

ID	StromalScore	ImmuneScore	ESTIMATEScore	
TCGA-CF-A47X-01A-31R-A23W-07	-1772.23869809142	-602.429051032574	-	
2374.66774912399				
TCGA-ZF-AA51-01A-21R-A39I-07	64.3441392254353	1450.54662334637		
1514.89076257181				
TCGA-BL-A0C8-01A-11R-A10U-07	-625.200675069726	-211.674358804004	-	
836.875033873729				
TCGA-BT-A42C-01A-11R-A23N-07	-1729.01589157274	-438.730301824338	-	
2167.74619339708				
TCGA-G2-A3IB-01A-11R-A20F-07	-1436.34728994	-218.627253281216	-	
1654.97454322122				
TCGA-2F-A9KP-01A-11R-A38B-07	-1630.63052327507	-674.193999823542	-	
2304.82452309861				
TCGA-DK-A3IT-01A-31R-A20F-07	-53.3954836772599	529.93283129294		
476.537347615681				
TCGA-FD-A43P-01A-31R-A23W-07	-257.918314092308	1960.04947408487		
1702.13115999257				
TCGA-DK-A3IV-01A-22R-A21D-07	-1488.33800517209	1268.08811578202	-	
220.249889390063				
TCGA-2F-A9KW-01A-11R-A38B-07	-18.8384464968865	357.681108801005		
338.842662304119				
TCGA-GU-A762-01A-11R-A33J-07	436.953392960058	2383.71665033574		
2820.6700432958				
TCGA-XF-AAME-01A-12R-A42T-07	1564.83999742588	2374.88671678768		
3939.72671421356				
TCGA-XF-AAN0-01A-11R-A42T-07	-433.471711504356	926.142039176469		
492.670327672113				
TCGA-CF-A47W-01A-11R-A23W-07	-1628.41563670245	-364.794427590086	-	
1993.21006429253				
TCGA-GC-A3I6-01A-11R-A20F-07	-483.413782656876	834.807380461024		
351.393597804149				
TCGA-FD-A6TA-01A-12R-A33J-07	538.860345099576	1265.02252638968		
1803.88287148925				
TCGA-DK-A1A7-01A-11R-A13Y-07	-1073.92465083149	58.2864381036851	-	
1015.6382127278				
TCGA-FD-A3SR-01A-11R-A22U-07	361.358864769324	993.789629045046		
1355.14849381437				
TCGA-GU-AATP-01A-11R-A39I-07	528.365798725223	759.807122468201		
1288.17292119342				
TCGA-DK-AA6X-01A-12R-A42T-07	-559.782348043752	878.575438424505		
318.793090380753				
TCGA-XF-A9T3-01A-11R-A42T-07	517.884018403117	1031.17078641073		
1549.05480481385				
TCGA-PQ-A6FN-01A-11R-A31N-07	-516.939276659981	705.863785487601		

188.92450882762			
TCGA-DK-A3WW-01A-22R-A23N-07	-432.686228255479	1973.5087331237	
1540.82250486822			
TCGA-XF-AAMY-01A-11R-A42T-07	186.511652334003	211.246976159031	
397.758628493034			
TCGA-K4-A3WS-01A-11R-A22U-07	1127.38075925364	1241.7727865668	
2369.15354582044			
TCGA-UY-A9PA-01A-11R-A38B-07	-1625.69938043669	831.079793038577	-
794.61958739811			
TCGA-G2-AA3F-01A-12R-A42T-07	-1119.97605350379	-443.460647735005	-
1563.4367012388			
TCGA-FJ-A871-01A-11R-A352-07	-842.415544805501	-485.807087926978	-
1328.22263273248			
TCGA-ZF-A9RN-01A-11R-A42T-07	-1127.82177767135	1053.21311558385	-
74.6086620875008			
TCGA-GC-A3RB-01A-12R-A220-07	-1314.19503076671	-180.545891778136	-
1494.74092254485			
TCGA-UY-A9PF-01A-11R-A38B-07	-445.634966376598	475.539642043842	
29.904675667244			
TCGA-YC-A89H-01A-11R-A36F-07	-646.889902122956	366.617780491821	-
280.272121631135			
TCGA-XF-AAMQ-01A-11R-A42T-07	-687.052164908733	1151.38113551108	
464.328970602352			
TCGA-CF-A1HR-01A-11R-A13Y-07	-800.926656101546	394.753596135759	-
406.173059965786			
TCGA-E7-A3X6-01A-12R-A22U-07	-640.818854292803	1095.32963835949	
454.510784066687			
TCGA-DK-A6AW-01A-11R-A30C-07	-1108.43371356432	-292.640683425998	-
1401.07439699032			
TCGA-GC-A3BM-01A-11R-A22U-07	-1498.32829552124	-25.2754104678103	-
1523.60370598905			
TCGA-GV-A6ZA-01A-12R-A33J-07	-1345.99152456011	400.943369803567	-
945.048154756548			
TCGA-G2-A2EJ-01A-11R-A180-07	-1304.13732027335	409.712642913094	-
894.424677360258			
TCGA-FD-A43N-01A-11R-A23W-07	-40.2218988865042	362.428193085891	
322.206294199386			
TCGA-UY-A8OD-01A-11R-A36F-07	556.062493748461	982.297243423872	
1538.35973717233			
TCGA-2F-A9KT-01A-11R-A38B-07	-936.774492675418	-92.6058276869062	-
1029.38032036232			
TCGA-BT-A20Q-01A-11R-A14Y-07	415.792071119799	1057.2686425733	
1473.0607136931			
TCGA-CU-A0YR-01A-12R-A10U-07	132.007546226705	1301.81023028688	

1433.81777651358		
TCGA-SY-A9G5-01A-11R-A38B-07	782.544867388454	1708.13074419519
2490.67561158365		
TCGA-4Z-AA84-01A-11R-A39I-07	-1002.54691088598	-335.878454891326 -
1338.4253657773		
TCGA-4Z-AA7Q-01A-11R-A39I-07	-495.605887182969	1804.00124132829
1308.39535414532		
TCGA-FD-A5BT-01A-11R-A26T-07	1480.22858209892	2385.29578281764
3865.52436491656		
TCGA-CF-A27C-01A-11R-A16R-07	-2154.7783267956	-413.555572104406 -
2568.3338989		
TCGA-E7-A6MF-01A-12R-A32O-07	-1829.58243603786	-280.732073207146 -
2110.31450924501		
TCGA-FT-A61P-01A-11R-A30C-07	665.471639835075	1202.08893064583
1867.5605704809		
TCGA-DK-AA77-01A-11R-A39I-07	-1416.70372058611	505.000899082875 -
911.702821503238		
TCGA-ZF-AA5N-01A-11R-A42T-07	-1527.70055102854	-157.085023827182 -
1684.78557485572		
TCGA-DK-AA6U-01A-11R-A39I-07	-1854.50461137816	-396.647392254239 -
2251.15200363239		
TCGA-BT-A20O-01A-21R-A14Y-07	1047.31838300991	3086.7190490448
4134.03743205471		
TCGA-GD-A3OS-01A-12R-A22O-07	-395.648328054756	-49.7914093022977 -
445.439737357054		
TCGA-XF-A9SZ-01A-11R-A39I-07	627.973212500302	845.836871465156
1473.81008396546		
TCGA-4Z-AA82-01A-11R-A39I-07	-176.62895426241	334.78769025177
158.158735989359		
TCGA-DK-AA76-01A-11R-A39I-07	-1808.12941570949	-1096.84214558378 -
2904.97156129327		
TCGA-DK-A3IL-01A-11R-A20F-07	-771.938911922325	-257.122150814334 -
1029.06106273666		
TCGA-E7-A678-01A-11R-A30C-07	-1881.91492363438	18.3914334381903 -
1863.52349019619		
TCGA-ZF-A9R1-01A-11R-A39I-07	-1205.23281809858	-139.801117845579 -
1345.03393594416		
TCGA-XF-A9SH-01A-11R-A39I-07	-874.429295631732	142.129309401516 -
732.299986230216		
TCGA-FD-A5BU-01A-31R-A26T-07	488.458718747592	1313.44550513484
1801.90422388243		
TCGA-C4-A0F7-01A-11R-A084-07	-943.004137572052	-441.07233417505 -
1384.0764717471		
TCGA-C4-A0F0-01A-12R-A10U-07	-175.336608722605	855.420613210572

680.084004487967			
TCGA-FD-A3N5-01A-11R-A21D-07	-900.477298493645	367.209423791031	-
533.267874702615			
TCGA-ZF-AA5H-01A-11R-A39I-07	-186.552659792117	1291.88632751138	
1105.33366771927			
TCGA-DK-A3WX-01A-22R-A22U-07	118.433107187052	1445.59972516426	
1564.03283235132			
TCGA-YF-AA3L-01A-11R-A38B-07	-1289.55461266317	-118.319795296147	-
1407.87440795932			
TCGA-BT-A2LA-01A-11R-A18C-07	-1390.28208103529	-1428.58349447607	-
2818.86557551136			
TCGA-4Z-AA87-01A-11R-A39I-07	-806.492710775063	704.33225437673	-
102.160456398333			
TCGA-BT-A2LB-01A-11R-A18C-07	231.692807708646	1020.59184216397	
1252.28464987262			
TCGA-XF-A8HB-01A-11R-A36F-07	-1906.58662517618	-385.181903710974	-
2291.76852888715			
TCGA-DK-A2I6-01A-12R-A18C-07	-936.359882672186	-228.128482391235	-
1164.48836506342			
TCGA-ZF-AA4X-01A-11R-A38B-07	-2432.85542937504	-358.01958120171	-
2790.87501057675			
TCGA-BT-A20P-01A-11R-A14Y-07	-1490.13142918067	-373.796045650345	-
1863.92747483101			
TCGA-BT-A20W-01A-21R-A14Y-07	-601.658466636404	609.619273929175	
7.96080729277082			
TCGA-FD-A5BX-01A-11R-A26T-07	820.859564215631	1854.84338592508	
2675.70295014072			
TCGA-BL-A13J-01A-11R-A10U-07	-99.876947942544	-92.4877997214408	-
192.364747663985			
TCGA-CF-A8HX-01A-11R-A36F-07	-1588.31639735985	-473.644692004299	-
2061.96108936415			
TCGA-PQ-A6FI-01A-11R-A31N-07	-1190.29295404381	474.266540076472	-
716.026413967338			
TCGA-FJ-A3Z7-01A-12R-A23N-07	131.687557044745	363.626546499494	
495.314103544238			
TCGA-E7-A7PW-01A-11R-A352-07	-1856.24600504095	-128.784586516948	-
1985.0305915579			
TCGA-4Z-AA7S-01A-11R-A39I-07	-1368.7235608233	-597.177547679784	-
1965.90110850309			
TCGA-CF-A3MH-01A-11R-A20F-07	-1948.40377192882	-105.080405193428	-
2053.48417712225			
TCGA-DK-A6B2-01A-11R-A30C-07	627.697874126739	1292.89255090424	
1920.59042503098			
TCGA-4Z-AA86-01A-11R-A39I-07	649.033347932914	1865.05391631594	

2514.08726424885		
TCGA-BL-A0C8-01B-04R-A277-07	-903.814619824186	-841.675248087716 -
1745.4898679119		
TCGA-5N-A9KI-01A-31R-A42T-07	-7.61895828693348	747.177131807088
739.558173520154		
TCGA-GU-AATO-01A-11R-A39I-07	-87.0765586366839	1160.9561159361
1073.87955729941		
TCGA-CF-A9FH-01A-11R-A38B-07	-1919.51909940743	-249.268545211843 -
2168.78764461927		
TCGA-FD-A6TG-01A-11R-A32O-07	538.620550088055	853.169437982637
1391.78998807069		
TCGA-4Z-AA7O-01A-31R-A39I-07	-613.506660434985	655.126392392588
41.6197319576032		
TCGA-GV-A3QI-01A-11R-A22O-07	-1848.14536149155	-1152.82072409293 -
3000.96608558448		
TCGA-DK-A6AV-01A-12R-A30C-07	-982.624237339837	332.311850279071 -
650.312387060766		
TCGA-DK-A1A3-01A-11R-A13Y-07	234.876844970719	675.634192571103
910.511037541822		
TCGA-GD-A6C6-01A-21R-A31N-07	-1022.44361443498	171.224473007284 -
851.219141427692		
TCGA-GC-A3RD-01A-12R-A22U-07	-1158.04707845745	-101.318992024398 -
1259.36607048185		
TCGA-BT-A20R-01A-12R-A16R-07	856.174396533834	598.027717692392
1454.20211422623		
TCGA-XF-A9T0-01A-11R-A39I-07	-198.49375700566	646.955169259925
448.461412254264		
TCGA-YF-AA3M-01A-11R-A42T-07	-1497.93343888491	-109.463571953721 -
1607.39701083863		
TCGA-4Z-AA7Y-01A-11R-A39I-07	-1716.5571124156	-470.628695568016 -
2187.18580798361		
TCGA-FD-A62O-01A-11R-A30C-07	-861.528937774776	-416.111606643086 -
1277.64054441786		
TCGA-BL-A3JM-01A-12R-A21D-07	-569.674823135513	-173.372752284253 -
743.047575419767		
TCGA-FJ-A3ZF-01A-11R-A23N-07	-1833.72550512973	-1010.51234510936 -
2844.23785023908		
TCGA-CU-A0YO-01A-11R-A10U-07	-332.658429454169	880.150664640368
547.492235186198		
TCGA-CF-A5UA-01A-11R-A28M-07	-1544.77020941995	-217.346377306724 -
1762.11658672668		
TCGA-K4-AAQO-01A-11R-A38B-07	452.013034635691	845.118753760633
1297.13178839632		
TCGA-XF-AAMJ-01A-11R-A42T-07	1198.45816053696	622.59367210835

1821.05183264531			
TCGA-GU-A763-01A-11R-A32O-07	-1940.23038134644	-41.6755553991329	-
1981.90593674557			
TCGA-G2-A2EC-01A-11R-A180-07	361.143434656282	971.885925806413	
1333.02936046269			
TCGA-FD-A3B7-01A-31R-A20F-07	1295.6682256484	2136.02755235085	
3431.69577799925			
TCGA-FD-A5C0-01A-11R-A28M-07	-428.897133366416	212.367709616357	-
216.529423750059			
TCGA-FD-A5BS-01A-21R-A26T-07	1668.8212482347	3164.37053676924	
4833.19178500395			
TCGA-CU-A0YN-01A-21R-A10U-07	-111.821500959118	916.942435966247	
805.12093500713			
TCGA-FD-A5BZ-01A-11R-A28M-07	1018.37986315376	157.720133847225	
1176.09999700098			
TCGA-UY-A9PE-01A-11R-A38B-07	-515.070402271291	-246.463799383914	-
761.534201655205			
TCGA-GV-A40E-01A-12R-A23N-07	-584.006482953346	413.859054461905	-
170.14742849144			
TCGA-BT-A2LD-01A-12R-A20F-07	-602.038937200312	222.210429842253	-
379.828507358059			
TCGA-UY-A9PD-01A-11R-A38B-07	-253.961053032468	-35.5836300214698	-
289.544683053938			
TCGA-G2-AA3B-01A-11R-A39I-07	-1707.76953223638	306.223249188435	-
1401.54628304795			
TCGA-K4-A54R-01A-11R-A26T-07	250.009467474398	1384.52457993991	
1634.53404741431			
TCGA-DK-A1AA-01A-11R-A13Y-07	-1422.60657077233	70.9970010821334	-
1351.60956969019			
TCGA-CU-A5W6-01A-11R-A28M-07	-942.174125293519	162.680335552978	-
779.493789740541			
TCGA-DK-AA6R-01A-11R-A42T-07	-896.952919698162	204.253299429789	-
692.699620268373			
TCGA-BT-A3PH-01A-11R-A220-07	-992.095740309142	-376.76183276733	-
1368.85757307647			
TCGA-BL-A13I-01B-04R-A277-07	1142.45976337523	2074.86217943835	
3217.32194281358			
TCGA-CF-A3MF-01A-12R-A21D-07	-1290.97814361958	-264.898707226835	-
1555.87685084641			
TCGA-CF-A47T-01A-11R-A23W-07	-1292.57828525093	-517.354105585169	-
1809.9323908361			
TCGA-YC-A8S6-01A-31R-A38B-07	607.974779097187	1324.76171792077	
1932.73649701796			
TCGA-DK-A3IS-01A-21R-A21D-07	-1814.67839483102	-171.590681531205	-

1986.26907636223			
TCGA-XF-A9SJ-01A-11R-A39I-07	217.375664309722	1411.41137534361	
1628.78703965333			
TCGA-DK-AA6T-01A-11R-A39I-07	-123.947939194131	2167.22856111362	
2043.28062191949			
TCGA-BT-A20N-01A-11R-A14Y-07	-1019.45064211244	-670.939395641637	-
1690.39003775408			
TCGA-C4-A0F6-01A-11R-A10U-07	-373.917212243134	113.835096354957	-
260.082115888178			
TCGA-CF-A7I0-01A-22R-A352-07	-471.129485076529	101.192747905829	-
369.9367371707			
TCGA-FD-A3B6-01A-21R-A20F-07	-180.940081292244	1718.70246422347	
1537.76238293123			
TCGA-GC-A3YS-01A-11R-A23N-07	486.693931652269	936.46362806001	
1423.15755971228			
TCGA-XF-A9T2-01A-11R-A42T-07	-164.244668498083	-72.2636552382903	-
236.508323736373			
TCGA-UY-A78O-01A-12R-A33J-07	-869.453721166465	-27.2651679011085	-
896.718889067574			
TCGA-GC-A3OO-01A-11R-A22U-07	-24.0139122263739	415.472522403669	
391.458610177295			
TCGA-E7-A6ME-01A-22R-A32O-07	-1589.43467695471	211.81862685483	-
1377.61605009988			
TCGA-XF-AAN5-01A-11R-A42T-07	-563.182557959682	1453.0727814455	
889.89022348582			
TCGA-FD-A3SN-01A-12R-A22U-07	-291.831287098834	319.256204416089	
27.4249173172552			
TCGA-ZF-A9R2-01A-11R-A39I-07	-2418.60351026673	-747.304096141287	-
3165.90760640802			
TCGA-ZF-AA4T-01A-11R-A38B-07	-1758.12203716159	-371.221484529669	-
2129.34352169126			
TCGA-E7-A4IJ-01A-31R-A26T-07	-1334.51874542549	539.823778542714	-
794.694966882781			
TCGA-FD-A6TE-01A-12R-A33J-07	-1905.55464847937	-88.8401841536066	-
1994.39483263298			
TCGA-H4-A2HO-01A-11R-A180-07	-793.78652913317	550.632754266554	-
243.153774866615			
TCGA-FD-A6TB-01A-12R-A33J-07	489.24396114357	1965.66752953793	
2454.9114906815			
TCGA-XF-AAN3-01A-11R-A42T-07	283.191439533779	739.142662585179	
1022.33410211896			
TCGA-XF-AAMH-01A-11R-A42T-07	-863.885897384193	-588.474104093356	-
1452.36000147755			
TCGA-FD-A3B8-01A-31R-A20F-07	1656.25973688676	2689.67969567099	

4345.93943255775			
TCGA-XF-A9SY-01A-21R-A42T-07	568.580293659178	2093.00884452631	
2661.58913818549			
TCGA-CF-A9FF-01A-11R-A38B-07	-625.082733799333	464.870711648536	-
160.212022150797			
TCGA-XF-A9ST-01A-11R-A42T-07	-1452.33494512298	-910.760543273716	-
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TCGA-FD-A6TF-01A-52R-A32O-07	461.656722401288	443.298894908113	
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TCGA-XF-AAMX-01A-11R-A42T-07	-375.471416658761	-239.550048645797	-
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TCGA-DK-A1AE-01A-11R-A13Y-07	-1228.79321888643	-360.855149512982	-
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TCGA-FJ-A3ZE-01A-11R-A23N-07	-2032.58769776254	-1008.63136943982	-

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3816.87371608646		
TCGA-G2-A2EO-01A-11R-A180-07	481.806384842526	1423.97030880791
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116.829790654565		
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TCGA-E7-A541-01A-11R-A26T-07	-812.952266735791	1269.41313334994
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TCGA-UY-A78N-01A-12R-A33J-07	-1172.83468229566	-869.392270788331	-
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TCGA-DK-AA75-01A-11R-A39I-07	-1882.35491414549	-727.72111841558	-
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442.555642853104			
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TCGA-K4-A5RH-01A-11R-A30C-07	891.464277888764	2493.92868210705	
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TCGA-BL-A13J-01A-11R-A277-07	344.380747623484	-42.5649875159941	
301.81576010749			
TCGA-XF-AAN7-01A-11R-A42T-07	-154.731999344926	63.1241284988687	-
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TCGA-2F-A9KO-01A-11R-A38B-07	-114.753831166899	1490.74693725784	
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TCGA-DK-A3IM-01A-11R-A20F-07	-1737.41573368933	-639.715983535885	-
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TCGA-FD-A3SS-01A-12R-A22U-07	-958.72325079688	-406.527065853809	-
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TCGA-4Z-AA7N-01A-11R-A39I-07	826.302726508366	2591.45437520603	
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TCGA-HQ-A2OE-01A-11R-A206-07	-1745.33654133416	-390.552031005961	-
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TCGA-UY-A8OC-01A-11R-A36F-07	350.970042512313	328.515162659298	
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TCGA-GV-A3JV-01A-11R-A220-07	-177.653164313987	632.429044599162	
454.775880285175			
TCGA-XF-A9T8-01A-11R-A39I-07	369.017844327711	1995.76792593932	
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TCGA-KQ-A41S-01A-12R-A33J-07	353.971710952567	303.416326172519	
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TCGA-CU-A3YL-01A-11R-A22U-07	-961.922583244866	-109.762621998064	-
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TCGA-E7-A7XN-01A-11R-A352-07	-895.821398563133	1911.59250164216	

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TCGA-DK-A2HX-01A-12R-A18C-07	974.057304470224	293.222654677199
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TCGA-FD-A43U-01A-11R-A23W-07	1033.45329488401	2301.74441945265
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3149.48797701752		
TCGA-XF-AAN2-01A-11R-A42T-07	-901.798831236067	948.311875314414
46.5130440783471		
TCGA-ZF-AA54-01A-11R-A39I-07	873.727549304878	1762.36268053392
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TCGA-BT-A20X-01A-11R-A16R-07	-223.947970053036	459.802028745757
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TCGA-CF-A9FL-01A-11R-A38B-07	-352.97179372608	24.1416699230391
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1291.45208193066		-
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TCGA-DK-A2I2-01A-11R-A180-07	248.762378948983	1599.57107133301
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TCGA-FD-A62S-01A-11R-A30C-07	1228.01053955981	1430.42634501072
2658.43688457054		
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TCGA-E5-A2PC-01A-11R-A206-07	-1523.62718741926	452.595072385873
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2732.59111958331		
TCGA-GD-A76B-01A-11R-A32O-07	-718.44362776124	1396.59807991946
678.154452158218		
TCGA-GC-A6I1-01A-12R-A31N-07	-166.131682816432	2365.04898254227
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TCGA-BL-A13J-01B-04R-A277-07	-202.208910011313	96.3841148638609 -
105.824795147453		
TCGA-XF-A9SK-01A-11R-A42T-07	745.382465182645	1242.28337236767
1987.66583755031		
TCGA-DK-A1AD-01A-11R-A13Y-07	-331.0121845321	310.168349833909 -
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338.135191240561		
TCGA-FD-A3SQ-01A-21R-A22U-07	803.541658254063	891.756762782574
1695.29842103664		
TCGA-GV-A3QF-01A-31R-A22U-07	-1693.48975167865	-428.639944514986 -
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TCGA-E7-A7DV-01A-11R-A33J-07	595.294169019933	2109.71002106544
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TCGA-G2-A2EL-01A-12R-A18C-07	-2040.28584853238	-1568.14746083726 -
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82.5512068771961		
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TCGA-XF-A9SM-01A-11R-A42T-07	666.28377128677	2459.52995822561
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TCGA-DK-A3IN-01A-11R-A20F-07	481.799794022937	1027.67921867083
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661.59653435808		-
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TCGA-G2-A2ES-01A-11R-A180-07	-27.312057183619	862.008122716481
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3696.64122660726		
TCGA-4Z-AA83-01A-11R-A39I-07	-833.78110129157	469.588299768067
364.192801523502		-
TCGA-E7-A5KE-01A-11R-A28M-07	-2171.9519261966	-953.389035873166
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409.967916899811		
TCGA-ZF-AA53-01A-11R-A39I-07	656.076765225657	1689.96893904514
2346.04570427079		
TCGA-ZF-A9RM-01A-11R-A38B-07	-2485.34263522628	-853.289509848077
3338.63214507436		-
TCGA-BL-A13I-01A-11R-A13Y-07	745.797096263816	2226.70862514418

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TCGA-CU-A72E-01A-12R-A33J-07	-148.207798363489	294.732762849119
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TCGA-2F-A9KR-01A-11R-A38B-07	-1435.12042202624	-210.880182178551
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TCGA-BL-A5ZZ-01A-31R-A30C-07	935.830069132174	1253.64892432889
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TCGA-BT-A20J-01A-11R-A14Y-07	-325.973402452671	1766.75835208646
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TCGA-DK-AA71-01A-31R-A39I-07	-1247.75247983422	-220.522373868609
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TCGA-KQ-A41O-01A-12R-A352-07	-2502.81683610988	-1426.77319398445
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TCGA-E7-A677-01A-11R-A30C-07	-1077.47670300041	167.589549739366
909.887153261041		-
TCGA-DK-A1A5-01A-11R-A13Y-07	334.520173901917	384.891273091952
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TCGA-HQ-A5NE-01A-12R-A28M-07	-436.961017941409	354.578787699562
82.3822302418473		-
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TCGA-XF-A9SU-01A-31R-A39I-07	455.149957590174	961.231276715512	
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TCGA-CF-A47S-01A-11R-A23W-07	-1481.40518224087	267.163316288429	-
1214.24186595244			
TCGA-FD-A6TK-01A-42R-A33J-07	904.790348518546	1598.65569786854	
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TCGA-E7-A5KF-01A-11R-A28M-07	-2385.07344194345	-526.199074894634	-
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TCGA-UY-A78L-01A-12R-A33J-07	-233.36122727095	226.736692537261	-
6.62453473368876			
TCGA-S5-A6DX-01A-11R-A31N-07	362.704896270794	1887.87861577723	
2250.58351204802			
TCGA-XF-A8HI-01A-11R-A38B-07	-1526.667462905	28.5389557869321	-
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TCGA-XF-A9T5-01A-11R-A42T-07	109.353541738119	2144.473106133	
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TCGA-XF-A9SX-01A-21R-A39I-07	977.305618013402	1911.62828751059	
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TCGA-G2-A2EK-01A-22R-A18C-07	-896.109348200544	344.419676264481	-
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TCGA-XF-A8HD-01A-11R-A36F-07	-255.093238502541	1428.60975449535	
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TCGA-XF-A9SP-01A-11R-A39I-07	941.019599083924	849.81682449322	
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