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In [ ]: # Imports & display options
import os
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns

from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler, LabelEncoder
from sklearn.pipeline import Pipeline
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import (
    accuracy_score, f1_score, roc_auc_score, average_precision_score,
    RocCurveDisplay, PrecisionRecallDisplay, ConfusionMatrixDisplay
)

pd.set_option("display.max_columns", 100)
pd.set_option("display.width", 120)
sns.set(context="notebook", style="whitegrid")

PATH_META = "GSE62944_metadata.csv"
PATH_EXPR = "C:/Users/james/OneDrive/Documents/GitHub/Comp_BME_Module_3/Comp_BME_Mo

ANGIO_GENES = ["VEGFA", "HIF1A", "ANGPT2", "FLT1"]
TP53_GENE = "TP53"

if not os.path.exists(PATH_META):
    raise FileNotFoundError(f"Metadata not found: {PATH_META}")
if not os.path.exists(PATH_EXPR):
    raise FileNotFoundError(f"Expression file not found: {PATH_EXPR}")
```

```
In [ ]: # Load metadata
meta = pd.read_csv(PATH_META)

colmap = {}
for want, candidates in {
    "sample": ["sample", "sample_id", "SAMPLE", "tcga_sample", "rna_sample"],
    "cancer_type": ["cancer_type", "project", "cancer", "type", "disease"],
    "tissue": ["tissue", "sample_type", "TISSUE", "source_name", "is_tumor"],
}.items():
    for c in candidates:
        if c in meta.columns:
            colmap[want] = c
            break

missing = [k for k in ["sample", "cancer_type"] if k not in colmap]
if missing:
    raise ValueError(f"Missing columns {missing} in metadata.")

meta = meta.rename(columns={colmap["sample"]: "sample_id", colmap["cancer_type"]:"cancer_type"})
if "tissue" in colmap:
    meta = meta.rename(columns={colmap["tissue"]:"tissue"})

lung_meta = meta[meta["cancer_type"].isin(["LUAD", "LUSC"])].copy()
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print(lung_meta["cancer_type"].value_counts())
print(f'Lung samples in metadata: {len(lung_meta)}')

expr_header = pd.read_csv(PATH_EXPR, nrows=0)
expr_cols = expr_header.columns.tolist()
gene_col = expr_cols[0]
lung_ids = set(lung_meta["sample_id"])
keep_cols = [gene_col] + [c for c in expr_cols if c in lung_ids]

if len(keep_cols) <= 1:
    print("Example lung IDs:", list(lung_meta["sample_id"].head(5)))
    print("Example expr columns:", expr_cols[:8])
    raise ValueError("Sample IDs did not match between metadata and expression.")

expr = pd.read_csv(PATH_EXPR, usecols=keep_cols).set_index(gene_col)
lung_expr = expr[[c for c in expr.columns if c in lung_ids]]
lung_meta = lung_meta[lung_meta["sample_id"].isin(lung_expr.columns)]

print(f'Expression genes: {lung_expr.shape[0]}:, lung samples: {lung_expr.shape[1]}

def normalize_gene_index(idx):
    s = pd.Index(idx)
    s = s.str.replace(r"\.\d+$", "", regex=True)
    s = s.str.upper()
    s = s.str.replace(r"[^A-Z0-9_-\.]", "", regex=True)
    return s

lung_expr.index = normalize_gene_index(lung_expr.index)

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cancer_type
LUAD     80
LUSC     80
Name: count, dtype: int64
Lung samples in metadata: 160
Expression genes: 15,716, lung samples: 160

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In [ ]: # Map genes
symbol_to_ensembl = {
    "TP53": "ENSG00000141510",
    "HIF1A": "ENSG00000100644",
    "ANGPT2": "ENSG00000114771",
    "FLT1": "ENSG00000102755",
    "VEGFA": "ENSG00000112715",
}

def resolve_gene_name(symbol, expr_index):
    sym = symbol.upper()
    if sym in expr_index:
        return sym
    ens = symbol_to_ensembl.get(sym)
    if ens and ens in expr_index:
        return ens
    if ens and ens.split(".")[0] in expr_index:
        return ens.split(".")[0]
    return None

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requested_genes = [TP53_GENE] + ANGIO_GENES
resolved_map = {g: resolve_gene_name(g, lung_expr.index) for g in requested_genes}
present_pairs = [(g, r) for g, r in resolved_map.items() if r is not None]

gene_mat = pd.DataFrame({sym: lung_expr.loc[r] for sym, r in present_pairs})
df = gene_mat.merge(
    lung_meta[["sample_id", "cancer_type"]],
    left_index=True, right_on="sample_id", how="left"
).set_index("sample_id")

print("df shape:", df.shape)
print("Columns:", df.columns.tolist())
print(df.head())

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df shape: (160, 6)
Columns: ['TP53', 'VEGFA', 'HIF1A', 'ANGPT2', 'FLT1', 'cancer_type']
          TP53      VEGFA      HIF1A      ANGPT2      FLT1  cancer
r_type
sample_id
TCGA-44-8117-01A-11R-2241-07  3.533095  9.701291  6.736848  3.030111  4.151444
LUAD
TCGA-50-5936-01A-11R-1628-07  5.960825  6.493070  6.753303  3.582496  4.130102
LUAD
TCGA-55-A494-01A-11R-A24X-07  6.236896  9.863876  5.849348  4.003857  4.178755
LUAD
TCGA-78-7160-01A-11R-2039-07  6.803066  6.842713  7.120642  2.753598  4.723887
LUAD
TCGA-78-7158-01A-11R-2039-07  7.446952  6.778299  6.417706  1.361158  2.384635
LUAD

```

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In [ ]: # Exploratory Data Analysis (EDA)
plot_vars = [g for g in requested_genes if g in df.columns]

if len(plot_vars) >= 1:
    _ = df[plot_vars].hist(bins=30, figsize=(10, 6))
    plt.suptitle("Expression Distributions (log2 TPM)", fontsize=14)
    plt.tight_layout()
    plt.show()

if len(plot_vars) >= 2:
    sns.pairplot(
        df.reset_index(),
        vars=plot_vars,
        hue="cancer_type",
        corner=True,
        plot_kws={"alpha": 0.6, "edgecolor": "k", "linewidth": 0.3},
    )
    plt.suptitle("Pairwise Expression Scatterplots", y=1.02)
    plt.show()

if len(plot_vars) >= 2:
    corr_all = df[plot_vars].corr(method="spearman")
    print("Spearman correlations (lung overall):\n", corr_all)
    sns.heatmap(corr_all, annot=True, cmap="coolwarm", fmt=".2f")
    plt.title("Spearman Correlation - All Lung Samples")
    plt.tight_layout()

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plt.show()

# Logistic Regression Model
features = [g for g in requested_genes if g in df.columns]
data_ml = df.dropna(subset=features + ["cancer_type"]).copy()
X = data_ml[features]
y = data_ml["cancer_type"]

# Encode LUAD/LUSC
le = LabelEncoder()
y_enc = le.fit_transform(y)
print("Label encoding:", dict(zip(le.classes_, le.transform(le.classes_)))))

# Train/test split
X_tr, X_te, y_tr, y_te = train_test_split(
    X, y_enc, test_size=0.2, stratify=y_enc, random_state=42
)

# Pipeline
pipe = Pipeline([
    ("scaler", StandardScaler()),
    ("clf", LogisticRegression(
        penalty="l2", solver="lbfgs", max_iter=5000, n_jobs=-1
    ))
])

# Fit/predict
pipe.fit(X_tr, y_tr)
y_pred = pipe.predict(X_te)
y_score = pipe.predict_proba(X_te)[:, 1]

acc = accuracy_score(y_te, y_pred)
f1 = f1_score(y_te, y_pred)
auc = roc_auc_score(y_te, y_score)
aupr = average_precision_score(y_te, y_score)

print("\n==== Logistic Regression (5-gene panel) - Test set ===")
print(f"Accuracy: {acc:.3f}")
print(f"F1-score: {f1:.3f}")
print(f"ROC AUC : {auc:.3f}")
print(f"PR AUC : {aupr:.3f}")

# validation
fig, ax = plt.subplots(1, 3, figsize=(18, 5))
RocCurveDisplay.from_predictions(y_te, y_score, name="LogReg", ax=ax[0])
ax[0].set_title("ROC Curve")

PrecisionRecallDisplay.from_predictions(y_te, y_score, name="LogReg", ax=ax[1])
ax[1].set_title("Precision-Recall Curve")

ConfusionMatrixDisplay.from_predictions(
    y_te, y_pred, normalize="true", display_labels=le.classes_, ax=ax[2]
)
ax[2].set_title("Confusion Matrix (normalized)")
plt.tight_layout()
plt.show()

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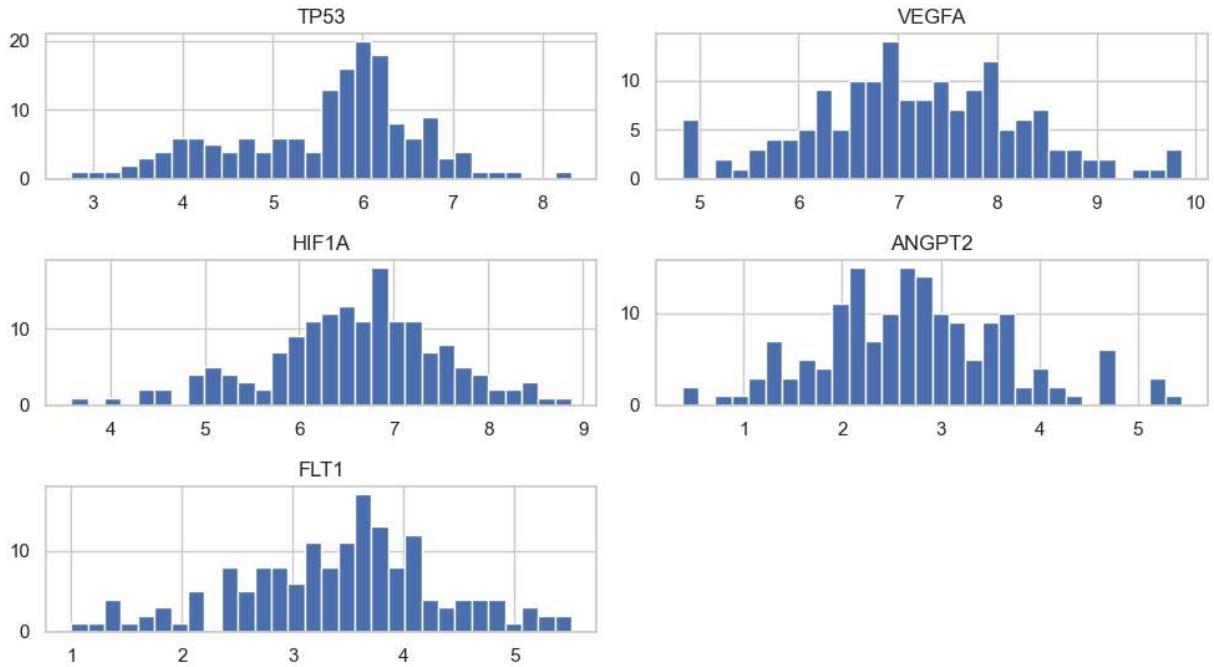
clf = pipe.named_steps["clf"]
coef_tbl = pd.DataFrame({"feature": features, "coef": clf.coef_[0]})
coef_tbl["abs_coef"] = coef_tbl["coef"].abs()
coef_tbl = coef_tbl.sort_values("abs_coef", ascending=False)

print("\nTop features by |coefficient|:")
print(coef_tbl[["feature", "coef"]].to_string(index=False))

plt.figure(figsize=(6,4))
plt.barh(coef_tbl["feature"], coef_tbl["coef"], color="steelblue")
plt.xlabel("Coefficient (standardized)")
plt.title("Logistic Regression - Coefficients")
plt.tight_layout()
plt.show()

```

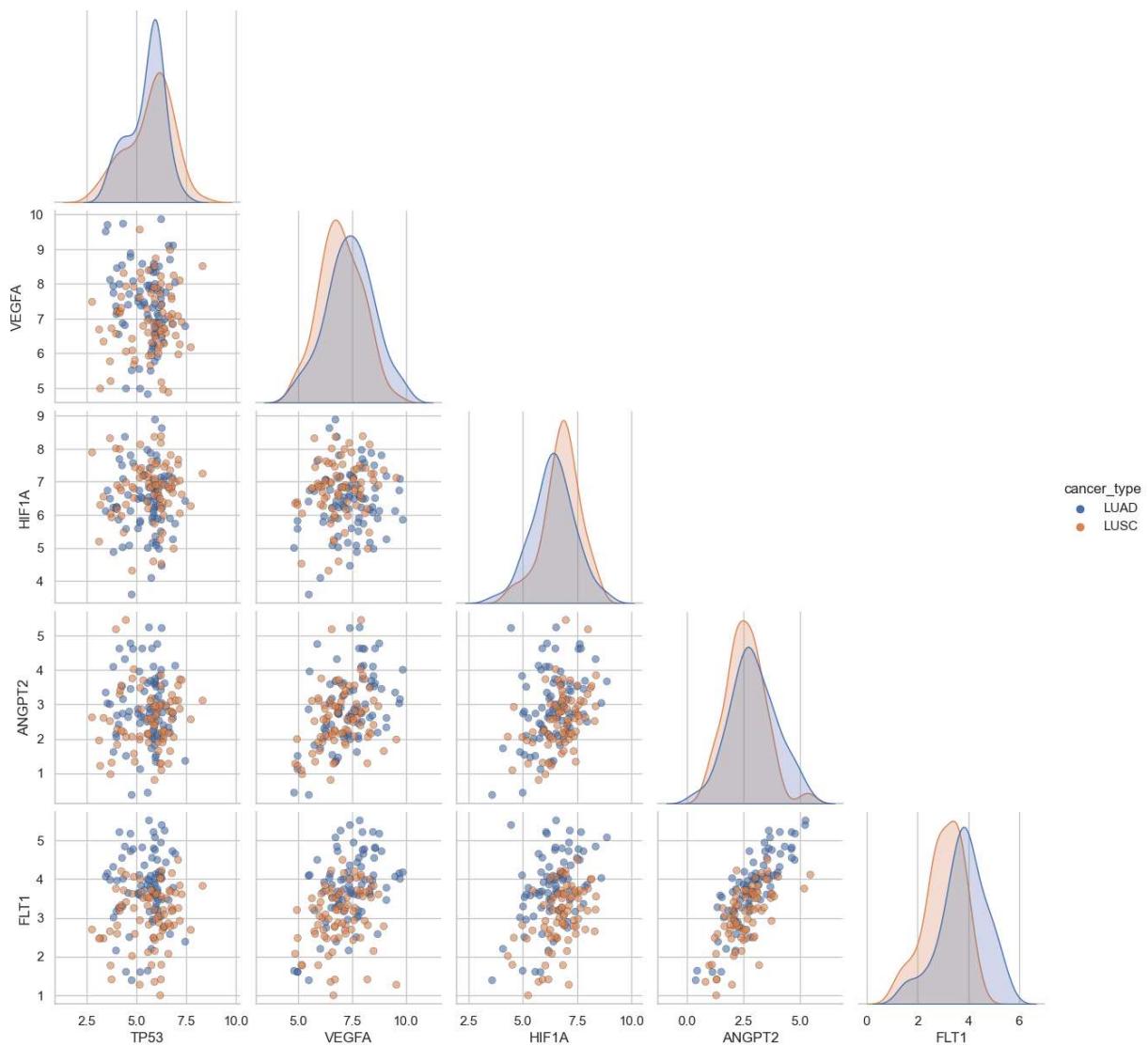
Expression Distributions (log2 TPM)



```
c:\Users\james\AppData\Local\Programs\Python\Python311\Lib\site-packages\seaborn\_ol
dcore.py:1119: FutureWarning: use_inf_as_na option is deprecated and will be removed
in a future version. Convert inf values to NaN before operating instead.
    with pd.option_context('mode.use_inf_as_na', True):
c:\Users\james\AppData\Local\Programs\Python\Python311\Lib\site-packages\seaborn\_ol
dcore.py:1075: FutureWarning: When grouping with a length-1 list-like, you will need
to pass a length-1 tuple to get_group in a future version of pandas. Pass `(name,)` 
instead of `name` to silence this warning.
    data_subset = grouped_data.get_group(pd_key)
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```

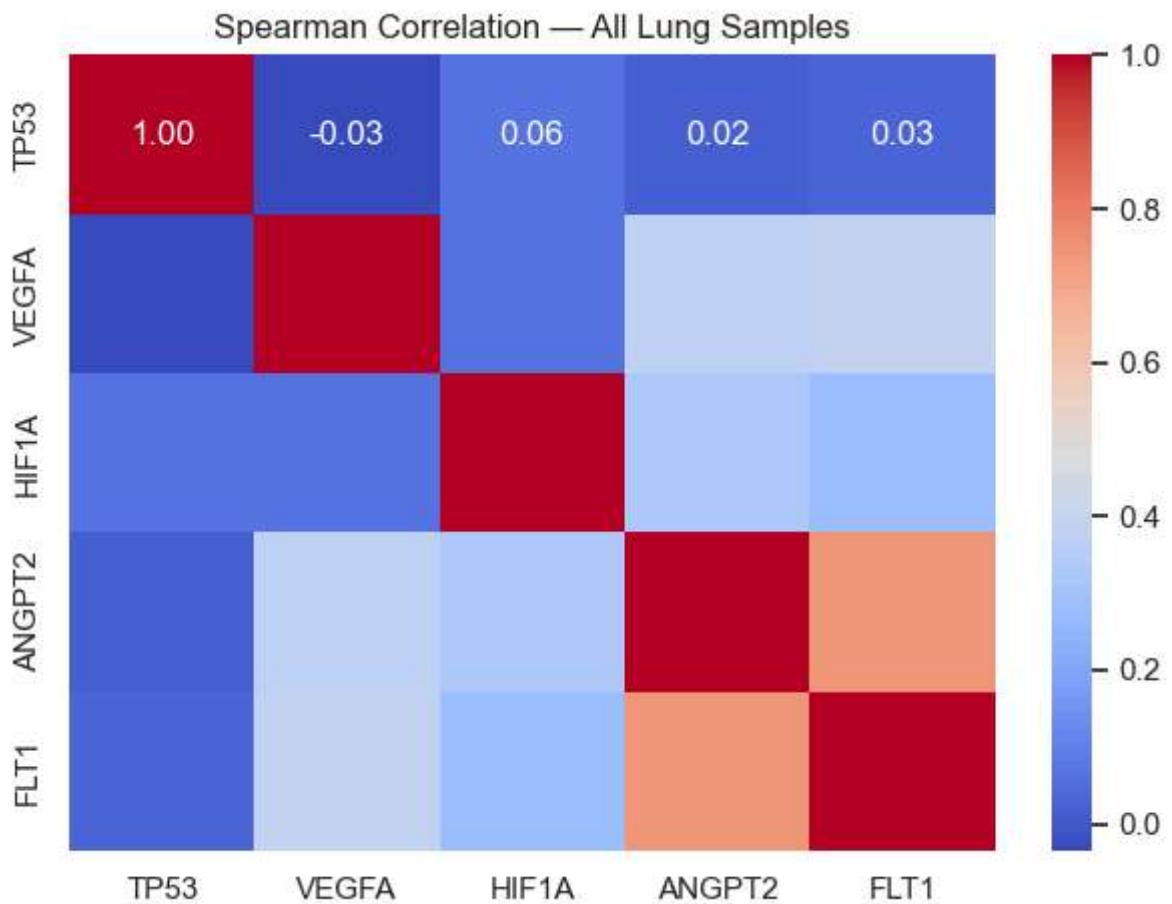
```
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instead of `name` to silence this warning.
```

### Pairwise Expression Scatterplots



Spearman correlations (lung overall):

	TP53	VEGFA	HIF1A	ANGPT2	FLT1
TP53	1.000000	-0.034616	0.062859	0.020315	0.032245
VEGFA	-0.034616	1.000000	0.062821	0.380810	0.394044
HIF1A	0.062859	0.062821	1.000000	0.333546	0.275217
ANGPT2	0.020315	0.380810	0.333546	1.000000	0.742614
FLT1	0.032245	0.394044	0.275217	0.742614	1.000000



Label encoding: {'LUAD': np.int64(0), 'LUSC': np.int64(1)}

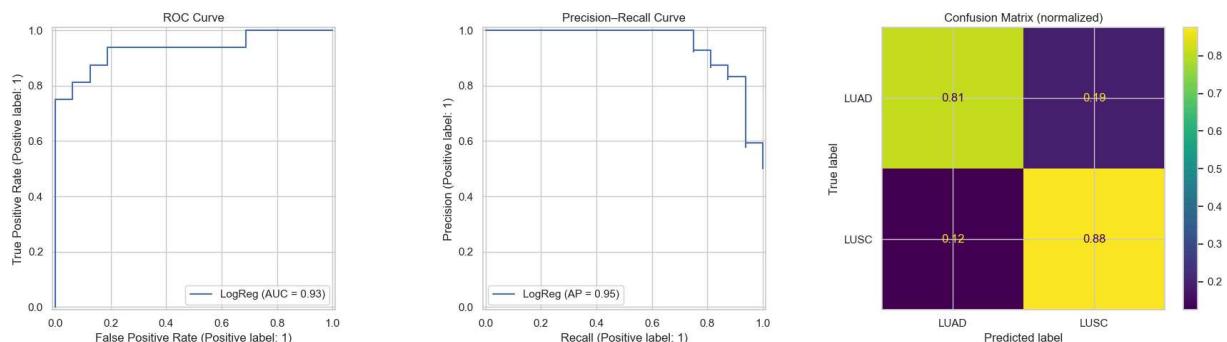
==== Logistic Regression (5-gene panel) – Test set ====

Accuracy: 0.844

F1-score: 0.848

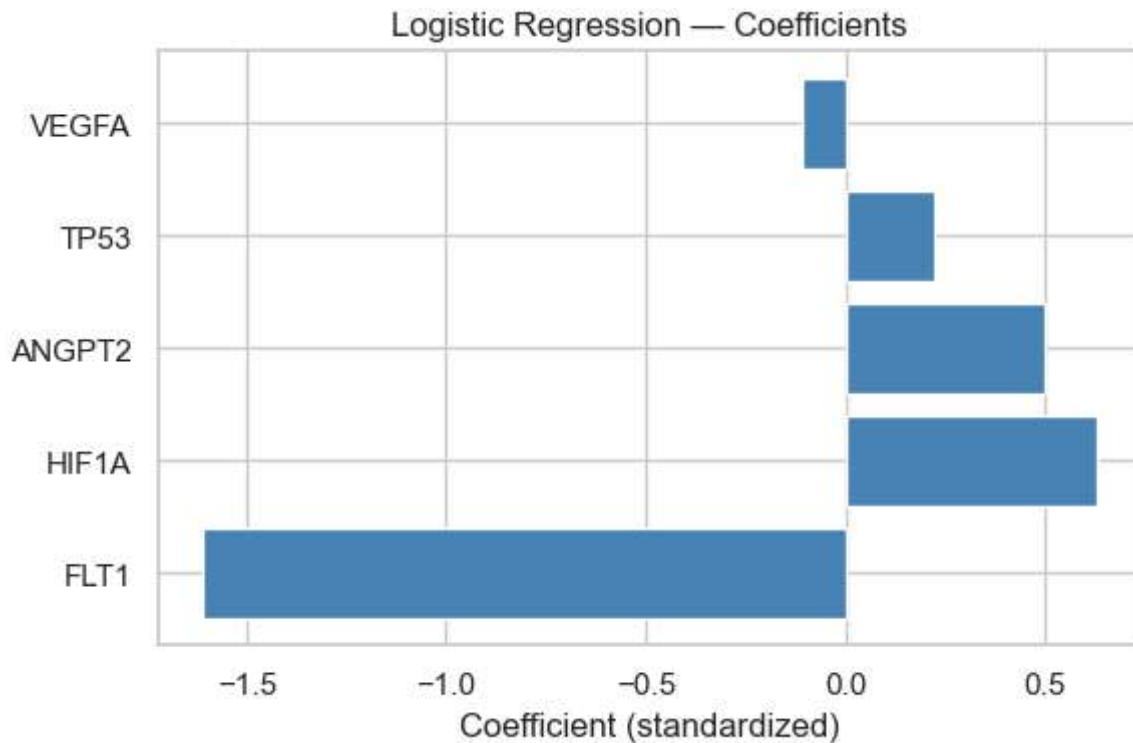
ROC AUC : 0.934

PR AUC : 0.952



Top features by |coefficient|:

feature	coef
FLT1	-1.608109
HIF1A	0.628050
ANGPT2	0.500068
TP53	0.222143
VEGFA	-0.108949



```
In [ ]: # LITERATURE VALIDATION:  
# TP53 mutations are more prevalent in LUSC compared to LUAD (reported ranges: ~75-  
# Both VEGFA and ANGPT2 are higher in Lung cancer compared to normal, but their pr  
# Increased VEGFA and ANGPT2 expression is associated with lower survival in LUAD p  
# Studies examining direct comparisons of expression levels between LUAD and LUSC e  
# This literature validation reinforces our finding that it is practical to use cer  
# With an AUC and AP values of 0.93 and 0.95 respectively, our validation suggests  
# In addition, our confidence matrix shows both labels to be correct over 80% of th
```