

1 Table S1. the primer sequences for lnc-HDAC9-8:2, lnc-GNB2L1-3:1,  
2 ENST00000609212 and lnc-NETO1-3:1.

Name	Sequence (5'-3')
lnc-HDAC9-8:2 Forward	5'- GCTGATTGGCACGACCTCTT -3'
lnc-HDAC9-8:2 Reverse	5'- CACCATCCTCACACCTCTGC -3'
lnc-GNB2L1-3:1 Forward	5'- CCTTCAGAGTCACCTCGCAGT -3'
lnc-GNB2L1-3:1 Reverse	5'- ACCGGAACACCTCACAGTCC -3'
lnc-NETO1-3:1 Forward	5'- AAGCCATGACTAAGGAGCCCA -3'
lnc-NETO1-3:1 Reverse	5'- TTCCGCTGAGGCATTGAAGG -3'
ENST00000609212 Forward	5'- TCCAGGAGGAGGACTGGAAG -3'
ENST00000609212 Reverse	5'- GCCATTGAGAGTCCACAGACA -3'

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Table S2. Mass spectrometry analysis of RNA pull down filtered.

Protein Group	Protein ID	Accession	-10kP	Coverage (%)	Coverage (%)	Area Sample	#Peptides	#Unique	#Spec Sample	PTM	Avg. Mass	Description
	84	150 sp Q 7KZ4 S	156.44	12	12	3.64E+06	10	10	10	13	101997	Staphylococcal nuclease domain-containing protein 1 O S=Hom o sapiens GN=SND1 PE=1 SV=1
	53	217 sp P06702 S	154.48	39	39	3.77E+07	5	5	5	25	Oxidation M	13242 Protein S100-A9 O S=Hom o sapiens GN=S100A9 PE=1 SV=1
	127	1033 H 3BRU 6 H 3B	119	21	21	1.61E+06	5	2	11	Carbamitom	31719 Poly(GC)-binding protein 2 (Fragment) O S=Hom o sapiens GN=PCBP2 PE=1 SV=1	
	127	1034 F8VZX2 F8VZ	119	20	20	1.61E+06	5	2	11	Carbamitom	33800 Poly(GC)-binding protein 2 O S=Hom o sapiens GN=PCBP2 PE=1 SV=1	
	127	1035 sp Q 15366 P	119	17	17	1.61E+06	5	2	11	Carbamitom	38580 Poly(GC)-binding protein 2 O S=Hom o sapiens GN=PCBP2 PE=1 SV=1	
	128	3129 sp Q 15365 P	117.03	18	18	1.95E+06	5	2	11	Carbamitom	37498 Poly(GC)-binding protein 1 O S=Hom o sapiens GN=PCBP1 PE=1 SV=2	
	151	1355 A0A0D9SF54	108.98	2	2	9.31E+05	5	5	5	5	282835	Spectrin alpha chain non-erythrocytic 1 O S=Hom o sapiens GN=SPTAN1 PE=1 SV=1
	151	1356 sp Q 13813 S	108.98	2	2	9.31E+05	5	5	5	5	284538	Spectrin alpha chain non-erythrocytic 1 O S=Hom o sapiens GN=SPTAN1 PE=1 SV=3
	151	1357 A0A0D9SG F6	108.98	2	2	9.31E+05	5	5	5	5	287604	Spectrin alpha chain non-erythrocytic 1 O S=Hom o sapiens GN=SPTAN1 PE=1 SV=1
	269	109 sp Q 02413 D	94.19	3	3	9.08E+05	2	2	3	Oxidation M	113748 Desmoglein-1 O S=Hom o sapiens GN=DSG1 PE=1 SV=2	
	330	23740 sp Q 96PZ0 P	90.2	5	5	5.73E+05	3	3	3	3	75035	Pseudouridylylase synthase 7 homolog O S=Hom o sapiens GN=PU57 PE=1 SV=2
	231	304 sp Q 08554 D	89.59	3	3	9.30E+05	2	2	2	3	99987	Desmoglein-1 O S=Hom o sapiens GN=DSG1 PE=1 SV=2
	337	29189 sp Q 87C J2 S	87.83	3	3	4.67E+05	2	2	3	3	93674	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B O S=Hom o sapiens GN=STT3B PE=1 SV=1
	179	830 M OQ X5S M O	86.57	5	5	1.80E+06	3	3	5	5	58481	Heterogeneous nuclear ribonucleoprotein L (Fragment) O S=Hom o sapiens GN=HNRNPL PE=1 SV=1
	179	831 sp P14866 H	86.57	5	5	1.80E+06	3	3	5	5	64133	Heterogeneous nuclear ribonucleoprotein L O S=Hom o sapiens GN=HNRNPL PE=1 SV=2
	271	296 sp Q 86Y23 H	86.52	1	1	1.32E+05	2	2	2	Pyro-glutro	282389	Homerin O S=Hom o sapiens GN=HRNR PE=1 SV=2
	268	3004 G 3XAC 6 G 3X	86.06	6	6	4.72E+05	2	2	2	2	48024	RNA-binding protein 39 O S=Hom o sapiens GN=RBM39 PE=1 SV=1
	268	3005 sp Q 14498 R	86.06	5	5	4.72E+05	2	2	2	2	59380	RNA-binding protein 39 O S=Hom o sapiens GN=RBM39 PE=1 SV=2
	229	3008 B3KM 87 B3K	85.17	5	5	1.06E+06	3	3	4	Deamidation	56736	Matrin-3 O S=Hom o sapiens GN=MATR3 PE=1 SV=1
	229	2918 G 6REM 6 D 6F	85.17	3	3	1.06E+06	3	3	4	Deamidation	88359	Matrin-3 O S=Hom o sapiens GN=MATR3 PE=1 SV=1
	229	2907 sp P43243 M	85.17	3	3	1.06E+06	3	3	4	Deamidation	94623	Matrin-3 O S=Hom o sapiens GN=MATR3 PE=1 SV=2
	229	2906 A0A0R4 J2 E8	85.17	3	3	1.06E+06	3	3	4	Deamidation	94623	Matrin-3 O S=Hom o sapiens GN=MATR3 PE=1 SV=1
	229	2908 A8M XP9 A8M	85.17	3	3	1.06E+06	3	3	4	Deamidation	99967	Matrin-3 O S=Hom o sapiens GN=MATR3 PE=1 SV=1
	276	3402 sp Q 01085 T	78.55	5	5	9.82E+05	2	2	4	4	41591	Nucleolin TAR O S=Hom o sapiens GN=TAL1 PE=1 SV=1
	184	533 sp Q 01081 U	77.96	10	10	2.34E+05	2	2	3	Acetylation (	27872	Splicing factor U2AF 35 kDa subunit O S=Hom o sapiens GN=U2AF1 PE=1 SV=3
	184	532 sp P0DN 76 U	77.96	10	10	2.34E+05	2	2	3	Acetylation (	27872	Splicing factor U2AF 35 kDa subunit-like protein O S=Hom o sapiens GN=U2AF1L5 PE=1 SV=1
	278	341 Q 2L6G 8 Q 2L	75.82	5	5	9.75E+05	2	2	4	4	51539	CDSN O S=Hom o sapiens GN=CDSN PE=1 SV=1
	278	340 sp Q 15517 C	75.82	5	5	9.75E+05	2	2	4	4	51522	Comedusomycin O S=Hom o sapiens GN=CDSN PE=1 SV=3
	278	339 G 8JL 2 G 8JL	75.82	5	5	9.75E+05	2	2	4	4	51607	CDSN O S=Hom o sapiens GN=CDSN PE=1 SV=1
	265	2981 sp Q 8N 3C0 J	72.01	1	1	2.01E+05	2	2	2	2	251458	Activating signal integrator 1 complex subunit 3 O S=Hom o sapiens GN=ASCC3 PE=1 SV=3
	333	43349 sp Q 9BPW 8 J	64.94	8	8	7.52E+05	3	2	3	3	33310	Protein Snap homolog 1 O S=Hom o sapiens GN=PSNAP1 PE=1 SV=1
	264	9079 H 7BY1 H 7B	63.99	12	12	1.02E+06	4	4	4	4	28747	Tropomyosin 1 (alpha) isoform CRA m O S=Hom o sapiens GN=TPM1 PE=1 SV=1
	336	23726 sp Q 6P H8 S Y	63.59	3	3	9.75E+05	2	2	2	2	73563	Aspartate--tRNA ligase mitochondrial O S=Hom o sapiens GN=DARS2 PE=1 SV=1
	456	3111 J3Q T54 J3Q T	62.78	9	9	4.03E+05	2	2	2	2	22620	Cleavage and polyadenylation-specificity factor subunit 7 (Fragment) O S=Hom o sapiens GN=CPSF7 PE=1 SV=8
	456	3112 F5H 6M O F5H	62.78	9	9	4.03E+05	2	2	2	2	24387	Cleavage and polyadenylation-specificity factor subunit 7 (Fragment) O S=Hom o sapiens GN=CPSF7 PE=1 SV=1
	456	3116 F5H 047 F5H	62.78	7	7	4.03E+05	2	2	2	2	31506	Cleavage and polyadenylation-specificity factor subunit 7 (Fragment) O S=Hom o sapiens GN=CPSF7 PE=1 SV=1
	456	2938 F5H 669 F5H	62.78	5	5	4.03E+05	2	2	2	2	41266	Cleavage and polyadenylation-specificity factor subunit 7 (Fragment) O S=Hom o sapiens GN=CPSF7 PE=1 SV=1
	456	2939 sp Q 8N 684 C	62.78	4	4	4.03E+05	2	2	2	2	52050	Cleavage and polyadenylation specificity factor subunit 7 O S=Hom o sapiens GN=CPSF7 PE=1 SV=1
	206	419 X6RD A4 X6R	60.45	14	14	6.40E+05	3	2	5	5	27274	Paraspeckle component 1 (Fragment) O S=Hom o sapiens GN=PSPC1 PE=1 SV=1
	206	422 sp Q 8W XF1 J	60.45	7	7	6.40E+05	3	2	5	5	58744	Paraspeckle component 1 O S=Hom o sapiens GN=PSPC1 PE=1 SV=1
	455	43354 sp Q 9Y3B7 R	57.8	12	12	1.72E+05	2	2	2	2	20683	39S ribosomal protein L11 mitochondrial O S=Hom o sapiens GN=M RPL11 PE=1 SV=1
	208	43350 sp Q 9Y2A7 N	55.81	2	2	3.25E+05	2	2	2	2	128790	Nck-associated protein 1 O S=Hom o sapiens GN=NCKAP1 PE=1 SV=1
	341	561 H 0YFC 6 H 0Y	54.22	21	21	2.62E+05	2	2	3	3	11687	GTP-binding nuclear protein Ran (Fragment) O S=Hom o sapiens GN=RAN PE=1 SV=1
	341	319 F5H 018 F5H	54.22	11	11	2.62E+05	2	2	3	3	22436	GTP-binding nuclear protein Ran (Fragment) O S=Hom o sapiens GN=RAN PE=1 SV=8
	341	226 sp P62826 R	54.22	10	10	2.62E+05	2	2	3	3	24423	GTP-binding nuclear protein Ran O S=Hom o sapiens GN=RAN PE=1 SV=3
	341	227 B5M D F5 B5M	54.22	9	9	2.62E+05	2	2	3	3	26224	GTP-binding nuclear protein Ran O S=Hom o sapiens GN=RAN PE=1 SV=1
	341	320 J3KQ E5 J3KQ	54.22	9	9	2.62E+05	2	2	3	3	26816	GTP-binding nuclear protein Ran (Fragment) O S=Hom o sapiens GN=RAN PE=1 SV=1
	230	43351 sp P42285 S F	51.98	2	2	4.89E+05	2	2	2	2	117805	Superkiller viral-like activity 2-like 2 O S=Hom o sapiens GN=SKM2L2 PE=1 SV=3
	457	2988 sp Q 02878 R	51.9	5	5	3.72E+05	2	2	2	2	32728	60S ribosomal protein L6 O S=Hom o sapiens GN=RPL6 PE=1 SV=3

Figure S1. qRT-PCR validation of four differentially expressed lncRNAs. (A) Comparison of fold change ( $\log_2(P_1/P_2)$ ) of lncRNAs between microarray and qRT-PCR results ( $P_1$ : primary tumor;  $P_2$ : spinal metastasis). (B) Relative expression levels of lncRNAs in tissues of patients with primary lung adenocarcinoma and lung adenocarcinoma spinal metastasis.

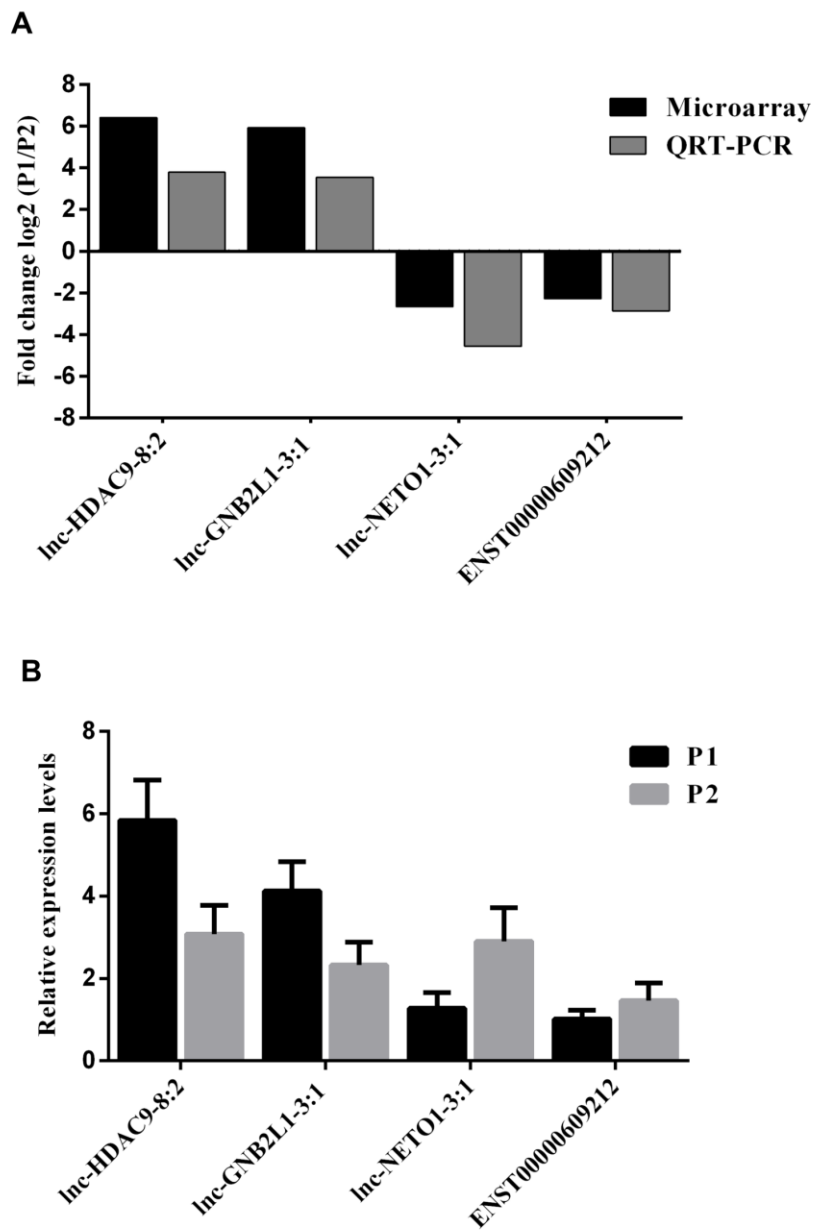


Figure S2. RNA pull-down assay for LINC00852 targeting S100A9. (A) Protein lysates obtained by RNA pull-down assays for mass spectrometry were analyzed by SDS-PAGE following silver staining. (B) Ion peak graph of S100A9.

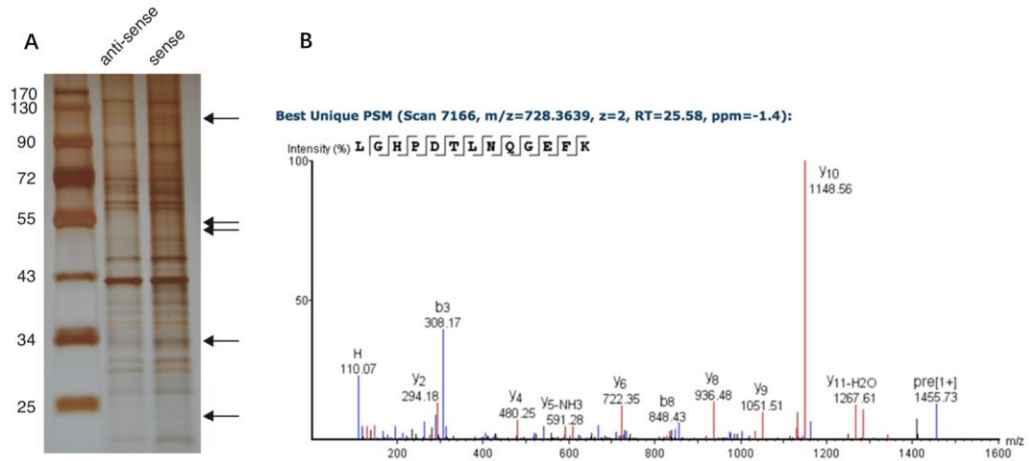


Figure S3. PET scan showing metastasis of other organs 6–8 weeks after ventricular injection in four groups of mice.

