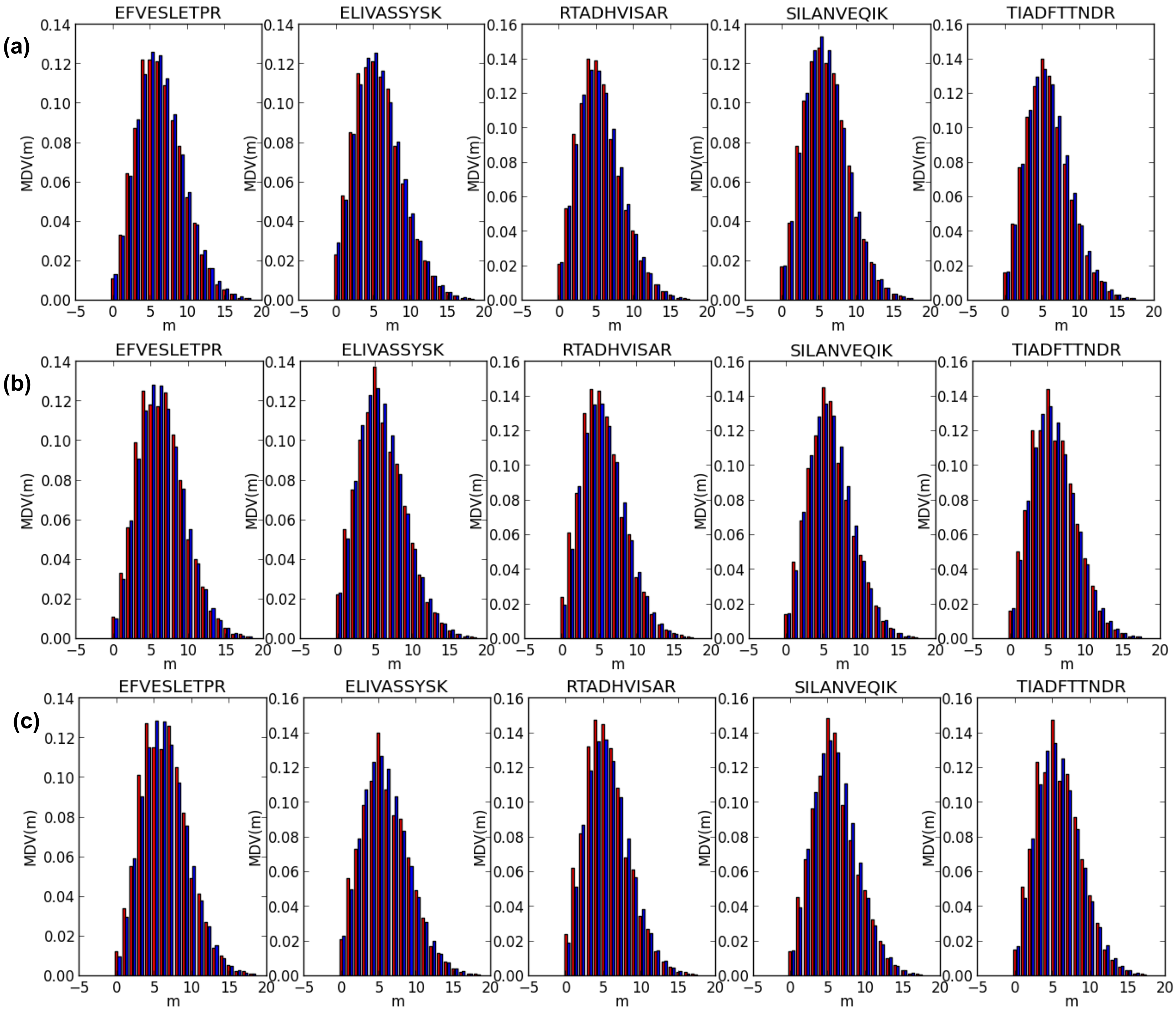
(a)
(b)
(c)
EFVESLETPR
ELIVASSYSK
RTADHVISAR
SILANVEQIK
TIADFTTNDR
MDV(m)
m
0.00
0.02
0.04
0.06
0.08
0.10
0.12
0.14
0.16
−5
0
5
10
15
20

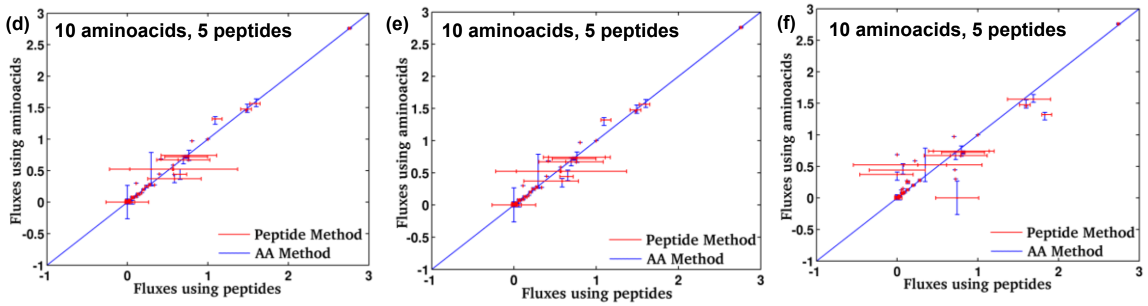

Figure S5. Peptide labeling data fit for the *E. coli* rf05 strain for 5 peptides and 10 amino acids. We have performed the same analysis as for figure S4 with following error rates (a) 0.05, (b) 0.08 and (c) 0.10, but using 5 peptides instead of 20. As can be observed the introduction noise has a much larger effect for this case than for the 20 peptides case.