

Supporting Information

Rapid determination of the presence of EGFR mutations with DNA-based nanocalipers

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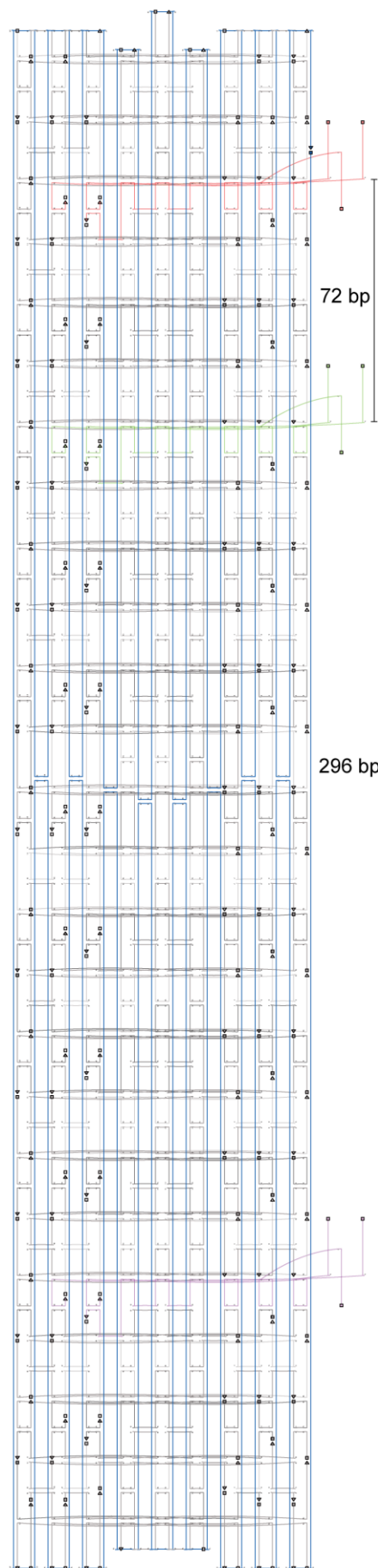
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Supporting Data S1.

A plane diagram of the three-layered rectangular structure (plotted by the software caDNAo). The essential elements for assembling DNA nanocalipers include M13mp18 scaffold ssDNA (blue) and massive staple strands, in which strands colored gray (named as structural strands) are designed to form the stable structure and 9 strands (colored red, green, and purple; named as positioning strands) are designed to create different given distances of EGF molecules. After being decorated by external nucleotide residues (5'-AAAAAAAAAAAAAAAA-3'), all positioning strands are bound to polyT-linked EGF molecules. For NC-25, the distance between red and green positioning strands is 72 bp \approx 25 nm; For NC-100, the distance between red and purple positioning strands is 296 bp \approx 100 nm.



Supporting Data S2. Detailed sequences of structural strands and positioning strands.

Staple strands	Sequence (5'-3')
structural strand 1	AACGGGTATTAACCAAGTACAAATAATACGTTAAATTGTAGCGGGAGCACGTATAAC
structural strand 2	TTGTAGCGTAAATGCTTTAAAATATTCCAGGAAGAAAT
structural strand 3	CGGAACGAGGGTACAACCTTCTGTTTAGAAAAAATCAGGTCACGTATCGATGA
structural strand 4	CGGAGTGAGAATACAGCAGCGGCTCATTAATTCATTAGCGGGGAGAGGCGGTT
structural strand 5	GATGATACAGGAGTGTCAAATGGTAGTTTGACCTATCAGGTGC
structural strand 6	TGCGTATTTCTGTGTAGGACGTTTTTTGCAACAACTAAAAACCCATG
structural strand 7	TAATTGCGTTGCGAACGAGTA
structural strand 8	CCGATAGTTGCGCATCAGCTTGCCAAAAGAAGCAAACGGAACGCCAATTCGCA
structural strand 9	CCACCCTCAGAGCCACATAGATAAAATACCAATCACACACGACCAGTA
structural strand 10	CAGTATTAACACCGCCACAGAGGTTCTGATTATTAATTTTACCAGAAAGTAAGCA
structural strand 11	CGGTCCACAAAACGACACATTCAACTAATCTAACAGCTTGGAG
structural strand 12	CAAAGGGCCCTAAAGGTAGGGCTTTTTATCAAAAATAGCACCCAAAAG
structural strand 13	AGCAATACTCCATCAGGATAGCTTATGTAATTATCAAGATTTGCGGGAGGTTTTGA
structural strand 14	TGAATCTTACAAAAACAATGAATCATAGTCAATATAACTCAAACAAAACATC
structural strand 15	GAATTTCTTAACATAAAAACAGTTAATTTTACAGAGGCGCAGATTCACCAGTGCT
structural strand 16	TAGGGTTGGGAAGAAAAAAGCCTGTATATGTCTAATATCATAATAA
structural strand 17	AGAGCCTAATTTGAGAATTGATCCGGCTTAATTACCTGAACAATATATTAGTC
structural strand 18	CACCAGTGAGCTCGAAAACGAACTAGACGACGACGTTGAACCCTCATT
structural strand 19	AGAACAAGCAAGCCGTTTTTATTTATCAATACTAGAAGCGAAAGGCAGAGCGGGAGCT
structural strand 20	ATAAAAGGACAACATAAAGGATTTAGAAGTATTGCCACCCTAAAGGGCG
structural strand 21	AAACAGGATGCAATGCGGCAAAGAATTAGCAACAGGTCAGGCGGGGTT
structural strand 22	ACCCTTCTGAAGGTTATCGACAACCTCGTATTAGAGCCACCAGGTAAAT
structural strand 23	AGGAAACGAGGCCGGATATACTTCTTATCAGATGCCACGCTGAGAGCC
structural strand 24	AAAACACTCATCTTTGACCCCAACCGGATTACCAGTCGAAATTGTCATTCAGGCTGCG
structural strand 25	AAGTCAGAGGGTACCCAATCCATCATAATCAATAGATAAAGAATAGCCCGAGA
structural strand 26	TGACAGGAGGTTGAGGAATTAAGCGGCTTAGATAAGCAAAGCCAGCTT
structural strand 27	TGTACCCCAAAAAGGGTAGCATTAAACATCCAACAAATAAAGCTGAGAC
structural strand 28	GCCATTAAATGAAAAAGCGGAATTATCATCATTTAGCGTCACCATTAC
structural strand 29	GGATTTGCTAAAGCAACGGCTTGTGAATTCATTCAGCGTGCCAGCTGCATTA
structural strand 30	GCGCATCGGCTGTCTTTTCCTTAGAAACCAGGTTTGAACCGCCGCGCTTAACAC
structural strand 31	GGAATCATTACCGCGCCAATACAACATGTTATACAACGGCGAACGGGATTTTAGACA
structural strand 32	AGTCCACTGGGAAAGCATTCTTACTTTTAACCGTTAAGCCTTACGCAG

structural strand 33	AGGTGGCAAAATTATTCGTCAGATGCCCCGAACAATCAACAGTTGAAAG
structural strand 34	TACCGTTCAGTAAGCCATTTGGGGTTGATTCACAAGAGATGGTGTAG
structural strand 35	AGGCTTGCAGGGAATTTTTTCATAAAAACAGAGGAAGTGAGCGAGAGCCCCAA
structural strand 36	TCACCGCCGCAGGTCGGAAGATTTAAGAGCAAGGAGCCTCACCTCA
structural strand 37	TAATAAGAGCAAGCGCTAACGAGCCAACGATTCTGTACGTGGACTCCAACGT
structural strand 38	TCTGAAACCACTGAGTATTATAGTTTGCCAGACCATTGCTATCCGCT
structural strand 39	CGCCTCCCTCAGAGCCAGACTTTAAGAAACAAGGCCAACATCTGAAAT
structural strand 40	AGAATCAAGTTTGCCTATTCCTGATGAATAATAACGAACCAACATCAC
structural strand 41	TATGTTAGACCGACTTAATAAAGAAACATTATCAAACCCCTCAATCAAT
structural strand 42	TTGTAAACTAAAAATTCTCAGAGCATAAAGCTGAGCCGCCCGCTCGA
structural strand 43	GAGGGTTGCCACCCTCCAGACCGGAATTACGGCGATTAACCAAGCTT
structural strand 44	ACGGTAATTCACCATCTGAAAAGGTGGCATCAGCGCAGTCCCTATTAT
structural strand 45	AGAGTCTGTTCTTTGACGCTATTAGTTTGATAACGTCACGTAGCGAC
structural strand 46	CCATCGATAACAAAGTTCCCTTAGAATCC
structural strand 47	AACCTAAAACGAAAGAGGCCAAAAAGCTGCTACCTTATATACGAGCTGGTGCCGGAAAC
structural strand 48	ACTACAACCCTGCCTAATATAACAGCGCGAGCAATATGATATTCAACC
structural strand 49	TGTCGTCTTCCAGACGT
structural strand 50	TAGACGGGAGAATACGTCAAAAAATAAGGTCCCATCCGTTCCGAAATCGGCAA
structural strand 51	TTCAGGGAAGAAGGATTAATGCTGACAGGCAACTGAGTAATGTGTAGG
structural strand 52	CAGCCTTACAGAGAGAATAAAATTTAATATCAATAAGCCCCAGCAGGCGAAA
structural strand 53	ACAGTATCGGCCTATTGAATCGTAAATTGTGAGGAAGTTTCC
structural strand 54	CAGTCGGGAAAGCCTGATTTCAACACTGCGGATTTTCTGTAGACAGCC
structural strand 55	CGCCACGCATAAGCTCCAAAACACTATCTTTAATCTTCTCTGTATATTTAAA
structural strand 56	ATTAAACGGGTAAAATACGTA
structural strand 57	TAGCTTTTTTCAGGCTTGAGAACACCAGCTCACTGCCCGCTTTC
structural strand 58	ACATTTGACTGGTAATAAGT
structural strand 59	TTAAATTTTTGCGGGAAAACATTATGACCCTGCACCCTCAGAATAGGT
structural strand 60	TGAGGACTAAAGATAAATGAAATCGTCATAACAGTTCGGTGCATCTCATTGCC
structural strand 61	ACATTCAATAAGTTTATACCTGAGGAAAACCTGCTTTGACTCACGCTG
structural strand 62	AGAAAATTCATATTCAAAATCGCGCATCTTCTAGTTGCGCCGCTACAGGGCGC
structural strand 63	TCACCGTCCAAACGTATTCATTTGAGGTTGGGCGATTAAAGTGGCGAG
structural strand 64	GAGTGAGCTAACTCACAT
structural strand 65	CCATATTATTTATATTGAGCGAAATGCTGACAAAATAAAACGCTAATACGTG
structural strand 66	AGATCTACAAAGGCATTAGATCCCCTCAACGATCTAAAGTTT
structural strand 67	ATTTTGCAAGCCCTTACGCTGAGTAAATCGTTTAGTAATACCAGCAG

structural strand 68	AGAGCCAGTGATTAAGTACATAAAGTCTGAGACCAGAATCGATTAGA
structural strand 69	TCCTCAAGTAGCAAGCAAAGATTACAAAATAGAAGGGCGACATGGTCA
structural strand 70	TACCGTAAATGAAAGTAACTAAAGAATAGTAGTGAGAAAGGCCGGAGA
structural strand 71	TTAACGGGGTCAGTGCC
structural strand 72	CAGATATAGAAGGCTTATCCGGTAAAGTACTCAACAGGAGCCCCCTGAGAAGTGTTT
structural strand 73	AAAATCACCGGAACCAAATCCTTTGAATATACAGCGTAAGCATGGAAA
structural strand 74	ATTGACGGACATATAATCAAGAAAATGCAAATGTTAGAATAGCGGGCG
structural strand 75	GAGATAACCCACACCAGTTACCATATGCGTTCAGCTATCCAGTTTGAACAAG
structural strand 76	AACTGGCACAAAATCAACCATATCCAGAAGGATCTAAAGCATCACCTT
structural strand 77	GGATCGTCACCCTGAAAGGAAAAGAAGTTCAGAAGCAGGAACAAACAATCATA
structural strand 78	ATGAATCGCACACAACGCGATTTTTAGTAAAAACAGTTTCAGTACAA
structural strand 79	CAGTTTGAGGGGACGACG
structural strand 80	CATTAGCACAATAATATGCTTCTGAAGAGTCAGAGGCCACAGCACTAA
structural strand 81	AGGAACCAATATCCAACAGGTCAGACACCGTACTCGGT
structural strand 82	TGAGAGTCTGATAAATTGTTTAGCTATATTTTGTCCATACATAAACAGT
structural strand 83	TATCATCGCCTGATAAATTGTGATGAACGTACAGGTAACCTAGAGGGCGAAAGGGGGA
structural strand 84	ATTGTATCGGTTTCGACAATGGAGATTTAACTGACCAAGAGAGTTGCAGCAAG
structural strand 85	CCAAGCGCGAAACAAAGTACAGGCTGACCGTTAATAATTCGTAATTCGGTGCGGGCCT
structural strand 86	AATCCCTTCTGGCAAGAAGAATAAAAGACAAACACCCTGACAAAGACA
structural strand 87	AAAGCCAGAATGAAAATTCTACTTACGGTGTTAGCATGTCGGCGGAT
structural strand 88	ACGCGAGGCGTTTTAGCGAACAGTAATAAAATTTAACATGCCGTAACGAGTAAA
structural strand 89	TTGAAAACATAGCGCAAATTTAAATCAAG
structural strand 90	GTAGGTTTACCAGCGCTTGCTTTGTACATTTGTAGATTAGAGCCGTCA
structural strand 91	CCACGGAACCGATTGAACATCGGGCAAACAATTCTAAAATATCTTTAG
structural strand 92	GCTATCTTACCGACCCAGCTAATCGCCATGAGAATATGTCTATCATGGGCGAT
structural strand 93	TAATGCCCGCCTGTAGCATAAATCCTGGATAGACCGCTCCGGAAGCA
structural strand 94	CTCCAAAAAAGCCGATATAAACATTATGTGTACAGAACAGCTGATTGCCCT
structural strand 95	ATCCTGTTACCCACACATACCGACATATTTAGGGAAGCGCAATCAAT
structural strand 96	TTGCTCAGACCCTCAGTATCGCGTATAACCCTCGCCAGCTGGATCCCC
structural strand 97	GGCCCACTGGTCGAGGACGCCAACAGATTAAGTTAAGAAAGGAAACCG
structural strand 98	CCCTTATTAGCGTTTGGTTTGAGTAATTGCGTTGAATGGCTTACCGCC
structural strand 99	ATTGCGAATAATAGTTAAAGGAAATCTACTTCATCAAGGGTGGTTTTTCTTTT
structural strand 100	GAACCGCCTACCAGGCTTGCGGATAATAAAGCTTTAGAACCCTCATAT
structural strand 101	TAAGAGGCGGTACCGTTGT
structural strand 102	GATTTTTGTTTATAACTGAAGAACGCGACAAAAGAAGTCAATCGGAGATAGA

structural strand 103	CCGCCACCAGAACCACCACCAAAATCGGTGCTCCTTTTTGTAAATCAAAA
structural strand 104	ATGCCACTTGACGAGAATGGTTTAGGGTGCCTTCGCACTCCAGCC
structural strand 105	GAGAGGGTAGCTATTTTTGAG
structural strand 106	CTCATAGTAGTAACAGGTAGATTCAATAACCTAATGCCG
structural strand 107	CCTTGATATTCACAAATAAATCATTAGCTCAAATCAGAAATAACAACC
structural strand 108	AAGATAAATGCAACAGTGATGGCAATTCATCACGTAATCACAATGAAA
structural strand 109	TTTTTTGGACGTGAACGAGGCATTTTCGAGCCCTCCCGACTAGTTGCT
structural strand 110	TTAATGCTCAAATATCATTGCGGAACAAAATTTTCGGTGGAATT
structural strand 111	AGGTTTAGTACCGATATAAGTCTTTAATTTGTACCAAGAAGCCTTTATTCAA
structural strand 112	GCGCGTTTTATCGGCGAAACCACAAAATTATATAGCCCTTATCGGCC
structural strand 113	GATAGCCGAGCCTTAATAG
structural strand 114	CGACCTGCTCCATGTTACTTAGGAACCGAGGAATACCGGCCAGTGGTTGGGTAACGCC
structural strand 115	GCACAGACAGTTGGCAGTTATTAATTTTAAAACCATCTTTGTGAATTA
structural strand 116	GCTTGACGATTAAAGACAGACGACGACAATAAAGCAAGCATCC
structural strand 117	GAGCACTAGACATTCTAACGGATATTCAATTTTGTACAT
structural strand 118	CGCAAGGAGTTAATATTGATAAGAAAGCGAACAGAACCGCTTA
structural strand 119	CGTCGGATCTGTTGGGCGAGAGGCGGAAGAACCGCTTTTATA
structural strand 120	GGATTATTCTATGGTTTTTCAAATCGTGTGATAATGAAAAAAG
structural strand 121	TAATTCGCGCTGCAAGAGGCATAGCATCAGTTACAACAACCCG
structural strand 122	GCATGCCTTGCCCTGACTTTGAAAGAGGACAGTCGAAATCAT
structural strand 123	ATGGGCGCTTCCGGCCGTCCAATTTAATCATAACAGAGGACC
structural strand 124	TAAAGATTGGTTGATACATGTTTTTGCATCAACCAATAGGGGA
structural strand 125	TACCTACACTTTCCTCCAATCGCACACCGGAAAATAAGATCG
structural strand 126	TTGCTGGTACGGTACGGACTACCTCAGTATAAAGCGTCTTAAT
structural strand 127	GCTGAACCGCGAACTGTTGCACGTGGAACAGACTCCTTACAA
structural strand 128	CTAGGGCGATAAATCAAAGTCCTGAACAAGAACGCACTCAAAC
structural strand 129	TAAAGTGTAACCTGTTGAATAAGGCTTGCCACGAAGGCCTT
structural strand 130	CGCGTAACTGATGGTGTAATTTACGAGCATGTATCATTCTAG
structural strand 131	TAGCTGTTGGGCGCCAGAGTAATCTTGACAAGCAGCGATTGCG
structural strand 132	GTTCTAGCTGGAGCAACCAATTCTAGAATGACCATTCCACATG
structural strand 133	GAATTGAGGACCTGAAAGTAACAGAACAACAAAGAAACGACA
structural strand 134	AAACAACAGGAAATTACATAGGTTTAAACATTAAGTCATAATC
structural strand 135	AGCATCGTAACAGAAAACGGCGAACGATGCCCCGATGGCTTTT
structural strand 136	CTTATTAATGCCCGAAAGGCTGAATATAGGATTAACGATTGG
structural strand 137	TTAGTAGAAGATGTGAGTGTAGAACCTCCAGTAGCAGACTGTA

structural strand 138	CAATCTCCGTGAAGCGGATAAATATGCATTAAGAGTCCTCATT
structural strand 139	GGAAATATCCATTTTTAATAAAACAGAGAGCCATTCATAGCC
structural strand 140	GTGTTTTGACGGATGATGATACCTTTTGGGAGGGAACCGGAAC
structural strand 141	CAGATGGGATAGGTCTTTATTCATTCTTTTCGGAATCTGAATT
structural strand 142	GTATACATTGGAATTATTCTCGCCTGACAAAGACACAGAACCG
structural strand 143	TGTGTCTGGCCGAGCTTCAGGTCATTTGGATAAGTGCCAGCAT
structural strand 144	TAATACTTTTGTAAAGTTGATTAGAGAGTACATAGCCCGGAG
structural strand 145	CATTTTTGTTCCTCCGACGCAGATAACATAACGCTTTCGAAGG
structural strand 146	GACGTTGTGCTGGTTTGACGGTCAATCATAAGGCCGGAACATA
structural strand 147	ATTTTAAAAGATTGTAGCTTAATTACTTCAAAGCCACCAAAT
structural strand 148	TCATCAACCGCTATTACGTTTACCAACGGAACCTTCGGTCGTTG
structural strand 149	GGGTACCGAGACGGGCACCAGGCGCATAGGCTACGGAGATCTG
0 nm positioning strand 1	AGCAGCAAAAATACCGGGAAGGGTAATAACCTACGGAATAATA
0 nm positioning strand 2	TG CCTGATAATCAGTATAGTGAAAATTGAGACAATTTAAGA
0 nm positioning strand 3	ATCGGAACGAAAAACCAAAGTACCGACAAAAGGTATTCTATCC
0 nm-A positioning strand 1	AAAAAAAAAAAAAAAAAAGCAGCAAAAATACCGGGAAGGGTAATAACCTACGGAATAATA
0 nm-A positioning strand 2	AAAAAAAAAAAAAAAAAATTGCCTGATAATCAGTATAGTGAAAATTGAGACAATTTAAGA
0 nm-A positioning strand 3	AAAAAAAAAAAAAAAAAATCGGAACGAAAAACCAAAGTACCGACAAAAGGTATTCTATCC
25 nm positioning strand 1	ATCTGGTCAATATTTTAGATTTTCTTAACAATGAAAATACAGA
25 nm positioning strand 2	AGCCATTGCAGGAGGCTTATATAATTTAGTATAAAAATAAAGTA
25 nm positioning strand 3	AAAGGAAGAGTGTTGTATGCAGAACGCGCCTGTTTTCATCCAG
25 nm-A positioning strand 1	AAAAAAAAAAAAAAAAAATCTGGTCAATATTTTAGATTTTCTTAACAATGAAAATACAGA
25 nm-A positioning strand 2	AAAAAAAAAAAAAAAAAAGCCATTGCAGGAGGCTTATATAATTTAGTATAAAAATAAAGTA
25 nm-A positioning strand 3	AAAAAAAAAAAAAAAAAAGGAAGAGTGTTGTATGCAGAACGCGCCTGTTTTCATCCAG
100 nm positioning strand 1	CAGTCAAACGTAAAACCTGGAAGTCCCTGACTTTCGTCACCAG
100 nm positioning strand 2	TGACCGTAGCAAAGCGGGGGTAAAAGAAGTAAAGACAGACT
100 nm positioning strand 3	CACAATTCGCCAACGCCCCAAATCAACGTAACAAGAATACCAT
100 nm-A positioning strand 1	AAAAAAAAAAAAAAAAACAGTCAAACGTAAAACCTGGAAGTCCCTGACTTTCGTCACCAG
100 nm-A positioning strand 2	AAAAAAAAAAAAAAAAATGACCGTAGCAAAGCGGGGGTAAAAGAAGTAAAGACAGACT
100 nm-A positioning strand 3	AAAAAAAAAAAAAAAAACACAATTCGCCAACGCCCCAAATCAACGTAACAAGAATACCAT
PolyT	TTTTTTTTTTTTTT-SH-C6

A

Genetic Site	Cell Bank information		Customer sample	
(Locus)	A-549		A549	
Amelogenin	X	Y	X	X
CSF1PO	10	12	10	12
D13S317	11	11	11	11
D16S539	11	12	11	12
D5S818	11	11	11	11
D7S820	8	11	8	11
THO1	8	9.3	8	9.3
TPOX	8	11	8	11
vWA	14	14	14	14
D21S11			29	29
Percent match between the sample and the database profile: 94.44%				

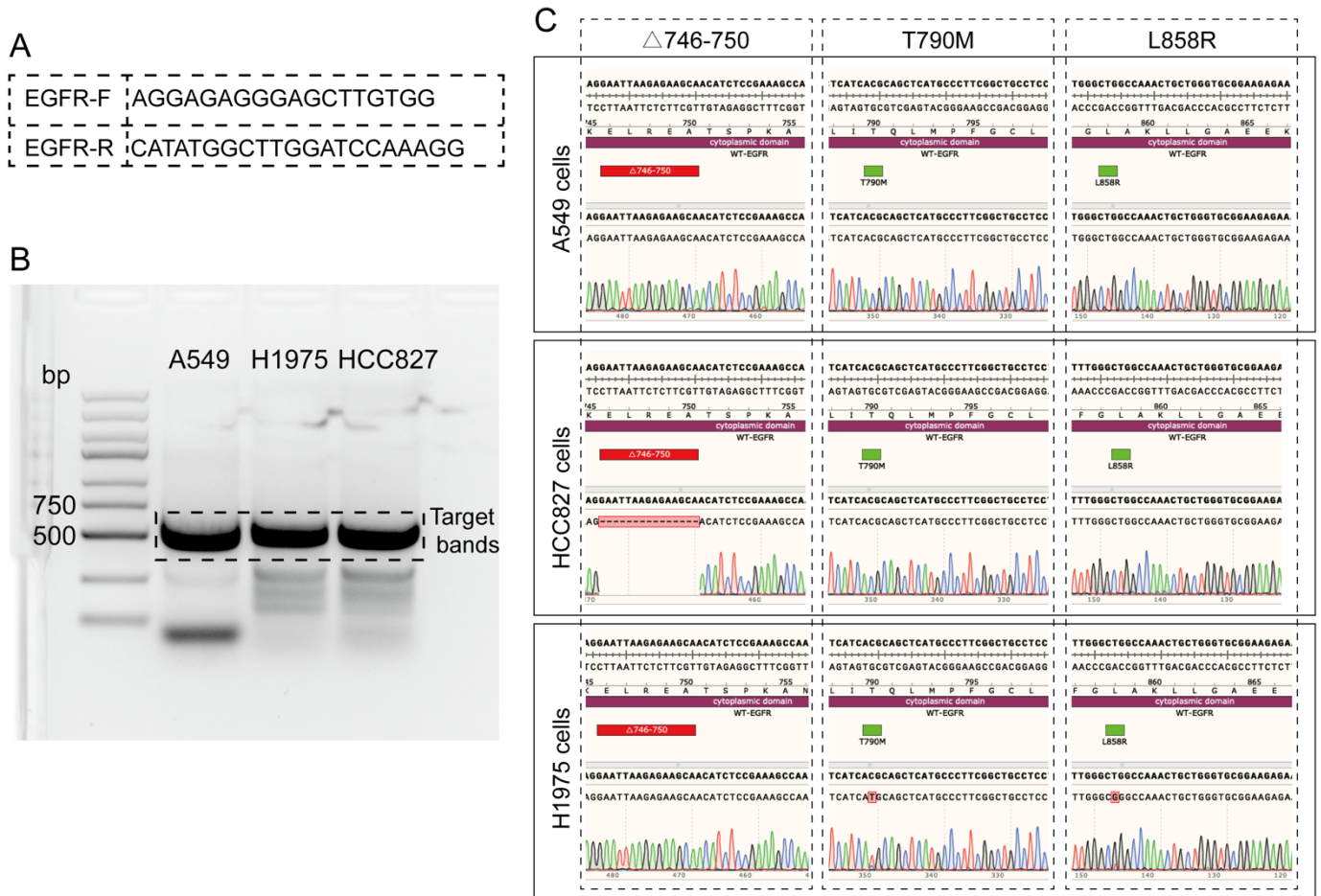
B

Genetic Site	Cell Bank information		Customer sample	
(Locus)	HCC827		HCC827	
Amelogenin	X	X	X	X
CSF1PO	11	11	11	11
D13S317	9	9	9	9
D16S539	12	12	12	12
D5S818	12	12	12	12
D7S820	11	12	11	12
THO1	6	6	6	6
TPOX	8	8	8	8
vWA	18	18	18	18
D21S11			31	31
Percent match between the sample and the database profile: 100%				

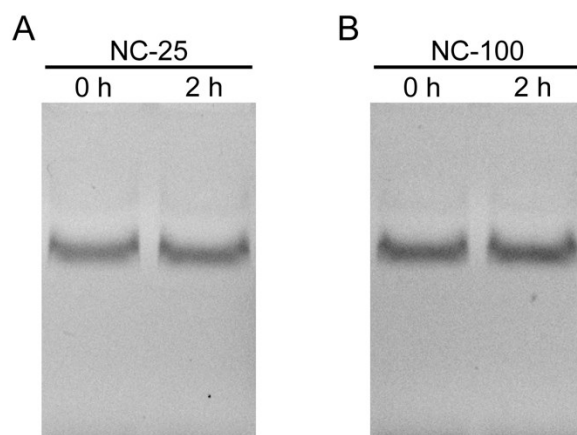
C

Genetic Site	Cell Bank information		Customer sample	
(Locus)	H1975		H1975	
Amelogenin	X	X	X	X
CSF1PO	12	12	12	12
D13S317	10	13	10	13
D16S539	9	12	9	12
D5S818	11	12	11	12
D7S820	8	11	8	8
THO1	7	7	7	7
TPOX	8	11	8	11
vWA	18	18	18	18
D21S11			28	28
Percent match between the sample and the database profile: 94%				

Supporting Data S3. STR identification results of various lung cancer cell lines. The purities of A549 (A), HCC827 (B) and H1975 (C) were verified by STR identification.



Supporting Data S4. Identification of A549, H1975, and HCC827 cell lines. (A) Nucleotide sequences of EGFR-F and EGFR-R primers. (B) The separation of PCR products (in 1% agarose gel) from EGFR-F and EGFR-R primers extensions. Marker: D2000 plus DNA Ladder. (C) Sequencing results of A549, HCC827, and H1975 cells exhibit their EGFR mutation status. The nucleotide sequence of EGFR (Human Gene, NM_005228.5) was downloaded from the *Ensembl website* and observed by the SnapGene software. Then, EGFR-F primers and EGFR-R primers at the corresponding positions of the shortest sequence fragments (approximately 500 bp) containing the E746_A750 deletion, L858R, and T790M were designed to compare the differences in the nucleotide sequence of EGFR in the three cell lines. These results demonstrate that no unwanted mutations or cell blending occurred during the culture period of three cell lines.



Supporting Data S5. Gel electrophoresis (1% agarose) results show the stability of DNA nanocalipers. (A) NC-25 was incubated in the detection environment for 0 h and 2 h. (B) NC-100 was incubated in the detection environment for 0 h and 2 h. The representative gel electrophoresis images show the respective signal expressions among various samples. The signal expression of DNA nanocalipers incubated in the detection environment for 0 h was consistent with that of the 2 h incubation, demonstrating that DNA nanocalipers remained structurally stable within the detection period.

Supporting Data S6. Identification of EGFR mutations by NGS and DNA nanocalipers.

Sample number	NGS		DNA nanocalipers
	Mutation type	Amino acid change	
1	Mutated EGFR	p. Leu858Arg	Mutated EGFR
	Mutated PTEN	p. Glu314fs	
2	Mutated EGFR	p. Glu746_Ser752delinsVal	Mutated EGFR
	Mutated BAP1	p. Ile47fs	
3	Mutated EGFR	E21	Mutated EGFR
	Mutated MET	E2	
4	Mutated EGFR	p. Glu746_Ala750del	Mutated EGFR
	Mutated TP53	p. Arg175His	
5	Mutated EGFR	p. Gly719Ser p. Glu709Ala	Mutated EGFR
	Mutated PMS1	p. Gln226*	
	Mutated RB1	p. Ser565*	
	Mutated WRN	p. Ser1141*	
	Mutated STK11	deletion	
6	Mutated EGFR	p. Leu861Gln	Mutated EGFR
	Mutated TP53	p. Trp53*	
	Mutated ERBB2	Amplification	
7	Mutated TP53	p. Ser166*	Wild-type EGFR
8	Wild-type EGFR	No mutation	Wild-type EGFR
9	Mutated KIF5B-RET	Fusion	Wild-type EGFR

Note: The standard of the quality examination offered by the service provider: The minimum DNA content requirement is 10 ng for NGS. The typical cancer/normal cell proportion should reach 25% for NGS.