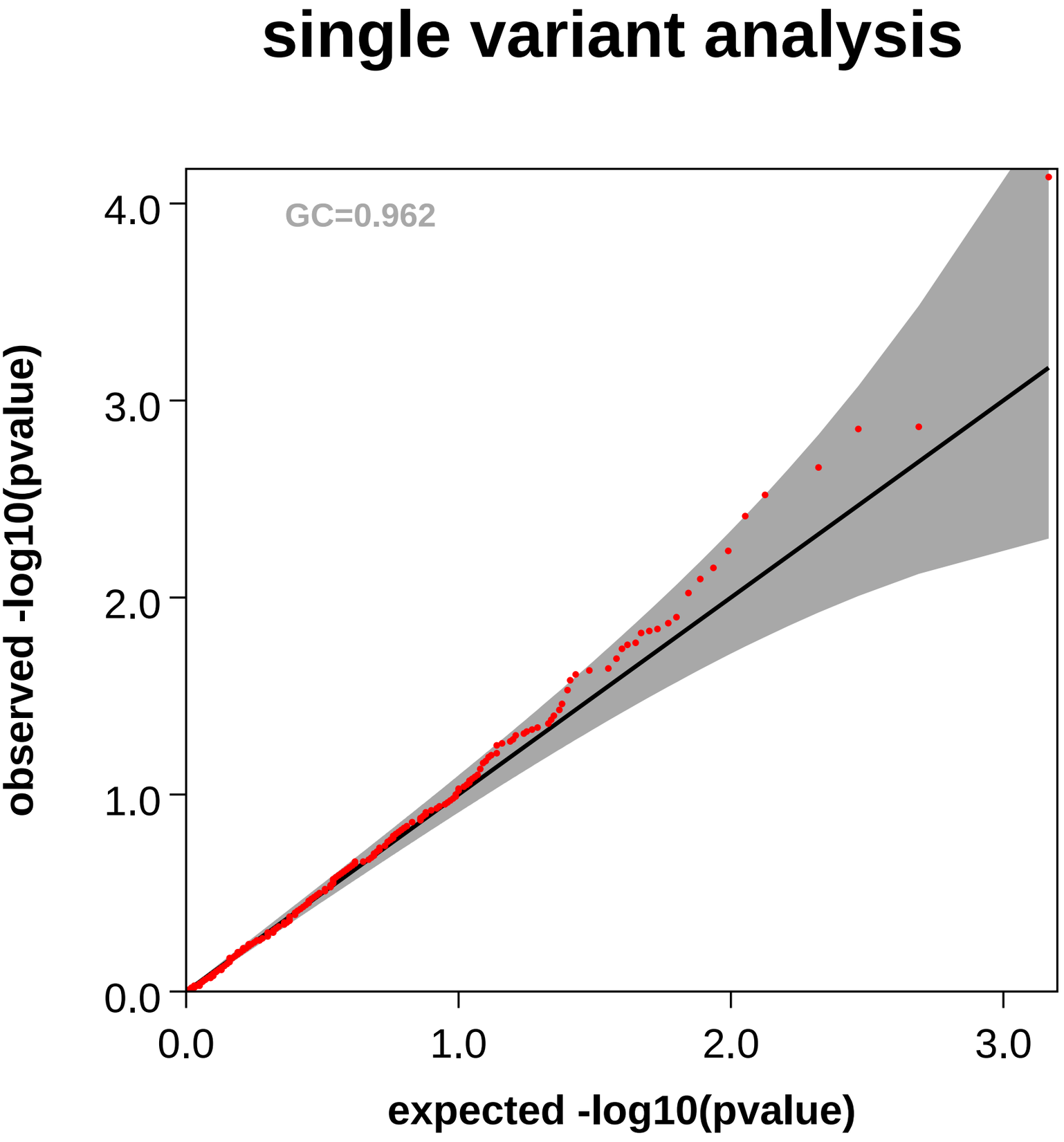
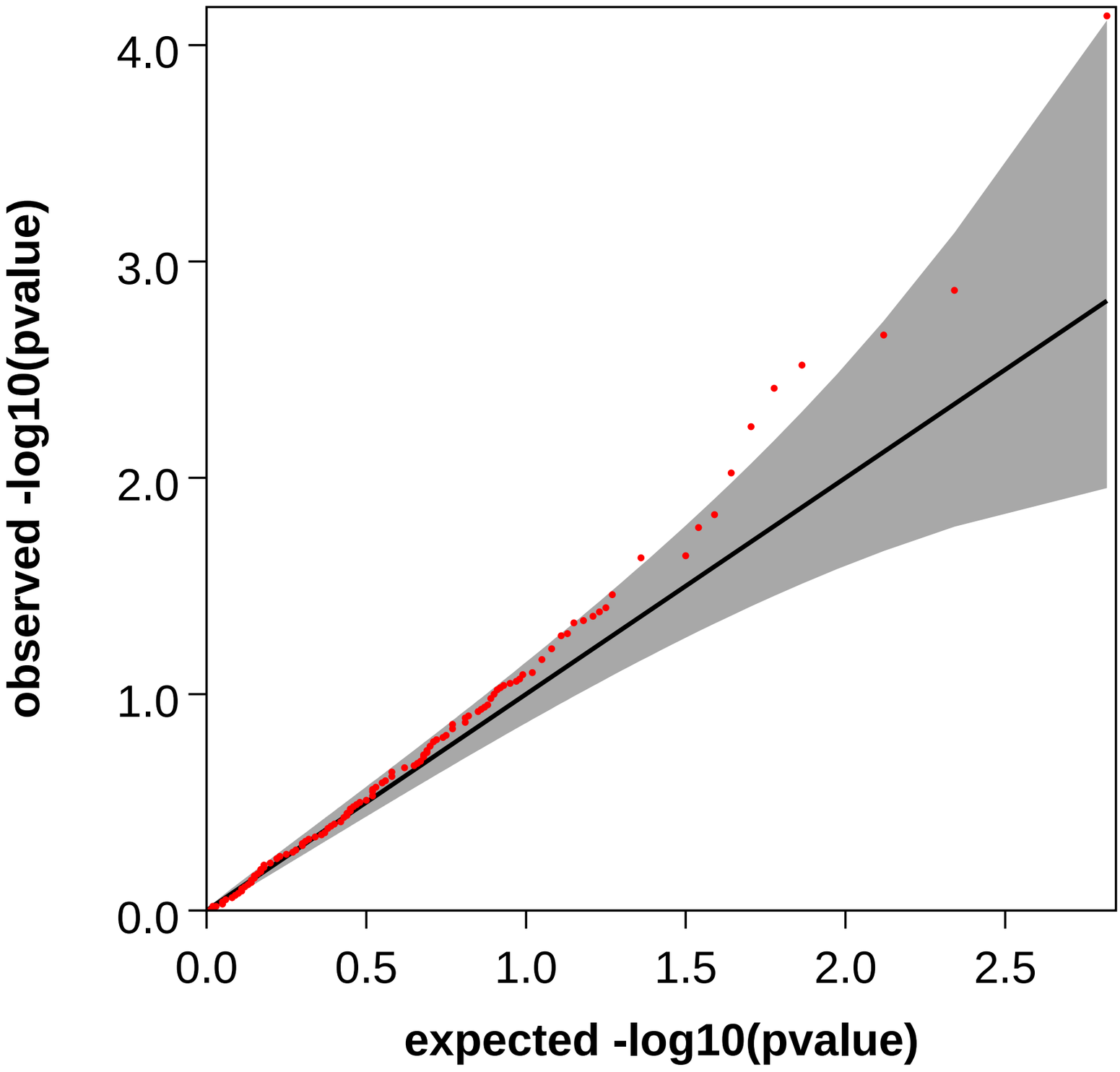
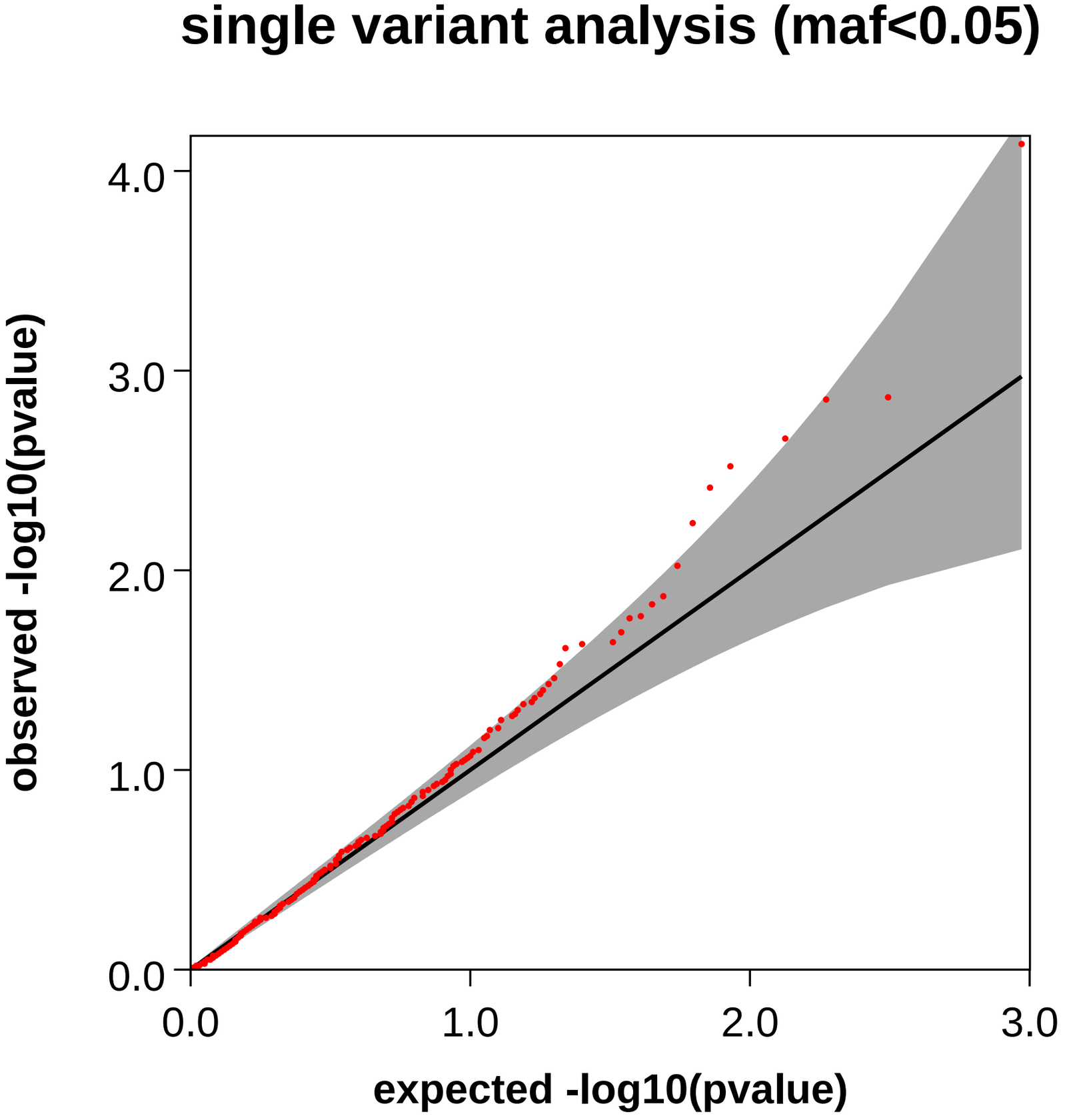
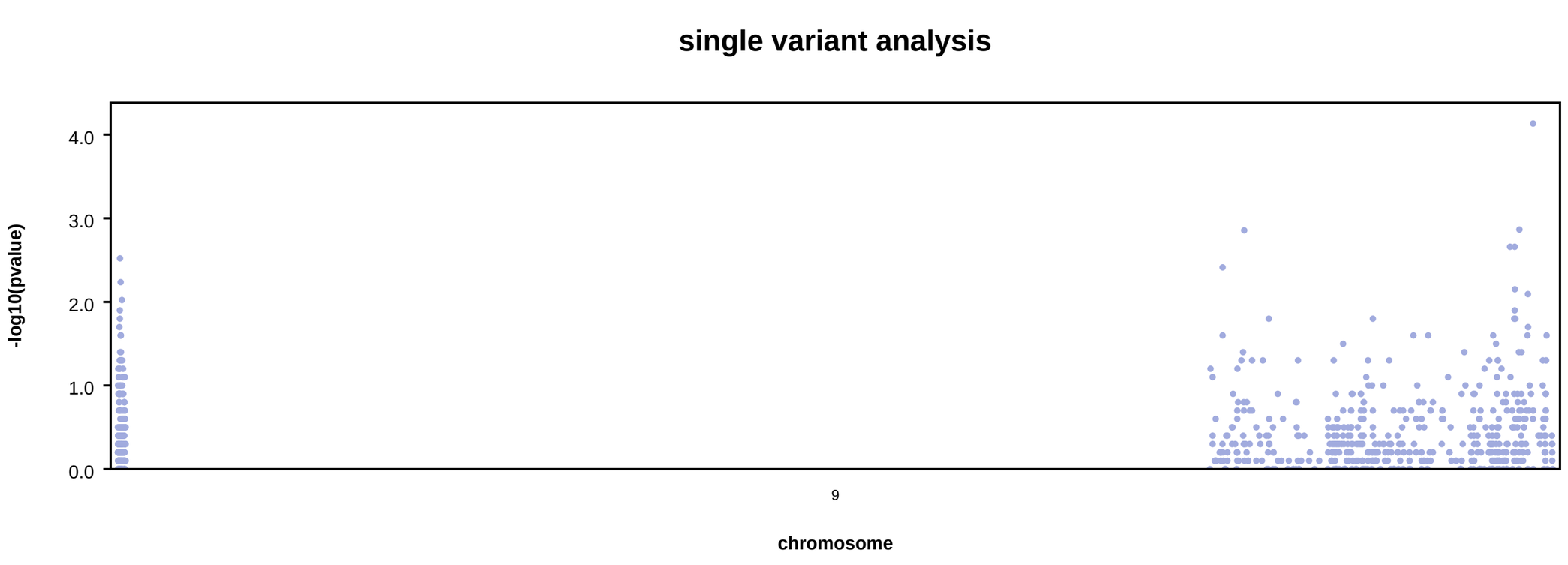
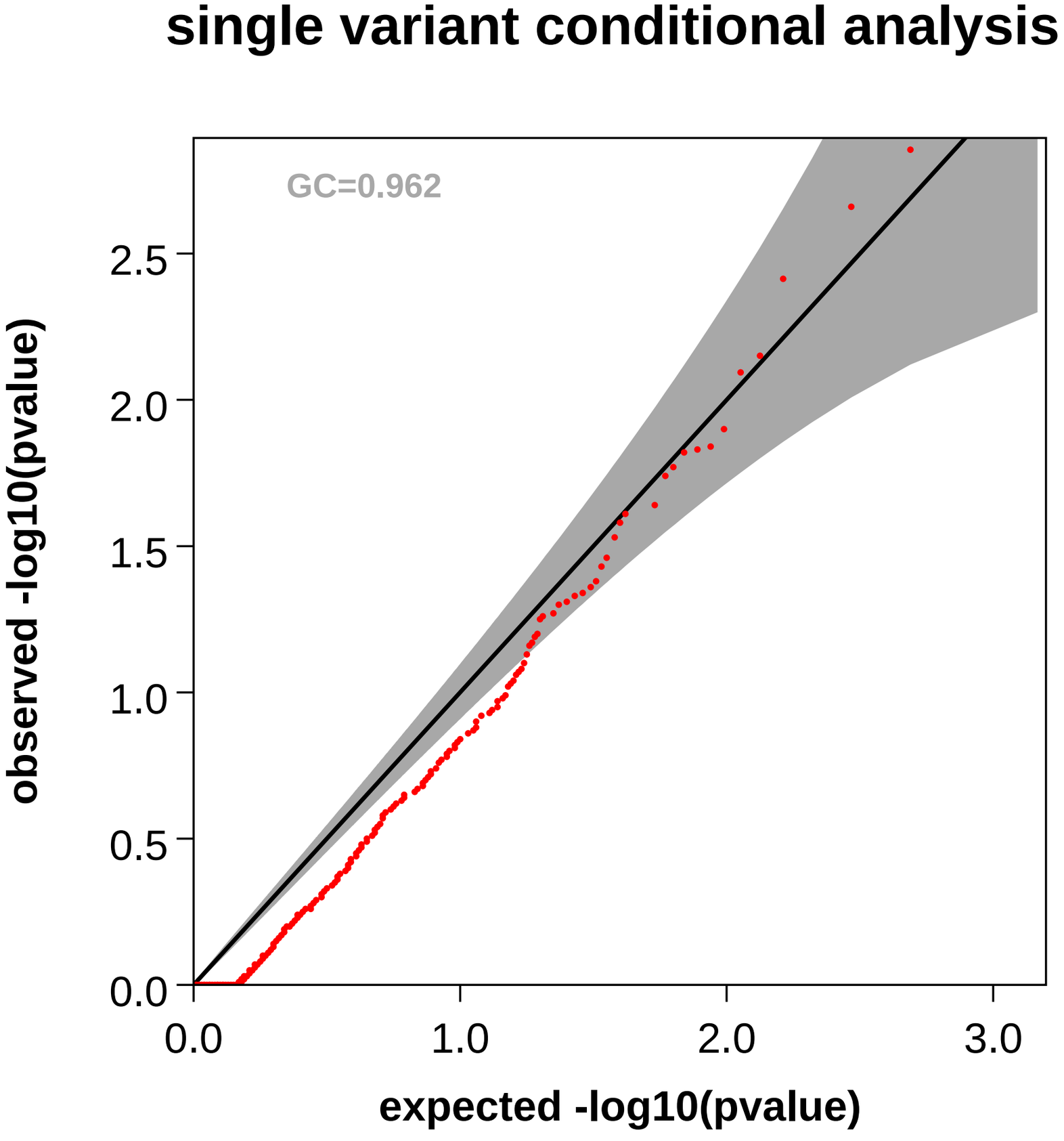
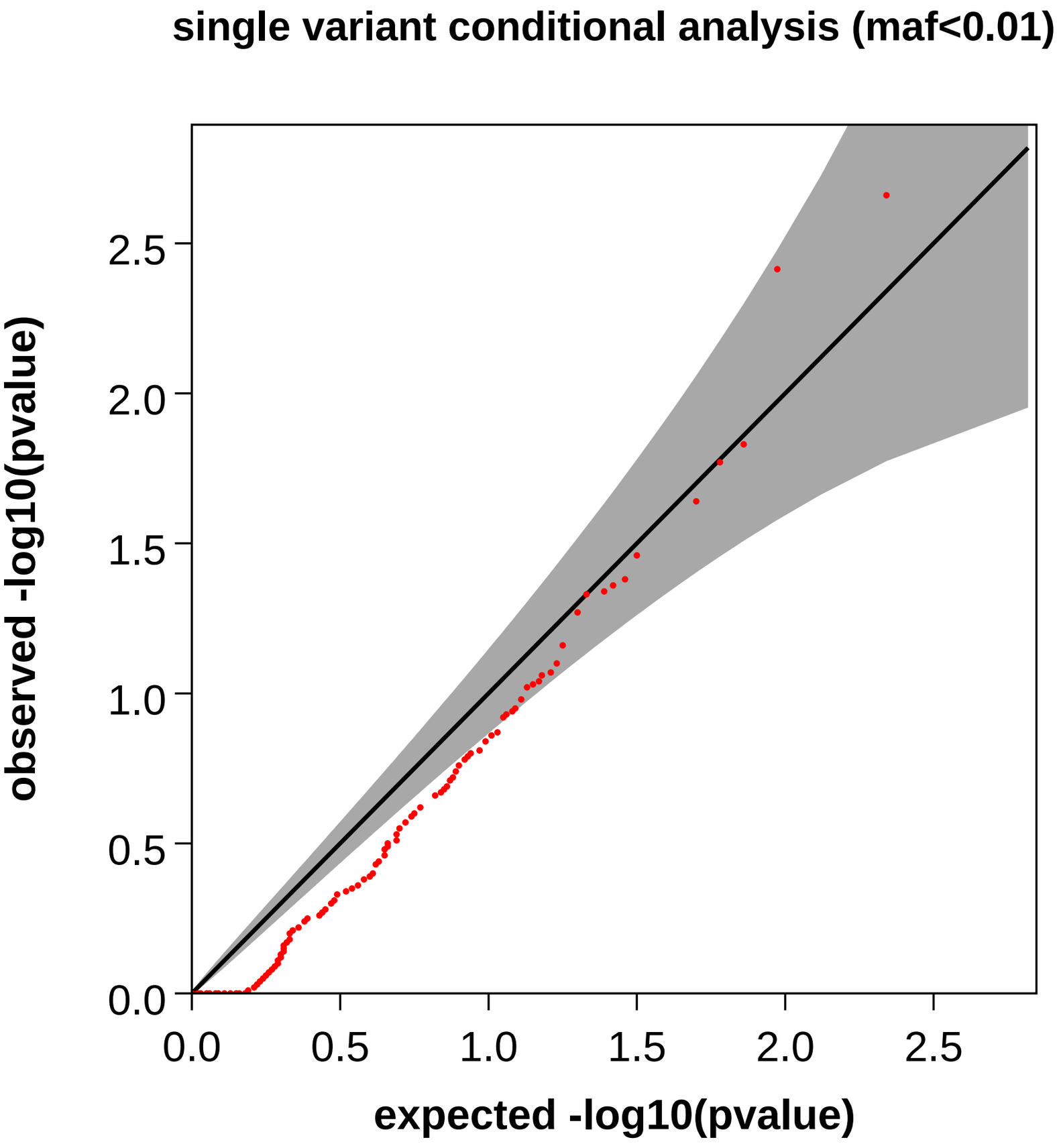

single variant analysis
GC=0.962
observed -log10(pvalue)
expected -log10(pvalue)
0.0
1.0
2.0
3.0
4.0

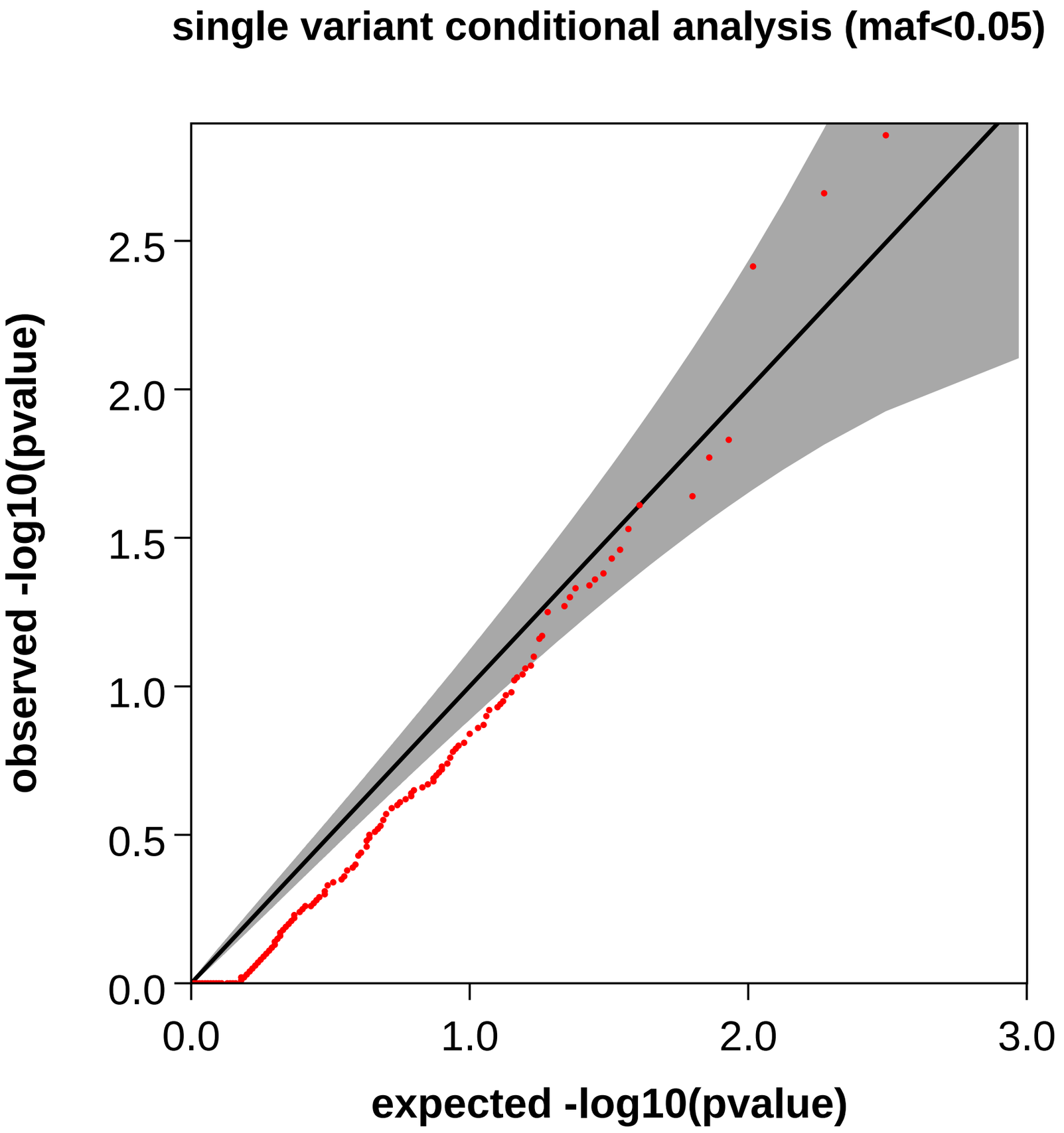

single variant analysis (maf<0.01)
observed -log10(pvalue)
expected -log10(pvalue)
0.0
1.0
2.0
3.0
4.0
0.0
0.5
1.0
1.5
2.0
2.5

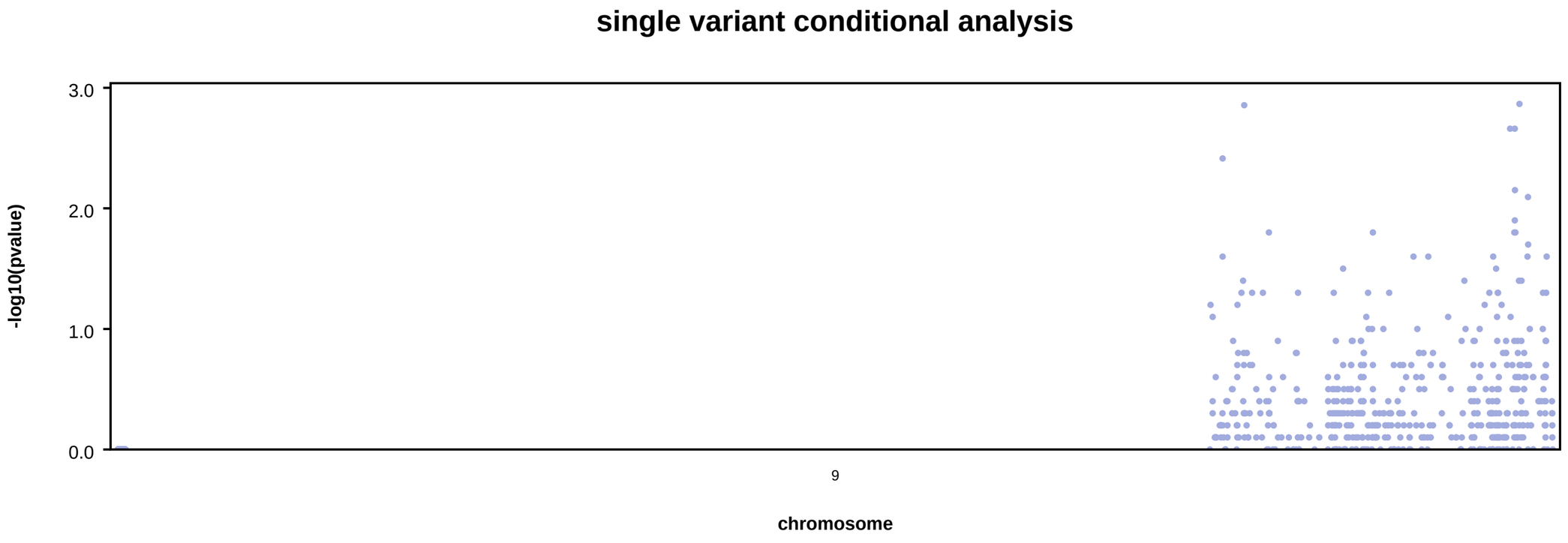

single variant analysis (maf<0.05)
observed -log10(pvalue)
expected -log10(pvalue)
0.0
1.0
2.0
3.0
4.0
0.0
1.0
2.0
3.0


single variant analysis
-log10(pvalue)
4.0
3.0
2.0
1.0
0.0
9
chromosome


single variant conditional analysis
GC=0.962
observed -log10(pvalue)
expected -log10(pvalue)
0.0
0.5
1.0
1.5
2.0
2.5
0.0
1.0
2.0
3.0


single variant conditional analysis (maf<0.01)
observed -log10(pvalue)
expected -log10(pvalue)
0.0
0.5
1.0
1.5
2.0
2.5


single variant conditional analysis (maf<0.05)
observed -log10(pvalue)
expected -log10(pvalue)
0.0
0.5
1.0
1.5
2.0
2.5
0.0
1.0
2.0
3.0


single variant conditional analysis
-log10(pvalue)
3.0
2.0
1.0
0.0
9
chromosome