Supplemental Table S1: STROBE Statement—checklist of items that should be included in reports of observational studies

	Item No.	Recommendation	Page No.
Title and abstract	1	(*a*) Indicate the study's design with a commonly used term in the title or the abstract	1
		(*b*) Provide in the abstract an informative and balanced summary of what was done and what was found	1
Introduction			
Background/rationale	2	Explain the scientific background and rationale for the investigation being reported	1-2
Objectives	3	State specific objectives, including any prespecified hypotheses	1-2
Methods			
Study design	4	Present key elements of study design early in the paper	2-4
Setting	5	Describe the setting, locations, and relevant dates, including periods of recruitment, exposure, follow-up, and data collection	2-4
Participants	6	(*a*) *Cohort study*—Give the eligibility criteria, and the sources and methods of selection of participants. Describe methods of follow-up *Case-control study*—Give the eligibility criteria, and the sources and methods of case ascertainment and control selection. Give the rationale for the choice of cases and controls *Cross-sectional study*—Give the eligibility criteria, and the sources and methods of selection of participants	2-4
		(*b*) *Cohort study*—For matched studies, give matching criteria and number of exposed and unexposed *Case-control study*—For matched studies, give matching criteria and the number of controls per case	
Variables	7	Clearly define all outcomes, exposures, predictors, potential confounders, and effect modifiers. Give diagnostic criteria, if applicable	2-4
Data sources/ measurement	8*	For each variable of interest, give sources of data and details of methods of assessment (measurement). Describe comparability of assessment methods if there is more than one group	*2-4*
Bias	9	Describe any efforts to address potential sources of bias	-
Study size	10	Explain how the study size was arrived at	-

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Quantitative variables	11	Explain how quantitative variables were handled in the analyses. If applicable, describe which groupings were chosen and why	3-4
Statistical methods	12	(*a*) Describe all statistical methods, including those used to control for confounding	3-4
		(*b*) Describe any methods used to examine subgroups and interactions	3-4
		(*c*) Explain how missing data were addressed	-
		(*d*) *Cohort study*—If applicable, explain how loss to follow-up was addressed *Case-control study*—If applicable, explain how matching of cases and controls was addressed *Cross-sectional study*—If applicable, describe analytical methods taking account of sampling strategy	3-4
		(*e*) Describe any sensitivity analyses	
Results			
Participants	13*	(a) Report numbers of individuals at each stage of study—eg numbers potentially eligible, examined for eligibility, confirmed eligible, included in the study, completing follow-up, and analysed	4-13
		(b) Give reasons for non-participation at each stage	-
		(c) Consider use of a flow diagram	-
Descriptive data	14*	(a) Give characteristics of study participants (eg demographic, clinical, social) and information on exposures and potential confounders	4-13
		(b) Indicate number of participants with missing data for each variable of interest	-
		(c) *Cohort study*—Summarise follow-up time (eg, average and total amount)	
Outcome data	15*	*Cohort study*—Report numbers of outcome events or summary measures over time	*4-13*
		Case-control study—Report numbers in each exposure category, or summary measures of exposure	
		Cross-sectional study—Report numbers of outcome events or summary measures	
Main results	16	(*a*) Give unadjusted estimates and, if applicable, confounder-adjusted estimates and their precision (eg, 95% confidence interval). Make clear which confounders were adjusted for and why they were included	Every figure
		(*b*) Report category boundaries when continuous variables were categorized	-
		(*c*) If relevant, consider translating estimates of relative risk into absolute risk for a meaningful time period	-

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Other analyses	17	Report other analyses done—eg analyses of subgroups and interactions, and sensitivity analyses	4-13
Discussion			
Key results	18	Summarise key results with reference to study objectives	13
Limitations	19	Discuss limitations of the study, taking into account sources of potential bias or imprecision. Discuss both direction and magnitude of any potential bias	15
Interpretation	20	Give a cautious overall interpretation of results considering objectives, limitations, multiplicity of analyses, results from similar studies, and other relevant evidence	13-16
Generalisability	21	Discuss the generalisability (external validity) of the study results	15-16
Other information			
Funding	22	Give the source of funding and the role of the funders for the present study and, if applicable, for the original study on which the present article is based	16

*Give information separately for cases and controls in case-control studies and, if applicable, for exposed and unexposed groups in cohort and cross-sectional studies.

Note: An Explanation and Elaboration article discusses each checklist item and gives methodological background and published examples of transparent reporting. The STROBE checklist is best used in conjunction with this article (freely available on the Web sites (13/07/2022) of PLoS Medicine at http://www.plosmedicine.org/, Annals of Internal Medicine at http://www.annals.org/, and Epidemiology at http://www.epidem.com/). Information on the STROBE Initiative is available at www.strobe-statement.org.

Supplemental Table S2: Details about bacterial findings (double naming feasible)

Location of the finding	Number of patients
Positive blood culture	35 (37.6%)
Bacterial drainage infection	32 (34.4%)
Pneumonia	13 (13.9%)
Urinary tract infection	11 (11.8%)
Positive blood culture with VRE	8 (8.6%)
Positive blood culture with MRGN	7 (7.5%)
Colonization with MRSA	2 (2.1%)
Colonization with VRE	12 (12.9%)
Colonization with MRGN	3 (3.2%)
Colonization with VRE and MRGN	9 (9.7%)
New acquisition of colonization with VRE*	8 (8.6%)
New acquisition of colonization with MRGN*	5 (5.4%)

Legend: VRE, vancomycin resistant *Enterococcus faecium*; MRGN, multiresistant gram-negative bacteria; MRSA, methicillin resistant *Staphylococcus aureus*; values are given as number (with the corresponding percentage value)

Supplemental Table S3: Risk factors for death within 90 days following LTX

Variable	Univariate analysis with 95% CI	*p*-value	Multivariate analysis with 95% CI	p-value
BChE d14	0.29 (0.09-0.96)	**0.045***	2.46 (0.04-32.06)	0.658
MR-proADM d7	0.07 (0..02-0.28)	**< 0.001*****	0.19 (0.00-8,86)	0.394
male	2.94 (0.91-6.83)	0.062	0.76 (0.03-19,16)	0.870
Transfusion of red blood cells	1.53 (0.53-4.41)	0.299	1.98 (0.04-94,43)	0.727
Transfusion of fresh frozen plasma	1.05 (0.31-3.64)	0.579	3.06 (0.10-91.63)	0.519
Acute renal failure following LTX	0.065 (0.19 – 0.22)	**< 0.001*****	0.04 (0.00-1.61)	0.086
Acute liver failure following LTX	0.02 (0.01-0.10)	**< 0.001*****	0.08 (0.00-2.06)	0.130
Need for surgical intervention	3.04 (2.19-4.22)	**< 0.001*****	0.00 (0.00-0.00)	0.996
Duration of surgery	0.89 (0.79-1,00)	0.111	0.99 (0.98-1.01)	0.332
SOFA-Score	0.91 (0.83-1.02)	**0.017***	1.15 (0.78-1.68)	0.465

Legends: LTX = liver transplantation, BChE = butyrylcholinesterase, MR-proADM = mid-regional proadrenomedullin, SOFA = Sequential Organ Failure Assessment score. Data given as Odds-Ratio with 95%-Confidence interval. Symbols of significance: $p < 0.05$: *, $p < 0.01$: **, $p < 0.001$***

Supplemental Table S4: Plasma values of transaminases and coagulation parameters

		d0	d1	d2	d7	d14	d21	d28
ALAT [U/L]	Non-survivors	990.0 (641.5 - 2626.0)	1354.5 (926.0 - 2185.8)	744.5 (451.5 - 1284.5)	56.0 (44.0 - 77.0)	33.5 (22.0 - 77.0)	29.0 (20.0 - 39.50)	34.0 (25.5 - 57.5)
	Survivors	1440.5 (814.0 - 2569.3)	1419.0 (748.0 - 2317.0)	1068.0 (398.8 - 1588.8)	60.0 (41.0 - 86.0)	36.0 (26.3v- 49.8)	25.0 (18.0 - 52.0)	25.5 (19.3 - 49.8)
ASAT [U/L]	Non-survivors	546.0 (350.5 - 1030.0)	896.0 (661.3 - 1231.3)	1047.5 (563.3 - 1604.0)	151.0 (98.5 - 268.5)	75.5 441.5 - 102.0)	43.0 (19.0 - 60.0)	43.0 (23.8 - 84.3)
	Survivors	620.0 (358.0 - 1074.8)	726.0 (408.0 - 1452.0)	773.0 (478.5 - 1665.5)	182.0 (124.5 – 329.5)	83.5 (49.8 - 116.5)	43.5 (27.3 - 66.3)	33.5 (20.3 - 72.0)
PTT [s]	Non-survivors	31.7 (29.0- 34.2)	31.9 (30.2- 34.4)	31.4 (29.1- 34.4)	27.2 (23.4- 32.3)	23.5 (22.7- 27.9)*	26.8 (24.6- 30.7)	29.0 (24.9- 32.2)
	survivors	30.9 (28.0- 36.3)	31.1 (28.5- 34.8)	30.3 (27.4- 34.2)	24.8 (22.4- 29.6)	23.4 (20.9- 27.1)	24.0 (21.7- 31.2)	27.1 (23.9- 36.4)
Prothrombin time [%]	Non-survivors	58.8 (52.9- 64.1)	51.1 (45.9- 61.2)	60.1 (45.6- 68.7)	78.6 (61.1- 92.8)	88.8 (74.9- 103.0	83.5 (65.5- 92.5)	83.5 (70.4- 89.2)
	survivors	44.8 (44.9- 65.1)	52.7 (44.1- 65.1)	58.2 (48.4- 67.3)	80.7 (69.1- 97.7)	88.9 (79.7- 95.5)	87.1 (72.4- 95.9)	82.5 (78.7- 89.6)

Legend: ALAT, alanine-aminotransferase; ASAT, aspartate-aminotransferase; PTT, partial thromboplastin time, values are given as median with accompanying quartiles.

Supplemental Table S5: Plasma values of the infection parameters adjusted to the timepoint of bacterial infection

		PreV0	V0	V1
PCT [µg/L]	Infection	2.23 (0.51 - 6.53)	1.28 (0.21 - 4.04)	0.94 (0.16 - 4.6)
	No Infection	2.78 (0.93 - 8.45)	1.24 (0.42 - 5.08)	0.59 (0.15 - 1.70)
CRP [mg/L]	Infection	30.35 (13.72 - 62.77)	44.4 (15.05 - 86.35)	56.4 (22.95 - 78.37)
	No Infection	51.15 (21.85 - 74.45)	42.2 (29.57 - 78.42)	51.2 (27.25 - 102.82)
IL-6 [ng/L]	Infection	67.30 (16.10 - 161.26)	52.75 (25.61 - 109.01)	44.69 (19.73 - 86.24)
	No Infection	51.81 (24.05 - 105.58)	64.28 (17.70 - 141.06)	37.96 (22.22 - 68.21)

Legend: PCT, procalcitonin; CRP, c-reactive protein; IL-6, interleukin 6; values are given as median with the first and third quartile,
In patients with a bacterial infection new timepoints were created by matching them to the first time of bacterial infection, whereas the control group without bacterial infection was built by matching them age and sex-related to the same timepoints of the patients with bacterial infection. The following virtual timepoints were created: first measurement before the first bacterial infection (preV0), the plasma level at time of the bacterial infection (V0) and next following measured plasma level (V1).