Breast Cancer Classification

ML 7641: Group 3 Final Project

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Breast Cancer Motivation

- One of the most prevalent and life-threatening forms of cancer among women worldwide
- 1 in 20 women worldwide will be diagnosed with breast cancer in their lifetime [1].
- High degree of heterogeneity @ molecular level [2].

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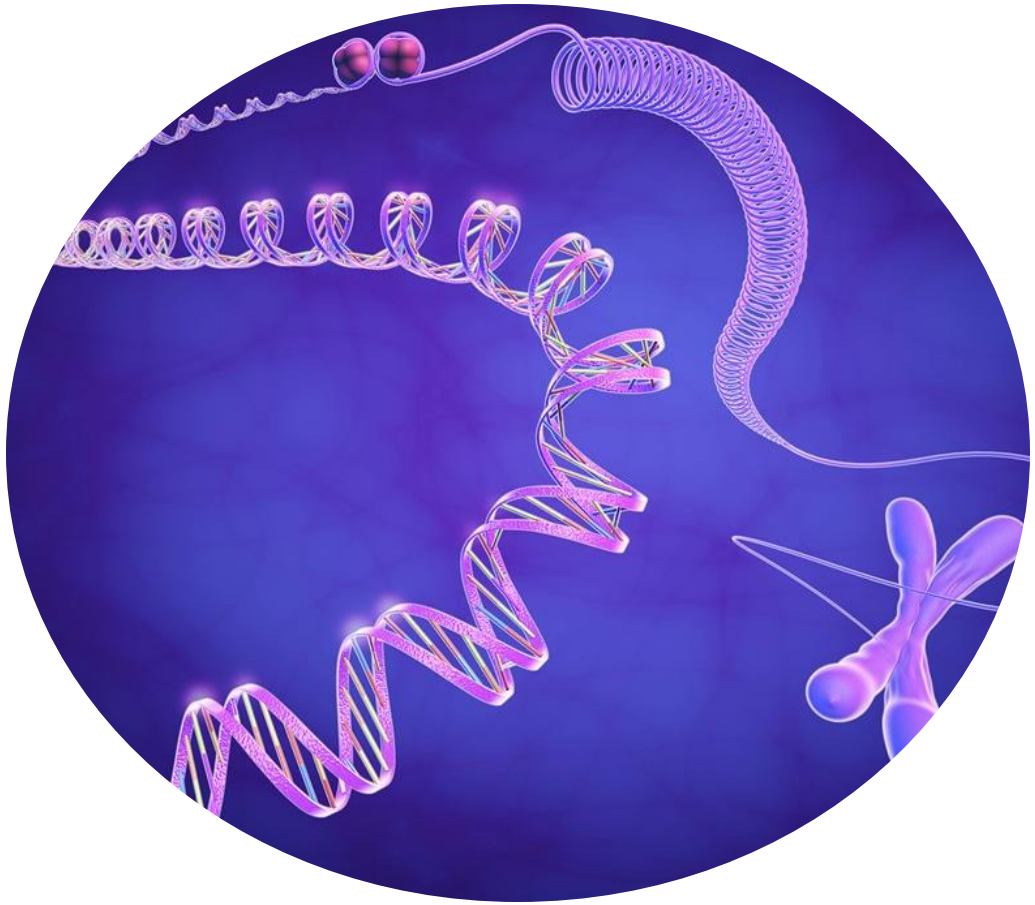
METABRIC Dataset [3]

- Breast cancer gene expression profiles for 1,904 breast cancer patients
  - Includes 31 clinical attributes
  - m-RNA levels z-score for 331 genes
  - mutation data for 175 genes



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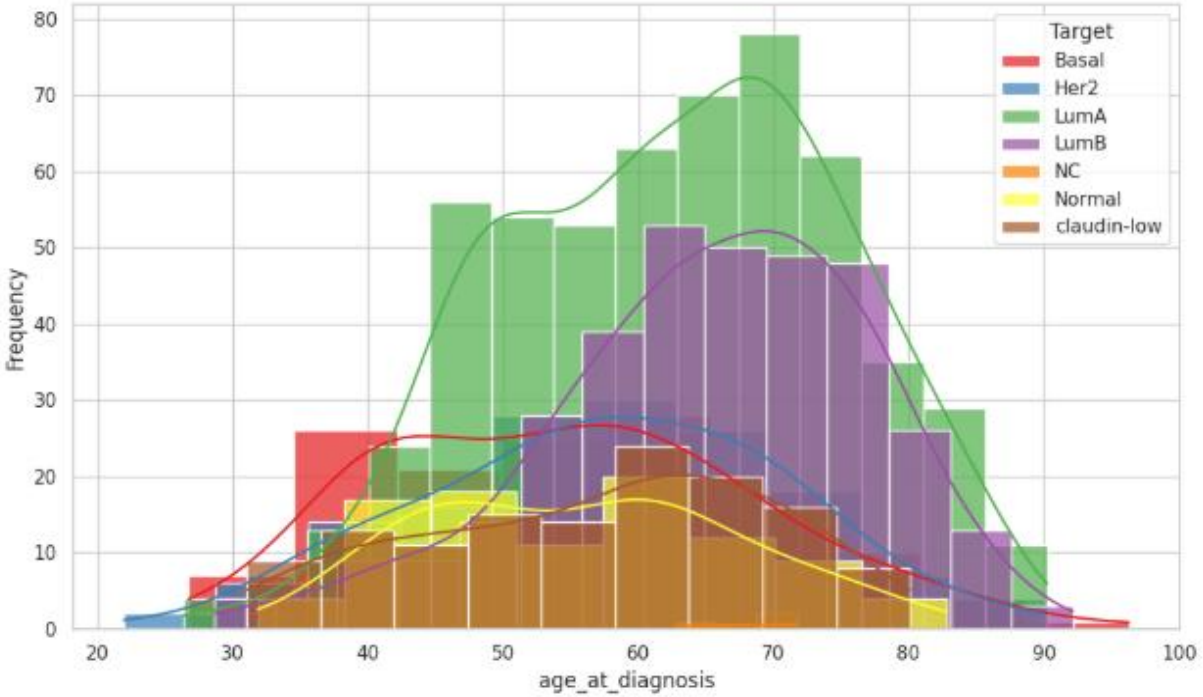
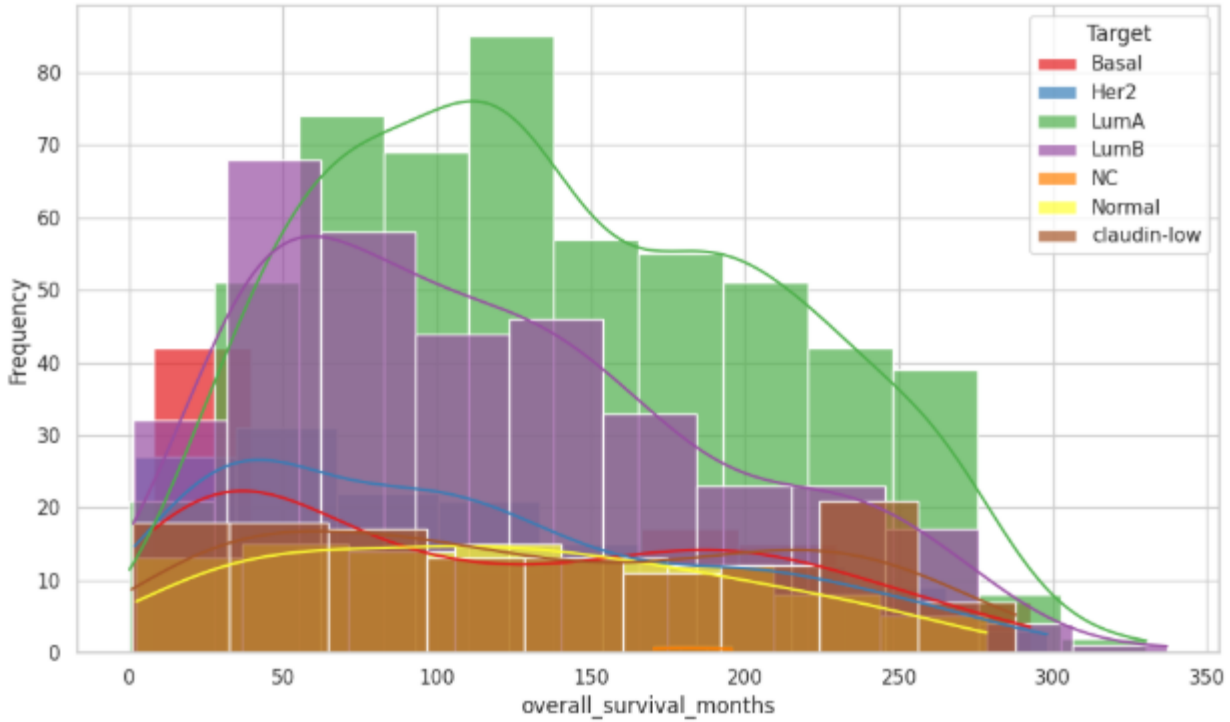
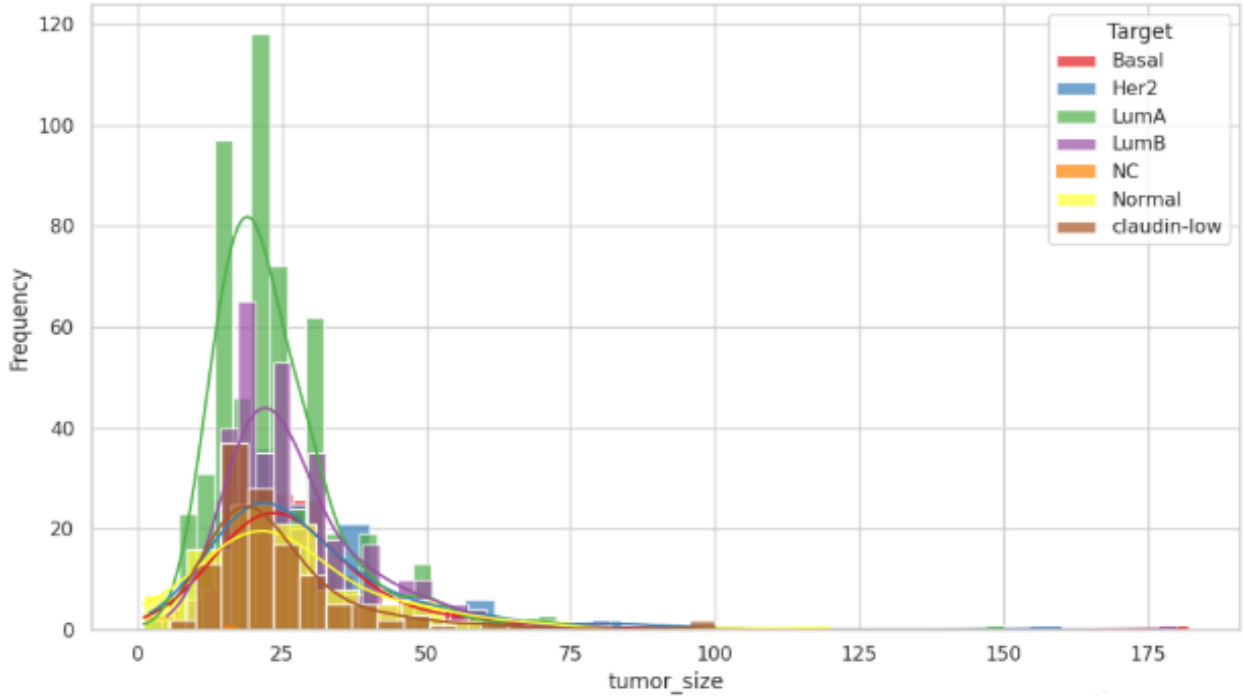
Exploratory Data Analysis

1. Split clinical and gene data
2. Visualized class distributions across clinical data attributes (via histograms & boxplots)
3. Pairplot of numerical columns of clinical data
4. Dropped NC class moving forward due to very low cases
5. Ran PCA & UMAP for dimensionality reduction
6. Ran K-Means & GMM clustering on UMAP
7. Selected top 50 features based on mutual information

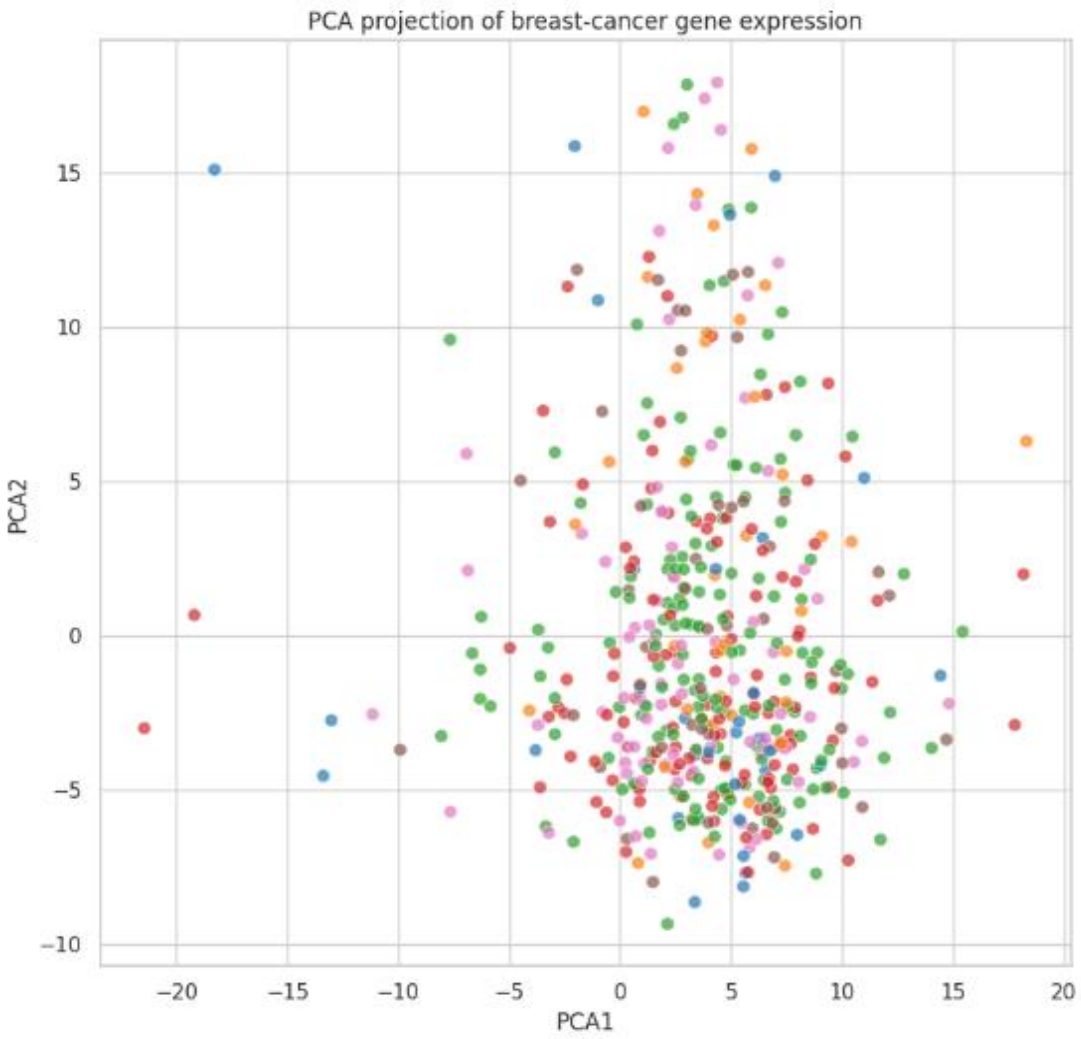
Exploratory Data Analysis

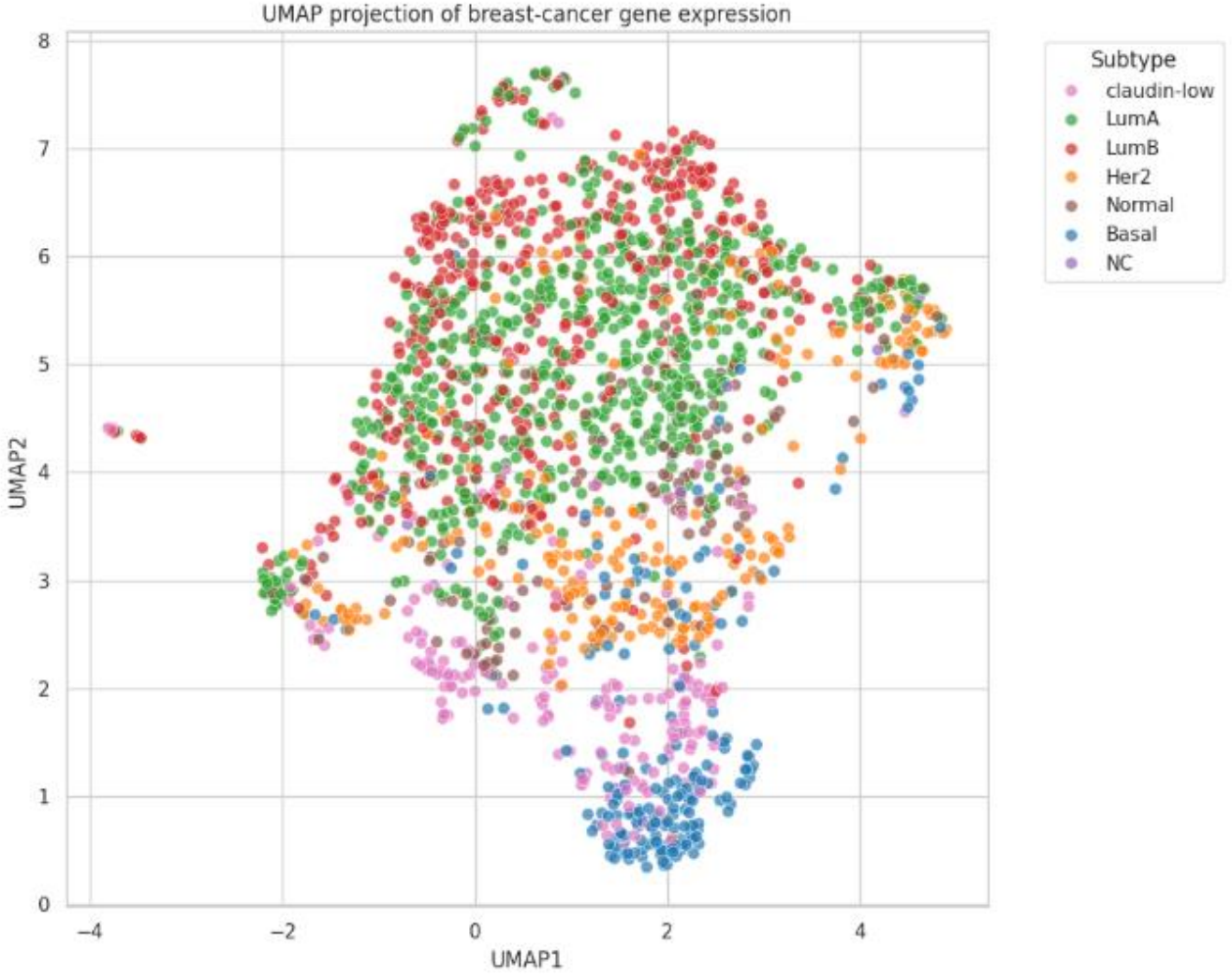






PCA & UMAP





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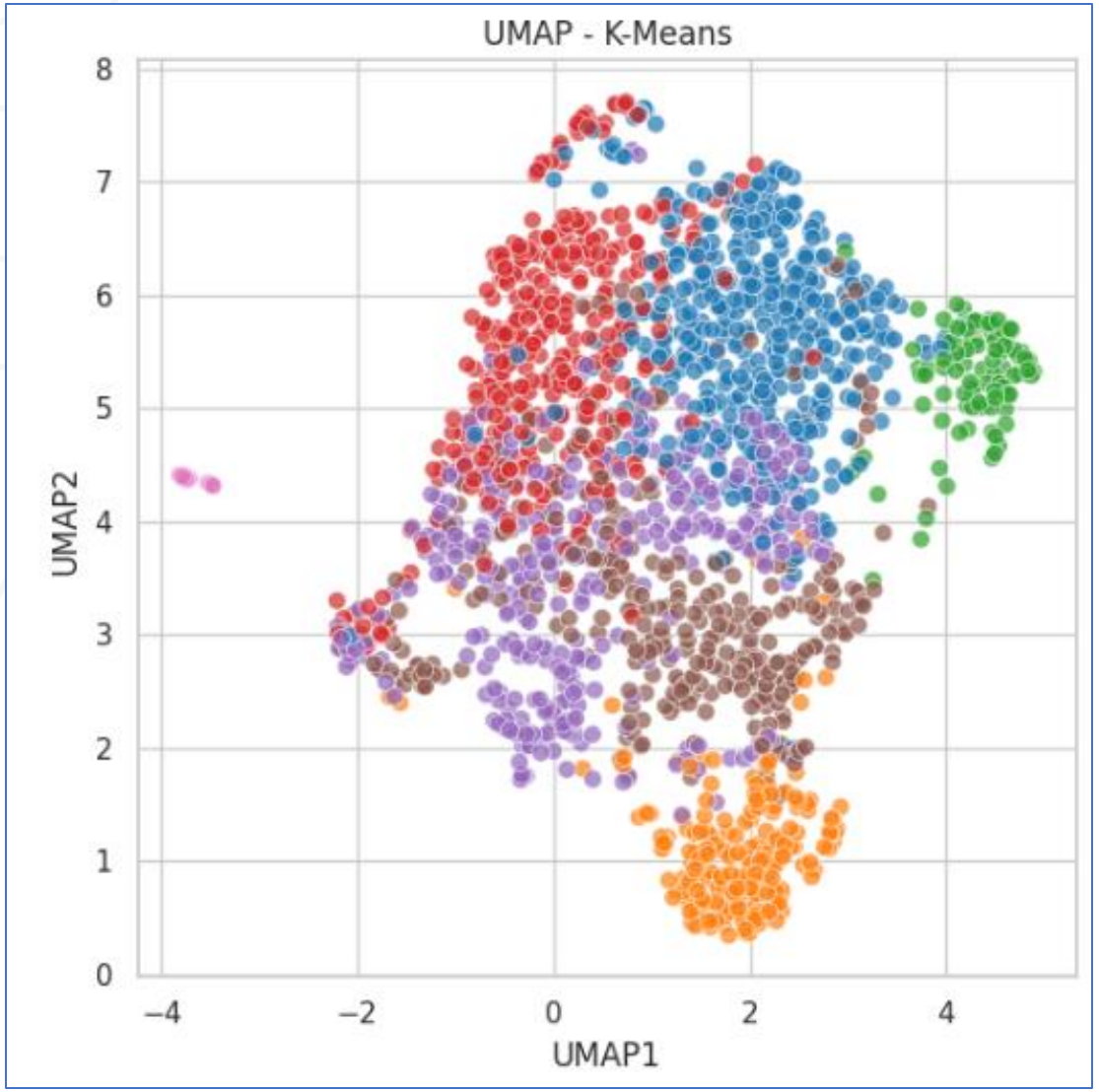
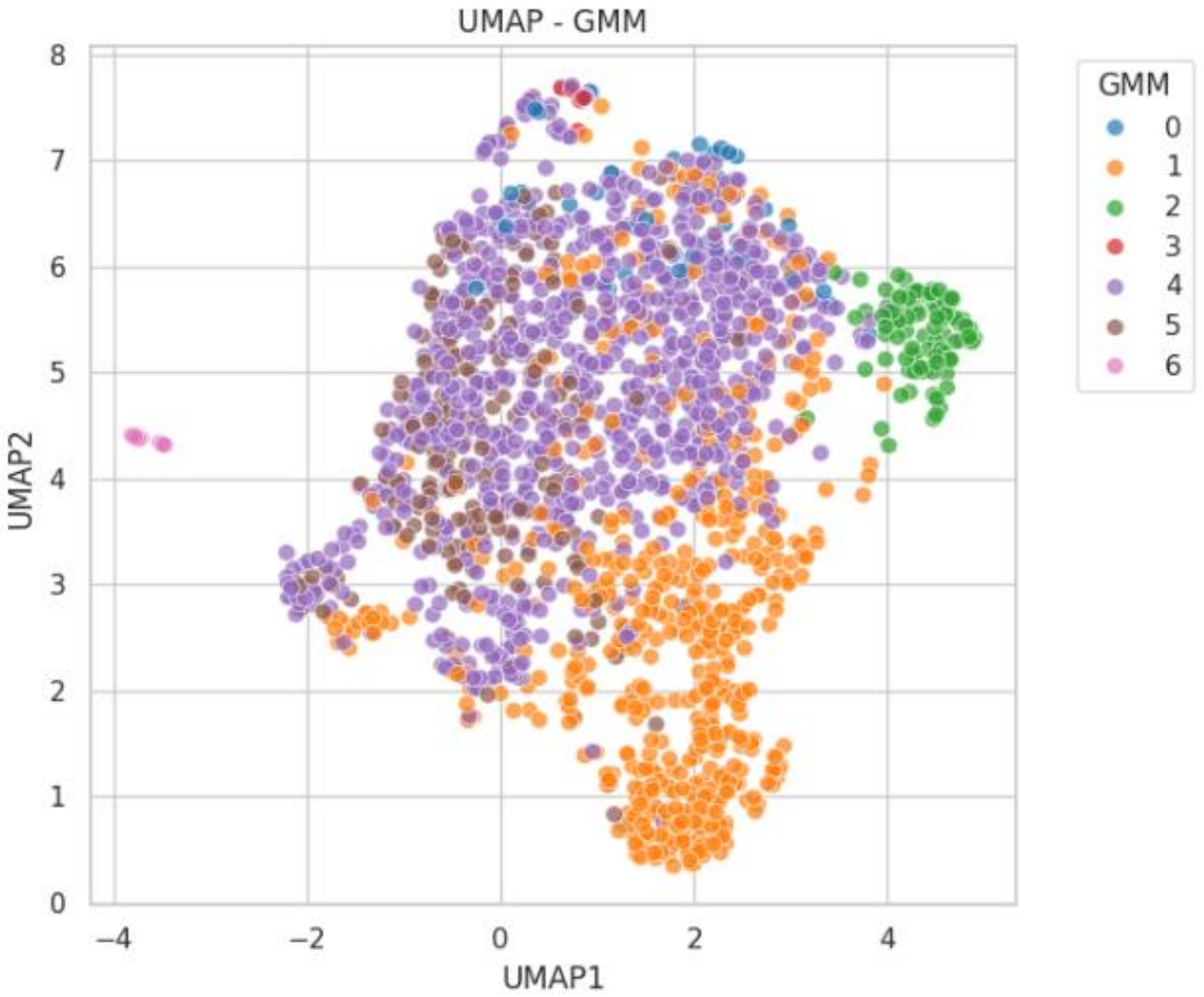
Clustering: K-Means vs GMM





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Data Preprocessing

- Train-Test Split (80% training, 20% testing)

- Clinical Data:
  - Imputation
  - Outlier treatment using IQR clipping
  - Scaling
  - Correlation Handling
  - Encoding Categorical Data

- Feature Selection

- No missing values in gene data, already in z-scale

Model Analysis 

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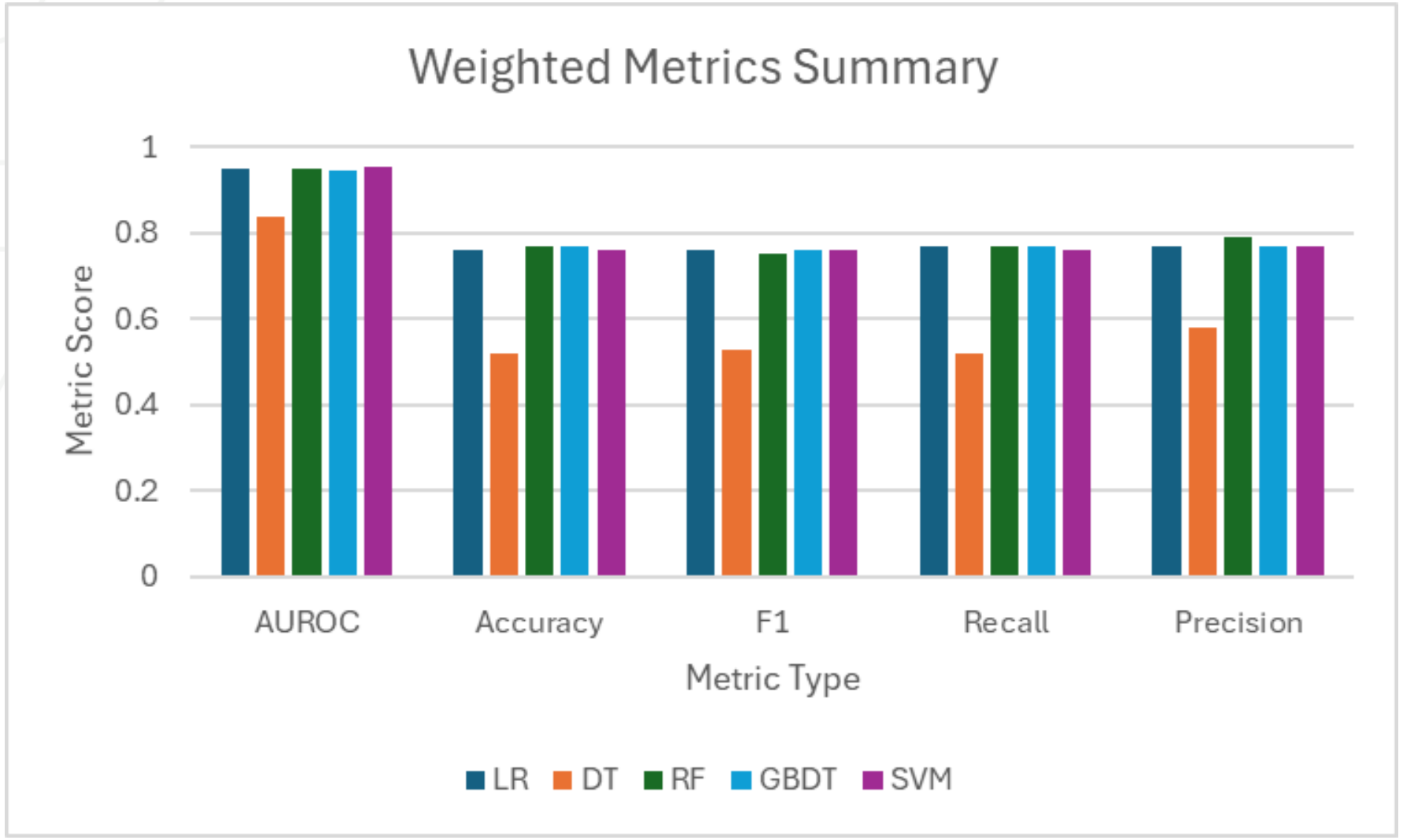
Aggregated Weighted Metrics Summary Across Models



SVM: Highest AUROC (0.9514)

LR is right behind (0.9475)

DT: Lowest metrics across the board

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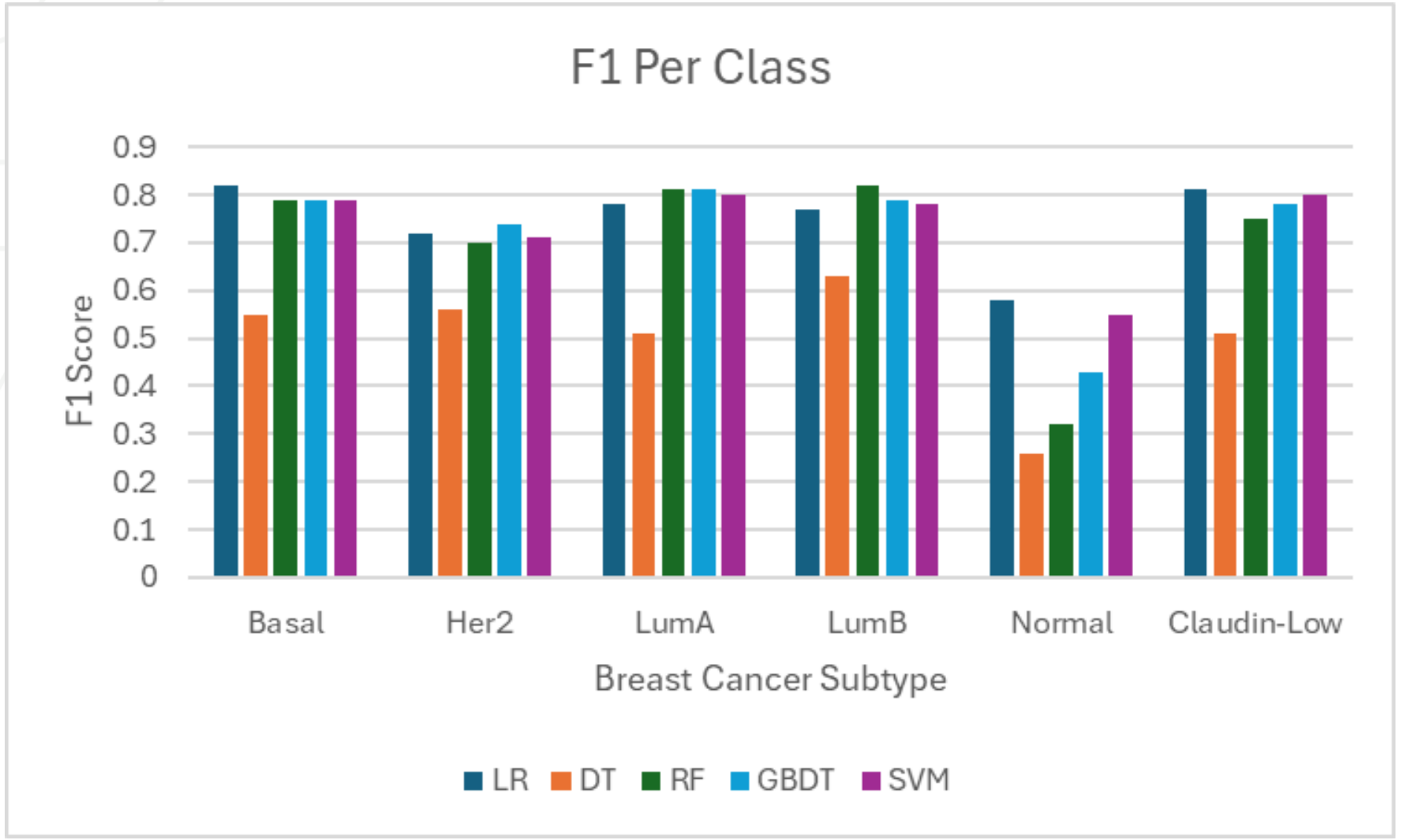
F1 Per Class Across Models



LR wins on 3 classes: Basal, Claudin-low & Normal

RF wins LumB & tied w/ GBDT on LumA

GBDT wins Her2

SVM sits firmly in the middle

DT lags far behind

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Best Model: SVM

Hyperparameters:

```
param_grid = {
    'C': [0.001, 0.01, 0.1, 1, 10, 100],  # Regularization parameter
    'kernel': ['linear', 'rbf', 'poly', 'sigmoid'],
    'gamma': ['scale', 'auto', 0.001, 0.01, 0.1, 1],  # Kernel coefficient
    'degree': [2, 3, 4, 5],  # Only for 'poly' kernel
    'coef0': [0.0, 0.1, 0.5, 1.0]  # For 'poly' and 'sigmoid' kernels
}
```

Hyperparameter	Chosen Value
Kernel	RBF
C	10
Gamma	0.001
Tolerance	0.001
Degree	2
Coef0	0.1
Probability	True

Classification Report (Weighted AUROC: 0.9475)

Class	Precision	Recall	F1-Score	Support
Basal	0.82	0.76	0.79	37
Her2	0.66	0.78	0.71	51
LumA	0.86	0.75	0.80	127
LumB	0.75	0.83	0.78	92
Normal	0.53	0.58	0.55	31
Claudin-low	0.83	0.77	0.80	39
Accuracy		**0.76**		**377**
Macro Avg	**0.74**	**0.74**	**0.74**	**377**
Weighted Avg	**0.77**	**0.76**	**0.76**	**377**

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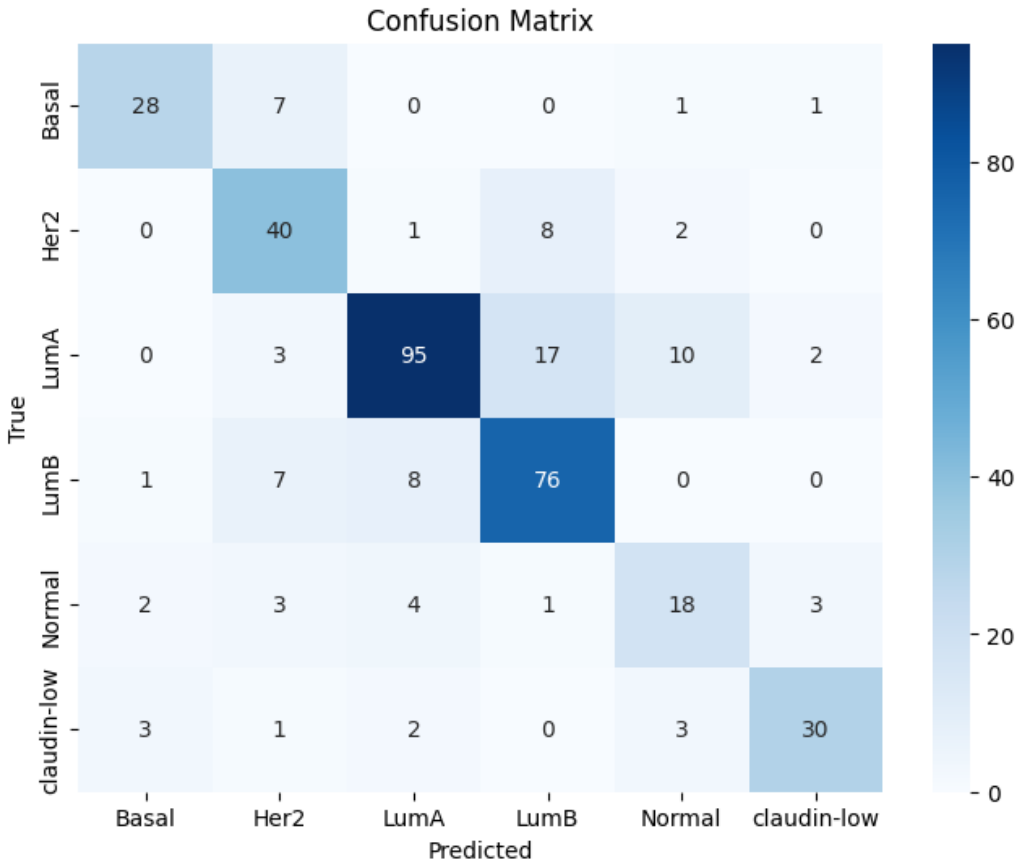
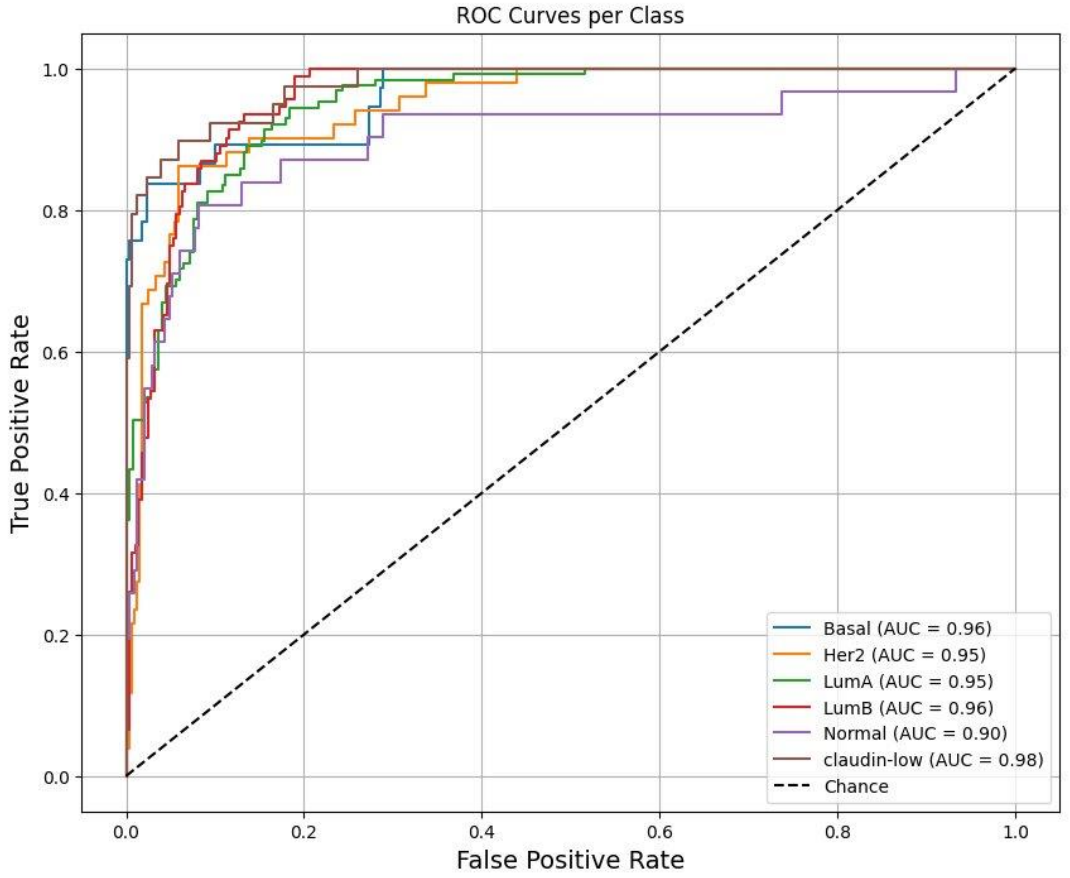
Best Model: SVM





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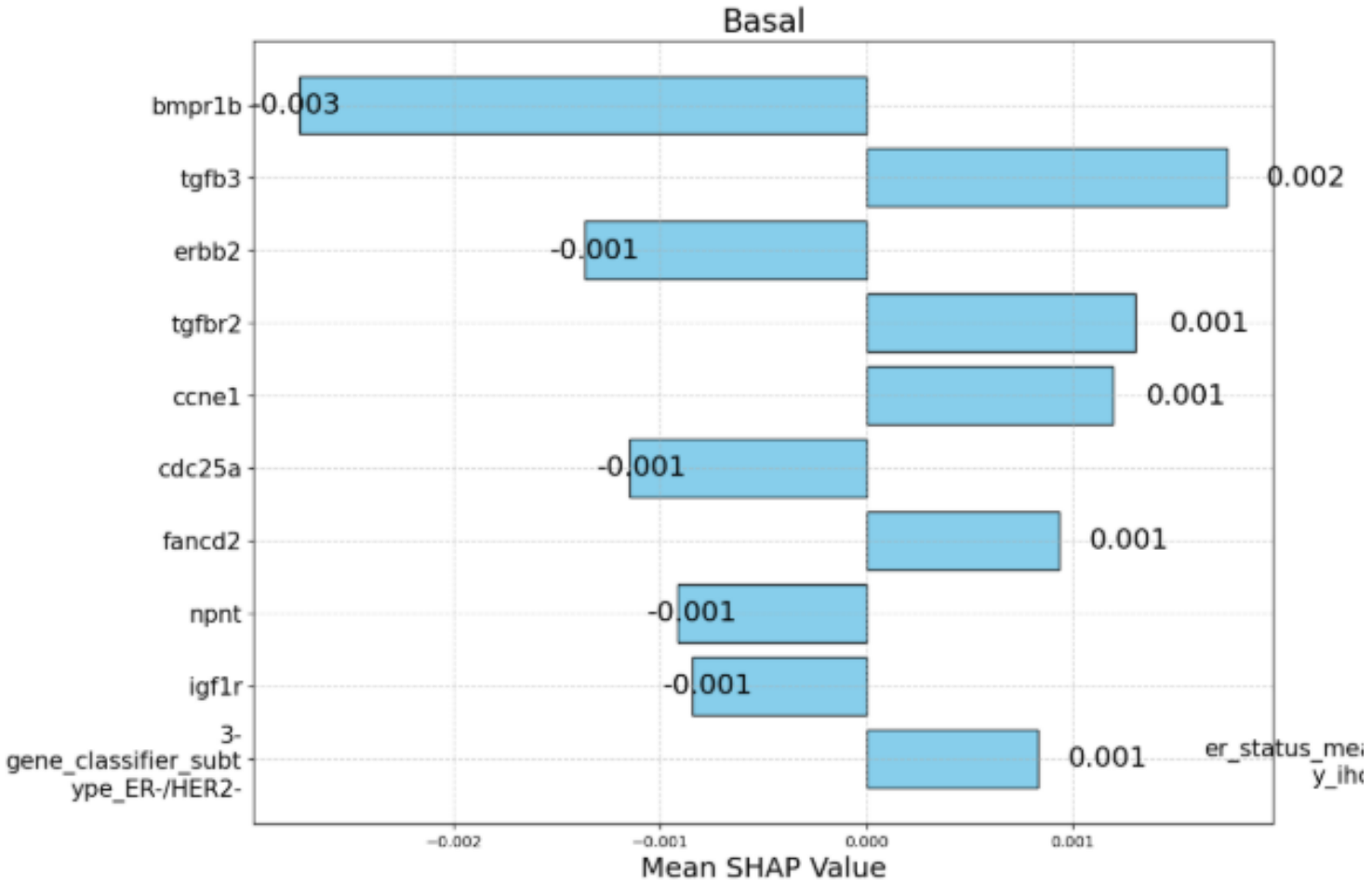
SVM: Top 10 Most Informative Features

- Plotted these distributions per class
- Sticking w/ Basal class for SHAP analysis b/c it's the most aggressive subtype



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SHAP Analysis: SVM

Gene	SHAP Value Sign	Coefficient's Sign Matches Clinical Literature?
bmpr1b	Negative	**Yes**, BMPR1B is significantly downregulated in basal-like breast cancers compared to other subtypes [4]
tgfb3	Positive	**No.** TGFB3 expression is documented to be lower in basal-like compared to HER-2 and LumA/B subtypes. In addition, our expression data shows the lowest expression for TGFB3 in basal-like [5].
erbb2	Negative	**Yes**, the sign of SHAP value and clinical literature's support that the gene is downregulated match [6] In addition, ERBB2 is the top feature for class HER2 according to the SHAP values obtained from the SVM model
tgfbr2	Positive	**No**, TGFBR2 is significantly downregulated across breast cancer subtypes, including basal-like ones, compared to normal tissue [7]
ccne1	Positive	**Yes**, CCNE1 amplification (copy-number gains) occurs in a subset (6–34%) of basal-like/TNBC cases [8]

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Close Second: LR

Hyperparameters:

```
# Hyperparameter space
param_grid_l2 = {
    'C': np.logspace(-4, 2, 10),
    'penalty': ['l2'],
    'solver': ['lbfgs', 'newton-cg', 'sag'],
    'max_iter': [1000]
}
```

```
param_grid = param_grid_l2
logreg = LogisticRegression(multi_class='multinomial', random_state=42)
search = RandomizedSearchCV(
    estimator=logreg,
    param_distributions=param_grid,
    n_iter=30, # 20
    scoring=scoring,
    refit='roc_auc_ovr',
    cv=5,
    n_jobs=-1,
    random_state=42
)
```

Hyperparameter	Chosen Value
Penalty	L2
Solver	Newton-cg
C	0.0464
Tolerance	0.0001
Fit Intercept	TRUE
Max Iter	1000
Multi-class	Multinomial

Classification Report (Weighted AUROC: 0.9475)

Class	Precision	Recall	F1-Score	Support
Basal	0.85	0.78	0.82	37
Her2	0.67	0.78	0.72	51
LumA	0.85	0.73	0.78	127
LumB	0.73	0.80	0.77	92
Normal	0.56	0.61	0.58	31
Claudin-low	0.82	0.79	0.81	39
Accuracy		**0.76**		**377**
Macro Avg	**0.75**	**0.75**	**0.75**	**377**
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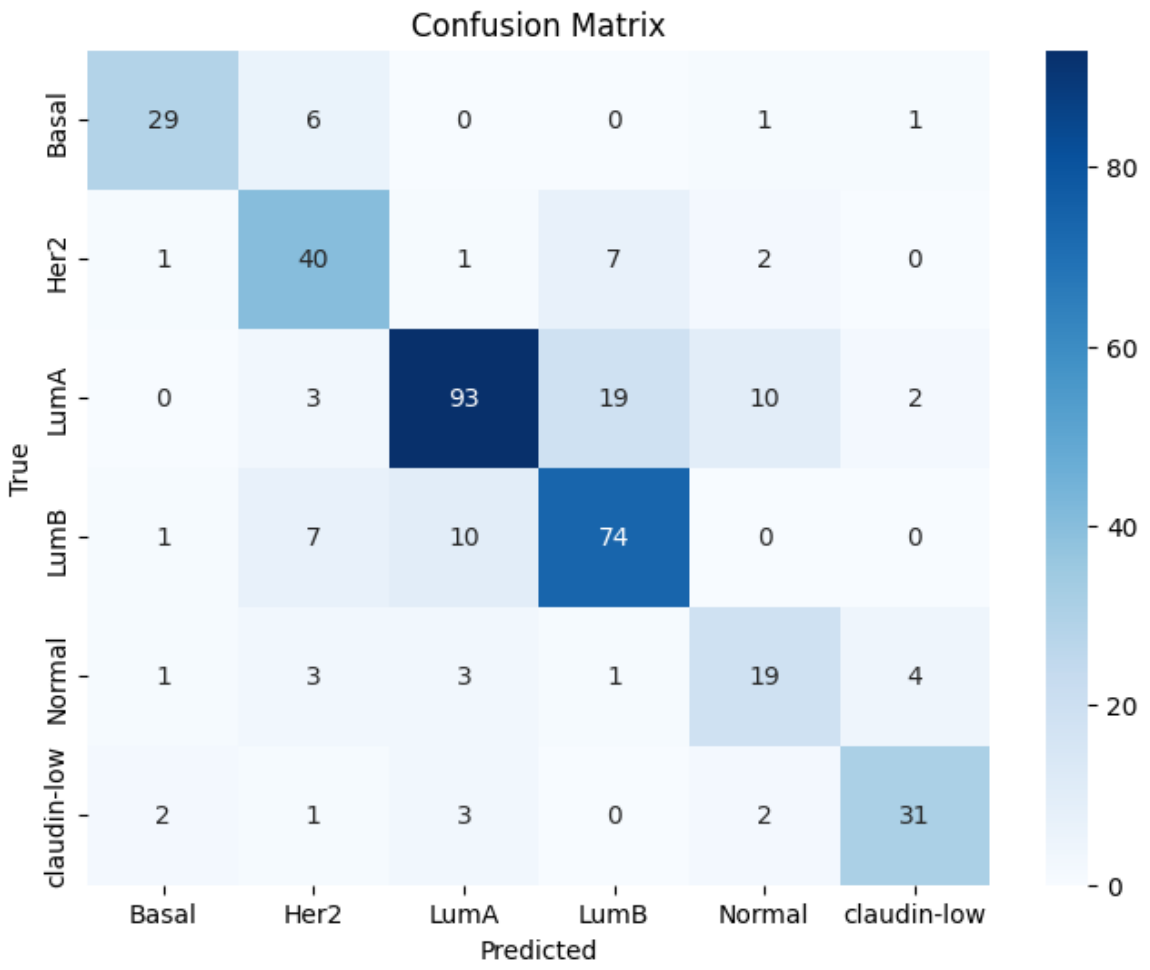
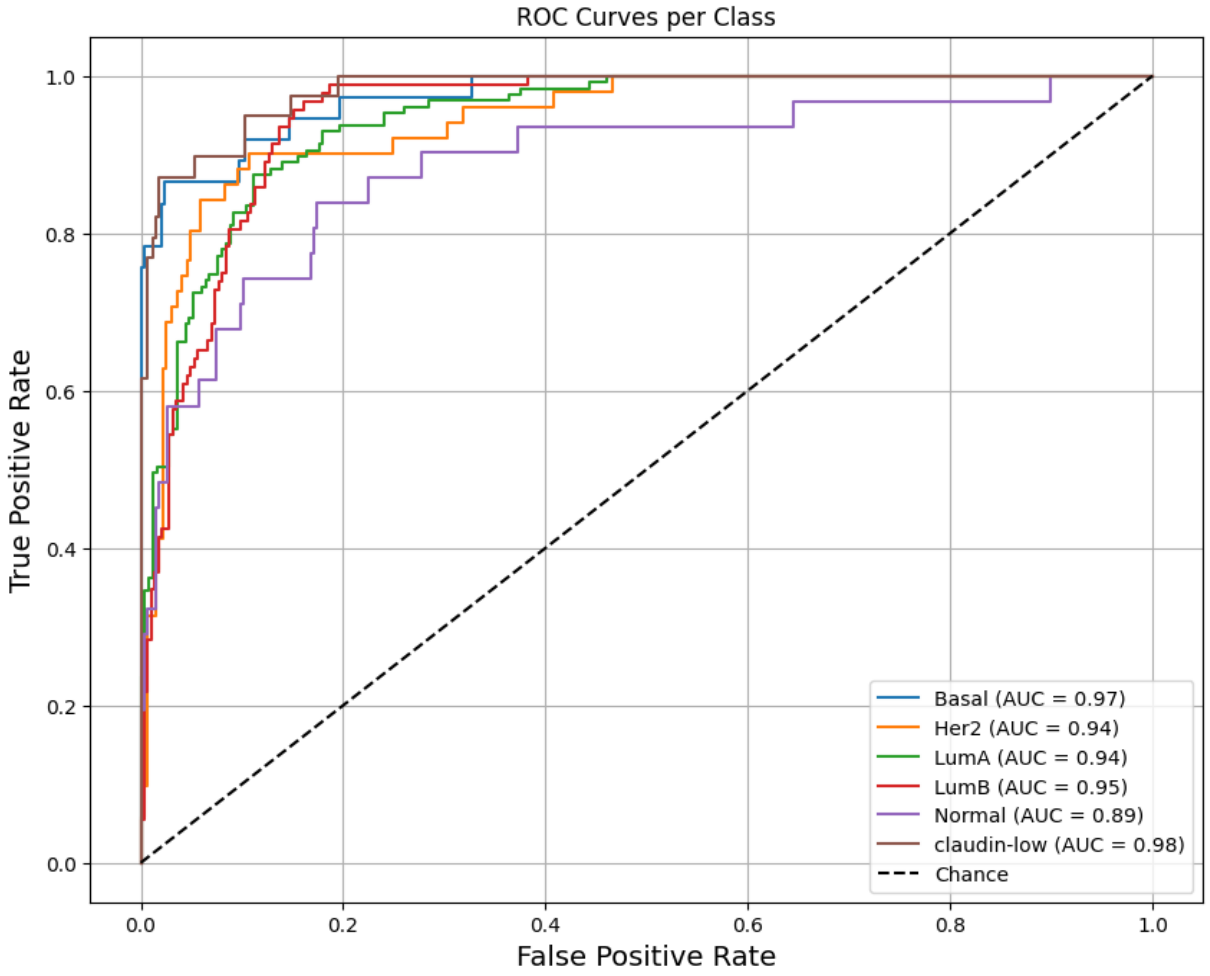
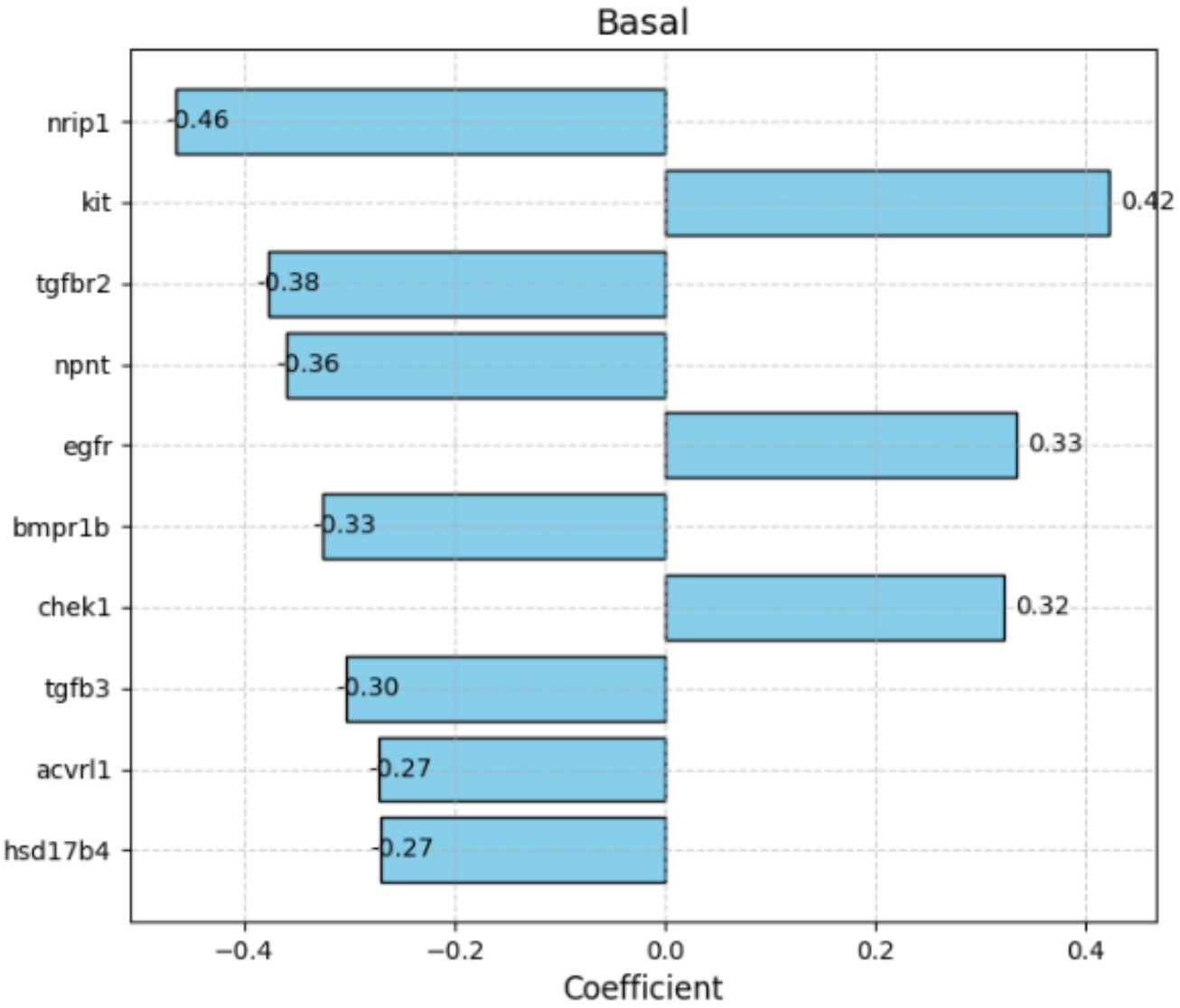
Close Second: LR





LR: Top 10 Most Informative Features

- Plotted these distributions per class
- Sticking w/ Basal class for SHAP analysis b/c it's the most aggressive subtype



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SHAP Analysis: LR

Gene	SHAP Value Sign	Coefficient's Sign Matches Clinical Literature?
nrip1	Negative	**Yes**, known to be lowly expressed in basal-like subtype [9].
kit	Positive	**Yes**, overexpressed in basal-like subtype [10].
tgfbr2	Negative	**Yes**, low expression in basal-like tissue compared to normal tissue [7].
nptnt	Negative	Not known to be a marker but consistent with our expression data (box-plots)
egfr	Positive	**Yes**, known to be overexpressed [11].
bmpr1b	Negative	**Yes**. Known to be downregulated in basal-like subtype compared to other breast cancer subtypes [4].

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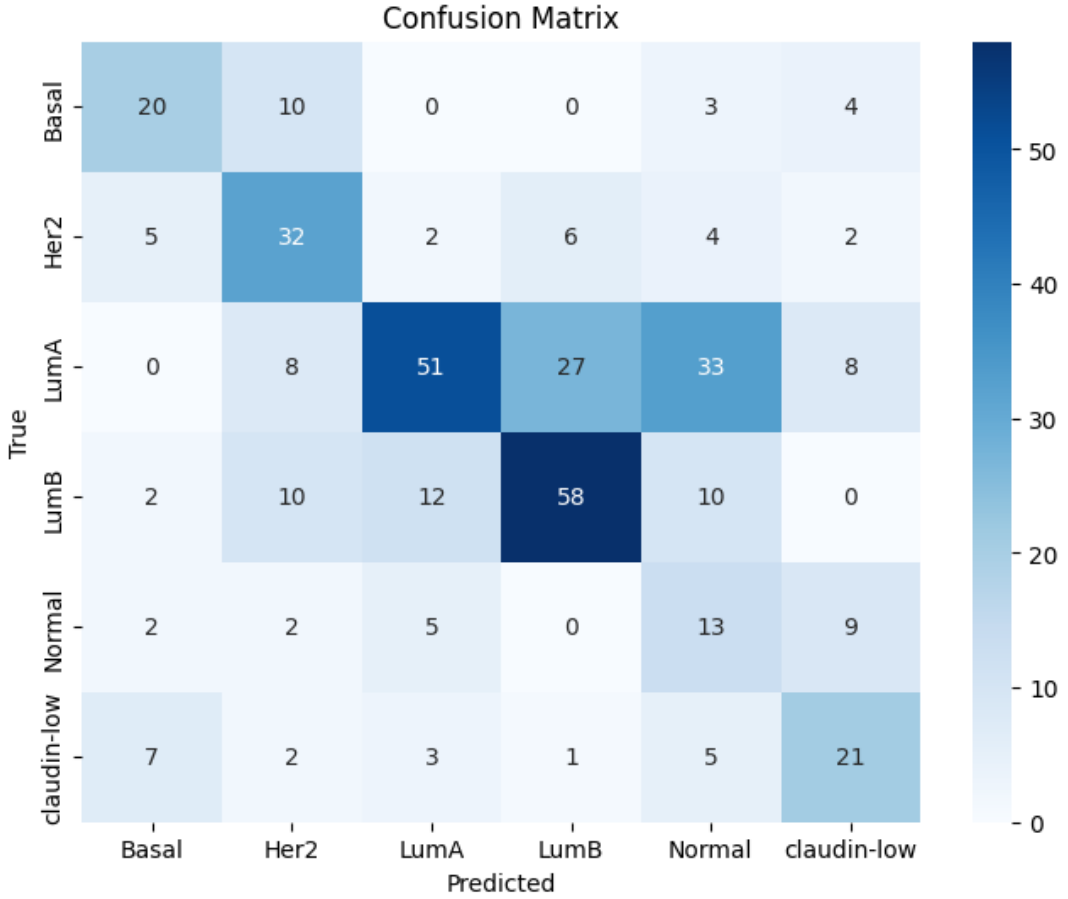
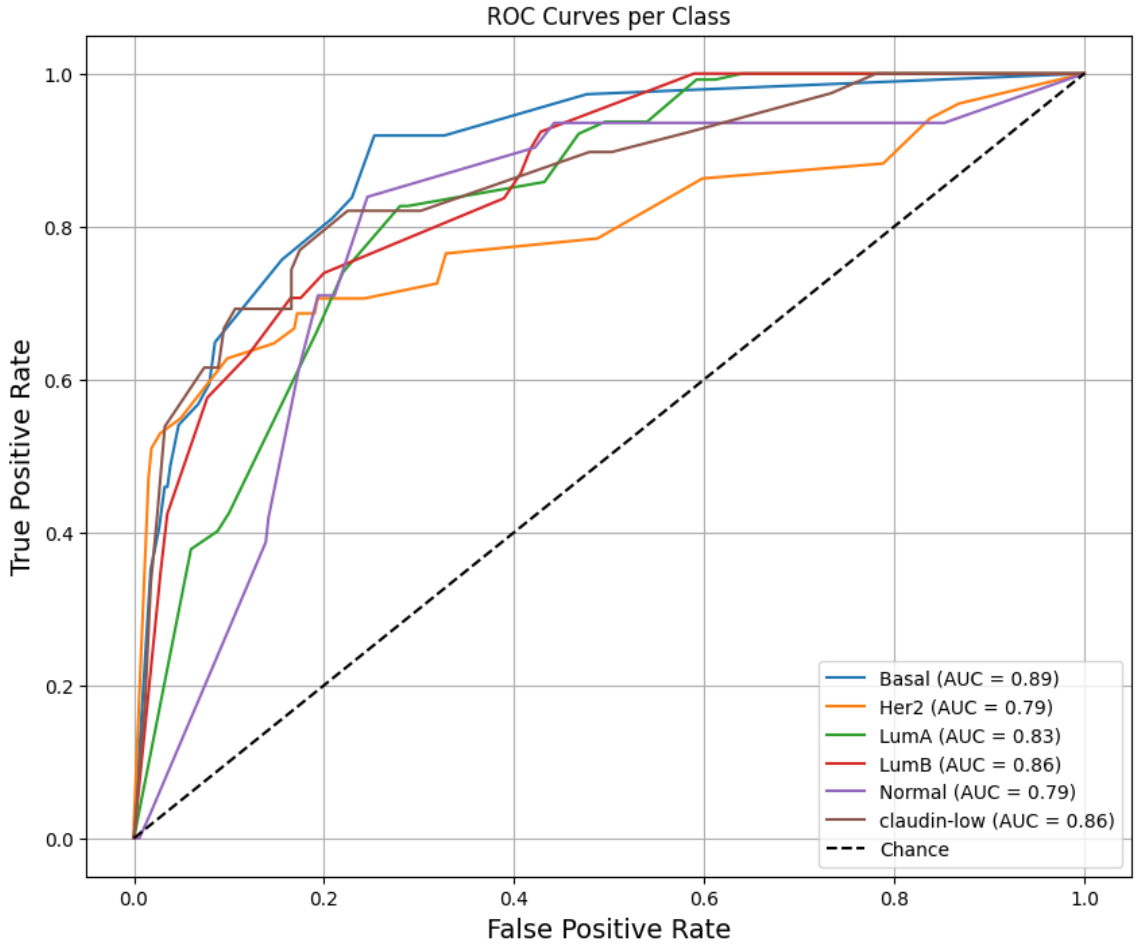
Worst Model: DT






```
param_grid_dt = {
    'max_depth': [3, 5, 10, 15, 20, None],
    'min_samples_split': [2, 5, 10, 20],
    'min_samples_leaf': [1, 2, 5, 10],
    'max_features': ['sqrt', 'log2', None],
    'criterion': ['gini', 'entropy']
}
```

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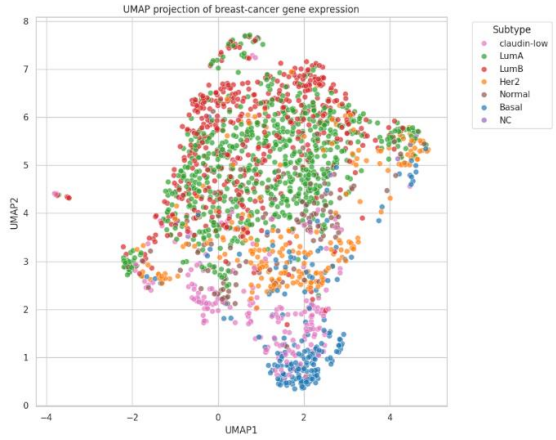
Worst Model: DT

- Shallow depth leading to high bias and underfitting as each split is only going to use a handful of the most obvious features
- Random Forest & GBDT also used depth ≤ 5, but they aggregated hundreds of such trees, letting later trees (or other bootstrap samples) pick different features and interactions
- Random Forest's bootstrap sampling and feature bagging smooth out noise; GBDT turns variance into bias-correction

Conclusion

- Our data is linearly separable (UMAP supports)
- SVM is the best model, followed by LR (Based on weighted test AUROC)
- For both SVM & LR, confusion matrices show high mismatch for LumA & LumB. LumA samples were also mostly misclassified as normal in both LR and SVM
- DT is the weakest model
- Optimized the ML pipeline for speed and low-resource systems, balancing simplicity with potential performance trade-offs.



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