

**Table S1.** Information of NCCLUAD patients

Sample ID	Histology	Tumor grade*	Gender	Age	Smoking	Pack-year	EGFR Mutation	KRAS Mutation	RNA-seq
NCCLUAD-002	Lung adenocarcinoma	PD	M	62	Ever	63	Not detected	Not detected	
NCCLUAD-003	Lung adenocarcinoma	PD	M	59	Ever	45	Not detected	Not detected	
NCCLUAD-004	Lung adenocarcinoma	PD	F	53	Never		Not detected	Not detected	
NCCLUAD-005	Lung adenocarcinoma	MD	F	60	Never		Not detected	Not detected	
NCCLUAD-006	Lung adenocarcinoma	PD	F	52	Never		Not detected	Not detected	
NCCLUAD-007	Lung adenocarcinoma	PD	F	44	Never		Not detected	Not detected	KIF5-RET
NCCLUAD-008	Lung adenocarcinoma	-	M	59	Ever	80	Not detected	Not detected	
NCCLUAD-009	Lung adenocarcinoma	PD	M	54	Ever	6	Not detected	Not detected	KIF5-RET
NCCLUAD-010	Lung adenocarcinoma	MD	F	53	Never		Not detected	Not detected	CD63-BCAR4
NCCLUAD-011	Lung adenocarcinoma	PD	M	51	Ever	1	Not detected	Not detected	
NCCLUAD-012	Lung adenocarcinoma	PD	F	77	Never		Not detected	Not detected	
NCCLUAD-014	Lung adenocarcinoma	-	M	40	Ever	4	Not detected	Not detected	EML4-ALK
NCCLUAD-018	Lung adenocarcinoma	PD	F	63	Never		Not detected	Not detected	EML4-ALK
NCCLUAD-019	Lung adenocarcinoma	MD	M	34	Never		Not detected	Not detected	
NCCLUAD-020	Lung adenocarcinoma	MD	M	69	Never		Not detected	Not detected	EML4-ALK
NCCLUAD-023	Lung adenocarcinoma	MD	F	54	Ever	10	Not detected	Not detected	
NCCLUAD-024	Lung adenocarcinoma	PD	M	43	Never		Not detected	Not detected	
NCCLUAD-030	Lung adenocarcinoma	PD	M	37	Ever	18	Not detected	Not detected	
NCCLUAD-031	Lung adenocarcinoma	PD	M	51	Ever	6.7	Not detected	Not detected	
NCCLUAD-032	Lung adenocarcinoma	PD	M	52	Ever	2	Not detected	Not detected	
NCCLUAD-033	Lung adenocarcinoma	PD	M	49	Ever	10	Not detected	Not detected	EML4-ALK
NCCLUAD-034	Lung adenocarcinoma	PD	M	53	Ever	0.25	Not detected	Not detected	
NCCLUAD-038	Lung adenocarcinoma	MD	F	38	Never		Not detected	Not detected	ROS1-SLC43A2
NCCLUAD-043	Lung adenocarcinoma	MD	F	53	Never		Not detected	Not detected	
NCCLUAD-045	Lung adenocarcinoma	WD	F	54	Never		Not detected	Not detected	KIF5B-REB
NCCLUAD-046	Lung adenocarcinoma	MD	F	55	Never		Not detected	Not detected	EML4-ALK
NCCLUAD-047	Lung adenocarcinoma	MD	F	55	Never		Not detected	Not detected	
NCCLUAD-049	Lung adenocarcinoma	MD	F	57	Never		Not detected	Not detected	
NCCLUAD-050	Lung adenocarcinoma	-	F	47	Never		Not detected	Not detected	

\* PD, poorly differentiated; MD, moderately differentiated; WD, well differentiated

**Table S2.** Differentially expressed genes between empty vector and CD63-BCAR4 identified by microarray

Category	Gene Symbol	Fold change			Gene Name
		CD63-BCAR4 Stable cell-1	CD63-BCAR4 Stable cell-2	BCAR4 Stable cell	
Cell migration	MMP1	8.722	7.810	0.661	matrix metalloproteinase 1
	LINC00473	7.024	3.935	2.282	long intergenic non-protein coding RNA 473
Cell differentiation	DCLK1	5.833	7.099	1.643	doublecortin-like kinase 1
Extracellular matrix	COL13A1	5.693	7.137	1.450	collagen, type XIII, alpha 1
Cell differentiation	DMBT1	5.634	7.108	1.606	deleted in malignant brain tumors 1
Cell differentiation, Neurogenesis	ACOX2	5.002	5.973	0.901	acyl-CoA oxidase 2, branched chain
	CACNG7	4.616	6.732	0.937	calcium channel, voltage-dependent, gamma subunit 7
	ETV4	4.588	6.487	0.793	ets variant 4
Extracellular matrix	SH3TC1	4.516	3.610	0.806	SH3 domain and tetratricopeptide repeats 1
	TGM2	3.975	5.945	1.527	transglutaminase 2
Inflammatory response	FAM196B	3.968	2.767	1.370	family with sequence similarity 196, member B
	CHST1	3.832	6.199	0.746	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1
Cell Proliferation	CyclinD1	3.822	4.067	1.028	cyclin D1
Apoptotic process, Cell differentiation, Neurogenesis	SPRY4	3.705	4.839	1.156	sprouty homolog 4 (Drosophila)
	PCSK9	3.654	3.277	13.917	proprotein convertase subtilisin/kexin type 9
Cell differentiation, Neurogenesis	ETV5	3.514	5.426	1.669	ets variant 5
Angiogenesis	ANGPTL4	3.469	6.646	0.467	angiopoietin-like 4
Cell Proliferation	SCD	3.421	4.286	5.813	stearoyl-CoA desaturase (delta-9-desaturase)
	DMKN	3.184	4.106	0.853	dermokine
	RORA	3.177	3.948	0.948	RAR-related orphan receptor A
	GALNT14	3.168	3.329	0.639	polypeptide N-acetylgalactosaminyltransferase 14
	RNA5-8S5	3.132	2.085	0.816	RNA, 5.8S ribosomal 5
Immune response, Secretion	MPP4	3.131	2.962	0.924	membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4)
	MPP4	3.129	3.108	1.209	membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4)
	TLR4	3.129	3.461	1.213	toll-like receptor 4
	DMKN	3.110	3.539	0.767	dermokine
	MEG3	2.982	3.224	1.549	maternally expressed 3 (non-protein coding)
Secretion	IL17RD	2.979	4.362	2.145	interleukin 17 receptor D
Cell migration	CA9	2.954	8.423	0.813	carbonic anhydrase IX
	DOCK4	2.941	3.805	0.742	dedicator of cytokinesis 4
	KCNMA1	2.917	3.281	1.259	potassium channel, calcium activated large conductance subfamily M alpha, member
	SEMA3A	2.915	3.098	1.235	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphori
	GOLGA6C	2.811	2.317	1.977	golgin A6 family, member C
	SYNE3	2.795	2.814	1.484	spectrin repeat containing, nuclear envelope family member 3
	TMEM233	2.762	3.304	0.598	transmembrane protein 233
	SPRED3	2.762	3.756	1.153	sprouty-related, EVH1 domain containing 3
	WNK2	2.752	3.502	1.408	WNK lysine deficient protein kinase 2
	FLJ41170	2.735	2.922	1.808	uncharacterized LOC440200

Cell Proliferation	HMGA2	2.709	2.550	1.069	high mobility group AT-hook 2
	NIM1K	2.700	6.135	1.219	NIM1 serine/threonine protein kinase
	MLPH	2.686	4.646	0.615	melanophilin
	AGPAT9	2.674	3.216	1.117	1-acylglycerol-3-phosphate O-acyltransferase 9
	NRG2	2.655	4.122	0.855	neuregulin 2
Cell differentiation, Neurogenesis	CDH4	2.641	2.864	0.982	cadherin 4, type 1, R-cadherin (retinal)
	TUBBP5	2.639	4.991	1.024	tubulin, beta pseudogene 5
	STXBP5L	2.598	2.679	2.051	syntaxin binding protein 5-like
	LRP3	2.537	3.018	1.453	low density lipoprotein receptor-related protein 3
	IRX4	2.513	2.795	1.651	iroquois homeobox 4
Cell differentiation, Neurogenesis	C2orf82	2.513	2.103	1.995	chromosome 2 open reading frame 82
	DPYSL5	2.512	2.755	1.046	dihydropyrimidinase-like 5
	LYPD1	2.494	2.870	1.751	LY6/PLAUR domain containing 1
Cell Proliferation	STC1	2.485	4.824	1.029	stanniocalcin 1
Immune response	LINC00637	2.466	2.579	2.171	long intergenic non-protein coding RNA 637
	APLN	2.463	4.369	1.117	apelin
	LOC101929056	2.457	2.450	1.843	uncharacterized LOC101929056
Cell migration	MEG8	2.447	3.255	1.438	maternally expressed 8 (non-protein coding)
	CAMK2N1	2.428	3.450	1.080	calcium/calmodulin-dependent protein kinase II inhibitor 1
	LAMA5	2.424	3.755	1.365	laminin, alpha 5
	CERS1	2.421	2.852	1.204	ceramide synthase 1
Cell cycle	FLJ32255	2.366	2.747	1.320	uncharacterized LOC643977
	SPRY1	2.316	5.727	0.653	sprouty homolog 1, antagonist of FGF signaling (Drosophila)
	SLC1A1	2.289	3.896	1.103	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system
Cell differentiation, Neurogenesis	DPYSL5	2.286	2.942	1.004	dihydropyrimidinase-like 5
	LOC284080	2.280	2.525	1.323	uncharacterized LOC284080
Cell differentiation	DMKN	2.276	2.712	0.868	dermokine
Cell Proliferation	DUSP6	2.266	2.786	1.089	dual specificity phosphatase 6
Cell Proliferation	BCL2	2.263	2.158	1.301	B-cell CLL/lymphoma 2
	NT5E	2.262	2.801	1.421	5'-nucleotidase, ecto (CD73)
	STEAP1	2.256	3.632	0.735	six transmembrane epithelial antigen of the prostate 1
	LINC01433	2.252	2.944	1.489	long intergenic non-protein coding RNA 1433
	DPF3	2.248	2.404	1.043	D4, zinc and double PHD fingers, family 3
Cell cycle	RRAGD	2.223	3.572	0.929	Ras-related GTP binding D
	BTBD11	2.223	3.522	0.726	BTB (POZ) domain containing 11
Angiogenesis, Cell differentiation	GPR4	2.193	3.423	1.136	G protein-coupled receptor 4
Cell differentiation, Neurogenesis	SLC12A7	2.182	2.346	1.181	solute carrier family 12 (potassium/chloride transporter), member 7
	LDLR	2.165	2.168	2.962	low density lipoprotein receptor
Extracellular matrix	TGM2	2.159	2.107	1.121	transglutaminase 2
	DUSP4	2.151	2.198	1.019	dual specificity phosphatase 4
	CELF2	2.149	2.351	0.265	CUGBP, Elav-like family member 2
Immune response, Secretion	PGF	2.146	3.154	0.979	placental growth factor
	TLR4	2.145	2.357	0.823	toll-like receptor 4
Cell cycle, Cell death, Neurogenesis	BRSK2	2.129	2.655	1.006	BR serine/threonine kinase 2

	KANK3	2.126	2.190	1.012	KN motif and ankyrin repeat domains 3
Cell migration	EPHB3	2.123	2.429	0.645	EPH receptor B3
	NALCN	2.109	2.372	1.328	sodium leak channel, non selective
	ST3GAL6	2.096	2.975	1.301	ST3 beta-galactoside alpha-2,3-sialyltransferase 6
	ANO7	2.086	2.211	2.191	anoctamin 7
	THSD4	2.074	2.322	1.255	thrombospondin, type I, domain containing 4
	EPHA1-AS1	2.074	3.433	0.791	EPHA1 antisense RNA 1
Apoptotic process, Immune response	LY96	2.067	2.328	0.757	lymphocyte antigen 96
Cell differentiation, Neurogenesis	NDRG1	2.059	4.576	0.958	N-myc downstream regulated 1
Cell Proliferation	HMGA2	2.058	2.522	0.694	high mobility group AT-hook 2
	ARHGEF4	2.047	3.437	0.968	Rho guanine nucleotide exchange factor (GEF) 4
Cell Proliferation, Cell migration, Apoptotic process	DDIT4	2.044	4.488	1.357	DNA-damage-inducible transcript 4
	LINC01291	2.042	2.981	0.807	long intergenic non-protein coding RNA 1291
	SETD3	2.041	2.043	1.495	SET domain containing 3
	PRRT1	2.037	2.139	1.700	proline-rich transmembrane protein 1
	TMEM74B	2.031	3.929	0.781	transmembrane protein 74B
	ITGB8	2.023	2.619	1.560	integrin, beta 8
	SFRP1	2.020	3.473	1.631	secreted frizzled-related protein 1
Cell differentiation	SULF2	2.014	2.460	0.685	sulfatase 2
Cell cycle	RASSF2	2.012	3.251	0.915	Ras association (RalGDS/AF-6) domain family member 2
Cell cycle	INHBA	0.500	0.493	0.821	inhibin, beta A
	ARSG	0.499	0.478	0.578	arylsulfatase G
	LOC392364	0.493	0.320	0.373	nuclear pore associated protein 1 pseudogene
	PRDM15	0.492	0.396	0.429	PR domain containing 15
	ARMCX4	0.490	0.315	0.234	armadillo repeat containing, X-linked 4
	SAMD11	0.484	0.487	1.013	sterile alpha motif domain containing 11
	LINC01124	0.471			long intergenic non-protein coding RNA 1124
Apoptotic process	TRIM39	0.471	0.464	0.473	tripartite motif containing 39
	SEPP1	0.470	0.304	0.226	selenoprotein P, plasma, 1
	DIO2	0.464	0.296	1.080	deiodinase, iodothyronine, type II
	PLEKHA7	0.461	0.430	0.827	pleckstrin homology domain containing, family A member 7
Apoptotic process	PRUNE2	0.460	0.477	1.691	prune homolog 2 (Drosophila)
	HCK	0.459	0.237	0.554	HCK proto-oncogene, Src family tyrosine kinase
	TBC1D22A	0.459	0.288	0.385	TBC1 domain family, member 22A
	KRT16P2	0.453	0.348	0.640	keratin 16 pseudogene 2
	C10orf120	0.447	0.497	0.362	chromosome 10 open reading frame 120
	ZCCHC6	0.443	0.317	0.526	zinc finger, CCHC domain containing 6
	GGTLC2	0.441	0.492	0.482	gamma-glutamyltransferase light chain 2
Cell migration	GREM1	0.441	0.434	0.687	gremlin 1, DAN family BMP antagonist
Cell differentiation	SOX3	0.439	0.492	0.299	SRY (sex determining region Y)-box 3
	LOC284950	0.436	0.298	1.146	uncharacterized LOC284950
	STEAP4	0.427	0.162	0.202	STEAP family member 4
	PTGFR	0.424	0.486	0.982	prostaglandin F receptor (FP)
	ZNF236	0.419	0.471	0.566	zinc finger protein 236

	GGTLC1	0.418	0.465	0.417	gamma-glutamyltransferase light chain 1
	ITFG3	0.415	0.405	0.379	integrin alpha FG-GAP repeat containing 3
Extracellular matrix	RARRES2	0.409	0.444	1.087	retinoic acid receptor responder (tazarotene induced) 2
Cell Proliferation	PDZK1	0.401	0.437	0.942	PDZ domain containing 1
Cell Proliferation	PRDM1	0.399	0.463	1.151	PR domain containing 1, with ZNF domain
Extracellular matrix	ADAMTS1	0.399	0.370	0.797	ADAM metalloproteinase with thrombospondin type 1 motif, 1
Extracellular matrix	EDIL3	0.391	0.400	0.846	EGF-like repeats and discoidin I-like domains 3
	LOC400743	0.389	0.498	0.266	uncharacterized LOC400743
Cell cycle	ZBTB49	0.389	0.292	0.372	zinc finger and BTB domain containing 49
	PTGFR	0.384	0.481	0.936	prostaglandin F receptor (FP)
	POU6F1	0.382	0.489	0.523	POU class 6 homeobox 1
Extracellular matrix	AEBP1	0.381	0.438	0.741	AE binding protein 1
Cell Proliferation	NR4A3	0.378	0.352	0.962	nuclear receptor subfamily 4, group A, member 3
Cell migration	GREM1	0.376	0.386	0.757	gremlin 1, DAN family BMP antagonist
Cell migration	AMOT	0.372	0.461	0.234	angiomin
Cell migration	CYP1B1	0.370	0.471	1.034	cytochrome P450, family 1, subfamily B, polypeptide 1
	Inc-STOM-2	0.367	0.328	0.255	Inc-STOM-2:2
	TMEM140	0.362	0.484	0.459	transmembrane protein 140
	NOSTRIN	0.361	0.447	0.770	nitric oxide synthase trafficking
Angiogenesis	ACKR3	0.360	0.473	0.782	atypical chemokine receptor 3
Cell Proliferation	ATOH8	0.359	0.400	1.052	atonal homolog 8 (Drosophila)
Inflammatory response	NCR3	0.356	0.452	0.476	natural cytotoxicity triggering receptor 3
Cell cycle	FGF9	0.353	0.295	0.267	fibroblast growth factor 9
	PROC	0.352	0.442	0.423	protein C (inactivator of coagulation factors Va and VIIIa)
	Inc-CLIC6-1	0.350	0.420	0.398	Inc-CLIC6-1:1
Cell migration	CCL7	0.349	0.386	0.262	chemokine (C-C motif) ligand 7
	KRT42P	0.346	0.329	0.585	keratin 42 pseudogene
Aging	KRT14	0.343	0.358	0.604	keratin 14, type I
	FAXC	0.342	0.449	0.377	failed axon connections homolog (Drosophila)
	MSL3	0.340	0.377	0.500	male-specific lethal 3 homolog (Drosophila)
	LOC400553	0.339		0.135	uncharacterized LOC400553
Cell differentiation, Cell death	KRT17	0.332	0.365	0.647	keratin 17, type I
	C7orf69	0.331	0.268	0.842	chromosome 7 open reading frame 69
Cell differentiation	TRPC4	0.329	0.370	1.011	transient receptor potential cation channel, subfamily C, member 4
Secretion	CPLX2	0.327	0.458	0.389	complexin 2
	NIPAL4	0.327	0.466	0.246	NIPA-like domain containing 4
	CRYM	0.326	0.247	0.368	crystallin, mu
Cell migration	NRG2	0.325	0.496	0.427	neuregulin 2
	TPH2	0.322	0.214	0.172	tryptophan hydroxylase 2
	LOC100268168	0.319	0.384	0.391	uncharacterized LOC100268168
	LOC100129027	0.319	0.214	0.324	uncharacterized LOC100129027
Extracellular matrix	ADAMTS1	0.314	0.303	0.861	ADAM metalloproteinase with thrombospondin type 1 motif, 1
	FAR2	0.304	0.476	0.793	fatty acyl CoA reductase 2
Cell migration	PDE4D	0.304	0.378	0.190	phosphodiesterase 4D, cAMP-specific

	RDH16	0.295	0.269	0.274	retinol dehydrogenase 16 (all-trans)
Cell differentiation	LIPN	0.295	0.282	0.235	lipase, family member N
	B3GALT4	0.294	0.411	1.203	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4
Cell migration	S100A1	0.291	0.282	0.276	S100 calcium binding protein A1
	MUC5AC	0.289	0.189	0.245	mucin 5AC, oligomeric mucus/gel-forming
Immune response	C4BPB	0.288	0.207	0.612	complement component 4 binding protein, beta
	FAM230B	0.283	0.331	0.173	family with sequence similarity 230, member B (non-protein coding)
	AMPH	0.278	0.374	0.846	amphiphysin
Cell differentiation	EGR2	0.277	0.321	0.733	early growth response 2
	TMPRSS15	0.276	0.287	0.271	transmembrane protease, serine 15
	TRABD2B	0.274	0.454	0.576	TraB domain containing 2B
Cell differentiation, Neurogenesis	GPR37L1	0.265	0.469	0.781	G protein-coupled receptor 37 like 1
	ECEL1P2	0.263	0.264	0.746	endothelin converting enzyme-like 1, pseudogene 2
Cell migration	NRP2	0.260	0.323	0.446	neuropilin 2
	MSC	0.258	0.414	0.815	musculin
	SPG20-AS1	0.253	0.315	0.464	SPG20 antisense RNA 1
Cell Proliferation	IGFN1	0.246	0.236	0.705	immunoglobulin-like and fibronectin type III domain containing 1
	CAMK1G	0.243		0.225	calcium/calmodulin-dependent protein kinase IG
Cell cycle	PAX6	0.236	0.381	1.077	paired box 6
Cell migration	OLR1	0.233	0.227	1.032	oxidized low density lipoprotein (lectin-like) receptor 1
Extracellular matrix	ABI3BP	0.231	0.219	0.864	ABI family, member 3 (NESH) binding protein
	OR10J5	0.226	0.165	0.150	olfactory receptor, family 10, subfamily J, member 5
	lnc-ENPP1-2	0.223	0.276	0.208	lnc-ENPP1-2:1
	CMA1	0.220			chymase 1, mast cell
Cell migration	NRP2	0.217	0.340	0.398	neuropilin 2
	EPDR1	0.216	0.325	0.358	ependymin related 1
	CNN1	0.213	0.251	0.267	calponin 1, basic, smooth muscle
Cell migration	SAA2	0.201	0.405	1.237	serum amyloid A2
Cell migration	SAA4	0.200	0.426	1.362	serum amyloid A4, constitutive
	CPE	0.198	0.247	0.182	carboxypeptidase E
Cell migration	EDN2	0.195	0.289	0.512	endothelin 2
Immune response	ENPP2	0.195	0.334	0.370	ectonucleotide pyrophosphatase/phosphodiesterase 2
Extracellular matrix	ABI3BP	0.193	0.219	0.939	ABI family, member 3 (NESH) binding protein
Cell cycle	PAX6	0.188	0.379	1.321	paired box 6
	PCDHB5	0.184	0.384	0.197	protocadherin beta 5
Cell Proliferation	DUSP2	0.179	0.156	0.655	dual specificity phosphatase 2
Neurogenesis	NPTX1	0.178	0.203		neuronal pentraxin I
Extracellular matrix	COL5A2	0.158	0.204	0.171	collagen, type V, alpha 2
	MAP3K14-AS1	0.154	0.208	0.189	MAP3K14 antisense RNA 1
	CACNA1G-AS1	0.153	0.259	1.211	CACNA1G antisense RNA 1
	MAN1A1		0.140	0.452	mannosidase, alpha, class 1A, member 1
	KANK4			0.941	KN motif and ankyrin repeat domains 4