

Table 1: Summary of Regression Analysis of the cell composition data

	Coefficient	Standard Error	z- value	P> z (>0.05)	[0.025	0.975]
Age	-0.0122	0.0015	-8.0492	8.3368 e-16 ****	-0.0152	-0.0092
Sex	-0.3263	0.1283	-2.5436	0.01097 *	-0.5778	-0.0749
Mesenchymal Stem cells	-61.2000	43.7957	-1.3974	0.1623	-147.0380	24.6380
Bronchial Epithelial Cells	0.5361	3.292	0.163	0.8706	-5.915	6.987
Fibroblasts	32.1632	37.925	0.848	0.3964	-42.168	106.495
Endothelial cells	18.2526	5.439	3.356	0.0007913***	7.592	28.913
Adipocytes	6.8374	5.997	1.140	0.2542	-4.916	18.591
Keratinocytes	-14.7111	18.027	-0.816	0.4145	-50.043	20.621
Schwann cells	-18.0620	14.929	-1.210	0.2263	-47.323	11.199
Smooth Muscle Cells	-2.0380	10.827	-0.188	0.8507	-23.259	19.184
CD34+	10.8900	3.406	3.197	0.001389**	4.214	17.566
Platelets	-0.1945	1.416	-0.137	0.8908	-2.971	2.582
Monocytes CD14+ CD16-	-5.9829	0.846	-7.075	1.4954 e-12****	-7.640	-4.325
Monocytes CD14- CD16+	-12.5595	4.203	-2.988	0.002809**	-20.798	-4.321
Macrophage	-6.5335	5.359	-1.219	0.2228	-17.036	3.96
M1 Macrophage (IFN γ)	-8.8978	3.206	-2.776	0.005507**	-15.181	-2.615
M2 Macrophage (IL4)	-50.7094	14.247	-3.559	0.0003718***	-78.633	-22.786
Monocyte derived Macrophages (IFN α)	20.2936	6.632	3.060	0.002213**	7.295	33.292
Dendritic cells (BDCA1+)	-78.2019	62.424	-1.253	0.2103	-200.551	44.147
Dendritic cells (BDCA3+)	-111.9394	93.014	-1.203	0.2288	-294.244	70.365
Dendritic cells (plasmacytoid+)	-3.0851	5.666	-0.544	0.5861	-14.190	8.020
T cells (CD4+)	-14.1071	1.845	-7.646	2.0712 e-14****	-17.723	-10.491
T cells (CD8+)	2.1898	3.791	0.578	0.5635	-5.240	9.620
T cells ($\gamma - \delta$)	-6.5137	2.067	-3.152	0.001622**	-10.564	-2.463
NK cells	-9.8719	2.659	-3.712	0.0002053***	-15.084	-4.660
Neutrophils	-3.9653	0.592	-6.696	2.1464 e-11****	-5.126	-2.805
B cells	-1.5695	1.901	-0.826	0.4089	-5.295	2.156

A

p = 8.3368 e-16 ****

B

p = 0.0007913***

C

p = 0.001389**

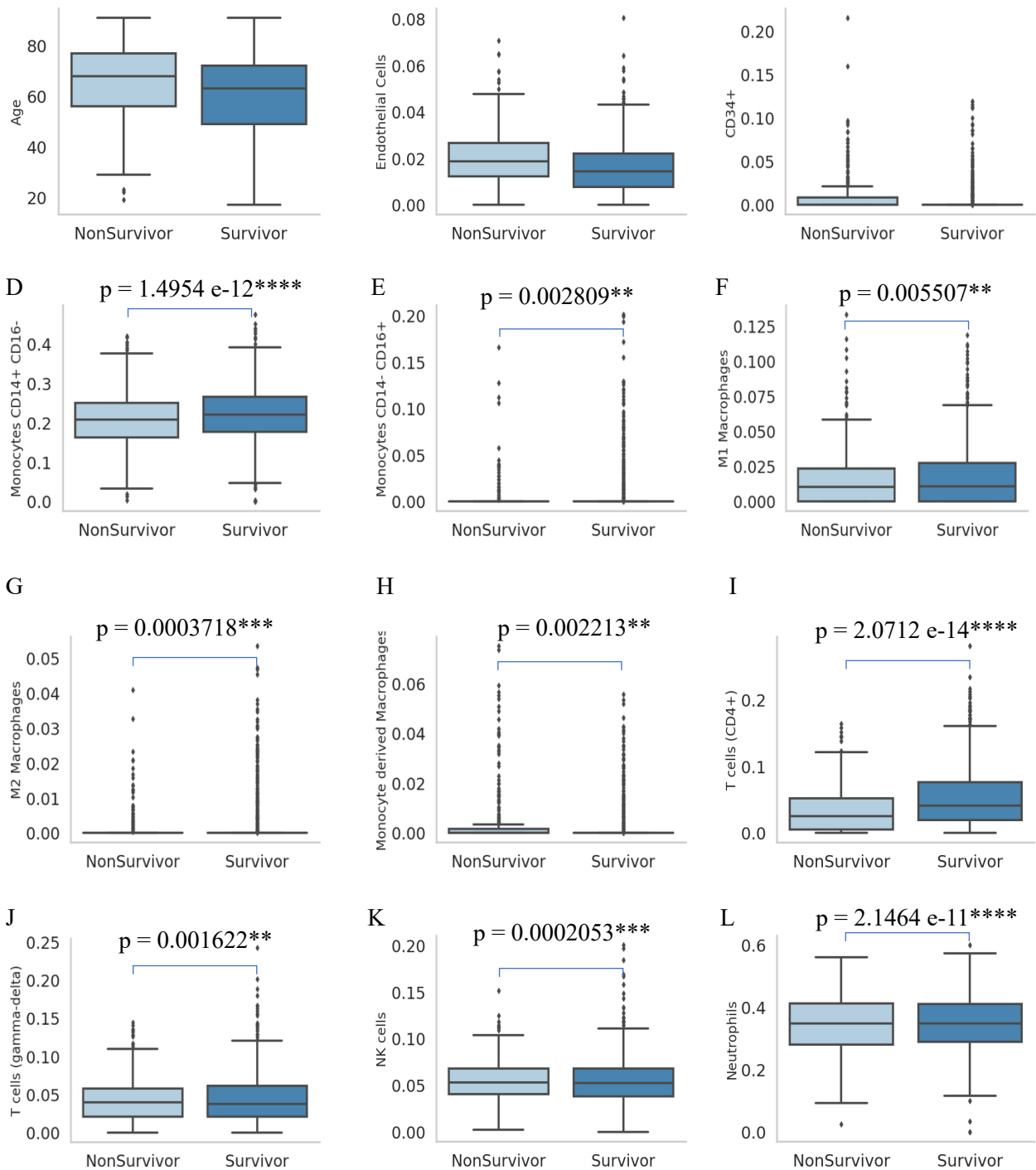


Figure 1: Comparison of between non-survivor and survivor based on (A) age distribution (B-L) relative composition of cells that has significant difference with respect to sepsis mortality.

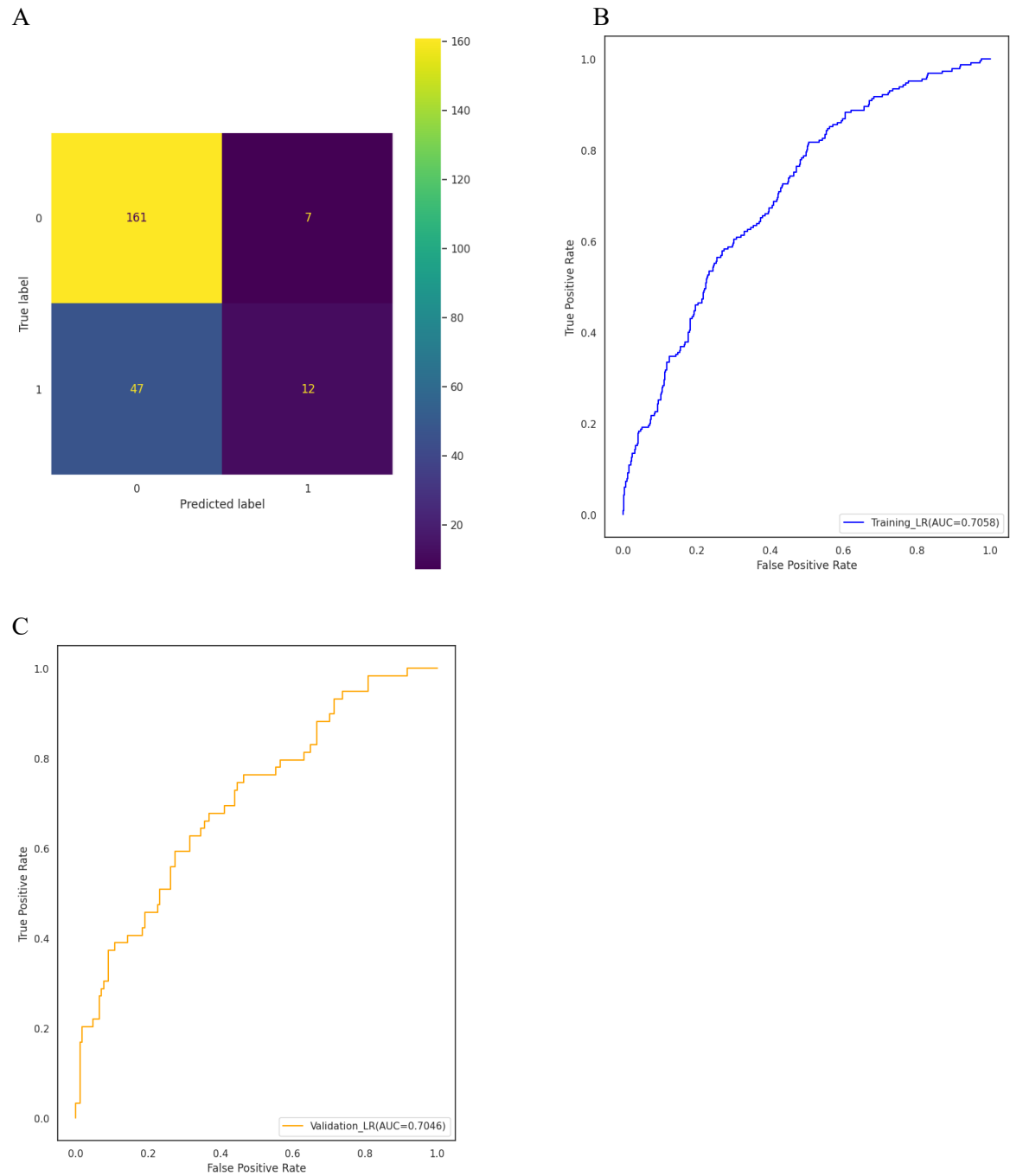
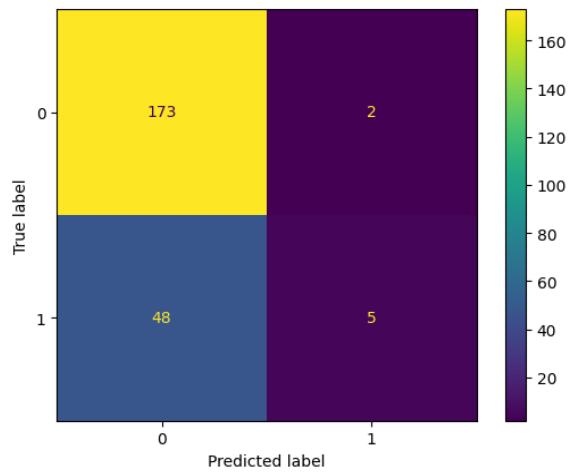
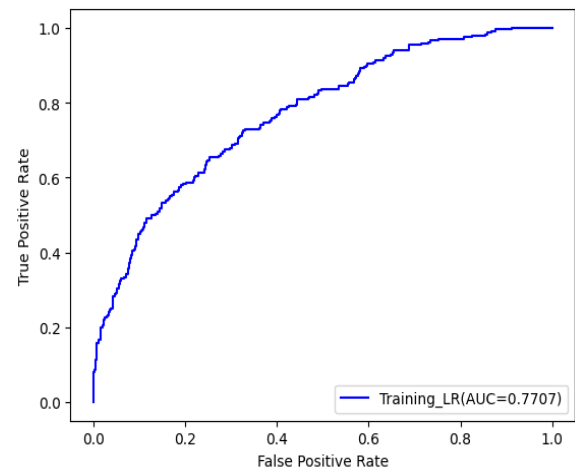


Figure 2: Logistic Regression of Cell composition data. (A) Summary of true and predicted labels in Confusion matrix (B) AUROC curve of Training Dataset (C) AUROC curve of Validation Dataset

A



B



C

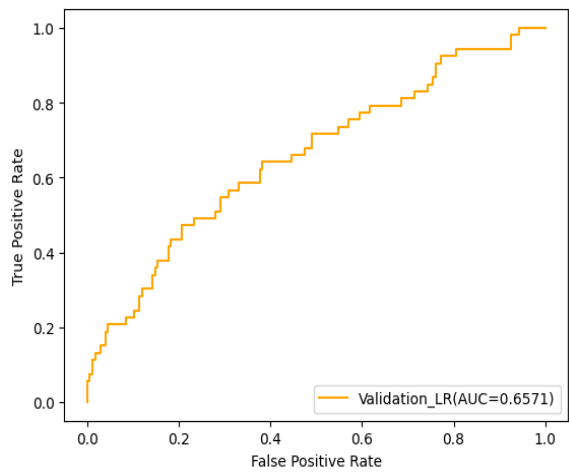
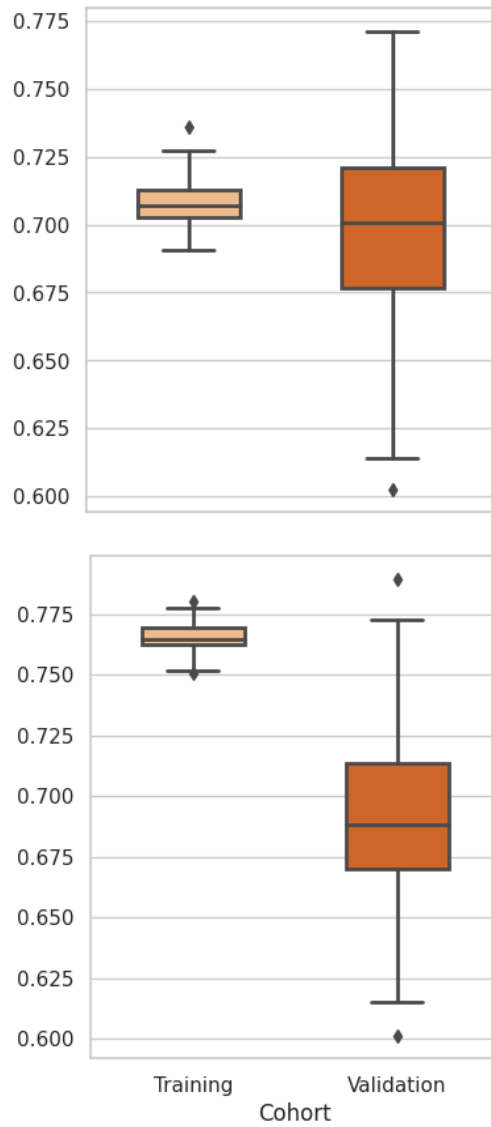


Figure 3: Logistic Regression of Gene Expression data. (A) Summary of true and predicted labels in Confusion matrix (B) AUROC curve of Training Dataset (C) AUROC curve of Validation Dataset

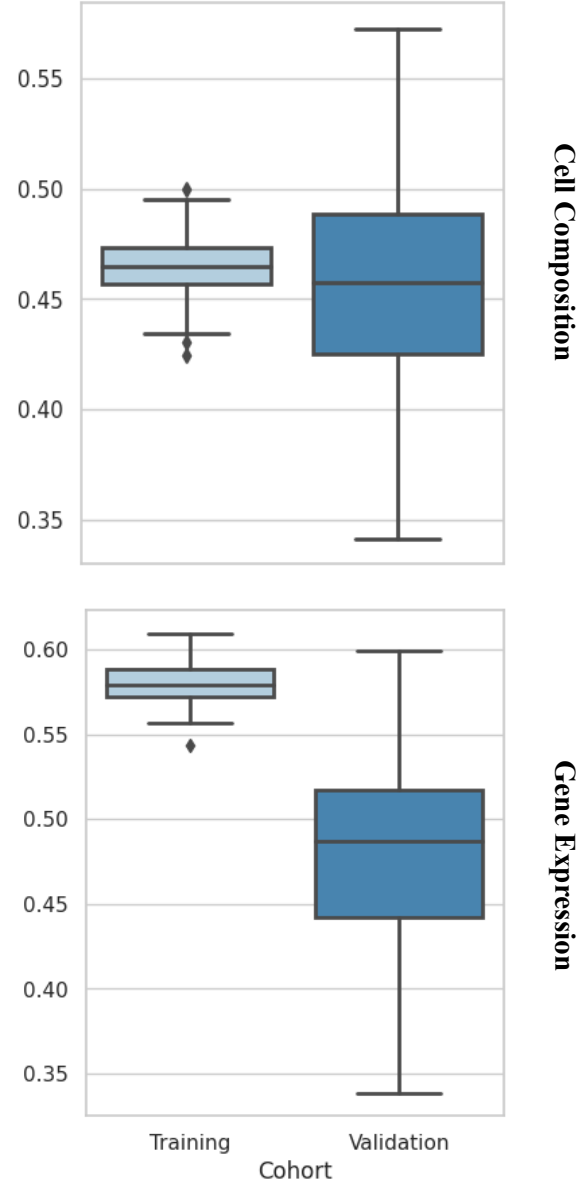
AUROC

AUPRC

A



B



Cell Composition

Gene Expression

Figure 4: Model performance of training and validation cohorts as measured by (A) AUROC and (B) AUPRC. The two panels (top and bottom) depict the model performance across cell composition and gene expression data respectively.