Supplementary

Table S1 RNA-seq QC files of micro-dissected LUAD tumor samples

Patient ID	Pathology subtype	Sample ID	Reads	Length	Total base (Mbases)	GC (%)	Q20 (%)	Q30 (%)
Patient-1	A	Sample-1	49752465	150	14,925.74	47.495	96.855	92.595
Patient-1	L	Sample-2	50771302	150	15,231.4	46.355	97.22	93.4
Patient-2	A	Sample-3	43921894	150	13,176.56	43.79	97.235	93.41
Patient-2	L	Sample-4	47953239	150	14,385.98	45.07	96.83	92.58
Patient-3	L	Sample-5	47528344	150	14,258.5	51.385	96.94	92.655
Patient-3	A	Sample-7	55983211	150	16,794.96	51.88	97.07	92.945
Patient-4	A	Sample-8	47523687	150	14,257.1	50.455	97.03	92.88
Patient-4	L	Sample-9	49002262	150	14,700.68	49.62	96.73	92.295
Patient-8	L	Sample-18	45848489	150	13,754.54	48.66	98.01	94.84
Patient-8	A	Sample-19	49679627	150	14,903.88	47.72	97.90	94.60
Patient-9	L	Sample-29	51816620	150	15,544.98	45.89	96.35	91.42
Patient-9	A	Sample-30	40922331	150	12,276.70	46.58	96.87	92.27
Patient-10	L	Sample-31	62936242	150	18,880.88	52.58	97.90	94.46
Patient-10	A	Sample-32	56744881	150	17,023.46	52.31	98.00	94.78
Patient-11	L	Sample-33	57603968	150	17,281.2	45.28	96.56	91.75
Patient-11	A	Sample-34	56029922	150	16,808.98	45.5	97.55	93.71
Patient-12	L	Sample-35	55155880	150	16,546.76	54.81	97.48	93.97
Patient-12	A	Sample-36	61039303	150	18,311.80	56.00	97.76	94.19
Patient-13	L	Sample-37	62780120	150	18,834.04	42.62	97.85	94.41
Patient-13	P	Sample-38	40263904	150	12,079.18	44.48	97.47	93.86
Patient-14	L	Sample-39	61066595	150	18,319.98	47.54	97.38	93.28
Patient-14	P	Sample-40	58994783	150	17,698.44	47.56	95.94	90.34
Patient-15	L	Sample-41	57257550	150	17,177.26	45.3	96.67	91.78
Patient-15	A	Sample-42	56206369	150	16,861.92	46.01	97.62	94.21
Patient-16	L	Sample-43	57072292	150	17,121.68	57.16	97.83	94.32
Patient-16	P	Sample-44	57501470	150	17,250.44	57.51	97.73	94.16
Patient-17	L	Sample-45	56634036	150	16,990.22	55.19	97.78	94.84
Patient-17	A	Sample-46	71545100	150	21,463.52	56.09	97.72	94.84
Patient-21	L	Sample-51	40863094	150	12,258.92	48.98	96.67	91.68
Patient-21	A	Sample-52	66474066	150	19,942.22	49.04	98.19	95.52
Patient-22	L	Sample-53	57835741	150	17,350.72	53.20	97.00	92.33
Patient-22	A	Sample-54	55088723	150	16,526.62	55.89	97.40	94.53
Patient-23	L	Sample-55	69087844	150	20,726.36	46.55	96.97	92.58
Patient-23	A	Sample-56	51693963	150	15,508.18	47.75	96.80	92.12
Patient-24	L	Sample-57	61497533	150	18,449.26	49.44	98.10	95.34
Patient-24	A	Sample-58	77679561	150	23,303.86	47.34	97.58	93.92
Patient-25	L	Sample-59	61736467	150	18,520.94	53.92	96.16	93.11
Patient-25	A	Sample-60	60198979	150	18,059.70	55.91	97.91	94.48
Patient-28	L	Sample-65	59316730	150	17,795.02	48.67	97.45	93.39
Patient-28	A	Sample-66	57369294	150	17,210.78	46.95	97.91	94.88
Patient-29	L	Sample-67	55111301	150	16,533.4	48.16	97.03	92.52
Patient-29	S	Sample-68	66639879	150	19,991.96	50.86	95.77	89.92

A, acinar; GC, percentage of G and C bases; L, lepidic; LUAD, lung adenocarcinoma; P, papillary; Q20, lower quality threshold, with a 1 in 100 probability of an incorrect base call (99% accuracy); Q30, high-quality benchmark, with a 1 in 1,000 probability of an incorrect base call (99.9% accuracy); QC, quality control; RNA-seq, RNA sequencing; S, solid.

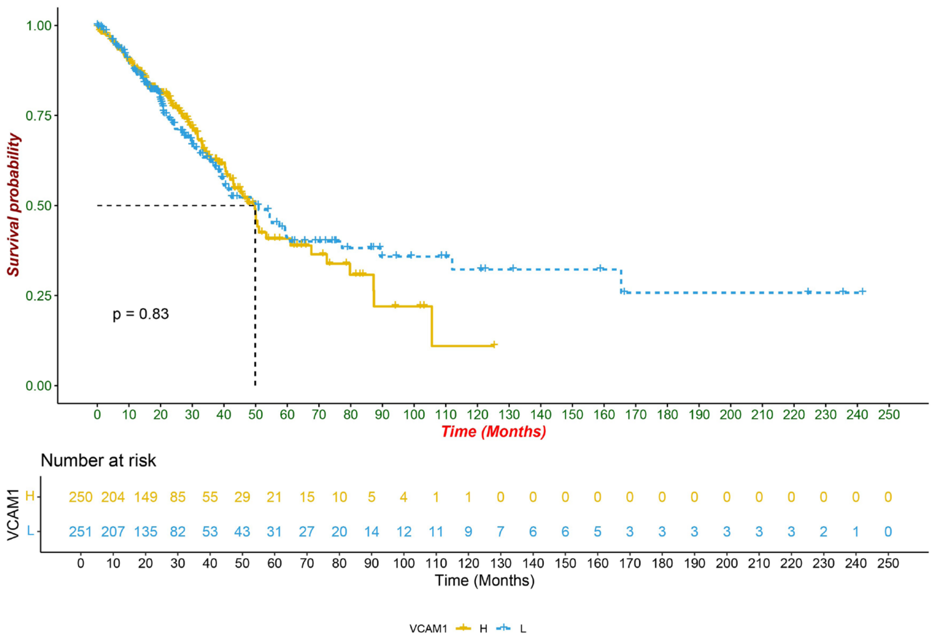

Figure S1 The K-M plot of 501 TCGA-LUAD patients showed no overall survival difference between high and low *VCAM1* expression groups. H, high expression; K-M, Kaplan-Meier; L, low expression; LUAD, lung adenocarcinoma; TCGA, The Cancer Genome Atlas.

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