

# EDGE-GWAS Quick Function Test (synthetic data)

2026-02-10 16:34

## Summary

All quick smoke tests passed.

## Functions exercised

all\_exports: OK  
calculate\_genomic\_inflation: OK  
get\_pc\_covariate\_list: OK  
format\_gwas\_output: OK  
create\_summary\_report: OK  
save\_results: OK  
load\_alpha\_values: OK  
EDGEAnalysis (continuous): OK  
EDGEAnalysis (binary): OK  
manhattan\_plot: OK  
qq\_plot: OK  
plot\_alpha\_distribution: OK  
check\_external\_tools: OK  
download\_test\_files: OK

Quick smoke tests (synthetic/small data)...

```
[OK] imports
[OK] calculate_genomic_inflation
[OK] get_pc_covariate_list
[OK] format_gwas_output
[OK] create_summary_report
[OK] save_results
[OK] load_alpha_values
[OK] EDGEAnalysis (continuous, synthetic)
[OK] EDGEAnalysis (binary, synthetic)
```

Manhattan plot saved to /Users/nicen/edge/edge-gwas/tests/output/quick\_manhattan.png

QQ plot saved to /Users/nicen/edge/edge-gwas/tests/output/quick\_qq.png

Genomic inflation factor ( $\lambda$ ): 2.261

Alpha distribution plot saved to /Users/nicen/edge/edge-gwas/tests/output/quick\_alpha\_dist.png

Total alpha values: 5

Alpha statistics:

Mean: -0.422

Median: 0.040

Std: 2.355

Min: -3.987

Max: 2.539

```
[OK] manhattan_plot, qq_plot, plot_alpha_distribution
```

✓ PLINK2: PLINK v2.0.0-a.7 64-bit (5 Dec 2025)

✓ GCTA: \*\*\*\*\*

✓ R: R version 4.3.3 (2024-02-29) -- "Angel Food Cake"

✓ R package GENESIS: Installed

✓ R package SNPRelate: Installed

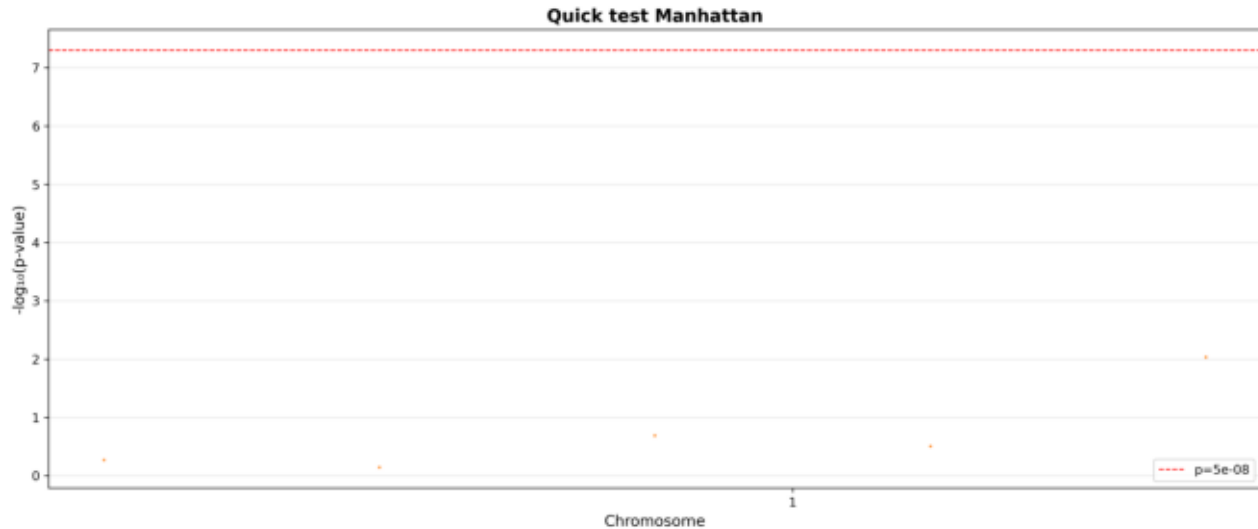
✓ R package gdsfmt: Installed

```
[OK] check_external_tools
```

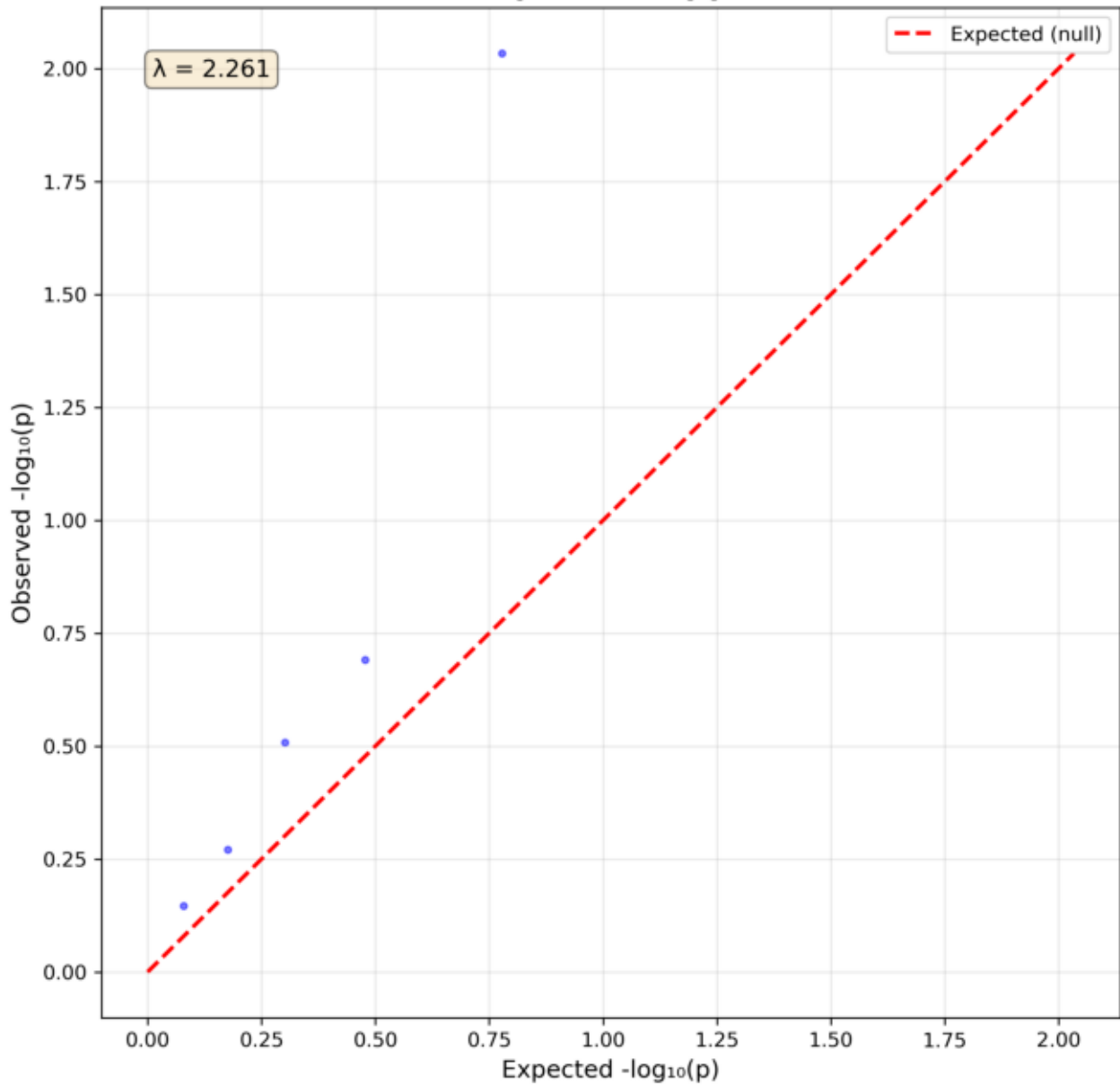
```
[OK] download_test_files
```

All quick smoke tests passed.

quick\_manhattan.png



## Quick test QQ



**Distribution of EDGE Alpha Values**