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Supplemental information

Risk assessment with gene expression markers in sepsis development

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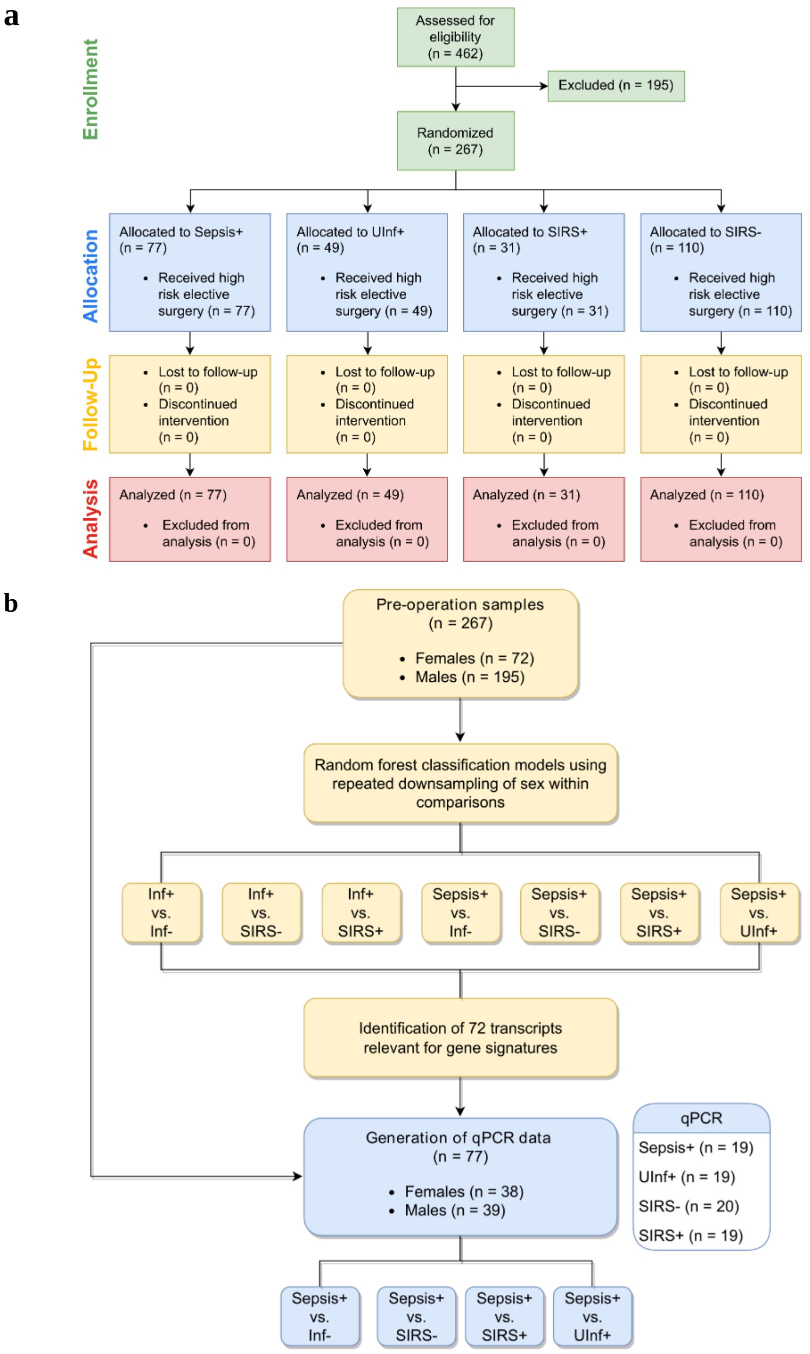
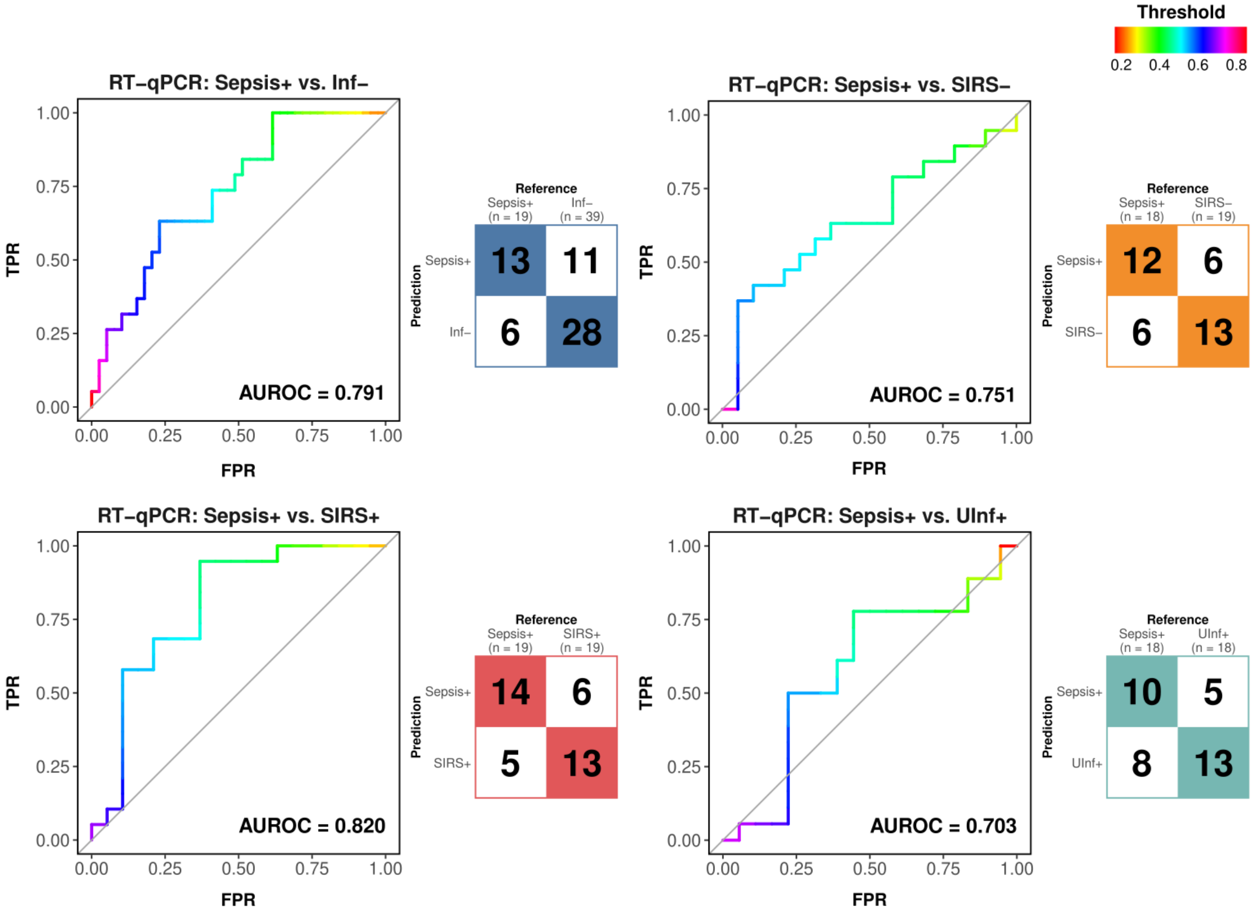
Supplementary Information



Supplementary Figure 1, Study Design to collect and process pre-operation samples of patients scheduled for elective surgery with different post-operative outcome, related to Table 1 and STAR methods. (a) CONSORT diagram and (b) flow chart of the study.



Supplementary Figure 2, Related to Figure 3. RT-qPCR based model classification performance. AUROC and confusion matrices are indicated. The color gradient denotes the probability threshold at any point along the AUROC curves over TPR and FPR. Mean performances for correct classification are indicated in respective confusion matrices. TPR/FPR: True/false positive rate. Further performance information is provided in Supplementary Table 5. RT-qPCR data is available in Supplementary Table 6.

Comparison of post-operative outcome	**Modules**	**Expression (p-value)**	**Correlation (p-value)**
Sepsis (♀♂) vs. SIRS+ (♀♂)	All	5.1e-14	0.04
Sepsis (♀) vs. SIRS+ (♀)	All	1.6e-14	2.8e-03
Sepsis (♂) vs. SIRS+ (♂)	All	1.9e-13	3.7e-08
UInf+ (♀♂) vs. SIRS+ (♀♂)	All	2.4e-13	0.12
UInf+ (♀) vs. SIRS+ (♀)	All	1.2e-13	0.47
UInf+ (♂) vs. SIRS+ (♂)	All	1.7e-10	6.1e-04
Sepsis (♀) vs. Sepsis (♂)	All	0.06	1.7e-05
UInf+ (♀) vs. UInf+ (♂)	All	9.3e-11	2.5e-09
SIRS+ (♀) vs. SIRS+ (♂)	All	0.18	2.8e-03
Sepsis (♀♂) vs. UInf+ (♀♂)	Cell. defense resp./T cell activation	2.5e-06	NA
Sepsis (♀) vs. UInf+ (♀)	Cell. defense resp./T cell activation	1.6e-07	NA
Sepsis (♂) vs. UInf+ (♂)	Cell. defense resp./T cell activation	1.1e-09	NA
SIRS+ (♀♂) vs. UInf+ (♀♂)	Cell. defense resp./T cell activation	1.1e-09	NA
SIRS+ (♀) vs. UInf+ (♀)	Cell. defense resp./T cell activation	1.1e-09	NA

SIRS+ (♂) vs. UInf+ (♂)	Cell. defense resp./T cell activation	6.2e-06	NA
Sepsis (♀♂) vs. SIRS+ (♀♂)	Cell. defense resp./T cell activation	1.1e-09	NA
Sepsis (♀) vs. SIRS+ (♀)	Cell. defense resp./T cell activation	1.7e-08	NA
Sepsis (♂) vs. SIRS+ (♂)	Cell. defense resp./T cell activation	1.1e-09	NA
Sepsis (♀) vs. Sepsis (♂)	Cell. defense resp./T cell activation	0.23	NA
UInf+ (♀) vs. UInf+ (♂)	Cell. defense resp./T cell activation	1.1e-09	NA
SIRS+ (♀) vs. SIRS+ (♂)	Cell. defense resp./T cell activation	0.15	NA
Sepsis (♀♂) vs. UInf+ (♀♂)	GTPase regulator activity	4.6e-11	NA
Sepsis (♀) vs. UInf+ (♀)	GTPase regulator activity	1.7e-12	NA
Sepsis (♂) vs. UInf+ (♂)	GTPase regulator activity	5.4e-09	NA
SIRS+ (♀♂) vs. UInf+ (♀♂)	GTPase regulator activity	1.8e-11	NA
SIRS+ (♀) vs. UInf+ (♀)	GTPase regulator activity	3.5e-11	NA
SIRS+ (♂) vs. UInf+ (♂)	GTPase regulator activity	4.6e-11	NA
Sepsis (♀♂) vs. SIRS+ (♀♂)	GTPase regulator activity	9.3e-11	NA
Sepsis (♀) vs. SIRS+ (♀)	GTPase regulator activity	9.5e-10	NA
Sepsis (♂) vs. SIRS+ (♂)	GTPase regulator activity	1.1e-10	NA

Sepsis (♀) vs. Sepsis (♂)	GTPase regulator activity	3.5e-08	NA
UInf+ (♀) vs. UInf+ (♂)	GTPase regulator activity	0.04	NA
SIRS+ (♀) vs. SIRS+ (♂)	GTPase regulator activity	1.4e-09	NA
Sepsis (♀♂) vs. UInf+ (♀♂)	N.-m. cilium assembly/Cytokinesis	1.6e-08	NA
Sepsis (♀) vs. UInf+ (♀)	N.-m. cilium assembly/Cytokinesis	5.2e-05	NA
Sepsis (♂) vs. UInf+ (♂)	N.-m. cilium assembly/Cytokinesis	4.6e-07	NA
SIRS+ (♀♂) vs. UInf+ (♀♂)	N.-m. cilium assembly/Cytokinesis	0.08	NA
SIRS+ (♀) vs. UInf+ (♀)	N.-m. cilium assembly/Cytokinesis	2.5e-03	NA
SIRS+ (♂) vs. UInf+ (♂)	N.-m. cilium assembly/Cytokinesis	0.29	NA
Sepsis (♀♂) vs. SIRS+ (♀♂)	N.-m. cilium assembly/Cytokinesis	0.05	NA
Sepsis (♀) vs. SIRS+ (♀)	N.-m. cilium assembly/Cytokinesis	0.15	NA
Sepsis (♂) vs. SIRS+ (♂)	N.-m. cilium assembly/Cytokinesis	3.7e-04	NA
Sepsis (♀) vs. Sepsis (♂)	N.-m. cilium assembly/Cytokinesis	0.31	NA
UInf+ (♀) vs. UInf+ (♂)	N.-m. cilium assembly/Cytokinesis	0.05	NA
SIRS+ (♀) vs. SIRS+ (♂)	N.-m. cilium assembly/Cytokinesis	7.4e-07	NA

Supplementary Table 4, Related to Figure 2. Statistical comparisons of co-expression network components. Expression differences were assessed separately by $\log_2$ of fold change against SIRS- for each indicated postoperative outcome group. Expression (p-value) and Correlation (p-value) refer to FDR corrected p-values after paired Wilcoxon test for gene expression differences and correlation differences between genes. ♀♂: all samples, ♀: female samples, ♂: male samples; UInf+: uncomplicated infection postoperative outcome; Cell. defense resp.: Cellular defense response; N.-m. cilium assembly: Non-motile cilium assembly (cf. Figure 2a); NA: test does not apply.