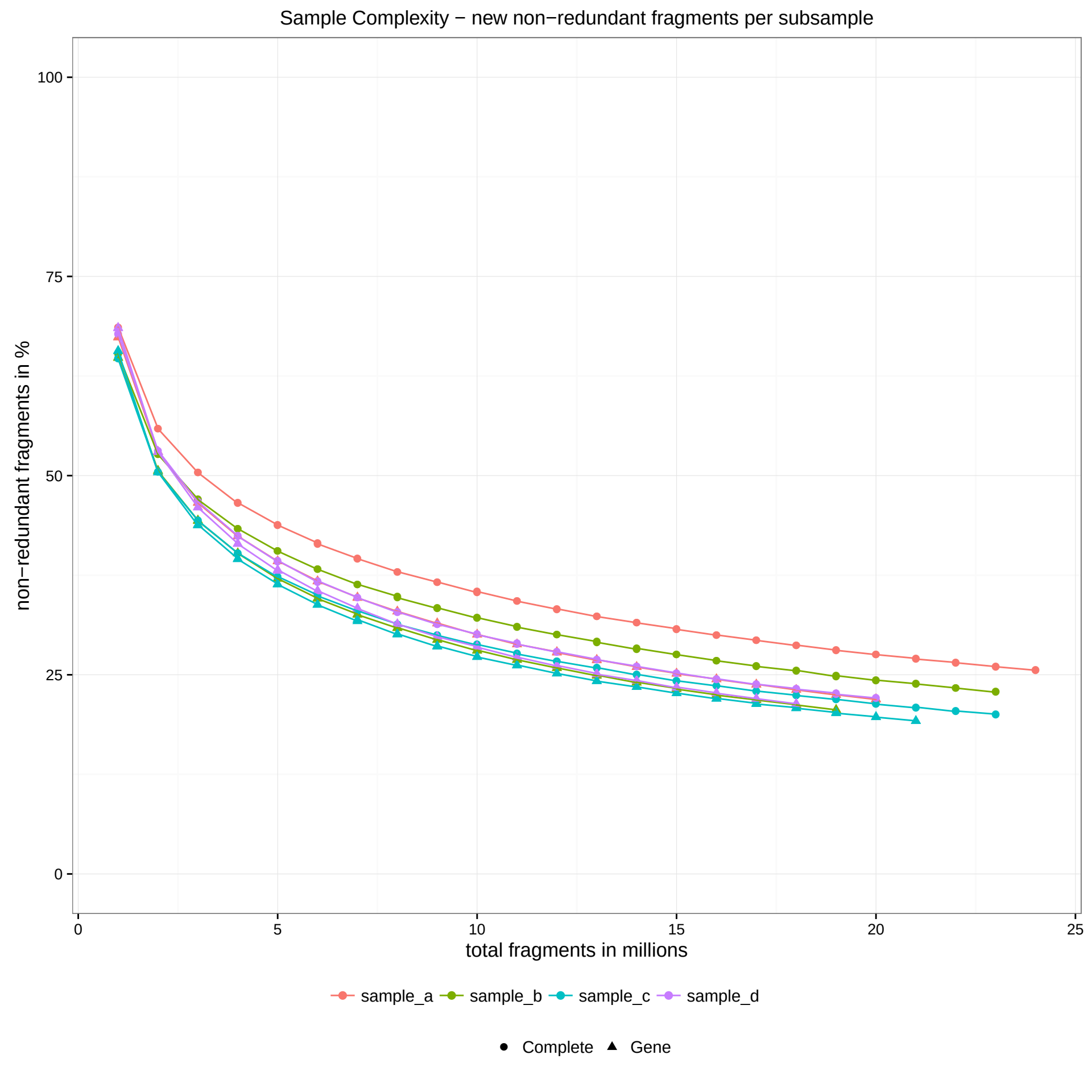

Sample Complexity − new non−redundant fragments per subsample
non−redundant fragments in %
100
75
50
25
0
0
5
10
15
20
25
total fragments in millions
sample_a
sample_b
sample_c
sample_d
Complete
Gene