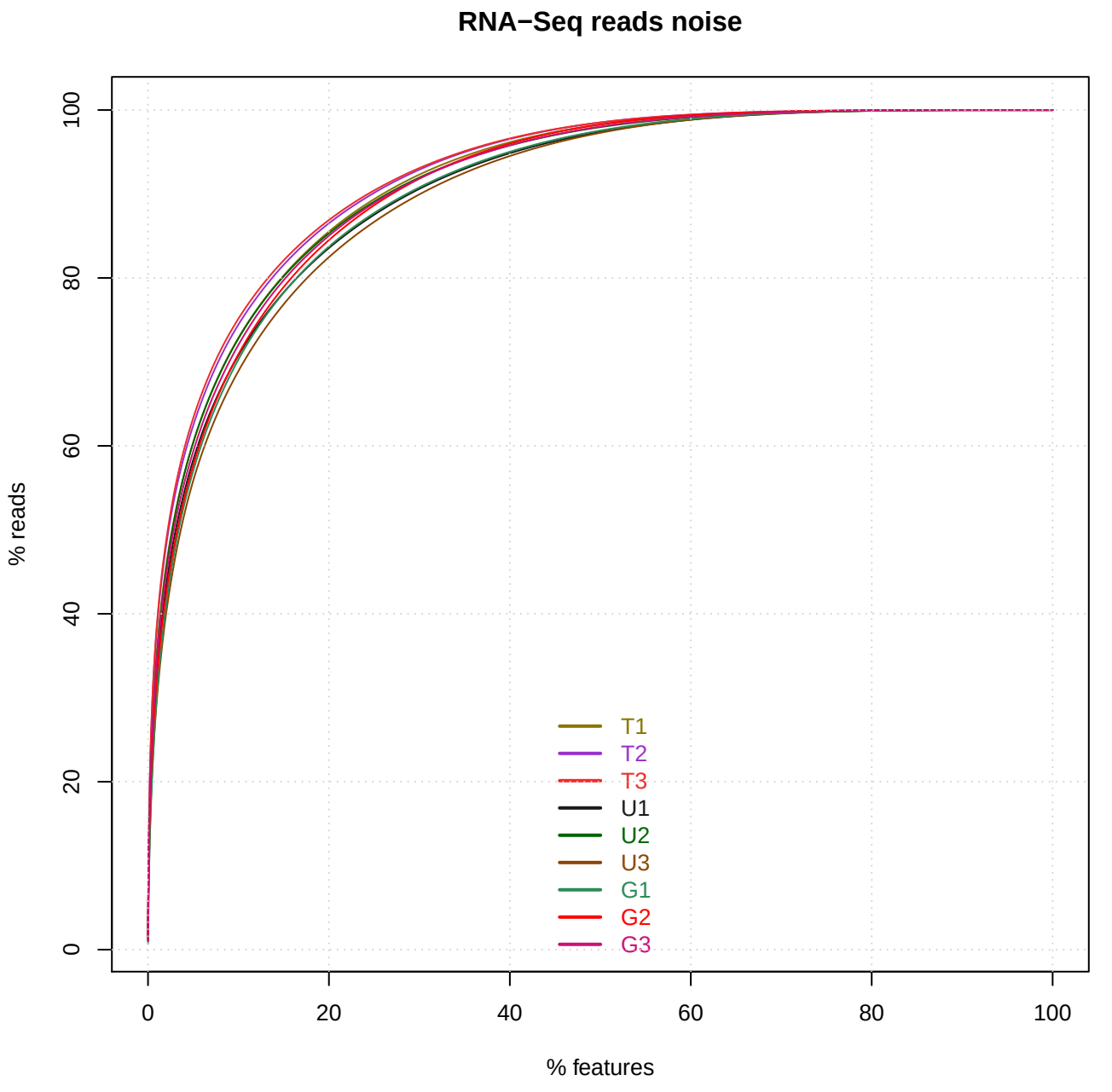
RNA−Seq reads noise
% reads
% features
0
20
40
60
80
100
T1
T2
T3
U1
U2
U3
G1
G2
G3