

THE EFFECT OF COPD ON GENE TRANSCRIPTION

	COPD subjects	Control subjects	P value
Male, n (%)	98 100.0	91 100.0	
Age, years	67.5 ± 6.4	60.9 ± 9.5	<0.0001
Smoking (py)	48.0 ± 22.0	35.2 ± 17.2	<0.0001
FEV1, %	71.9 ± 13.4	91.0 ± 12.4	<0.0001
FEV1/FVC	57.1 ± 7.8	74.8 ± 4.3	<0.0001
DLCO, %	77.4 ± 13.8	92.8 ± 13.2	<0.0001

COPD: chronic obstructive pulmonary disease; DLCO: diffusing capacity of the lung for CO₂; pack-years; FEV1: forced expiratory volume in 1 second. Unless otherwise stated, the mean ± standard deviation is shown.

INTRODUCTION

- CHRONIC OBSTRUCTIVE PULMONARY DISEASE (COPD) IS A GROUP OF DISORDERS THAT IMPAIR LUNG FUNCTION (ALFAHAD ET AL., 2021).
- ASSOCIATED CONDITIONS INCLUDE EMPHYSEMA, DAMAGE TO ALVEOLAR WALLS, AND CHRONIC BRONCHITIS (ZHANG ET AL., 2021).
- IT AFFECTS AN ESTIMATED 65 MILLION PEOPLE WORLDWIDE, CAUSING ABOUT 3 MILLION DEATHS ANNUALLY (WHO., 2024).
- COMMON SYMPTOMS INCLUDE SHORTNESS OF BREATH, CHRONIC COUGH, AND PROGRESSIVE LOSS OF LUNG FUNCTION.
- MAJOR RISK FACTORS INCLUDE CIGARETTE SMOKING, OCCUPATIONAL EXPOSURE, BIOMASS SMOKE, AND, MORE RECENTLY, NORMAL AGEING (LANGE ET AL., 2015).

Heatmap of Top 10 Up & Down Regulated Genes in Control vs COPD

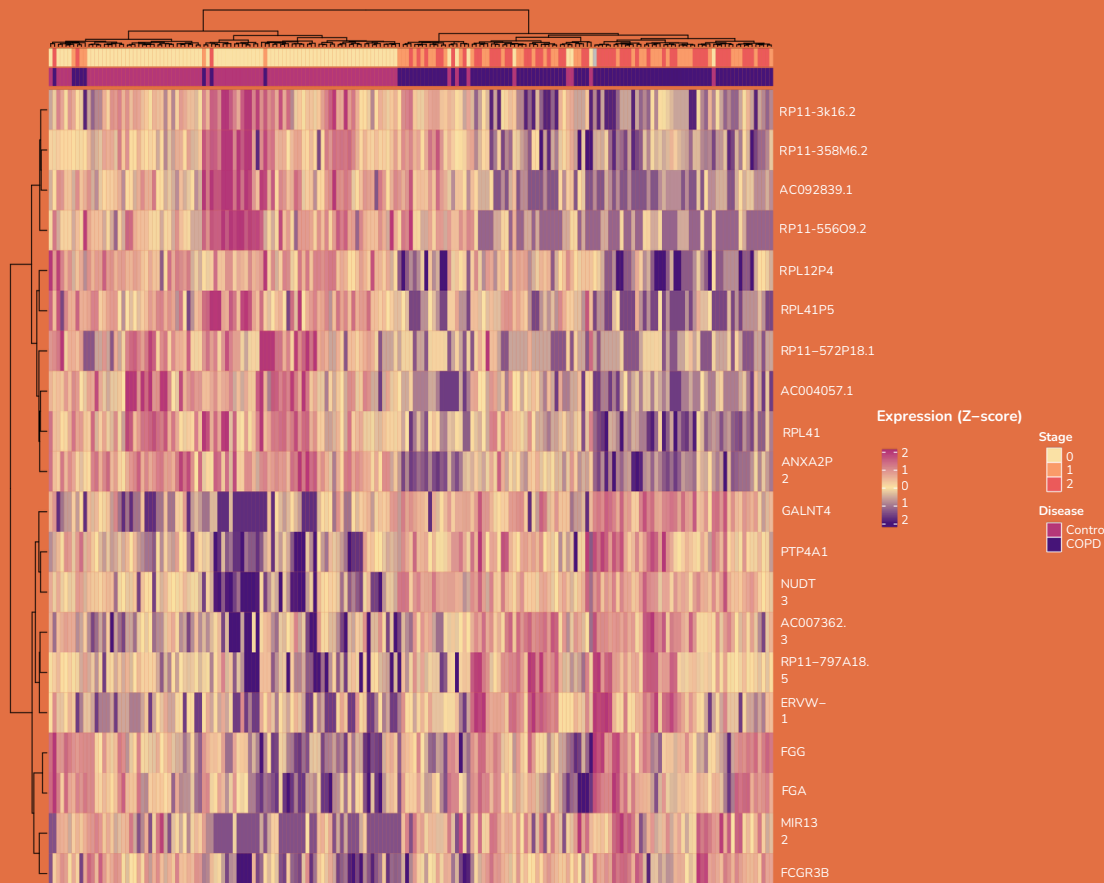


Figure Heatmap: X-axis portrays the disease and stage of disease: Control(0), COPD(Stage 1 and 2). Y-axis lists Top 10 up and Top 10 down regulated genes. These genes are significantly changed in regulation. Top 10 Up and Top 10 Down regulated genes are selected based on their log expression values.

PCA Plot Control vs COPD

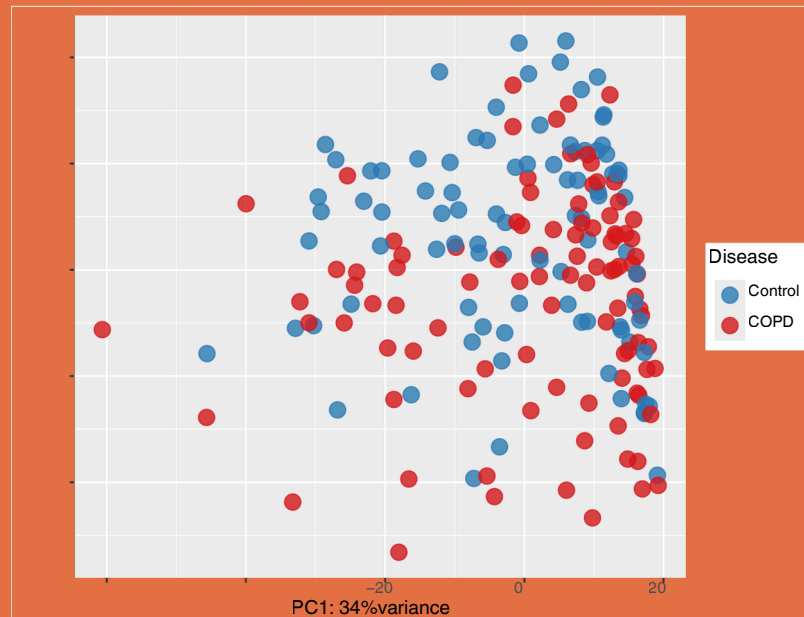


Figure: Principal component analysis of RNA sequencing data. PC1 is on the x-axis (34% variance) and PC2 is on the y-axis (14% variance). Each point represents a sample, colored by COPD (Red) vs control (Blue).

Interesting genes:

ANXA2P2
FTH1
GALNT4
FGG

Genes involved in aerobic electron transport chain

Vulcano plot of Top 10 Up & Down Regulated Gene Expression in Control vs COPD

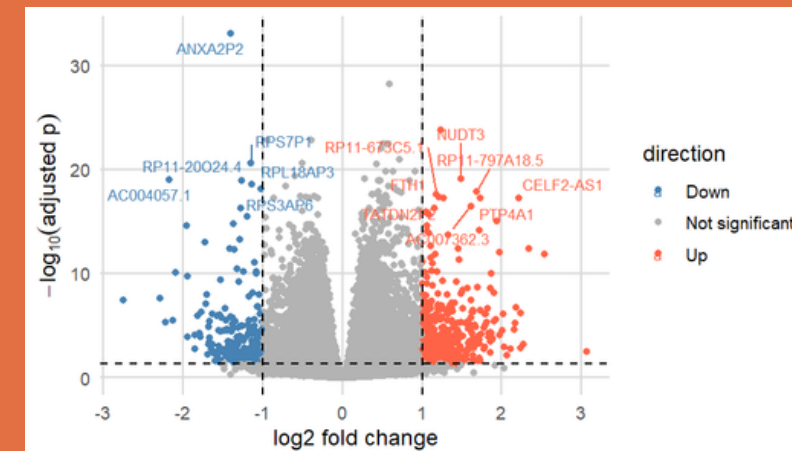


Figure Volcanoplot: X-axis portrays the change in expression between COPD and Controls. Y-axis shows significance of difference as log₁₀(adjusted p-value)(adjusted for multiple testing error). Top 10 most significant upregulated and downregulated genes are annotated on either side.

CONCLUSION

- FGG, FGA, AND PTP4A1 FORM A STRONGLY CONNECTED CLUSTER, SUGGESTING A MECHANISTIC SHIFT IN CELLULAR DIFFUSION AND RESULTING IN FIBRIN DEPOSITION.
- FTH1 MAY INDICATE MITOCHONDRIAL DYSREGULATION, AS SEVERAL DOWNREGULATED GENES ARE LINKED TO THESE PROCESSES.
- GALNT4 PROMOTES MUCIN HYPERSECRETION, INFLUENCING CELL PROLIFERATION AND INVASION (GUO ET AL., 2025).
- FGG HAS BEEN REPEATEDLY IDENTIFIED AS A POTENTIAL COPD BIOMARKER (ZHANG ET AL., 2021; KIM ET AL., 2015).
- COLLECTIVELY, THESE GENES ARE ASSOCIATED WITH INFLAMMATORY RESPONSES SIMILAR TO CHRONIC BRONCHITIS (YU ET AL., 2021), APPEAR TO DRIVE DISEASE PROGRESSION, AND INDICATE ALVEOLAR CELLULAR DYSFUNCTION, THOUGH THEIR SPECIFIC ROLES REQUIRE FURTHER INVESTIGATION.

REFERENCES

