

**Table S1:** Questionnaire with epidemiological risk factors

	healthy blood donors (n = 216)	outpatients after solid-organ transplantation (n = 280)
residence	city/town: 141 (65%) countryside: 67 (31%) ambiguous answer: 4 (2%) NA: 4 (2%)	city/town: 88 (31%) countryside: 186 (66%) ambiguous answer: 1 (< 1%) NA: 4 (2%)
residence in village < 10.000 inhabitants	no: 160 (74%) yes: 52 (24%) NA: 4 (2%)	no: 93 (33%) yes: 177 (63%) ambiguous answer: 1 (< 1%) NA: 9 (3%)
property with direct access to fields, meadows or forests	no: 117 (54%) yes: 94 (44%) NA: 5 (2%)	no: 91 (33%) yes: 185 (66%) ambiguous answer: 2 (< 1%) NA: 2 (< 1%)
practicing gardening	no: 114 (53%) yes: 95 (44%) ambiguous answer: 1 (< 1%) NA: 4 (2%)	no: 98 (35%) Yes: 178 (64%) ambiguous answer: 1 (< 1%) NA: 3 (1%)
garden with stone wall	no: 149 (69%) yes: 61 (28%) NA: 6 (3%)	no: 174 (62%) yes: 92 (33%) NA: 14 (5%)
animal contact	no: 96 (44%) yes: 113 (52%) NA: 5 (2%)	no: 132 (47%) yes: 145 (52%) NA: 2 (< 1%)
contact to cats	yes: 66 (31%)	yes: 61 (22%)
contact to shrews	no: 179 (83%) yes: 32 (15%) NA: 4 (2%)	no: 210 (75%) yes: 61 (22%) NA: 9 (3%)
walking barefoot outdoors	no: 148 (69%) yes: 63 (29%) NA: 4 (2%)	no: 195 (70%) yes: 80 (29%) NA: 5 (2%)

**Table S2:** Contingency analysis of clinical signs (questionnaire) and reactive ELISA screening (reactivity against  $\geq 1$  antigen)

new onset/aggravation of	healthy blood donors	outpatients after solid-organ transplantation
headache	OR not defined/not calculated p = 1.00	OR: 2.18 95% CI: 0.79-5.91 p = 0.09
short-time memory impairment	OR: 1.67 95% CI: 0.16-9.36 p = 0.63	OR: 0.75 95% CI: 0.20-2.30 p = 0.80
long-time memory impairment	OR not defined/not calculated p = 1.00	OR: 1.59 95% CI: 0.57-4.22 p = 0.34
visual impairment	OR not defined/not calculated p = 0.36	OR: 1.54 95% CI: 0.76-3.09 p = 0.23
smelling/tasting impairment	OR not defined/not calculated p = 1.00	OR: 1.47 95% CI: 0.42-4.81 p = 0.57
behavioral/personality change	OR not defined/not calculated p = 1.00	OR: 2.15 95% CI: 0.39-11.83 p = 0.28
frequent falls	not defined/not calculated	OR: 1.31 95% CI: 0.27-5.32 p = 0.74
gait ataxia	OR not defined/not calculated p = 1.00	OR: 0.76 95% CI: 0.21-2.34 p = 0.80
numbness of extremities	OR not defined/not calculated p = 1.00	OR: 1.44 95% CI: 0.62-3.24 p = 0.33
unable to walk long distance	OR not defined/not calculated p = 0.15	OR: 1.09 95% CI: 0.52-2.20 p = 0.86
paresis	OR not defined/not calculated p = 1.00	OR: 1.43 95% CI: 0.66-3.03 p = 0.35

statistical analysis with Fisher's exact test

(OR = odds ratio, 95% CI = 95% confidence interval of OR)

**Table S3:** Peptides specific for patients with BoDV-1 infection

protein	peptide position on membrane	amino acids of protein	peptide sequence	no. of positive samples	homology, human proteins (taxid: 9606)	E value
N	2-4	5-27	RRLVDDADAMEDQDLYEPPASLP	4	leptin receptor overlapping transcript like 1	0.058
N	23-28	89-123	AFVHGGVPRESYLSTPVTRGEQTVVKTAIFYGEKT	3	leucine rich repeat containing 5 variant	5.7
N	43-45	169-191	MMAALNRPSHGETATLLQMFNPH	2	endogenous Bornavirus like nucleoprotein 2	0.084
N	57-58	225-239	QIKLVASYAQMTTYTTIKE	1	endogenous Bornavirus like nucleoprotein 1	0.13
N	65	257-271	VVAYEIRDELEVS AK	1	ribosomal protein S6 kinase alpha-5	4.6
N	77-78	305-319	AAFYWSKKENPTMAGYRAS	2	olfactory receptor 4B1	3.0
N	89	353-367	LSGEISAIMKMIGVT	1	fibrous sheath-interacting protein 2	9.3
X	2-3	5-23	LRLTLLELVRRLLNGNATIE	3	immunoglobulin heavy chain junction region	7.8
P	6-8	21-43	LRRERP GSPRPRKVPRNALTQPV	4	Ras association domain family member 5	0.06
					PDCD7 protein	0.17
					DNA-binding protein A	0.33
					HYA22	0.47
					zinc finger protein 335	0.93
P	18	69-83	LSNDELIKKLVTELA	2	zinc finger protein 469	0.009
P	39	153-167	KLMMEKVDLLYASTA	2	hCG2036668	9.2
P	42	165-179	STAVGTSAPMLPSHP	2	mediator complex subunit 13L	9.3
P	44	173-187	PMLPSHPAPPRIYPQ	2	alternative protein KLC2	0.4
P	46	181-195	PPRIYPQLPSAPTTD	3	immunoglobulin heavy chain junction region	2.8

Peptides that were found to be specific for samples of patients with BoDV-1 infection in a linear epitope mapping were blasted against a human protein database (<https://blast.ncbi.nlm.nih.gov>). All results with E values < 1 are given. For peptides with insignificant alignments (E value > 1), the lowest E value is shown.

**Table S4:** Peptides associated with false-reactive ELISA results

protein	peptide position on membrane	amino acids of protein	peptide sequence	cohort	no. of positive samples	homology, human proteins (taxid: 9606)	E value	homology, organism-independent, exclusion of <i>Bornaviridae</i> (taxid: 178830)	E value
N	5-6	17-35	QDLYEPPASLPKLPKGFLQ	blood donor (BoDV-1)	1 (4)	4-hydroxy-phenylpyruvate-dioxygenase	2.1	CehA/McbA family metallohydrolase [Deltaproteobacteria bacterium]	8.8
N	12-13	45-63	PGIGHEKDIRQNAVALLDQ	transplant	1	G protein subunit beta 2	1.5	endogenous Bornavirus-like nucleoprotein 2 [Ictidomys tridecemlineatus]	0.78
N	32	125-139	QRDLTELEISSIFSH	transplant	1	calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase 1C	9.2	pseudouridine synthase [unclassified Clostridium]  endogenous Bornavirus-like nucleoprotein 2 [Ictidomys tridecemlineatus]	0.14  0.56
N	36-38	141-163	CSLLIGVVIGSSSKIKAGAEQIK	transplant blood donor NEG (BoDV-1)	3 2 (2)	endogenous Bornavirus like nucleoprotein 2	0.65	endogenous Bornavirus-like nucleoprotein 2 [Ictidomys tridecemlineatus]  endogenous Bornavirus-like nucleoprotein 1-like [Chrysochloris asiatica]	2E-09  3E-07

								endogenous Bornavirus-like nucleoprotein 1 [Mus caroli]	0.092
								hypothetical protein B5V03_18725 [Bradyrhizobium betae]	0.51
N	41	161-175	QIKKRFKTMMAALNR	transplant	1	endogenous Bornavirus like nucleoprotein 2	0.28	endogenous Bornavirus-like nucleoprotein 2 [Ictidomys tridecemlineatus]	0.05
N	47-48	185-203	LQMENPHEAIDWINGQPWV	blood donor neg ctrl (BoDV-1)	1 1 (3)	endogenous Bornavirus like nucleoprotein 1	0.006	endogenous Bornavirus-like nucleoprotein 2 [Ictidomys tridecemlineatus]	2E-06
N	68-82	269-339	SAKLKEDHADLPFLGAIRHPDAIKLAP RSFPNLASAAFYWSKKENPTMAGYR ASTIQPGASVKETQLARY	transplant blood donor blood donor NEG (BoDV-1)	5 2 2 3	endogenous Bornavirus like nucleoprotein 1	2E-05	endogenous Bornavirus-like nucleoprotein 2 [Ictidomys tridecemlineatus]  endogenous Bornavirus-like nucleoprotein 1- like [Chrysochloris asiatica]  endogenous Bornavirus-like nucleoprotein 1 of several other species	5E-48   6E-21
X	1	1-15	MSSDLRLTLLELVRR	transplant	1	coiled-coil domain- containing protein 157	0.57	hypothetical protein C5Q97_08165 [Victivallales bacterium]	3.2
X	4	13-27	VRRLNGNATIESGRL	blood donor	1	NFIL3 like protein	3.2	AsmA-like C- terminal domain- containing protein	0.28

								[Deltaproteobacteria bacterium]	
X	5-7	17-35	NGNATIESGRLPGGRRRSPDTT	transplant blood donor (BoDV-1)	1 1 2	gamma-taxilin	0.47	ABC transporter [Aeromicrobium sp.]	2.0
X	15-19	57-87	PTSRPAPEGPQEEPLHLRPRPANRK GAAVE	transplant blood donor (BoDV-1)	4 2 (8)	germinal-center associated nuclear protein	1.1	hypothetical protein [Methylobacterium sp.]	0.99
P	1-5	1-31	MATRPSSLVDSLEDEEDPQTLRRERP GSPRP	transplant blood donor blood donor NEG (BoDV-1)	3 1 1 (6)	PDCD7 protein  CDK5 and ABL1 enzyme substrate  CABLES	0.40  0.79  0.79	unnamed protein product [Mytilus coruscus]  hypothetical protein [Azospirillum ramasamyi]  Rab-GTPase-TBC domain [Phytophthora infestans]  neurotrophin receptor- interacting factor homolog [Chrysochloris asiatica]  tbc1 domain family member 23-like partial [Plasmopara halstedii]	0.067  0.19  0.26  0.72  0.72
P	9	33-47	KVPRNALTQPVDQLL	transplant blood donor blood donor NEG (BoDV-1)	1 1 1 (4)	protein sprouty homolog 2	9.2	malto- oligosyltrehalose synthase [Proteobacteria bacterium]	6.3
P	11-13	41-63	QPVDQLLKDLRKNPSMISDPDQR	transplant blood donor (BoDV-1)	3 1 (6)	MLF1IP protein	0.91	methyltransferase [Pontibacter korlensis]	0.71

P	16-17	61-79	DQRTGREQLSNDELIKKLV	transplant blood donor NEG neg ctrl (BoDV-1)	3 1 3 (4)	la-related protein 6	1.5	golgin subfamily B member 1 [Mugil cephalus]	0.78
P	19	73-87	ELIKKLVTELAENSM	transplant blood donor (BoDV-1)	1 1 (1)	zinc finger protein 469	6.5	sugar ABC transporter ATP- binding protein [Subtercola sp.]	6.3
P	23-24	89-107	EAEVVRGTLGDISARIEAG	transplant (BoDV-1)	4 (2)	cytochrome P450 4X1	4.3	precorrin-4 C(11)- methyltransferase [Planctomycetota bacterium]	0.39
								precorrin-4 C(11)- methyltransferase [Moorella sp.]	0.78
P	29-37	113-159	ALQVETIQTAQRCDHSDSIRILGENIKI LDRSMKTMMEKLMMEKV	transplant blood donor blood donor NEG neg ctrl	5 1 2 1	alternative protein RBM28	2.7	hypothetical protein 3 [Bitis gabonica]	0.002
								TPA: MMPL family transporter [Acholeplasmatace ae bacterium]	0.21
								TPA: GTPase HflX [candidate division Zixibacteria bacterium]	0.55
								TPA: anion permease [Elusimicrobia bacterium]	0.75
								MMPL family transporter [Acholeplasmatace ae bacterium]	0.77
								hypothetical protein [Cryomorpha ignava]	0.98

P	43	169-183	GTSAPMLPSHPAPPR	transplant (BoDV-1)	1 (3)	alternative protein KLC2	0.4	unnamed protein product [Taenia asiatica]  hypothetical protein F4802DRAFT_2757 47 [Xylaria palmicola]  Os09g0532600 [Oryza sativa Japonica Group]	0.56  0.79  0.8
P	48	189-203	QLPSAPTTDEWDIIP	blood donor (BoDV-1)	1 (4)	immunoglobulin heavy chain junction region	0.29	carboxypeptidase regulatory-like domain-containing protein [Deltaproteobacter ia bacterium]	6.3

Peptides that were identified in a linear epitope mapping to be associated with false-reactive ELISA results were blasted against a human protein database and an organism-independent database (after exclusion of *Bornaviridae*), respectively (<https://blast.ncbi.nlm.nih.gov>). All results with E values < 1 are given. For peptides with insignificant alignments (E value > 1), the lowest E value is shown.