

Gwas Result Result #29 — Analysis Report

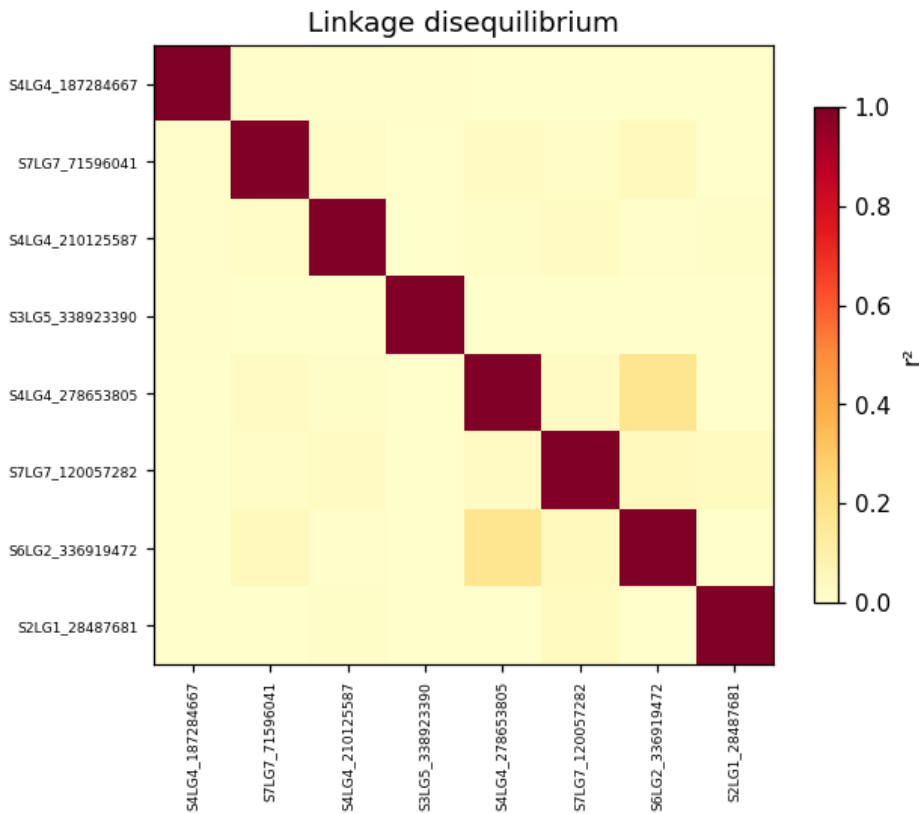
Generated 2026-09-21 02:39:37 · 1 run(s) · CAT-G Data Analyzer

1. gwas result (#29)

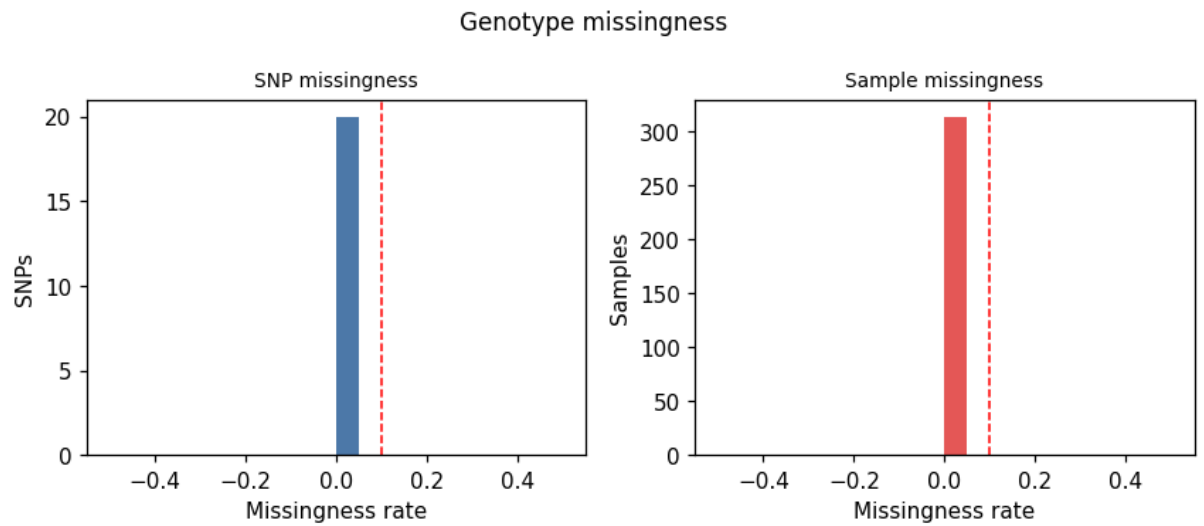
2026-09-21 02:18:47 · gwas_result · status: completed

GWAS tested 8 SNPs after QC (of 20 input); 0 passed significance.

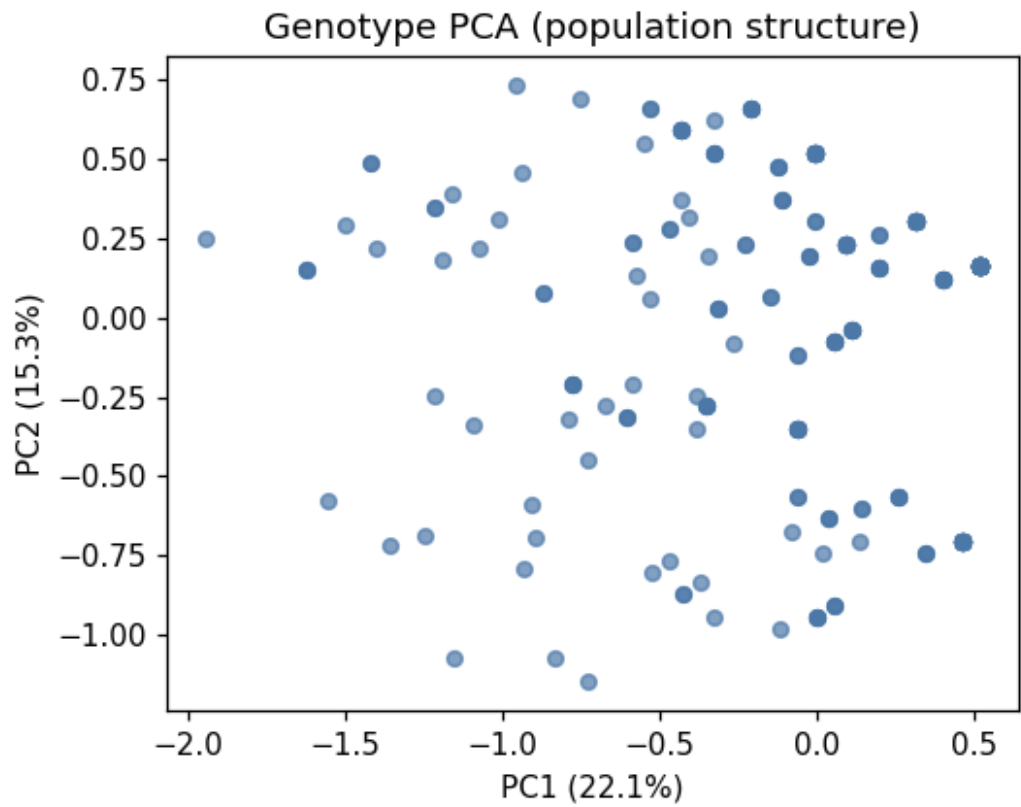
n_snps_input	20
n_snps_after_qc	8
maf_filtered	0
missingness_filtered	0
hwe_filtered	12
hwe_not_testable	0
ld_pruned	0



ld heatmap



missingness plot



genotype pca

Method & Provenance

method	GWAS — association analysis
engine	Python · scikit-learn/statsmodels 1.8.0
datasets	gallery — cat_g_gwas_real_data.csv
started	2026-09-21 02:18:47.650556
permanent link	https://cat-g-omxpert.wishartlab.com/results/by-token/bb45ab95d37f40eb83d4d8e3b198

Parameter	Value
target_column	Protein_Y19
encoding_model	additive
significance_threshold	0.00625
n_snps_input	20
n_snps_after_qc	8
n_samples	283
n_significant	0
lambda_gc	33.578415

Command history

```
# python
# app.services.gwas_qc_service - SNP QC + allele encoding

# python
from sklearn.linear_model import LogisticRegression

# python
for snp in snp_matrix.columns: # per-SNP association test

# python
    model = LogisticRegression(max_iter=1000).fit(X_snp, y)

# python
    p = association_pvalue(model)

# python
fdr = statsmodels.stats.multitest.multipletests(p_values, method='fdr_bh')
```