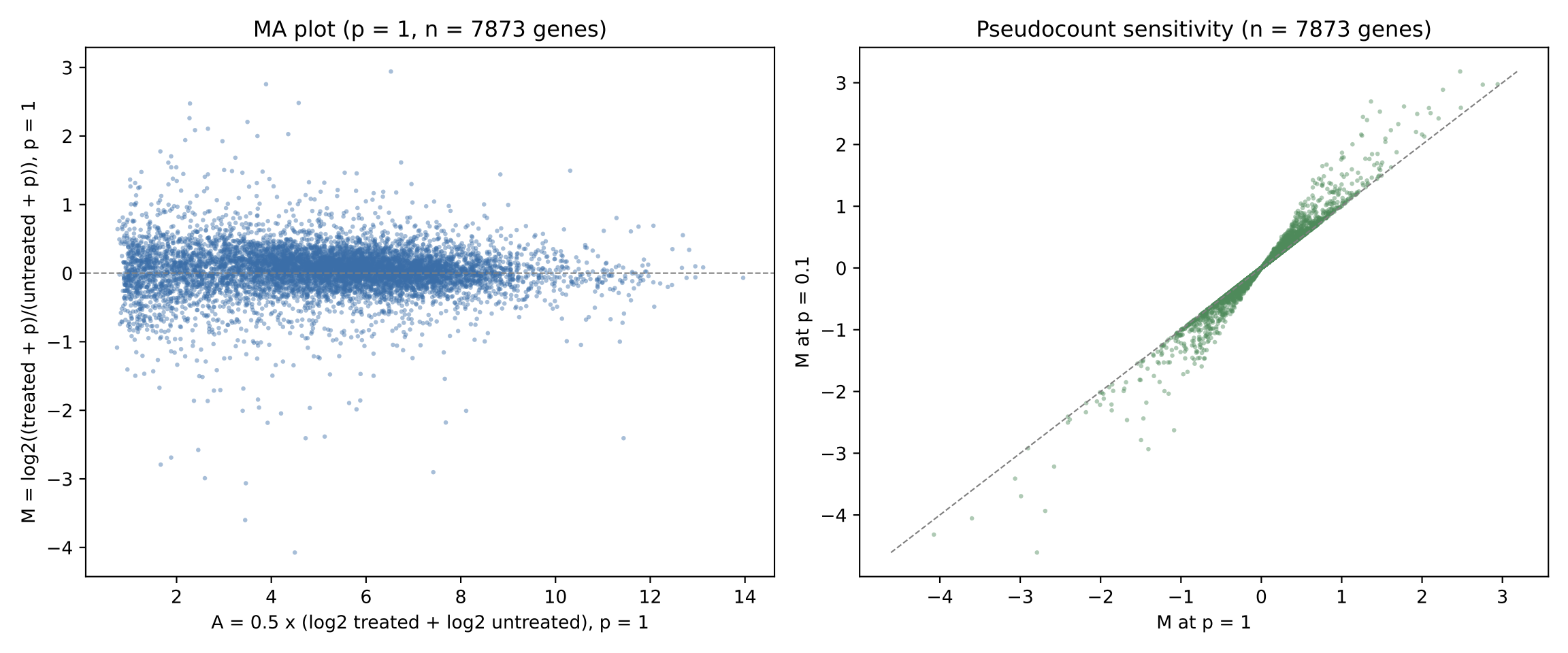

MA plot (p = 1, n = 7873 genes)
M = log2((treated + p)/(untreated + p)), p = 1
A = 0.5 x (log2 treated + log2 untreated), p = 1
Pseudocount sensitivity (n = 7873 genes)
M at p = 0.1
M at p = 1