

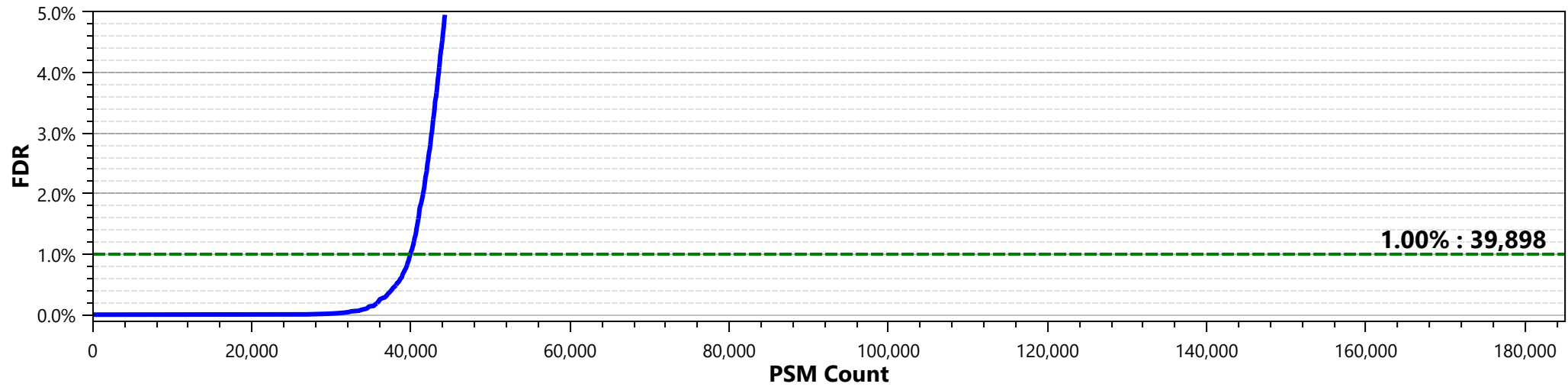
Property	Value
Peptide Level:	
spectra number	39,654
scans number	36,912
peptides number	19,176
sequences number	16,161
proteins number	23,200
protein groups number	4,363
decoy spectra number	244
decoy peptides number	191
decoy proteins number	5,573
decoy protein groups number	43
Cleavage:	
Specific	93.03% (17,840/19,176)
C-term specific	4.84% (928/19,176)
N-term specific	2.11% (405/19,176)
Non specific	0.02% (3/19,176)
Modifications:	
TMT6plex[AnyN-term]	87.09% (16,701/19,176)
TMT6plex[K]	40.48% (7,762/19,176)
Oxidation[M]	13.13% (2,517/19,176)
Deamidated[N]	5.77% (1,107/19,176)
Carbamyl[AnyN-term]	5.77% (1,106/19,176)
Carbamidomethyl[C]	3.36% (644/19,176)
Succinyl[AnyN-term]	1.20% (231/19,176)
Gln->pyro-Glu[AnyN-termQ]	0.77% (147/19,176)
Acetyl[ProteinN-term]	0.65% (124/19,176)
Iodoacetanilide[K]	0.13% (24/19,176)
Missed Cleavage:	
number=0	79.88% (15,317/19,176)
number=1	18.26% (3,502/19,176)
number=2	1.37% (262/19,176)
number=3	0.28% (54/19,176)
number=4	0.13% (25/19,176)
number=5	0.05% (10/19,176)
number=6	0.03% (5/19,176)
number=10	0.01% (1/19,176)
Mixed Spectra:	
number=1	92.68% (34,209/36,912)
number=2	7.22% (2,664/36,912)
number=3	0.11% (39/36,912)
Charge:	
charge=2	72.66% (13,934/19,176)
charge=3	23.00% (4,411/19,176)
charge=4	3.81% (730/19,176)
charge=5	0.48% (92/19,176)
charge=6	0.05% (9/19,176)
MassError:	
Precursor mass error: (mean)	0.59ppm
Precursor mass error: (std)	±1.53ppm
ID Rate:	
GMHJYZ_DeqMSvalidation_300ug_TMT10_IPG3-10_fr07	36.26% (12,500/34,474)
GMHJYZ_DeqMSvalidation_300ug_TMT10_IPG3-10_fr08	35.01% (12,000/34,275)
GMHJYZ_DeqMSvalidation_300ug_TMT10_IPG3-10_fr09	36.50% (12,412/34,005)
Overall	35.92% (36,912/102,754)



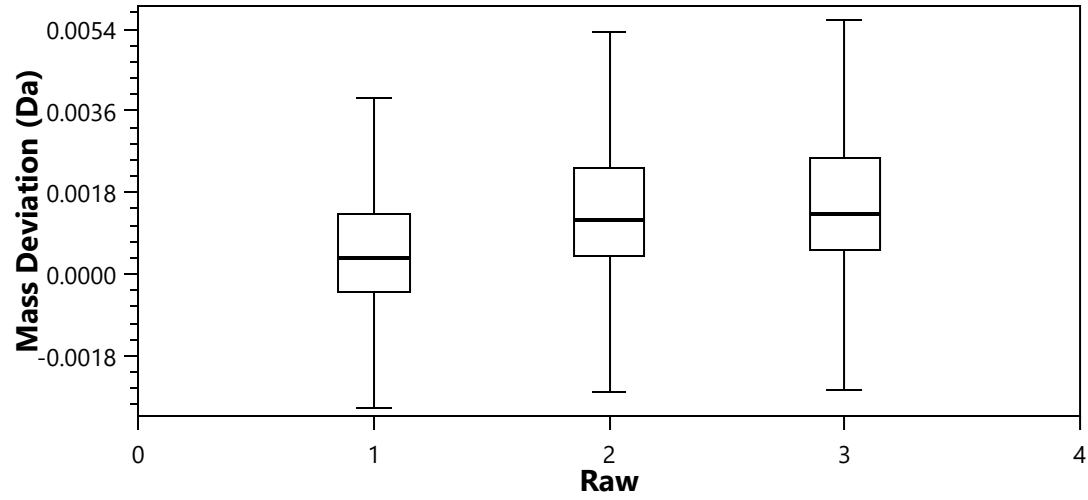
Parameter

Property	Value	
Param:		
thread number	2	
ms tolerance	10ppm	
msms tolerance	0.02Da	
open search	True	
input format	raw	
fix modification	Carbamidomethyl[C];TMT6plex[AnyN-term];TMT6plex[K];	
variable modification	Oxidation[M];	
enzyme	Trypsin_P KR P C	
max missing cleavage number	1	
co elute	True	
ll info label	1 none;	
File:		
aa path 1	F:\Yanbo\workshop_pFindTask1\result\1.aa	
modification path	F:\Yanbo\pFind3\bin\modification.ini	
fasta path	F:\Yanbo\Human_Ecoli_target.fasta	
contaminant path	NULL	
task path	F:\Yanbo\workshop_pFindTask1\result\workshop_pFindTask1	
Raws:		
raw path 1	F:\Yanbo\GMHJYZ_DeqMSvalidation_300ug_TMT10_IPG3-10_fr07.raw	
raw path 2	F:\Yanbo\GMHJYZ_DeqMSvalidation_300ug_TMT10_IPG3-10_fr08.raw	
raw path 3	F:\Yanbo\GMHJYZ_DeqMSvalidation_300ug_TMT10_IPG3-10_fr09.raw	

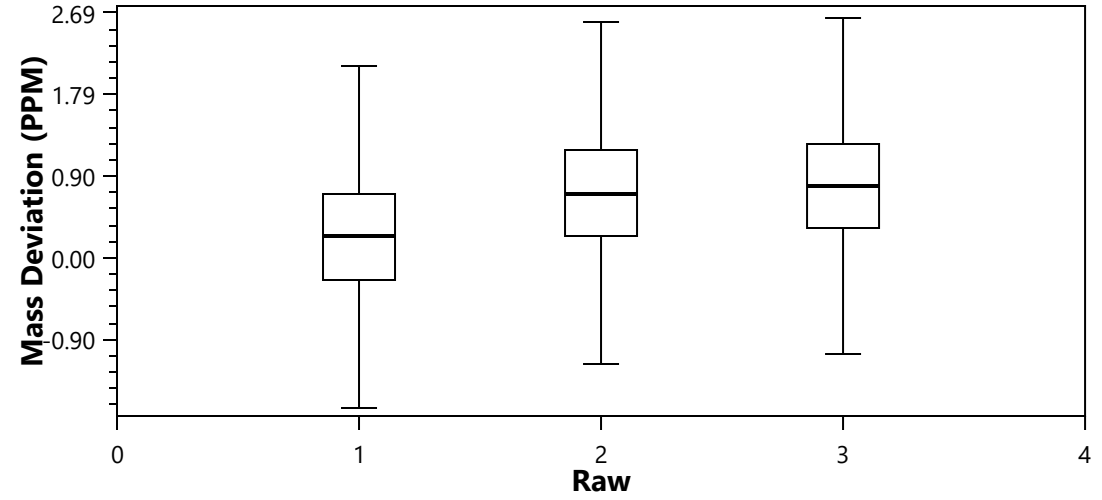
FDR Curve



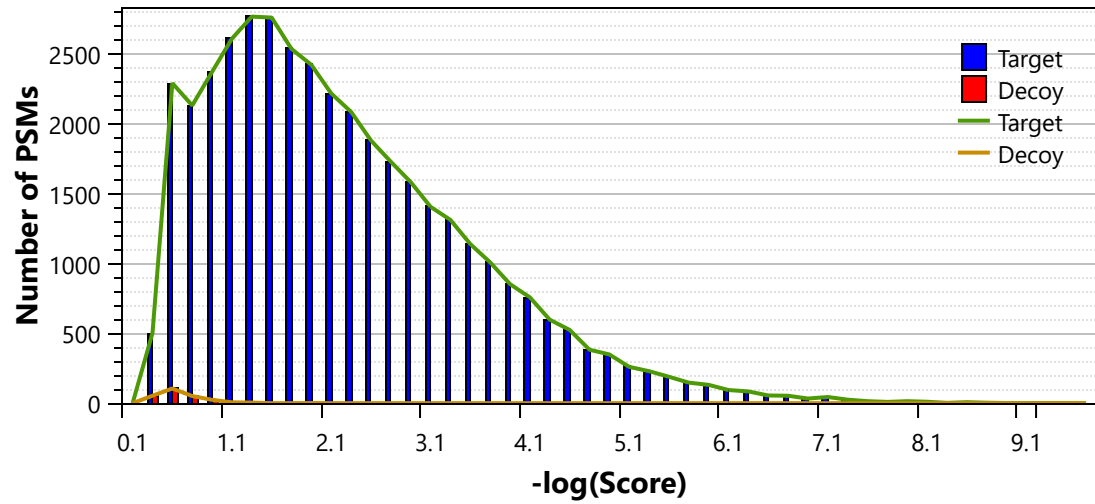
Mass Deviation



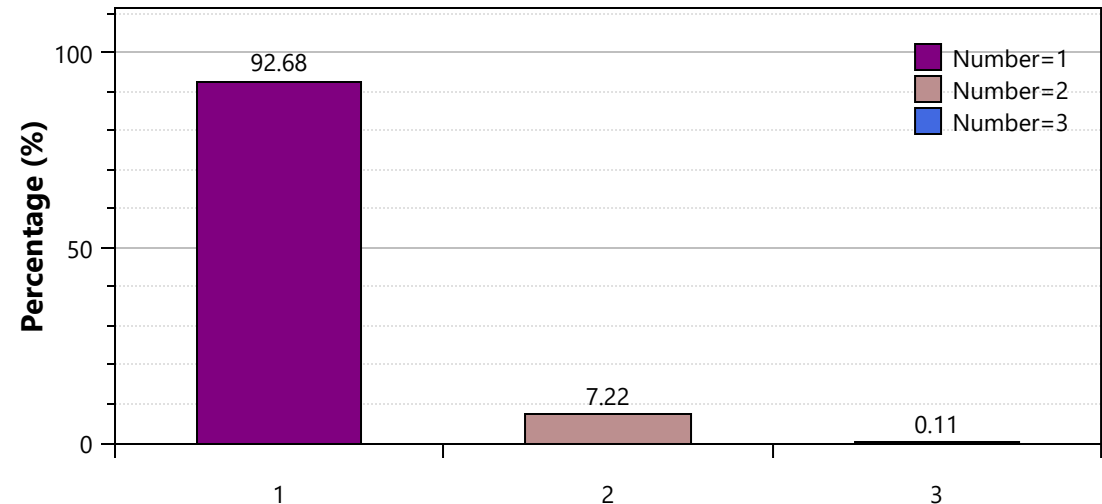
Mass Deviation



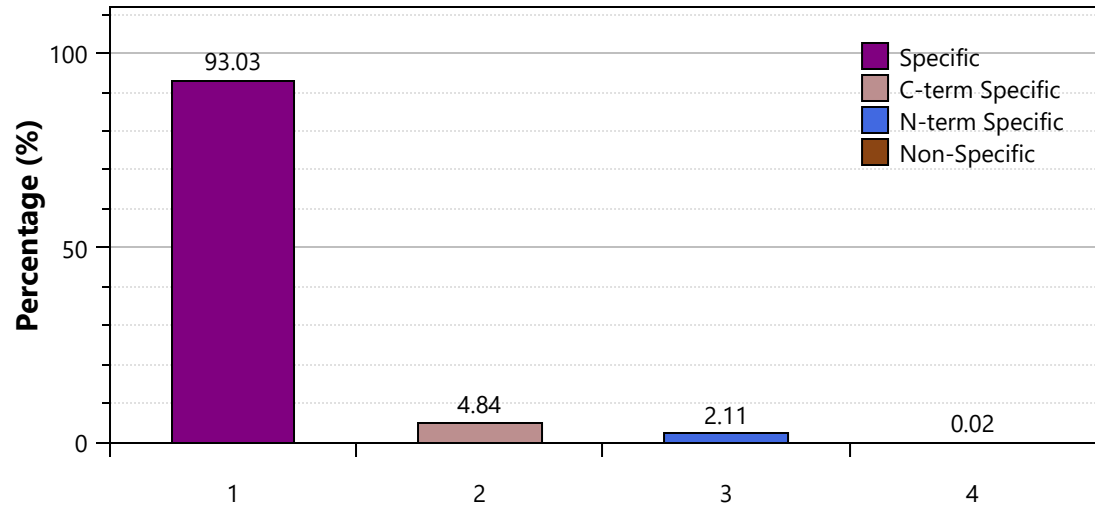
Score Distribution



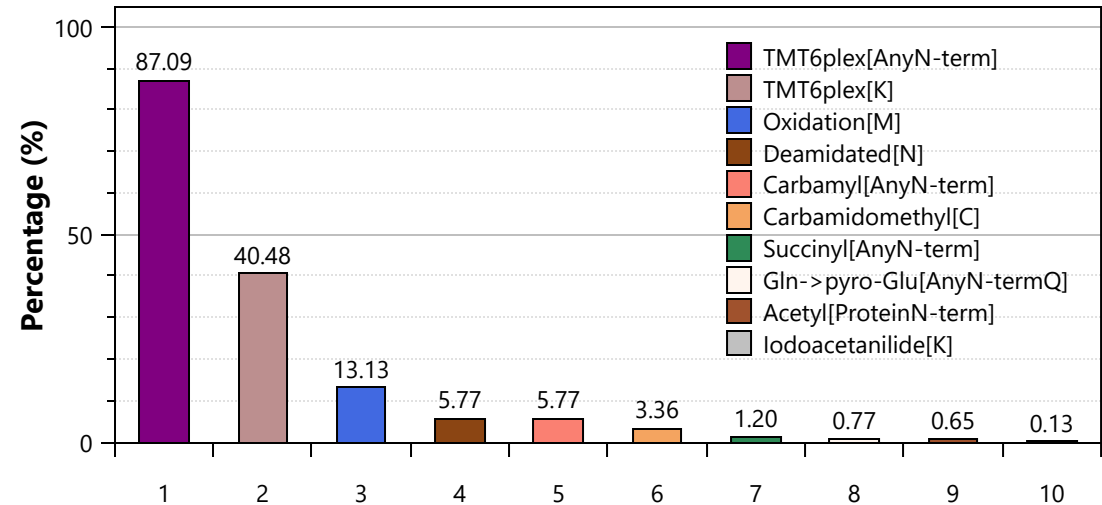
Mixture Spectra Percentage (%)



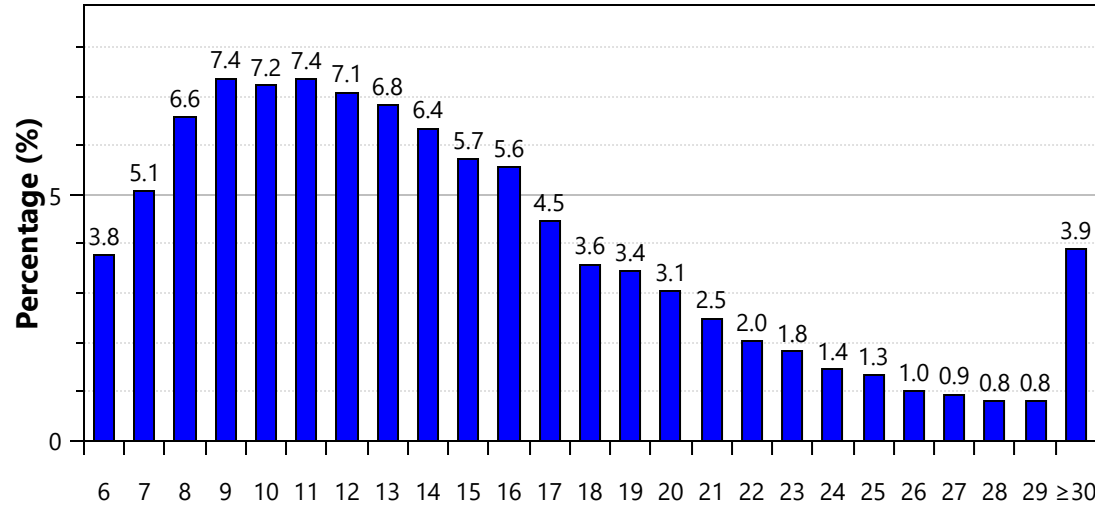
Cleavage Specific Percentage (%)



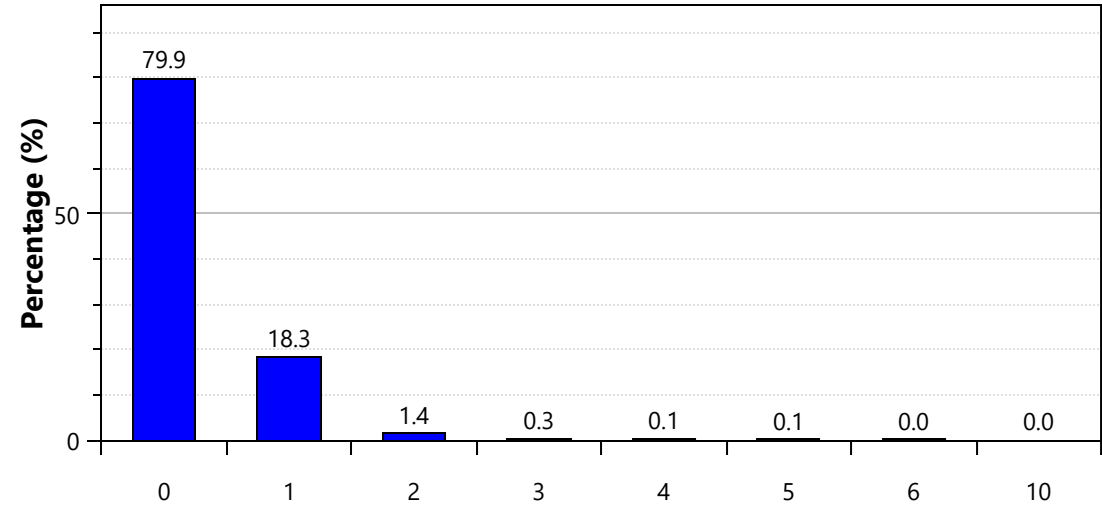
Modification Percentage (%)



Length Percentage (%)



Missed Cleavage Percentage (%)



ID Rate (%)

