Immune scores, stromal scores and ESTIMATE scores of LGG patients

Sample ID	Stromal score	Immune score	ESTIMATE score
TCGA-CS-4938-01	−860.8	−527.55	−1,388.35
TCGA-CS-4941-01	−495.9	405.97	−89.93
TCGA-CS-4942-01	−605.66	599.15	−6.51
TCGA-CS-4943-01	−1,002.81	−587.15	−1,589.96
TCGA-CS-4944-01	−861.48	−351.29	−1,212.76
TCGA-CS-5393-01	−909.49	−85.91	−995.4
TCGA-CS-5394-01	−1,495.84	−1,443.56	−2,939.41
TCGA-CS-5395-01	−905.05	−1,073.51	−1,978.55
TCGA-CS-5396-01	−795.4	−726.98	−1,522.38
TCGA-CS-5397-01	−529.49	−363.32	−892.81
TCGA-CS-6186-01	−1,096.77	−730.63	−1,827.39
TCGA-CS-6188-01	−516.2	−42.5	−558.69
TCGA-CS-6290-01	−384.26	918.79	534.53
TCGA-CS-6665-01	−30.83	1,018.62	987.79
TCGA-CS-6666-01	−581.55	−519.77	−1,101.32
TCGA-CS-6667-01	−969.46	−637.55	−1,607.02
TCGA-CS-6668-01	−1,706.34	−1,457.66	−3164
TCGA-CS-6669-01	−1,340.83	−1,808.82	−3,149.65
TCGA-CS-6670-01	−1,351.35	−1,361.95	−2,713.3
TCGA-DB-5270-01	−531.28	−528.28	−1,059.56
TCGA-DB-5273-01	−346.21	161.3	−184.91
TCGA-DB-5274-01	−797.92	−235.67	−1,033.59
TCGA-DB-5275-01	−1,299.75	−780.75	−2,080.5
TCGA-DB-5276-01	−348.13	144.04	−204.09
TCGA-DB-5277-01	−1,164.42	−1,144.4	−2,308.82
TCGA-DB-5278-01	−1,059	−1,097.18	−2,156.18
TCGA-DB-5279-01	−1,108.21	−984.2	−2,092.41
TCGA-DB-5280-01	−902.12	−879.82	−1,781.93
TCGA-DB-5281-01	−744.05	−936.73	−1,680.77
TCGA-DB-A4X9-01	−1,374.48	−837.83	−2,212.32
TCGA-DB-A4XA-01	−934.1	−535.06	−1,469.15
TCGA-DB-A4XB-01	−1,405.68	−862.82	−2,268.5
TCGA-DB-A4XC-01	−953.45	−266.97	−1,220.42
TCGA-DB-A4XD-01	−1,180.42	−854.89	−2,035.31
TCGA-DB-A4XE-01	−1,321.33	−916.24	−2,237.57
TCGA-DB-A4XF-01	−835.98	−539.39	−1,375.38

TCGA-DB-A4XG-01	−1,664.23	−1,707.76	−3,371.99
TCGA-DB-A4XH-01	−1,377.36	−1,533.12	−2,910.49
TCGA-DB-A64L-01	−1,388.76	−821.66	−2,210.42
TCGA-DB-A64O-01	−742.69	−561.98	−1,304.68
TCGA-DB-A64P-01	−975.23	−761.61	−1,736.84
TCGA-DB-A64Q-01	−1,473.88	−1,074.77	−2,548.65
TCGA-DB-A64R-01	−1,465.49	−1,478.32	−2,943.81
TCGA-DB-A64S-01	−441.99	298.15	−143.84
TCGA-DB-A64U-01	−1,297.03	−1,114.43	−2,411.46
TCGA-DB-A64V-01	−655.53	303.41	−352.12
TCGA-DB-A64W-01	−1,752.59	−2,012.46	−3,765.05
TCGA-DB-A64X-01	−1,316.74	−931.47	−2,248.2
TCGA-DB-A75K-01	−787.17	−220.88	−1,008.04
TCGA-DB-A75L-01	−1,041.01	−663.03	−1,704.03
TCGA-DB-A75M-01	−1,001.63	−426.24	−1,427.87
TCGA-DB-A75O-01	−893.93	225.73	−668.19
TCGA-DB-A75P-01	−794.59	−731.76	−1,526.35
TCGA-DH-5140-01	−1,019.7	−1,031.36	−2,051.06
TCGA-DH-5141-01	−1,107.77	−788.57	−1,896.34
TCGA-DH-5142-01	−364.35	768.43	404.08
TCGA-DH-5143-01	−885.48	−391.72	−1,277.19
TCGA-DH-5144-01	−1,473.56	−1,102.24	−2,575.8
TCGA-DH-A669-01	−1,126.61	−492.43	−1,619.05
TCGA-DH-A66B-01	−668.61	392.06	−276.55
TCGA-DH-A66D-01	−832.21	−9.09	−841.31
TCGA-DH-A66F-01	−1,367.59	−1,173.52	−2,541.11
TCGA-DH-A66G-01	−506.69	−312.17	−818.86
TCGA-DH-A7UR-01	−1,187.12	−1,427.5	−2,614.62
TCGA-DH-A7US-01	−1,355.79	−969.78	−2,325.56
TCGA-DH-A7UT-01	−1,138.17	−366.72	−1,504.89
TCGA-DH-A7UU-01	−1,175.89	−821.64	−1,997.53
TCGA-DH-A7UV-01	−1,052.32	−372.67	−1,424.98
TCGA-DU-5847-01	−339.9	454.94	115.04
TCGA-DU-5849-01	−1,247.75	−1,067.4	−2,315.15
TCGA-DU-5851-01	−1,024.39	−834.89	−1,859.27
TCGA-DU-5852-01	−321.45	8.49	−312.96
TCGA-DU-5853-01	−715.41	107.77	−607.64
TCGA-DU-5854-01	−141.58	199.16	57.58

TCGA-DU-5855-01	−791.76	129.71	−662.05
TCGA-DU-5870-01	−794.7	−625.3	−1,420
TCGA-DU-5871-01	−996.39	−202.55	−1,198.94
TCGA-DU-5872-01	−516.06	−140.1	−656.15
TCGA-DU-5874-01	−1,422.91	−1,484.8	−2,907.7
TCGA-DU-6392-01	−378.75	−218.66	−597.41
TCGA-DU-6393-01	−1,524.43	−1,400.74	−2,925.17
TCGA-DU-6394-01	−1,221.01	−910.23	−2,131.24
TCGA-DU-6395-01	−1,010.85	−513.84	−1,524.7
TCGA-DU-6396-01	−40.43	1,199.57	1,159.13
TCGA-DU-6397-01	−953.26	−771.98	−1,725.25
TCGA-DU-6399-01	−621.11	−50.9	−672.01
TCGA-DU-6400-01	−1,476.58	−1,179.76	−2,656.34
TCGA-DU-6401-01	−587.1	−467.47	−1,054.57
TCGA-DU-6402-01	−199.18	341.4	142.22
TCGA-DU-6403-01	−947.08	−56.31	−1,003.39
TCGA-DU-6404-01	−697.14	−794.32	−1,491.46
TCGA-DU-6405-01	−1,063.47	−422.01	−1,485.48
TCGA-DU-6406-01	−824.7	−253.43	−1,078.13
TCGA-DU-6407-01	−1,010.85	−723	−1,733.85
TCGA-DU-6408-01	−1,079.39	−339.87	−1,419.26
TCGA-DU-6410-01	−1,541.86	−1,797.1	−3,338.96
TCGA-DU-6542-01	−653.3	81.57	−571.73
TCGA-DU-7006-01	−211.49	598.93	387.44
TCGA-DU-7007-01	30.78	226.32	257.1
TCGA-DU-7008-01	−1,498.4	−1,224.84	−2,723.24
TCGA-DU-7009-01	−1,502.94	−1,546.72	−3,049.66
TCGA-DU-7010-01	−798.43	−927.21	−1,725.64
TCGA-DU-7011-01	33.49	347.29	380.77
TCGA-DU-7012-01	614.23	1,207.1	1,821.33
TCGA-DU-7013-01	−777.27	−318.29	−1,095.56
TCGA-DU-7014-01	−902.06	−550.46	−1,452.52
TCGA-DU-7015-01	−677.34	370.38	−306.96
TCGA-DU-7018-01	−1,340.22	−1,469.91	−2,810.13
TCGA-DU-7019-01	−591.31	−442.35	−1,033.66
TCGA-DU-7290-01	−180.56	782.48	601.91
TCGA-DU-7292-01	−1,010.42	−1,244.38	−2,254.8
TCGA-DU-7294-01	−1,268.89	−1,184.9	−2,453.8

TCGA-DU-7298-01	−1,107.98	−518.43	−1,626.41
TCGA-DU-7299-01	−1,088.14	−393.54	−1,481.68
TCGA-DU-7300-01	−874.04	−893.14	−1,767.18
TCGA-DU-7301-01	−420.62	62.26	−358.36
TCGA-DU-7302-01	−1,445.28	−1,476.98	−2,922.26
TCGA-DU-7304-01	−778.99	−193.52	−972.51
TCGA-DU-7306-01	−708.97	−460.26	−1,169.22
TCGA-DU-7309-01	−831.3	−864	−1,695.3
TCGA-DU-8158-01	−167.4	408.25	240.85
TCGA-DU-8161-01	−92.35	615.44	523.09
TCGA-DU-8162-01	−850.5	−1,064.51	−1,915
TCGA-DU-8163-01	−626.39	147.46	−478.92
TCGA-DU-8164-01	−1,432.72	−1,502.9	−2,935.62
TCGA-DU-8165-01	−42.77	198.44	155.67
TCGA-DU-8166-01	−960.87	−574.16	−1,535.03
TCGA-DU-8167-01	−457.74	−0.74	−458.48
TCGA-DU-8168-01	−1,628.67	−1,383.5	−3,012.18
TCGA-DU-A5TP-01	−629.15	931	301.86
TCGA-DU-A5TR-01	−270.98	1,274.49	1,003.51
TCGA-DU-A5TS-01	−1,204.98	−588.31	−1,793.29
TCGA-DU-A5TT-01	−753	−530.5	−1,283.5
TCGA-DU-A5TU-01	−615.13	461.18	−153.95
TCGA-DU-A5TW-01	−1,307.37	−915.91	−2,223.29
TCGA-DU-A5TY-01	−36.87	852.85	815.98
TCGA-DU-A6S2-01	−1,462.66	−1,377.35	−2,840
TCGA-DU-A6S3-01	−1,560.04	−1,599.28	−3,159.32
TCGA-DU-A6S6-01	−1,555.81	−1,736.71	−3,292.52
TCGA-DU-A6S7-01	−1,023.95	−201.27	−1,225.22
TCGA-DU-A6S8-01	−1,461.4	−1,285.8	−2,747.2
TCGA-DU-A76K-01	−1,237.81	−1,684.19	−2,922
TCGA-DU-A76L-01	263.97	327.27	591.24
TCGA-DU-A76O-01	−916.89	404.94	−511.95
TCGA-DU-A76R-01	−898.9	−1,141.1	−2,040.01
TCGA-DU-A7T6-01	−990.38	−1,218.78	−2,209.17
TCGA-DU-A7T8-01	−545.36	−194.6	−739.96
TCGA-DU-A7TA-01	−599.22	−24.03	−623.24
TCGA-DU-A7TB-01	−1,287.23	−1,152.06	−2,439.29
TCGA-DU-A7TC-01	−1,451.72	−1,206.92	−2,658.64

TCGA-DU-A7TD-01	−285.77	515.56	229.78
TCGA-DU-A7TG-01	−946.07	−1,008.66	−1,954.73
TCGA-DU-A7TI-01	−807.65	97.31	−710.34
TCGA-DU-A7TJ-01	−772.43	−267.98	−1,040.41
TCGA-E1-5302-01	−691.73	107.61	−584.12
TCGA-E1-5303-01	−482.36	662.4	180.04
TCGA-E1-5304-01	−1,832.4	−1,576	−3,408.4
TCGA-E1-5305-01	−960.48	−702.24	−1,662.72
TCGA-E1-5307-01	−1,200.6	−492.5	−1,693.11
TCGA-E1-5311-01	−1,333.32	−1,436.27	−2,769.59
TCGA-E1-5318-01	−823	−911.28	−1,734.28
TCGA-E1-5319-01	−913.78	−743.21	−1,656.99
TCGA-E1-5322-01	−740.37	265.16	−475.21
TCGA-E1-A7YD-01	−1,075.35	−721.31	−1,796.66
TCGA-E1-A7YE-01	−116.72	666.7	549.98
TCGA-E1-A7YH-01	−1,202.62	−466.72	−1,669.35
TCGA-E1-A7YI-01	−1,468.5	−959.47	−2,427.97
TCGA-E1-A7YJ-01	−839.69	253.91	−585.78
TCGA-E1-A7YK-01	−360.96	804.95	443.99
TCGA-E1-A7YL-01	−269.06	526.3	257.24
TCGA-E1-A7YM-01	−1,239.6	−853.89	−2,093.49
TCGA-E1-A7YN-01	361.51	1,572.89	1,934.4
TCGA-E1-A7YO-01	−1,254.39	−1,430.01	−2,684.4
TCGA-E1-A7YQ-01	263.14	959.02	1,222.16
TCGA-E1-A7YS-01	−1,737.49	−1,385.5	−3,122.98
TCGA-E1-A7YU-01	−1,244.94	−869.45	−2,114.39
TCGA-E1-A7YV-01	−1,426.86	−1,418.74	−2,845.6
TCGA-E1-A7YW-01	−1,118.84	−465.38	−1,584.23
TCGA-E1-A7YY-01	−1,116.18	−1,287.16	−2,403.34
TCGA-E1-A7Z2-01	−1,312.74	−1,369.83	−2,682.57
TCGA-E1-A7Z3-01	−777.81	−619.17	−1,396.98
TCGA-E1-A7Z4-01	−1,176.77	−72.09	−1,248.86
TCGA-E1-A7Z6-01	−1,058.56	−602.95	−1,661.51
TCGA-EZ-7264-01	−1,511.79	−1,479.51	−2,991.3
TCGA-F6-A8O3-01	−1,685.51	−1,538.7	−3,224.21
TCGA-F6-A8O4-01	−1,520.59	−1,381.51	−2,902.09
TCGA-FG-5962-01	−1,185.04	−1,186.74	−2,371.78
TCGA-FG-5963-01	−256.19	724.09	467.9

TCGA-FG-5964-01	–970.77	–115.31	–1,086.08
TCGA-FG-5965-01	–863.38	–317.11	–1,180.49
TCGA-FG-6688-01	–525.21	344.24	–180.97
TCGA-FG-6689-01	–965.83	–257	–1,222.82
TCGA-FG-6690-01	–864.34	–117.85	–982.19
TCGA-FG-6691-01	–324.38	516.1	191.72
TCGA-FG-6692-01	–807.08	–160.03	–967.11
TCGA-FG-7634-01	–85.45	40.53	–44.92
TCGA-FG-7636-01	–1,323.43	–690.42	–2,013.85
TCGA-FG-7637-01	–1,068.93	–1,082.39	–2,151.33
TCGA-FG-7638-01	–1,199.13	–1,050.21	–2,249.34
TCGA-FG-7641-01	–1,578.93	–1,747.32	–3,326.25
TCGA-FG-7643-01	–863.63	–1,092.41	–1,956.03
TCGA-FG-8181-01	–969.73	–1,352.85	–2,322.58
TCGA-FG-8182-01	–875.43	–186.52	–1,061.95
TCGA-FG-8185-01	–1,302.01	–810.12	–2,112.13
TCGA-FG-8186-01	–796.37	–62.39	–858.76
TCGA-FG-8187-01	–1,061.2	–722.38	–1,783.58
TCGA-FG-8188-01	–849.84	–537.58	–1,387.43
TCGA-FG-8189-01	–1,362.55	–1,873.35	–3,235.9
TCGA-FG-8191-01	–783.45	–187.47	–970.92
TCGA-FG-A4MT-01	–1,255.8	–845.92	–2,101.72
TCGA-FG-A4MU-01	–231.53	387.22	155.69
TCGA-FG-A4MW-01	–982.79	–797.95	–1,780.74
TCGA-FG-A4MX-01	–1,377.64	–676.27	–2,053.91
TCGA-FG-A4MY-01	–1,196.89	–809.82	–2,006.7
TCGA-FG-A60J-01	–911.04	–444.14	–1,355.17
TCGA-FG-A60K-01	–1,396.11	–776.46	–2,172.57
TCGA-FG-A60L-01	–824.67	129.61	–695.06
TCGA-FG-A6IZ-01	–1,515.4	–697.15	–2,212.55
TCGA-FG-A6J1-01	–1,086.49	–498.02	–1,584.51
TCGA-FG-A6J3-01	–312.65	749.8	437.15
TCGA-FG-A70Y-01	–798.94	–110.07	–909.01
TCGA-FG-A70Z-01	–76.78	35.71	–41.07
TCGA-FG-A710-01	–766.69	170.45	–596.24
TCGA-FG-A711-01	–1,539.6	–902.96	–2,442.57
TCGA-FG-A713-01	–1,196.11	–1,564.62	–2,760.73
TCGA-FG-A87N-01	–1,372.02	–874.06	–2,246.08

TCGA-FG-A87Q-01	−89.09	584.2	495.11
TCGA-FN-7833-01	−97.08	820.42	723.34
TCGA-HT-7467-01	−1,067.52	−1,192.2	−2,259.73
TCGA-HT-7468-01	−1,181.44	−989.24	−2,170.69
TCGA-HT-7469-01	−1,218.55	−959.74	−2,178.28
TCGA-HT-7470-01	−1,010.64	−952.03	−1,962.67
TCGA-HT-7471-01	−582.97	−149.6	−732.57
TCGA-HT-7472-01	−534.72	94.07	−440.65
TCGA-HT-7473-01	−157.99	893.87	735.88
TCGA-HT-7474-01	−1,168.87	−1,205.1	−2,373.97
TCGA-HT-7475-01	−1,573.82	−1,546.94	−3,120.76
TCGA-HT-7476-01	−446.2	−847.01	−1,293.21
TCGA-HT-7477-01	−1,027.46	−934.49	−1,961.95
TCGA-HT-7478-01	−81.62	975.89	894.27
TCGA-HT-7479-01	−488.94	−70.49	−559.43
TCGA-HT-7480-01	−1,306.37	−1,324.7	−2,631.07
TCGA-HT-7481-01	−1,241.87	−1,327.33	−2,569.2
TCGA-HT-7482-01	−594.18	25.93	−568.25
TCGA-HT-7483-01	−772.78	−982.65	−1,755.43
TCGA-HT-7485-01	−999.53	−523.04	−1,522.57
TCGA-HT-7601-01	72.55	971.77	1,044.32
TCGA-HT-7602-01	−901.74	−377.68	−1,279.42
TCGA-HT-7603-01	−1,416.31	−1,405.42	−2,821.73
TCGA-HT-7604-01	−1,111.1	−914.27	−2,025.36
TCGA-HT-7605-01	−1,168.87	−1,211.25	−2,380.12
TCGA-HT-7606-01	−1,331.3	−968.44	−2,299.74
TCGA-HT-7607-01	−915.92	−1,069.9	−1,985.81
TCGA-HT-7608-01	−917.26	−643.37	−1,560.63
TCGA-HT-7609-01	−988.37	−201.98	−1,190.35
TCGA-HT-7610-01	−1,188.53	−1,274.85	−2,463.38
TCGA-HT-7611-01	−734.02	−256.45	−990.47
TCGA-HT-7616-01	−241.1	356.45	115.35
TCGA-HT-7620-01	−1,191.95	−653.46	−1,845.41
TCGA-HT-7676-01	−829.99	193.58	−636.41
TCGA-HT-7677-01	−1,202.98	−1,140.78	−2,343.76
TCGA-HT-7680-01	−370.63	208.38	−162.25
TCGA-HT-7681-01	−1,058.14	−784.62	−1,842.76
TCGA-HT-7684-01	−780.14	−51.19	−831.32

TCGA-HT-7686-01	−378.5	891.17	512.67
TCGA-HT-7687-01	−1,044.69	−780.21	−1,824.9
TCGA-HT-7688-01	−1,407.4	−1,478.03	−2,885.43
TCGA-HT-7689-01	−1,036.96	−456.16	−1,493.11
TCGA-HT-7690-01	−298.8	271.02	−27.78
TCGA-HT-7691-01	−220.96	228.92	7.95
TCGA-HT-7692-01	−1,286.67	−889.47	−2,176.13
TCGA-HT-7693-01	−808.23	103.59	−704.63
TCGA-HT-7694-01	−1,417.17	−1,587.57	−3,004.73
TCGA-HT-7695-01	−1,247.51	−1,428.42	−2,675.93
TCGA-HT-7854-01	−406.64	269.14	−137.51
TCGA-HT-7855-01	−1,147.12	−673.18	−1,820.3
TCGA-HT-7856-01	−1,189.57	−1,486.93	−2,676.5
TCGA-HT-7857-01	978.57	1,791.16	2,769.73
TCGA-HT-7858-01	−692.34	275.04	−417.3
TCGA-HT-7860-01	−404.53	224.62	−179.9
TCGA-HT-7873-01	−957.5	−660.43	−1,617.93
TCGA-HT-7874-01	−1,203.71	−1,454.62	−2,658.33
TCGA-HT-7875-01	−1,369.58	−1,524.42	−2,894.01
TCGA-HT-7877-01	−1,243.57	−1,290.89	−2,534.46
TCGA-HT-7879-01	−771.46	−477.83	−1,249.29
TCGA-HT-7880-01	−1,129.74	−1,115.53	−2,245.27
TCGA-HT-7881-01	−1,431.44	−1,598.21	−3,029.65
TCGA-HT-7882-01	1,759.22	1,636.15	3,395.36
TCGA-HT-7884-01	−1,257.46	−1,239.09	−2,496.55
TCGA-HT-7902-01	−1,142.49	−903.27	−2,045.76
TCGA-HT-8010-01	−948.05	−893.59	−1,841.64
TCGA-HT-8011-01	−1,182.58	−954.57	−2,137.15
TCGA-HT-8012-01	−1,242.17	−1,006.66	−2,248.82
TCGA-HT-8013-01	−582.45	796.6	214.15
TCGA-HT-8015-01	−717.61	−576.73	−1,294.34
TCGA-HT-8018-01	85.93	−41.1	44.82
TCGA-HT-8019-01	−1,241.92	−1,716.45	−2,958.37
TCGA-HT-8104-01	−692.12	−687.58	−1,379.7
TCGA-HT-8105-01	−1,243.22	−1,045.39	−2,288.61
TCGA-HT-8106-01	509.56	2,236.6	2,746.16
TCGA-HT-8107-01	−1,088.84	−1,484.63	−2,573.47
TCGA-HT-8108-01	−828.75	128.33	−700.42

TCGA-HT-8109-01	−1,047.19	−935.78	−1,982.97
TCGA-HT-8110-01	−206.77	1,092.11	885.34
TCGA-HT-8111-01	−855.71	58.4	−797.31
TCGA-HT-8113-01	−1,415.29	−1,621.17	−3,036.47
TCGA-HT-8114-01	−217.96	404.7	186.74
TCGA-HT-8558-01	−1,284.24	−1,665.07	−2,949.31
TCGA-HT-8563-01	764.08	1,815.67	2,579.75
TCGA-HT-8564-01	−800.02	−683.71	−1,483.72
TCGA-HT-A4DS-01	−930.43	358.62	−571.81
TCGA-HT-A4DV-01	−1,212.45	−799.68	−2,012.14
TCGA-HT-A5R5-01	−583.68	204.32	−379.36
TCGA-HT-A5R7-01	−1,226.91	−1,073.73	−2,300.63
TCGA-HT-A5R9-01	−1,261.5	−1,406.31	−2,667.81
TCGA-HT-A5RA-01	−473.94	−303.61	−777.55
TCGA-HT-A5RB-01	−1,310.67	−1,416.78	−2,727.46
TCGA-HT-A5RC-01	−705.68	−205.94	−911.62
TCGA-HT-A614-01	−1,306.56	−723.53	−2,030.1
TCGA-HT-A615-01	−946.56	36.96	−909.59
TCGA-HT-A616-01	−1,216.88	−1,235.83	−2,452.71
TCGA-HT-A617-01	−200.78	286.65	85.87
TCGA-HT-A618-01	−527.16	811.31	284.16
TCGA-HT-A619-01	−1,483.79	−1,373.94	−2,857.73
TCGA-HT-A61A-01	−1,172.86	−1,389.44	−2,562.3
TCGA-HT-A61B-01	−414.65	873.82	459.17
TCGA-HT-A61C-01	−792.6	−188.11	−980.71
TCGA-HT-A74H-01	−382.14	−61.58	−443.72
TCGA-HT-A74J-01	−1,262.63	−638.75	−1,901.37
TCGA-HT-A74K-01	−706.3	−467.69	−1,173.99
TCGA-HT-A74L-01	−1,101.74	−584.33	−1,686.07
TCGA-HT-A74O-01	−580.23	602.13	21.9
TCGA-HW-7486-01	−941.99	−596.94	−1,538.93
TCGA-HW-7487-01	−1,481.14	−1,428.66	−2,909.8
TCGA-HW-7489-01	−1,197.34	−1,075.64	−2,272.98
TCGA-HW-7490-01	−811.02	−425.06	−1,236.09
TCGA-HW-7491-01	−1,278.5	−1,212.1	−2,490.6
TCGA-HW-7493-01	−400.44	−323.81	−724.25
TCGA-HW-7495-01	−1,251	−1,426.79	−2,677.78
TCGA-HW-8319-01	−1,220.74	−1,009.89	−2,230.63

TCGA-HW-8320-01	−931.29	−447.09	−1,378.38
TCGA-HW-8321-01	−831.77	−523.96	−1,355.73
TCGA-HW-8322-01	−1,299.43	−880.16	−2,179.59
TCGA-HW-A5KJ-01	−1,486.45	−1,256.24	−2,742.69
TCGA-HW-A5KK-01	−404.53	688.45	283.92
TCGA-HW-A5KL-01	−1,009.87	−448.03	−1,457.9
TCGA-HW-A5KM-01	24.21	1,638.1	1,662.31
TCGA-IK-7675-01	−1,182.45	−1,181.51	−2,363.96
TCGA-IK-8125-01	−1,162.92	−1,046.49	−2,209.41
TCGA-KT-A74X-01	−1,413.92	−965.62	−2,379.54
TCGA-KT-A7W1-01	−1,135.7	−756.52	−1,892.23
TCGA-P5-A5ET-01	−1,465.03	−1,508.97	−2,974
TCGA-P5-A5EU-01	−433.04	263.17	−169.87
TCGA-P5-A5EV-01	−1,109.3	−549.64	−1,658.95
TCGA-P5-A5EW-01	−892.27	−483.06	−1,375.33
TCGA-P5-A5EX-01	−90.23	690.32	600.1
TCGA-P5-A5EY-01	−946.45	−770.69	−1,717.14
TCGA-P5-A5EZ-01	−817.02	−227.02	−1,044.04
TCGA-P5-A5F0-01	−1,674.24	−1,734.33	−3,408.57
TCGA-P5-A5F1-01	−795.1	−312.74	−1,107.84
TCGA-P5-A5F2-01	−1,418.04	−1,310.13	−2,728.17
TCGA-P5-A5F4-01	−1,374.84	−1,535.32	−2,910.16
TCGA-P5-A5F6-01	−740.26	−817.19	−1,557.46
TCGA-P5-A72U-01	266.08	209.44	475.52
TCGA-P5-A72W-01	−1,351.54	−728.56	−2,080.1
TCGA-P5-A72X-01	−776.09	−776.64	−1,552.73
TCGA-P5-A72Z-01	−1,541.91	−1,373.65	−2,915.56
TCGA-P5-A730-01	−1,072.03	−1,083.27	−2,155.3
TCGA-P5-A731-01	−619.42	−720.44	−1,339.85
TCGA-P5-A733-01	−1,263.06	−1,119.3	−2,382.37
TCGA-P5-A735-01	−1,415.2	−764.69	−2,179.89
TCGA-P5-A736-01	−362.69	548.97	186.28
TCGA-P5-A737-01	−1,367.72	−972.58	−2,340.3
TCGA-P5-A77W-01	−1,535.04	−1,383.73	−2,918.77
TCGA-P5-A77X-01	−1,532.69	−1,561.94	−3,094.63
TCGA-P5-A780-01	−694.36	−428.34	−1,122.7
TCGA-P5-A781-01	−1,201.94	−1,072.56	−2,274.49
TCGA-QH-A65R-01	−1,353.7	−1,186.38	−2,540.08

TCGA-QH-A65S-01	–1,062.96	–322.71	–1,385.67
TCGA-QH-A65V-01	–1,274.05	–755.71	–2,029.75
TCGA-QH-A65X-01	–975.5	–608.25	–1,583.75
TCGA-QH-A65Z-01	–1,541.98	–1,202.12	–2,744.1
TCGA-QH-A6CS-01	–673.04	–290.01	–963.05
TCGA-QH-A6CU-01	–938.8	–300.66	–1,239.46
TCGA-QH-A6CV-01	–735.67	184.66	–551
TCGA-QH-A6CW-01	–984.75	–177.47	–1,162.23
TCGA-QH-A6CX-01	–710.64	–52.41	–763.05
TCGA-QH-A6CY-01	–1,371.75	–1,232.16	–2,603.91
TCGA-QH-A6CZ-01	–1,451.16	–1,470.54	–2,921.71
TCGA-QH-A6X3-01	–1,084.89	–648.74	–1,733.63
TCGA-QH-A6X4-01	–1,699.18	–1,082.55	–2,781.73
TCGA-QH-A6X5-01	–1,320.34	–972.82	–2,293.16
TCGA-QH-A6X8-01	–1,404.35	–950.28	–2,354.63
TCGA-QH-A6X9-01	–1,274.95	–1,058.12	–2,333.07
TCGA-QH-A6XA-01	–1,038.9	–641.29	–1,680.19
TCGA-QH-A6XC-01	–1,027.72	–672.72	–1,700.43
TCGA-QH-A86X-01	–1,382.09	–1,118.83	–2,500.92
TCGA-QH-A870-01	–1,347.08	–925.92	–2,273
TCGA-R8-A6MK-01	–1,448.65	–936.37	–2,385.02
TCGA-R8-A6ML-01	–1,574.98	–1,277.8	–2,852.78
TCGA-R8-A6MO-01	–1,229.5	–566.9	–1796.41
TCGA-R8-A73M-01	–1,703.21	–1,322.8	–3,026
TCGA-RY-A83X-01	–1,445.37	–1,272.95	–2,718.32
TCGA-RY-A83Y-01	–1,308.62	–516.19	–1,824.8
TCGA-RY-A83Z-01	–1,640.34	–564.34	–2,204.68
TCGA-RY-A840-01	–1,529.97	–1,144.09	–2,674.07
TCGA-RY-A843-01	–1,206.98	–809.56	–2,016.54
TCGA-RY-A845-01	–1,240.89	–848.17	–2,089.06
TCGA-RY-A847-01	–918.97	–303.41	–1,222.38
TCGA-S9-A6TS-01	–1,065.09	–461.92	–1,527.01
TCGA-S9-A6TU-01	–755.62	18.1	–737.52
TCGA-S9-A6TV-01	–121.68	672.08	550.4
TCGA-S9-A6TW-01	–814.02	–863.14	–1,677.15
TCGA-S9-A6TX-01	–1,228.96	–923.37	–2,152.33
TCGA-S9-A6TY-01	–1,742.83	–1,710.75	–3,453.58
TCGA-S9-A6TZ-01	–712.44	–410.05	–1,122.49

TCGA-S9-A6U0-01	182.44	714	896.44
TCGA-S9-A6U1-01	−999.37	−552.32	−1,551.69
TCGA-S9-A6U2-01	−934.54	−679.98	−1,614.52
TCGA-S9-A6U5-01	−1,137.94	−133.52	−1,271.46
TCGA-S9-A6U6-01	−1,214.68	−786	−2,000.68
TCGA-S9-A6U8-01	−828.88	−83.3	−912.18
TCGA-S9-A6U9-01	−342.72	416.98	74.26
TCGA-S9-A6UA-01	404.87	1,076.13	1,481
TCGA-S9-A6UB-01	−1,677.69	−1,508.57	−3,186.26
TCGA-S9-A6WD-01	−1,572.88	−1,280.31	−2,853.19
TCGA-S9-A6WE-01	−1,282.54	−952.98	−2,235.53
TCGA-S9-A6WG-01	293.14	273.84	566.98
TCGA-S9-A6WH-01	−1,533.65	−1,232.33	−2,765.98
TCGA-S9-A6WI-01	−1,227.14	−1,579.53	−2,806.67
TCGA-S9-A6WL-01	−685.52	−1,227.77	−1,913.29
TCGA-S9-A6WM-01	−632.29	−725.25	−1,357.53
TCGA-S9-A6WN-01	−240.86	580.93	340.07
TCGA-S9-A6WO-01	−1,049.23	−123.61	−1,172.84
TCGA-S9-A6WP-01	−1,115.25	−318.96	−1,434.21
TCGA-S9-A6WQ-01	−866.95	34.43	−832.52
TCGA-S9-A7IQ-01	−1,453.22	−1,817.48	−3,270.7
TCGA-S9-A7IS-01	−1,412.79	−912.21	−2,325
TCGA-S9-A7IX-01	−387.44	17.31	−370.13
TCGA-S9-A7IY-01	−981.72	−98.77	−1,080.49
TCGA-S9-A7IZ-01	−931.09	−359.14	−1,290.22
TCGA-S9-A7J0-01	−1,646.84	−1,156.53	−2,803.37
TCGA-S9-A7J1-01	−1,082.66	−878.06	−1,960.72
TCGA-S9-A7J2-01	−1,455.84	−1,312.86	−2,768.7
TCGA-S9-A7J3-01	−1,227.81	−737.31	−1,965.12
TCGA-S9-A7QW-01	−1,652.97	−1,307.36	−2,960.32
TCGA-S9-A7QX-01	−1,198.04	−253.25	−1,451.29
TCGA-S9-A7QY-01	−1,505.27	−1,251	−2,756.27
TCGA-S9-A7QZ-01	−1,512.15	−1,586.46	−3,098.6
TCGA-S9-A7R1-01	−1,418.7	−1,442.38	−2,861.09
TCGA-S9-A7R2-01	−408.69	509.9	101.21
TCGA-S9-A7R3-01	−869.7	−288.96	−1,158.66
TCGA-S9-A7R4-01	−186.88	−114.95	−301.84
TCGA-S9-A7R7-01	175.79	699.25	875.04

TCGA-S9-A7R8-01	−923.33	−74.69	−998.02
TCGA-S9-A89V-01	−786.08	−403.95	−1,190.03
TCGA-S9-A89Z-01	−393.33	418.64	25.31
TCGA-TM-A7C3-01	−989.68	−1,110.65	−2,100.32
TCGA-TM-A7C4-01	−1,392.49	−1,489.4	−2,881.89
TCGA-TM-A7C5-01	−1,433.22	−1,243.37	−2,676.59
TCGA-TM-A7CA-01	−1,426.79	−1,091.23	−2,518.02
TCGA-TM-A7CF-01	−1,508.77	−1,393.18	−2,901.96
TCGA-TM-A84B-01	−949.88	−1,189.92	−2,139.8
TCGA-TM-A84C-01	−466.44	−78.95	−545.39
TCGA-TM-A84F-01	−424.4	931	506.59
TCGA-TM-A84G-01	−1,571.25	−1,570.48	−3,141.73
TCGA-TM-A84H-01	−1,440.68	−995.33	−2,436.01
TCGA-TM-A84I-01	−1,242.81	−685.37	−1,928.18
TCGA-TM-A84J-01	−926.97	−1,339.27	−2,266.24
TCGA-TM-A84L-01	−646.57	−95.41	−741.98
TCGA-TM-A84M-01	−1,598.16	−1,414.83	−3,012.99
TCGA-TM-A84O-01	−1,045.45	−758.73	−1,804.18
TCGA-TM-A84Q-01	−747.4	84.12	−663.28
TCGA-TM-A84R-01	−1,286.25	−1,682.92	−2,969.17
TCGA-TM-A84S-01	−1,164.3	−684.1	−1,848.4
TCGA-TM-A84T-01	−1,047.6	−526.79	−1,574.39
TCGA-TQ-A7RF-01	−1,314.84	−556.93	−1,871.77
TCGA-TQ-A7RG-01	−1,095.09	−712.47	−1,807.56
TCGA-TQ-A7RH-01	−777.39	−93.46	−870.85
TCGA-TQ-A7RI-01	−1,269.94	−778.06	−2,048
TCGA-TQ-A7RJ-01	−1,030.7	−285.24	−1,315.94
TCGA-TQ-A7RK-01	−1,460.74	−1,049.87	−2,510.61
TCGA-TQ-A7RM-01	−1,379.21	−1,561.1	−2,940.32
TCGA-TQ-A7RN-01	−1,396.68	−1,171.12	−2,567.8
TCGA-TQ-A7RO-01	−1,359.46	−1,076.65	−2,436.11
TCGA-TQ-A7RP-01	−586.44	−569.96	−1,156.4
TCGA-TQ-A7RQ-01	−1,624.29	−1,691.39	−3,315.67
TCGA-TQ-A7RR-01	−981.2	−339.66	−1,320.86
TCGA-TQ-A7RS-01	−1,551.17	−1,337.43	−2,888.6
TCGA-TQ-A7RU-01	−1,378.11	−1,319.65	−2,697.76
TCGA-TQ-A7RV-01	−1,331.73	−1,044.22	−2,375.95
TCGA-TQ-A7RW-01	−605.94	331.99	−273.95

TCGA-TQ-A8XE-01	−1,333.68	−738.64	−2,072.32
TCGA-VM-A8C8-01	−993.85	−390.91	−1,384.77
TCGA-VM-A8C9-01	−230.84	933.74	702.9
TCGA-VM-A8CA-01	−784.83	−453.16	−1,237.99
TCGA-VM-A8CB-01	−1,672.41	−1,267.99	−2,940.4
TCGA-VM-A8CD-01	−596.51	−21.76	−618.26
TCGA-VM-A8CE-01	−1,070.13	−976.71	−2,046.83
TCGA-VM-A8CF-01	−707.79	585.3	−122.49
TCGA-VM-A8CH-01	−833.82	−148.47	−982.28
TCGA-VV-A829-01	−1,031.76	−509.24	−1,541
TCGA-VV-A86M-01	−1,077.43	−108.46	−1,185.88
TCGA-VW-A7QS-01	−1,349.46	−1,281.57	−2,631.03
TCGA-VW-A8FI-01	−1,018.94	−110.58	−1,129.51
TCGA-W9-A837-01	−1,468.21	−1,433.28	−2,901.49
TCGA-WH-A86K-01	−1,107.97	−572.4	−1,680.37
TCGA-WY-A858-01	−186.91	673.64	486.73
TCGA-WY-A859-01	−1,543.28	−1,602.86	−3,146.14
TCGA-WY-A85A-01	−1348	−679.52	−2,027.52
TCGA-WY-A85B-01	−772.63	143.59	−629.04
TCGA-WY-A85C-01	−1,127.53	−653.42	−1,780.95
TCGA-WY-A85D-01	−1,188.95	−385.44	−1,574.39
TCGA-WY-A85E-01	−1,565.53	−1,247.25	−2,812.78