Supplementary data for

Real-Time Kinetic Analysis and Detection of Glycated Hemoglobin A1c using Quartz Crystal Microbalance-Based Aptasensor

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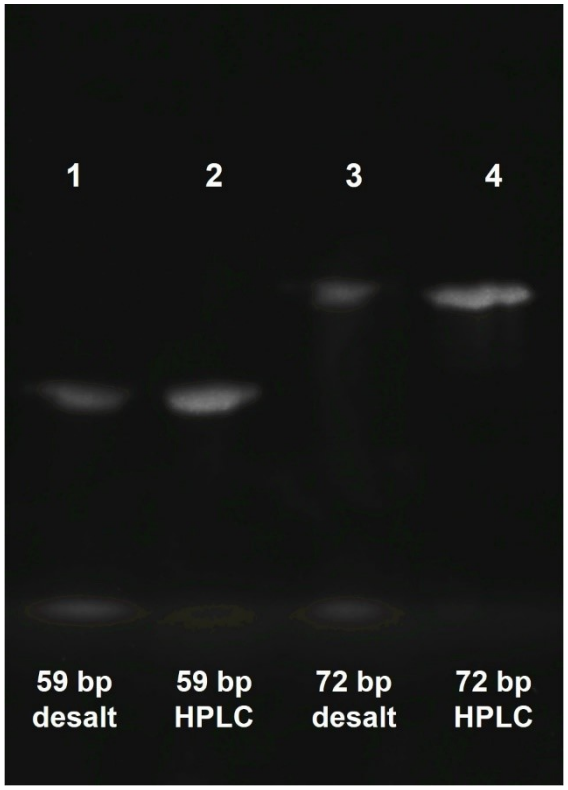


Fig. S1 Denatured polyacrylamide gel electrophoresis of HbA1c aptamers. 59-base aptamer desalt grade (lane 1), 72-base aptamer desalt grade (lane 2), 59-base HPLC grade (lane 3), 72-base HPLC grade (lane 4)

Table S1 Secondary structure simulation of each aptamer at the lowest ΔG value

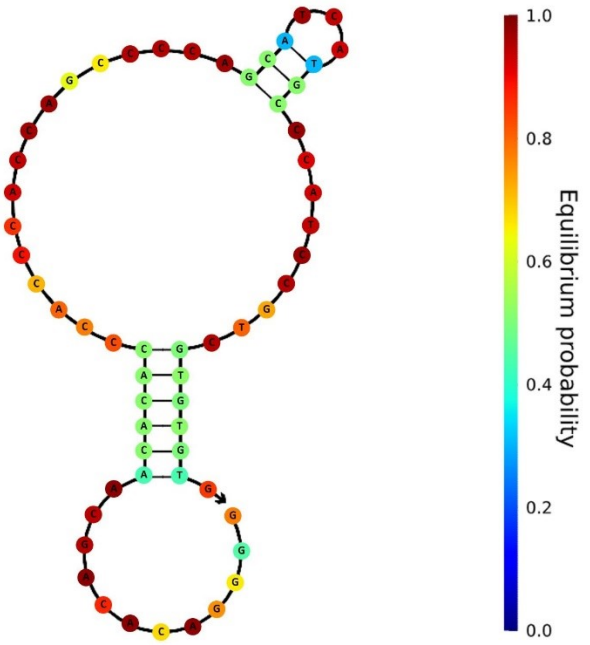
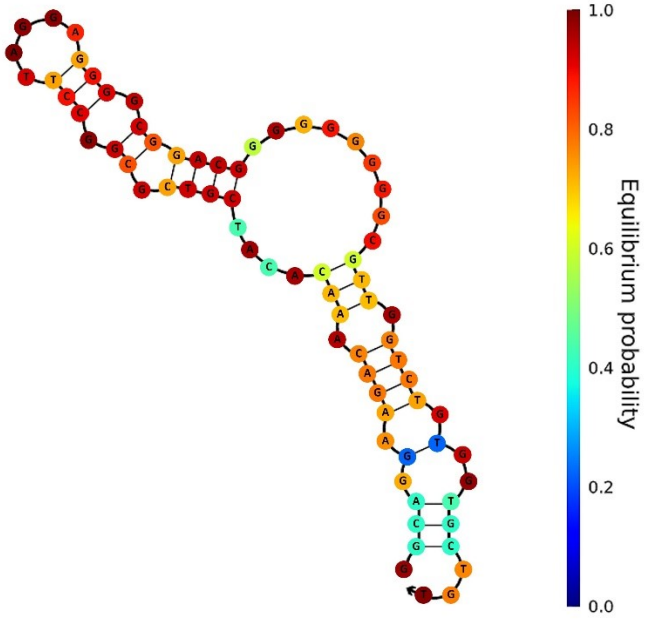
Structure	ΔG (kcal.mole^{-1})
59-base aptamer: 5′- GGG GAC ACA GCA ACA CAC CCA CCC ACC AGC CCC AGC ATC ATG CCC ATC CGT CGT GTG TG-3′ 	-3.22
72-base aptamer: 5′-GGC AGG AAG ACA AAC ACA TCG TCG CGG CCT TAG GAG GGG CGG ACG GGG GGG GGC GTT GGT CTG TGG TGC TGT-3′ 	-9.47

Table S2 Summary of the analyzed data using the Plot profile function from ImageJ.

Lane	Area	Mean	Min	Max	Integrated Density	Difference Integrated Density
1	64	65.649	46.50	70.965	4201.536	1557.824
2	64	41.308	37.98	45.728	2643.712	
3	64	87.673	56.925	94.157	5611.072	1981.632
4	64	56.710	52.519	61.658	3629.440	

The gel image (Fig. 2) was analyzed by the Plot profile function of ImageJ software. The integrated intensity of each lane was calculated from the product of the area (64 pixels for all lanes) and the mean gray value.

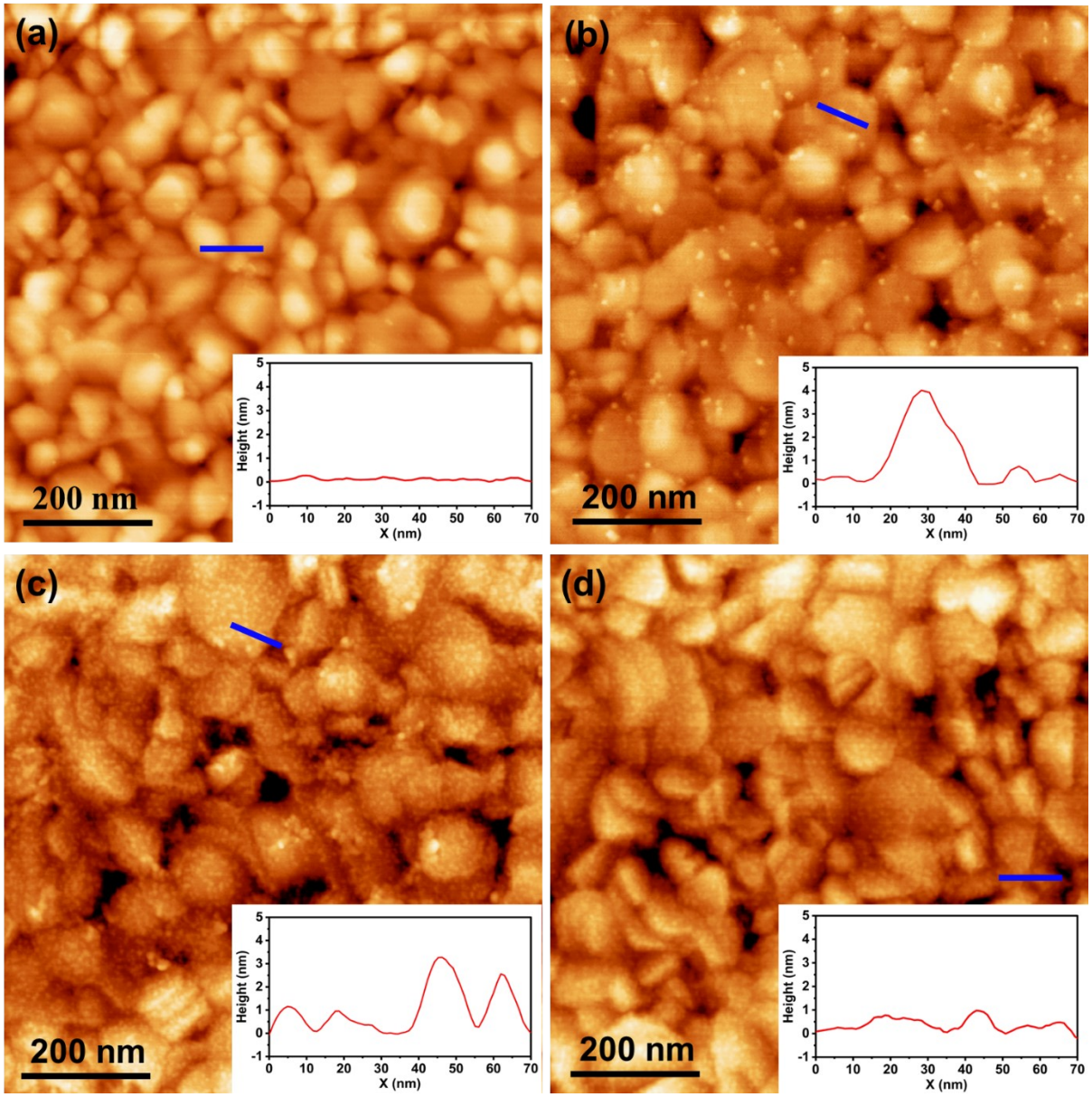


Fig. S2 Atomic force microscope (AFM) images of mixed SAMs-modified QCM substrates under different pretreatment processes: (a) bare gold (Au) on a quartz crystal, (b) normal preparation conditions (without pretreating the mixture), (c) ultrasonic pretreatment of the mixture for 1 min, and (d) ultrasonic pretreatment with horizontal shaking at 100 rpm during incubation overnight. The insets represent the height profile of the surface corresponding to the blue lines.

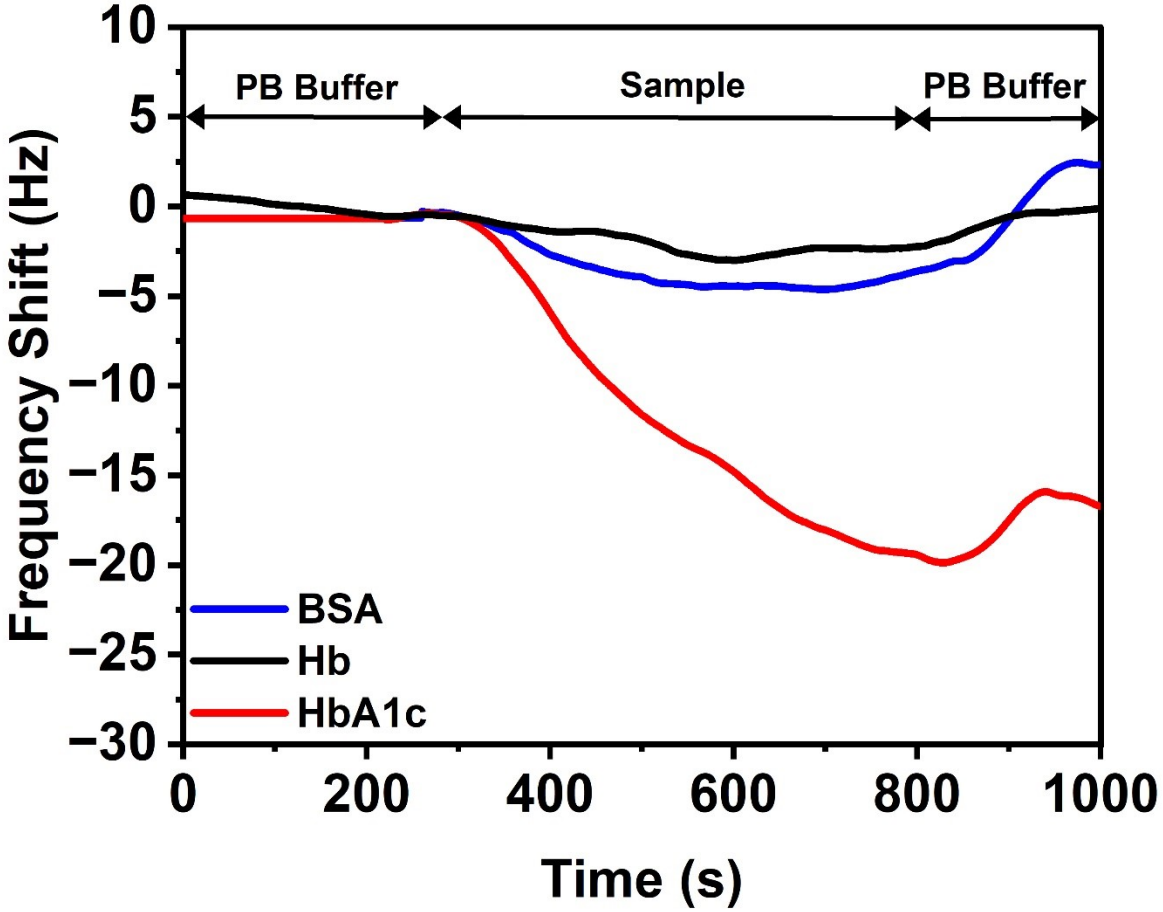


Fig. S3 QCM signals of non-specific adsorption of BSA (blue), Hb (black), and HbA1c (red) on aptamer functionalized surfaces.

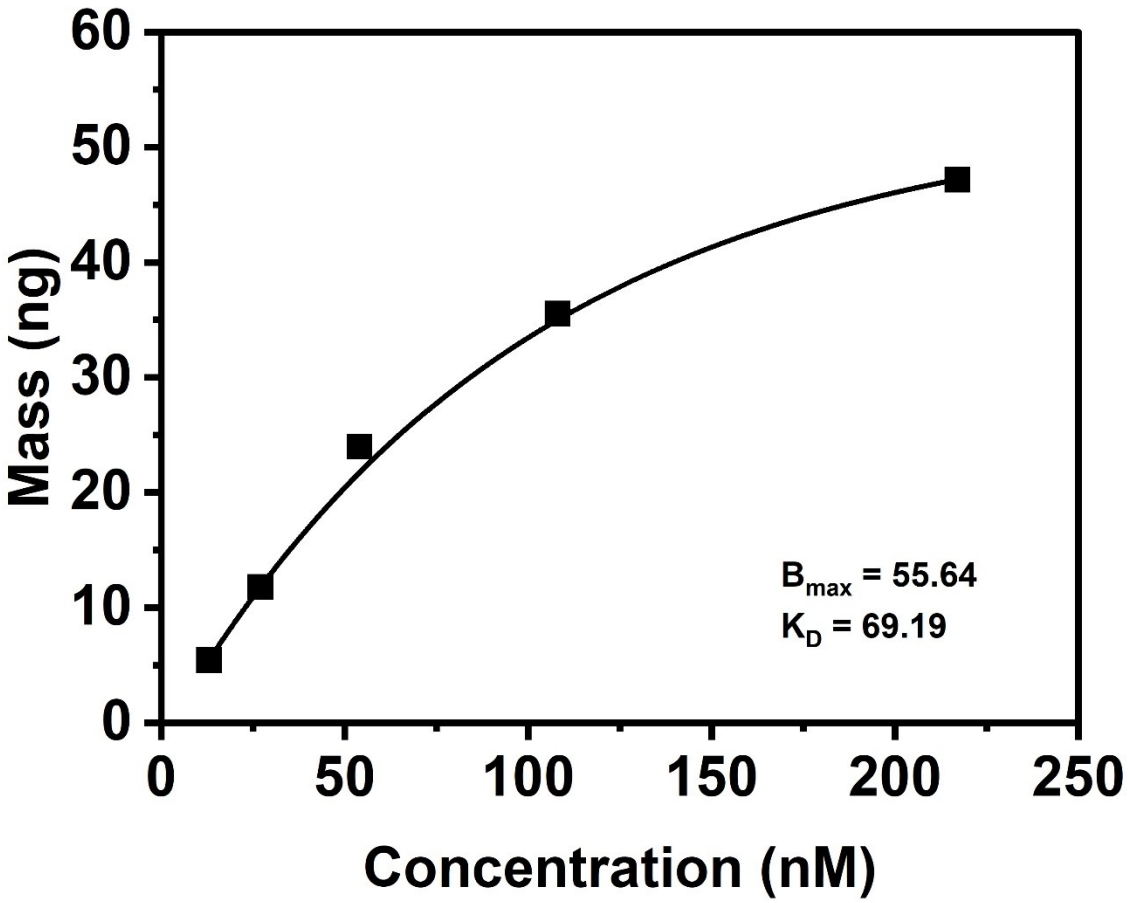


Fig. S4 The equilibrium characterization by using the saturation binding curve. Fitting the mass and HbA1c concentrations with the one-site specific binding model gave the K_D of 69.19 nM.

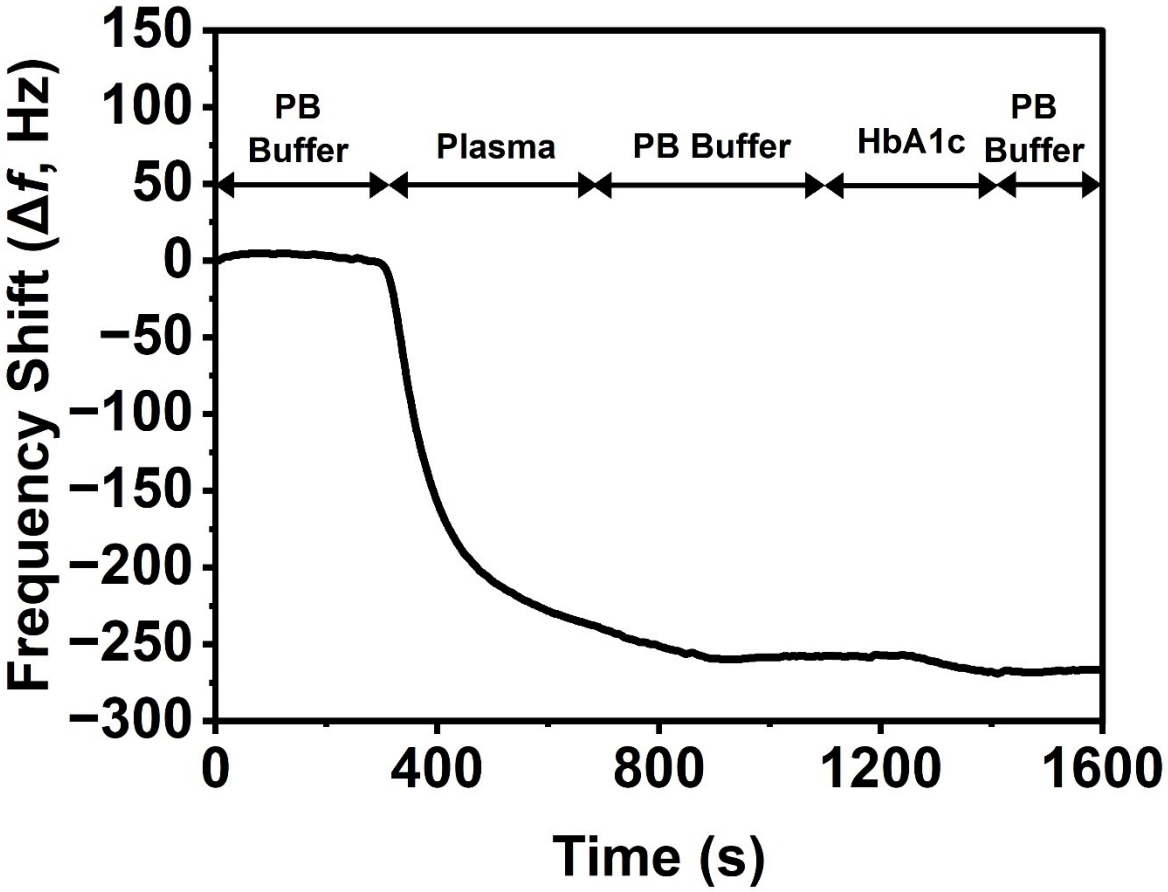


Fig. S5 A representative QCM measurement of spiked samples in real human plasma. The diluted human plasma was first introduced for 10 min to establish a baseline, followed by the injection of spiked sample.