

Electronic Supplementary Information

Aptamer AS411 interacts with the KRAS promoter/hnRNP A1 complex and shows increased potency against drug-resistant lung cancer

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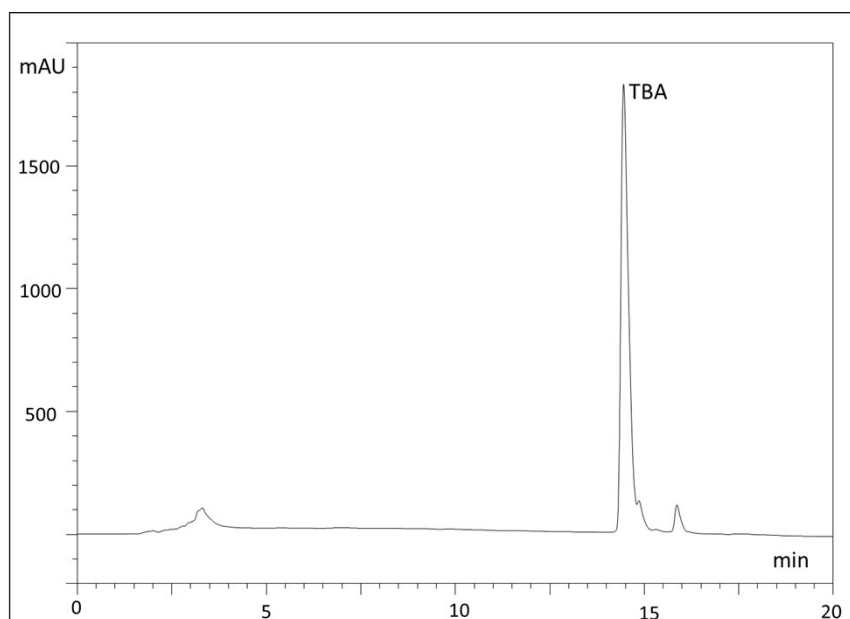


Figure S1. HPLC purification of nucleotide sequences, TBA as example. (Linear gradient using 5–35% acetonitrile–TEAB 100 mM in 20 min, XBridge™ OST C18 2.5 μ m 10 \times 50 mm Column, 60°C, 1.5 mL/min, 260 nm).

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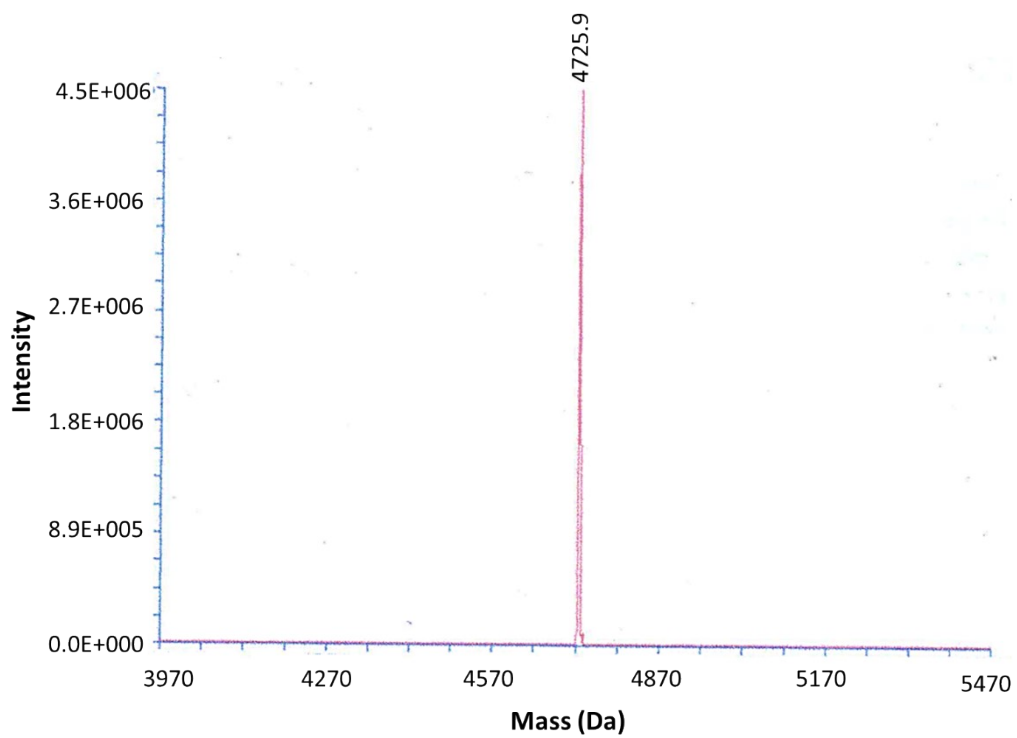


Figure S2. ESI-TOF spectrum of TBA

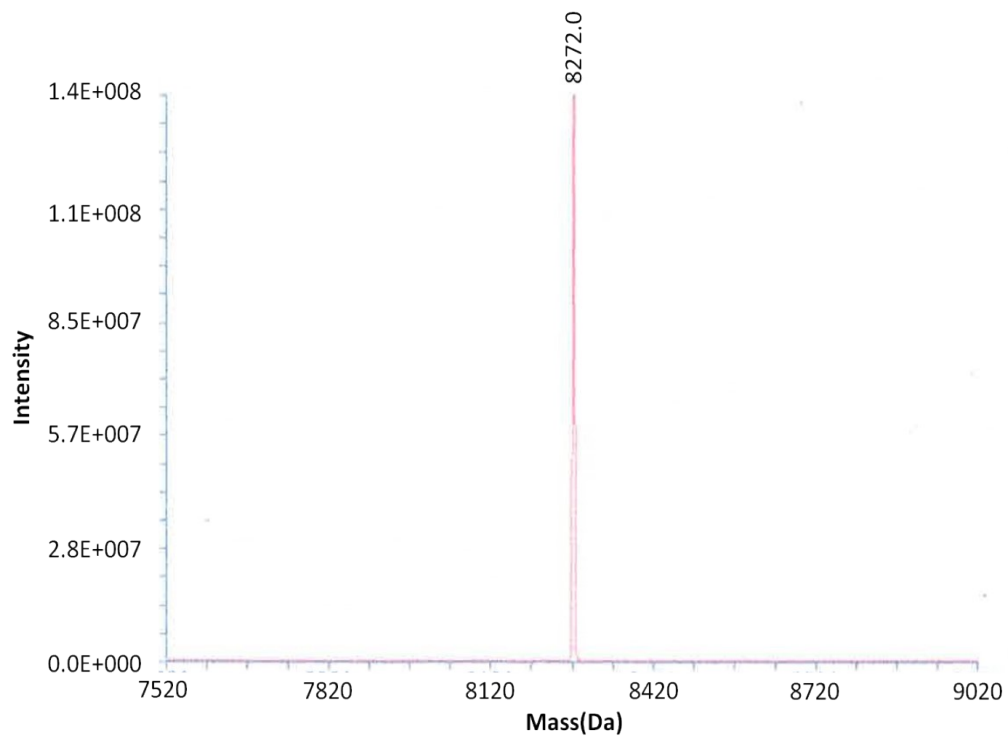


Figure S3. ESI-TOF spectrum of AS1411.

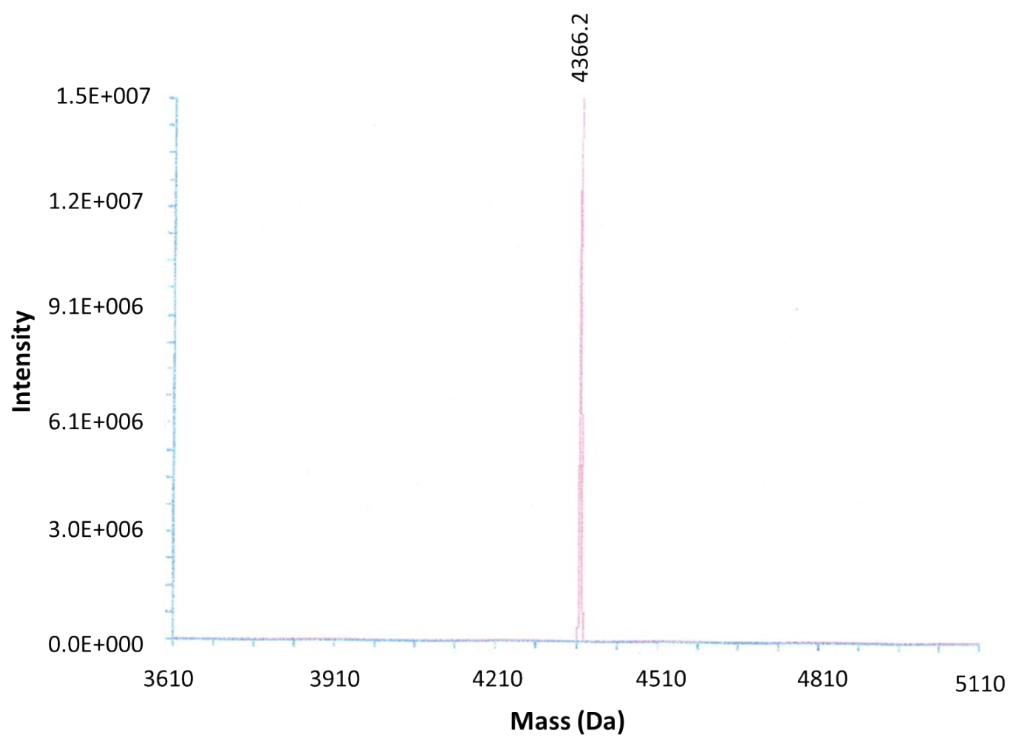


Figure S4. ESI-TOF spectrum of NC

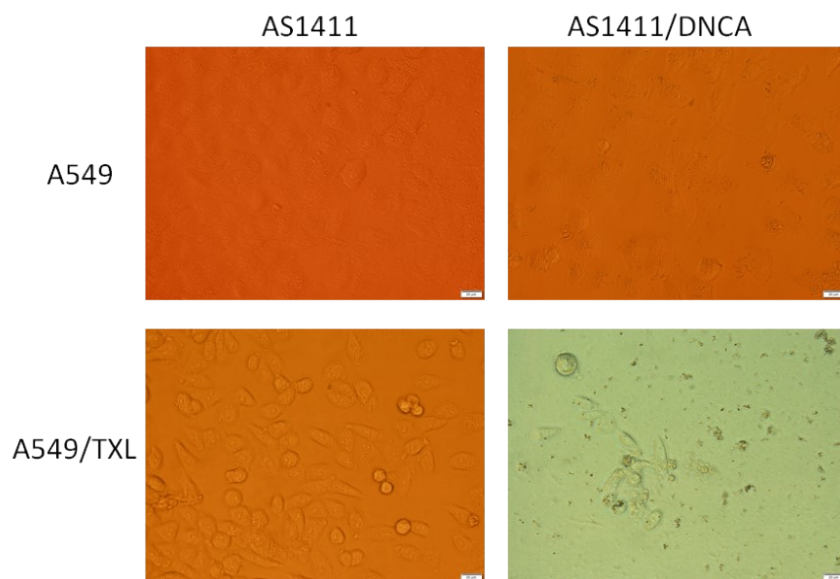


Figure S5. Inverted microscopy of A549 and A549/TXL cells 48 h after treated with AS1411 or AS1411/DNCA (AS1411: 200 nM, DNCA: 26 μ M). The microscopy was performed 2 h after addition of CCK-8 agent.

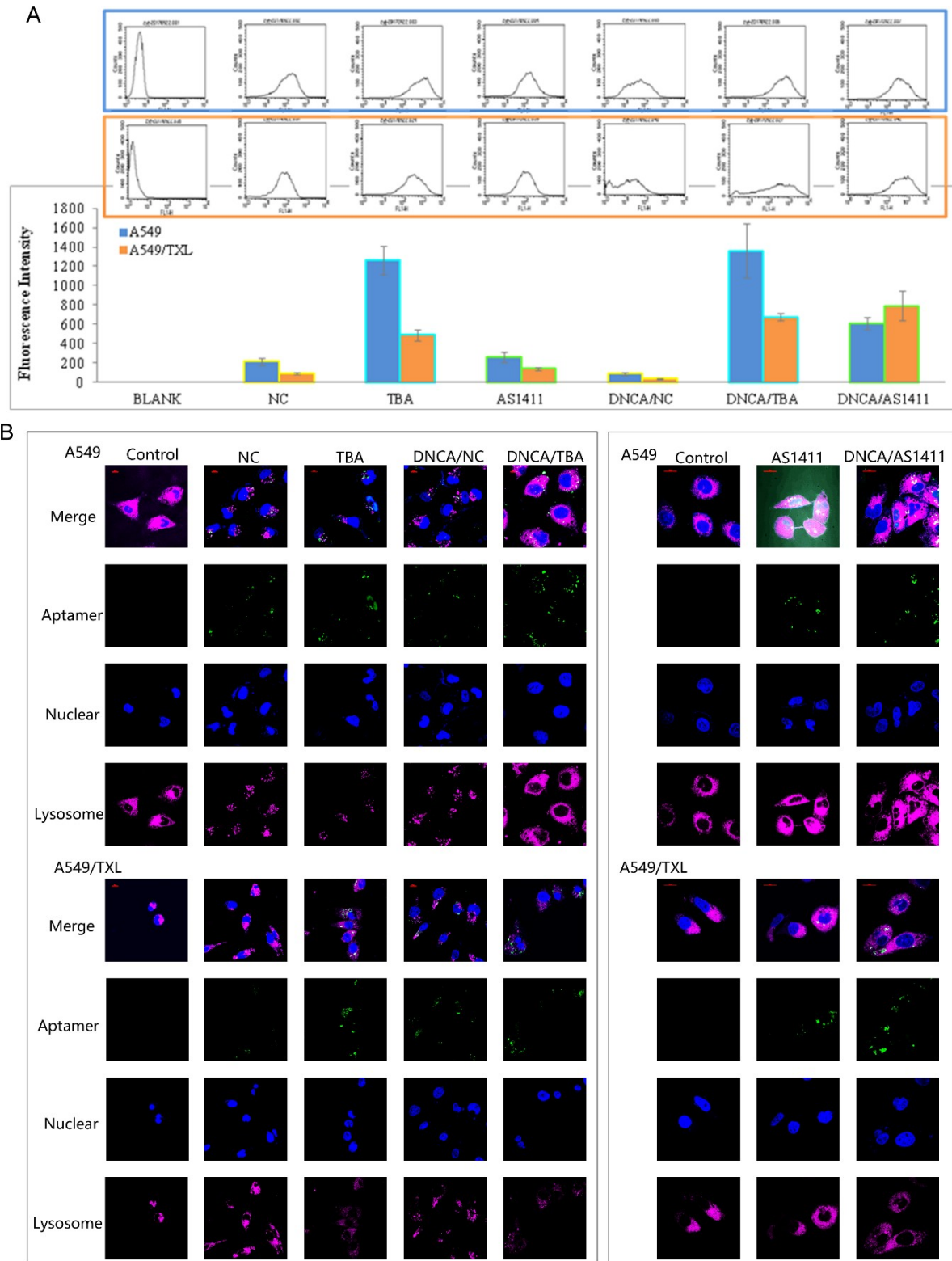


Figure S6. Cellular uptake of TBA and AS1411 by A549 and A549/TXL cells (aptamer or NC: 100 nM, DNCA: 7.5 μ M). Cellular uptake was analyzed 4 h after addition of FAM-labelled aptamer (encapsulated by DNCA) by flow cytometry (**A**) and confocal microscopy (**B**). A pool of three different sets of experiments (each repeated in triplicate) was performed, and each value expressed as mean \pm Standard Deviation.

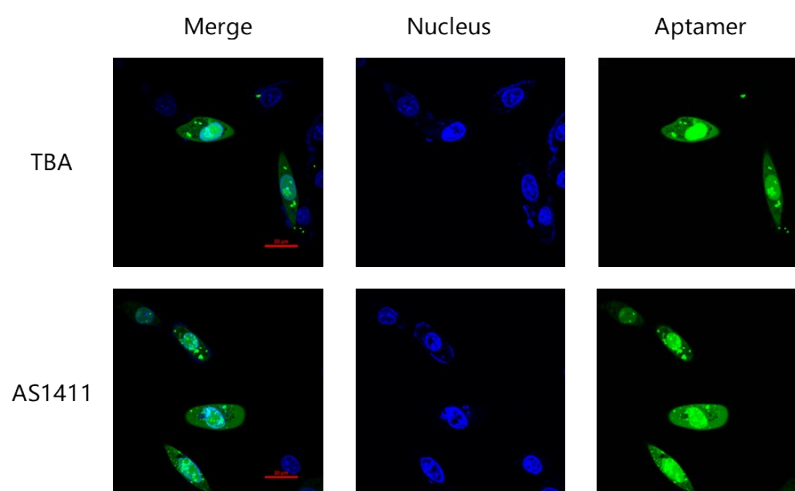


Figure S7. Distribution of TBA and AS1411 in the nucleus of A549/TXL cell. Cellular distribution was analyzed 8 h after addition of FAM-labelled aptamer by confocal microscopy (aptamer or NC: 100 nM, DNCA: 7.5 μ M).

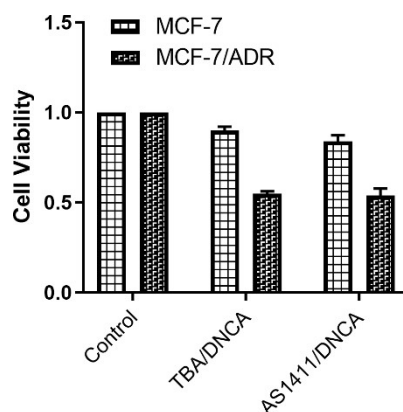


Figure S8. Effect of TBA and AS1411 on the growth of MCF-7, MCF-7/ADR cells. Cell viability was assayed 48 h after addition of aptamer (aptamer: 200 nM, DNCA: 15 μ M) using the CCK-8 assay.

Table S1. Ribosome associated proteins with significant change in TBA/DNCA vs Control

protein	ratio	P-value	protein	ratio	P-value	protein	ratio	P-value
RPL9	1.232	0.036	RPS15A	1.554	0.013	RPL11	1.268	0.024
MRPS23	0.770	0.002	RPS23	0.752	0.012	MRPS5	0.711	0.006
RPL21	0.795	0.041	RPS18	1.238	0.022	RPL6	1.514	0.003
RPLP1	0.492	0.011	RPL7A	1.295	0.042	MRPS31	1.416	0.009
RPS9	1.224	0.008	RPS26	1.206	0.011	MRPL20	1.345	0.023
RPL14	1.940	0.005	RPS28	2.015	0.039	MRPL18	1.692	0.041
RPL15	1.673	0.010	RPL24	1.763	0.021			
RPS8	1.349	0.000	RPL18A	1.398	0.002			

Table S2. Ribosome associated proteins with significant change in AS1411/DNCA vs Control

protein	ratio	P-value	protein	ratio	P-value	protein	ratio	P-value
RPL9	1.347	0.013	RPL26	1.211	0.044	RPL7A	1.339	0.044
MRPL22	0.730	0.049	RPL15	1.666	0.018	RPS6	1.237	0.028
RPL18	0.727	0.010	RPL37A	0.795	0.002	RPL11	1.374	0.008
RPLP1	0.471	0.006	RPL37	0.798	0.038	MRPS5	0.674	0.006
RPL7	1.207	0.029	RPS8	1.255	0.019	RPL6	1.520	0.028
RPS9	1.294	0.004	RPS15A	1.674	0.015	MRPL13	0.752	0.033
RPL34	1.282	0.028	RPS23	0.817	0.042	MRPL18	1.660	0.001
RPL14	1.949	0.030	RPS18	1.216	0.043	MRPL39	1.213	0.038

Table S3. Ubiquitination related proteins with significant change in TBA/DNCA vs Control

protein	ratio	P-value	protein	ratio	P-value	protein	ratio	P-value
UCHL5	1.201	0.027	MTOR	0.825	0.035	ZSWIM2	0.699	0.027
OTUB1	1.378	0.047	RAD23B	0.793	0.026	DTX3L	0.177	0.015
EIF3F	1.223	0.001	FKBP1A	0.703	0.001	CDK5RAP3	1.204	0.003
SNX3	1.268	0.041	MAD2L1	0.755	0.009	PSMB7	0.76	0.013
LATS1	0.772	0.034	UBE2V1	0.572	0.014	RNF126	0.601	0.041
PSMA5	0.667	0.002	TRIM25	0.746	0.022	TRIM4	0.125	0.042
PSMB6	1.306	0.031	RBBP6	1.29	0.043	PDCL3	0.733	0.036
CDC27	0.778	0.015	SYVN1	1.533	0.002	PEF1	0.806	0.03

Table S4. Ubiquitination related proteins with significant change in AS1411/DNCA vs control

protein	ratio	P-value	protein	ratio	P-value	protein	ratio	P-value
USP39	1.476	0.009	RAD23A	0.774	0.021	UBR7	1.481	0.040
OTUB1	1.373	0.011	FKBP1A	0.698	0.001	ZSWIM2	0.656	0.009
EIF3F	1.263	0.018	FOXK1	1.239	0.017	DTX3L	0.165	0.009
FBXO21	0.746	0.006	CDK5	0.753	0.047	CDK5RAP3	1.281	0.013
FBXO45	1.567	0.032	MAD2L1	0.765	0.039	PSMB7	0.791	0.011
PSMA1	1.212	0.005	UBE2V1	0.588	0.009	RNF126	0.641	0.022
PSMA5	0.643	0.002	TRIM25	0.769	0.009	RBCK1	0.757	0.039
MTOR	0.818	0.018	UBE2R2	0.796	0.048	TRIM4	0.168	0.044
PSMB3	1.220	0.012	RBBP6	1.326	0.040	PDCL3	0.671	0.039

Table S5. Sequences of primer used

Primer	Sequence(5'-3')
GAPDH-forward	CAT CAC TGC CAC CCA GAA GAC TG
GAPDH-reverse	ATG CCA GTG AGC TTC CCG TTC AG
KRAS- forward	CAG TAG ACA CAA AAC AGG CTC AG
KRAS- reverse	TGT CGG ATC TCC CTC ACC AAT G