597.6456557 | 0.869177494 |
| TCGA-DD-AAW3-01A | -891.0234378 | -295.2713892 | -1186.294827 | 0.908609877 |
| TCGA-ED-A7PY-01A | -1282.975889 | -227.7547837 | -1510.730672 | 0.927461921 |
| TCGA-ZP-A9D2-01A | -495.5722382 | 254.5435385 | -241.0286997 | 0.842112994 |
| TCGA-G3-A25Y-01A | -161.1180822 | 604.0649774 | 442.9468952 | 0.783817525 |
| TCGA-G3-A3CI-01A | -311.6511467 | 971.0721823 | 659.4210356 | 0.763692616 |
| TCGA-K7-A5RG-01A | -188.1317082 | 2461.046434 | 2272.914725 | 0.590898087 |
| TCGA-EP-A3RK-01A | -77.84511918 | 1763.478732 | 1685.633613 | 0.658164123 |
| TCGA-CC-A7IJ-01A | 822.6309678 | 1925.221374 | 2747.852342 | 0.533265686 |
| TCGA-MI-A75H-01A | -503.7418631 | 1058.053179 | 554.3113155 | 0.773561906 |
| TCGA-G3-AAV5-01A | -1067.743349 | 102.0170355 | -965.7263133 | 0.894613971 |
| TCGA-ED-A7XP-01A | -326.901279 | 512.4410633 | 185.5397842 | 0.806716264 |
| TCGA-DD-A1ED-01A | -68.3663328 | 1134.742642 | 1066.376309 | 0.72378879 |
| TCGA-ED-A5KG-01A | 574.1775101 | 3133.830775 | 3708.008286 | 0.409144703 |
| TCGA-ED-A459-01A | -829.0366935 | 556.5898677 | -272.4468258 | 0.844591187 |
| TCGA-2Y-A9GX-01A | 733.017093 | 1691.828852 | 2424.845945 | 0.572760793 |
| TCGA-DD-A73E-01A | -1137.816249 | -748.8420291 | -1886.658278 | 0.946673185 |
| TCGA-QA-A7B7-01A | -1302.622499 | -33.85298177 | -1336.475481 | 0.917595272 |
| TCGA-DD-AACL-01A | -465.5726788 | 1775.561778 | 1309.989099 | 0.698656479 |
| TCGA-MR-A520-01A | -714.3762684 | 219.6935092 | -494.6827591 | 0.861604752 |
| TCGA-DD-A1EF-01A | -622.8497116 | 614.817872 | -8.031839663 | 0.823179352 |
| TCGA-G3-A25T-01A | -434.3069845 | 359.7541719 | -74.55281263 | 0.828684127 |
| TCGA-FV-A4ZP-01A | -710.4532724 | 1228.744805 | 518.2915324 | 0.77690174 |
| TCGA-WX-AA44-01A | -885.4733497 | 392.7452987 | -492.728051 | 0.861459078 |
| TCGA-DD-A4NE-01A | -695.6878335 | -215.9073009 | -911.5951344 | 0.891035254 |
| TCGA-CC-A7IG-01A | -920.6932925 | 481.984152 | -438.7091405 | 0.8574053 |
| TCGA-ZP-A9D0-01A | -704.3279521 | -173.6346945 | -877.9626466 | 0.888783396 |
| TCGA-G3-A25X-01A | -58.37293525 | 1493.927426 | 1435.554491 | 0.685351573 |
| TCGA-BC-4072-01B | -308.6789897 | 1382.680754 | 1074.001765 | 0.723015976 |
| TCGA-XR-A8TC-01A | -781.5387679 | -203.4556248 | -984.9943928 | 0.895874202 |
| TCGA-BC-A3KF-01A | -801.7848335 | -72.95181192 | -874.7366454 | 0.88856626 |
| TCGA-O8-A75V-01A | -204.7669994 | 1185.510049 | 980.7430498 | 0.732404932 |
| TCGA-DD-AADI-01A | -154.2508348 | 1578.087643 | 1423.836808 | 0.686603098 |
| TCGA-BC-A8YO-01A | -874.4586513 | 1204.36598 | 329.9073292 | 0.794013196 |
| TCGA-DD-A39V-01A | -362.4906909 | 1382.55782 | 1020.067129 | 0.728462557 |
| TCGA-DD-A1EC-01A | -159.200144 | 2406.694949 | 2247.494805 | 0.593904219 |
| TCGA-DD-AACQ-01A | -1449.8008 | -525.4717459 | -1975.272546 | 0.950783953 |
| TCGA-DD-A1EB-01A | -556.1432268 | 124.7206139 | -431.4226128 | 0.856854361 |
| TCGA-KR-A7K7-01A | -1075.131556 | 1202.134754 | 127.0031979 | 0.811764059 |
| TCGA-DD-AAVV-01A | 87.20933597 | 1455.428913 | 1542.638249 | 0.673820861 |
| TCGA-DD-AADN-01A | -1075.52099 | 1996.490737 | 920.9697473 | 0.73835063 |
| TCGA-LG-A9QC-01A | -926.1633716 | -366.160623 | -1292.323995 | 0.914999748 |
| TCGA-RC-A7S9-01A | -1147.995527 | 546.6813776 | -601.3141499 | 0.869443653 |
| TCGA-BC-A112-01A | -263.2886167 | 466.3344774 | 203.0458608 | 0.805195073 |
| TCGA-2Y-A9H0-01A | -1041.922228 | 807.7220499 | -234.2001779 | 0.841572004 |
| TCGA-CC-A7IL-01A | -1511.854751 | -444.2429275 | -1956.097679 | 0.949908056 |
| TCGA-KR-A7K2-01A | -357.5168935 | 602.7551514 | 245.2382579 | 0.801506932 |
| TCGA-DD-AADU-01A | -1241.503166 | 15.95323559 | -1225.549931 | 0.911001337 |
| TCGA-ED-A66Y-01A | -1203.507144 | -813.3963089 | -2016.903453 | 0.952659689 |
| TCGA-CC-A8HT-01A | -1026.914436 | 821.8273135 | -205.0871229 | 0.839256039 |
| TCGA-DD-AADY-01A | -639.8796356 | -379.5346821 | -1019.414318 | 0.898107599 |
| TCGA-BC-A216-01A | -951.3994215 | 874.0088825 | -77.39053898 | 0.828917202 |
| TCGA-RC-A7SF-01A | -944.666002 | 323.2723919 | -621.3936101 | 0.870896 |
| TCGA-RC-A7SK-01A | -1127.901567 | -339.4386975 | -1467.340264 | 0.925061566 |
| TCGA-DD-AAD8-01A | -942.6628574 | 139.4823551 | -803.1805023 | 0.88369882 |
| TCGA-DD-AAEE-01A | -944.9483546 | -208.6526594 | -1153.601014 | 0.906595109 |
| TCGA-DD-A119-01A | -326.5496302 | 358.0561111 | 31.50648089 | 0.819870236 |
| TCGA-G3-AAV6-01A | -1052.54879 | -306.1088236 | -1358.657613 | 0.918884749 |
| TCGA-DD-A73F-01A | -135.9647882 | 1786.109383 | 1650.144595 | 0.662077181 |
| TCGA-DD-A4NP-01A | -690.4312667 | 210.3089719 | -480.1222948 | 0.860517931 |
| TCGA-DD-AAEK-01A | -151.728812 | 1518.341852 | 1366.61304 | 0.692685721 |
| TCGA-DD-A11D-01A | -630.4371858 | 57.03490974 | -573.4022761 | 0.867412243 |
| TCGA-DD-A1EG-01A | 0.874244221 | 1384.668919 | 1385.543163 | 0.690678925 |
| TCGA-PD-A5DF-01A | 174.851736 | 895.4036672 | 1070.255403 | 0.72339577 |
| TCGA-DD-A3A9-01A | -39.92701542 | 875.7602232 | 835.8332077 | 0.746720982 |
| TCGA-2Y-A9H4-01A | -753.8387221 | 582.7101557 | -171.1285664 | 0.836535248 |
| TCGA-DD-A118-01A | -347.1006153 | 58.47918169 | -288.6214337 | 0.845860004 |
| TCGA-DD-A4NL-01A | -184.4444533 | 420.1460291 | 235.7015758 | 0.802343251 |
| TCGA-5C-A9VH-01A | -276.4746398 | 78.63619033 | -197.8384495 | 0.838677017 |
| TCGA-3K-AAZ8-01A | -999.2002148 | 445.3274109 | -553.8728039 | 0.865982239 |
| TCGA-MI-A75G-01A | -1060.213192 | -266.8101179 | -1327.02331 | 0.917042848 |
| TCGA-DD-A3A6-01A | 701.7306563 | 1301.42137 | 2003.152027 | 0.622372099 |
| TCGA-CC-A5UD-01A | -1130.263343 | -195.3227268 | -1325.586069 | 0.916958695 |
| TCGA-DD-A3A3-01A | -1329.55492 | 302.3703767 | -1027.184544 | 0.898608614 |
| TCGA-CC-A7IH-01A | -946.2526887 | -431.0009671 | -1377.253656 | 0.919958256 |
| TCGA-DD-A4NH-01A | -595.3577132 | 933.1019211 | 337.7442079 | 0.793313365 |
| TCGA-K7-A6G5-01A | -335.9171554 | 857.5813509 | 521.6641955 | 0.77658994 |
| TCGA-DD-AACU-01A | -669.1111972 | 439.2789942 | -229.832203 | 0.841225507 |
| TCGA-BW-A5NO-01A | -659.875596 | 528.9046695 | -130.9709265 | 0.833290963 |
| TCGA-XR-A8TG-01A | -463.7617985 | 300.273367 | -163.4884315 | 0.835920247 |
| TCGA-DD-A1EJ-01A | -1008.421899 | 305.9847408 | -702.4371584 | 0.876680858 |
| TCGA-CC-5259-01A | -1267.867271 | 590.0216275 | -677.8456436 | 0.874938599 |
| TCGA-2Y-A9H3-01A | -131.7293981 | 1776.851519 | 1645.122121 | 0.662629516 |
| TCGA-UB-AA0V-01A | 147.7365312 | 624.1345223 | 771.8710535 | 0.752932889 |
| TCGA-GJ-A9DB-01A | -194.4264379 | 358.6043245 | 164.1778866 | 0.808565289 |
| TCGA-DD-A4NK-01A | -691.1915456 | -76.9848233 | -768.1763689 | 0.881282199 |
| TCGA-2Y-A9H6-01A | -3.713690655 | 1074.581975 | 1070.868284 | 0.723333653 |
| TCGA-BD-A2L6-01A | -658.4037563 | 419.2849093 | -239.118847 | 0.841961771 |
| TCGA-G3-A5SM-01A | 91.12524608 | 990.966709 | 1082.091955 | 0.722195072 |
| TCGA-DD-AAD5-01A | -946.7543483 | 833.4321929 | -113.3221554 | 0.831855976 |
| TCGA-BD-A3EP-01A | 178.8321923 | 1471.988173 | 1650.820365 | 0.662002838 |
| TCGA-CC-5260-01A | 72.25967024 | 699.2335726 | 771.4932428 | 0.752969385 |
| TCGA-WQ-A9G7-01A | -1253.58673 | -248.8050427 | -1502.391773 | 0.927003531 |
| TCGA-FV-A2QR-01A | -214.1939389 | 219.2255903 | 5.03165145 | 0.822089079 |
| TCGA-DD-AAW2-01A | -789.5935899 | -225.9676219 | -1015.561212 | 0.897858722 |
| TCGA-DD-AA3A-01A | -1432.104043 | -20.14615171 | -1452.250194 | 0.924217984 |
| TCGA-CC-5263-01A | -769.6030149 | 643.0709785 | -126.5320363 | 0.832930572 |
| TCGA-FV-A495-01A | 82.20113898 | 1325.609186 | 1407.810325 | 0.688311542 |
| TCGA-BC-A10U-01A | -1223.213156 | 72.34409316 | -1150.869062 | 0.906425806 |
| TCGA-ZS-A9CE-01A | -1167.418143 | -490.3895614 | -1657.807704 | 0.935317743 |
| TCGA-G3-A7M8-01A | -259.8326843 | 310.9709068 | 51.13822249 | 0.818216911 |
| TCGA-5R-AA1D-01A | 1168.839177 | 1036.075742 | 2204.914918 | 0.598921122 |
| TCGA-ED-A82E-01A | -370.377108 | 273.0438202 | -97.33328778 | 0.830551132 |
| TCGA-DD-A3A1-01A | -994.5150852 | 912.0905119 | -82.42457338 | 0.829330317 |
| TCGA-MI-A75E-01A | -127.2731581 | 941.4796522 | 814.2064941 | 0.748828729 |
| TCGA-DD-AAEA-01A | -982.7723215 | 713.5648225 | -269.207499 | 0.844336506 |
| TCGA-ZS-A9CF-01A | -829.9625121 | 402.947474 | -427.0150381 | 0.856520625 |
| TCGA-G3-A25V-01A | 71.13392112 | 1161.761136 | 1232.895057 | 0.706708051 |
| TCGA-CC-A9FS-01A | -921.4734248 | 36.53115608 | -884.9422687 | 0.889252499 |
| TCGA-BC-A69H-01A | -787.5911255 | 928.1257927 | 140.5346672 | 0.81060251 |
| TCGA-DD-A3A7-01A | -1090.111588 | 325.9118023 | -764.1997853 | 0.88100619 |
| TCGA-CC-5261-01A | 87.67305527 | 1121.15398 | 1208.827035 | 0.709203185 |
| TCGA-G3-AAV0-01A | -789.3238965 | 250.0531927 | -539.2707038 | 0.864908381 |
| TCGA-DD-AAE4-01A | 69.72265024 | 1759.580231 | 1829.302881 | 0.642141591 |
| TCGA-CC-A7II-01A | -741.2466927 | -318.9554786 | -1060.202171 | 0.900724505 |
| TCGA-DD-A3A8-01A | -1110.162804 | -151.5191968 | -1261.682001 | 0.913175805 |
| TCGA-G3-A7M5-01A | -916.0053373 | 378.5297333 | -537.4756039 | 0.864776092 |
| TCGA-CC-A3MC-01A | -523.700351 | 343.0712035 | -180.6291475 | 0.837298541 |
| TCGA-2V-A95S-01A | -383.5199206 | 2158.28224 | 1774.762319 | 0.648258175 |
| TCGA-ED-A66X-01A | 339.1897442 | 931.0858216 | 1270.275566 | 0.702815332 |
| TCGA-G3-A6UC-01A | -1132.018827 | -255.6538292 | -1387.672656 | 0.920556725 |
| TCGA-BD-A3ER-01A | 106.090091 | 616.9275615 | 723.0176526 | 0.757632779 |
| TCGA-DD-A3A5-01A | -626.0101683 | 131.2411816 | -494.7689867 | 0.861611177 |
| TCGA-DD-AACH-01A | -727.1543497 | 364.9420899 | -362.2122597 | 0.851572531 |
| TCGA-CC-5262-01A | 247.2359178 | 1181.879056 | 1429.114974 | 0.686039607 |
| TCGA-DD-AADG-01A | -1020.521027 | -388.1713443 | -1408.692372 | 0.921757545 |
| TCGA-DD-AAW0-01A | 6.968045482 | 1091.685524 | 1098.65357 | 0.720511406 |
| TCGA-DD-AACJ-01A | -1223.538899 | -7.504847379 | -1231.043747 | 0.911333614 |
| TCGA-DD-AADL-01A | -1193.682424 | -313.2322642 | -1506.914688 | 0.927252328 |
| TCGA-RC-A6M6-01A | -1372.566911 | 1.598101791 | -1370.968809 | 0.919596212 |
| TCGA-DD-A4NO-01A | -340.0793453 | 181.4001807 | -158.6791646 | 0.835532581 |
| TCGA-CC-A5UE-01A | -1477.643499 | 9.623409863 | -1468.020089 | 0.925099463 |
| TCGA-G3-A7M7-01A | -775.0477817 | -43.08643863 | -818.1342203 | 0.884724088 |
| TCGA-ES-A2HT-01A | -187.3089569 | 734.8099906 | 547.5010337 | 0.774195031 |
| TCGA-DD-AACX-01A | -1232.792205 | 204.9866222 | -1027.805583 | 0.898648607 |
| TCGA-2Y-A9GV-01A | -100.2398516 | 898.0236241 | 797.7837725 | 0.750424252 |
| TCGA-DD-AACF-01A | -958.767093 | 711.2207602 | -247.5463329 | 0.842628565 |
| TCGA-BW-A5NP-01A | -1318.758164 | -514.4904296 | -1833.248593 | 0.944118131 |
| TCGA-UB-A7MA-01A | -792.2713033 | -13.43132466 | -805.702628 | 0.883872042 |
| TCGA-G3-A25Z-01A | -439.3070176 | 452.6965043 | 13.38948663 | 0.821389952 |
| TCGA-MI-A75C-01A | -1411.570619 | 628.8951863 | -782.6754331 | 0.882286014 |
| TCGA-DD-A4NA-01A | -390.3867858 | 584.2756962 | 193.8889103 | 0.80599143 |
| TCGA-ZP-A9CV-01A | -130.549689 | 951.5741108 | 821.0244218 | 0.748165065 |
| TCGA-T1-A6J8-01A | -487.4580468 | 210.1207836 | -277.3372632 | 0.84497532 |
| TCGA-DD-A1EK-01A | -335.7185559 | 816.3182261 | 480.5996701 | 0.780373358 |
| TCGA-5C-AAPD-01A | -240.5124029 | 1719.018914 | 1478.506511 | 0.680746706 |
| TCGA-KR-A7K8-01A | -158.8476757 | 1618.562887 | 1459.715211 | 0.682764653 |
| TCGA-DD-AAD6-01A | -1410.327648 | 71.44365343 | -1338.883995 | 0.917735753 |
| TCGA-DD-A4NB-01A | 995.4099243 | 891.1419425 | 1886.551867 | 0.635676998 |
| TCGA-DD-A11C-01A | -88.93998015 | 471.4234416 | 382.4834615 | 0.789298084 |
| TCGA-WJ-A86L-01A | -1331.701406 | -131.6691075 | -1463.370513 | 0.924840084 |
| TCGA-ED-A8O6-01A | -920.9283025 | 23.72959007 | -897.1987124 | 0.890073999 |
| TCGA-DD-AAEB-01A | -744.6154909 | 399.3203435 | -345.2951474 | 0.850268103 |
| TCGA-2Y-A9GU-01A | -982.8430972 | -168.7551374 | -1151.598235 | 0.906471008 |
| TCGA-DD-A73A-01A | -869.0855229 | 868.7461149 | -0.339408092 | 0.822537712 |
| TCGA-RC-A6M4-01A | -1240.048013 | -626.0045866 | -1866.052599 | 0.94569432 |
| TCGA-BW-A5NQ-01A | -777.8618013 | 1401.76586 | 623.9040592 | 0.76704794 |
| TCGA-DD-AAVY-01A | -1130.063324 | -272.6093831 | -1402.672707 | 0.921414548 |
| TCGA-DD-A1EL-01A | -1269.215618 | 229.9812578 | -1039.23436 | 0.899383259 |
| TCGA-DD-A4NJ-01A | -168.1573221 | 854.4752017 | 686.3178797 | 0.761137827 |
| TCGA-G3-A5SL-01A | -641.8832623 | -36.39959161 | -678.282854 | 0.874969674 |
| TCGA-DD-AACG-01A | -1165.281926 | 782.5942702 | -382.6876558 | 0.853144302 |
| TCGA-DD-AAC8-01A | -887.3175438 | 427.6224317 | -459.6951121 | 0.858986582 |
| TCGA-ED-A7XO-01A | -134.6716099 | 799.4636284 | 664.7920185 | 0.763183404 |
| TCGA-DD-AACB-01A | -656.4871893 | 1425.170784 | 768.6835952 | 0.753240718 |
| TCGA-G3-A7M6-01A | -624.5410774 | 280.8908536 | -343.6502238 | 0.850140988 |
| TCGA-ED-A97K-01A | -336.1303648 | 541.3155019 | 205.1851371 | 0.805008815 |
| TCGA-DD-A73C-01A | -104.9772983 | 254.9461381 | 149.9688398 | 0.809790783 |
| TCGA-DD-AAW1-01A | -903.6554614 | -123.0912986 | -1026.74676 | 0.898580417 |
| TCGA-XR-A8TF-01A | -1071.514723 | -94.02545986 | -1165.540183 | 0.907333288 |
| TCGA-CC-A5UC-01A | -242.7106663 | 414.9106651 | 172.1999988 | 0.807871849 |
| TCGA-DD-A39Y-01A | -1166.395572 | 33.43257862 | -1132.962993 | 0.90531253 |
| TCGA-DD-A114-01A | 297.7206221 | 1801.592965 | 2099.313587 | 0.611262037 |
| TCGA-NI-A8LF-01A | -357.7886783 | 84.42067565 | -273.3680026 | 0.844663577 |
| TCGA-DD-AADF-01A | -1125.393518 | 315.6277853 | -809.7657323 | 0.884150846 |
| TCGA-DD-AAEI-01A | -620.4066958 | 749.8088007 | 129.4021049 | 0.811558369 |
| TCGA-2Y-A9H5-01A | -289.3146243 | 286.2971259 | -3.017498359 | 0.822761215 |