

Supplementary materials

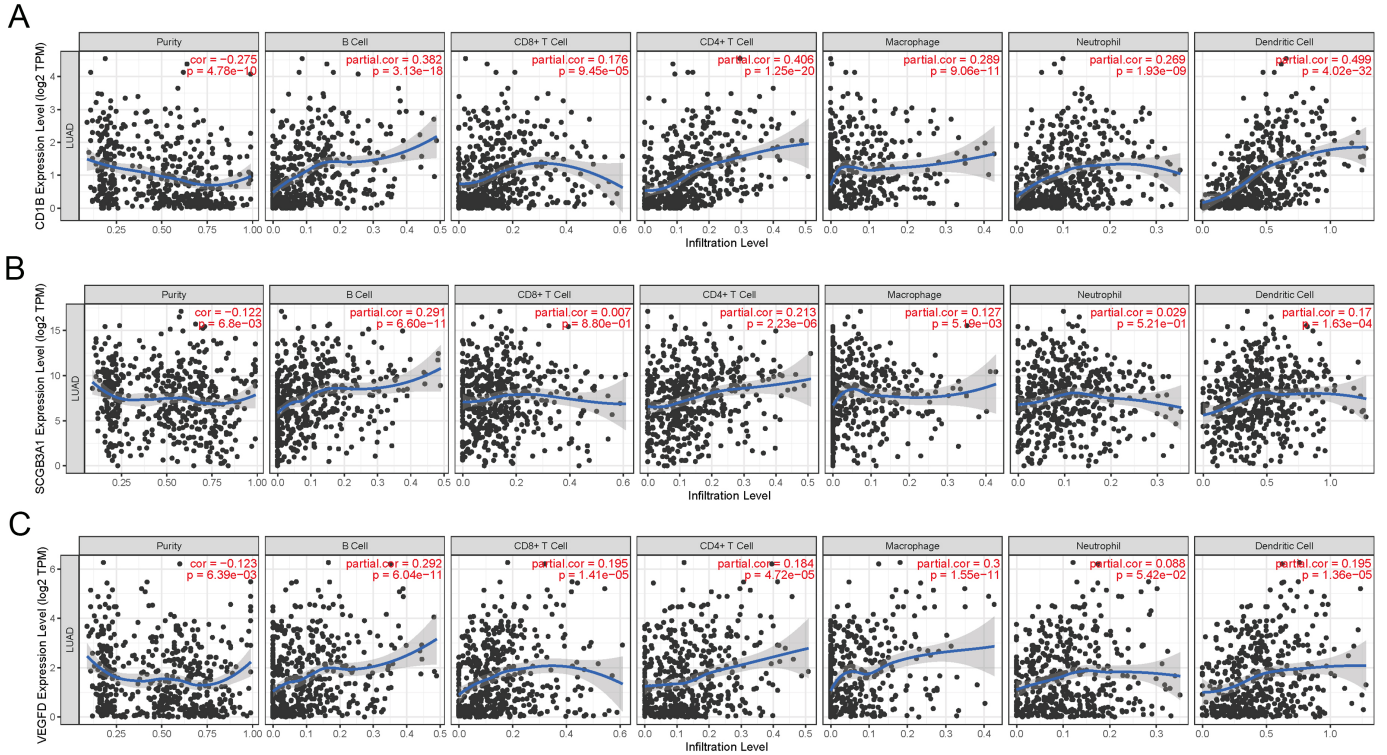


Figure S1. Correlation between expression of three hub genes and immune cell infiltration.

Scatter plots of the correlation of immune cells with CD1B(A), SCGB3A1(B) and VEGFD(C) are shown.

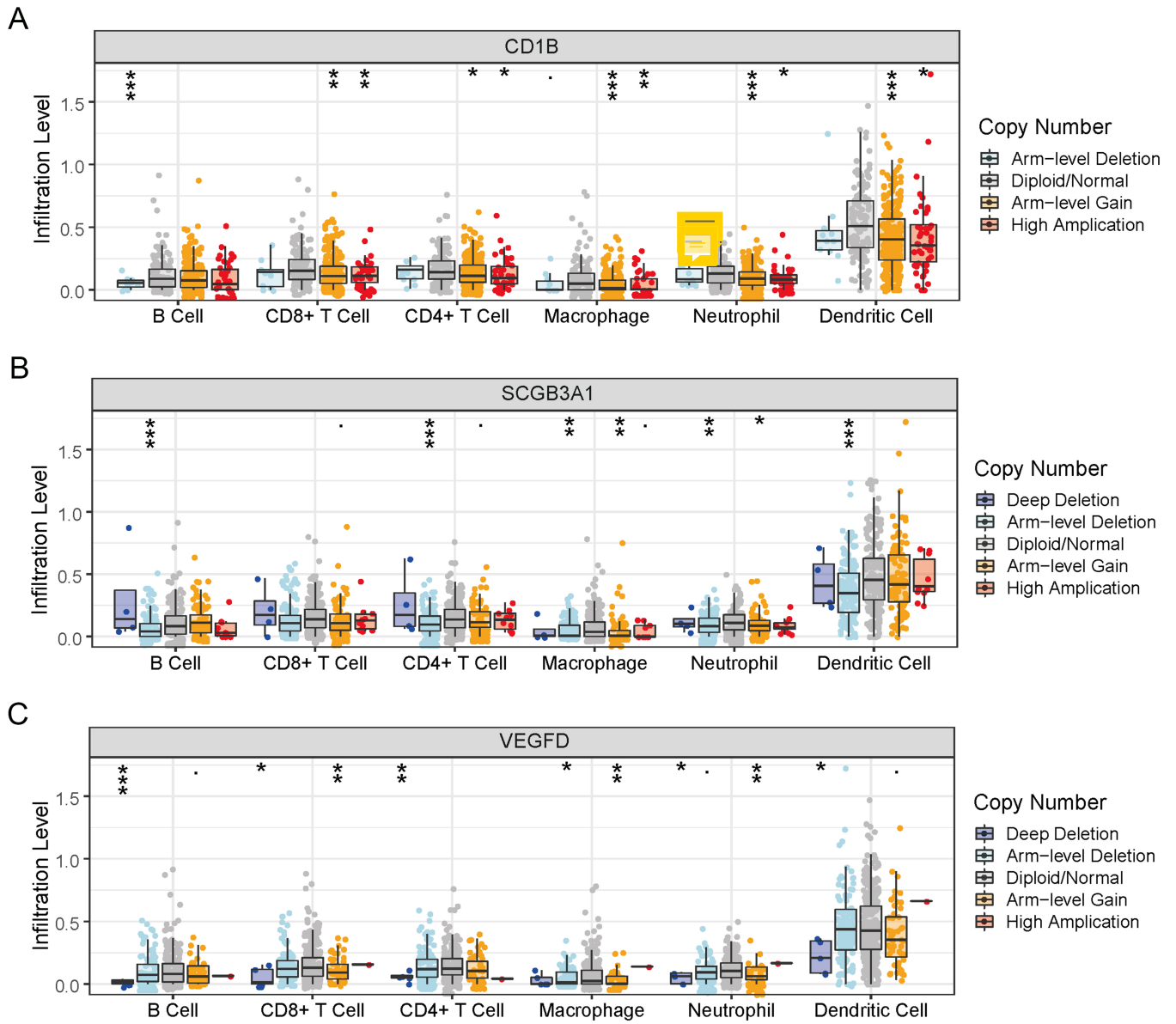


Figure S2. Correlation between mutants of hub gene and immune cell infiltration. Boxplots indicated that diverse forms of mutation carried by CD1B(A), SCGB3A1(B) and VEGFD(C) were related to lower immune cell infiltrates. *** $p < 0.001$, ** $p < 0.01$, * $p < 0.05$.

Table S1. TMB scores calculated for each LUAD sample in TCGA.

Patient ID	TMB value
TCGA-75-7027-01A-11D-1945-08	5.894736842
TCGA-91-8496-01A-11D-2393-08	0.473684211
TCGA-MP-A4TJ-01A-51D-A25L-08	1.394736842
TCGA-64-5778-01A-01D-1625-08	12.13157895
TCGA-62-A46O-01A-11D-A24D-08	21.78947368
TCGA-55-6972-01A-11D-1945-08	6.157894737
TCGA-55-8621-01A-11D-2393-08	0.157894737
TCGA-55-8090-01A-11D-2238-08	2.315789474
TCGA-99-7458-01A-11D-2036-08	10.21052632
TCGA-05-5429-01A-01D-1625-08	0.710526316
TCGA-97-7938-01A-11D-2167-08	9.184210526
TCGA-55-A57B-01A-12D-A397-08	0.842105263
TCGA-55-7994-01A-11D-2184-08	37.60526316
TCGA-05-4425-01A-01D-1753-08	0.894736842
TCGA-MN-A4N5-01A-11D-A24P-08	10.81578947
TCGA-86-7701-01A-11D-2167-08	4.526315789
TCGA-93-A4JN-01A-11D-A24P-08	1.473684211
TCGA-38-4632-01A-01D-1753-08	11.34210526
TCGA-97-7553-01A-21D-2036-08	0.631578947
TCGA-50-5935-01A-11D-1753-08	0.815789474
TCGA-99-AA5R-01A-11D-A397-08	0.105263158
TCGA-38-4629-01A-02D-1265-08	6.973684211
TCGA-55-7907-01A-11D-2167-08	28.52631579
TCGA-86-8073-01A-11D-2238-08	31.05263158
TCGA-73-A9RS-01A-11D-A410-08	23.23684211
TCGA-44-7660-01A-11D-2063-08	7.868421053
TCGA-69-7765-01A-11D-2167-08	12
TCGA-NJ-A4YF-01A-12D-A25L-08	14.92105263
TCGA-55-1595-01A-01D-0969-08	7.473684211
TCGA-50-5044-01A-21D-1855-08	1.578947368
TCGA-86-8671-01A-11D-2393-08	0.026315789
TCGA-73-4662-01A-01D-1265-08	5.131578947
TCGA-50-5049-01A-01D-1625-08	13.57894737
TCGA-MP-A5C7-01A-11D-A25L-08	1.684210526
TCGA-55-7576-01A-11D-2063-08	7.842105263
TCGA-55-8505-01A-11D-2393-08	0.736842105
TCGA-99-8033-01A-11D-2238-08	3.842105263
TCGA-17-Z050-01A-01W-0747-08	3.710526316
TCGA-91-6831-01A-11D-1855-08	6.763157895
TCGA-86-8054-01A-11D-2238-08	5.552631579

TCGA-75-5147-01A-01D-1625-08	0.868421053
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TCGA-69-A59K-01A-11D-A25L-08	11.76315789
TCGA-MP-A4T7-01A-11D-A24P-08	2.973684211
TCGA-17-Z041-01A-01W-0746-08	2.605263158
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TCGA-17-Z019-01A-01W-0746-08	0.052631579
TCGA-49-AAR0-01A-21D-A397-08	2.131578947
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TCGA-95-7944-01A-11D-2184-08	5.5
TCGA-44-6148-01A-11D-1753-08	0.105263158
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TCGA-86-8358-01A-11D-2323-08	27.42105263
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TCGA-49-4505-01A-01D-1931-08	4.552631579
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TCGA-97-8176-01A-11D-2393-08	3.236842105
TCGA-55-A48X-01A-11D-A24D-08	7.131578947
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TCGA-55-7725-01A-11D-2167-08	3.263157895
TCGA-44-2665-01A-01D-A271-08	0.710526316
TCGA-17-Z052-01A-01W-0747-08	1.157894737
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TCGA-55-6969-01A-11D-1945-08	8.921052632
TCGA-55-8615-01A-11D-2393-08	2.736842105
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TCGA-55-8208-01A-11D-2238-08	2.473684211
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TCGA-38-6178-01A-11D-1753-08	0.815789474
TCGA-86-8674-01A-21D-2393-08	7.342105263
TCGA-49-4487-01A-21D-1855-08	5.447368421
TCGA-44-2662-01A-01D-A271-08	3.421052632
TCGA-49-AAR2-01A-11D-A397-08	9.947368421
TCGA-NJ-A4YG-01A-22D-A25L-08	2.578947368
TCGA-17-Z026-01A-01W-0746-08	16.71052632
TCGA-75-6207-01A-11D-1753-08	1.263157895
TCGA-44-8119-01A-11D-2238-08	14.63157895

TCGA-64-5815-01A-01D-1625-08	3.868421053
TCGA-73-4668-01A-01D-1265-08	14.68421053
TCGA-95-7567-01A-11D-2063-08	19.26315789
TCGA-44-6774-01A-21D-1855-08	6.842105263
TCGA-78-8662-01A-11D-2393-08	29.10526316
TCGA-91-6840-01A-11D-1945-08	2.842105263
TCGA-NJ-A55R-01A-11D-A25L-08	5.763157895
TCGA-17-Z061-01A-01W-0747-08	4.368421053
TCGA-55-7281-01A-11D-2036-08	10.65789474
TCGA-MP-A4T6-01A-32D-A25L-08	1.421052632
TCGA-55-7724-01A-11D-2167-08	2.5
TCGA-62-8394-01A-11D-2323-08	1.842105263
TCGA-73-4670-01A-01D-1265-08	9.605263158
TCGA-86-8281-01A-11D-2284-08	5.526315789
TCGA-55-8616-01A-11D-2393-08	11.13157895
TCGA-05-4410-01A-21D-1855-08	22.23684211
TCGA-97-8547-01A-11D-2393-08	1.315789474
TCGA-95-A4VK-01A-11D-A25L-08	6.157894737
TCGA-55-A48Z-01A-12D-A24P-08	0.947368421
TCGA-49-6767-01A-11D-1855-08	10.31578947
TCGA-44-2661-01A-01D-1105-08	0.657894737
TCGA-17-Z055-01A-01W-0747-08	9.394736842
TCGA-78-7163-01A-12D-2063-08	0.421052632
TCGA-50-8457-01A-11D-2323-08	1.210526316
TCGA-69-7973-01A-11D-2184-08	6.552631579
TCGA-64-1679-01A-21D-2063-08	11.15789474
TCGA-95-A4VN-01A-11D-A25L-08	8.157894737
TCGA-78-7147-01A-11D-2036-08	7.763157895
TCGA-75-6203-01A-11D-1753-08	0.184210526
TCGA-50-5055-01A-01D-1625-08	0.131578947
TCGA-44-3919-01A-02D-1458-08	0.789473684
TCGA-55-8511-01A-11D-2393-08	11.84210526
TCGA-97-8172-01A-11D-2284-08	5.815789474
TCGA-49-4486-01A-01D-1265-08	2.736842105
TCGA-17-Z037-01A-01W-0746-08	2.894736842
TCGA-44-A47B-01A-11D-A24D-08	1.263157895
TCGA-78-7146-01A-11D-2036-08	9.210526316
TCGA-44-7671-01A-11D-2063-08	5.947368421
TCGA-17-Z049-01A-01W-0746-08	15.21052632
TCGA-44-3917-01A-01D-A271-08	4.736842105
TCGA-17-Z023-01A-01W-0746-08	9.263157895
TCGA-55-6985-01A-11D-1945-08	9.710526316
TCGA-49-AAQV-01A-11D-A397-08	0.789473684

TCGA-55-8094-01A-11D-2238-08	11.15789474
TCGA-44-6145-01A-11D-1753-08	7
TCGA-55-6971-01A-11D-1945-08	1.894736842
TCGA-55-7573-01A-11D-2036-08	1.157894737
TCGA-L9-A443-01A-12D-A24D-08	6.052631579
TCGA-62-A46R-01A-11D-A24D-08	3.789473684
TCGA-55-7914-01A-11D-2167-08	4.052631579
TCGA-L9-A50W-01A-12D-A397-08	0.736842105
TCGA-50-6595-01A-12D-1855-08	1.157894737
TCGA-55-6543-01A-11D-1753-08	0.447368421
TCGA-05-4390-01A-02D-1753-08	13.52631579
TCGA-44-A47A-01A-21D-A24D-08	4.236842105
TCGA-17-Z059-01A-01W-0747-08	3.868421053
TCGA-05-4418-01A-01D-1265-08	6.657894737
TCGA-69-7978-01A-11D-2184-08	9.684210526
TCGA-91-8497-01A-11D-2393-08	0.947368421
TCGA-44-7662-01A-11D-2063-08	12.78947368
TCGA-55-8619-01A-11D-2393-08	0.078947368
TCGA-55-A494-01A-11D-A24P-08	6.157894737
TCGA-50-5931-01A-11D-1753-08	7.289473684
TCGA-55-7727-01A-11D-2167-08	4.894736842
TCGA-50-5068-01A-01D-1625-08	1.842105263
TCGA-53-7626-01A-12D-2063-08	8.973684211
TCGA-91-8499-01A-11D-2393-08	8.315789474
TCGA-05-5420-01A-01D-1625-08	1.421052632
TCGA-78-7161-01A-11D-2036-08	4.052631579
TCGA-50-5939-01A-11D-1625-08	1.789473684
TCGA-17-Z021-01A-01W-0746-08	2.078947368
TCGA-97-A4LX-01A-11D-A24P-08	2.078947368
TCGA-55-7815-01A-11D-2167-08	2.868421053
TCGA-50-6673-01A-11D-1945-08	1.263157895
TCGA-44-7661-01A-11D-2063-08	5
TCGA-75-5126-01A-01D-1753-08	11.26315789
TCGA-55-8512-01A-11D-2393-08	0.947368421
TCGA-44-4112-01A-31D-A27T-08	10.42105263
TCGA-50-5936-01A-11D-1625-08	2.473684211
TCGA-49-6742-01A-11D-1855-08	5.710526316
TCGA-17-Z051-01A-01W-0747-08	6.5
TCGA-55-8091-01A-11D-2238-08	0.5
TCGA-75-6212-01A-11D-1753-08	0.421052632
TCGA-73-4659-01A-01D-1265-08	5.289473684
TCGA-44-6775-01A-31D-A27T-08	1.105263158
TCGA-44-6144-01A-11D-1753-08	4.684210526

TCGA-55-7284-01B-11D-2238-08	0.868421053
TCGA-05-4417-01A-22D-1855-08	7.105263158
TCGA-17-Z000-01A-01W-0746-08	2.815789474
TCGA-05-5715-01A-01D-1625-08	2.894736842
TCGA-78-7145-01A-11D-2036-08	4.815789474
TCGA-55-8510-01A-11D-2393-08	6.5
TCGA-55-8205-01A-11D-2238-08	9.552631579
TCGA-44-8117-01A-11D-2238-08	18.76315789
TCGA-78-7166-01A-12D-2063-08	5.210526316
TCGA-05-4395-01A-01D-1265-08	6.684210526
TCGA-69-7760-01A-11D-2167-08	1.5
TCGA-4B-A93V-01A-11D-A397-08	3.526315789
TCGA-50-5942-01A-21D-1753-08	0.763157895
TCGA-55-1594-01A-01D-1040-01	4.684210526
TCGA-53-7813-01A-11D-2167-08	3.657894737
TCGA-44-2668-01A-01D-A271-08	6.631578947
TCGA-86-8672-01A-21D-2393-08	6.526315789
TCGA-73-7499-01A-11D-2184-08	1.315789474
TCGA-50-5941-01A-11D-1753-08	6.421052632
TCGA-NJ-A4YI-01A-11D-A25L-08	11.13157895
TCGA-78-8660-01A-11D-2393-08	4.973684211
TCGA-91-6830-01A-11D-1945-08	3.552631579
TCGA-MP-A4SV-01A-11D-A24P-08	5.184210526
TCGA-64-5781-01A-01D-1625-08	24.81578947
TCGA-73-4658-01A-01D-1753-08	4.157894737
TCGA-75-7025-01A-12D-1945-08	0.526315789
TCGA-55-6987-01A-11D-1945-08	3.210526316
TCGA-49-AAR4-01A-12D-A410-08	7.315789474
TCGA-73-4677-01A-01D-1265-08	6.394736842
TCGA-MP-A4TI-01A-21D-A24P-08	3.026315789
TCGA-38-4627-01A-01D-1553-08	0.473684211
TCGA-55-1596-01A-01D-1040-01	4.763157895
TCGA-05-4427-01A-21D-1855-08	23.71052632
TCGA-53-A4EZ-01A-12D-A24P-08	13.10526316
TCGA-17-Z045-01A-01W-0746-08	16.02631579
TCGA-05-4405-01A-21D-1855-08	7.289473684
TCGA-91-6836-01A-21D-1855-08	12.21052632
TCGA-49-AAR9-01A-21D-A410-08	16.26315789
TCGA-78-7159-01A-11D-2036-08	7.289473684
TCGA-78-8648-01A-11D-2393-08	0.026315789
TCGA-44-A47F-01A-11D-A24D-08	1.473684211
TCGA-50-5933-01A-11D-1753-08	10.47368421
TCGA-97-8171-01A-11D-2284-08	1.263157895

TCGA-L9-A743-01A-43D-A397-08	1.342105263
TCGA-38-4631-01A-01D-1753-08	17.55263158
TCGA-05-4434-01A-01D-1265-08	0.684210526
TCGA-05-4420-01A-01D-1265-08	6.921052632
TCGA-44-2666-01A-41D-A27T-08	0.578947368
TCGA-38-4630-01A-01D-1265-08	3.105263158
TCGA-05-4382-01A-01D-1931-08	31.36842105
TCGA-05-5423-01A-01D-1625-08	3.710526316
TCGA-62-A46S-01A-11D-A24D-08	2.657894737
TCGA-75-5125-01A-01D-1753-08	3.368421053
TCGA-64-5775-01A-01D-1625-08	12.36842105
TCGA-97-7554-01A-11D-2036-08	9.894736842
TCGA-MP-A4T4-01A-11D-A25L-08	6.842105263
TCGA-55-A48Y-01A-11D-A24D-08	6.763157895
TCGA-78-7152-01A-11D-2036-08	3.815789474
TCGA-78-7154-01A-11D-2036-08	5.789473684
TCGA-95-A4VP-01A-21D-A25L-08	2.657894737
TCGA-49-6761-01A-31D-1945-08	3.842105263
TCGA-71-6725-01A-11D-1855-08	1.131578947
TCGA-05-4433-01A-22D-1855-08	0.894736842
TCGA-17-Z018-01A-01W-0746-08	6.026315789
TCGA-MP-A4TF-01A-11D-A25L-08	9.552631579
TCGA-64-5774-01A-01D-1625-08	3.315789474
TCGA-NJ-A55O-01A-11D-A25L-08	1.894736842
TCGA-86-6851-01A-11D-1945-08	20.55263158
TCGA-78-7156-01A-11D-2036-08	7
TCGA-62-A46V-01A-11D-A24D-08	1.131578947
TCGA-17-Z057-01A-01W-0747-08	8.5
TCGA-44-A4SS-01A-11D-A24P-08	8.078947368
TCGA-49-4494-01A-01D-1265-08	4.210526316
TCGA-86-8056-01A-11D-2238-08	5.684210526
TCGA-67-3774-01A-01D-1040-01	2.605263158
TCGA-MN-A4N4-01A-12D-A24P-08	29.5
TCGA-17-Z016-01A-01W-0746-08	8.210526316
TCGA-93-A4JP-01A-11D-A24P-08	0.421052632
TCGA-64-1680-01A-02D-0969-08	0.947368421
TCGA-50-6592-01A-11D-1753-08	5.763157895
TCGA-17-Z027-01A-01W-0746-08	2.210526316
TCGA-78-8640-01A-11D-2393-08	16.39473684
TCGA-S2-AA1A-01A-12D-A397-08	2.447368421
TCGA-78-7162-01A-21D-2063-08	1.157894737
TCGA-69-7764-01A-11D-2167-08	1.921052632
TCGA-55-7728-01A-11D-2184-08	2.263157895

TCGA-38-7271-01A-11D-2036-08	0.605263158
TCGA-17-Z043-01A-01W-0746-08	4.763157895
TCGA-50-5930-01A-11D-1753-08	25.5
TCGA-55-8092-01A-11D-2238-08	12.31578947
TCGA-97-A4M7-01A-11D-A24P-08	6.263157895
TCGA-62-A46Y-01A-11D-A24D-08	0.894736842
TCGA-55-8614-01A-11D-2393-08	4.868421053
TCGA-17-Z002-01A-01W-0746-08	0.105263158
TCGA-J2-A4AD-01A-11D-A24D-08	6.157894737
TCGA-MP-A4TH-01A-31D-A25L-08	2.605263158
TCGA-78-7158-01A-11D-2036-08	5.921052632
TCGA-91-6829-01A-21D-1855-08	14.94736842
TCGA-55-8299-01A-11D-2284-08	0.315789474
TCGA-MP-A4TC-01A-11D-A24P-08	5.921052632
TCGA-78-7148-01A-11D-2036-08	5.026315789
TCGA-17-Z056-01A-01W-0747-08	6.973684211
TCGA-44-6777-01A-11D-1855-08	7.026315789
TCGA-55-6712-01A-11D-1855-08	2.078947368
TCGA-49-4512-01A-21D-1855-08	0.763157895
TCGA-MP-A4TE-01A-22D-A25L-08	3.421052632
TCGA-55-7911-01A-11D-2167-08	4.789473684
TCGA-50-5051-01A-21D-1855-08	2.236842105
TCGA-55-7570-01A-11D-2036-08	9.421052632
TCGA-86-8673-01A-11D-2393-08	10.63157895
TCGA-62-8402-01A-11D-2323-08	1.157894737
TCGA-55-6980-01A-11D-1945-08	0.236842105
TCGA-75-5122-01A-01D-1753-08	1.789473684
TCGA-17-Z011-01A-01W-0746-08	2.657894737
TCGA-49-4490-01A-21D-1855-08	0.526315789
TCGA-44-7667-01A-31D-2063-08	10.31578947
TCGA-86-7953-01A-11D-2184-08	1.105263158
TCGA-05-4250-01A-01D-1105-08	8.684210526
TCGA-17-Z020-01A-01W-0746-08	1.657894737
TCGA-97-A4M0-01A-11D-A24P-08	9.342105263
TCGA-75-5146-01A-01D-1625-08	4.421052632
TCGA-MN-A4N1-01A-11D-A24P-08	10.36842105
TCGA-71-8520-01A-11D-2393-08	2.026315789
TCGA-86-8280-01A-11D-2284-08	0.842105263
TCGA-55-A4DF-01A-11D-A24D-08	16.55263158
TCGA-55-6983-01A-11D-1945-08	1.894736842
TCGA-38-4625-01A-01D-1553-08	13.76315789
TCGA-64-1677-01A-01W-0928-08	4.105263158
TCGA-91-6848-01A-11D-1945-08	13.44736842

TCGA-44-2655-01A-01D-1553-08	2.763157895
TCGA-44-7670-01A-11D-2063-08	27.10526316
TCGA-17-Z010-01A-01W-0746-08	6.263157895
TCGA-50-8459-01A-11D-2323-08	1.789473684
TCGA-44-2659-01A-01D-0969-08	10.10526316
TCGA-49-4501-01A-01D-1265-08	0.973684211
TCGA-44-7659-01A-11D-2063-08	3.605263158
TCGA-78-7537-01A-11D-2063-08	3.710526316
TCGA-05-4430-01A-02D-1265-08	4.578947368
TCGA-69-7763-01A-11D-2167-08	1.5
TCGA-91-A4BD-01A-11D-A24D-08	0.605263158
TCGA-17-Z031-01A-01W-0746-08	60.02631579
TCGA-97-7546-01A-11D-2036-08	6.684210526
TCGA-17-Z004-01A-01W-0746-08	0.421052632
TCGA-93-A4JQ-01A-11D-A24P-08	0.973684211
TCGA-97-A4M2-01A-12D-A24P-08	0.078947368
TCGA-17-Z032-01A-01W-0746-08	2.342105263
TCGA-05-4397-01A-01D-1265-08	21.13157895
TCGA-05-4426-01A-01D-1265-08	1.236842105
TCGA-MP-A4TK-01A-11D-A24P-08	6.842105263
TCGA-64-5779-01A-01D-1625-08	8.5
TCGA-67-4679-01B-01D-1753-08	7
TCGA-86-8278-01A-11D-2284-08	1.447368421
TCGA-80-5611-01A-01D-1625-08	4.631578947
TCGA-86-7955-01A-11D-2184-08	7.421052632
TCGA-55-7903-01A-11D-2167-08	3.315789474
TCGA-78-7160-01A-11D-2036-08	0.684210526
TCGA-55-8087-01A-11D-2238-08	0.605263158
TCGA-05-4403-01A-01D-1265-08	3.394736842
TCGA-44-3918-01A-01D-A271-08	18.60526316
TCGA-49-AARO-01A-12D-A410-08	12.84210526
TCGA-50-8460-01A-11D-2323-08	0.631578947
TCGA-17-Z009-01A-01W-0746-08	0.184210526
TCGA-53-7624-01A-11D-2063-08	20.55263158
TCGA-91-6847-01A-11D-1945-08	1.394736842
TCGA-55-8301-01A-11D-2284-08	5.131578947
TCGA-44-6778-01A-11D-1855-08	8.657894737
TCGA-17-Z013-01A-01W-0746-08	1.473684211
TCGA-MP-A4T2-01A-11D-A24P-08	1.368421053
TCGA-86-7713-01A-11D-2063-08	4.052631579
TCGA-91-6835-01A-11D-1855-08	0.947368421
TCGA-55-6986-01A-11D-1945-08	0.394736842
TCGA-49-AARE-01A-11D-A410-08	34.15789474

TCGA-35-3615-01A-01D-1040-01	3.078947368
TCGA-86-A4JF-01A-11D-A24P-08	27.68421053
TCGA-05-5425-01A-02D-1625-08	11.42105263
TCGA-17-Z060-01A-01W-0747-08	6.894736842
TCGA-J2-8194-01A-11D-2238-08	3.710526316

Abbreviations: TMB, tumor mutation burden; LUAD, lung adenocarcinoma.