Supporting Information

Label-free, multiplexed detection of bacterial tmRNA using

silicon photonic microring resonators

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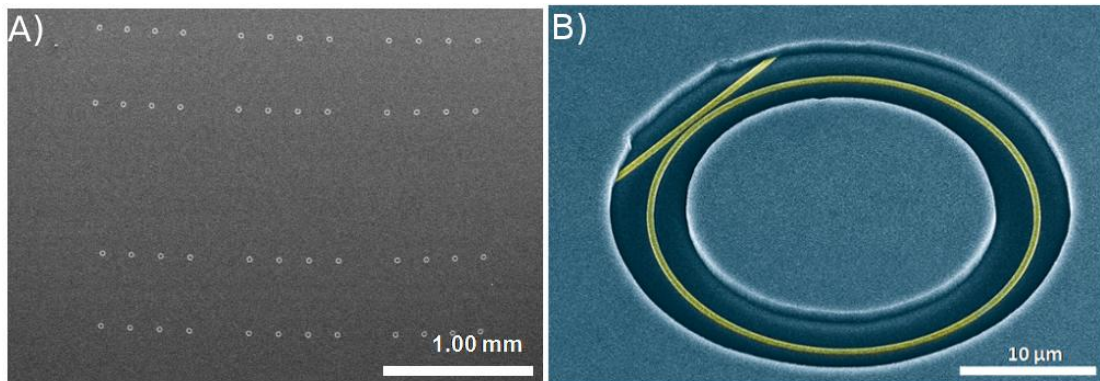
SEM Image of Microring Resonator

Figure S1. A) Each 6 x 6 mm sensor chip contains an array of 32 microring sensors, of which 24 are active and 8 are thermal reference controls. The 200 µm spacing between sensors enables the rings to be individually addressed with standard spotting technologies. B) False color SEM image of the interface between the microring structure and the adjacent linear waveguide as seen through the annular opening in the fluoropolymer cladding layer. The microring diameter is 30 µm and the waveguide separation is 200 nm.

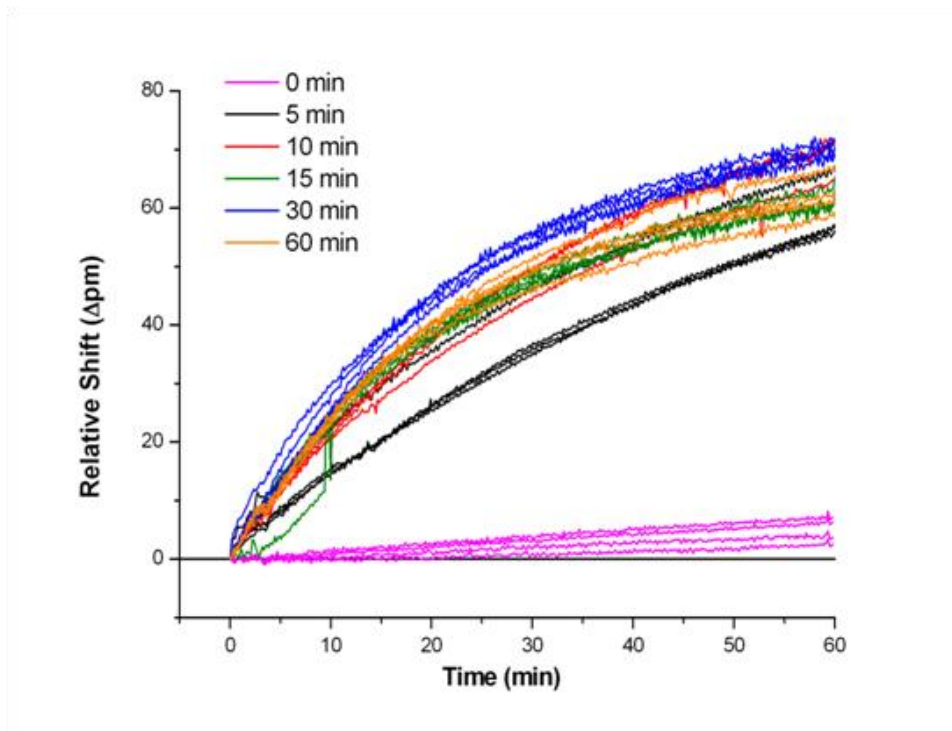**Hybridization response as a function of fragmentation time**

Figure S2. Varied hybridization responses as a function of fragmentation time, ranging from 0 to 60 minutes. 15 minutes was used in experiments, as it was the minimal time required to achieve complete fragmentation. The results of at least three separate identically modified microrings are plotted.

Sequences of ssrA genes: Genes were cloned into plasmid vectors, and degenerate ssrA primers were used to prepare and sequence amplicons from target organisms. Sequences have been edited to remove ambiguous readings from ends.

>*Streptococcus pneumoniae* ATCC 33400
TTCGACAGGCATTATGAGGCATATTTTGCGACTCGTGTGGCGACGTAAACGCTCAGTTAAATATAACTGCAAAAAA
TAACACTTCTTACGCTCTAGCTGCCTAAAAACCAGCAGGCGTGACCCGATTTGGATTGCTCGTGTTCAATGACAGG
TCTTATTATTAGCGAGATACGATTAAGCCTTGTCTAGCGGCTTGATAAGAGATTGATAGACTCGCAGTTTCTAGACT
TGAGTTATGTGTCGAGGGGCTGTTAAAATAATACATAACCTATGGTTGTAGACAAATATGTTGGCAGGTGTTTGGA
CG

>*Streptococcus agalactiae*
TTCGACAGGCATTATGAGGTATATTTCGCGACTCATCGGCAGATGTAAAATGCCAGTTAAATATAACTGCAAAAAA
TACAAATTCTTACGCATTAGCTGCCTAAAAAACAGCCTGCGTGATCTTCACAAGATTGTTTGCGTTTTGCTAGAAGG
TCTTATTTATCAGCAAACTACGTTTGGCTACTGTCTAGTTAGTTAAAAAGAGATTTATAGACTCGCTATGTGAGGGC
TTGAGTTATGTGTCATCACCTAGTTAAATCAATACATAACCTATAGTTGTAGACAAATATATTAGCAGATGTTTGGA
CG

>*Enterococcus faecium*
GGGGACGTTACGGATTCGACAGGCACAGTCGAGCTTGAATTGCGTTTCGTAGGTTACGTCTACGTAAAAACGTTA
CAGTTAAATATAACTGCTAAAAACGAAACAACTCTTACGCTTTAGCTGCCTAAAAACAGTTAGCGTAGATCCTCTC
GGCATCGCCCATGTGCTCGAGTAAGGGTCCTAACTTTAGTGGGATACGTTTCAACTTTCCGTCTGTAAGTTGAAAA
AGAGAACATCAGACTAGCGATACAGAATGCCTGTCACTCGGCAAGCTGTAAAGTGAATCCTTAAATGAGTTGACT
ATGAACGTAGATTTTTAAGTGGCGATGTGTTTGGACGCGGGTTCGACTCCCGCCGTCTCCACCA

>*Klebsiella pneumoniae* ATCC 13883
TTCGACGGGATTTGCGAAACCCAAGGTGCATGCCGAGGGGCGGTTGGCCTCGTAAAAAGCCGCAAAAAATAGTC
GCAAACGACGAAAACTACGCTTTAGCAGCTTAATAACCTGCTCTGAGCCCTCTCTCCCTAGCTTCCGCTCTTAAGAC
GGGGATCAAAGAGAGGTCAAACCCAAAAGAGATCGCGTGGATGCCCTGCCTGGGGTTGAAGCGTTAAATCTAAT
CAGGCTAGTTTGTTAGTGGCGTGTCTGTCCGCAGCTGGCAAGCGAATGTAAAGACTGACTAAGCATGTAGTGCCG
AGGATGTAGGAATTTCGGACC

Table S1. Fitting parameters utilized for the 1:1 Langmuir kinetic binding isotherm for varying concentrations of tmRNA.

tmRNA	A (pm)	B (min^{-1})	t_0 (min)	AB (pm/min)	χ^2	R^2
16.6 pmol	92.5754	0.1730	-1.2423	16.0156	9.8382	0.9577
	89.5685	0.1652	-1.2827	14.7967	8.7604	0.9612
	91.9702	0.1854	-1.1798	17.0513	7.7875	0.9638
5.24 pmol	81.8943	0.0894	-0.7974	7.3173	3.2140	0.9909
	87.7340	0.0805	-0.8410	7.0582	1.8900	0.9955
	80.7949	0.0928	-0.6570	7.4953	1.7206	0.9950
1.66 pmol	77.6464	0.0334	-0.0376	2.5942	0.3331	0.9991
	79.0721	0.0351	0.0541	2.7723	0.3133	0.9992
	95.7390	0.0280	1.1308	2.6826	7.4294	0.9859
	67.4506	0.0442	0.2027	2.9779	0.3974	0.9987
524 fmol	84.9326	0.0108	0.8607	0.9207	0.6647	0.9953
	64.3997	0.0138	-0.0996	0.8900	0.6270	0.9943
	75.1582	0.0103	-0.1769	0.7704	0.5990	0.9940

Table S2. Fitting parameters utilized for linear fits for varying concentrations of tmRNA

tmRNA	Slope (pm/min)	Slope Error (pm/min)	Intercept (pm)	Intercept Error (pm)	R^2
166 fmol	0.5270	0.0817	0.1612	0.0024	0.9253
	-1.3564	0.0877	0.2047	0.0025	0.9455
	1.0046	0.0845	0.1403	0.0024	0.8976
	-0.1234	0.0828	0.1295	0.0024	0.8863
0 fmol	-0.7517	0.0767	0.0079	0.0022	0.0297
	-0.0098	0.0804	-0.0265	0.0023	0.2538
	-0.6313	0.0858	-0.0504	0.0025	0.5217
	-1.4223	0.0780	-0.0592	0.0023	0.6449