Denyes et al. - Supplemental Material

Table S1: Optimization of LTF-MB enrichment protocol. A generalized setup of 7.00 x 10^4 beads/µL, 10^4 *S.* Typhimurium DB7155 cells, PBS buffer pH 7.0, 250 mM NaCl, was used to analyze three variables: density beads per assay, pH, and NaCl concentration. Recovery rates are reported as a percentage of bead-enriched *Salmonella* cells / total *Salmonella* cells. Experiments were performed in triplicate and presented as mean ± Standard Deviation (SD).

Tested variable		Rate of Recovery % (mean ± SD)
Bead density (beads/µL)	1.75 x 10^4	90 ± 2
	7.0 x 10^4	98 ± 2
	1.75 x 10^5	98 ± 1
	2.45 x 10^5	98 ± 1
	3.5 x 10^5	98 ± 2
Buffer and pH	Citrate pH 3	2 ± 0.1
	Citrate pH 4	21 ± 2
	Citrate pH 5	98 ± 0.5
	Citrate pH 6	97 ± 2
	PBS pH 7	98 ± 1
	PBS pH 8	98 ± 1.5
	PBS pH 9	96 ± 2
Buffer NaCl concentration	0 mM	98 ± 1
	125 mM	98 ± 1
	250 mM	98 ± 1.1
	500 mM	93 ± 1
	750 mM	95 ± 1
	1 M	90 ± 5

Table S2: Calculating $A.U._{450nm}$ / initial *Salmonella* cell numbers ($log_{10}CFU$) to quantify the discrepancy in labeling efficiency of ELLTA. The mean $A.U._{450nm}$ data from duplicate measurements was blank subtracted and divided by the mean number of cells per assay ($log_{10}CFU$). The $A.U.log_{10}CFU^{-1}$ per strain is tabulated in order of binding strength. $A.U.log_{10}CFU^{-1}$ values of 0.01 or negative indicate no labeling by HRP-LTF.

Salmonella strains	Designation	$A.U._{450nm}$ (raw)	$Absorbance_{raw}$ -0.24_{blank}	$log_{10}CFU$ per assay	$Abs_{correct}$/ $log_{10}CFU$ ($AU.log_{10}CFU^{-1}$)
S. Typhimurium	DB7155	3.02	2.79	5.86	0.48
S. Javiana	N2427-08	2.92	2.69	5.84	0.46
S. Indiana		2.81	2.58	5.90	0.44
S. Typhimurium	N11-2063	2.82	2.59	6.11	0.42
S. Typhimurium LT2	ATCC 14028	2.43	2.19	5.68	0.39
Salmonella bongori	N268-08	2.59	2.36	6.10	0.39
S. Newport	N2932-08	2.43	2.20	5.82	0.38
S. Typhimurium	N11-2679	2.46	2.23	6.05	0.37
Salmonella enterica ssp. *diarizonae*	N09-2338	2.50	2.27	6.27	0.36
S. Heidelberg	N2743-08	2.22	1.99	6.25	0.32
Salmonella enterica ssp. *salamae*	N09-2794	2.13	1.90	6.36	0.30
S. Typhimurium	N11-2388	1.94	1.70	6.09	0.28
S. Typhimurium	N07-1209	1.86	1.63	6.22	0.26
S. Typhimurium	N11-2663	1.74	1.50	6.22	0.24
S. Newport	WS2681	1.69	1.46	6.22	0.23
S. Enteritidis C		1.55	1.31	5.99	0.22
Salmonella enterica ssp. *houtenae*	N09-2589	1.25	1.02	6.39	0.16
S. Infantis		1.14	0.91	6.25	0.15
S. Hadar	WS 2691	0.97	0.74	5.62	0.13
Salmonella enterica ssp. *arizonae*	N09-0860	0.79	0.55	6.36	0.09
S. Montevideo	WS2678	0.62	0.39	6.27	0.06
Non-*Salmonella* strains					
Bacillus cereus	HER 1399	0.29	0.05	5.37	0.01
Cronobacter sakazakii	ATCC 29544	0.27	0.03	6.43	0.01
Citrobacter freundii	N 0106	0.24	0.00	6.25	0.00
Bacillus atrophaeus (subtilis)	ATCC 9372	0.16	-0.07	5.24	-0.01
Enterobacter aerogenes	DSM 30053	0.17	-0.07	6.30	-0.01
Escherichia coli	CGSC4401	0.17	-0.06	5.62	-0.01
Escherichia vulneris	DSM 4564	0.15	-0.09	6.21	-0.01
Listeria monocytogenes	WSLC 1001	0.15	-0.08	6.20	-0.01
Klebsiella	1319	0.13	-0.10	6.54	-0.02
Staphylococcus aureus	ATCC 19685	0.08	-0.16	N/A	N/A

Figure S1: Enzyme-linked LTF Assay (ELLTA) workflow. **1)** LTF-MBs are incubated for 45 minutes with aliquots of (**A**) pre-enriched food samples or (**B**) bacterial dilutions. **2)** LTF-MBs are magnetically separated and washed with PBS-T. **3)** Either LTF-MBs are resuspended in PBS-T and plated on selective agar for colony counting to determine initial contamination numbers, or **4)** for ELLTA, after washing the LTF-MBs are incubated for 30 minutes with the HRP-LTF probe. **5)** After magnetic separation and washing, TMB solution is incubated with the beads for 15 minutes and is converted by the bacteria-bound HRP-LTF probe to the blue chromogen. **6)** The LTF-MBs are magnetically separated and the catalyzed TMB solution dispensed into 96 well plates for spectrophotometric absorbance measurements after acidification with H_2SO_4 to produce a yellow chromogen for increased measurement sensitivity.