

Gwas Result Result #28 — Analysis Report

Generated 2026-09-21 02:39:33 · 1 run(s) · CAT-G Data Analyzer

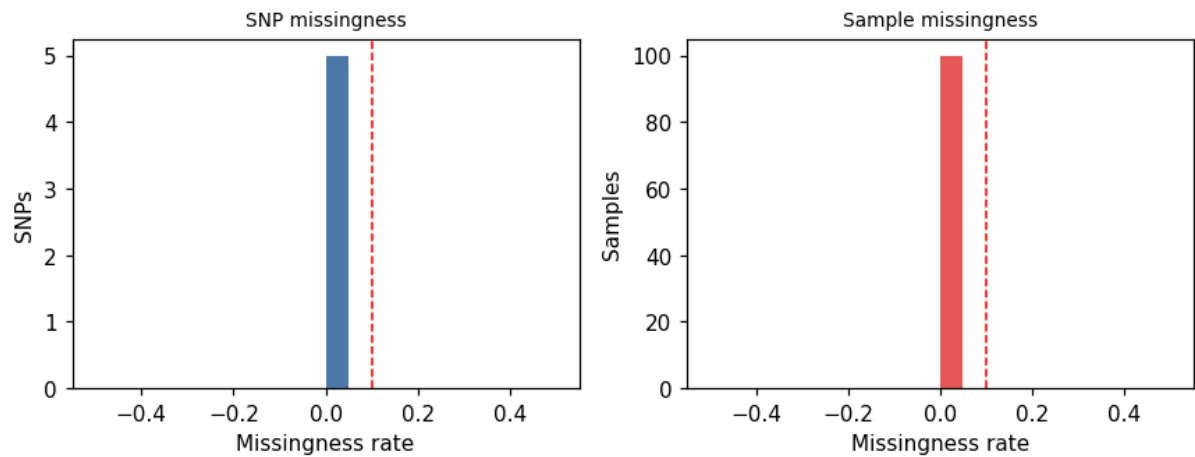
1. gwas result (#28)

2026-09-21 02:18:44 · gwas_result · status: completed

GWAS tested 1 SNPs after QC (of 7 input); 0 passed significance.

n_snps_input	7
n_snps_after_qc	1
maf_filtered	2
missingness_filtered	0
hwe_filtered	4
hwe_not_testable	0
ld_pruned	0

Genotype missingness



missingness plot

Method & Provenance

method	GWAS — association analysis
engine	Python · scikit-learn/statsmodels 1.8.0
datasets	gallery — example_gwas_protein.csv
started	2026-09-21 02:18:44.740736
permanent link	https://cat-g-omxpert.wishartlab.com/results/by-token/abdb9fb3c3284f0dbf813675034bb

Parameter	Value
target_column	Protein_Y19
encoding_model	additive
significance_threshold	0.05

n_snps_input	7
n_snps_after_qc	1
n_samples	95
n_significant	0
lambda_gc	0.032914

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')
```