SUPPLEMENTARY MATERIAL

Supplements

Data S1. Supplemental Methods

Imputation and Data Processing

Imputation was carried out in the CSWG-MI and CSWG-HF cohorts using the MissForest function from the missingpy package for Python.[26] Random forest imputation has been shown to perform well in epidemiological datasets and is able to deal with categorical variables.[27] Before random forest (RF) imputation, we removed variables and patients with high missingness (cutoffs: more than 40% missingness for CSWG-MI and 34% for CSWG-HF, which was picked to ensure that overall missingness in the dataset did not exceed 10%) from the derivation dataset to ensure that our results are not driven by patients or variables with most missingness. Hemodynamic variables were gathered for patients in the CSWG but excluded from cluster analysis because the full set of hemodynamics was solely available in the CSWG registry (with a degree of missingness that was acceptable for descriptive statistics but insufficient for clustering which requires complete data), but not in the DRR registry thus using them for clustering would have prevented us from thoroughly validating the clusters. Hemodynamics are also hardly imputable in patients with all hemodynamic variables missing.

We performed a sensitivity analyses of the clustering results by deriving the clusters from CSWG MI datasets imputed with five different random seeds. After imputation, outliers, defined by adapted Tukey's criteria (>3 interquartile ranges away from the 1st or 3rd quartile), were removed from further analyses and visual representation (Supplemental Figure 1). Variables with log-normal distributions were log-transformed. For cluster analyses, all continuous variables were normalized to the minimum of 0 and the maximum of 1. Only for the parallel coordinate plots and radar plots, variables were subsequently standardized to a mean of 0 and an SD of 1.

Variable selection

Correlating (non-orthogonal) variables can distort clustering, as several algorithms tend to weigh these variables higher than orthogonal variables, so they are important to identify and remove when running these analyses.[21] Furthermore, especially in small datasets, clustering on too many variables can add too much granularity to the algorithm without achieving model generalizability.[28] While no strict threshold exists to identify the optimal

number of variables to cluster on for a specific number of cases, a possible hint may be deduced from latent class analysis, where similar dimensionality problems occur[29]: Formann proposed the minimal sample size to include no less than 2^n cases (n = number of variables), preferably 5*2^n.[30] For datasets of approximately 400-500 cases, this suggests that the maximum number of variables to cluster on is eight, preferably six variables. Therefore, to eliminate non-orthogonal variables and appropriately reduce the dimensionality of our model, we employed a classification algorithm to variable selection.

Based on the assumption, that variables driving mortality are clinically the most interesting variables in CS, we identified important variables by supervised ML based on mortality association prior to applying an unsupervised clustering algorithm (semi-supervised learning). We used a random forest classifier to predict in-hospital mortality in 10 bootstrapped samples of 75% of the CSWG-MI derivation cohort. Unlike most regression models the random forest classifier does not assume linear relationships between variables. We identified mortality-predicting variables as variables with the highest average predictive importance in the 10 samples using the RandomForestClassifier function from sklearn.ensemble for Python. In a first run we used all continuous variables (including clinical and laboratory data) that remained after preprocessing independent of their correlation (Supplemental Figure 2). We then trained the random forest classifier again after removal of correlating variables and identified the six most predictive ones for the actual clustering process. Of note, based on the lab values collected, abnormal renal function did not discriminate between acute and chronic kidney injury.

Clustering Procedures

Before clustering, variables were normalized to a minimum of 0 and a maximum of 1. Distance measurement for all clustering algorithms was Euclidean distance. Consensus *k* means clustering was performed on 1000 bootstrap samples of the whole cohorts of the size of 80% of the overall cohort in CSWG-MI and DRR. Consensus clustering provides several benefits including comprehensive cluster visualization, assessment of cluster stability, and estimation of an optimal *k* (number of clusters).[18, 22] The optimal *k* was determined as the *k* achieving highest consensus of the derivation cohort samples, as well as using the Silhouette score, the Calinski-Harabasz criterion, the Davies-Bouldin index and the elbow method for *k* Means clustering in the total derivation cohort. For sensitivity analyses we tested if *k*, cluster

consensus, and cluster distribution remained stable when (a) between five and eight variables were chosen for clustering instead of the identified six and (b) when imputed datasets with five different random seeds were used.

To be of clinical use, clusters would need assignable to patients individually without de-novo clustering of a full cohort.[17, 20] We validated the applicability of our cluster assignment in individual patients using the centroids of the clusters in the derivation cohort to assign clusters to patients in the DRR and CSWG-HF validation cohorts to their respective nearest centroid using the NearestCentroid classifier from the sklearn.neighbors package. Composition of phenotypes and outcomes was compared in the different cohorts to externally validate the phenotypes gathered by the classifier.

Figure S1: Flow Chart of Study Populations and Data Processing

CSWG: Cardiogenic Shock Working Group (Registry); DRR: Danish Retroshock Registry; MI: Myocardial Infarction; HF: Heart Failure

Figure S2: Variable Importance in Random Forest Classifier

A Random Forest Classifier was trained on in-hospital mortality in the derivation cohort to identify the most mortality-driving variables. A and C: Variable importance was calculated as average importance of a variable in the random classifier in 10 runs with different seeds. Importance of the most predictive variable was set to 100%, and the others relative to this variable. A) shows the result using all variables (including correlating variables). Out of the most predictive variables, the correlating (i.e. "non-orthogonal") variables were identified using a correlation matrix (B). In pairs of correlating (|r|>0.6) variables the variable with lower predictive value than the respective other variable was removed. The result is shown in C: The six variables with the highest predictive importance were the same in both instances, before and after removal of the non-orthogonal variables. ALT: Alanine Aminotransferase; BUN: Blood urea nitrogen; Crea: Serum Creatinine; GFR (CKDEPI): Glomerular Filtration Rate; Hgb: Hemoglobin; INR: International Normalized Ratio; WBC: White Blood Cell Count.

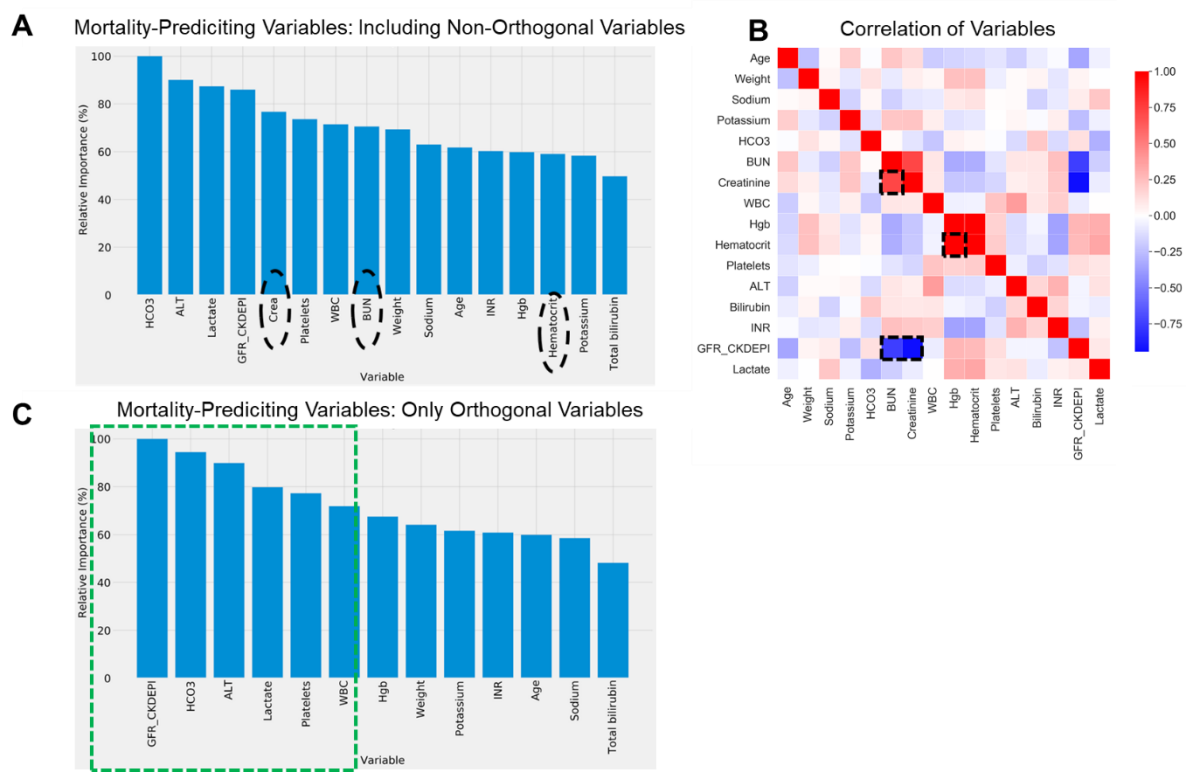

Figure S3: Specifying the Optimal Number of Clusters (*k)* from the CSWG-MI Derivation Cohort

A: Cluster-Consensus Plot showing the *cluster-consensus* values of clusters at each *k*. High values indicate cluster stability[22]. B: Cumulative Distribution Function (CDF) plot for each *k* to determine where the CDF reaches a maximum without expense of consensus. Higher and "flatter" curves are favorable[22]. C: Tracking plot for each *k* showing the cluster assignment of each case. Changing colors within a column indicate unstable cluster assignment, as these samples are changing clusters often in repeated runs[22]. D: Different metrics for the quality of the clustering to determine the optimal *k.* Unlike A-C, this panel depicts the scores/criteria for *k* Means clustering on the full cohort and not the consensus *k* Means clusters. The scores determine, how well the variables entered in the clustering are clustered with different *k*. Higher silhouette scores and lower Davies-Bouldin scores indicate better clustering and relatively higher Calinski-Harabasz scores estimate the optimal *k*. Finally, the "elbow" in the elbow plot can be used to estimate the optimal *k*. The Silhouette, the Davies-Bouldin criterion and the elbow plot indiciate an optimal *k* of 3 clusters. The Calinski-Harabasz suggests an optimal *k* at 2 or 3.

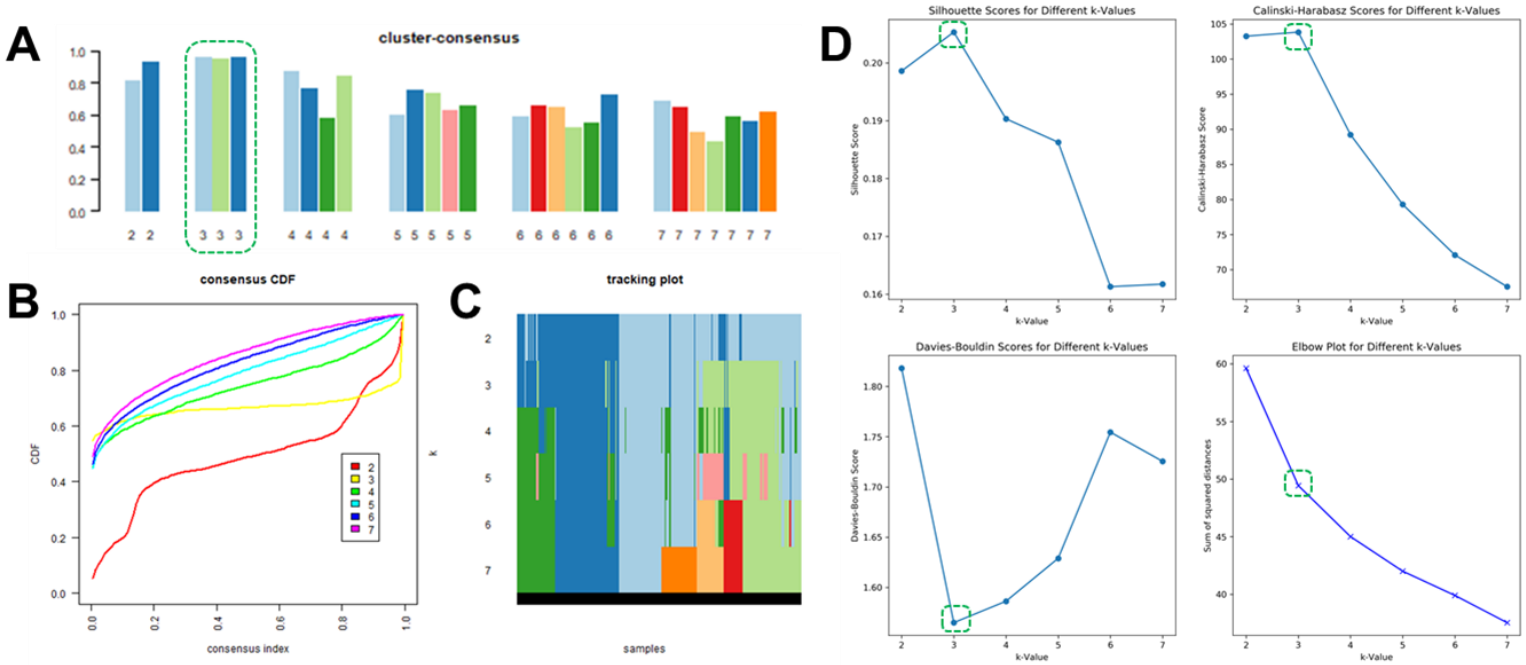

Table S1: Patient Characteristics in the Clusters of CSWG-MI, DRR and CSWG-HF

Table displays only non-imputed data. Mean (SD) or n (%). ALT: Alanine Aminotransferase; BUN: Blood urea nitrogen; CI: Cardiac Index; CO: Cardiac Output; COPD: Chronic obstructive pulmonary disease; CPI: Cardiac Power Index; CPO: Cardiac Power Output, CSWG-HF: Cardiogenic Shock Working Group registry Heart Failure cohort; Creatinine: Serum creatinine; CSWG-MI: Cardiogenic Shock Working Group registry Myocardial Infarction cohort; CVA/TIA: Cerebrovascular accident/Transient Ischemic Attack; DBP: Diastolic blood pressure; DM2: Type 2 Diabetes Mellitus; DRR: Danish Retroshock Registry; ECMO: Extracorporeal membrane oxygenation; GFR: Glomerular Filtration Rate; Hgb: Hemoglobin; HTN: Hypertension; IABP: Intra-Aortic Balloon Pump; INR: International Normalized Ratio; LVEDD: Left ventricular end-diastolic dimension; MAP: Mean arterial pressure; PA Sat: Pulmonary Arterial Saturation; PADP: Pulmonary Artery Diastolic Pressure; PAP: Pulmonary Artery Pressure; PAPI: Pulmonary Artery Pulsatility Index; PASP: Pulmonary Artery Systolic Pressure; PCWP: Pulmonary Capillary Wedge Pressure; PVD: Peripheral vascular disease; RAP: Right atrial pressure; SBP: Systolic blood pressure; WBC: White Blood Cell Count.

	CSWG MI						DRR INDEPENDENTLY CLUSTERED						DRR WITH ASSIGNED CLUSTERS						CSWG HF					
	I		II		III		I		II		III		I		II		III		I		II		III	
	N	(%)	N	(%)	N	(%)	N	(%)	N	(%)	N	(%)	N	(%)	N	(%)	N	(%)	N	(%)	N	(%)	N	(%)
Non-Survivors	30	20.55	65	45.14	66	55	101	29.36	147	45.51	230	57.21	90	28.21	83	40.29	305	56.07	19	10.5	74	31.76	34	51.52
Male	103	70.55	95	65.97	81	67.5	271	78.78	232	71.83	316	78.61	247	77.43	151	73.3	421	77.39	131	72.38	191	81.97	40	60.61
IABP	89	60.96	88	61.11	72	60	44	12.79	43	13.31	40	9.95	43	13.48	29	14.08	55	10.11	59	32.6	110	47.21	31	46.97
ECMO	36	24.66	38	26.39	54	45	8	2.33	6	1.86	29	7.21	10	3.13	0	0	33	6.07	22	12.15	41	17.6	30	45.45
Impella	55	37.67	67	46.53	48	40	40	11.63	33	10.22	79	19.65	37	11.6	18	8.74	97	17.83	27	14.92	58	24.89	24	36.36
Mechanical ventilation	77	52.74	79	54.86	86	71.67													42	23.2	75	32.19	46	69.7
Vasopressor/Inotrope Use	98	67.12	116	80.56	104	86.67	329	95.64	307	95.05	396	98.51	302	94.67	201	97.57	529	97.24	139	76.8	192	82.4	53	80.3
Vasodilators	23	15.75	20	13.89	19	15.83													93	51.38	96	41.2	12	18.18
History of HTN	84	57.53	119	82.64	78	65	129	37.5	209	64.71	174	43.28	132	41.38	134	65.05	246	45.22	57	31.49	119	51.07	40	60.61
History of CKD (any stage)	2	1.37	56	38.89	15	12.5													33	18.23	116	49.79	20	30.3
History of COPD	6	4.11	13	9.03	5	4.17	30	8.72	42	13	32	7.96	27	8.46	23	11.17	54	9.93	18	9.94	23	9.87	8	12.12
History of CVA/TIA	17	11.64	23	15.97	17	14.17	24	6.98	37	11.46	24	5.97	23	7.21	25	12.14	37	6.8	28	15.47	41	17.6	7	10.61
Prior HF	35	23.97	39	27.08	18	15													144	79.56	181	77.68	38	57.58
Prior MI	30	20.55	52	36.11	28	23.33	39	11.34	60	18.58	53	13.18	37	11.6	41	19.9	74	13.6	36	19.89	77	33.05	19	28.79
History of PCI	41	28.08	50	34.72	47	39.17													28	15.47	56	24.03	10	15.15
History of CABG	8	5.48	17	11.81	8	6.67													10	5.52	28	12.02	7	10.61
History of Diabetes	40	27.4	89	61.81	50	41.67	41	11.92	60	18.58	72	17.91	39	12.23	42	20.39	92	16.91	36	19.89	82	35.19	24	36.36
History of PVD	6	4.11	8	5.56	6	5	17	4.94	29	8.98	31	7.71	22	6.9	14	6.8	41	7.54	3	1.66	12	5.15	3	4.55
	Mean	**SD**	**Mean**	**SD**	**Mean**	**SD**	**Mean**	**SD**	**Mean**	**SD**	**Mean**	**SD**	**Mean**	**SD**	**Mean**	**SD**	**Mean**	**SD**	**Mean**	**SD**	**Mean**	**SD**	**Mean**	**SD**
Age (years)	61.95	13.94	69.03	11.56	64.28	13.27	62.84	10.86	71.29	9.16	64.44	11.09	63.44	10.8	71.38	9.15	65.46	11.17	51.4	15.26	60.41	12.1	59.39	14.87
Weight (kg)	82.02	20.38	82.47	18.22	80.97	17.43	79.56	15.21	80.37	16.17	83.13	15.75	79.23	14.8	80.59	16.37	82.43	16	83.17	21.31	88.55	21.54	90.64	26.62
Sodium (mEq/L)	137.17	3.85	136.52	4.47	137.81	4.25	137.65	4.49	137.63	4.42	138.28	4.59	137.61	4.5	137.41	4.08	138.22	4.66	135.01	5.19	133.22	5.59	135.34	5.77
Potassium (mEq/L)	4.16	0.57	4.44	0.71	4.31	0.89	3.88	0.6	4.15	0.82	4.17	0.85	3.88	0.6	4.21	0.83	4.13	0.83	4.12	0.57	4.26	0.65	4.78	0.93
HCO3 (mEq/L)	22.4	4.2	21.48	3.83	16.55	4.11	20.95	3.93	19.61	3.72	15.45	4.34	21.5	3.88	20.15	3.38	16.07	4.23	26.38	3.59	25.18	4.12	16.61	4.08
BUN (mg/dL)	18.21	7.56	42.01	19.29	24.9	10.93	17.92	7.67	31.03	19.85	25.13	15.98	6.56	2.79	12.49	7.93	8.68	5.37	24.31	10.54	49.55	24.3	37	21.22
Creatinine (mg/dL)	0.94	0.22	2.49	1.39	1.47	0.5	0.94	0.2	2.01	1.51	1.53	0.85	83.37	18.25	194.23	148.99	135.31	79.16	1.09	0.25	2.38	1.33	2.02	1.06
WBC ($10^3/mm^3$)	12.36	5.54	13.94	5.87	18	8.58	15.09	5.89	15.93	6.81	17.86	7.03	14.53	5.82	15.61	6.57	17.77	6.95	9.48	4.4	10.07	4.82	16.57	7.68
Hgb (g/dL)	13.21	2.37	11.27	2.3	12.98	2.67	13.78	1.79	12.99	2.06	13.77	2.31	8.52	1.12	7.98	1.25	8.5	1.4	12.5	2.27	11.68	2.25	11.51	2.57
Hematocrit (%)	39.05	7.05	33.74	7.08	39.01	7.27	39.58	6.88	37.45	6.97	39.84	7.79	0.39	0.07	0.37	0.07	0.39	0.08	38.48	6.39	35.52	6.36	35.9	8.29
Platelets ($10^3/mm^3$)	218.5	70.53	187.96	75.91	248.58	109.59	250.06	87.37	263.2	96.3	232.08	81.75	249.07	87.3	241.19	96.71	248.51	87.01	219.49	75.66	182.16	76.08	197.26	82.32
ALT (U/L)	73.57	121.42	147.98	316.97	290.73	561.28	109.77	151.8	69.39	122.74	378.98	700.65	97.88	150.87	123.74	268.22	286.41	607.24	61.23	103.66	166.85	476.27	1106.4	1798.8
Total bilirubin (mg/dL)	0.89	0.53	0.91	0.56	0.82	0.55	0.74	1.09	0.72	0.53	0.85	1.03	12.53	18.97	12.95	9.71	13.72	15.95	1.7	2.41	1.67	1.78	2.33	1.81
INR	1.24	0.29	1.44	0.51	1.49	0.54	1.2	0.35	1.27	0.53	1.33	0.59	1.19	0.31	1.27	0.58	1.31	0.57	1.82	1.01	1.88	1.03	2.48	1.78
GFR (mL/min/1.73 m^2)	81.47	16.47	30.34	13.8	50.72	16.98	81.93	14.31	39.79	15.27	52.93	18.18	80.95	15.37	36.65	15.27	53.2	18.94	76.26	20.66	33.14	12.4	39.37	17.4

	CSWG MI						DRR INDEPENDENTLY CLUSTERED						DRR WITH ASSIGNED CLUSTERS						CSWG HF					
	I		II		III		I		II		III		I		II		III		I		II		III	
Lactate (mEq/L)	3.45	3.15	2.17	1.27	7.89	4.21	3.81	2.61	3.54	2.2	9.21	4.69	3.54	2.4	2.36	1.24	8.35	4.43	2.17	1.21	2.15	1.27	9.9	4.82
pH	7.3	0.13	7.35	0.12	7.21	0.16	7.31	0.11	7.29	0.1	7.18	0.14	7.32	0.1	7.3	0.09	7.2	0.14	7.41	0.1	7.38	0.1	7.26	0.16
MAP (mmHg)	79.63	16.5	74.98	15.7	68.42	16.21	66.07	11.44	63.4	11.96	62.9	11.76	65.78	11.85	63.95	11.21	63.12	11.88	72.92	10.48	74.09	13.89	69.64	16.41
DBP (mmHg)	64.71	15.46	58.46	14.47	57.25	16.91	54.82	10.54	52.32	12.03	51.86	11.16	85.11	13.72	84.3	13.34	82.69	14.86	62.03	10.64	62.55	13.63	57.84	15.33
SBP (mmHg)	104.65	23.76	103.57	23.97	93.19	22.2	85.35	13.8	83.59	13.79	82.42	14.94	54.32	10.89	52.56	10.75	52.31	11.7	92.79	13.66	96.65	16.54	91.24	20.08
CI (L/min/m²)	1.92	0.62	1.93	0.55	1.76	0.57													1.84	0.42	1.96	0.65	1.92	0.72
CO (L/min)	3.72	1.3	3.88	1.67	3.45	1.41													3.81	2.86	4.22	2.73	4.08	2.95
CPI (W/m$^{2)}$	0.33	0.14	0.32	0.11	0.27	0.14													0.30	0.07	0.32	0.13	0.30	0.12
CPO (W)	0.64	0.27	0.64	0.29	0.53	0.31													0.61	0.42	0.69	0.41	0.67	0.58
LVEDD (mm)	4.88	0.93	4.98	0.95	4.45	0.77													6.66	1.12	6.5	1.2	5.93	1.11
Heart rate (1/min)	87.97	22.03	89.84	19.48	96.39	24.64	86.37	24.97	86.2	24.25	85.56	22.94	86.42	25.66	83.43	22.67	86.78	23.44	90.41	20.34	91.86	23.23	94.54	25.27
PCWP (mmHg)	23.91	8.66	25.78	9.95	23.36	9.45													23.16	9.3	24.4	8.01	26.48	9.31
PADP (mmHg)	22.67	7.84	24.82	6.85	23.65	8.38													25.07	8.36	26.68	8.14	27.53	9.65
PASP (mmHg)	42.6	13.9	47.12	13.53	41.57	13.86													47.14	13.47	50.47	14.64	47.91	15.57
mean PAP (mmHg)	29.29	9.19	32.32	8.42	29.6	9.69													32.46	9.48	34.61	9.71	34.32	11.04
RAP (mmHg)	12.98	5.77	14.8	7.13	16.81	6.48	12.31	5.19	12.48	5.3	12.83	4.79	12.39	5.48	11.99	5.11	12.86	4.79	11.4	6.91	14.68	6.87	16.81	8.06
PAPI (arbitrary units)	2.38	3.84	1.82	1.03	1.11	0.59													3.46	4.51	2.36	2.55	1.65	1.46
RVSWI (mmHg * ml/m²)	5.00	2.84	5.33	2.78	3.41	3.07													5.99	2.71	6.03	3.63	4.86	3.06

Figure S4: Sources of Each Cluster's Baseline Differences from the Other Clusters

Chord Plots illustrate the association between clusters and clinically relevant groups of variables based on organ system function. A connection (or "chord") from a cluster to a category signifies that at least one variable in this cluster was different from the other two clusters combined. Relative chord thickness corresponds to the relative influence of each organ system in determining the characteristics of each phenotype. Only non-imputed data was used for these graphs. Panel A shows all the phenotypes and panels B-D highlight each phenotype individually.

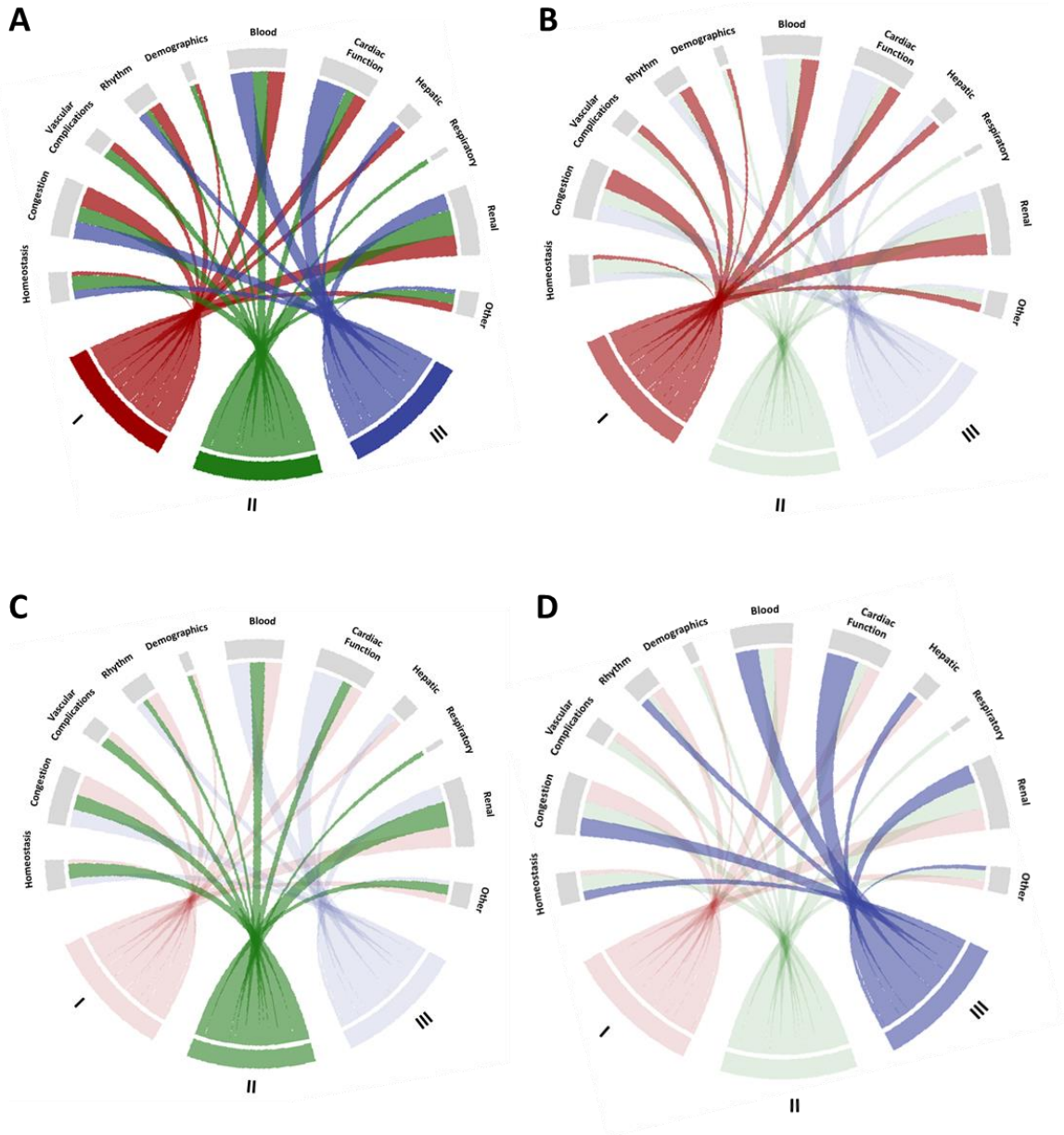

Figure S5: Independent *de novo* Consensus k-Means Clustering in DRR

To assess external reproducibility of the derived clusters we applied consensus k-Means clustering to patients in the DRR validation cohort independently on the same variables. In these representative plots, each column represents one patient while each row displays the assigned clusters. Well-defined squares indicate stable clusters. These figures suggest stability of the clusters when 3 is picked as the number of clusters (k). DRR: Danish Retroshock Registry.

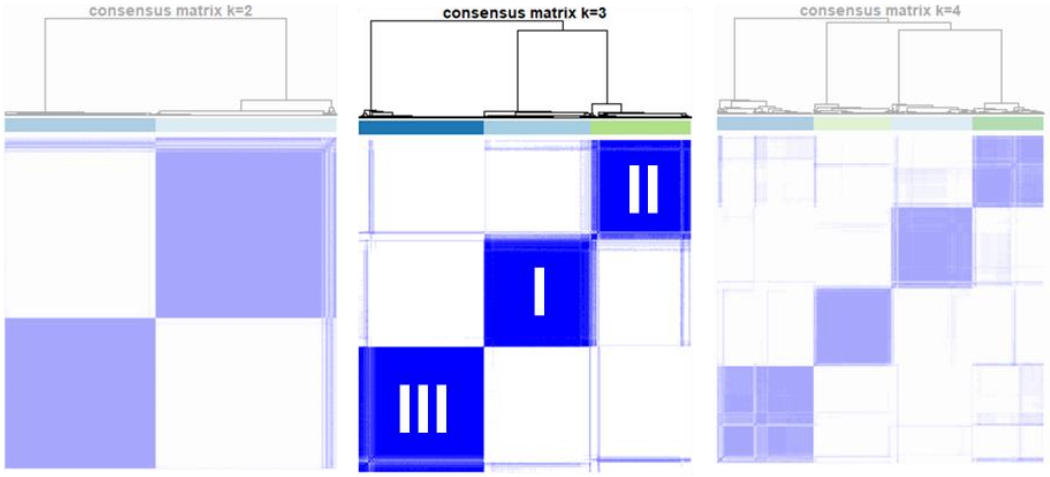

Figure S6: Similarity of Clusters in the CSWG-MI Derivation and the DRR Validation Cohort

Parallel coordinate plots comparing the tendencies of clinical parameters throughout the CSWG MI and DRR validation cohorts with respect to different clusters. A value of 1 signifies that the mean value for one cluster was one standard deviation higher than the mean value of the two cluster that are compared in the respective graph. The plots indicate how similar the properties of the clusters in CSWG-MI and DRR were, when clustered and analyzed separately. Furthermore, they reveal the resemblance of the clusters assigned to the validation cohort using the nearest centroid classifier ("DRR predicted") as compared to the clusters from independent consensus K means clustering ("DRR clustered"). CSWG: Cardiogenic Shock Working Group; DRR: Danish Retroshock Registry.

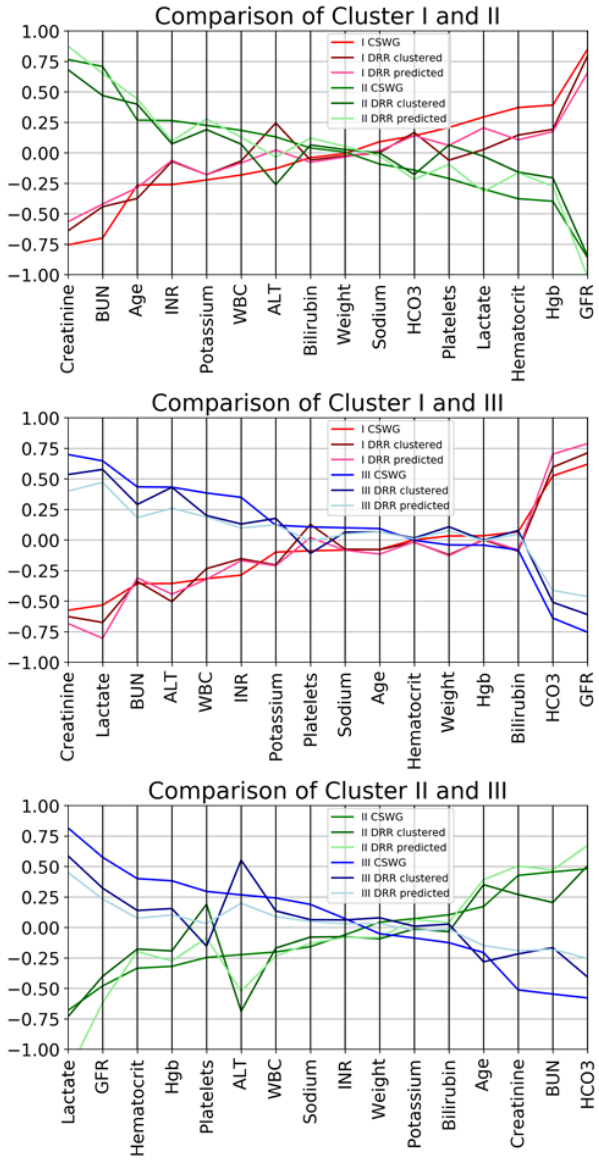

Figure S7: Distribution of Patients in the Clusters by Cohort

Top panel: Pie charts depicting the percentage of patients per cluster in each cohort. For DRR, the results are shown twice: "DRR clustered" depicts the clusters of the patients when DRR was independently *de novo* clustered, while "DRR predicted" depicts the clusters when they were applied based on the centroids of the clusters in the CSWG MI derivation cohort. Patients in "DRR clustered" and "DRR predicted" were in the same cluster in 82% of the cases, indicating the similarity of the two methods. Bottom Panel: The t-distributed stochastic neighbor embedding (t-SNE) plots for a visual representation of the clustering in each cohort. For these plots, the 6 variables that were used for clustering were reduced to 2 variables which enables plotting the results in a two-dimensional graph. CSWG: Cardiogenic Shock Working Group (Registry); DRR: Danish Retroshock Registry; MI: Myocardial Infarction; HF: Heart Failure

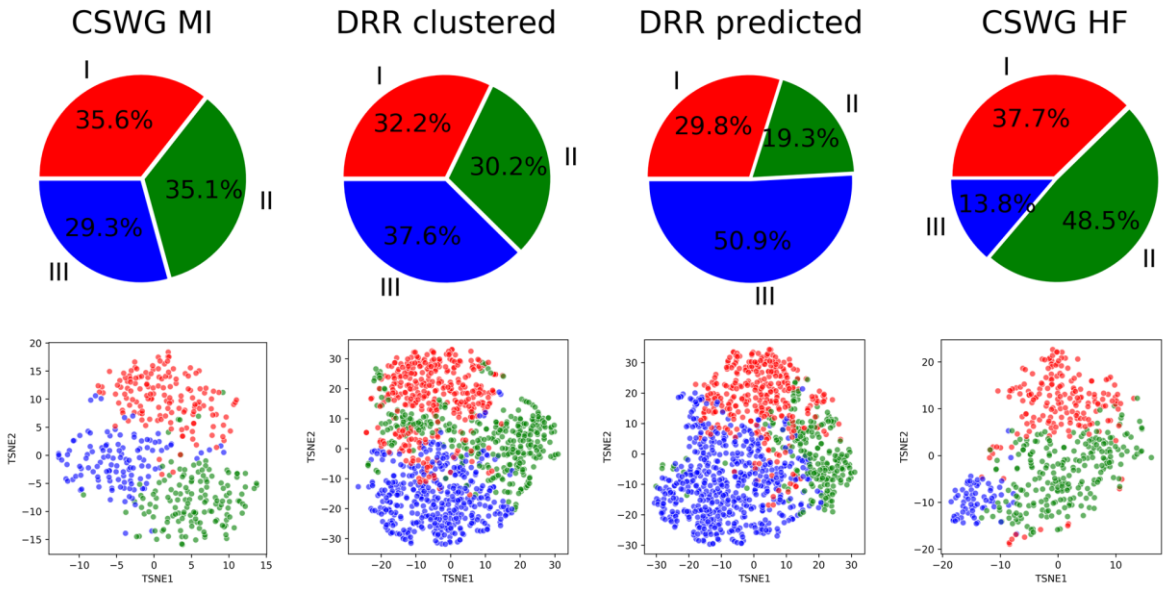

Figure S8: Phenotype Characteristics in the Validation Cohorts

Radar plots illustrate the specific characteristics of the cardiogenic shock phenotypes in the validation cohorts DRR and CSWG HF. Data was normalized across all phenotypes to a mean of 0 and an SD of 1. The dashed black line marks the mean (0), while every concentric gray line signifies a 0.1 SD difference from the overall mean. ALT: Alanine Aminotransferase; BUN: Blood urea nitrogen; CI: Cardiac Index; CO: Cardiac Output; CPI: Cardiac Power Index; CPO: Cardiac Power Output; CSWG HF: Cardiogenic Shock Working Group Registry Heart Failure Cohort; DBP: Diastolic Blood Pressure; DRR: Danish Retroshock Registry; GFR: Glomerular Filtration Rate; Hgb: Hemoglobin; INR: International Normalized Ratio; MAP: Mean Arterial Pressure; LVEDD: Left ventricular end-diastolic dimension; PA Sat: Pulmonary Arterial Saturation; PADP: Pulmonary Artery Diastolic Pressure; PAP: Pulmonary Artery Pressure; PAPI: Pulmonary Artery Pulsatility Index; PASP: Pulmonary Artery Systolic Pressure; PCWP: Pulmonary Capillary Wedge Pressure; RAP: Right atrial pressure; RVSWI: Right ventricular stroke work index; SBP: Systolic blood pressure; SVI: Stroke Volume Index WBC: White Blood Cell Count

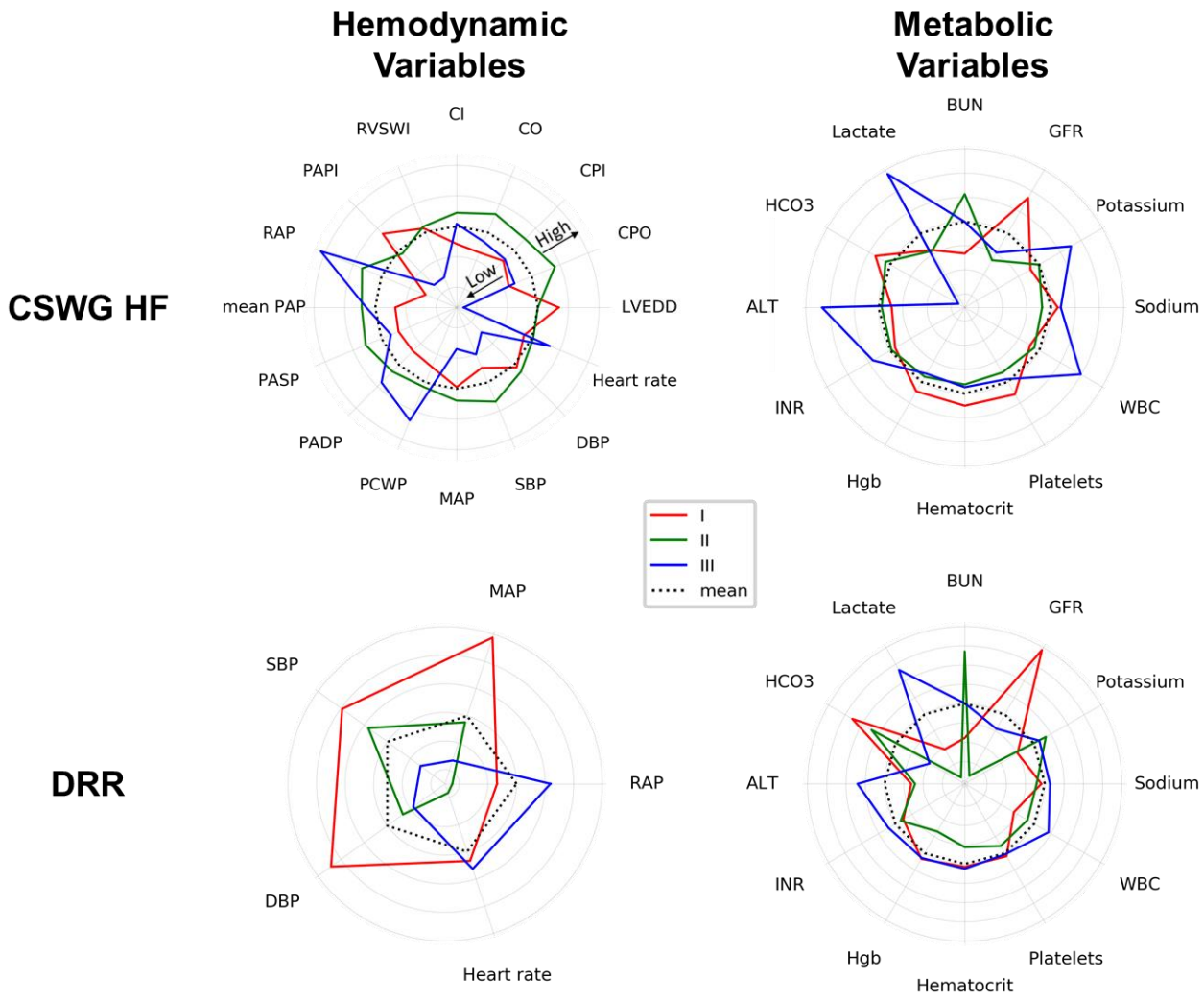

Table S2: Sensitivity Analysis of DRR including all Patients

No patients were excluded for this analysis but missing values (overall missingness 4717 values = 8.1%) in DRR were imputed. The results resemble the results of the main analysis. ALT: Alanine Aminotransferase; BUN: Blood urea nitrogen; CABG: Coronary artery bypass graft; COPD: Chronic obstructive pulmonary disease; CVA/TIA: Cerebrovascular accident/Transient Ischemic Attack; DM2: Type 2 Diabetes Mellitus; DRR: Danish Retroshock Registry; ECMO: Extracorporeal membrane oxygenation; GFR: Glomerular Filtration Rate; Hgb: Hemoglobin; HTN: Hypertension; IABP: Intra-Aortic Balloon Pump; INR: International Normalized Ratio; MI: Myocardial infarction; PCI: Percutaneous coronary intervention; WBC: White Blood Cell Count.

		Non-congested	**Cardiorenal**	**Cardiometabolic**
variable	level			
n		512	316	888
Age		65.0 (12.0)	72.6 (10.1)	66.9 (11.9)
Gender		386 (75.4)	222 (70.3)	670 (75.5)
Weight		78.2 (14.2)	78.6 (15.3)	81.2 (14.9)
DM2		59 (11.5)	64 (20.3)	150 (16.9)
Prior MI		69 (13.5)	59 (18.7)	124 (14.0)
HTN		242 (47.3)	216 (68.4)	440 (49.5)
CVA/TIA		38 (7.4)	37 (11.7)	61 (6.9)
COPD		50 (9.8)	40 (12.7)	87 (9.8)
Prior PCI		483 (94.3)	300 (94.9)	842 (94.8)
Prior CABG		38 (7.4)	16 (5.1)	47 (5.3)
Pressors or Inotropes		437 (85.4)	275 (87.0)	780 (87.8)
IABP		64 (12.5)	40 (12.7)	84 (9.5)
ECMO		13 (2.5)		45 (5.1)
Mortality		183 (36.6)	155 (50.3)	558 (63.9)
Lactate	mEq/L	3.7 (2.6)	2.5 (1.3)	8.7 (4.6)
HCO3	mEq/L	21.5 (3.8)	20.3 (3.5)	16.2 (4.2)
GFR	mL/min/1.73 m^2	80.2 (16.3)	35.8 (15.4)	52.5 (18.7)
Creatinine	mg/dL	0.9 (0.2)	2.3 (1.8)	1.5 (0.9)
BUN	mg/dL	18.4 (7.4)	36.4 (23.2)	24.7 (15.2)
Platelets	$10^3/mm^3$	246.3 (86.5)	240.5 (92.1)	248.6 (87.8)
Total bilirubin	mg/dL	0.7 (0.9)	0.7 (0.5)	0.7 (0.8)
WBC	$10^3/mm^3$	14.1 (5.9)	15.1 (6.1)	17.2 (6.5)
Hematocrit	%	38.7 (6.5)	36.9 (6.4)	39.2 (7.2)
Potassium	mEq/L	3.9 (0.6)	4.2 (0.8)	4.2 (0.9)
Sodium	mEq/L	137.7 (4.5)	137.3 (4.1)	138.2 (4.6)
Hemoglobin	g/dL	13.5 (1.9)	12.6 (2.0)	13.5 (2.2)
ALT	U/L	89.5 (132.1)	106.7 (225.3)	255.5 (556.0)
INR		1.2 (0.4)	1.3 (0.5)	1.3 (0.6)

Table S3: Sensitivity Analysis of CSWG HF including all Patients

No patients were excluded for this analysis but missing values (overall missingness 6161 values = 20.4%) in CSWG HF were imputed. The results resemble the results of the main analysis. ALT: Alanine Aminotransferase; BUN: Blood urea nitrogen; CABG: Coronary artery bypass graft; COPD: Chronic obstructive pulmonary disease; CSWG-HF: Cardiogenic Shock Working Group registry Heart Failure cohort; CVA/TIA: Cerebrovascular accident/Transient Ischemic Attack; DM2: Type 2 Diabetes Mellitus; ECMO: Extracorporeal membrane oxygenation; GFR: Glomerular Filtration Rate; Hgb: Hemoglobin; HTN: Hypertension; IABP: Intra-Aortic Balloon Pump; INR: International Normalized Ratio; MI: Myocardial infarction; PCI: Percutaneous coronary intervention; WBC: White Blood Cell Count.

		Non-congested	**Cardiorenal**	**Cardiometabolic**
variable	level			
n		227	379	80
Age	Years	52.1 (15.0)	60.5 (12.3)	61.2 (15.0)
Gender	Male	169 (74.4)	300 (79.2)	52 (65.0)
Weight	kg	81.5 (19.7)	86.5 (19.8)	88.4 (22.4)
DM2		49 (21.6)	136 (35.9)	30 (37.5)
Prior MI		52 (22.9)	128 (33.8)	25 (31.2)
HTN		75 (33.0)	207 (54.6)	53 (66.2)
CVA/TIA		28 (12.3)	49 (12.9)	7 (8.8)
COPD		20 (8.8)	31 (8.2)	10 (12.5)
Prior PCI		51 (22.5)	124 (32.7)	15 (18.8)
Prior CABG		11 (4.8)	48 (12.7)	11 (13.8)
Pressors or Inotropes		177 (78.0)	319 (84.2)	66 (82.5)
IABP		103 (45.4)	234 (61.7)	39 (48.8)
ECMO		22 (9.7)	44 (11.6)	34 (42.5)
Mortality		36 (16.4)	89 (24.3)	40 (50.6)
Lactate	mEq/L	2.3 (1.0)	2.1 (1.0)	9.2 (4.6)
HCO3	mEq/L	26.0 (2.9)	25.0 (2.9)	17.2 (4.0)
GFR	mL/min/1.73 m^2	76.1 (20.1)	33.6 (12.2)	39.3 (17.7)
Creatinine	mg/dL	1.1 (0.2)	2.3 (1.2)	2.1 (1.2)
BUN	mg/dL	24.7 (9.3)	48.5 (20.6)	37.6 (20.0)
Platelets	$10^3/mm^3$	216.7 (66.9)	186.4 (60.2)	200.1 (78.1)
Total bilirubin	mg/dL	1.6 (1.9)	1.5 (1.3)	2.1 (1.5)
WBC	$10^3/mm^3$	9.4 (3.8)	10.2 (4.2)	18.5 (13.7)
Hematocrit	%	37.7 (5.5)	35.9 (4.8)	36.2 (6.9)
Potassium	mEq/L	4.1 (0.5)	4.3 (0.5)	4.9 (0.9)
Sodium	mEq/L	134.8 (4.6)	133.3 (4.2)	135.3 (5.4)
Hemoglobin	g/dL	12.4 (1.9)	11.8 (1.7)	11.8 (2.4)
ALT	U/L	82.9 (122.8)	163.4 (428.6)	838.1 (1344.1)
INR		1.8 (0.9)	1.7 (0.9)	2.4 (1.6)

Figure S9: Sensitivity Analysis of DRR including all Patients

Patients in the Danish Retroshock Registry were excluded if missing any of the six values that were necessary for clustering (n=633). Depicted in this figure is the comparison of de novo consensus k means clustering and the cluster assignment based on the nearest centroids of the CSWG derivation cohort within the full (partially imputed) DRR cohort (n=1716). Cluster distribution differed between both methods, but the tendencies of the variables that were clustered on remained stable, underlining the external validity of the clusters.

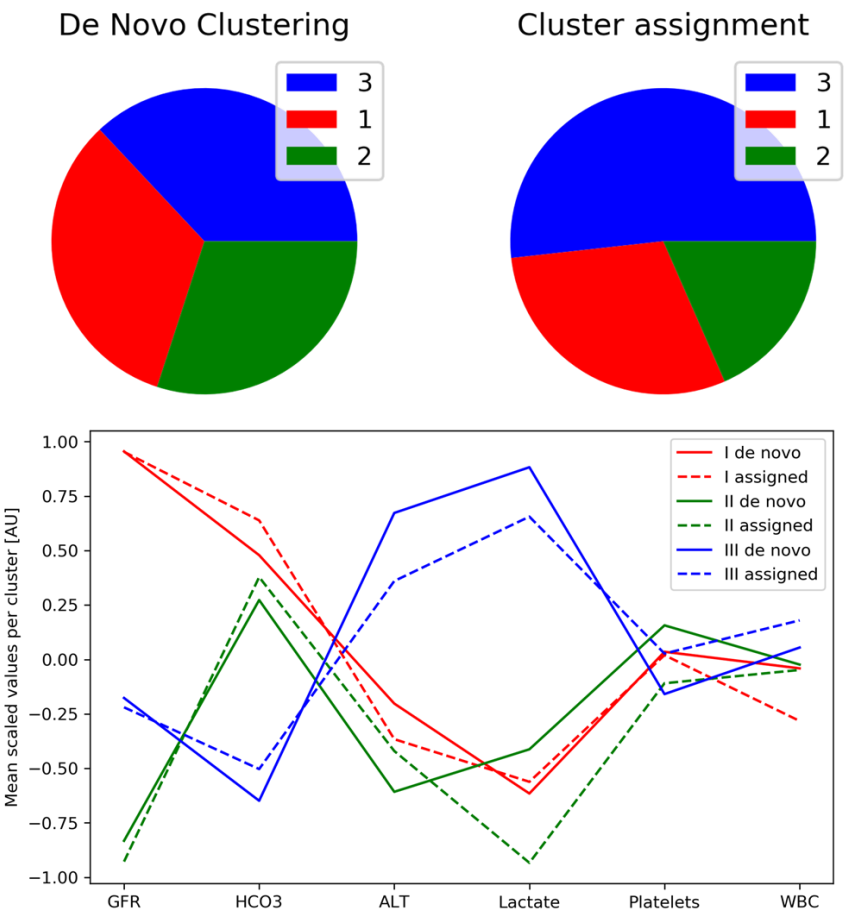

Table S4. Odds of Mortality Associated with SCAI Stage and Phenotypes.

	CSWG MI				CSWG HF				CSWG MI+HF			
	OR	(95% CI)	aOR*	(95% CI)	OR	(95% CI)	aOR*	(95% CI)	OR	(95% CI)	aOR*	(95% CI)
SCAI												
B	0	-	0	-	0	-	0	-	0	-	0	-
C	1.0	-	1.0	-	1.0	-	1.0	-	1.0	-	1.0	-
D	3.8	(1.9-7.7)	3.4	(1.7-6.9)	6.1	(2.8-13.0)	5.6	(2.6-12.2)	4.8	(2.8-8.0)	4.3	(2.6-7.2)
E	7.9	(3.7-16.8)	6.3	(2.9-13.6)	14.2	(5.7-35.4)	9.3	(3.6-23.7)	10.9	(6.1-19.4)	8.2	(4.5-14.7)
Phenotypes												
I	1.0	-	1.0	-	1.0	-	1.0	-	1.0	-	1.0	-
II	3.3	(2.3-4.8)	2.9	(1.7-4.9)	3.2	(1.9-5.3)	2.9	(1.6-5.2)	3.3	(2.3-4.8)	2.7	(1.9-4.0)
III	6.6	(4.3-10.0)	4.0	(2.3-7.1)	4.7	(2.8-8.1)	6.1	(2.9-12.7)	6.6	(4.3-10.0)	4.8	(3.0-7.5)

*aORs adjusted by SCAI stage and CSWG derived clusters. aOR: adjusted odds ratio; CSWG: Cardiogenic Shock Working Group (Registry); HF: Heart Failure; MI: Myocardial Infarction; OR: odds ratio