

Table 1: Summary Statistics for Age by Sample Type

Sample Type	Count	Mean Age	Standard Deviation (Std)	Min Age	25th Percentile (Q1)	Median (Q2)	75th Percentile (Q3)	Max Age
Mucosa	50	62.50	14.20	25.0	52.0	63.0	74.0	88.0
Normal	98	70.54	9.02	43.0	65.0	71.0	78.0	87.0
Tumor	98	70.54	9.02	43.0	65.0	71.0	78.0	87.0

The Mucosa group has the lowest mean age (62.5 years) with higher variability (Std = 14.2), whereas the Normal and Tumor groups share the same mean (70.54 years) and standard deviation (9.02 years), suggesting a similar age distribution between normal and tumor samples.

Table 2: Top 10 differentially expressed genes for Therapeutic category

Probe ID	Gene Symbol	Expression young	Expression old	Log2FC	p-value
11728717_at	CXCL5	5.918118	4.105307	-0.438382	0.013276
11735589_at	PTGDR	3.552500	2.521276	-0.370561	0.005766
11753482_a_at	NPSR1	3.717673	2.697807	-0.351406	0.026773
11720607_a_at	SFRP2	3.112845	4.133139	0.319705	0.001297
11724085_at	DAPL1	4.528591	3.613004	-0.261205	0.025055
11729429_a_at	KIF26A	5.296464	4.263292	-0.258576	0.028254
11725749_a_at	GAL	7.929245	6.538249	-0.244309	0.002680
11724296_a_at	BMP7	6.773573	5.592282	-0.237800	0.016174
11727113_at	EGF	3.963832	3.236774	-0.228488	0.068713
11737992_s_at	GPR37	2.633223	3.239288	0.222572	0.005562

Table 3: Top 10 differentially expressed genes for Immune category:

Probe ID	Gene Symbol	Expression young	Expression old	Log2FC	p-value
11728717_at	CXCL5	5.918118	4.105307	-0.438382	0.013276
11756083_x_at	HLA-DQA1	3.776973	5.057379	0.342597	0.059841
11760799_x_at	HLA-DPB1	3.933745	4.932211	0.265887	0.078121
11743087_at	PPBP	4.399341	3.539138	-0.250365	0.278924
11725749_a_at	GAL	7.929245	6.538249	-0.244309	0.002680
11754033_a_at	PLA2G2A	7.120886	5.938443	-0.227025	0.095815
11727103_at	IGF2BP1	3.543495	2.906887	-0.217783	0.171347
11721911_at	SOX8	2.277223	2.795233	0.211715	0.006539
11720251_at	CCL18	6.111650	7.205966	0.206489	0.062271
11763253_x_at	IGKC	3.659786	4.359717	0.201893	0.040434

Table 4: Top 10 differentially expressed genes for Glycosylation category

Probe ID	Gene Symbol	Expression young	Expression old	Log2FC	p-value
11725764_a_at	COL11A1	3.015918	3.511118	0.167755	0.138753
11756588_a_at	ST6GALNAC1	7.894650	7.059149	-0.142310	0.028164
11738332_a_at	B3GALT5	2.908309	2.555133	-0.136641	0.086865
11753059_x_at	UGGT2	4.360405	4.883962	0.134446	0.023663
11735900_s_at	HS3ST4	2.501800	2.206416	-0.127135	0.158236
11739179_s_at	ST6GALNAC4	3.337355	3.714764	0.120370	0.031803
11740238_a_at	SULF2	8.647855	9.480913	0.119484	0.001935
11751294_a_at	ST6GALNAC5	2.626532	2.904714	0.106627	0.061446
11751484_x_at	BGN	3.787586	4.120529	0.096994	0.066748
11738408_a_at	SPACA3	2.507564	2.738896	0.092143	0.058830

Table 5: Top 10 Selected Features (Therapeutic Young <65)

Probe_ID	Gene_Symbol	Importance
11743444_s_at	RHOB	0.016434
11719561_s_at	SOX4	0.014702
11744422_s_at	CRADD	0.012035
11757319_x_at	HINT1	0.011385
11763250_x_at	CXCL1 /// CXCL2	0.010337
11758071_s_at	SULF1	0.010127
11758526_s_at	RELN	0.010074
11715355_at	COL1A2	0.010017
11715983_a_at	ADNP	0.009959
11715584_a_at	CAV1	0.009694

Table 6: Top 10 Selected Features (Therapeutic Old ≥ 65)

Probe_ID	Gene_Symbol	Importance
11737854_at	P2RY1	0.024957
11750512_x_at	CDK4	0.024067
11729750_a_at	LPAR1	0.016495
11741376_a_at	LRP8	0.012825
11744707_a_at	ANGPTL1	0.012820
11719110_a_at	TMEM161A	0.012813
11721357_at	NMB	0.012580
11757924_s_at	SIPA1L2	0.012421
11741113_a_at	PDCD4	0.012407
11715882_s_at	DAP3	0.011713

Table 7

Category	AgeGroup	Classifier	ModelType	CVAccuracy	PermutationPValue	TrainAccuracy	TestAccuracy
Glycosylation	Young (<65)	RandomForest	Full	0.99	0	1	0.90
Glycosylation	Young (<65)	RandomForest	Top3	0.91		1	0.81
Glycosylation	Old (>=65)	RandomForest	Full	0.98	0	1	1.00
Glycosylation	Old (>=65)	RandomForest	Top3	0.85		1	0.85
Glycosylation	Young (<65)	GBM	Full	0.93	0	1	0.76
Glycosylation	Young (<65)	GBM	Top3	0.89		1	0.76
Glycosylation	Old (>=65)	GBM	Full	0.92	0	1	0.98
Glycosylation	Old (>=65)	GBM	Top3	0.95		1	0.96
Glycosylation	Young (<65)	SVM	Full	0.99	0	1	1.00
Glycosylation	Young (<65)	SVM	Top3	0.91		0.96	0.81
Glycosylation	Old (>=65)	SVM	Full	0.99	0	1	1.00
Glycosylation	Old (>=65)	SVM	Top3	0.89		0.93	0.91
Immune	Young (<65)	RandomForest	Full	0.99	0	1	1.00
Immune	Young (<65)	RandomForest	Top3	0.69		1	0.71
Immune	Old (>=65)	RandomForest	Full	0.97	0	1	0.96
Immune	Old (>=65)	RandomForest	Top3	0.84		1	0.85
Immune	Young (<65)	GBM	Full	1.00	0	1	1.00
Immune	Young (<65)	GBM	Top3	0.96		1	0.95
Immune	Old (>=65)	GBM	Full	0.94	0	1	1.00
Immune	Old (>=65)	GBM	Top3	0.91		1	0.92
Immune	Young (<65)	SVM	Full	0.99	0	1	0.95
Immune	Young (<65)	SVM	Top3	0.61		0.65	0.67
Immune	Old (>=65)	SVM	Full	0.98	0	1	1.00
Immune	Old (>=65)	SVM	Top3	0.66		0.71	0.64
Therapeutic	Young (<65)	RandomForest	Full	0.99	0	1	1.00
Therapeutic	Young (<65)	RandomForest	Top3	1.00		1	0.86
Therapeutic	Old (>=65)	RandomForest	Full	0.97	0	1	0.98
Therapeutic	Old (>=65)	RandomForest	Top3	0.96		1	0.92
Therapeutic	Young (<65)	GBM	Full	1.00	0	1	1.00
Therapeutic	Young (<65)	GBM	Top3	0.91		1	0.90
Therapeutic	Old (>=65)	GBM	Full	0.94	0	1	0.98
Therapeutic	Old (>=65)	GBM	Top3	0.96		1	0.96
Therapeutic	Young (<65)	SVM	Full	0.99	0	1	1.00
Therapeutic	Young (<65)	SVM	Top3	0.81		0.86	0.81
Therapeutic	Old (>=65)	SVM	Full	0.98	0	1	1.00
Therapeutic	Old (>=65)	SVM	Top3	0.73		0.75	0.74