Result

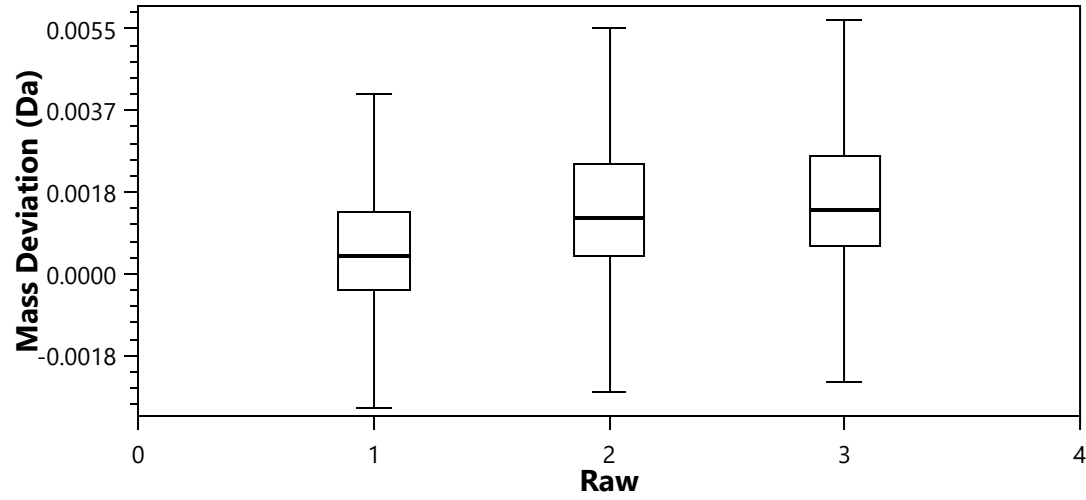| Property	Value	
Peptide Level:		
spectra number	44,734	
scans number	40,692	
peptides number	20,343	
sequences number	17,563	
proteins number	7,058	
protein groups number	6,154	
decoy spectra number	256	
decoy peptides number	203	
decoy proteins number	408	
decoy protein groups number	61	
Cleavage:		
Specific	98.50% (20,038/20,343)	
C-term specific	1.50% (305/20,343)	
N-term specific	0.00% (0/20,343)	
Non specific	0.00% (0/20,343)	
Modifications:		
TMT6plex[AnyN-term]	99.16% (20,172/20,343)	
TMT6plex[K]	54.80% (11,147/20,343)	
Oxidation[M]	14.81% (3,013/20,343)	
Carbamidomethyl[C]	3.77% (767/20,343)	
Missed Cleavage:		
number=0	81.26% (16,531/20,343)	
number=1	18.74% (3,812/20,343)	
Mixed Spectra:		
number=1	90.28% (36,735/40,692)	
number=2	9.52% (3,873/40,692)	
number=3	0.20% (83/40,692)	
number=4	0.00% (1/40,692)	
Charge:		
charge=2	71.32% (14,508/20,343)	
charge=3	25.58% (5,204/20,343)	
charge=4	2.92% (593/20,343)	
charge=5	0.18% (37/20,343)	
charge=6	0.00% (1/20,343)	
MassError:		
Precusor mass error: (mean)	0.60ppm	
Precusor mass error: (std)	±1.54ppm	
ID Rate:		
GMHJYZ_DeqMSvalidation_300ug_TMT10_IPG3-10_fr07	38.08% (13,128/34,474)	
GMHJYZ_DeqMSvalidation_300ug_TMT10_IPG3-10_fr08	40.74% (13,964/34,275)	
GMHJYZ_DeqMSvalidation_300ug_TMT10_IPG3-10_fr09	39.99% (13,600/34,005)	
Overall	39.60% (40,692/102,754)	

Parameter

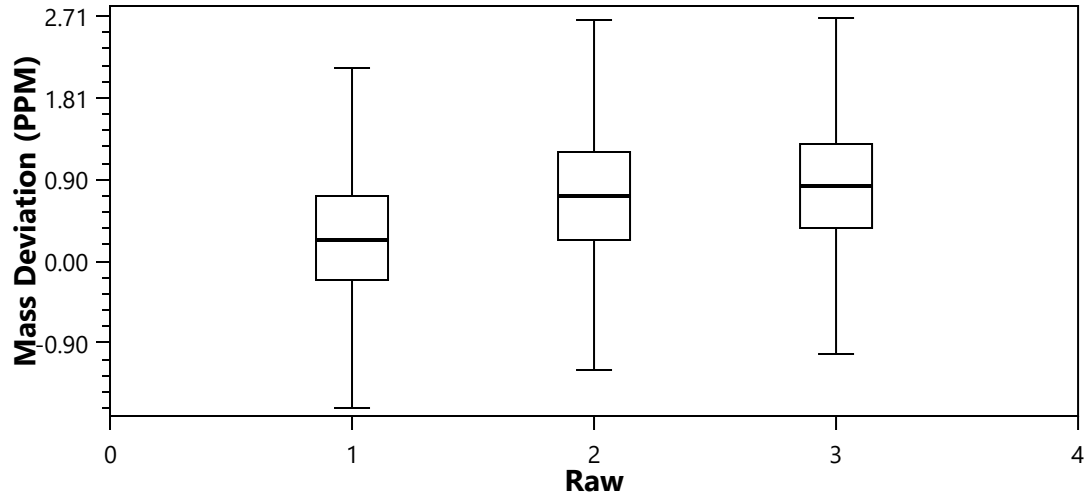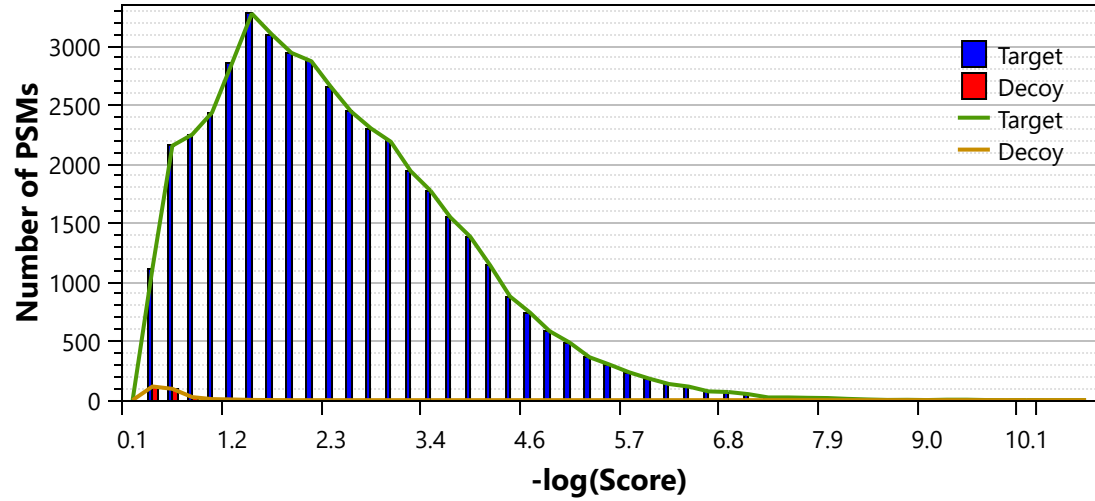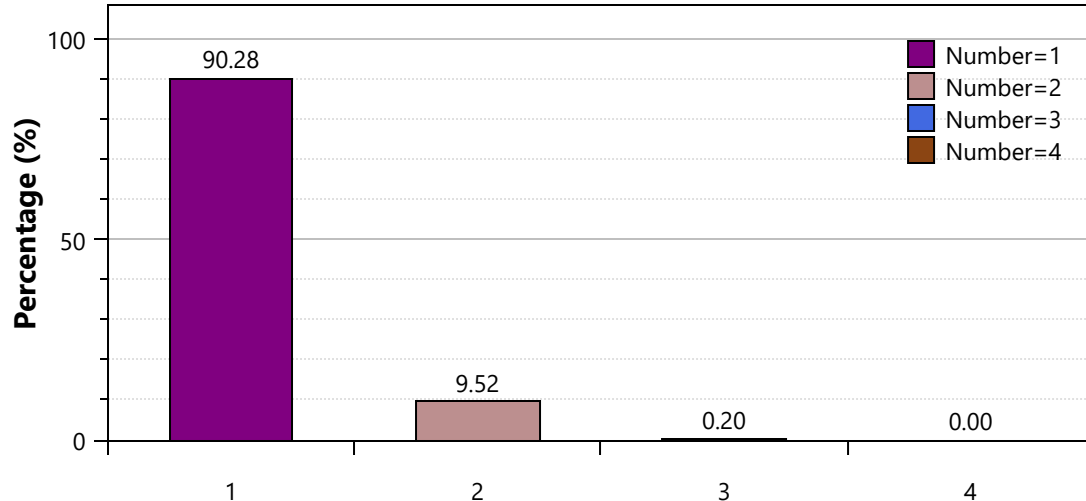| Property	Value	
Param:		
thread number	2	
ms tolerance	10ppm	
msms tolerance	0.02Da	
open search	False	
input format	raw	
fix modification	TMT6plex[K];TMT6plex[AnyN-term];Carbamidomethyl[C];	
variable modification	Oxidation[M];	
enzyme	Trypsin KR _ C	
max missing cleavage number	1	
co elute	True	
ll info label	1|none;	
File:		
aa path 1	C:\pFindTask3\result\1.aa	
modification path	F:\Yanbo\pFind3\bin\modification.ini	
fasta path	C:\pFindTask3\Work\Uniprot_sp-Human_refp-EcoliK12_20190626.fasta	
contaminant path	NULL	
task path	C:\pFindTask3\result\pFindTask3	
Raws:		
raw path 1	C:\pFindTask3\Work\GMHJYZ_DeqMSvalidation_300ug_TMT10_IPG3-10_fr07.raw	
raw path 2	C:\pFindTask3\Work\GMHJYZ_DeqMSvalidation_300ug_TMT10_IPG3-10_fr08.raw	
raw path 3	C:\pFindTask3\Work\GMHJYZ_DeqMSvalidation_300ug_TMT10_IPG3-10_fr09.raw	

Graph

FDR Curve

FDR

5.0%
4.0%
3.0%
2.0%
1.0%
0.0%

0   20,000   40,000   60,000   80,000   100,000   120,000   140,000   160,000   180,000

PSM Count

1.00% : 44,990

Mass Deviation

Mass Deviation (Da)

0.0055
0.0037
0.0018
0.0000
-0.0018

0   1   2   3   4

Raw

Mass Deviation

Mass Deviation (PPM)

2.71
1.81
0.90
0.00
-0.90

0   1   2   3   4

Raw

Score Distribution

Number of PSMs

3000
2500
2000
1500
1000
500

0.1   1.2   2.3   3.4   4.6   5.7   6.8   7.9   9.0   10.1

-log(Score)

- Target (blue)
- Decoy (red)
- Target (green line)
- Decoy (orange line)
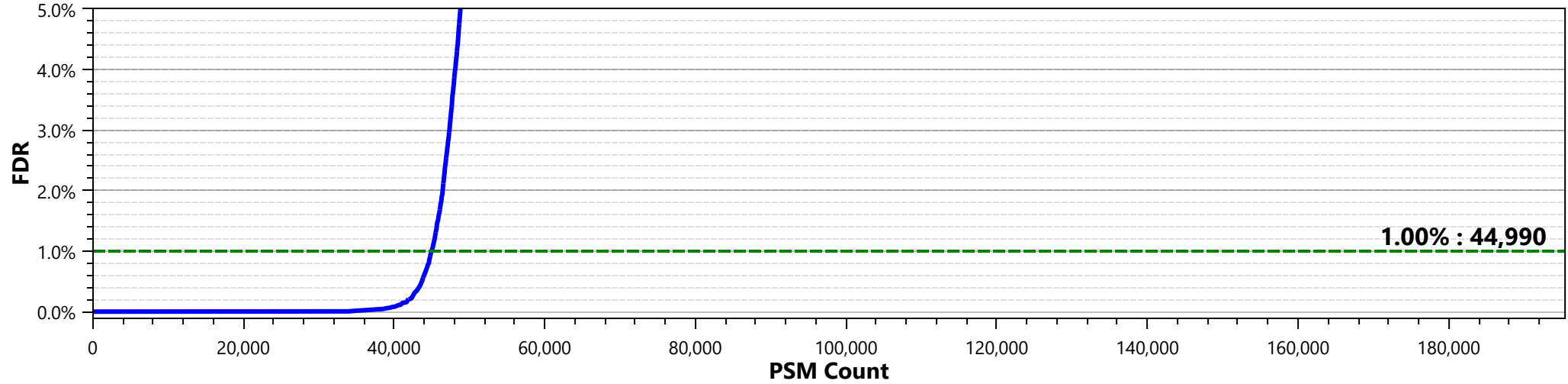
Mixture Spectra Percentage (%)

Percentage (%)

100
50
0

1: 90.28   2: 9.52   3: 0.20   4: 0.00

- Number=1
- Number=2
- Number=3
- Number=4

Cleavage Specific Percentage (%)

Percentage (%)

100
50
0

1: 98.50   2: 1.50   3: 0.00   4: 0.00

- Specific
- C-term Specific
- N-term Specific
- Non-Specific
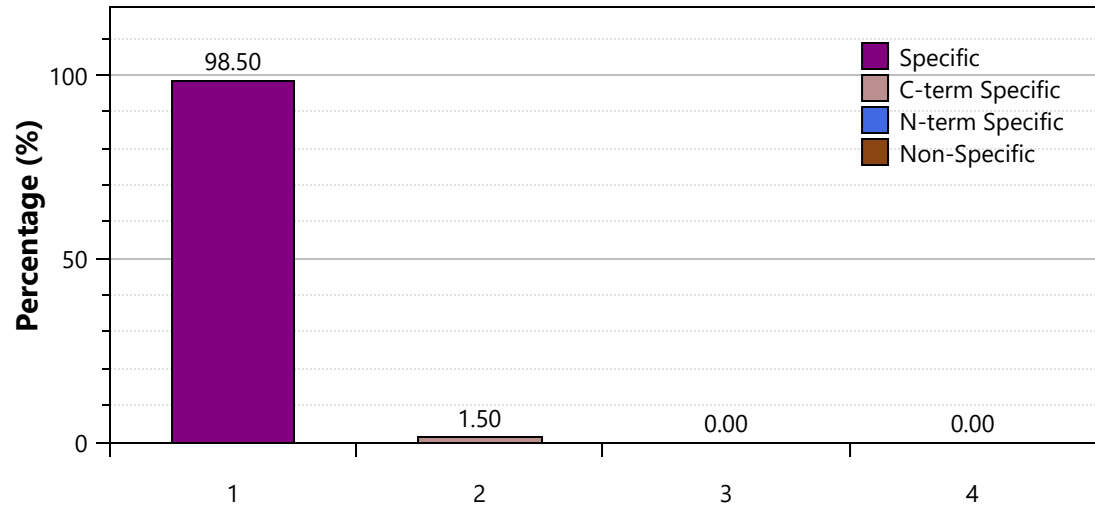
Modification Percentage (%)

Percentage (%)

100
50
0

1: 99.16   2: 54.80   3: 14.81   4: 3.77

- TMT6plex[AnyN-term]
- TMT6plex[K]
- Oxidation[M]
- Carbamidomethyl[C]

Length Percentage (%)

Percentage (%)

7: 5.7   8: 7.2   9: 8.0   10: 7.9   11: 7.9   12: 7.8   13: 7.3   14: 6.5   15: 6.0   16: 5.6   17: 4.5   18: 3.7   19: 3.7   20: 3.3   21: 2.5   22: 2.0   23: 1.7   24: 1.4   25: 1.3   26: 1.0   27: 0.9   28: 0.7   29: 0.7   ≥30: 2.7
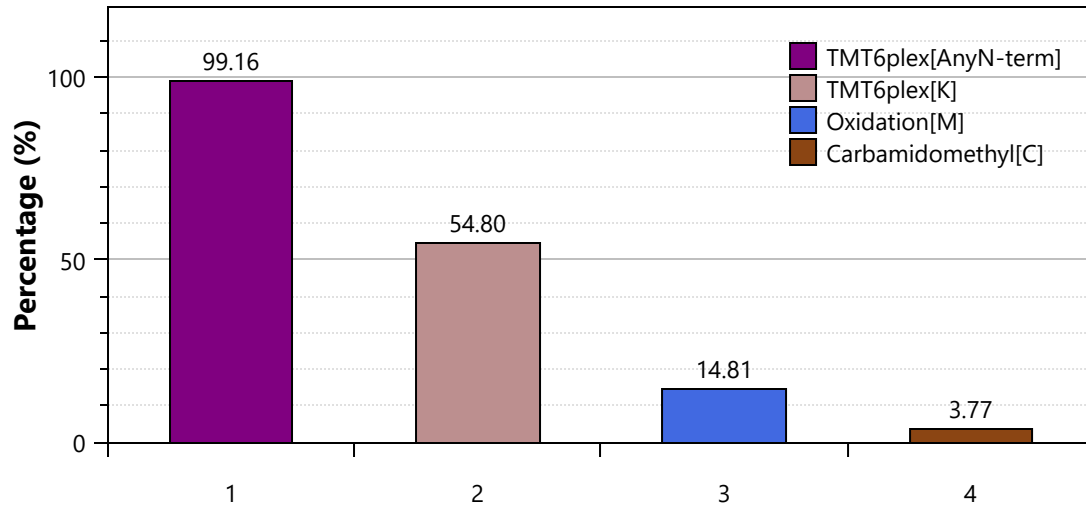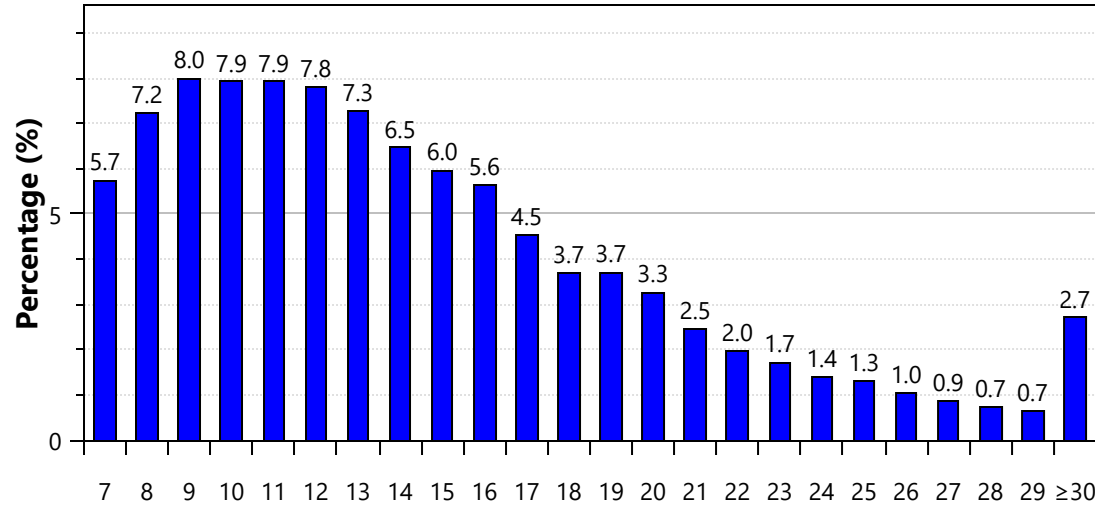
Missed Cleavage Percentage (%)

Percentage (%)

100
50
0

0: 81.3   1: 18.7

ID Rate (%)

Number of Spectra

40000
20000
0

1: 13128/34474 38.08%   2: 13964/34275 40.74%   3: 13600/34005 39.99%

Raw