

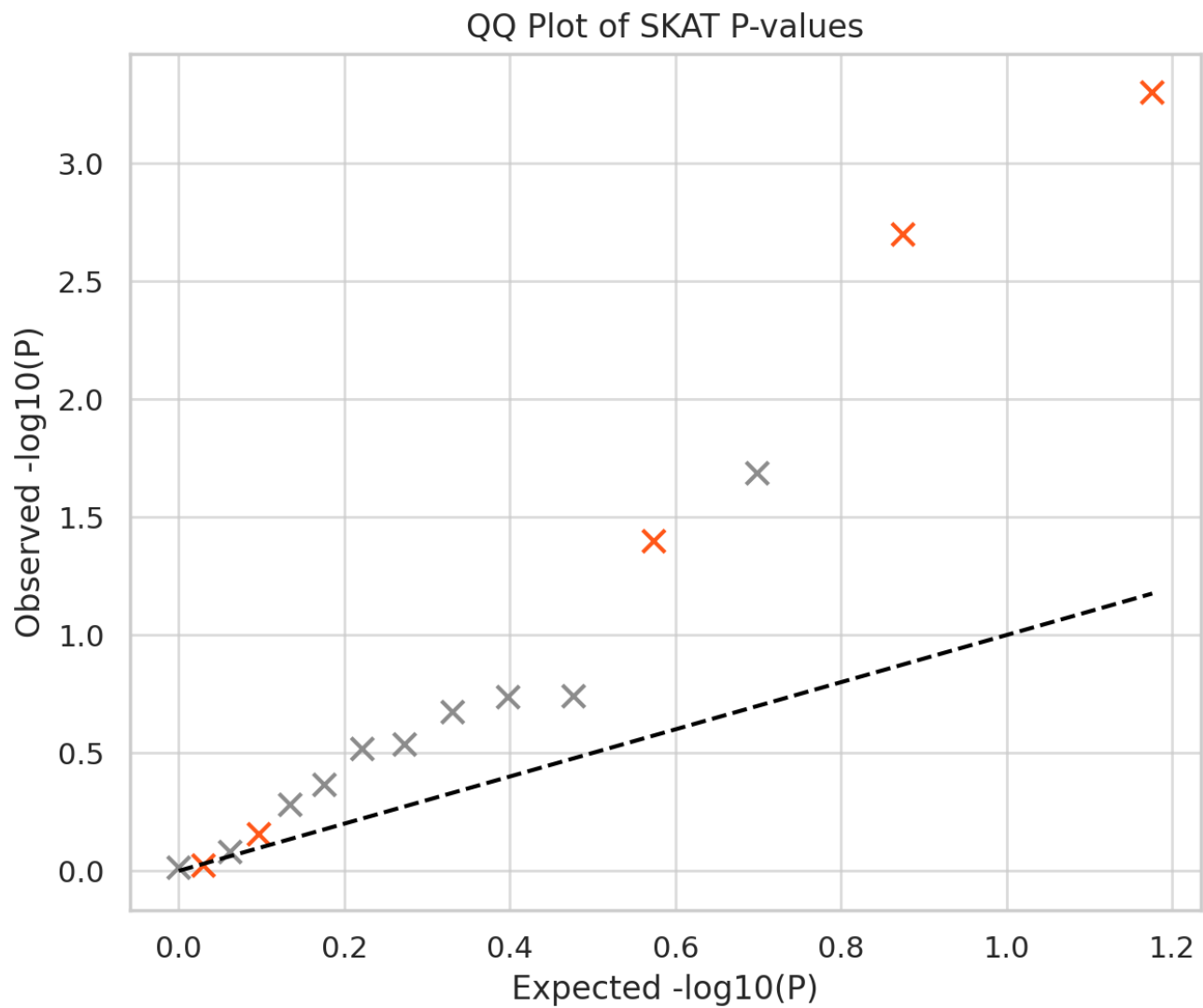
**Volcano Plot Interpretation:**

GeneA and GeneE clearly stand out in the upper corners -they have large effect sizes and low p-values, indicating strong associations.

GeneB appears further left (negative beta), but still high on the y-axis, showing that directional burden (CAST) detects a strong negative

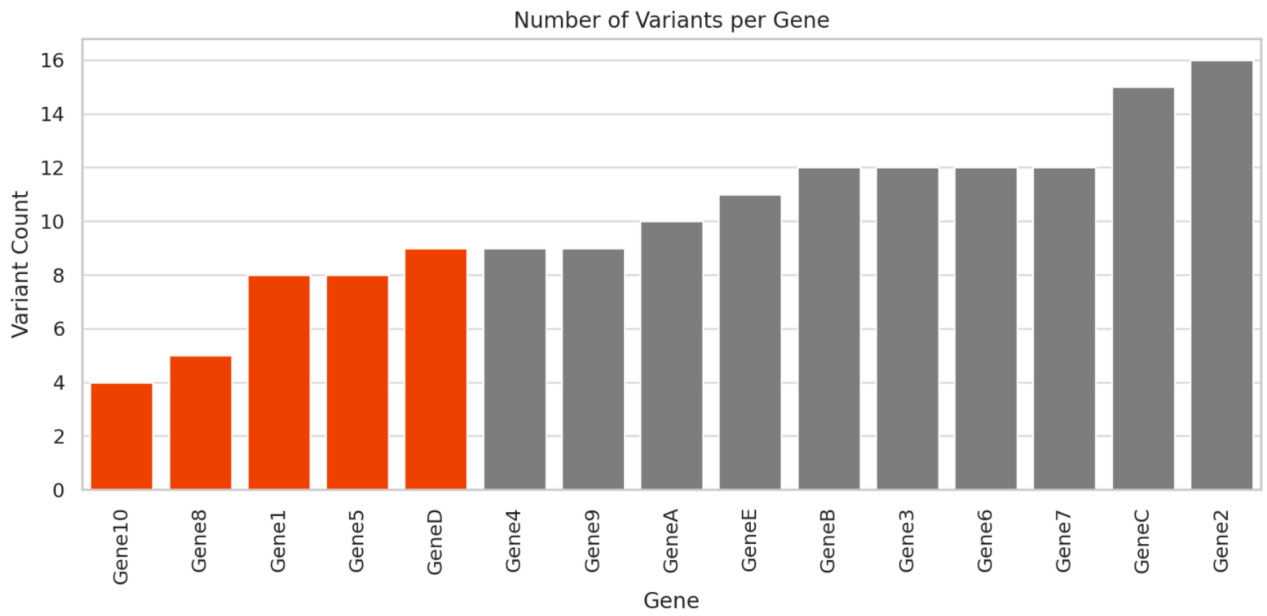
GeneC has modest signal in SKAT (moderate y-axis) but low effect size possibly a gene with weak or inconsistent burden.

GeneD lies near the bottom, no evidence of association in any test.



**QQ Plot Interpretation:**

Early upward deflection in the plot (above the diagonal) is driven by GeneA, GeneE, and to a lesser extent GeneC. The rest of the points follow the diagonal closely, suggesting a well-behaved null distribution.

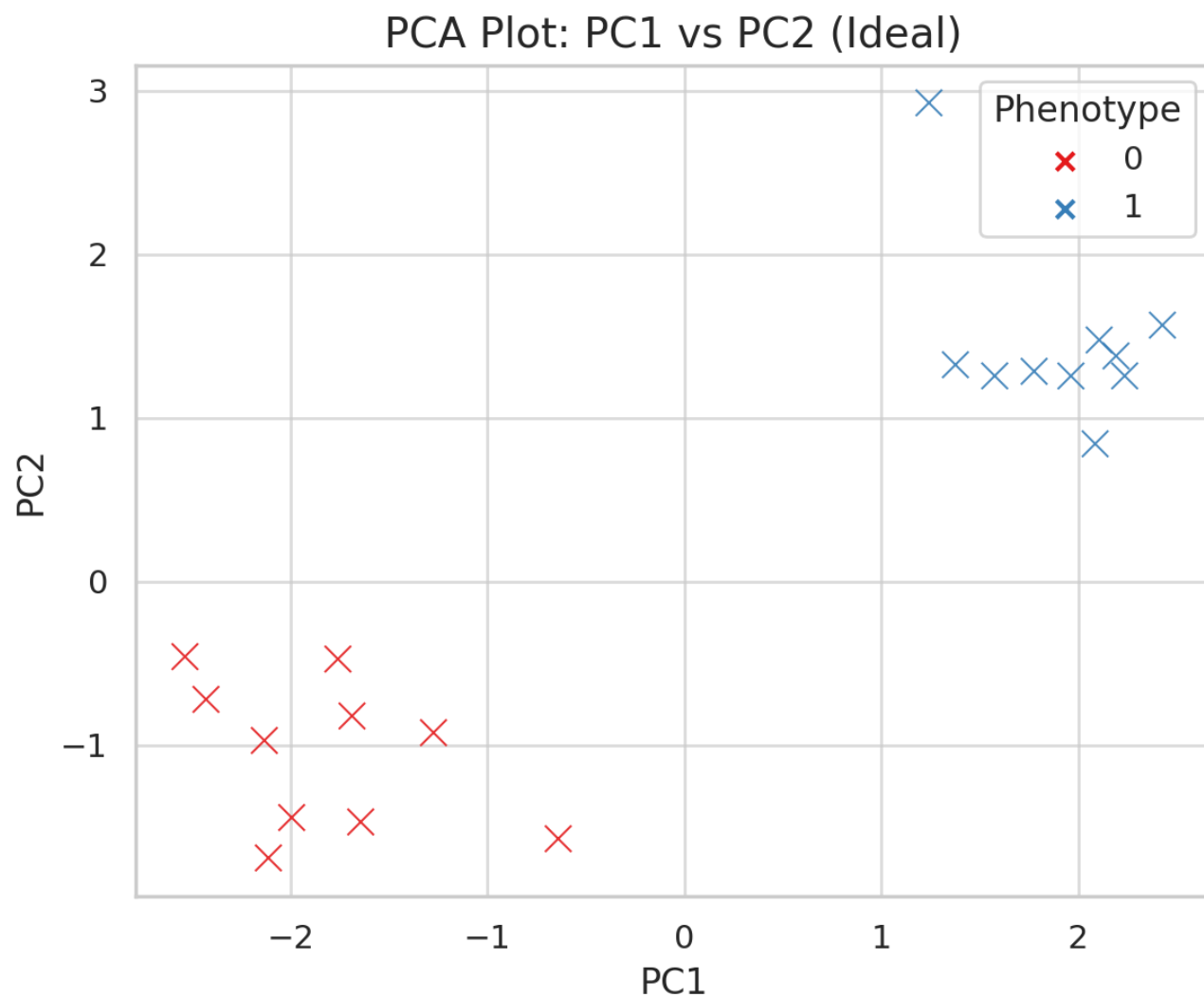


**Bar Plot Interpretation:**

GeneE has a high number of variants, likely increasing statistical power.

GeneA has fewer variants but still reaches significance, suggesting strong per-variant effects.

GeneD shows an average count but no association, underscoring the importance of burden effect, not just variant count.



PCA Plot Interpretation: Shows sample clustering by PC1 and PC2. Separation may indicate population structure or batch effects; overlap suggests minimal confounding.