Table SI. Bioinformatics tools applied to analyze the roles of adenosine deaminase RNA specific B1 in lung squamous cell carcinoma biological processes.

Author (year)	Database	URL link	Version no./release date	(Refs.)
Barrett T (2008)	GEO	www.ncbi.nlm.nih.gov/geoprofiles	NA/year	(14)
Tang Z (2017)	GE-mini	gemini.cancer-pku.cn	NA/year	(15)
Barretina J (2012)	CCLE	portals.broadinstitute.org/ccle/about	NA/year	(16)
Rhodes DR (2004)	Oncomine	www.oncomine.org/resource/login.html	Version 4.5/2015	(17)
Chandrashekar DS (2017)	UALCAN	ualcan.path.uab.edu/index.html	NA/year	(18)
Tang Z (2017)	GEPIA	gepia.cancer-pku.cn	GEPIA2/2019	(19)
Diez-Villanueva A (2015)	Wanderer	maplab.imppc.org/wanderer	NA/year	(20)
Xiong Y (2017)	DiseaseMeth	bio-bigdata.hrbmu.edu.cn/diseasemeth	NA/year	(21)
Modhukur V (2018)	MethSurv	biit.cs.ut.ee/methsurv	NA/year	(22)
Gao J (2013)	cBioPortal	www.cbioportal.org	NA/year	(24)
Szklarczyk D (2017)	STRING	string-db.org/cgi/input.pl	Version 11.0/2019	(25)
Reimand J (2019)	Cytoscape	cytoscape.org	NA/year	(26)
Kanehisa M (2017)	KEGG	www.kegg.jp	Version 93.0/2020	(27)
Wang J (2017)	WebGestalt	www.webgestalt.org	WebGestalt 2019/2019	(28)
Huang da W (2009)	DAVID	david.ncifcrf.gov	Version 6.8/2019	(29)

GEO, Gene Expression Omnibus; GE-mini, Genome Mining; CCLE, Cancer Cell Line Encyclopedia; UALCAN, University of Alabama Cancer Database; GEPIA, Gene Expression Profiling Interactive Analysis; STRING, Search Tool for the Retrieval of Interacting Genes/Proteins; KEGG, Kyoto Encyclopedia of Genes and Genomes; WebGestalt, Web-based Gene Set Analysis Toolkit; DAVID, Database for Annotation, Visualization and Integrated Discovery. NA/year, No updated version.

Table SII. Methylation values of CpG islands in adenosine deaminase RNA specific B1.

Probe	Chr	cg-start	cg-end	Percentage	Tum-mean	Tum-SD	Wilcox-stat	P-value
cg24063645	chr21	46553953	46553954	0.72	0.983350	0.033901	14,239	$3.60\text{x}10^{-19}$
cg11987819	chr21	46495389	46495390	0.70	0.028680	0.052133	1,494	$4.79\text{x}10^{-18}$
cg14194835	chr21	46640872	46640873	0.62	0.971891	0.059063	13,320	$1.61\text{x}10^{-14}$
cg05516004	chr21	46496180	46496181	0.42	0.872400	0.067490	2,370	$9.47\text{x}10^{-14}$
cg22635096	chr21	46550644	46550645	0.52	0.349856	0.152502	13,057	$2.57\text{x}10^{-13}$
cg16358576	chr21	46644306	46644307	0.60	0.796056	0.150458	13,007	$4.28\text{x}10^{-13}$
cg23662138	chr21	46495607	46495608	0.44	0.323296	0.192591	2,517	$4.32\text{x}10^{-13}$
cg08222185	chr21	46494823	46494824	0.72	0.027146	0.006026	2,610	$1.11\text{x}10^{-12}$
cg01603980	chr21	46521050	46521051	0.66	0.783528	0.067256	12,712	$7.99\text{x}10^{-12}$
cg19810954	chr21	46496510	46496511	0.46	0.742912	0.129804	2,972	$3.68\text{x}10^{-11}$
cg23919038	chr21	46554352	46554353	0.68	0.905925	0.053238	12,232	$6.59\text{x}10^{-10}$
cg15885953	chr21	46520883	46520884	0.70	0.962073	0.078048	11,663	$7.09\text{x}10^{-8}$
cg18501409	chr21	46553607	46553608	0.52	0.891189	0.085023	10,964	$9.70\text{x}10^{-6}$
cg12703219	chr21	46556392	46556393	0.56	0.823143	0.081602	4,602	$1.27\text{x}10^{-5}$
cg25894939	chr21	46521281	46521282	0.66	0.912348	0.094557	10,511	0.000146
cg18570853	chr21	46557241	46557242	0.62	0.324062	0.106233	9,889	0.003297
cg05575217	chr21	46518030	46518031	0.62	0.771849	0.152190	5,833	0.007729
cg21217129	chr21	46554127	46554128	0.66	0.831651	0.061263	9,665	0.008560
cg14526825	chr21	46646076	46646077	0.48	0.590036	0.171898	8,517	0.296906

Chr, chromosome containing the CpG; Tum, tumor; Wilcox-stat, if there are enough samples, Wilcoxon Rank Sum Test W parameter (nonparametric comparison of normals vs tumors).

Table SIII. Adenosine deaminase RNA specific B1-associated co-differentially expressed genes in lung squamous cell carcinoma.

Gene	Cytoband	Log ratio	P-value	q-value	Expression tendency
MIA3	1q41	0.21	2.75×10^{-4}	0.398	Upregulated
CSNK1D	17q25.3	0.22	4.40×10^{-4}	0.398	Upregulated
SUGP1	19p13.11	0.16	1.57×10^{-3}	0.503	Upregulated
TRAPPC12	2p25.3	0.28	2.11×10^{-3}	0.504	Upregulated
FAM53C	5q31.2	0.29	2.74×10^{-3}	0.515	Upregulated
BIRC6	2p22.3	0.24	3.14×10^{-3}	0.534	Upregulated
NELFA	4p16.3	0.29	4.77×10^{-3}	0.592	Upregulated
FLYWCH2	16p13.3	0.27	4.91×10^{-3}	0.592	Upregulated
ANAPC4	4p15.2	0.24	5.29×10^{-3}	0.605	Upregulated
SNX27	1q21.3	0.25	7.00×10^{-3}	0.605	Upregulated
BAZ2A	12q13.3	0.26	7.09×10^{-3}	0.605	Upregulated
TM2D3	15q26.3	-0.27	7.27×10^{-3}	0.605	Downregulated
PRUNE1	1q21.3	0.18	9.19×10^{-3}	0.605	Upregulated
LUC7L2	7q34	0.29	9.39×10^{-3}	0.605	Upregulated
MAP2K4	17p12	-0.16	9.62×10^{-3}	0.605	Downregulated
ATG3	3q13.2	0.29	9.64×10^{-3}	0.605	Upregulated
PDIA3P1	1q21.1	-0.28	9.97×10^{-3}	0.608	Downregulated
AP1B1	22q12.2	0.24	9.97×10^{-3}	0.608	Upregulated
CTNNB1	3p22.1	-0.28	9.99×10^{-3}	0.608	Downregulated
MAU2	19p13.11	0.26	0.0106	0.614	Upregulated
BNIP2	15q22.2	-0.28	0.0117	0.619	Downregulated
MSL1	17q21.1	0.24	0.0121	0.621	Upregulated
ZC3HAV1	7q34	0.27	0.0121	0.621	Upregulated
RBM39	20q11.22	0.26	0.0124	0.621	Upregulated
ZNF669	1q44	0.25	0.0125	0.621	Upregulated
TASOR	3p14.3	0.23	0.0130	0.624	Upregulated
RBM33	7q36.3	0.22	0.0138	0.624	Upregulated
CTBP1	4p16.3	0.22	0.0144	0.624	Upregulated
SLC5A6	2p23.3	0.28	0.0146	0.624	Upregulated
PELO	5q11.2	-0.27	0.0146	0.624	Downregulated
MICU2	13q12.11	-0.29	0.0149	0.624	Downregulated
EXOC7	17q25.1	0.28	0.0154	0.624	Upregulated
DUSP12	1q23.3	-0.26	0.0155	0.624	Downregulated
ELL	19p13.11	0.22	0.0155	0.624	Upregulated
METTL8	2q31.1	-0.30	0.0159	0.624	Downregulated
COPS3	17p11.2	-0.30	0.0159	0.624	Downregulated
SCO1	17p13.1	-0.23	0.0161	0.624	Downregulated
ACTR8	3p21.1	0.23	0.0168	0.624	Upregulated
MAEA	4p16.3	0.18	0.0182	0.636	Upregulated
ATP6V1A	3q13.31	0.28	0.0183	0.636	Upregulated
DHX33	17p13.2	0.27	0.0187	0.639	Upregulated
DCP1A	3p21.1	0.22	0.0188	0.639	Upregulated
EIF3J	15q21.1	-0.27	0.0193	0.648	Downregulated
SETD2	3p21.31	0.28	0.0193	0.648	Upregulated
RBM14	11q13.2	0.20	0.0203	0.649	Upregulated
INTS3	1q21.3	0.26	0.0209	0.649	Upregulated
LRRC57	15q15.2	-0.24	0.0209	0.649	Downregulated
SF3A1	22q12.2	0.14	0.0214	0.649	Upregulated
TOR1AIP2	1q25.2	0.20	0.0215	0.649	Upregulated
ROCK2	2p25.1	0.28	0.0216	0.649	Upregulated
ATP13A1	19p13.11	0.21	0.0217	0.649	Upregulated
RHBDD2	7q11.23	-0.24	0.0224	0.649	Downregulated
MBD4	3q21.3	0.29	0.0229	0.649	Upregulated
PPFIBP1	12p11.23-p11.22	-0.28	0.0230	0.649	Downregulated
ASXL2	2p23.3	0.28	0.0230	0.649	Upregulated
NRBF2	10q21.3	-0.26	0.0231	0.649	Downregulated

Table SIII. Continued.

Gene	Cytoband	Log ratio	P-value	q-value	Expression tendency
WDTC1	1p36.11	0.25	0.0233	0.649	Upregulated
TFCP2	12q13.12-q13.13	0.20	0.0235	0.649	Upregulated
SUOX	12q13.2	0.29	0.0236	0.649	Upregulated
ZNF621	3p22.1	0.27	0.0240	0.649	Upregulated
RYBP	3p13	0.26	0.0244	0.649	Upregulated
LARP4B	10p15.3	0.29	0.0253	0.649	Upregulated
NR2C2	3p25.1	0.24	0.0254	0.649	Upregulated
DAZAP1	19p13.3	0.28	0.0258	0.649	Upregulated
TP53BP1	15q15.3	-0.21	0.0259	0.649	Downregulated
RPUSD2	15q15.1	-0.28	0.0261	0.649	Downregulated
PSPC1	13q12.11	0.23	0.0266	0.649	Upregulated
ZNF2	2q11.1	0.28	0.0274	0.649	Upregulated
S100PBP	1p35.1	0.29	0.0277	0.649	Upregulated
SLC15A4	12q24.33	-0.28	0.0278	0.649	Downregulated
PTBP1	19p13.3	0.21	0.0280	0.649	Upregulated
WDCP	2p23.3	0.27	0.0286	0.651	Upregulated
SOS1	2p22.1	0.22	0.0286	0.651	Upregulated
UBE3B	12q24.11	0.25	0.0287	0.651	Upregulated
ZBTB14	18p11.31	0.19	0.0291	0.651	Upregulated
GZF1	20p11.21	0.25	0.0293	0.651	Upregulated
ZCCHC17	1p35.2	-0.28	0.0293	0.651	Downregulated
NIPAL3	1p36.11	0.25	0.0301	0.653	Upregulated
PCIF1	20q13.12	0.29	0.0302	0.654	Upregulated
HMBOX1	8p21.1-p12	-0.28	0.0305	0.654	Downregulated
ATXN2	12q24.12	0.23	0.0306	0.654	Upregulated
HNRNPU	1q44	0.26	0.0310	0.654	Upregulated
ADD1	4p16.3	0.26	0.0311	0.654	Upregulated
BRMS1	11q13.2	-0.23	0.0316	0.654	Downregulated
NEPRO	3q13.2	0.19	0.0318	0.654	Upregulated
GIGYF2	2q37.1	0.29	0.0321	0.655	Upregulated
C2CD5	12p12.1	0.26	0.0325	0.655	Upregulated
TIGAR	12p13.32	-0.18	0.0325	0.655	Downregulated
PCNX2	1q42.2	0.26	0.0325	0.655	Upregulated
PHF12	17q11.2	0.26	0.0328	0.655	Upregulated
TRIP12	2q36.3	0.25	0.0329	0.655	Upregulated
TXNRD2	22q11.21	0.26	0.0330	0.656	Upregulated
PPP2CB	8p12	-0.29	0.0340	0.659	Downregulated
EIF5A	17p13.1	-0.25	0.0344	0.659	Downregulated
BRD2	6p21.32	0.29	0.0344	0.659	Upregulated
GRK6	5q35.3	0.23	0.0346	0.659	Upregulated
CSPP1	8q13.1-q13.2	0.29	0.0346	0.659	Upregulated
SRGAP1	12q14.2	0.29	0.0349	0.659	Upregulated
SYNRG	17q12	0.29	0.0353	0.659	Upregulated
YBEY	21q22.3	-0.30	0.0355	0.659	Downregulated
TAGLN2	1q23.2	-0.24	0.0362	0.659	Downregulated
DDX47	12p13.1	-0.26	0.0366	0.659	Downregulated
PGRMC2	4q28.2	0.17	0.0366	0.659	Upregulated
GTDC1	2q22.3	-0.28	0.0366	0.659	Downregulated
BRPF1	3p25.3	0.28	0.0369	0.662	Upregulated
COQ7	16p12.3	0.23	0.0377	0.664	Upregulated
RPF2	6q21	-0.30	0.0378	0.664	Downregulated
OSTC	4q25	-0.27	0.0382	0.664	Downregulated
PSMD9	12q24.31	-0.23	0.0382	0.664	Downregulated
ING1	13q34	-0.24	0.0390	0.669	Downregulated
AQR	15q14	-0.18	0.0391	0.669	Downregulated
CEP104	1p36.32	0.23	0.0392	0.669	Upregulated
HDDC2	6q22.31	-0.29	0.0392	0.669	Downregulated

Table SIII. Continued.

Gene	Cytoband	Log ratio	P-value	q-value	Expression tendency
ZBTB21	21q22.3	0.27	0.0394	0.669	Upregulated
ZNF302	19q13.11	0.26	0.0395	0.669	Upregulated
RSPH3	6q25.3	-0.28	0.0395	0.669	Downregulated
ANP32E	1q21.2	0.27	0.0398	0.669	Upregulated
PHACTR4	1p35.3	0.27	0.0399	0.669	Upregulated
HECTD4	12q24.13	0.28	0.0402	0.669	Upregulated
ITPRID2	2q31.3	-0.26	0.0402	0.669	Downregulated
PDS5A	4p14	0.23	0.0412	0.672	Upregulated
ACADVL	17p13.1	-0.20	0.0413	0.672	Downregulated
PPP3CB	10q22.2	-0.21	0.0415	0.672	Downregulated
RPL24	3q12.3	-0.28	0.0420	0.672	Downregulated
AKIRIN2	6q15	-0.27	0.0420	0.672	Downregulated
HEXA	15q23	-0.17	0.0421	0.672	Downregulated
DHTKD1	10p14	0.29	0.0423	0.672	Upregulated
FBXL14	12p13.33	0.24	0.0430	0.672	Upregulated
PNPLA6	19p13.2	0.29	0.0430	0.672	Upregulated
KANSL3	2q11.2	0.23	0.0431	0.672	Upregulated
JMJD4	1q42.13	0.25	0.0433	0.672	Upregulated
MED26	19p13.11	0.24	0.0438	0.672	Upregulated
YIPF5	5q31.3	-0.20	0.0440	0.672	Downregulated
DAD1	14q11.2	-0.26	0.0448	0.676	Downregulated
THOC6	16p13.3	-0.27	0.0448	0.676	Downregulated
ATP5F1E	20q13.32	-0.29	0.0450	0.676	Downregulated
SAFB	19p13.3	0.22	0.0457	0.680	Upregulated
UBAC2	13q32.3	-0.27	0.0461	0.680	Downregulated
TMEM129	4p16.3	0.28	0.0465	0.680	Upregulated
CAPZA1	1p13.2	-0.28	0.0465	0.680	Downregulated
FEM1C	5q22.3	-0.23	0.0467	0.680	Downregulated
PFN1	17p13.2	-0.18	0.0471	0.680	Downregulated
SGPL1	10q22.1	-0.28	0.0471	0.680	Downregulated
SIAH1	16q12.1	-0.29	0.0472	0.680	Downregulated
REEP3	10q21.3	-0.28	0.0475	0.680	Downregulated
GORASP1	3p22.2	0.20	0.0477	0.681	Upregulated
TMEM258	11q12.2	-0.25	0.0478	0.682	Downregulated
SDF2	17q11.2	-0.27	0.0481	0.682	Downregulated
ERCC4	16p13.12	0.28	0.0483	0.682	Upregulated
ODR4	1q31.1	-0.23	0.0485	0.682	Downregulated
HNRNPM	19p13.2	0.14	0.0486	0.682	Upregulated
MECR	1p35.3	0.21	0.0489	0.682	Upregulated
TBCD	17q25.3	0.19	0.0490	0.682	Upregulated
ZBTB24	6q21	0.20	0.0490	0.682	Upregulated
SSR2	1q22	-0.30	0.0491	0.682	Downregulated
VPS50	7q21.2-q21.3	0.26	0.0494	0.682	Upregulated
C19ORF53	19p13.13	-0.26	0.0496	0.682	Downregulated
AMFR	16q13	-0.27	0.0498	0.682	Downregulated

Table SIV. Kyoto Encyclopedia of Genes and Genomes pathway enrichment of adenosine deaminase RNA specific B1-associated co-differentially expressed genes in lung squamous cell carcinoma.

Term	Count	P-value	Genes
hsa04120:Ubiquitin mediated proteolysis	5	0.014	UBE3B, ANAPC4, BIRC6, SIAH1, TRIP12
hsa04310:Wnt signaling pathway	5	0.014	CTBP1, ROCK2, PPP3CB, SIAH1, CTNNB1
hsa03040:Spliceosome	4	0.062	HNRNPM, AQR, SF3A1, HNRNPU