

Supporting information

Use of a large Stokes-shift fluorophore to increase the multiplexing capacity of a point-of-care DNA diagnostic device

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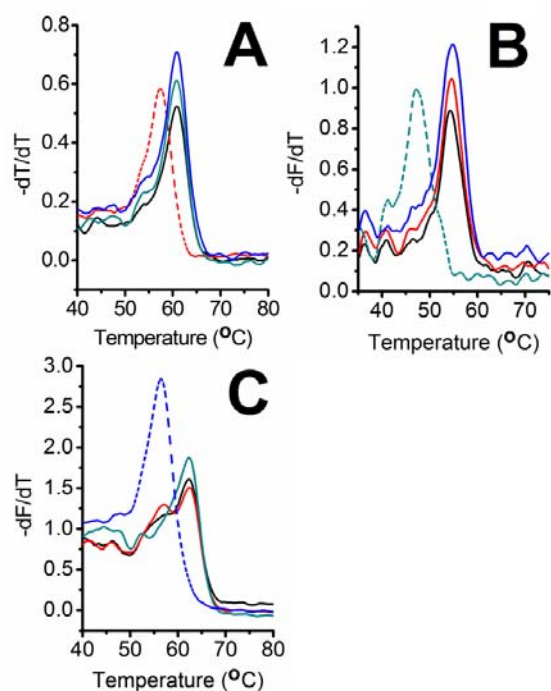


Figure S1; Melting curve derivatives of four samples performed on a Rotogene 3000 instrument, one containing wild-type targets for all three probes (Black), and three containing two wild-type and one mutant target, either C524X (Red), Δ F508 (Blue) or S466X (Cyan). Three channel combinations were used to analyze each sample, CH1 ex - CH1 em (A), Ch2 ex - CH2 em (B) and CH1 ex - CH2 em (C). Recognition of the mutant sequence by the corresponding probe is shown by dashed lines.

Table S1; Melting temperatures ($^{\circ}$ C) of samples containing three probes with either complementary target sequences, or one of the three available mutations, performed on a Rotogene 3000 instrument. T_m values of mismatched probes are underlined and mismatch/deletion is in parenthesis. (-TTT = triple T deletion).

Mutation located at	P-C524X/ C524X T_m	P-S466X/ S466X T_m	P- Δ F508/ Δ F508 T_m
No mutation	60.9	54.5	62.4
C524X	<u>57.4 (AG)</u>	54.5	62.5
S466X	60.8	<u>47.4 (GG)</u>	62.4
Δ F508	60.8	54.6	<u>56.5 (-TTT)</u>

Table S2; Sequences of target oligonucleotides used for probes in study, mutation sites in bold and underlined.

Name	Sequence
C524X WT	GTCATCAAAGCATG <u>C</u> CAACTAGAAGAG
C524X MT	GTCATCAAAGCATG <u>A</u> CAACTAGAAGAG
S466X WT	GACTT <u>C</u> ACTTCTAATGATGATTATGGGA
S466X MT	GACTT <u>G</u> ACTTCTAATGATGATTATGGGA
Δ F508 WT	CACCATTAAAGAAAATATCATC <u>TTT</u> GGTGTT
Δ F508 MT	CACCATTAAAGAAAATATCATCGGTGTT

Deconvoluted ESI⁺ mass spectra of probes acquired on Bruker micrOTOF

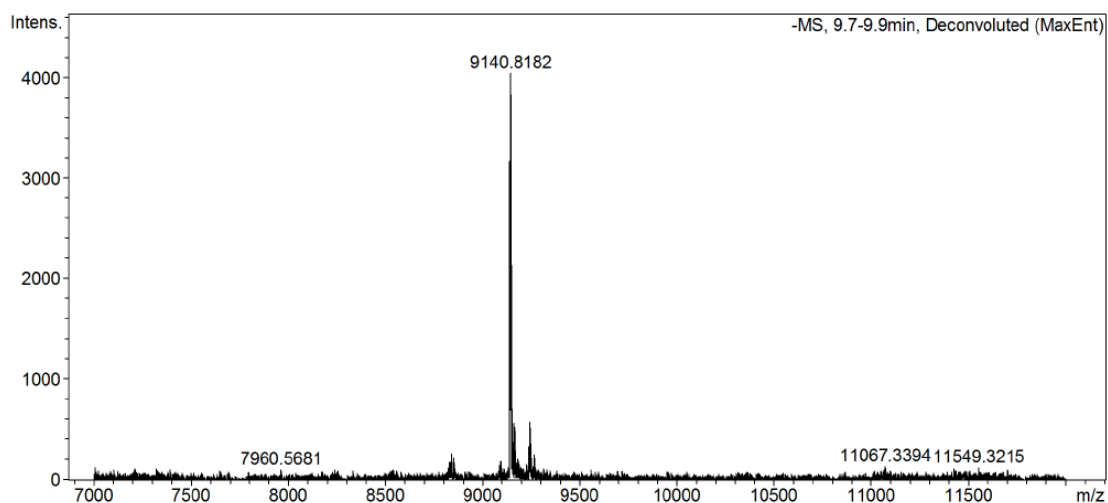


Figure S2; probe P- Δ F508. Found 9141, requires 9142.

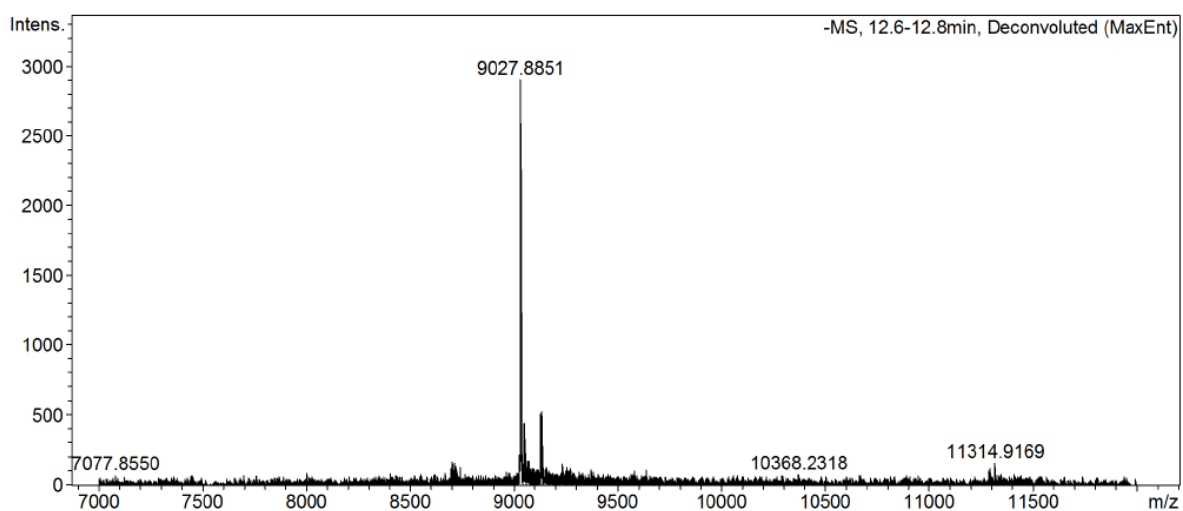


Figure S3; probe P-S466X. Found 9028, requires 9030.

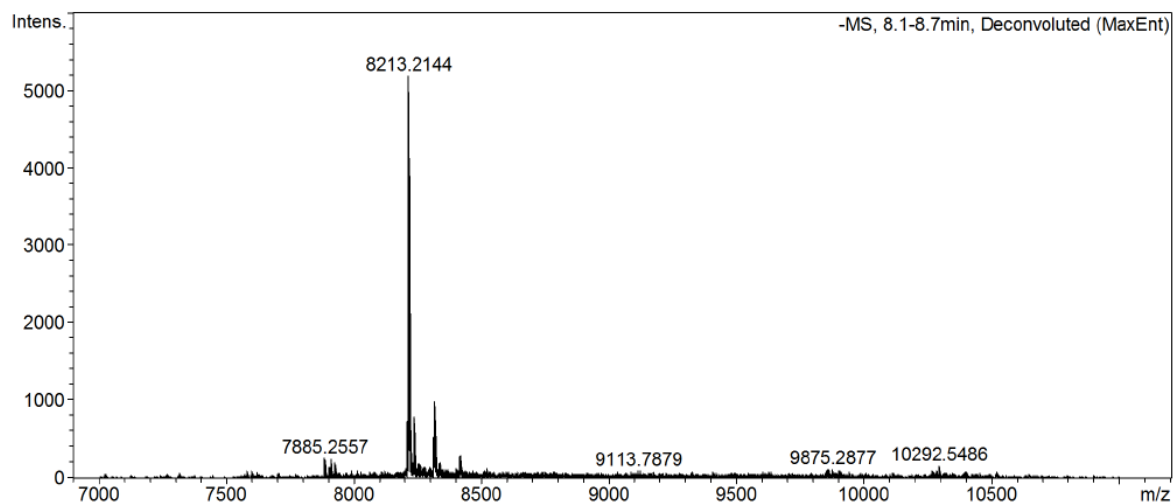


Figure S4; probe P-C524X. Found 8213, requires 8214.