Electronic Supplementary Information (ESI)

Single Particle ICP-MS-Based Absolute and Relative Quantification of E. coli O157 16sRNA using sandwich hybridization capture

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Table S1. Oligonucleotide sequences employed in the experiments.

Name	Antisense sequences (5′-3′)
Cracking primers	SS-TTTTTTTT-PC-TTTT-PC-TTTTTTGGCAGCACCGACGTAGAC
Detector probe	TCTTCCTGTTACCGTTCGACTTGCATTTTTTGTCTACGTCGGTG CTGCC
Capture probe	Biotin-TTTTTTTTTTACTCGTCAGCAAAGAAGCAAGCT
Target	TGCAAGTCGAACGGTAACAGGAAGAAGCTTGCTTCTTTGCTG ACGAGT
Single-base-mismatched target	TGCAGGTCGAACGGTAACAGGAAGAAGCTTGCTTCTTTGCTG ACGAGT

Note: Sequences that are labeled with the same color represent the same or complementary sequences.

Table S2. ICP-MS operational conditions

Parameter	Value
RF power (W)	1750 W
Plasma Gas (L/min)	17
Aux Gas (L/min)	1
Neb Gas (L/min)	1.05
Sample Uptake Rate (mL/min)	0.3
Dwell time (ms)	3 ms
Duration time	60 s

Table S3. Comparison of different assays for DNA/RNA detection.

Methods	Limit of detection	Specificity	RSD	Absolute quantification ability
Inductively coupled plasma mass spectrometry (ICP-MS) [1]	6 pM	High	Not reported	Yes
Single Particle inductively coupled plasma mass spectrometry （SP-ICP-MS)[2]	1 pM	High	Not reported	No
LAMP [3]	1 aM	High	Not reported	No
Rolling circle amplification (RCA) [4]	10 fM	High	4.30%	No
Helicase dependent amplification (HDA) [5]	12.8 fM	High	~10%	No
SHC-SP-ICP-MS	10 fM	High	<35%	Yes

References

1 K. Brückner, K. Schwarz, S. Beck and M. W. Linscheid, *Anal. Chem.*, 2014, **86**, 585–591.

2 G. Han, Z. Xing, Y. Dong, S. Zhang and X. Zhang, *Angew. Chemie - Int. Ed.*, 2011, **50**, 3462–3465.

3 C. Ma, D. Han, M. Deng, J. Wang and C. Shi, *Chem. Commun.*, 2015, **51**, 553–556.

4 P. Zhang, X. Wu, R. Yuan and Y. Chai, *Anal. Chem.*, 2015, **87**, 3202–3207.

5 F. Ma, M. Liu, B. Tang and C. Zhang, *Rapid and Sensitive Quantification of MicroRNAs by Isothermal Helicase-Dependent Amplification*, 2017, vol. 89.

Figure S1. The transport efficiency evaluation of the method performance : correlation between theoretical number of particles and the actual number of particles measured by SP-ICP-MS. The linearity range was evaluated in terms of particle number concentration. Suspensions of standards with 30 nm size were used to prepare dilutions containing (2×10^2, 2×10^3, 2×10^4, 2×10^5, 5×10^5, 2×10^6) particles mL^{-1}, respectively. Error bars are standard deviation of three repetitive experiments.

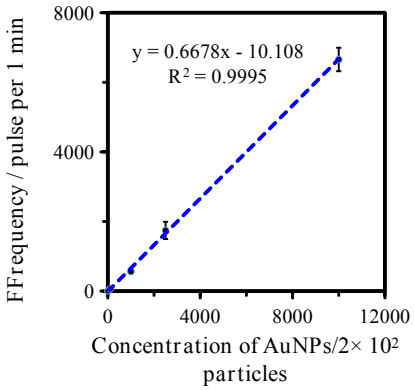

Figure S2. Comparison of the performance of pegylated colloidal gold, mix-labeled colloidal gold, and DNA labeled colloidal gold in enabling a low blank value assay. Bars represent the frequency intensity per 1 min of the different labeled colloidal gold nanoparticles in a no-target sandwich hybridization reaction-capture. Error bars represent the standard deviation of three experiments.

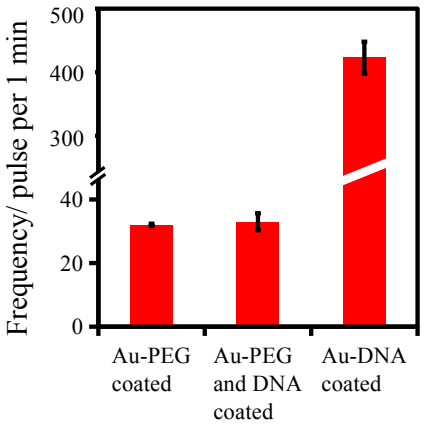

Figure S3. Au signal counts with different ratios of AuNP/target (2.5:1, 250:1, 1250:1, 2500:1) at a 500 fM target concentration. Error bars represent the standard deviation of three experiments.

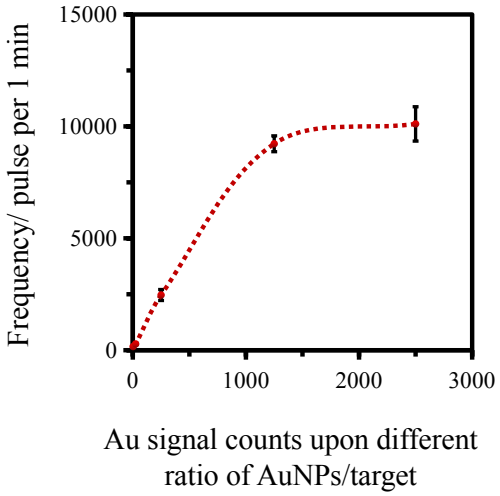

Figure S4. Au signal counts frequency upon illumination for 10 min, 30 min, 60 min, 90 min and 120 min, at a 500 fM target concentration. The ratio of AuNPs to target was 1000:1. Error bars represent the standard deviation of three experiments.