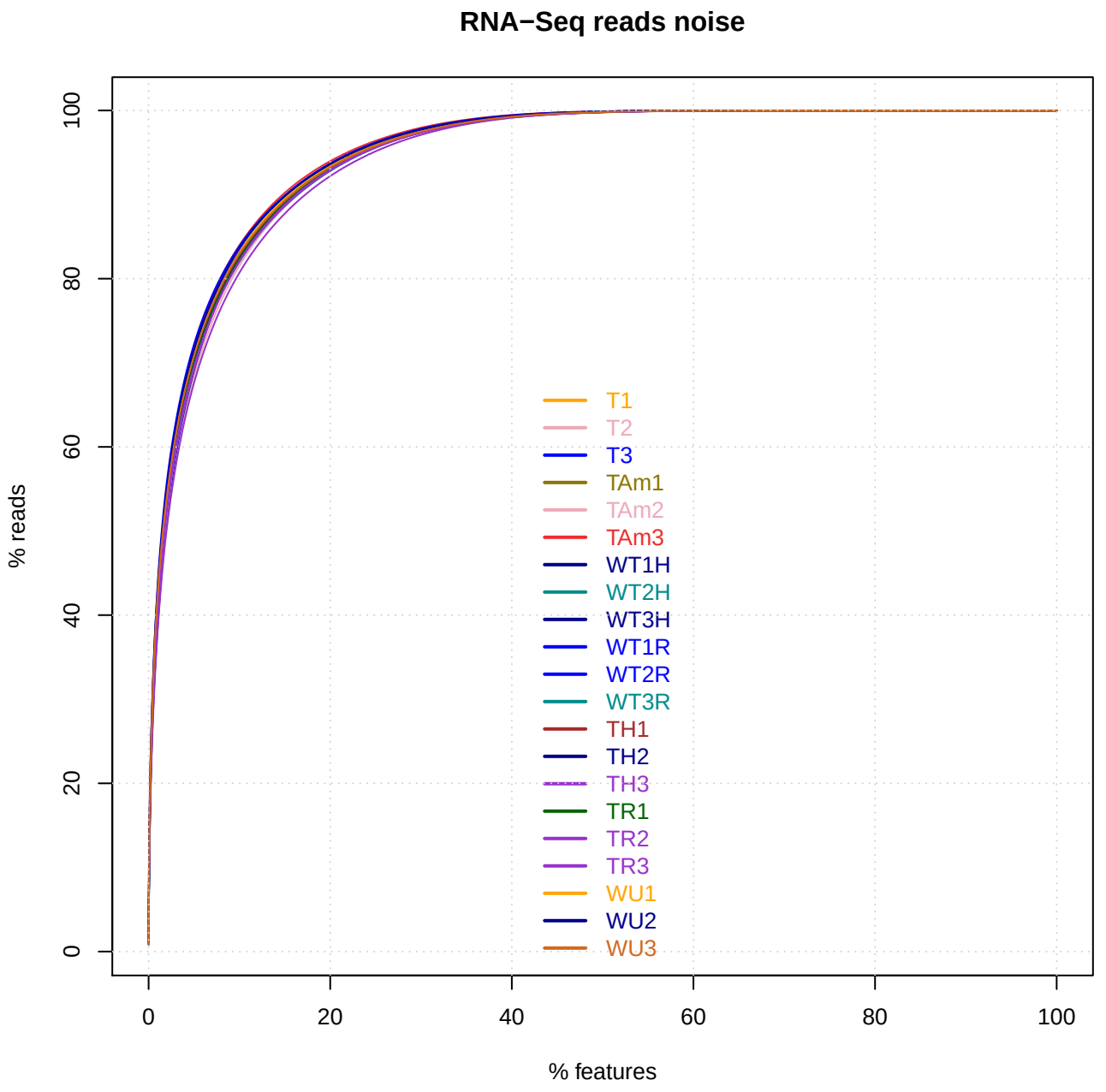
RNA−Seq reads noise
% reads
% features
0
20
40
60
80
100
T1
T2
T3
TAm1
TAm2
TAm3
WT1H
WT2H
WT3H
WT1R
WT2R
WT3R
TH1
TH2
TH3
TR1
TR2
TR3
WU1
WU2
WU3