Supporting Information

Multianalyte lateral flow immunoassay for simultaneous detection of protein-based inflammation biomarkers and pathogen DNA

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Table of Content:

Figure S1. Optimization of the IAC-DNA concentration

Figure S2. Analysis of the fluorescence signal at the DNA- and Protein-TL and representative lateral flow strips of the Multianalyte-Assay.

Table S1. Primers, probes and internal amplification control-DNA sequences.

Table S2. Mean, standard deviation (SD), and coefficient of variation (CV) of the "IL-6 added after RPA" assay.

Table S3. Comparing Multianalyte-Assay, reference assays, and "IL-6 added after RPA" assay regarding signal differences at the Protein- and DNA-TL.

 Table S4. Sigmoidal fit curve analysis.

Table S5. Mean, standard deviation (SD), coefficient of variation (CV) and limit of detection (LOD) of the Multianalyte-Assay and reference assays.



Figure S1. Optimization of the IAC-DNA concentration. To exclude false negative amplification results, a competitive IAC was designed that is co-amplified with the target DNA. This means, the same set of primers was used to amplify IAC- and target DNA. A specific IAC-probe allowed the separate detection of the IAC-DNA amplicons. Since, IAC- and target DNA compete for the same primers, the IAC-DNA concentration needs to be held at the lowest concentration leading to reproducible IAC-DNA amplification. We added 23 cp/reaction, 230 cp/reaction, or 2,300 cp/reaction of IAC-DNA to the Multianalyte-Assay (200 ng/ml IL-6 and 0 cp/reaction *P. aeruginosa* gDNA). A minimum of 230 cp/reaction was required for a clear IAC signal. cp, copies; TL, test line; IAC, internal amplification control; FC, flow control.



Figure S2. Analysis of the fluorescence signal at the DNA- and Protein-TL and representative lateral flow strips of the Multianalyte-Assay. **(A)** Analysis of the DNA-TL (red) for samples (Sample 1-9) containing 10^6 copies/reaction *P. aeruginosa* gDNA combined with 1-200 ng/mL IL-6. Since, the same amount of gDNA was added to each sample we observed a constant fluorescence signal at 16,877,612±1,470,312 RFU (CV of 8.7 %). The analysis of the Protein-TL (yellow) – 1-200 ng/mL were

added to each sample – is shown in Figure 3. **(B)** Analysis of the Protein-TL (yellow) for samples (Sample 1-9) containing 200 ng/mL IL-6 combined with 10^{0} - 10^{6} copies/reaction gDNA. Since, the same amount of IL-6 was added to each sample we observed a constant fluorescence signal at 9,371,882±1,242,955 RFU (CV of 13.3 %). The analysis of the DNA-TL (red) – 10^{0} - 10^{6} copies/reaction were added to each sample – is shown in Figure 3. The IAC (red) excluded false negative results and together with the FCs (yellow and red) ensured the validity of the test result. The experiments were conducted three times in triplicates. The error bars indicate one standard deviation. cp, copies; TL, test line; IAC, internal amplification control; FC, flow control; CV, coefficient of variation.

Name	Sequence (5'-3')
lasB-fwd primer	GAGAATGACAAAGTGGAACTGGTGATCCGCCTG
lasB-rev primer	Dig-GCCAGGCCTTCCCACTGATCGAGCACTTCGCCG
lasB probe	Biotin-GAACAACATCGCCCAACTGGTCTA CAACGT[THF]TCCTACCTGATTCCC-C3 spacer
IAC-probe	DNP-CAACTGCAGGGACGATTCCTTTGTCC CGAT[THF]CGACCAGCTCAACTC-C3 spacer
IAC-DNA	AAGACCGAGAATGACAAAGTGGAACTGGTGATCCGCCTGGGCGATATAC ACTCATCCCTC <u>CAACTGCAGGGACGATTCCTTTGTCCCGATTCGACCAGC</u> <u>TCAACTCAGGTGTCCTCATGAA</u> GGCGAGGGACTGTCGCGGCCGCATTTCG TCATCGACGCCAAGACCGGCGAAGTGCTCGATCAGTGGGAAGGCCTGGC CCACGC

Table S1. Primers, probes and internal amplification control-DNA sequences.

Dig, digoxigenin; THF, tetrahydrofuran; C3 spacer, polymerase extension blocking group; DNP, dinitrophenyl; IAC-DNA, internal amplification control-DNA; underlined sequence, fish virus DNA sequence.

Table S2. Mean, standard deviation (SD), and coefficient of variation (CV) of the "IL-6 added after RPA" assay. The IL-6 was added after the RPA reaction directly to the LFIA.

Mean, SD, and CV of "IL-6 added after RPA" Assay (Figure 2)										
Sample (IL-6 was added after RPA to the LFIA)										
IL-6 [ng/mL]	0	10	50	200	200	200	200			
gDNA [cp/react.]	106	106	10 ⁶	10 ⁶	104	10 ²	0			
Analysis of the Pr	otein-TL									
Mean [RFU]	159,896	1,327,839	5,646.520	12,148,815	12,552,290	12,713,553	12,694,232			
SD [RFU]	52,154	232,325	677,719	1,599,146	1,884,486	1,633,700	1,695,599			
CV [%] 33 17 12 13 15 13 13										
Analysis of the DNA-TL										

Mean [RFU]	16,741,322	19,800,875	19,919,971	20,158,056	19,471,840	8,747,130	3,575,449
SD [RFU]	1,418,412	904,239	889,147	1,049,164	1,129,021	1,511,582	1,029,275
CV [%]	8	5	4	5	6	17	29

Table S3. Comparing Multianalyte-Assay, reference assays, and "IL-6 added after RPA" assay regarding signal differences at the Protein- and DNA-TL.

	Signal difference: Protein-TL								
	IL-6 Referen Multianal	ice Assay vs. yte-Assay	IL-6 Referer "IL-6 added ass	nce Assay vs. after RPA" say	"IL-6 added after RPA" assay vs. Multianalyte- Assay				
IL-6 [ng/mL]] Δ [RFU] Δ [%] Δ [RFU] Δ [%]		Δ [%]	Δ[RFU]	Δ [%]				
0	30,530	16	30,530	16	0	0			
10	1,089,513	63	401,985	23	687,527	52			
50	3,207,760	50	789,537	12	2,418,223	43			
200	5,291,471	37	2,107,866	15	3,183,605	26			
			Signal differe	nce: DNA-TL					
	IL-6 Referen Multianal	ice Assay vs. yte-Assay	Signal differe IL-6 Referer "IL-6 added ass	nce: DNA-TL nce Assay vs. after RPA" say	"IL-6 added assay vs. M Ass	after RPA" ultianalyte- say			
gDNA [cp/reaction]	IL-6 Referen Multianal Δ [RFU]	ice Assay vs. yte-Assay Δ [%]	Signal differe IL-6 Referer "IL-6 added ass Δ [RFU]	nce: DNA-TL nce Assay vs. after RPA" say Δ [%]	"IL-6 added assay vs. M Ass Δ [RFU]	after RPA" ultianalyte- say Δ[%]			
gDNA [cp/reaction] 0	IL-6 Referen Multianal Δ [RFU] 138,362	ice Assay vs. yte-Assay Δ[%] 6	Signal differe IL-6 Referer "IL-6 added ass Δ [RFU] -534,032	nce: DNA-TL nce Assay vs. after RPA" say Δ [%] 22	"IL-6 added assay vs. M Ass Δ [RFU] 395,671	after RPA" ultianalyte- say Δ [%] 13			
gDNA [cp/reaction] 0 10 ²	IL-6 Referen Multianal Δ [RFU] 138,362 2,089,428	ice Assay vs. yte-Assay Δ[%] 6 30	Signal differe IL-6 Referer "IL-6 added ass Δ [RFU] -534,032 -1,789,996	nce: DNA-TL nce Assay vs. after RPA" say Δ [%] 22 26	 "IL-6 added assay vs. M Ass Δ [RFU] 395,671 3,879,423 	after RPA" ultianalyte- say Δ[%] 13 44			
gDNA [cp/reaction] 0 10 ² 10 ⁴	IL-6 Referen Multianal Δ [RFU] 138,362 2,089,428 194,218	ice Assay vs. yte-Assay Δ[%] 6 30	Signal differe IL-6 Referer "IL-6 added ass Δ [RFU] -534,032 -1,789,996 -1,013,333	nce: DNA-TL nce Assay vs. after RPA" say Δ [%] 22 26 5	 "IL-6 added assay vs. M Ass Δ [RFU] 395,671 3,879,423 1,207,551 	after RPA" ultianalyte- say Δ [%] 13 44 6			

 Table S4. Sigmoidal fit curve analysis.

Sigmoidal fi	it curve analysis (Figure 3a, IL-6 Reference Assay)
Function	$y = A2 + (A1-A2)/(1 + (x/x0)^{p})$ $A1 = 191684.28107 \pm 24356.00949$ $A2 = 2.19379E7 \pm 3074376.6902$ $x0 = 112.58296 \pm 26.19409$ $p = 1.10708 \pm 0.05592$
R ²	0.99768
Sigmoidal fi	t curve analysis (Figure 3a, Multianalyte-Assay, IL-6 Detection)
Function	$y = A2 + (A1-A2)/(1 + (x/x0)^{p})$ $A1 = 181540.24919 \pm 19802.54785$ $A2 = 1.42862E7 \pm 2207058.25379$ $x0 = 129.15303 \pm 28.70075$ $p = 1.31798 \pm 0.07849$
R ²	0.99624
Sigmoidal fi	it curve analysis (Figure 3b, DNA Reference Assay)
Function	$y = A2 + (A1-A2)/(1 + (x/x0)^{p})$ $A1 = 2437591.22467 \pm 249738.02004$ $A2 = 1.99388E7 \pm 403727.7639$ $x0 = 382.3198 \pm 65.46922$ $p = 0.63236 \pm 0.05258$
R ²	0.99798
Sigmoidal fi	t curve analysis (Figure 3b, Multianalyte-Assay, DNA detection)
Function	$y = A2 + (A1-A2)/(1 + (x/x0)^{p})$ $A1 = 2560822.58359 \pm 99063.43614$ $A2 = 1.8367E7 \pm 325327.72593$ $x0 = 466.35795 \pm 50.61403$ $p = 1.10038 \pm 0.07435$
\mathbf{R}^2	0.99839

Table S5. Mean, standard deviation (SD), coefficient of variation (CV) and limit of detection (LOD) of the Multianalyte-Assay and reference assays.

Mean, SD, CV, and LOD of sigmoidal fit curve analysis (Figure 3a, IL-6 Reference Assay)									
Sample									
IL-6 [ng/mL]	0	1	5	10	25	50	75	100	200
Analysis of the Protein-TL									
Mean [RFU]	190,426	316,137	782,135	1,729,825	3,485,327	6,436,057	8,473,509	10,688,265	14,256,681
SD [RFU]	38,281	41,837	84,614	128,118	355,295	284,760	763,074	673,234	1,080,644
CV [%]	20	13	11	7	10	4	9	6	8
LOD [RFU]	y _{LOD} = (190,4	26 + 1.645 *	38,281) + 1.64	45 * 41,837 =	322,219 RFU				
LOD [ng/mL]	1.1 ng/mL (9	5 % confiden	ce interval: n.	a.)					
Mean, SD, CV, a	and LOD of sig	moidal fit cu	rve analysis (Figure 3a, Mu	Itianalyte-As	say)			
Sample									
IL-6 [ng/mL]	0	1	5	10	25	50	75	100	200
gDNA [cp/react.]	10 ⁶	10 ⁶	10 ⁶	10 ⁶	10 ⁶	10 ⁶	10 ⁶	10 ⁶	10 ⁶
Analysis of the	Protein-TL								
Mean [RFU]	159,896	212,279	396,569	640,312	1,604,045	3,228,297	4,775,894	6,994,765	8,965,210
SD [RFU]	52,154	41,125	61,961	76,463	169,471	412,994	379,893	896,651	856,333
CV [%]	33	19	16	12	11	13	8	13	10
LOD [RFU]	y _{LOD} = (159,8	96 + 1.645 *	52,154) + 1.64	45 * 41,125 =	313,339 RFU				
LOD [ng/mL]	3.8 ng/mL (9	5 % confiden	ce interval: 2.	8 – 4.8 ng/ml	_)				
Analysis of the	DNA-TL								
Mean [RFU]	16,741,322	16,060,913	17,734,881	16,165,793	16,278,912	16,071,960	17,675,860	17,548,963	17,619,909
SD [RFU]	1,418,412	1,509,803	1,423,857	1,209,138	1,337,528	824,342	1,553,131	1,418,774	1,341,056
CV [%]	8	9	8	7	8	5	9	8	8
Mean, SD, CV, a	and LOD of sig	moidal fit cu	rve analysis (Figure 3b, DN	IA Reference	Assay)			
Sample									
gDNA [cp/react.]	0	10 ⁰	10 ¹	5x10 ¹	10 ²	10 ³	104	10 ⁵	10 ⁶
Analysis of the	Analysis of the DNA-TL								

Mean [RFU]	2,398,743	2,703,332	4,407,848	6,416,298	6,957,134	13,593,458	18,458,507	19,419,882	19,452,793	
SD [RFU]	606,206	520,165	721,782	556,069	954,023	916,495	868,245	759,026	999,109	
CV [%]	25	19	16	9	14	7	5	4	5	
LOD [RFU]	y _{LOD} = (2,398,743 + 1.645 * 606,206) + 1.645 * 520,165 = 4,251,623 RFU									
LOD [cp/react.]	12.6 copies/r	reaction (95 %	6 confidence i	nterval: 7.5 –	- 20.1 copies/	reaction)				
Mean, SD, CV, a	nd LOD of sig	moidal fit cu	rve analysis (I	Figure 3b, Mı	ultianalyte-As	say)				
Sample										
IL-6 [ng/mL]	200	200	200	200	200	200	200	200	200	
gDNA [cp/react.]	0	10 ⁰	10 ¹	5x10 ¹	10 ²	10 ³	104	10 ⁵	10 ⁶	
Analysis of the I	Protein-TL									
Mean [RFU]	9,059,397	9,084,745	8,983,850	9,437,570	9,750,352	9,791,736	9,813,015	9,461,062	8,965,210	
SD [RFU]	1,375,290	898,075	619,273	622,289	810,591	1,622,034	1,642,591	2,027,554	856,333	
CV [%]	15	10	7	7	8	17	17	21	10	
Analysis of the I	DNA-TL									
Mean [RFU]	2,537,105	2,481,734	2,807,802	3,919,639	4,867,706	13,519,583	18,264,289	18,949,951	17,619,909	
SD [RFU]	438,398	639,229	298,594	553,610	810,443	1,261,376	1,155,971	2,064,743	1,341,056	
CV [%]	17	26	11	14	17	9	6	11	8	
LOD [RFU]	y _{LOD} = (2,537)	,105 + 1.645 '	* 438,398) + 1	L.645 * 639,2	29 = 4,309,80	1 RFU				
LOD [cp/react.]	70.2 copies/reaction (95 % confidence interval: 55.9 – 90.8 copies/reaction)									