

Table S1. Array probes for detection of Lassa virus and internal control sequences.

No.	Spot on array ^a	Sequence (5'-3')	T _m (°C) ^b	Minimum no. of mismatches to off-target sites in: ^c			
				Viruses	Bacteria	Plasmodium	Human
1	A-01a	CATTCTTTCAAGAGGTGCCTCATGTG	41.6	5	6	6	4
2	A-01b	CATTCTTCCAAGAGGTGCCTCATGT	41.1	8	4	7	4
3	A-02a	TTCTTCCAGGAAGTGCCTCATGTAATAG	40.9	6	5	7	5
4	A-02b	CATTCTTTCAAGAGGTGCCTCATGTAATAG	41.5	7	7	6	5
5	A-03	CATTCTTTCAAGAGGTGCCTCACGT	41.3	4	4	6	3
6	A-04	CATTCTTTCAAGAGGTGCCCCATG	42.2	4	3	5	3
7	A-05a	CTTCCAGGAGGTGCCCCATGTA	41.4	3	2 ^d	4	3
8	A-05b	ATTCTTCCAGGAAGTGCCCCATG	41.7	3	2 ^e	5	2 ^f
9	A-06a	ACATTTTTCCAGGAAGTCCCTCATGT	40.9	5	4	5	4
10	A-06b	ACATTTTTCCAGGAAGTACCTCATGTCATA	41.2	7	7	8	5
11	A-07a	ACATTCTTTCAAGAGGTGCCTCATGTAATAGA	41.8	8	7	9	5
12	A-07b	ACATTCTTTCAAGAGGTGCCACATGTAATAG	41.1	7	6	9	5
13	A-08	CAAGAAGTACCTCATGTGATAGAGGAAGTGA	41.2	7	6	8	5
14	A-09	ACATTCTTTCAAGAGGTTCCCTCATGTCA	41.1	6	5	7	5
15	A-10a	CATTCTTCCAAGAAGTTCCTCATGTTATTG	41.4	7	6	7	6
16	A-10b	ACATTCTTCCAAGAAGTCCCTCATGTTAT	40.6	7	5	8	6
17	A-11a	ACATTCTTTCAAGAGGTTCCCTCATGTCAT	41.4	7	5	8	6
18	A-11b	ACATTCTTCCAGGAAGTTCCTCATGTTAT	40.6	6	5	8	5
19	A-12	CACCCTTCCAGGAAGTCCCTCAT	40.9	4	3	5	3
20	A-13	CATTCTTCCAAGAAGTACCACATGTTATCG	42.0	6	6	7	6
21	A-14	CAAGAAGTGCCTCATGTAATAGAGGAAGTAAT	40.9	7	7	7	6
22	A-15	ATTTTCCAGGAGGTGCCTCATGTC	42.1	4	4	5	3
23	A-16	CTTCTTCCAGGAGGTGCCTCACGT	41.4	5	3	5	3
24	B-01a	GCCTCATGTGATAGAAAGAGGTGATGAAC	41.1	5	5	6	5
25	B-01b	GCCCCATGTAATAGAAAGAGGTGATGAAC	41.9	7	5	8	6
26	B-02a	GCCTCATGTAATAGAGGAGGTGATGAACA	42.4	8	6	8	5
27	B-02b	GCCTCATGTAATAGAAAGAGGTGATGAACAT	41.0	8	5	6	6
28	B-03a	GTGCCTCATGTAATAGAGGAGGTAAATGAACA	42.6	8	7	9	6
29	B-03b	GTCCCTCATGTAATAGAGGAGGTGATGAAC	42.2	6	6	7	6
30	B-04	ACCTCATGTGATAGAGGAAGTGAATGAACA	41.0	6	5	7	6
31	B-05	GTCCCTCATGTTATAGAGGAGGTGATGAAC	42.2	7	6	6	6
32	B-06a	GCCTCATGTGATAGAGGAGGTGATGA	41.1	5	4	6	4
33	B-06b	TCCTCATGTGATAGAGGAGGTAAATGAACAT	41.3	7	6	8	6
34	B-07	GCCACATGTAATAGAGGAAGTGAATGAACA	41.4	6	6	7	6
35	B-08	AGTTCCTCATGTTATTGAGGAAGTGAATGAACA	41.4	7	5	7	5
36	B-09a	CCCTCATGTTATTGAGGAGGTAAATGAACA	42.2	6	5	7	5
37	B-09b	CCTCATGTGATTGAGGAGGTAAATGAACA	42.0	6	5	8	5
38	B-10a	GTTCCCTCATGTGATTGAGGAAATTAATGAAC	41.2	7	6	8	6
39	B-10b	GTTCCCTCATGTTATTGAGGAAATCATGAAC	41.2	7	6	8	6
40	B-11a	GCCTCATGTGATAGAGGAGGTGATGA	41.1	6	4	6	4
41	B-11b	GCCTCATGTGATTGAGGAGGTGATG	42.2	4	4	7	3
42	B-12	GCCCCATGTTATAGAGGAGGTGATGA	42.0	5	4	6	4
43	B-13	GTGCCTCATGTGATAGAGGAGGTAAATGA	41.4	7	5	6	5
44	B-14	CATGTTATCGAGGAAGTGAATATCGT	40.6	6	5	9	6
45	B-15a	GCCTCACGTTATAGAGGAAGTGAATGAACA	42.6	6	5	8	6
46	B-15b	GCCACAGGTTATAGAGGAAGTGAATGAACA	42.5	6	6	7	6
47	B-16	CCTCATGTGATAGAAAGTGAATGAACATTG	42.0	8	7	7	7
48	IC-01	GAACATTTTCGCAGCCTACCGTAG	38.6	Internal control			
49	IC-02	CAAATCACAGAATCGTCGTATGCAG	39.2	Internal control			

^a The positions of the spots on the array are shown in Fig. 1. Small letters (a, b) following the spot number indicate that two probes were mixed and spotted at the same position.

- ^b Melting temperature (T_m) was calculated using Vector NTI software (Invitrogen) considering the hybridization buffer composition.
- ^c Potential off-target sites in relevant microorganism and in humans were searched for by using BLASTN 2.2.26+ at <http://blast.ncbi.nlm.nih.gov/>. Each probe was run as a query sequence against the nr/nt database with expect threshold 50, word size 7, and match/mismatch score 1,-1. The search was run separately for the organisms: Viruses (taxid: 10239; 1.3 Mio entries) NOT Arenaviridae (taxid: 11617), Bacteria (taxid: 2; 6.2 Mio entries), Plasmodium (taxid: 5820; 0.4 Mio entries), and Human genomic plus transcript. Sites matching best to the query sequence were identified and the number of mismatches was counted.
- ^d Single site in *Desulfotomaculum kuznetsovii* DSM 6115 (CP002770.1).
- ^e Single site in *Pseudomonas putida* GB-1 (CP000926.1).
- ^f Three sites (chromosome 3, 16, 17).

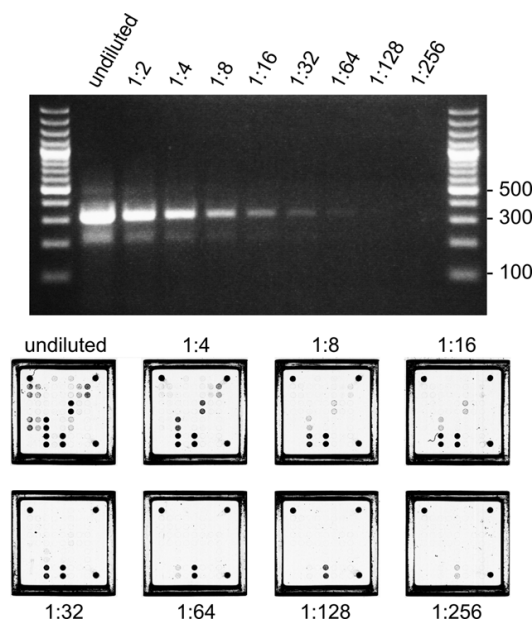


Fig. S1. Sensitivity of detection of amplified Lassa virus sequences on the array compared to agarose gel separation and ethidium bromide staining. Lassa virus RNA of strain Lib05-1580/121 was amplified and the PCR product was diluted in 1:2 steps and subjected to agarose gel (upper panel; the numbers on the right are base pairs) and array detection (lower panel). The diffuse minor bands running in the agarose gel with a virtual size of 220 base pairs probably represent single-stranded amplicon. Double stranded amplicon runs at 320 base pairs.

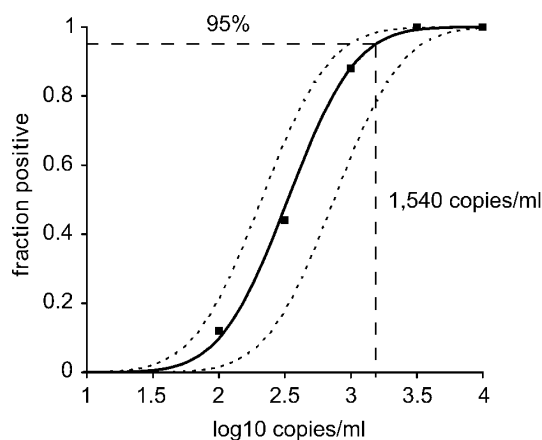


Fig. S2. Analytical sensitivity of the GPC RT-PCR with array hybridization determined by probit analysis. The analysis was performed with pooled data ($n = 150$ data points) of 5 virus strains shown in Table 1. Filled squares represent the experimentally determined fractions of positive results (y axis) at a given RNA concentration (x axis). The solid line represents the regression curve for the probability of obtaining a positive RT-PCR result at a given concentration of Lassa virus RNA in plasma. The dotted lines left and right of the regression curve depict the 95%-confidence interval for the curve.