

Appendix

Detection of Patient-Level distances from single cell genomics and pathomics data with Optimal Transport (PILOT)

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Appendix Table S1. Benchmarking of clustering results (ARI and Silhouette Scores), and area under the PR curve (AUCPR). Results in bold indicate the best value per method.

Methods	Pseudobulk			Phemd			Proportions			PILOT			Pro.Phate
Datasets/Metrics	ARI	Sil	AUCPR	ARI	Sil	AUCPR	ARI	Sil	AUCPR	ARI	Sil	AUCPR	AUCPR
PDAC	1.00	0.73	1.00	0.51	0.04	0.87	0.51	0.56	1.00	1.00	0.59	1.00	1.00
Lupus PBMC	0.57	0.34	0.92	0.51	0.02	0.58	0.70	0.39	0.91	0.61	0.28	0.89	0.91
Kidney IgAN (G)	0.50	0.01	0.51	0.50	-0.04	0.34	0.51	0.00	0.55	0.55	0.07	0.60	0.27
Myoc. Infarc	1.00	0.86	1.00	0.47	-0.06	0.26	0.81	0.70	0.98	0.90	0.73	0.98	0.94
Kidney AC (T)	0.57	0.21	0.54	0.51	0.00	0.76	0.53	0.25	0.87	0.68	0.30	0.93	0.88
Kidney AC (G)	0.51	0.25	0.59	0.51	-0.01	0.66	0.57	0.25	0.96	0.64	0.36	0.96	0.96
COVID-19	0.51	-0.25	0.92	0.51	-0.06	0.88	0.52	-0.14	0.95	0.55	-0.14	0.94	0.93
Kidney	0.71	0.16	0.77	0.76	0.44	1.00	0.70	0.24	0.92	0.62	0.11	0.81	0.71
Kidney IgAN (T)	0.48	0.07	0.54	0.49	-0.03	0.48	0.56	0.00	0.54	0.58	0.10	0.59	0.56
Lung	0.69	-0.17	0.59	0.29	-0.02	0.85	0.67	-0.03	0.90	0.67	-0.01	0.90	0.57
Diabetes	0.67	0.19	0.74	0.62	-0.13	0.51	0.64	-0.03	0.50	0.67	-0.01	0.71	0.54
Foll. lym.	0.50	0.29	0.90	0.52	0.09	0.97	0.48	0.95	1.00	0.76	0.60	1.00	1.00

Appendix Table S2. Benchmarking of Ordered Trajectory Analysis (Spearman Correlation). Spearman correlation values in bold indicate the best performing method per data set.

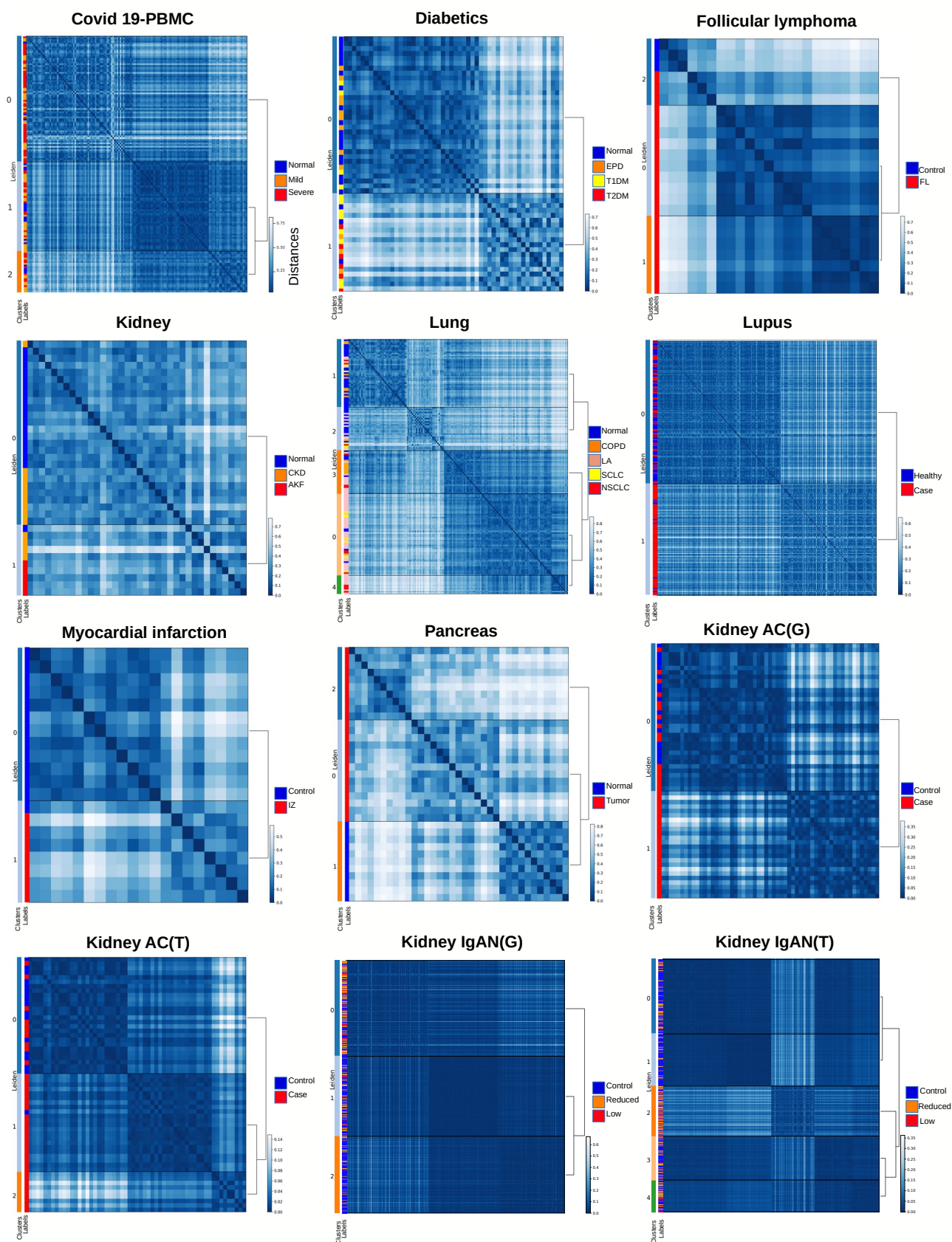
Datasets/Metrics	Pseudobulk	Phemd	Pro. Phate	Proportions	PILOT
Myoc. Infarc	0.83	-0.15	0.77	0.81	0.81
PDAC	0.80	0.34	0.80	0.80	0.80
Lupus PBMC	0.62	0.11	0.61	0.66	0.55
Diabetes	0.34	-0.30	-0.20	0.45	0.55
Foll. lym.	0.23	0.37	0.58	0.58	0.58
Kidney	0.50	0.91	0.22	0.73	0.66
Lung	-0.31	0.54	-0.28	0.52	0.57
COVID-19	0.16	-0.09	0.13	0.25	0.26
Kidney AC (G)	0.49	0.12	0.63	0.64	0.62
Kidney AC (T)	0.57	0.12	0.48	0.47	0.57
Kidney IgAN (G)	0.12	-0.09	0.31	0.37	0.38
Kidney IgAN (T)	0.26	0.27	0.39	0.36	0.39

Appendix Table S3. We used distinct statistical tests (Chi-Square for discrete and ANOVA for continuous variables) to evaluate association between detected clusters, biological or technical variables for all data sets. We only shown results with adjusted p -value < 0.05 . The variables were sorted first by data and then by increasing p -values.

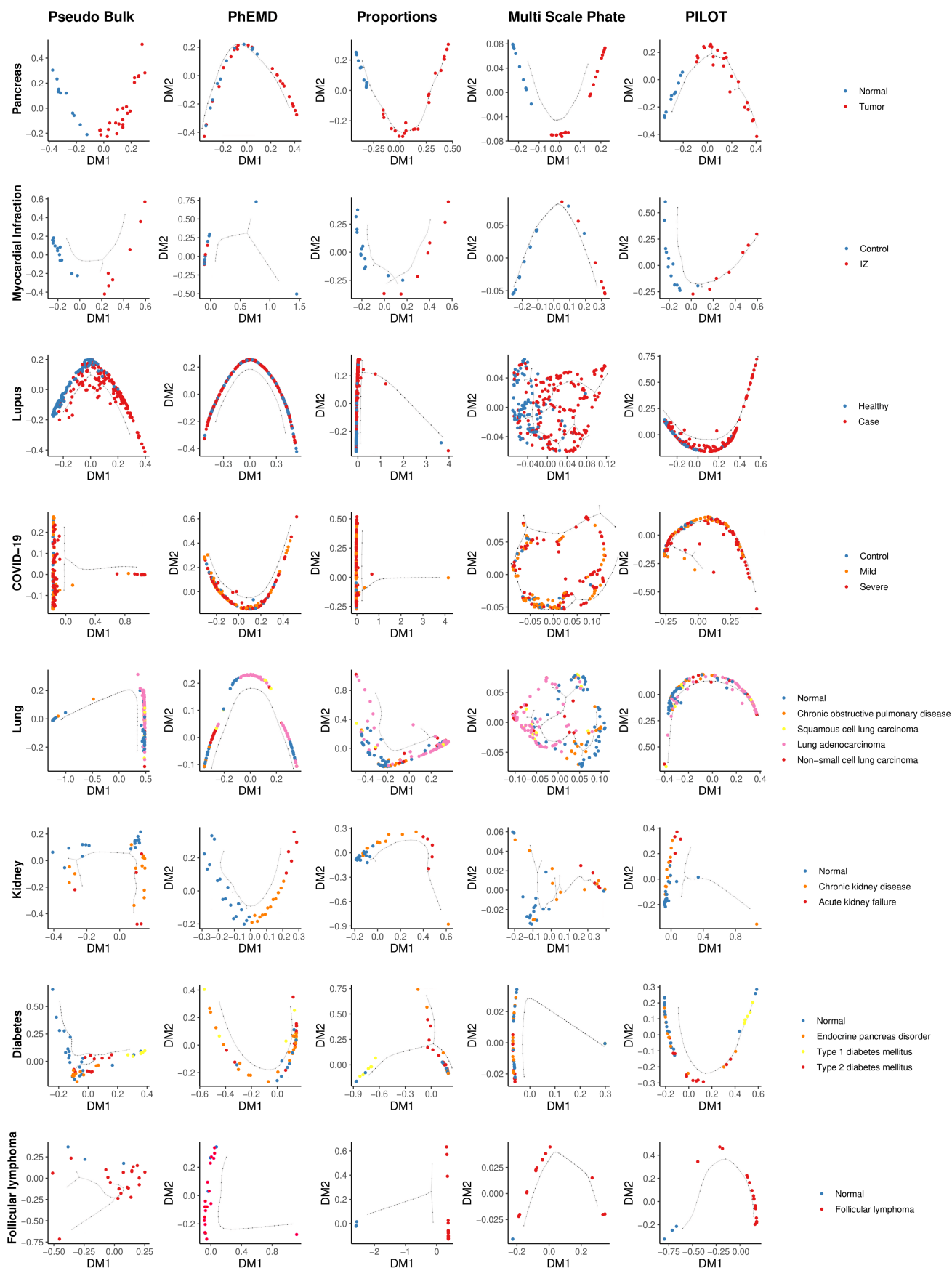
Data set	Variable	Test	P-value
Myocardial Infarction	Status	Chi-Squared	3.990000e-4
Follicular Lymphoma	Status	Chi-Squared	2.057900e-2
Diabetes	Status	Chi-Squared	1.480000e-4
Diabetes	Strain	Chi-Squared	3.190000e-4
Diabetes	Development stage	Chi-Squared	1.481000e-3
PDAC	Status	Chi-Squared	2.510999e-8
PDAC	Staging	Chi-Squared	4.156157e-5
PDAC	pathologic_diagnoses	Chi-Squared	4.719115e-3
PDAC	Location	Chi-Squared	3.329660e-2
PDAC	Diabetes	Chi-Squared	3.995506e-2
PDAC	vascular_invasion	Chi-Squared	4.639490e-2
Lupus	Status	Chi-Squared	6.020011e-15
Lupus	Processing_Cohort	Chi-Squared	4.852031e-6
Lupus	batch_cov	Chi-Squared	3.462091e-4
Kidney	Status	Chi-Squared	1.590000e-4
Kidney	diabetes_history	Chi-Squared	9.195000e-3
Kidney	BMI	Chi-Squared	4.905700e-2
Lung	study	Chi-Squared	3.067563e-25
Lung	Status	Chi-Squared	9.319169e-13
Lung	origin	Chi-Squared	1.630440e-12
Lung	ever_smoker	Chi-Squared	1.765099e-2
Lung	sex	Chi-Squared	2.977980e-2
Kidney IgAN Tubuli	Status	Chi-Squared	1.450070e-17
Kidney IgAN Tubuli	Sex	Chi-Squared	1.407880e-2
Kidney IgAN Tubuli	Age	ANOVA	9.756758e-8
Covid	City	Chi-Squared	2.300698e-9
Covid	Status	Chi-Squared	6.018506e-4
Covid	Age	ANOVA	4.270000e-4
Covid	Sampling day (Days after symptom onset)	ANOVA	1.863300e-2
Kidney IgAN Glomeruli	Status	Chi-Squared	1.057934e-15
Kidney IgAN Glomeruli	Age	ANOVA	1.682000e-3

Appendix Table S4. Log likelihood test and hazard ratios (HR) of cox regression for disease progression and morphometric variables

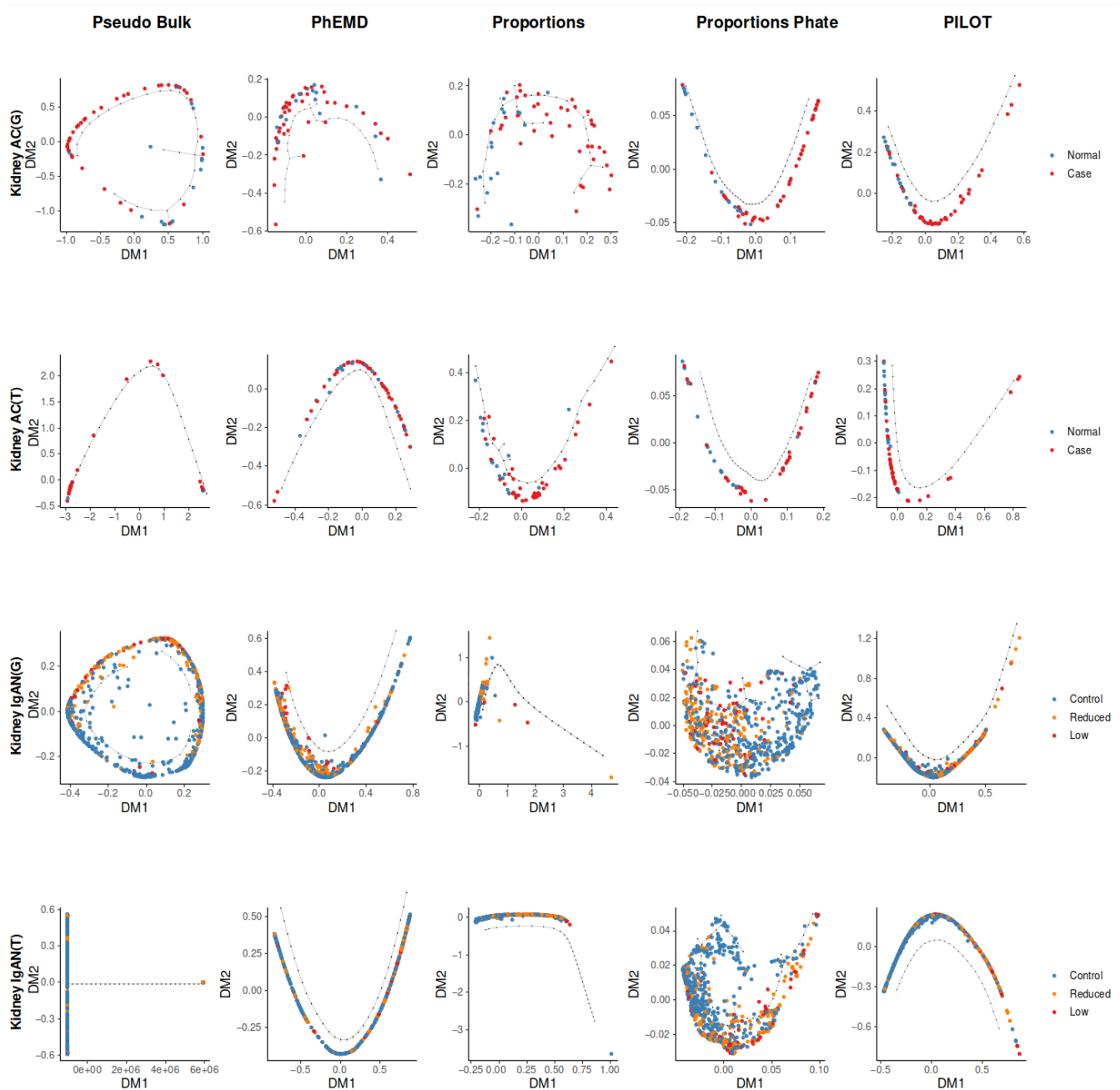
Features	p_value	HR	HR_lower_95	HR_higher_95
Disease_Progression	2.38E-11	14.22285964	6.133761376	32.97972059
Tuft-Area-Fraction	6.55E-06	0.006096	0.000754147	0.049275825
Age	0.000161201	1.026118273	1.012515212	1.03990409
Tuft Elongation	0.035174436	0.995855111	0.991024645	1.000709122
Tuft Area	0.059838632	0.99999991	0.999999796	1.000000024
Glomerular Area	0.084688986	0.99999995	0.999999883	1.000000017
Tuft Circularity	0.120647357	0.997847514	0.99474223	1.000962492
Tuft Eccentricity	0.193320223	0.99911608	0.99765839	1.0005759
Bowman Area	0.285387443	0.999999915	0.999999741	1.000000088
Glomerular Circularity	0.292065233	0.998989099	0.996929139	1.001053316
Glomerular Diameter	0.295112885	0.999996112	0.999988267	1.000003957
Tubular Distance	0.334379046	0.999806135	0.999357973	1.000254498
Tubular Area	0.361417305	1.000000128	0.999999865	1.000000392
Tuft Solidity	0.468203891	0.999443691	0.997818499	1.001071531
Glomerular Distance	0.55738282	1.000000526	0.999998905	1.000002148
Glomerular Solidity	0.594992091	0.999714882	0.998620471	1.000810492
Glomerular Eccentricity	0.721397871	1.000225975	0.999008779	1.001444655
Glomerular Elongation	0.944083375	0.999862207	0.995995708	1.003743715
Tubular Diameter	0.954027614	0.999999227	0.999972858	1.000025597



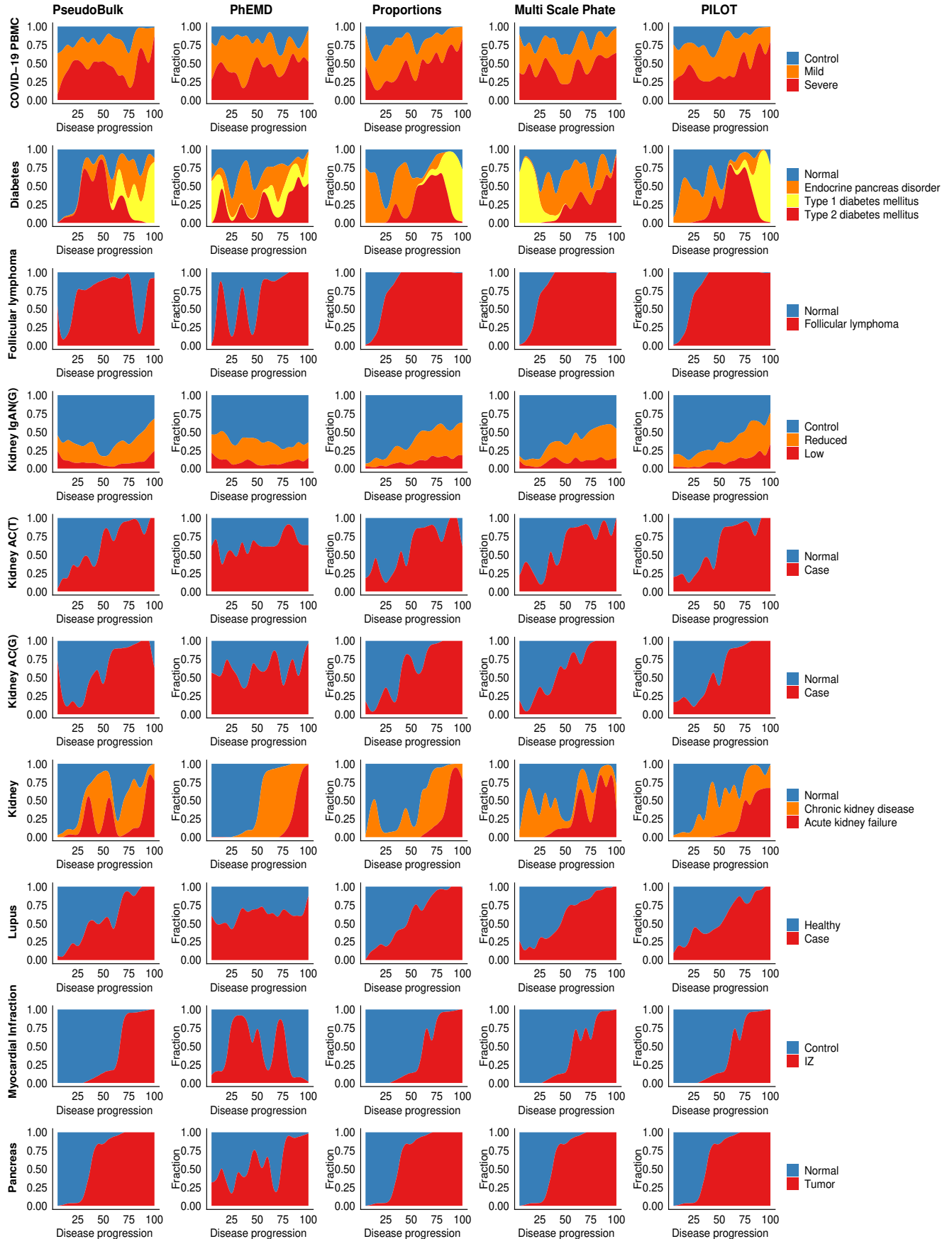
Appendix Figure S1. Heatmap representation of PILOT estimated Wasserstein distance and clustering using the Leiden algorithm. Color bars in the left of each heatmap shown respectively the cluster and the class labels.



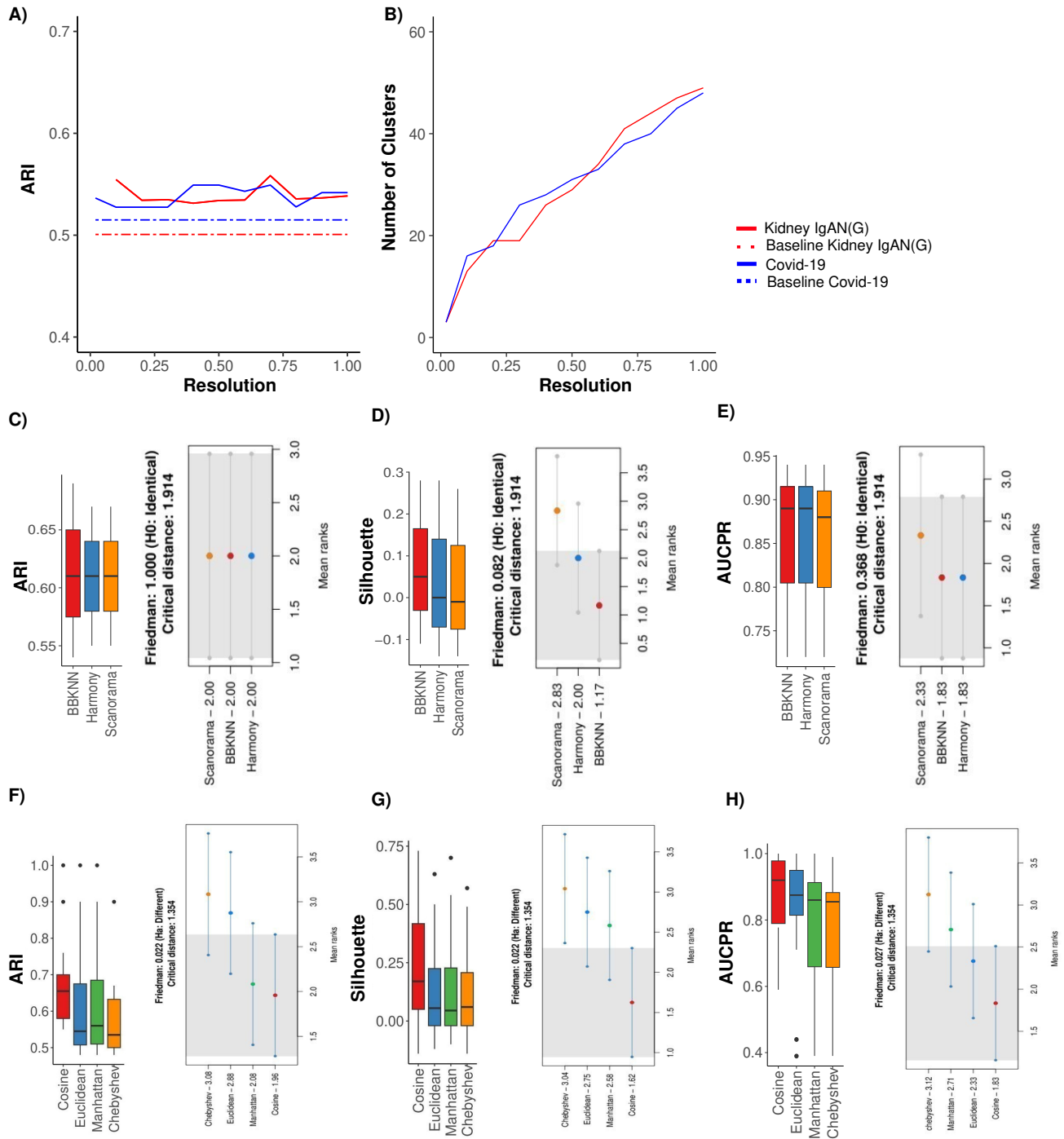
Appendix Figure S2. Diffusion maps of single cell data sets (rows) for Pseudo Bulk, PhEMD, Proportions, Multiscale Phate, and PILOT (columns). Dotted lines represent backbones of the estimated trajectories.



Appendix Figure S3. Diffusion maps of pathomics data sets (rows) for Pseudo Bulk, PhEMD, Proportions, Multiscale Phate, and PILOT (columns). Dotted lines represent backbones of the estimated trajectories.

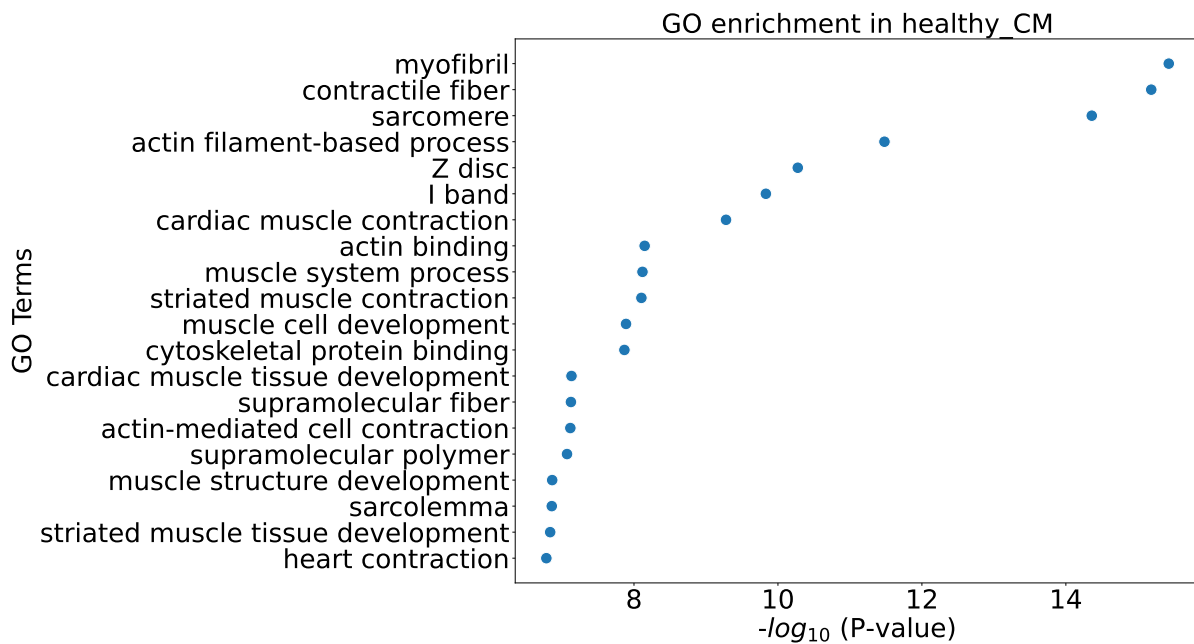


Appendix Figure S4. Fraction samples (y-axis) for distinct sample labels over the pseudo-time (x-axis) for disease progression trajectories.

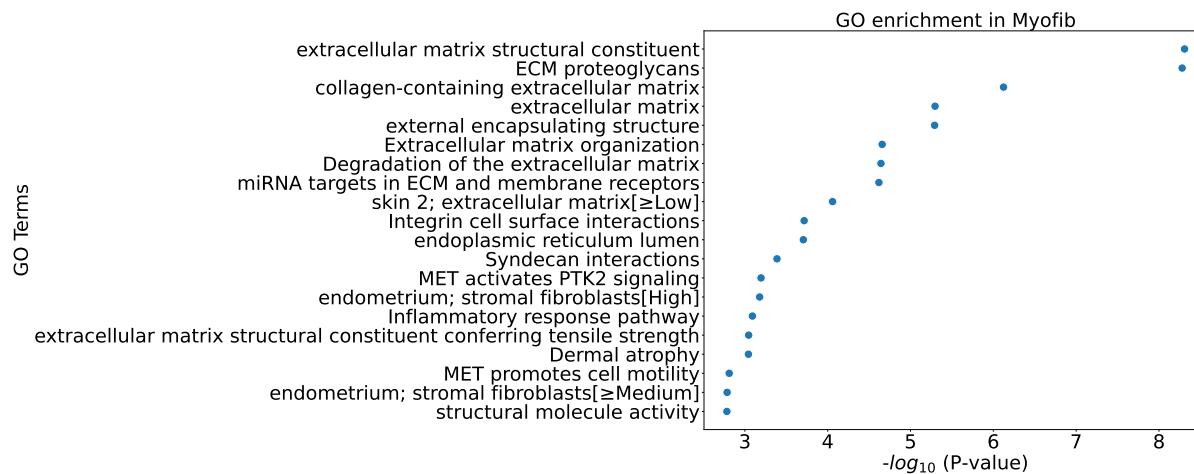


Appendix Figure S5. A - Clustering performance (measured by ARI) for PILOT (solid lines) and pseudo-bulk (traced lines) for distinct cluster resolution. We observe that for both Kidney IgAN and COVID-19, the number of clusters did not impacted the results from PILOT. B - Number of clusters for distinct Leiden algorithm resolution parameters. C-E - Benchmarking on the effect of distinct batch correction methods for data sets, where raw count matrices were available (Lupus, COVID, and Diabetes). F-H Benchmarking on the use of distinct distance/similarity metrics as cost matrix C for EMD. Low ranking values in the Friedman scores indicates best performing approaches.

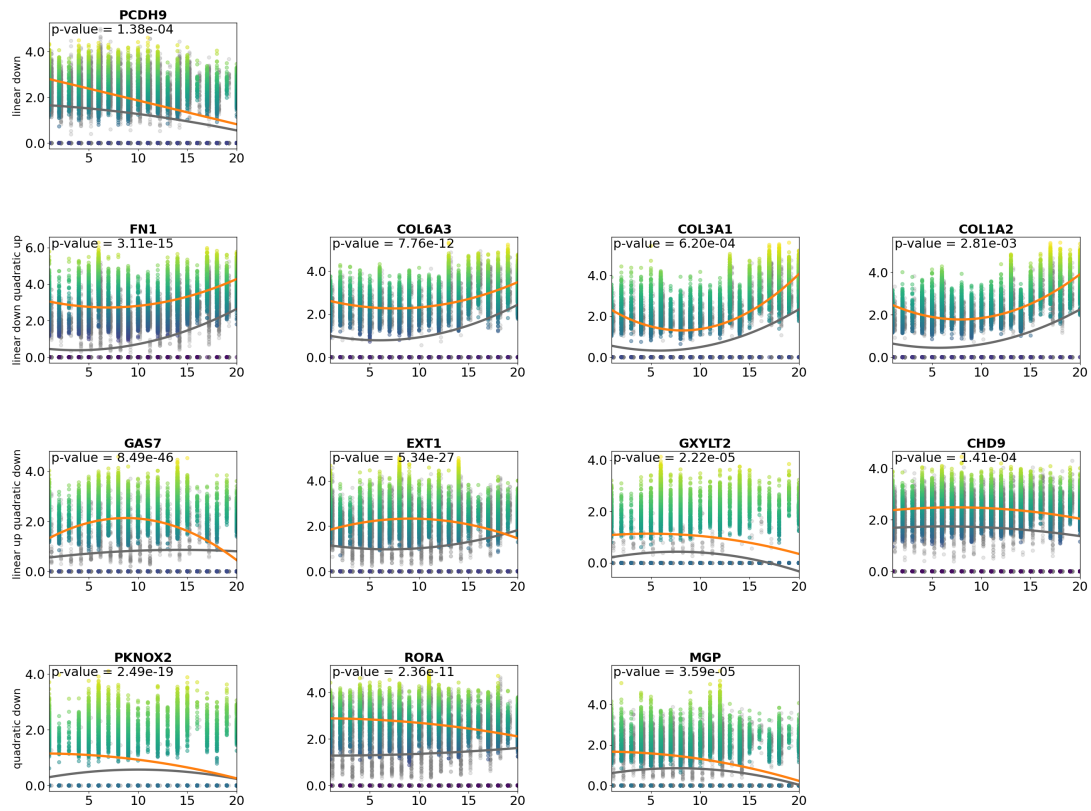
A) Healthy cardiomyocytes



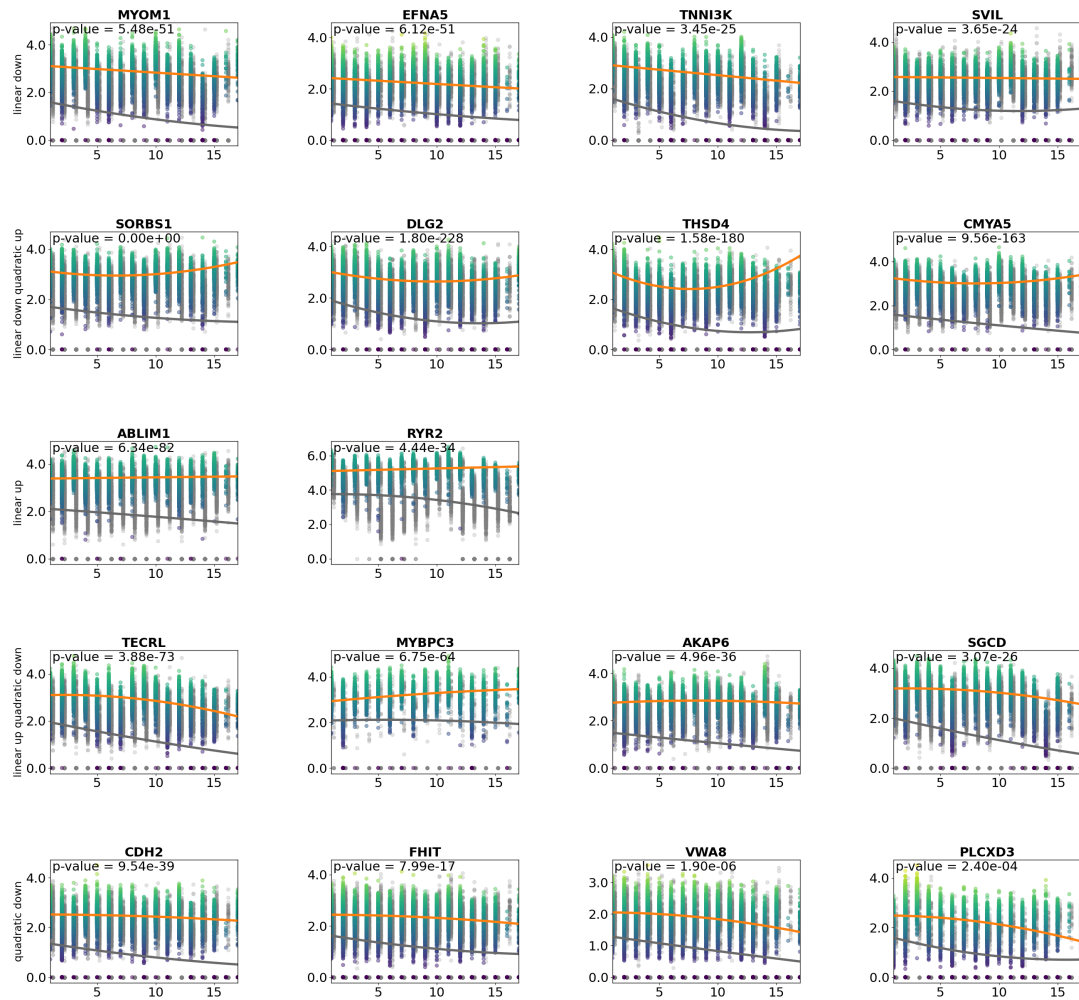
B) Myofibroblasts



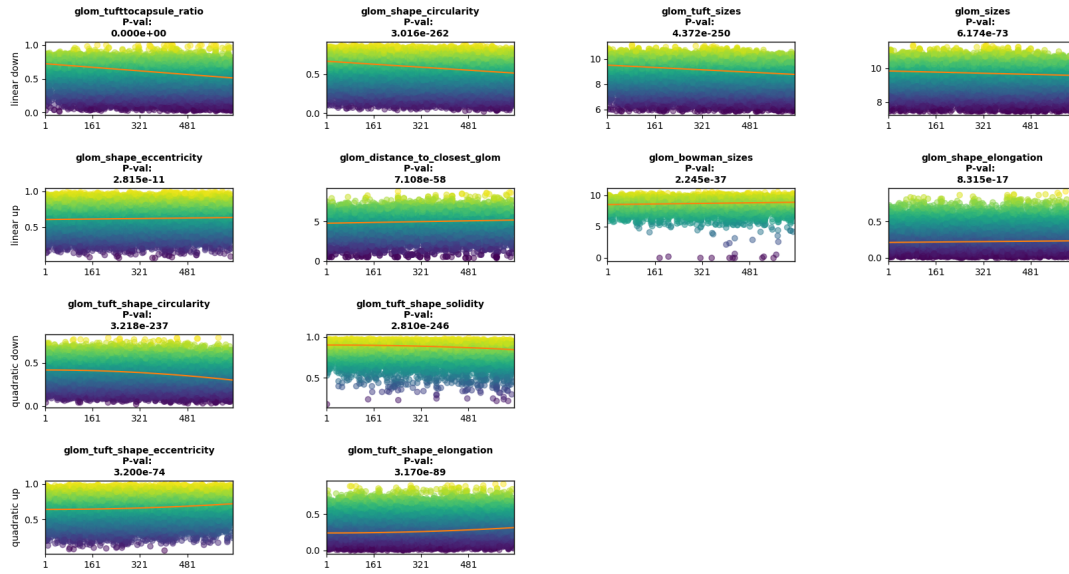
Appendix Figure S6. Top 20 terms of the enrichment analysis by using selected genes for Healthy cardiomyocytes and myofibroblasts (based on the first 50 genes with FC > 0.5 and Wald-test p -value < 0.01). The analysis was performed with g:profiler <https://biit.cs.ut.ee/gprofiler/gost>.



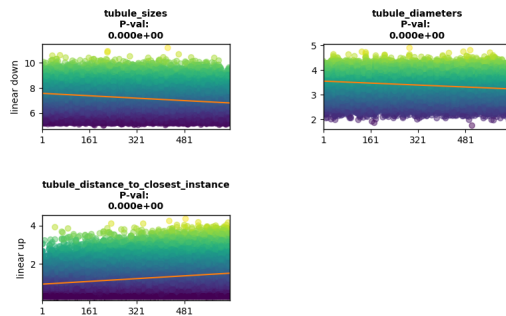
Appendix Figure S7. Top genes associated ($FC > 0.5$ and ranked by p -value of the Wald-test) from Myofibroblasts of the Myocardial infarction scRNA-seq. Every line corresponds to distinct models (linear, quadratic, linear-quadratic) and patterns (up vs. down). Only significant genes (p -value < 0.01) are shown.



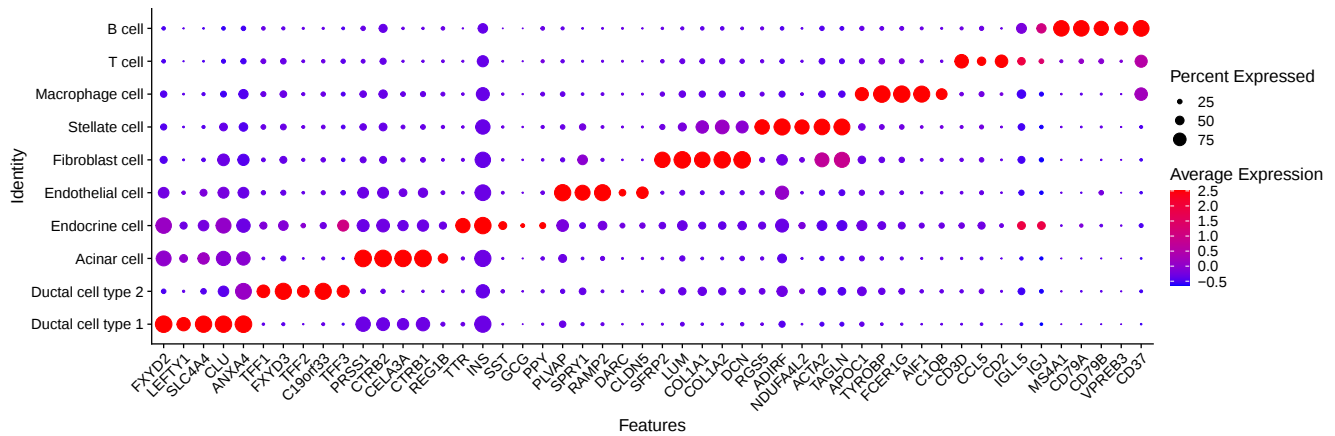
Appendix Figure S8. Top genes associated ($FC > 0.5$ and ranked by p -value of the Wald-test) from Healthy cardiomyocytes of the myocardial infarction scRNA-seq. Every line corresponds to distinct models (linear, quadratic, linear-quadratic) and patterns (up vs. down). Only significant genes (p -value < 0.01) are shown.



Appendix Figure S9. Top morphological features associated (ranked by adjusted R2) from Kidney IgA glomeruli. Every line corresponds to distinct models (linear, quadratic, linear-quadratic) and patterns (up vs. down). Significant features (p -value < 0.05) are marked in bold.



Appendix Figure S10. Top morphological features associated (ranked by adjusted R2) from Kidney IgA tubule. Every line corresponds to distinct models (linear, quadratic, linear-quadratic) and patterns (up vs. down). Significant features (p -value < 0.05) are marked in bold.



Appendix Figure S11. Markers used to characterize clusters in the PDAC single cell data set.

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