



Result

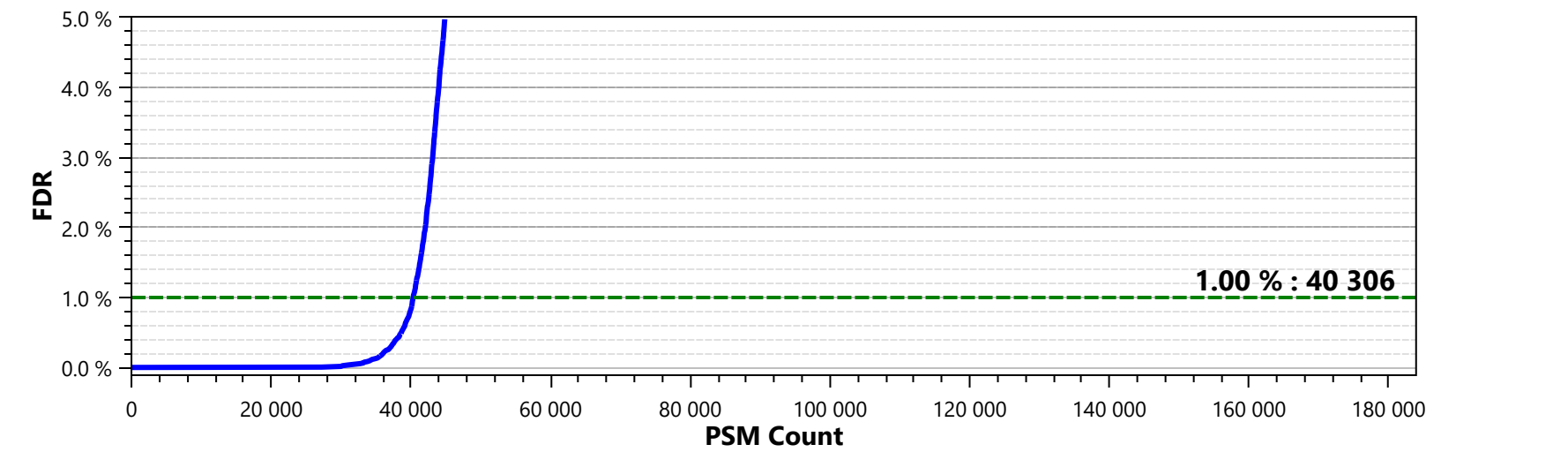
Property	Value	
Peptide Level:		
spectra number	40 047	
scans number	37 249	
peptides number	19 277	
sequences number	16 237	
proteins number	5 966	
protein groups number	4 368	
decoy spectra number	259	
decoy peptides number	192	
decoy proteins number	1 481	
decoy protein groups number	43	
Cleavage:		
Specific	93.68 % (18 058/19 277)	
C-term specific	4.44 % (856/19 277)	
N-term specific	1.87 % (361/19 277)	
Non specific	0.01 % (2/19 277)	
Modifications:		
TMT6plex[AnyN-term]	87.19 % (16 807/19 277)	
TMT6plex[K]	40.18 % (7 746/19 277)	
Oxidation[M]	13.18 % (2 540/19 277)	
Carbamyl[AnyN-term]	5.84 % (1 125/19 277)	
Deamidated[N]	5.75 % (1 108/19 277)	
Carbamidomethyl[C]	3.35 % (646/19 277)	
Succinyl[AnyN-term]	1.19 % (230/19 277)	
Gln->pyro-Glu[AnyN-termQ]	0.74 % (142/19 277)	
Acetyl[ProteinN-term]	0.57 % (109/19 277)	
Iodoacetanilide[K]	0.12 % (24/19 277)	
Missed Cleavage:		
number=0	80.23 % (15 466/19 277)	
number=1	18.38 % (3 544/19 277)	
number=2	0.90 % (173/19 277)	
number=3	0.26 % (50/19 277)	
number=4	0.13 % (25/19 277)	
number=5	0.06 % (11/19 277)	
number=6	0.03 % (5/19 277)	
number=7	0.01 % (2/19 277)	
number=10	0.01 % (1/19 277)	
Mixed Spectra:		
number=1	92.59 % (34 490/37 249)	
number=2	7.30 % (2 720/37 249)	
number=3	0.10 % (39/37 249)	
Charge:		
charge=2	72.85 % (14 044/19 277)	
charge=3	23.12 % (4 456/19 277)	
charge=4	3.50 % (675/19 277)	
charge=5	0.47 % (91/19 277)	
charge=6	0.05 % (10/19 277)	
charge=7	0.01 % (1/19 277)	
MassError:		
Precursor mass error: (mean)	0.59ppm	
Precursor mass error: (std)	±1.52ppm	
ID Rate:		
GMHJYZ_DeqMSvalidation_300ug_TMT10_IPG3-10_fr07	36.55 % (12 599/34 474)	
GMHJYZ_DeqMSvalidation_300ug_TMT10_IPG3-10_fr08	35.37 % (12 124/34 275)	
GMHJYZ_DeqMSvalidation_300ug_TMT10_IPG3-10_fr09	36.84 % (12 526/34 005)	
Overall	36.25 % (37 249/102 754)	



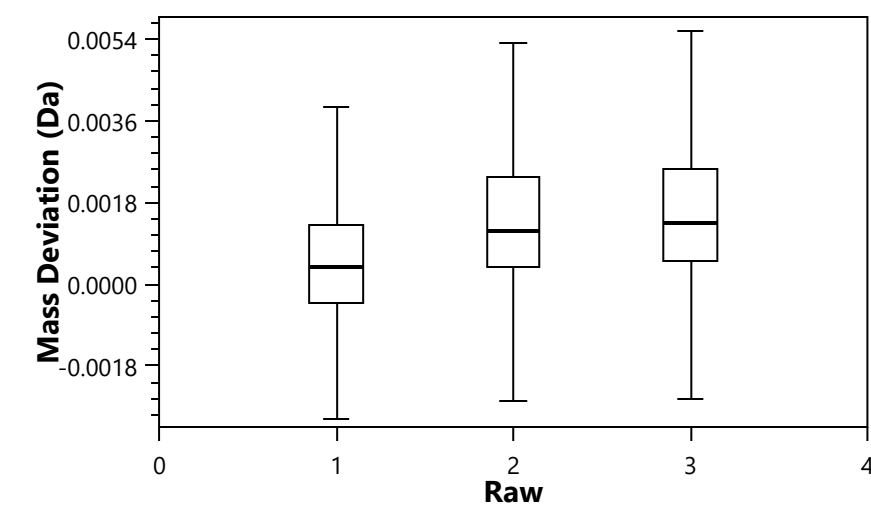
Parameter

Property	Value
Param:	
thread number	2
ms tolerance	10ppm
msms tolerance	0.02Da
open search	True
input format	raw
fix modification	TMT6plex[AnyN-term];TMT6plex[K];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:\pFindWorkspace\pFindTask1\result\1.aa
modification path	C:\pFindStudio\pFind3\bin\modification.ini
fasta path	C:\Users\maan\Desktop\Workshop\Uniprot_sp-Human_refp-EcoliK12_20190620.fasta
contaminant path	NULL
task path	C:\pFindWorkspace\pFindTask1\result\pFindTask1
Raws:	
raw path 1	C:\Users\maan\Desktop\Workshop\GMHJYZ_DeqMSvalidation_300ug_TMT10_IPG3-10_fr07.raw
raw path 2	C:\Users\maan\Desktop\Workshop\GMHJYZ_DeqMSvalidation_300ug_TMT10_IPG3-10_fr08.raw
raw path 3	C:\Users\maan\Desktop\Workshop\GMHJYZ_DeqMSvalidation_300ug_TMT10_IPG3-10_fr09.raw

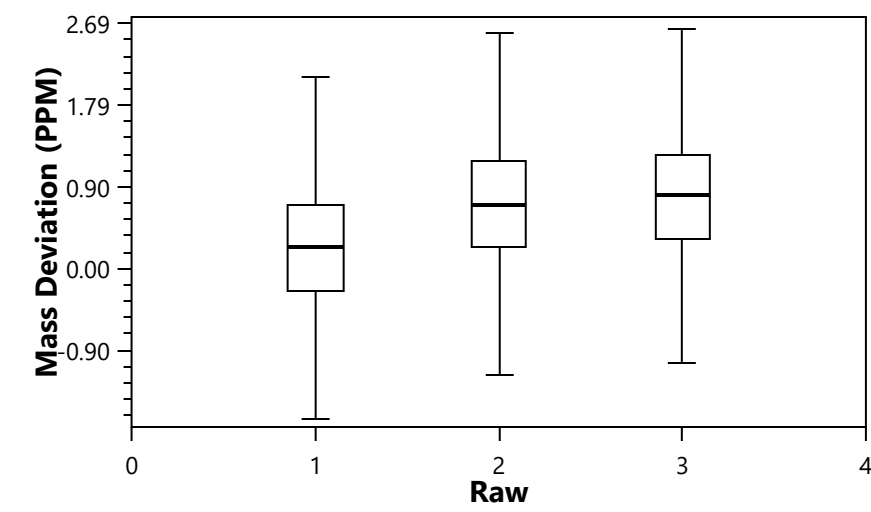
FDR Curve



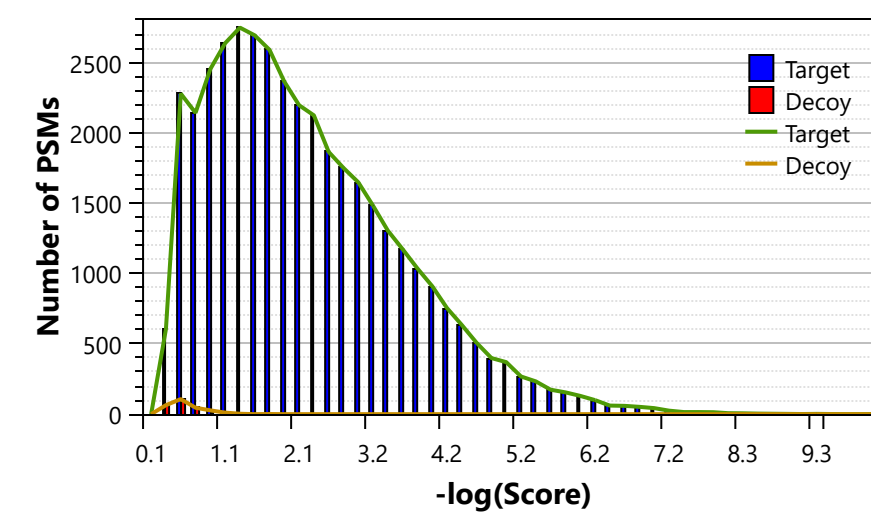
Mass Deviation



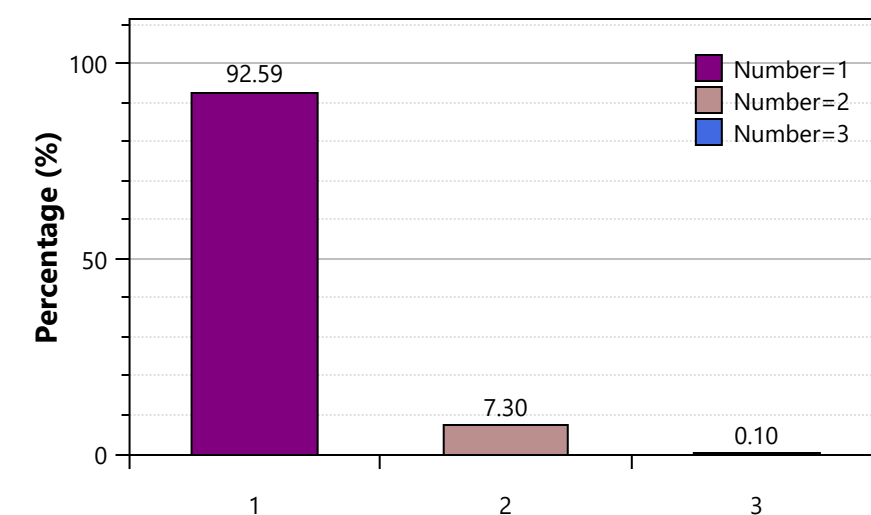
Mass Deviation



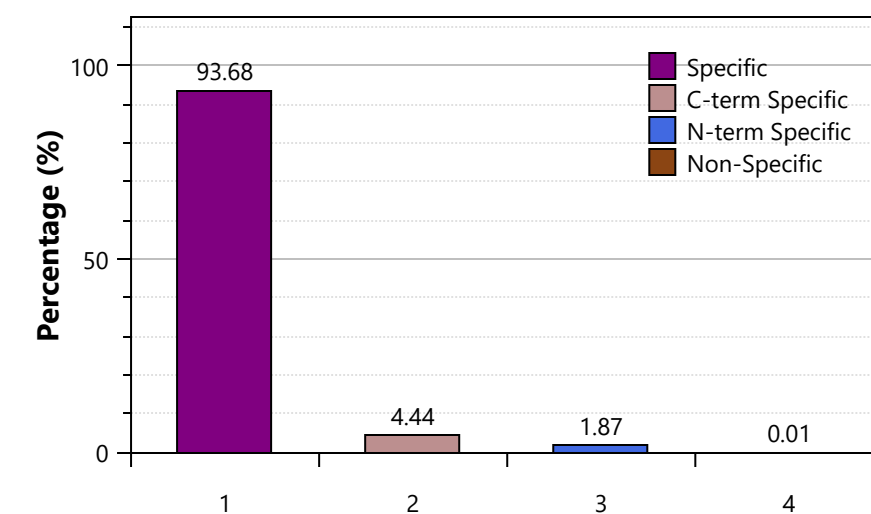
Score Distribution



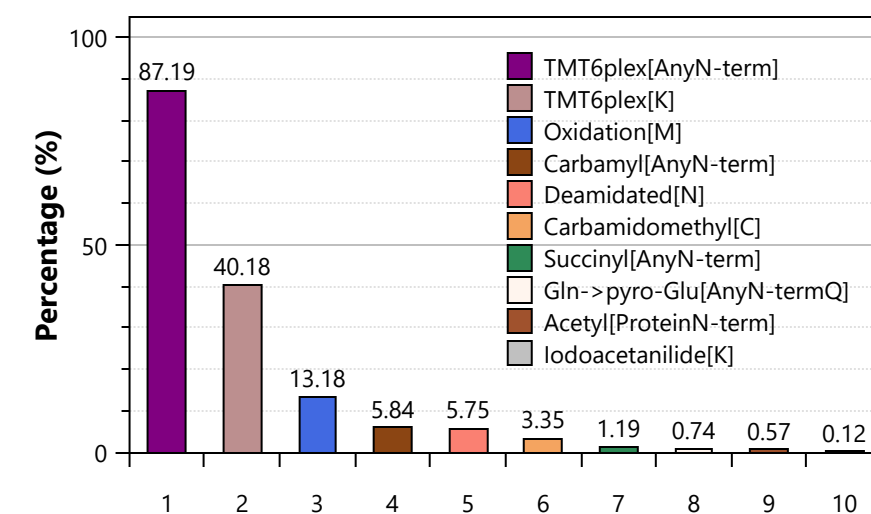
Mixture Spectra Percentage (%)



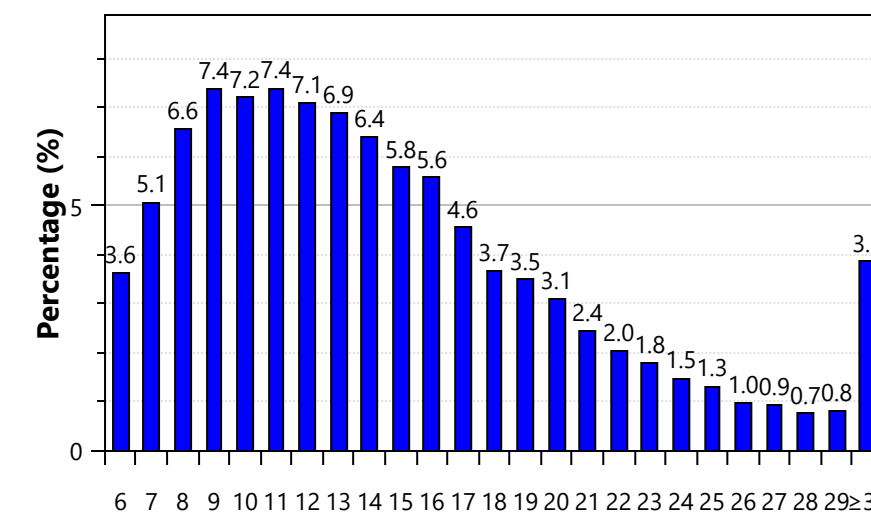
Cleavage Specific Percentage (%)



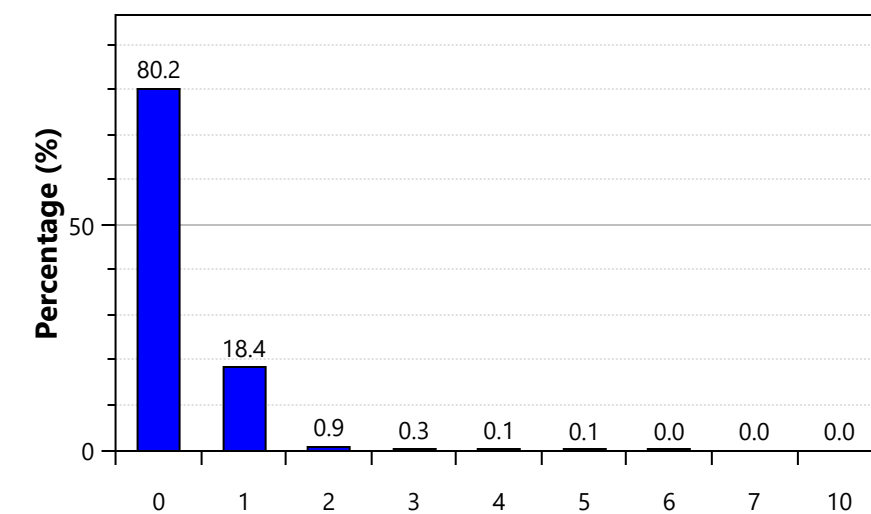
Modification Percentage (%)



Length Percentage (%)



Missed Cleavage Percentage (%)



ID Rate (%)

