

Supporting Information

LIPS method for the detection of SARS-CoV-2 antibodies to spike and nucleocapsid proteins

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Methods and materials

SARS-CoV-2 (NCBI Acc # NC_045512.2) two S (S1 aa 1-680 and S2 aa 820-1211) and N (aa 2-419) gene fragments were cloned into in-house modified pNanoLuc vector, the full sequences of the vector and cloned inserts are given below. After the transfection into HEK293 cells, the cell lysates containing NanoLuc-fusion proteins were collected at 72 h and stored at -20°C.

For Western blot, the cell lysates containing NanoLuc-fusion proteins were loaded to a 10% SDS-polyacrylamide gel and subjected to gel electrophoresis (1 h at 50 V and 2 h at 100 V). Proteins were then electrotransferred to a PVDF membrane (Millipore, 0,45 µm pore diameter) for 15 min at 10 V and 1 hour at 15 V at room temperature. Non-specific binding was blocked by incubation with 5% non-fat milk in TBST (Tris-buffered saline containing 0,1% Tween-20) for 1 h at room temperature, followed by an overnight incubation at 4 °C with primary antibodies diluted in 5% non-fat milk in TBST. The following primary antibodies were used: anti-Spike1 (diluted 1:2000, GeneTex), anti-NanoLuc (diluted 1:500, Promega). The membranes were washed three times with TBST, followed by an 1 hour incubation at room temperature with HRP-labeled secondary antibodies (Jackson ImmunoResearch) diluted in 5% non-fat milk in TBST. The chemiluminescent signal was produced using the Amersham ECL Reagents (GE Healthcare) and later detected using ImageQuant™ RT ECL™ Imager (GE Healthcare).

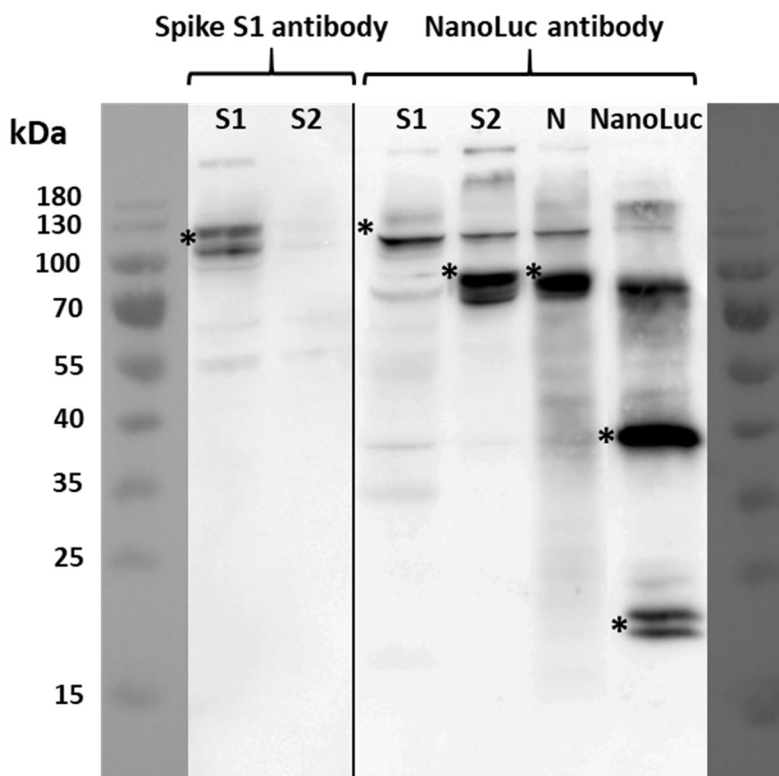
Plasma samples were obtained from 26 COVID-19 patients (age range 33-91 years) hospitalized at the Tartu University Hospital, Estonia. The diagnosis were confirmed by PCR analysis for SARS-CoV-2 virus. In addition, we studied 26 healthy controls (age range 23-54 years) without recent infection or COVID-19 symptoms (fever or cough) for last month. The study was conducted in accordance with the Helsinki Declaration, with the approval from the Ethics Committee of the University of Tartu.

The plasma samples were incubated with lysates containing S1, S2 and N fusion protein solutions (0.5 - 1×10^6 luminescence units; LU) for 1 h at RT. The Protein G Sepharose beads (25 µl of 4% suspension, Creative BioMart) were added and incubated at room temperature for 1 h in 96-well microfilter plates (Merck Millipore) to capture antibodies (in 1:40 dilution) and immune complexes to the beads. After the washing to remove unbound fusion proteins, luciferase substrate was added (Nano-Glo™ Luciferase Assay Substrate, Promega), and luminescence was measured in VICTOR X Multilabel Plate Reader (PerkinElmer Life Sciences). Results are expressed as fold changes (FC) of luminescence units (LU) ($FC = LU_{\text{sample}} / \text{average } LU_{\text{5 healthy control samples}}$). The positive/negative discrimination level was set to the mean plus 2 standard deviations of the healthy control samples. The experiments were performed three times in three experimental replicates. Statistics was performed using unpaired Student's t-test and Pearson correlation analysis in Graphpad Prism.

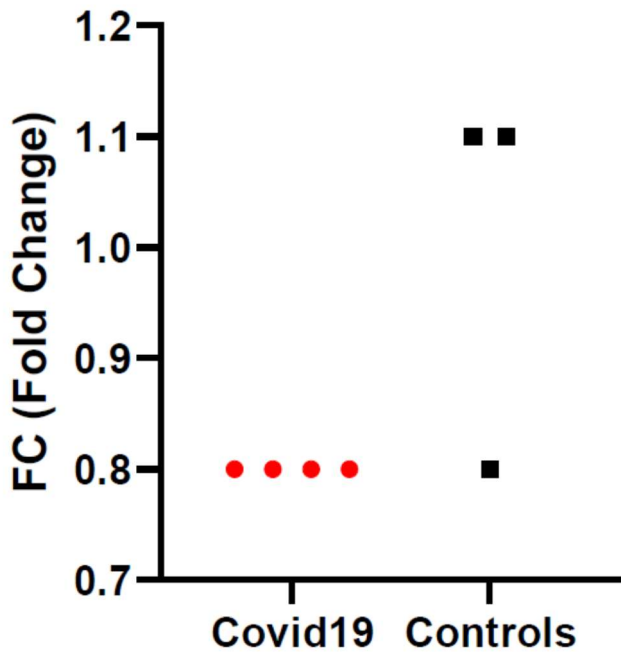
The Anti-SARS-CoV-2 IgG ELISA (Euroimmun Medizinische Labordiagnostika; Cat # EI 2668-9601 G) was performed according to the manufacturer's instructions. In semi-quantitative ELISA, IgG antibodies against SARS-CoV-2 S1 protein subunit S1 were detected. Briefly, 1:101 diluted plasma samples were added to wells coated with recombinant SARS-CoV-2 antigen and incubated for 60 minutes at 37 °C. Wells were washed three times followed by the addition of HRP-conjugated anti-human IgG and subsequent incubation for 30 minutes at 37 °C. Wells were washed three times again and a chromogen solution was added. Following 30 minutes of incubation at room temperature, the reaction was stopped and the resultant absorbance was read on a microplate reader at 450 nm with reference at 620 nm. A ratio between the extinction of the sample and calibrator on plate was calculated. According to the manufacturer's recommendations, a ratio <0.8 is considered negative, ≥0.8 and <1.1 borderline, and ≥1.1 positive.

Supporting Table 1. Main characteristics, LIPS and ELISA results of each studied patient. Patient sex, age and plasma sampling day, SARS-CoV-2 antibody values in LIPS with three antigens and EUROIMMUNE ELISA assay optical density (OD) values and its ratios to controls are given.

Patient nr	Sex (M/F)	Age (years)	Sample day	LIPS			ELISA	
				SP1	SP2	N	OD	Ratio
Pat1	M	33	11	0.8	1	3.7	0.4	1.7
Pat2	F	50	14	2.4	6.7	9.1	2.4	11.6
Pat3	M	55	12	5.1	3.9	8.4	3.4	16.2
Pat4	M	56	21	6.5	4.5	7.9	3.0	14.5
Pat5	F	58	26	11	9.3	7.7	3.4	16.6
Pat6	M	60	17	4.7	8	9	3.0	14.7
Pat7	M	61	14	2	3.3	5.2	1.0	4.8
Pat8	M	63	29	1.4	15.3	7.8	2.0	9.5
Pat9	M	70	16	3.9	7.4	10.2	2.8	13.4
Pat10	M	73	18	1.3	2.7	5.2	1.1	5.4
Pat11	M	83	20	4	2.6	7.2	3.0	14.5
Pat12	F	63	15	2.3	2.7	3.8	1.9	9.4
Pat13	F	83	17	1.5	1.2	2.7	2.4	11.5
Pat14	M	73	22	3.2	1.9	4.6	3.2	15.3
Pat15	M	57	22	2.4	1	3.4	2.9	14.2
Pat16	M	58	21	2.9	2.1	4.2	2.9	13.8
Pat17	M	63	37	2	5.1	4.9	2.1	10.2
Pat18	F	62	14	1.6	2.1	3.3	2.6	12.6
Pat19	F	62	14	2.4	2.2	5.7	2.9	13.8
Pat20	M	72	13	1.3	2.2	2.7	1.0	4.8
Pat21	F	91	14	1.1	5.6	4.4	0.8	4.1
Pat22	M	65	16	4.1	5.7	5.7	3.4	16.6
Pat23	F	55	25	2.3	1.9	5.1	2.8	13.7
Pat24	M	90	8	1.9	4.6	3.4	2.6	12.8
Pat25	M	60	15	1.5	1.6	3.5	2.1	10.2
Pat26	M	42	15	2.4	2.5	3.2	3.1	14.7

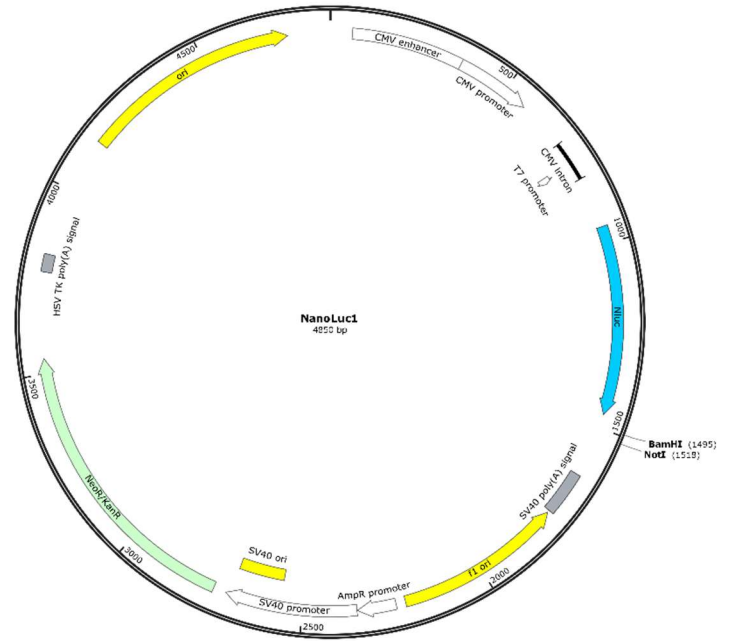


Supporting Figure 1. Western blot for the detection of NanoLuc-S1, NanoLuc-S2 and NanoLuc-N fusion proteins. The cell lysates were run a single 10% polyacrylamide gel, transferred to PVDF membrane, which was cut into two after the transfer. Left side: transfected HEK293 cell lysates of NanoLuc-S1 (S1) and NanoLuc-S2 (S2) were probed with anti-Spike1 antibody (diluted 1:2000, GeneTex). Right side: transfected HEK293 cell lysates of NanoLuc-S1, NanoLuc-S2, NanoLuc-N (N) and NanoLuc were probed with anti-NanoLuc antibody (diluted 1:500, Promega). The membranes were further incubated with HRP-labeled anti-rabbit (for S1) and anti-mouse (for NanoLuc) (both from Jackson ImmunoResearch). The detected proteins are shown by asterisks. The molecular marker lanes are shown on both sides of the membrane. The anti-S1 antibody (on left side) detects NanoLuc-S1 protein as a double band at approximately 110-120 kDa. The anti-NanoLuc antibody detects NanoLuc-S1 protein at the same location albeit weaker than seen with anti-S1 antibody. NanoLuc-S2 and NanoLuc-N are seen as strong bands at 75-80kDa. NanoLuc is seen at 20kDa but also at 38-40kDa. The predicted molecular mass of the proteins without post-translational modifications are 100kDa (NanoLuc-S1), 62kDa (NanoLuc-S2) and 59kDa (NanoLuc-N).



Supporting Figure 2. Empty NanoLuc vector without SARS-CoV-2 antigens was assayed with 4 Covid-19 and 3 control plasma samples. The NanoLuc (Promega) gene was expressed in HEK293 cells. The cell lysates were incubated with plasma samples (in 1:40 dilution) and bound to Protein G Sepharose to capture antibody complexes with viral proteins. After the washing, luciferase substrate Nano-Glo™ (Promega) was added and luminescence was measured in VICTOR X multilabel reader (PerkinElmer Life Sciences). Results are expressed as fold changes (FC) of luminescence units (LU) ($FC = \text{LU sample} / \text{average LU of 3 control samples}$). The luminescence values were in low range in LIPS assay and similar in Covid-19 and control individuals.

pNanoLuc1 vector



ID pNanoLuc1; linear; unassigned DNA; STD; UNC; 4850 BP.

SQ Sequence 4850 BP; 1159 A; 1276 C; 1262 G; 1153 T; 0 other;

TAGTTATTAA	TAGTAATCAA	TTACGGGGTC	ATTAGTTCAT	AGCCCATATA	TGGAGTTCGG	60
CGTTACATAA	CTTACGGTAA	ATGGCCCGCC	TGGCTGACCG	CCCAACGACC	CCCGCCCAT	120
GACGTCAATA	ATGACGTATG	TTCCCATAGT	AACGCCAATA	GGGACTTTCC	ATTGACGTCA	180
ATGGGTGGAG	TATTTACGGT	AAACTGCCCA	CTTGCCAGTA	CATCAAGTGT	ATCATATGCC	240
AAGTACGCCC	CCTATTGACG	TCAATGACGG	TAAATGGCCC	GCCTGGCATT	ATGCCCAGTA	300
CATGACCTTA	TGGGACTTTC	CTACTTGGCA	GTACATCTAC	GTATTAGTCA	TCGCTATTAC	360
CATGGTGATG	CGGTTTTGGC	AGTACATCAA	TGGGCTGGA	TAGCGTTTG	ACTCACGGGG	420
ATTTCCAAGT	CTCCACCCCA	TTGACGTCAA	TGGGAGTTTG	TTTTGGCACC	AAAATCAACG	480
GGACTTTCCA	AAATGTCGTA	ACAACCTCCG	CCCATTGACG	CAAATGGGCG	GTAGGCGTGT	540
ACGGTGGGAG	GTCTATATAA	GCAGAGCTCG	TTTAGTGAAC	CGTCAGATCG	CCTGGAGACG	600
CCATCCACGC	TGTTTTGACC	TCCATAGAAG	ACACCGGGAC	CGATCCAGCC	TCCGCGGCCG	660
GGAACGGTGC	ATTGGAACGC	GGATTCCCCG	TGCCAAGAGT	GACGTAAGTA	CCGCCTATAG	720
ACTCTATAGG	CACACCCCTT	TGGCTCTTAT	GCATGAATTA	ATACGACTCA	CTATAGGGAG	780
ACAGACTGTT	CCTTTCCTGG	GTCTTTTCTG	CAGGCACCGT	CGTCGACTTA	ACAGATCTCG	840
AGCTCAAGCT	TCGAATTCTC	GCCACCATGA	ACTCCTTCTC	CACAAGCGCC	TTCGGTCCAG	900
TTGCCTTCTC	CCTGGGCCTG	CTCCTGGTGT	TGCCTGTGTC	CTTCCCTGCC	CCAGTCTTCA	960
CACTCGAAGA	TTTCGTTGGG	GACTGGCGAC	AGACAGCCGG	CTACAACCTG	GACCAAGTCC	1020
TTGAACAGGG	AGGTGTGTCC	AGTTTGTTTT	AGAATCTCGG	GGTGTCCGTA	ACTCCGATCC	1080
AAAGGATTGT	CCTGAGCGGT	GAAAATGGGC	TGAAGATCGA	CATCCATGTC	ATCATCCCCT	1140
ATGAAGTCT	GAGCGGCGAC	CAAATGGGCC	AGATCGAAAA	AATTTTTAAG	GTGGTGTACC	1200
CTGTGGATGA	TCATCACTTT	AAGGTGATCC	TGCACTATGG	CACACTGGTA	ATCGACGGGG	1260
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TGATCAACCC	CGACGGCTCC	CTGCTGTTC	GAGTAACCAT	CAACGGAGTG	ACCGGCTGGC	1440
GGCTGTGCGA	ACGCATTCTG	GCGGAATTCT	GCAGTCGACG	GTACCGCGGG	CCCGGGATCC	1500
ACCGGGTACA	AGTAAAGCGG	CCGCGACTCT	AGATCATAAT	CAGCCATAAC	ACATTTGTAG	1560
AGGTTTTACT	TGCTTTAAAA	AACCTCCCAC	ACCTCCCCCT	GAACCTGAAA	CATAAAATGA	1620
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CTAAATCGGA	ACCCTAAAGG	GAGCCCCCGA	TTTAGAGCTT	GACGGGGAAA	GCCGGCGAAC	2100
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CACCTTGCTC	CTGCCGAGAA	AGTATCCATC	ATGGCTGATG	CAATGCGGCG	GCTGCATACG	3120
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TTCATCGACT	GTGGCCGGCT	GGGTGTGGCG	GACCGCTATC	AGGACATAGC	GTTGGCTACC	3420
CGTGATATTG	CTGAAGAGCT	TGGCGGCGAA	TGGGCTGACC	GCTTCCTCGT	GCTTTACGGT	3480
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TTCTGCGT	ATCCCCTGAT	TCTGTGGATA	ACCGTATTAC	CGCCATGCAT		4850

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Spike 1 gene fragment with BamHI and NotI restriction enzyme sites

ID Spike 1 fragment; linear; unassigned DNA; 2059 BP.
 SQ Sequence 2059 BP; 482 A; 623 C; 517 G; 437 T; 0 other;

GGATCCTAat	gttcgtcttc	ctggctctgc	tgctctgtgt	ctcctcacag	tgcgtcaatc	60
tgacaactcg	gactcagctg	ccacctgctt	atactaatag	cttcaccaga	ggcgtgtact	120
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gcaacatcat	cagaggctgg	atctttggca	ccacactgga	ctccaagaca	cagtctctgc	360
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ccgaggtgcc	cgtggctatc	cacgccgatc	agctgacccc	aacatggcgg	gtgtacagca	1920
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atccctatga	gtgcgacatc	ccaatcggcg	ccggcatctg	tgctctttac	cagaccaga	2040
caaactctTA	AGCGGCCG					2059

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Spike 2 gene fragment with BamHI and NotI restriction enzyme sites

ID Spike 2 fragment; linear; unassigned DNA; 1192 BP.
 SQ Sequence 1192 BP; 277 A; 363 C; 333 G; 219 T; 0 other;

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acaacacctt	cgtgagcggc	aactgtgacg	tggtcatcgg	catcgtgaac	aataccgtgt	960
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acatccagaa	ggagatcgac	cgccctgaac	aggtggctaa	gaatctgaac	gagagcctga	1140
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Nucleocapsid gene fragment with BamHI and NotI restriction enzyme sites

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ID   N gene; linear; unassigned DNA; 1273 BP.
SQ   Sequence 1273 BP; 300 A; 438 C; 336 G; 199 T; 0 other;
GGATCCTAtc tgacaacggc cctcagaacc agcggaacgc tcctcggatc accttcggcg      60
gcccttctga ctctaccggc tccaaccaga acggcgagag atccggagcc agatctaagc      120
agcggagacc ccagggcctg cccaacaaca ccgctcttg gtttaccgcc ctgacccagc      180
acggcaagga ggacctgaag ttccccagag gcccaaggggt gcccatcaac accaactcct      240
ccccagacga ccagatcggc tactaccggc gggctaccag aagaatcaga ggcgggcgacg      300
gcaagatgaa ggacctgtcc ccacggtggt acttctacta cctcggcaca ggacctgagg      360
ctggcctgcc ttacggagct aacaaggacg gaatcatctg ggtggctacc gagggagctc      420
tgaacacccc taaggaccac atcggaacct gcaaccccgc caacaacgct gctatcgtgc      480
tgcagctgcc tcaggggaaca accctgccta agggattcta cgctgagggg tctagaggag      540
ggtctcaggc ctcttctcgc tcttctctcc gctcccgcaa ctcttctcgc aactccaccc      600
caggggtcttc tagagggacc tctcctgcca gaatggctgg aaacggaggc gatgctgctc      660
tggctctgct gtcctcgcac cgcctcaacc agctcgagtc caagatgtct ggaaagggcc      720
agcaacagca ggggcagaca gtgacaaaaga agtctgctgc tgaagcctct aagaagcctc      780
gccagaagcg caccgctacc aaggcttaca acgtgaccca ggccttcggg aggaggggac      840
ctgagcagac acagggcaac ttcggggatc agggagctcat ccgccagggg acagactaca      900
agcaactggcc ccagatcgcc cagttcgccc ctagtgcctc tgccttcttc gggatgtccc      960
gcatcgggat ggaggtgacc cttcttgga cctggctgac ctacaccggg gccatcaagc     1020
tcgacgacaa ggaccccaac ttcaaggacc aggtcatcct cctcaacaag cacatcgacg     1080
cctacaagac cttcccaccc accgagccca agaaggacaa gaagaagaag gctgacgaga     1140
cccaggccct ccctcagagg cagaagaaac agcagaccgt gaccctgctg cctgctgctg     1200
acctcgacga cttctccaag cagctccagc agtcocatgtc ctctgctgac tctaccagg     1260
ctTAAGCGGC CGC

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