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Supporting Information

Molecular Recognition of Small Cell Lung Cancer Cells Using Aptamers

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Supporting Information

Multiple sequence alignment analysis (selected sequences studied in this work)

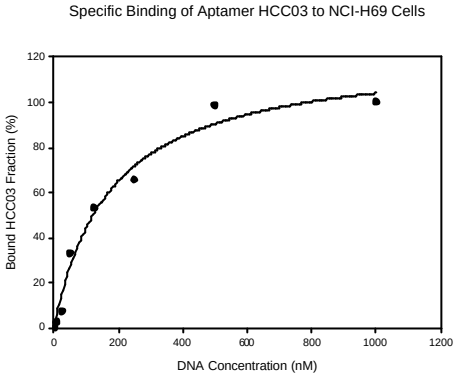
Motif 1	NAME	START	P-VALUE	SITES
	C2-7-40-A12	2	1.92e-16	G TGGATTGTTGTGTTCTGTTGGTTTTTGTG TTGTC
	C2-8-40-F10	2	1.92e-16	G TGGATTGTTGTGTTCTGTTGGTTTTTGTG TTGTC
	C2-4-20-E08	2	1.92e-16	G TGGATTGTTGTGTTCTGTTGGTTTTTGTG TTGTC
	C2-2-20-G02	5	5.07e-13	GGTG TGTGTTTTTGTTTTTGCTTGGTGTTTGTG TC
	C2-4-20-F04	6	3.46e-11	GCGGT TCTGTGGTTGTTGTTGTGTTGTTTTTTTG G
	C2-4-20-G08	7	4.06e-11	GGTCGG TGTTTTTGTTTGTTTTTTGTGCTTTTTTC
	C2-3-20-D02	1	6.41e-11	GGGTGTGTTGTTTTGTTTGTTCTTTGGTG ATTTTG
	C2-4-20-F03	4	6.73e-11	CGG TGTTTGTTCGTCGTGTTTTGTTGTATGTG TG

Motif 2	NAME	START	P-VALUE	SITES
	C2-5-40-C03	7	3.44e-15	TCCGTG CCACTGGCCCCCGGTGCCCCGGTCCCCGG
	C2-5-40-C09	7	3.44e-15	TCCGTG CCACTGGCCCCCGGTGCCCCGGTCCCCGG
	C2-5-40-A10	7	3.44e-15	TCCGTG CCACTGGCCCCCGGTGCCCCGGTCCCCGG
	C2-2-20-H12	1	2.16e-10	ACACCAGCGTACCTTGGTCGGGTCCCTGG GCGCAT
	C2-8-40-G03	3	2.35e-10	GC ACCTTCGTACCCCCACCTCCGGCCCGTGC TCC
	C2-8-40-G06	3	2.35e-10	GC ACCTTCGTACCCCCACCTCCGGCCCGTGC TCC
	C2-2-20-G06	1	2.35e-10	ACACCAGCGTACCTTGGTCGGGTCCCTGC TCTGAT
	C2-5-40-B08	2	1.12e-08	C CACCCGACACTTCGTCGTCCGTCCCCTTT TCCCG
	C2-3-20-B05	5	1.12e-08	CCGA CCTCTCGTTCCTCGTGTCCCATCCCCCCG CT
	C2-2-20-F09	4	1.21e-08	GGC TCCGTTACCCTCGTTCGACCTGCCCCCGC GTG

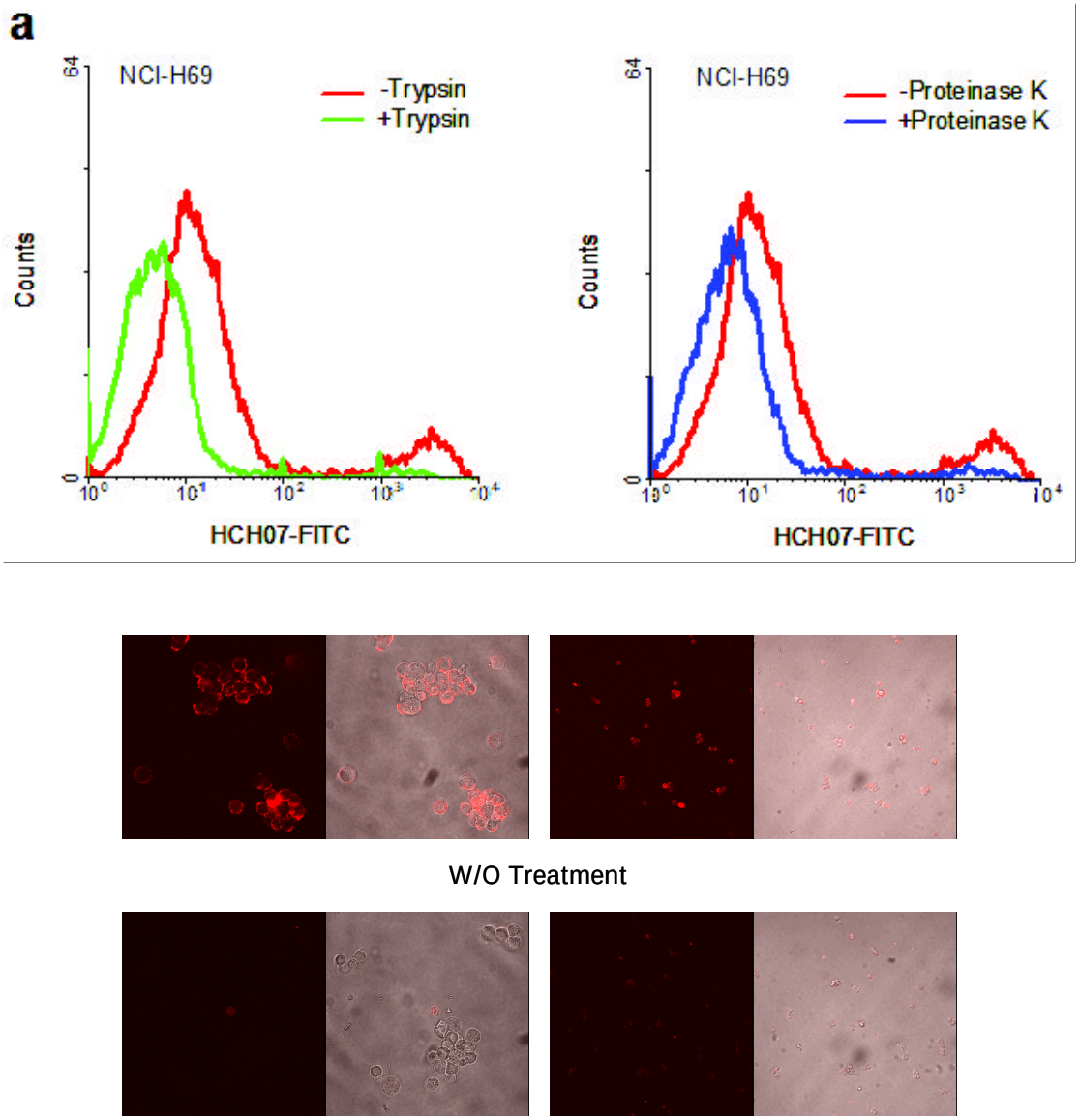
Motif 3	NAME	START	P-VALUE	SITES
	C2-6-40-H02	5	1.89e-18	GCCG ATGTCAACTTTTTCTAACTCACTGGTTTT GC
	C2-7-40-C06	5	1.89e-18	GCCG ATGTCAACTTTTTCTAACTCACTGGTTTT GC
	C2-2-20-E04	5	1.89e-18	GCCG ATGTCAACTTTTTCTAACTCACTGGTTTT GC
	C2-2-20-G08	5	1.89e-18	GCCG ATGTCAACTTTTTCTAACTCACTGGTTTT GC
	C2-2-20-H02	5	1.89e-18	GCCG ATGTCAACTTTTTCTAACTCACTGGTTTT GC
	C2-4-20-H07	5	1.89e-18	GCCG ATGTCAACTTTTTCTAACTCACTGGTTTT GC
	C2-6-40-G02	5	3.94e-18	GCCG ATGTCATCTTTTTCTAACTCACTGGTTTT GC
	C2-2-20-E11	1	5.75e-13	GCAACCTCTCTTTCAACTTCACTGGTTCT ATTCTC

Motif 4	NAME	START	P-VALUE	SITES
	C2-2-20-G11	3	3.39e-14	GC GGAAAATTAAGTTATTCTGCCCCCTCGA CTCAGCTGAG
	C2-1-20-D07	3	4.61e-14	CT GGATCTTAAAGATTGCATGCGCTCACTA TGGGA
	C2-4-20-H01	3	4.61e-14	CT GGATCTTAAAGATTGCATGCGCTCACTA TGGGA
	C2-2-20-F11	3	1.06e-13	GC AGAAAATTAAGTTATTCTGCCCCCTCGA CTCCG

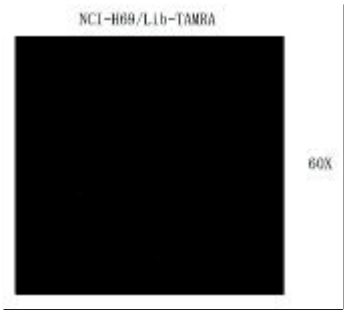
Supporting Figure 1. Multiple Sequence Alignment Analysis of Sequencing Results with MEME Version 3.5.3 (motif 1 refers to aptamer HCA12, motif 2 refers to aptamer HCC03, motif 3 refers to aptamer HCH07, motif 4 refers to aptamer HCH01)



Supporting Figure 2. Saturation Analysis of HCC03 (Saturation analysis was performed to measure the relative cell surface binding affinities of developed aptamers. Cells were incubated with FITC labeled aptamers at 4? for 30 minutes, washed three times with 400 µL washing buffer, and finally re-suspended in 400 µL binding buffer containing 20% FBS. Cells were then assayed using flow cytometry. Concentrations of FITC labeled aptamers for the relative affinity measurements varied from 0 to 1 µM. The FITC labeled ssDNA library was used to determine nonspecific binding. The mean fluorescence intensity of aptamer bound cells (nonspecific binding of DNA library subtracted) was used to calculate bound aptamer fraction at different concentrations. All affinity measurements were performed in triplicate. The results are described as mean ± s.e.m. The equilibrium dissociation constants (Kd) were obtained by fitting the cell surface binding data of aptamers to a one-site saturation model with SigmaPlot 9.0 (Jandel Scientific). In addition, the appearent Kd obtained in this experiment is considered to be higher than the accurate kd due to the error brought in by population of dead cell.)



Supporting Figure 3. Flow Cytometry Assay of Aptamer Target Protein Studies and Confocal Imaging of Aptamer Target Protein Studies



Supporting Figure 4. Fluorescent ssDNA library stained SCLC cell line tissue array as control by magnified confocal imaging (60× magnification).