

# MaxQuant report

## parameter.txt info

Version: 1.6.3.3run at: 12/04/2020 22:18:06

Fasta File: C:\Massspec Software\MaxQuant\_1.6.3.3\fasta\201014\_Human\_Uniprot-Reviewed.fasta, Match between runs: False

Min. to Max. peptide length for unspecific search: 8 to 25

## summary.txt info

Used Enzyme: Trypsin/P

Variable modifications: Oxidation (M);Acetyl (Protein N-term)

Mass Standard Deviation: mean 1.12359 ppm, max 1.14830 ppm

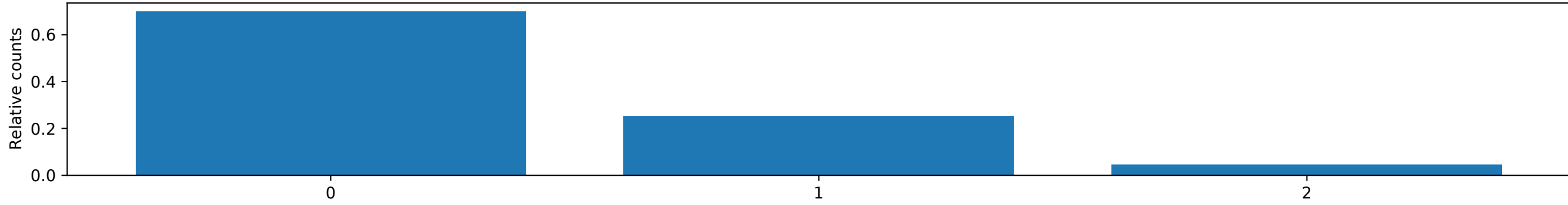
Identified proteins (without contaminants): 5027

Identified peptides (without contaminants): 54945

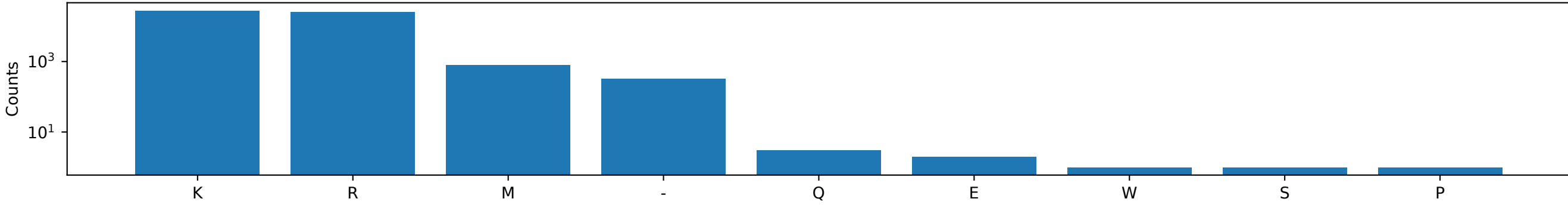
Has LFQ intensities: True

Has iBAQ: False

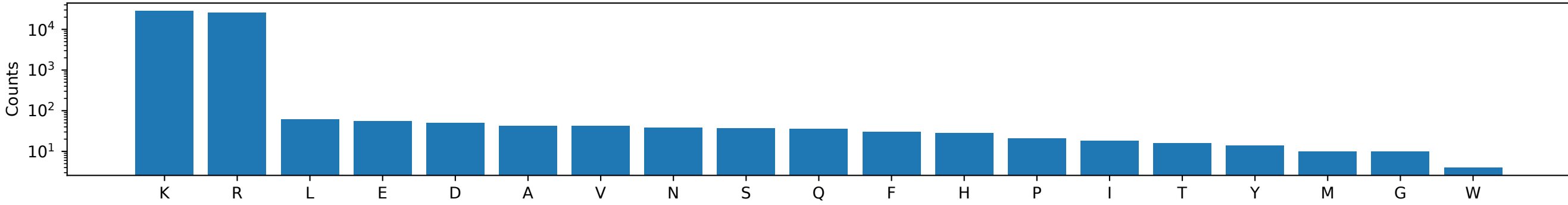
Missed Cleavages



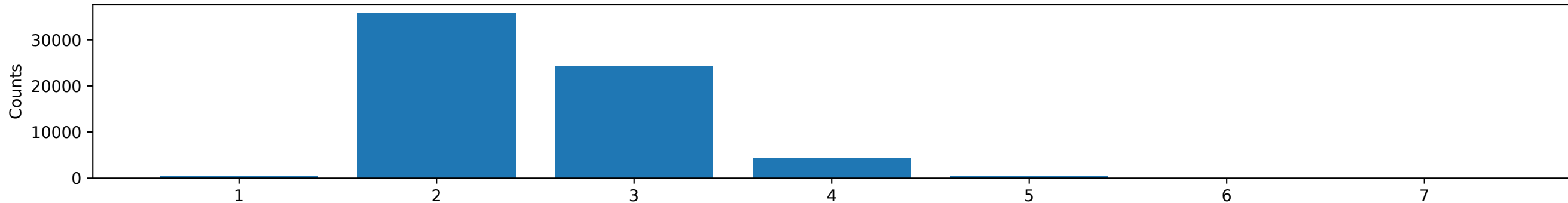
Amino acid before



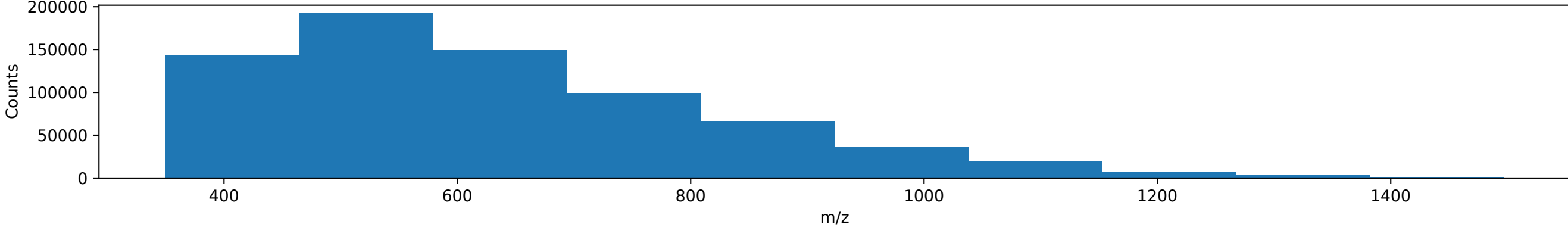
Last amino acid



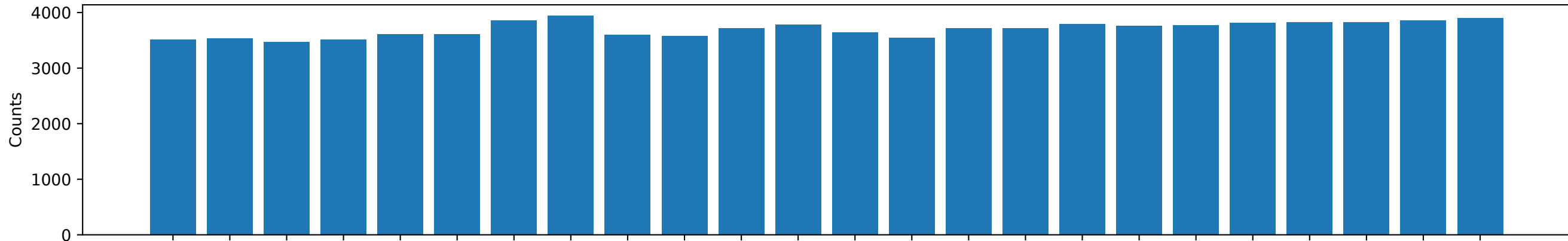
Peptide Charges



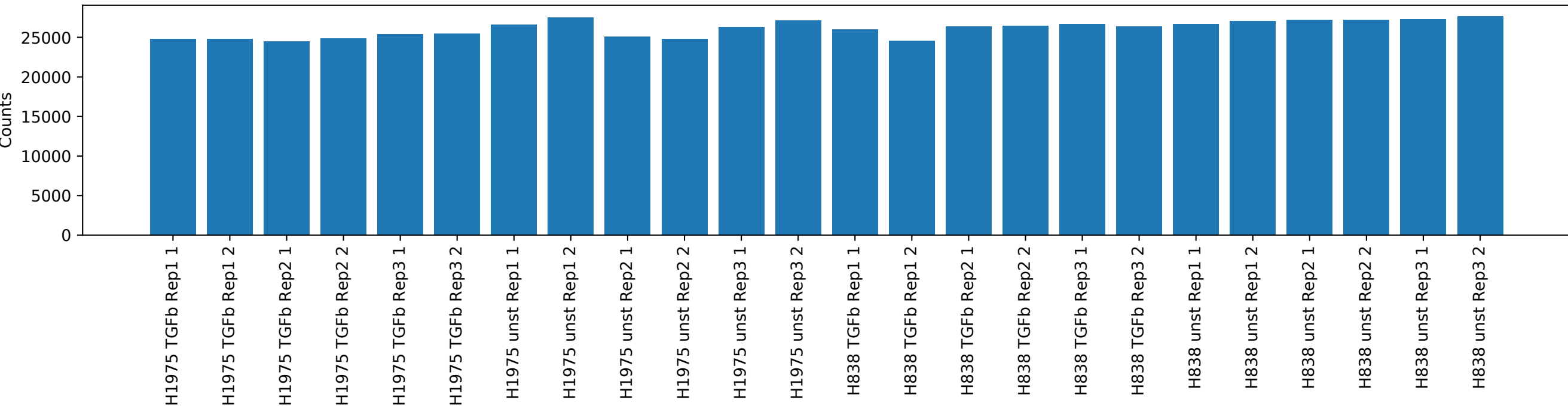
Peptide m/z



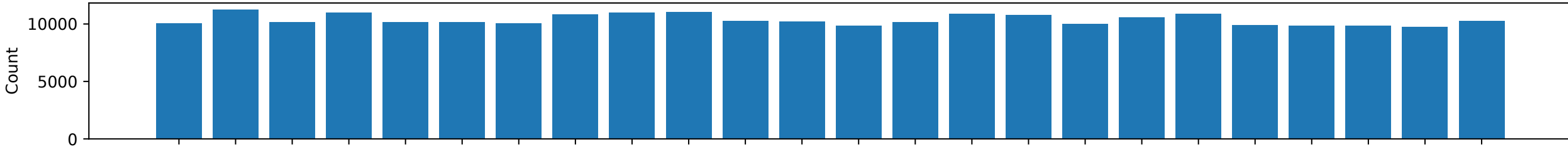
Identified proteins



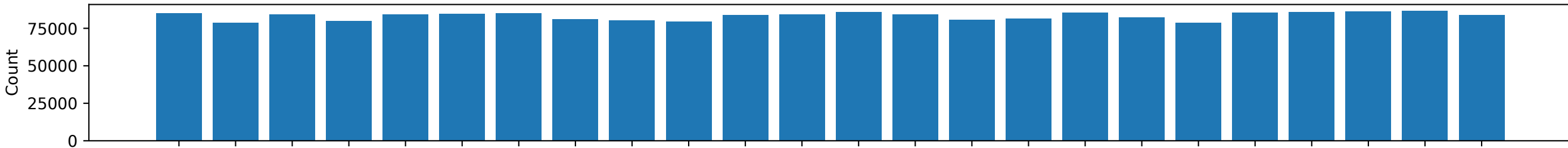
Identified peptides



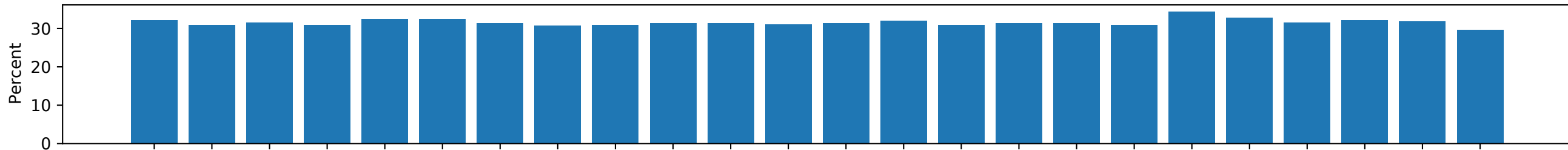
MS scans



MS/MS scans



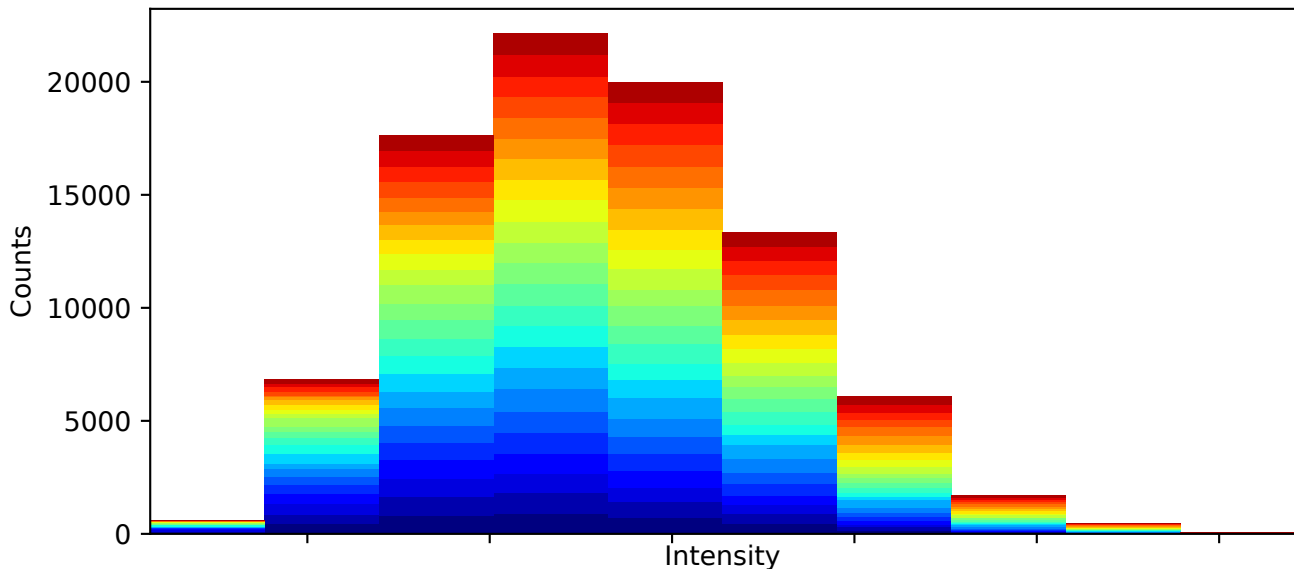
MS/MS identified [%]



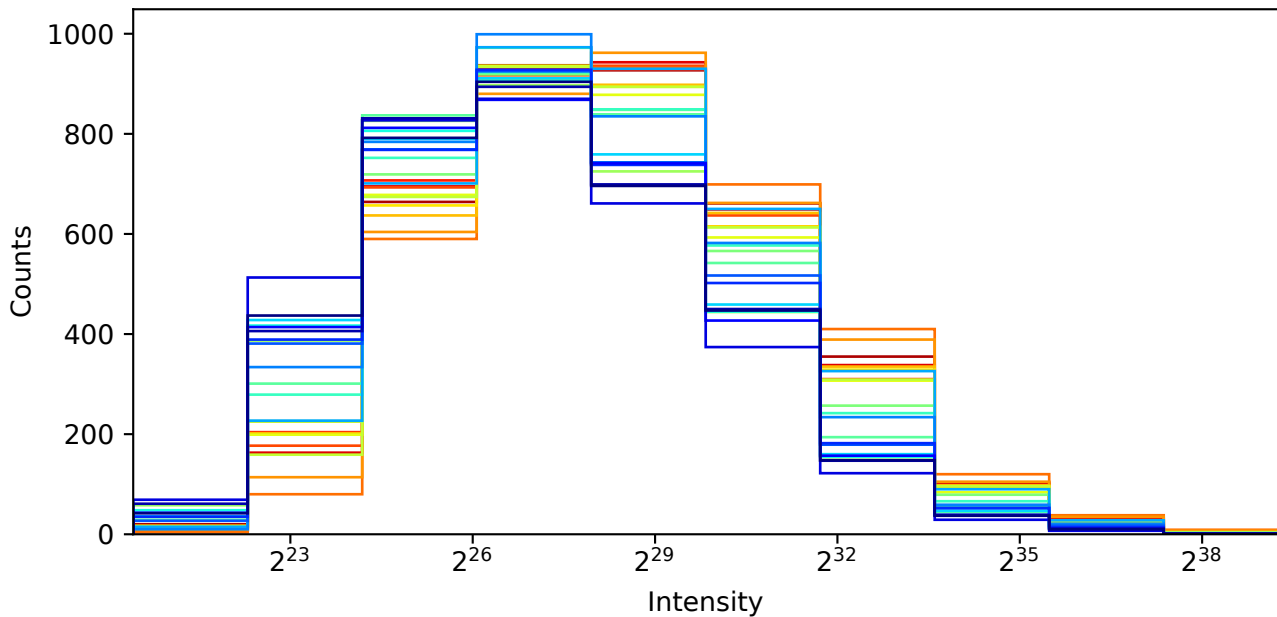
Intensity of contaminants from total intensity



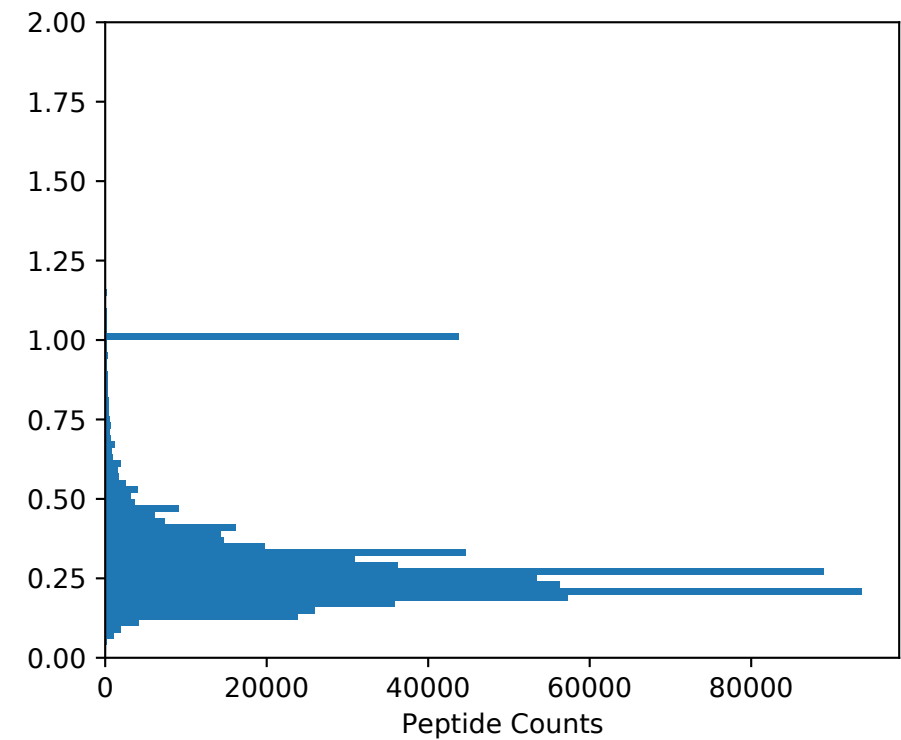
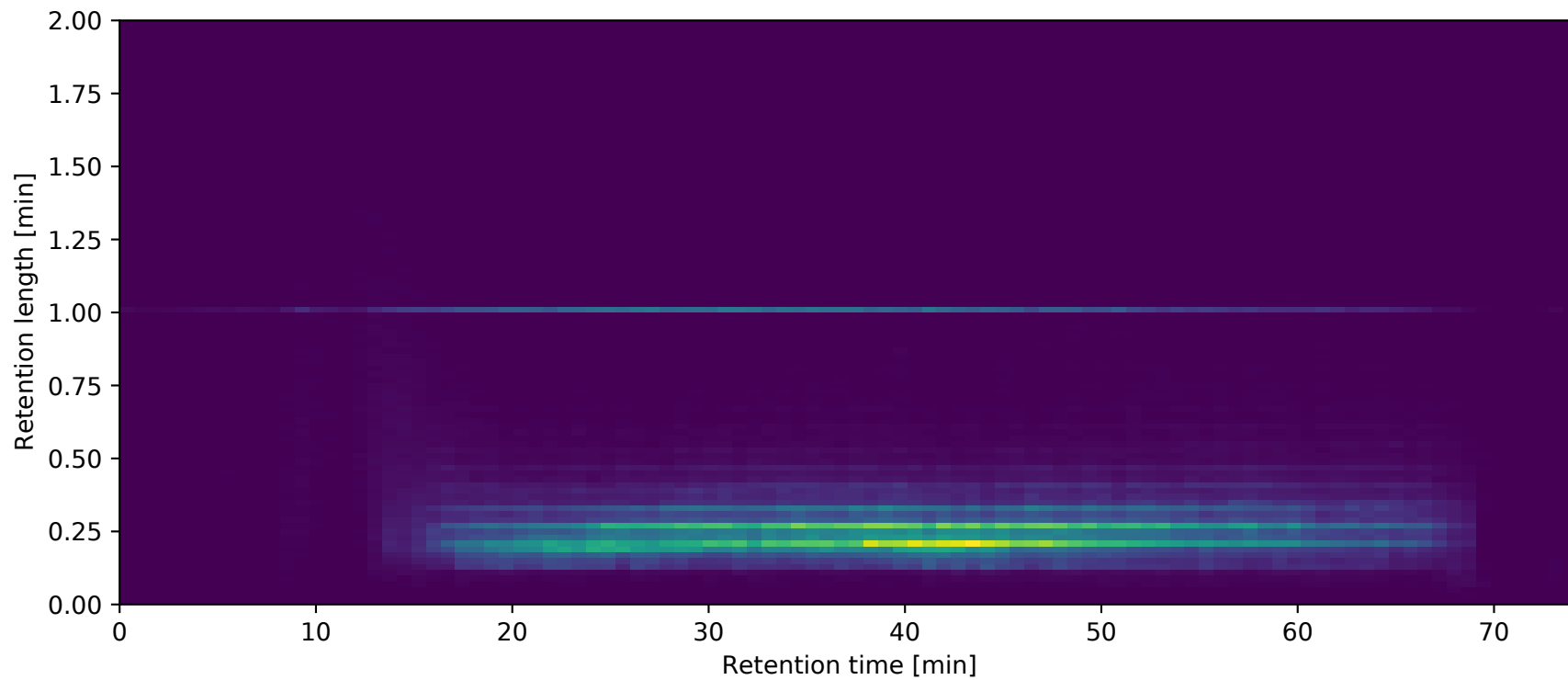
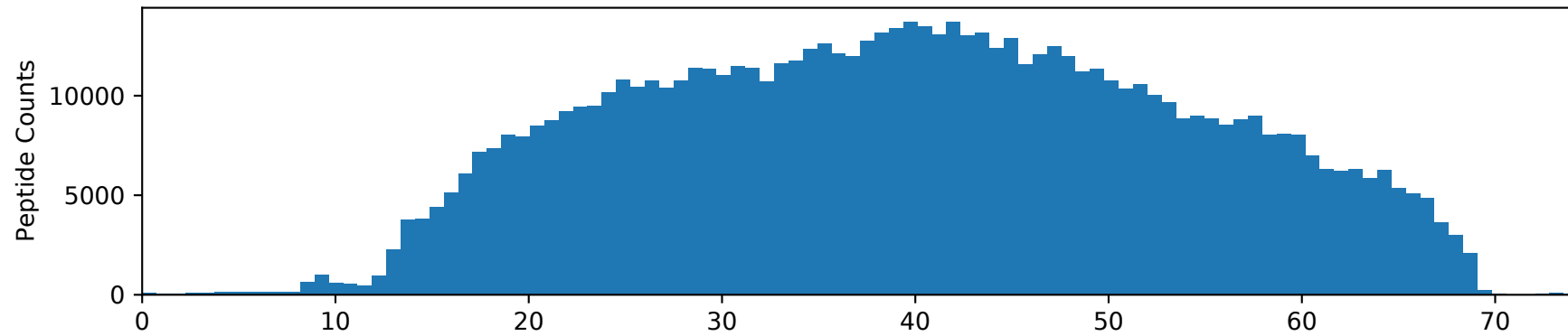
Grouped Intensity



Grouped Intensity

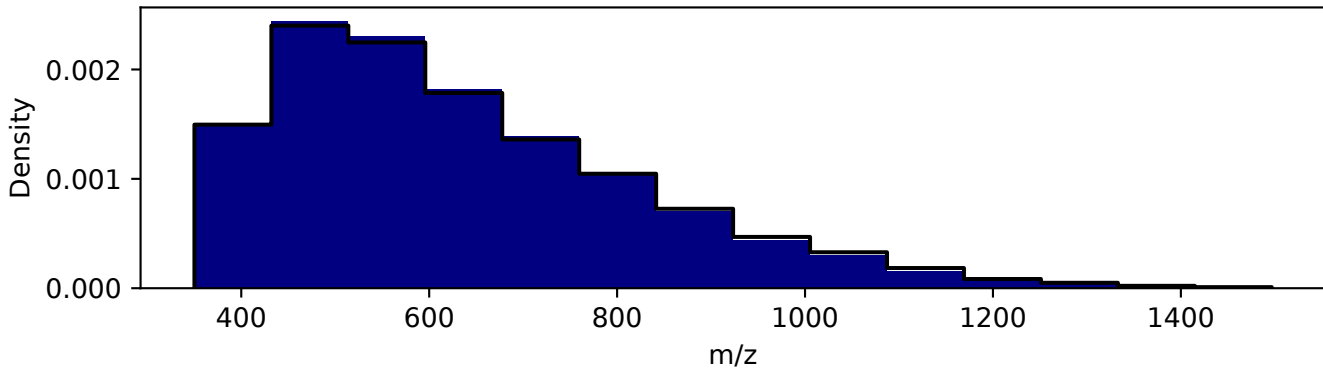


Overall Retention time vs Retention length

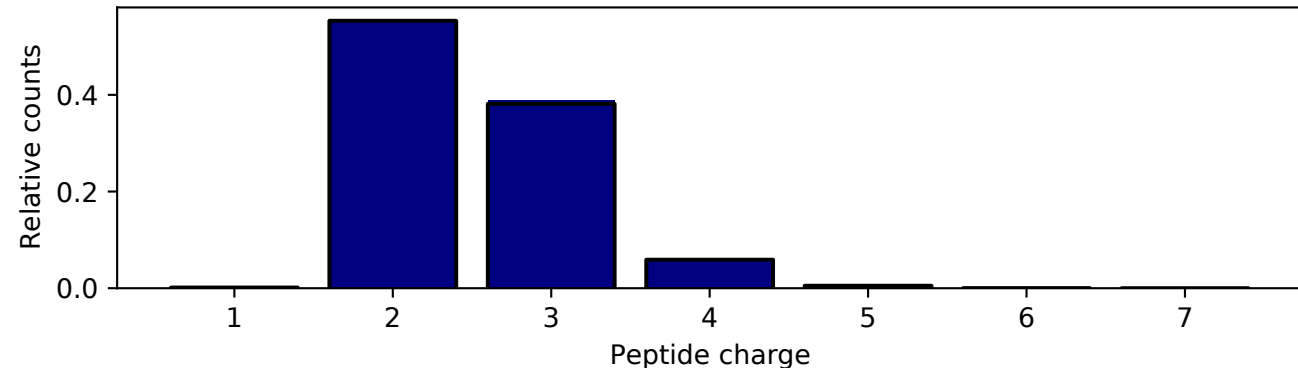


# H1975 TGFb Rep1 1

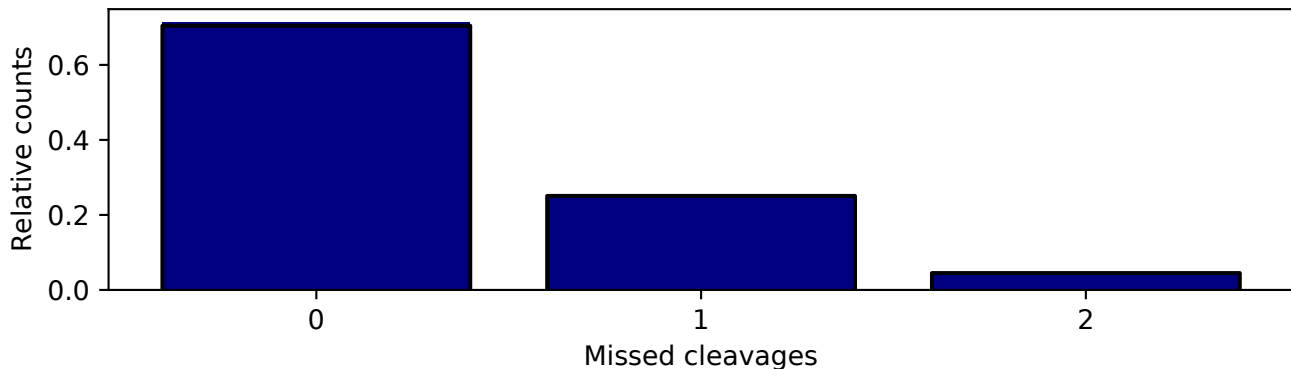
## Peptide m/z



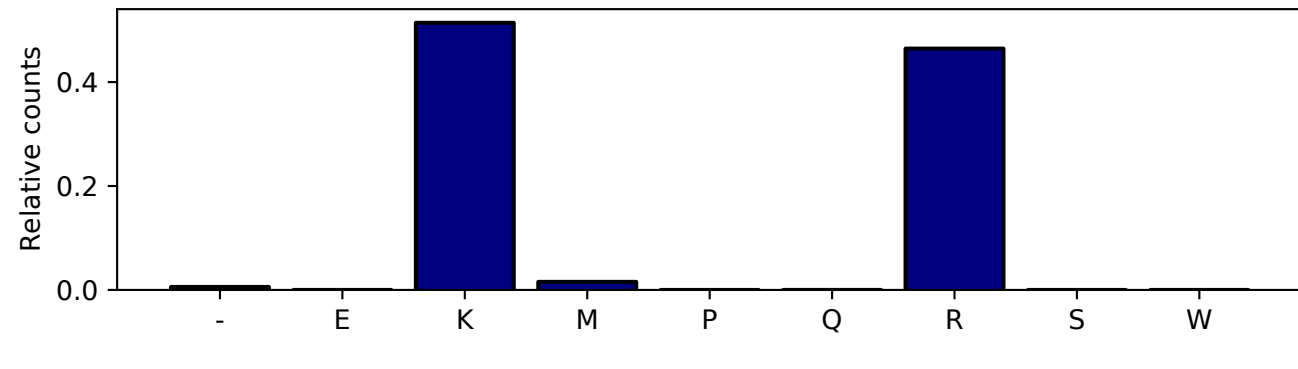
## Peptide charges



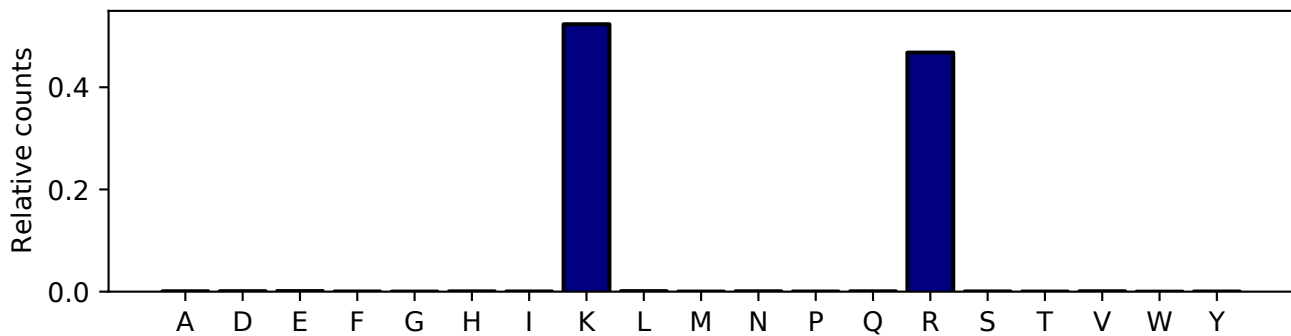
## Number of missed cleavages



## Amino acid before

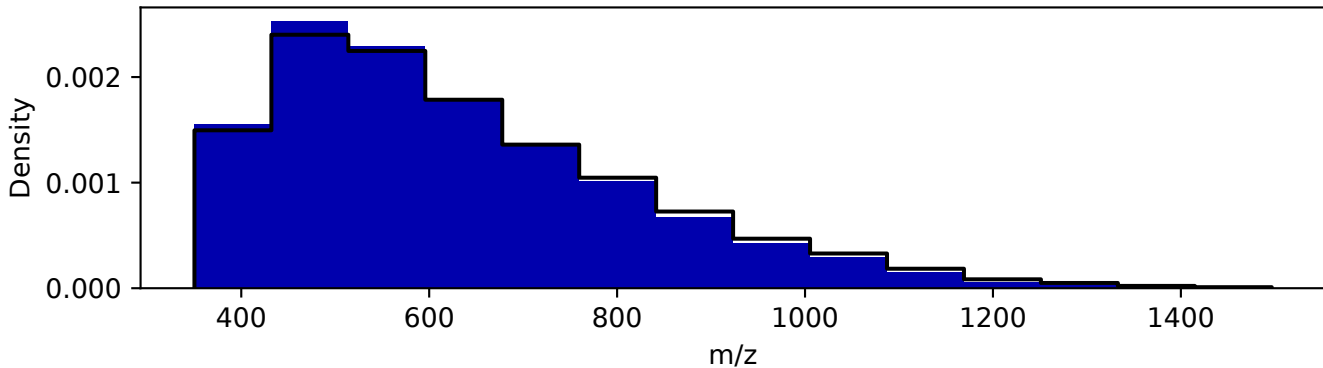


## Last amino acid

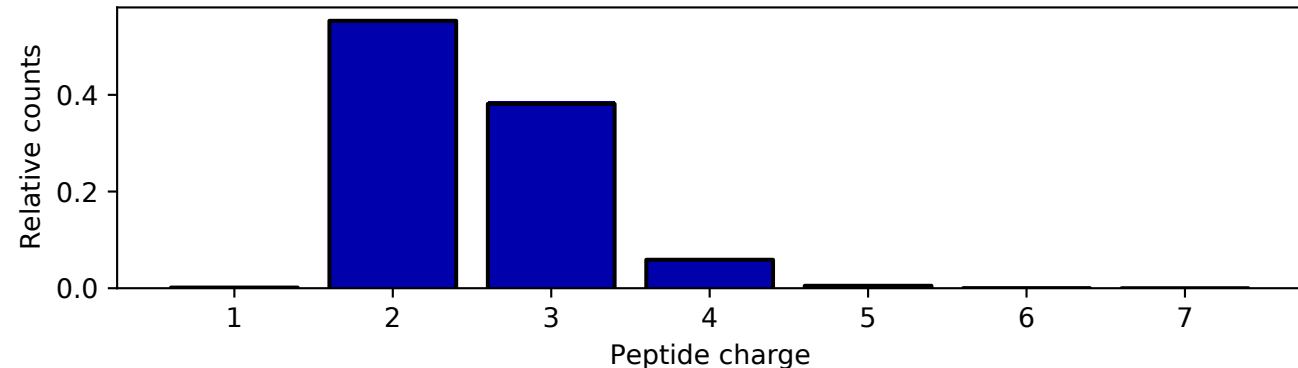


# H1975 TGFb Rep1 2

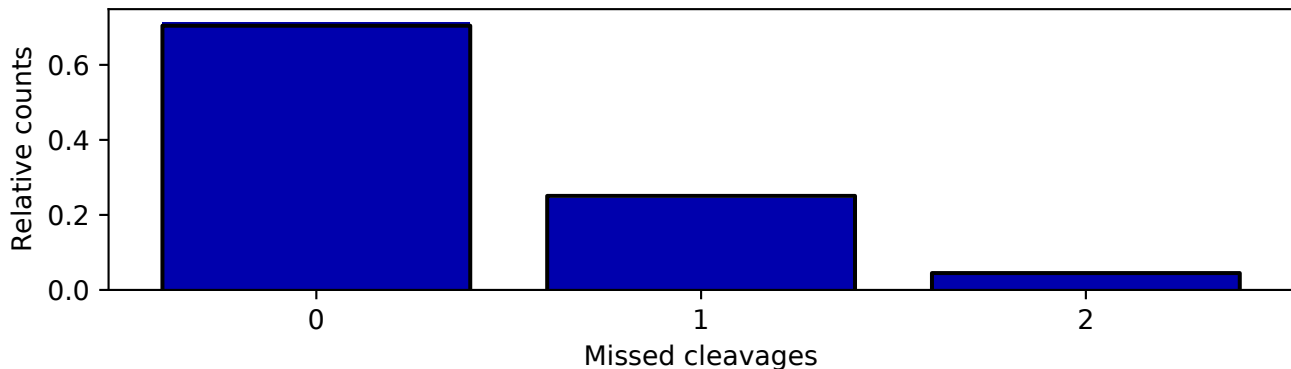
## Peptide m/z



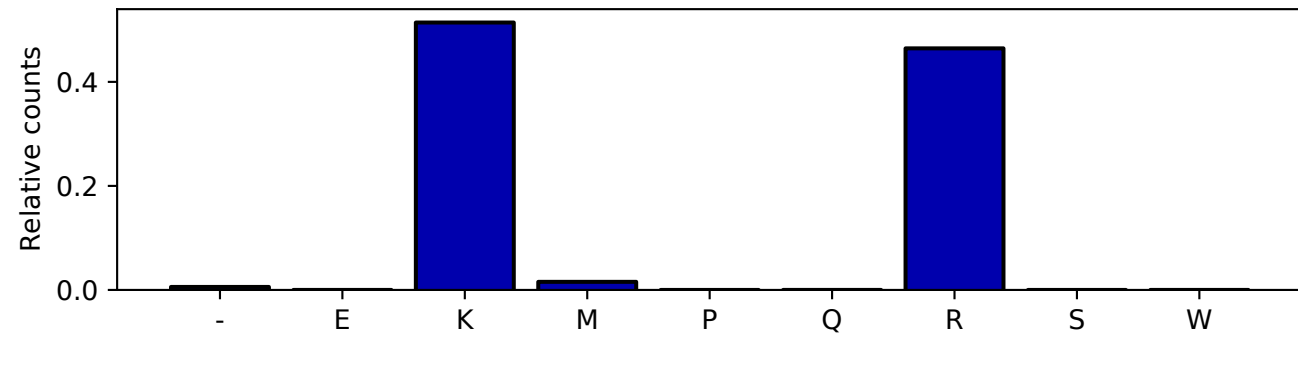
## Peptide charges



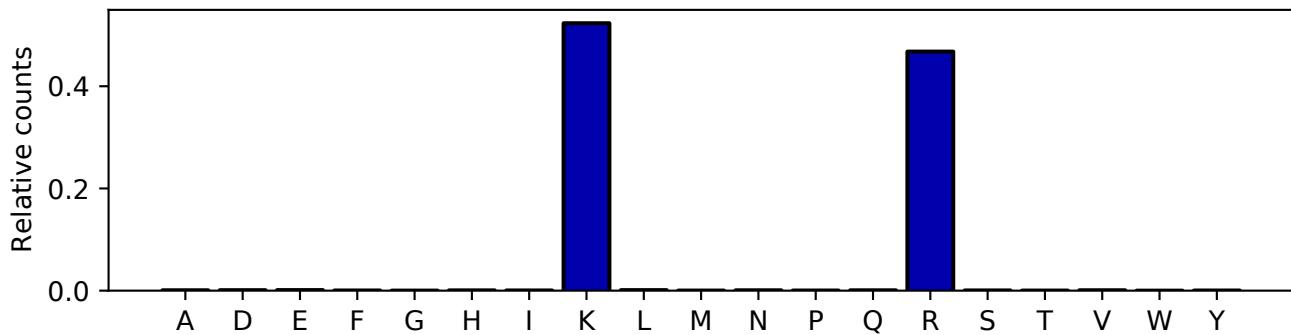
## Number of missed cleavages



## Amino acid before

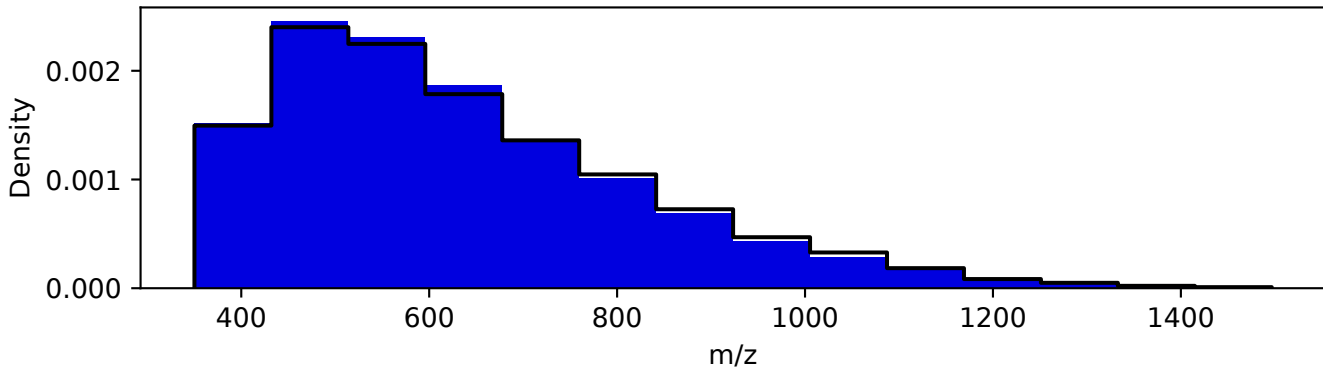


## Last amino acid

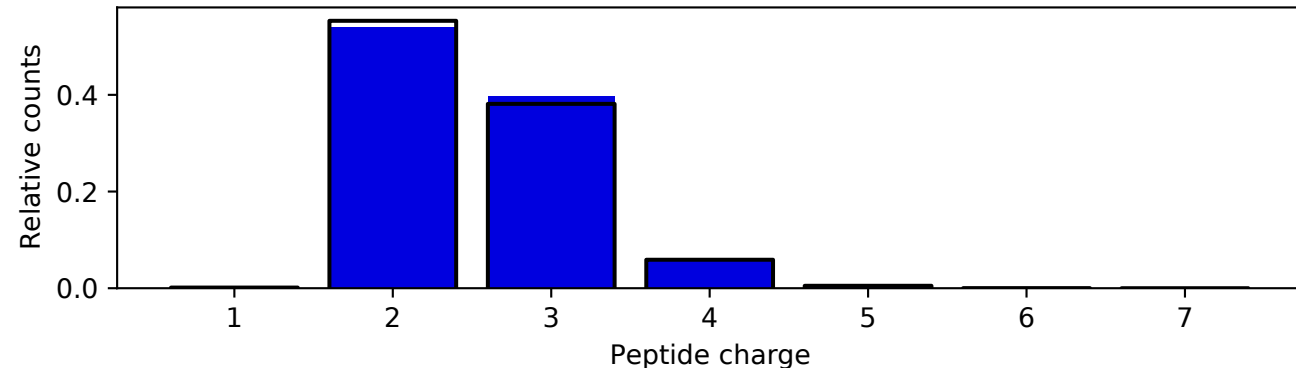


# H1975 TGFb Rep2 1

## Peptide m/z



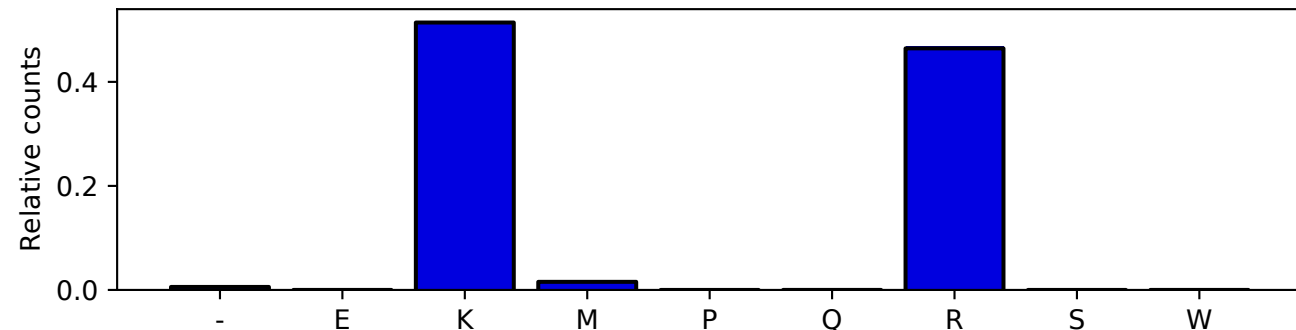
## Peptide charges



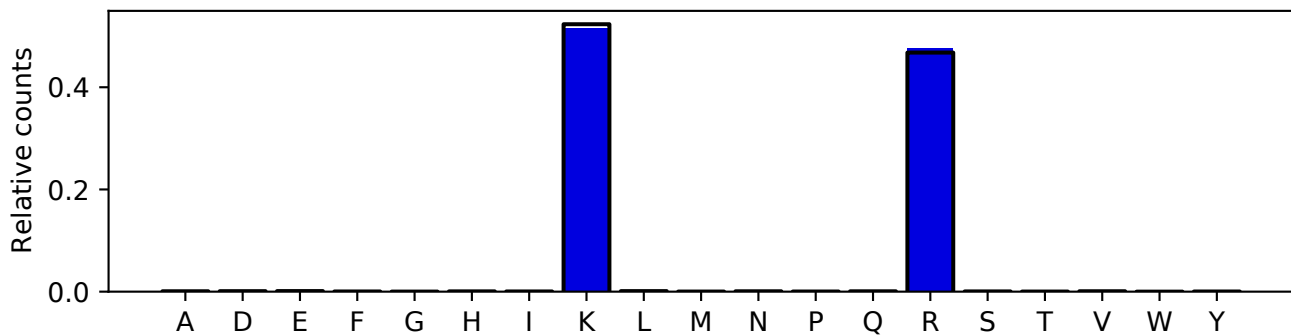
## Number of missed cleavages



## Amino acid before

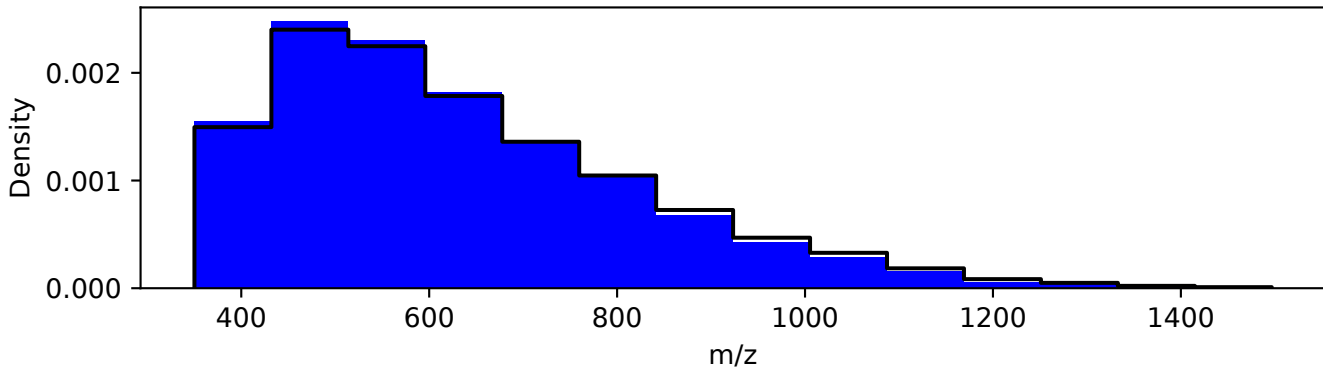


## Last amino acid

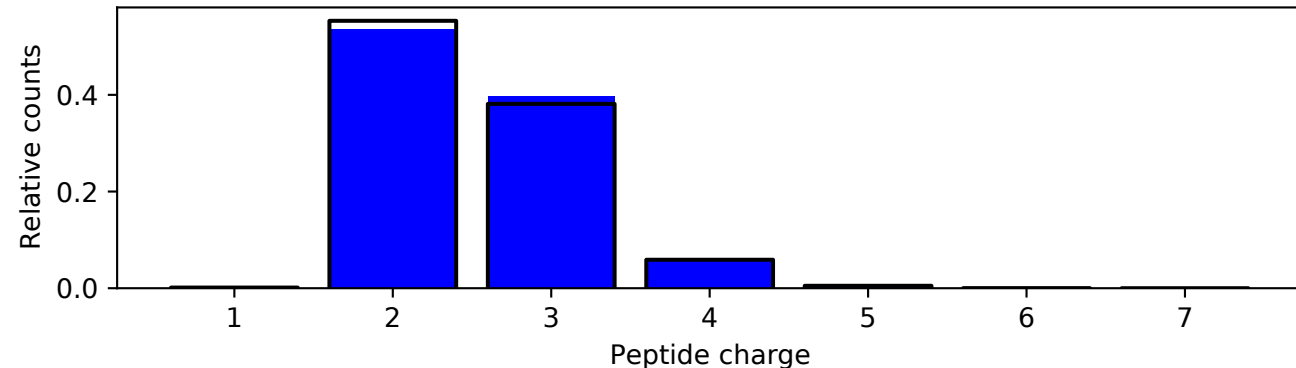


# H1975 TGFb Rep2 2

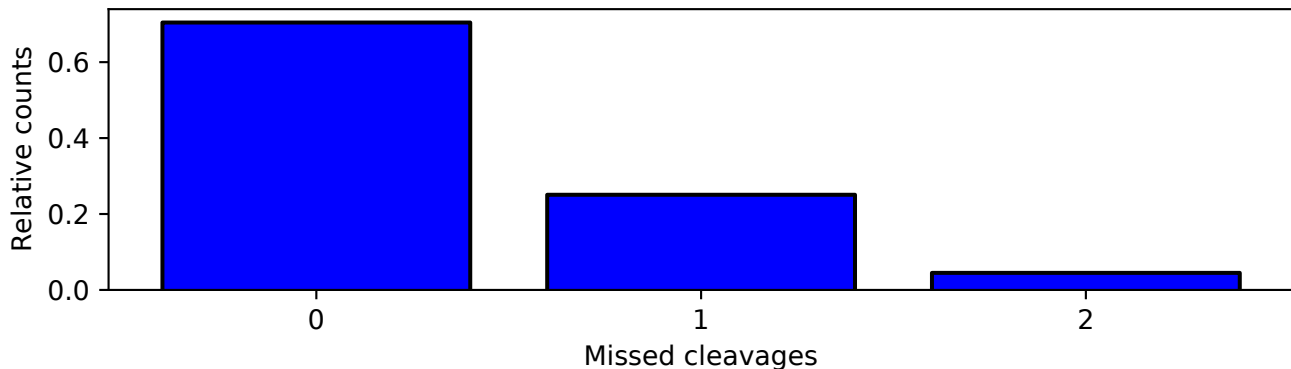
## Peptide m/z



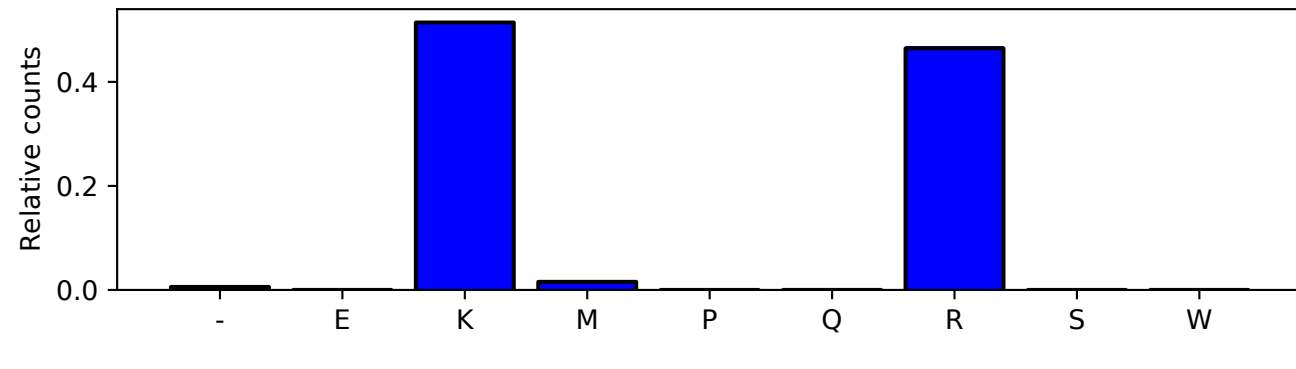
## Peptide charges



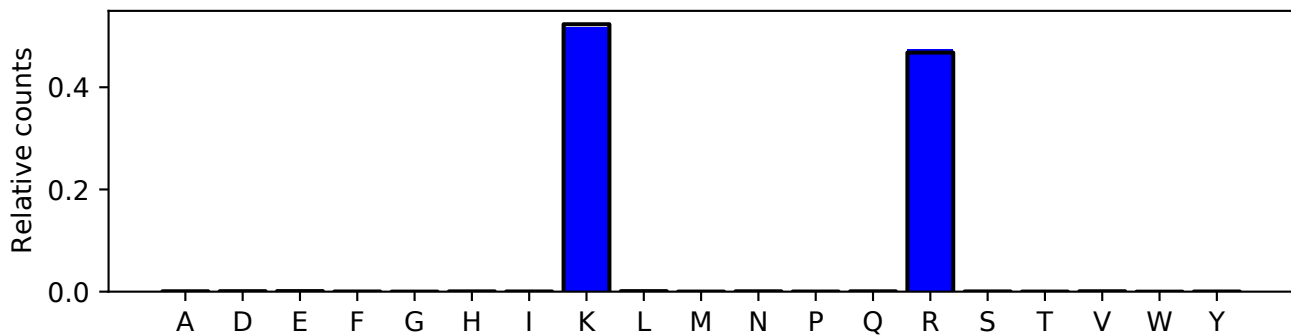
## Number of missed cleavages



## Amino acid before

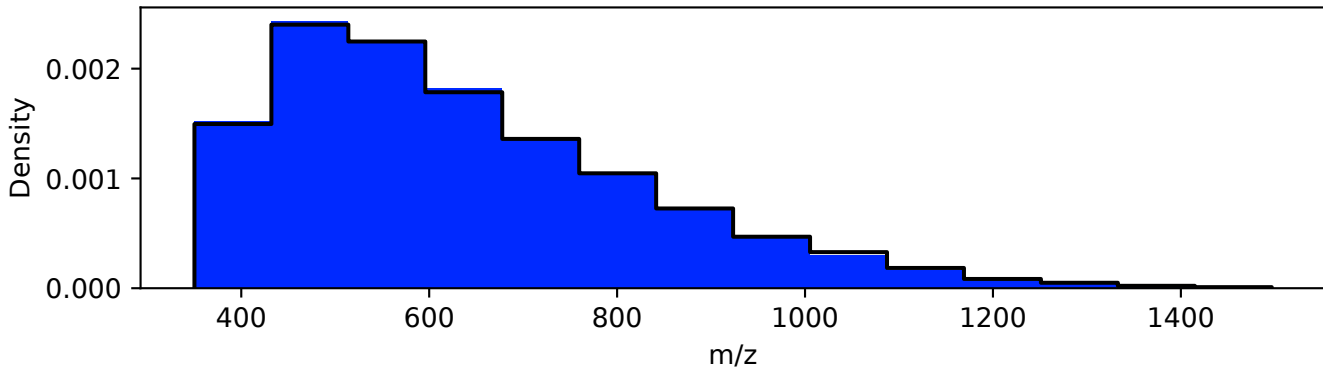


## Last amino acid

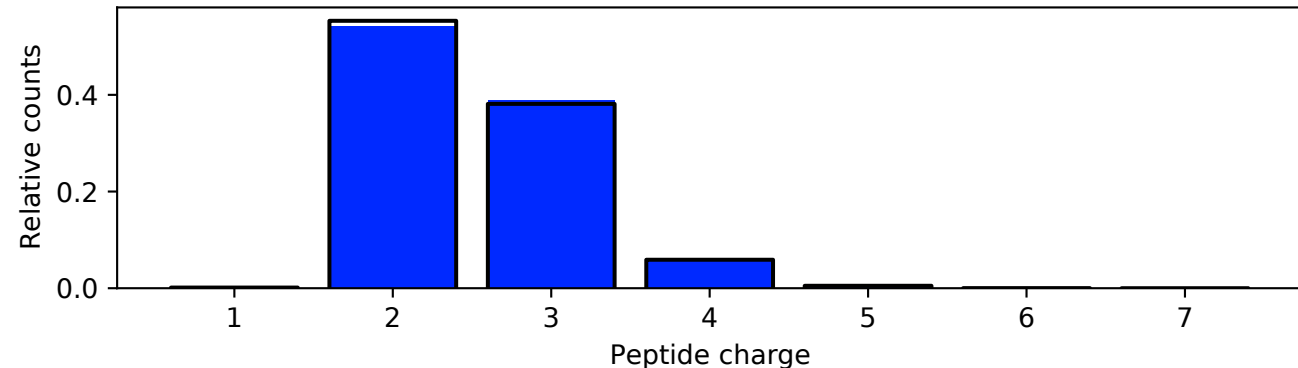


# H1975 TGFb Rep3 1

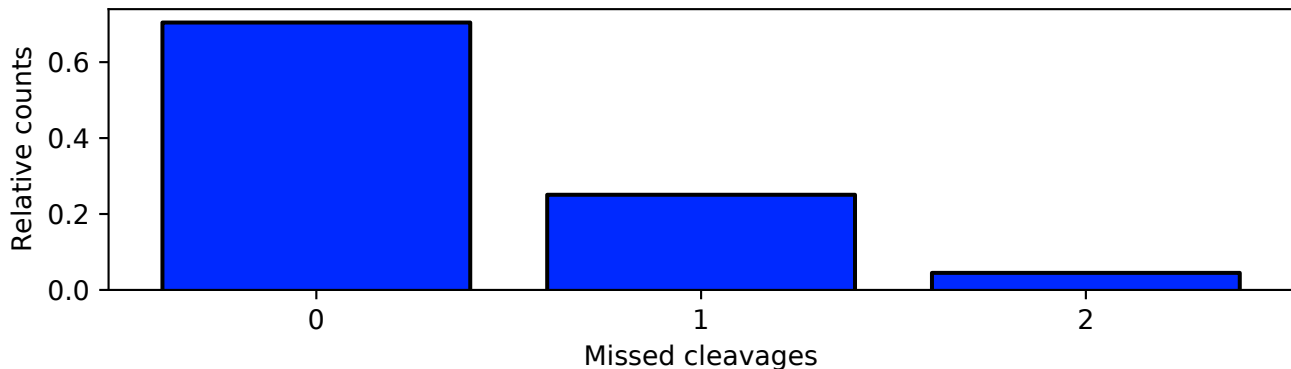
## Peptide m/z



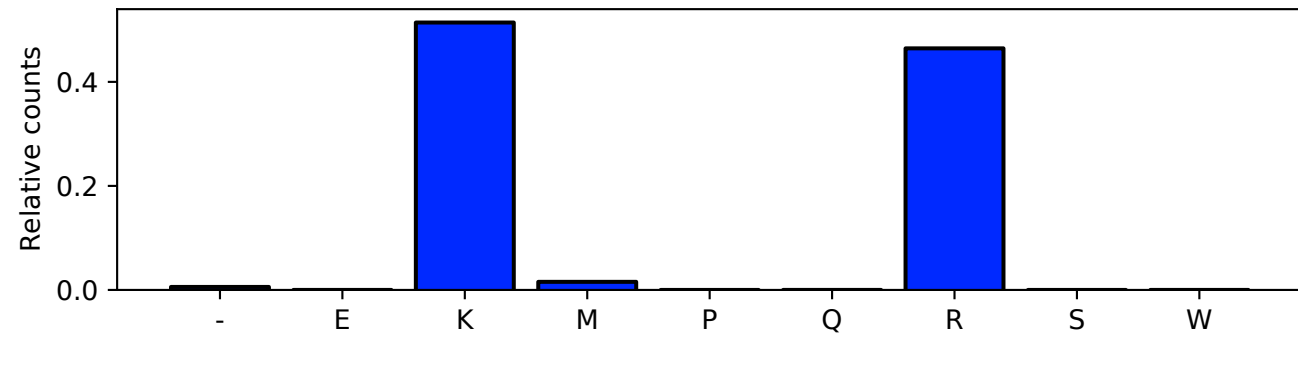
## Peptide charges



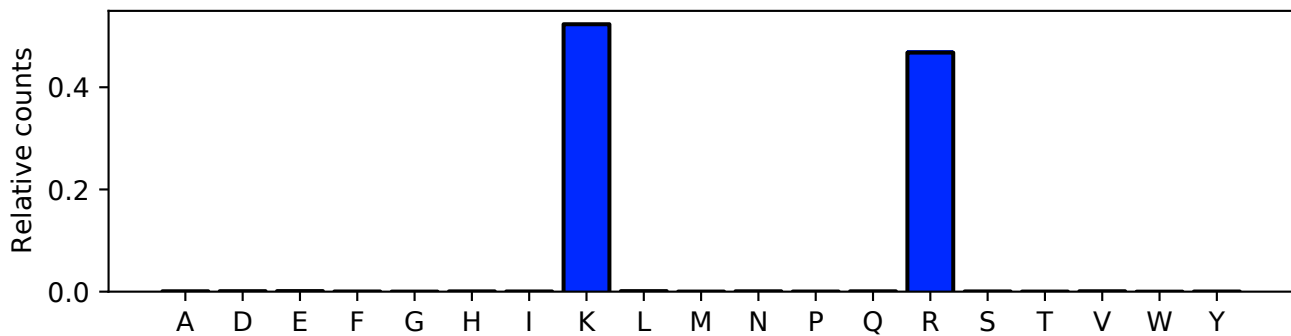
## Number of missed cleavages



## Amino acid before

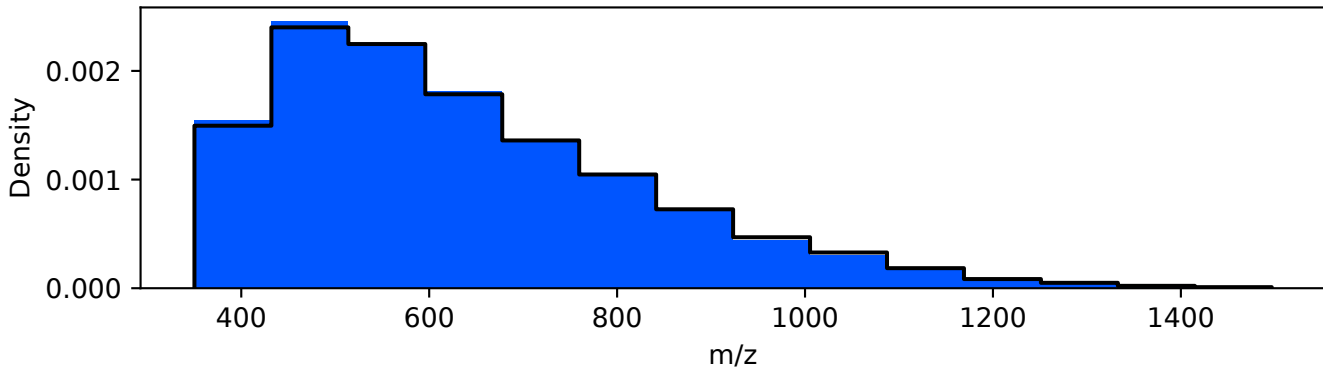


## Last amino acid

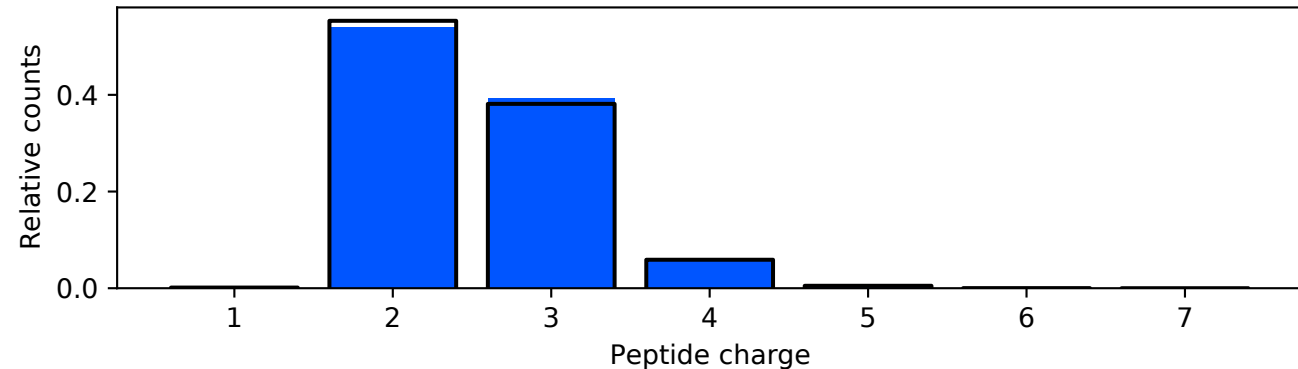


# H1975 TGFb Rep3 2

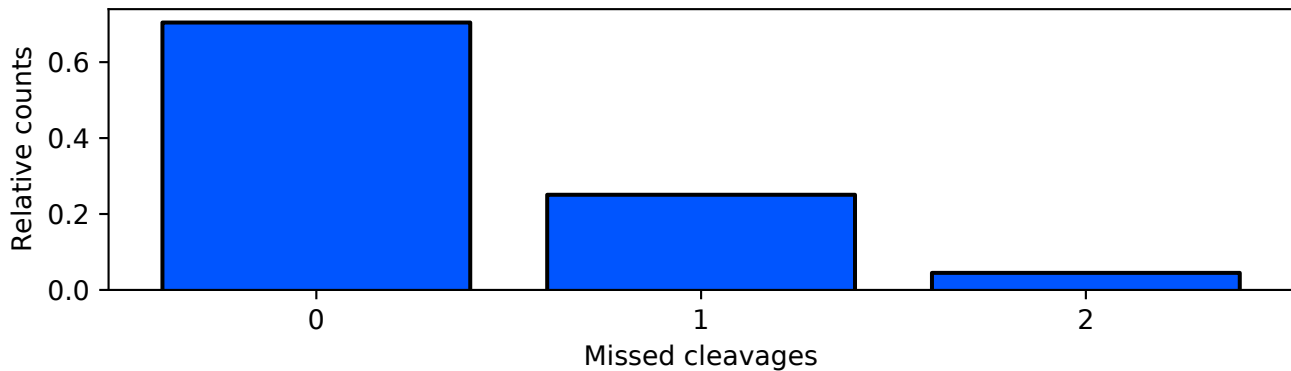
## Peptide m/z



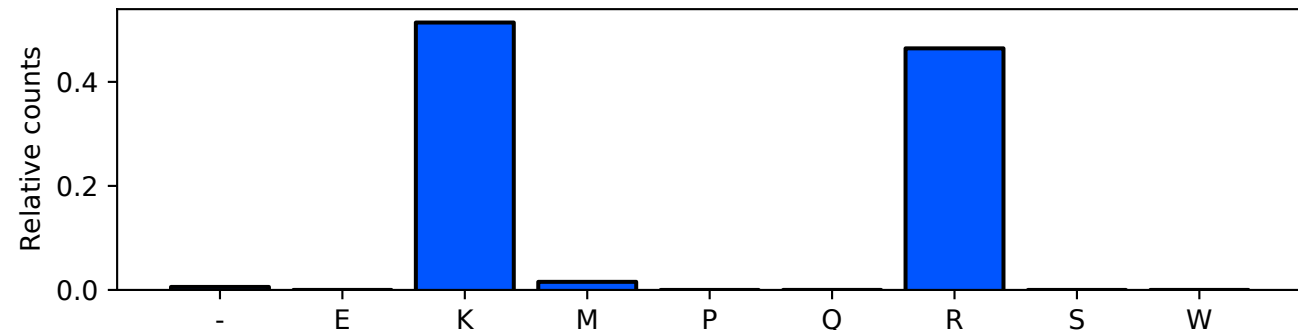
## Peptide charges



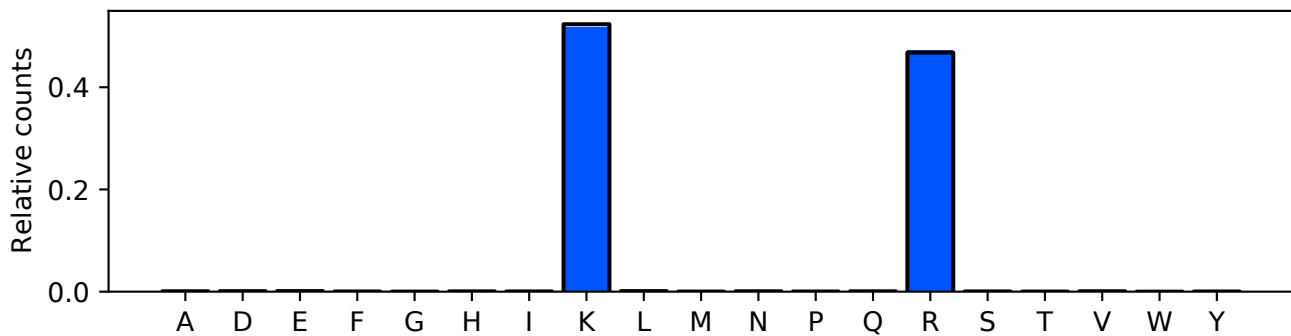
## Number of missed cleavages



## Amino acid before

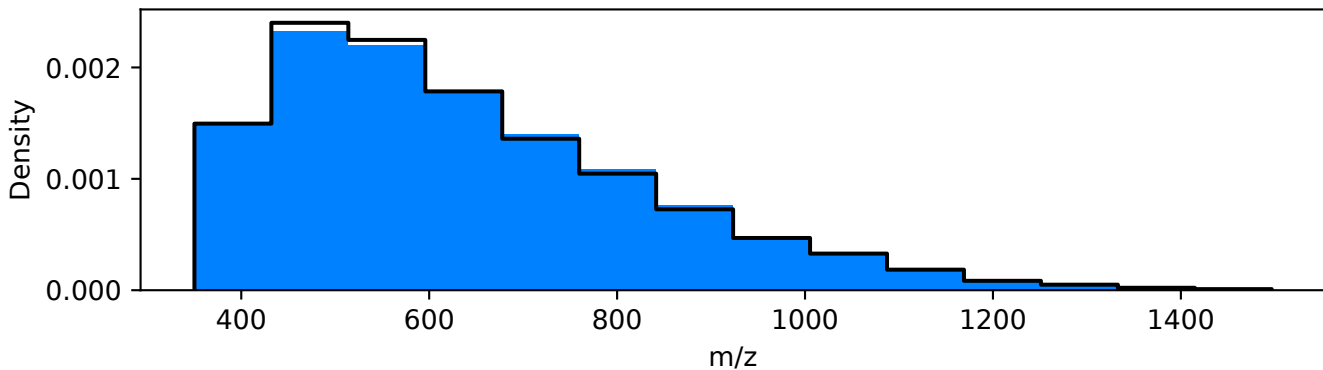


## Last amino acid

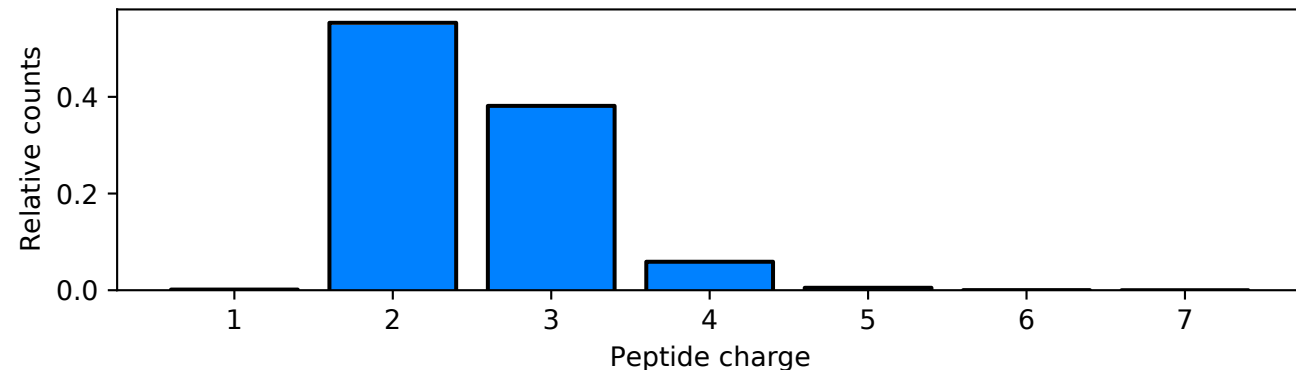


# H1975 unst Rep1 1

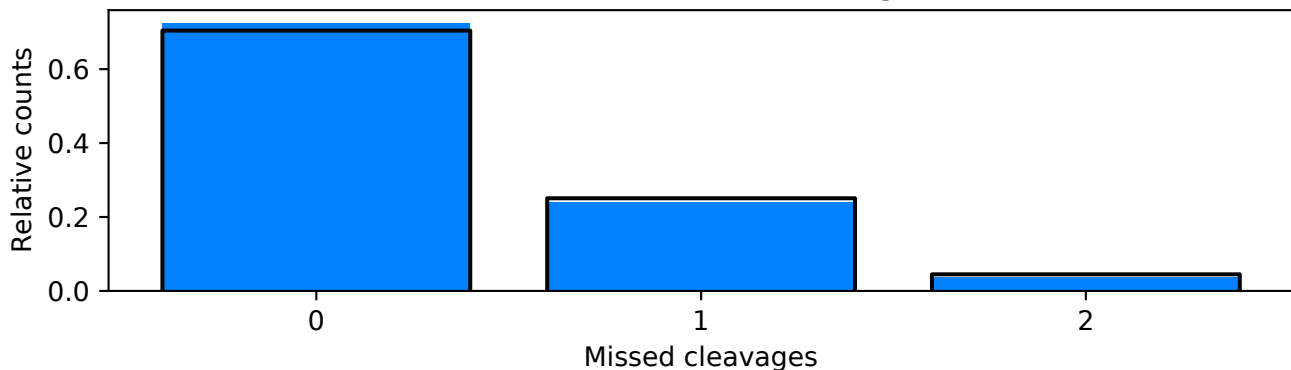
## Peptide m/z



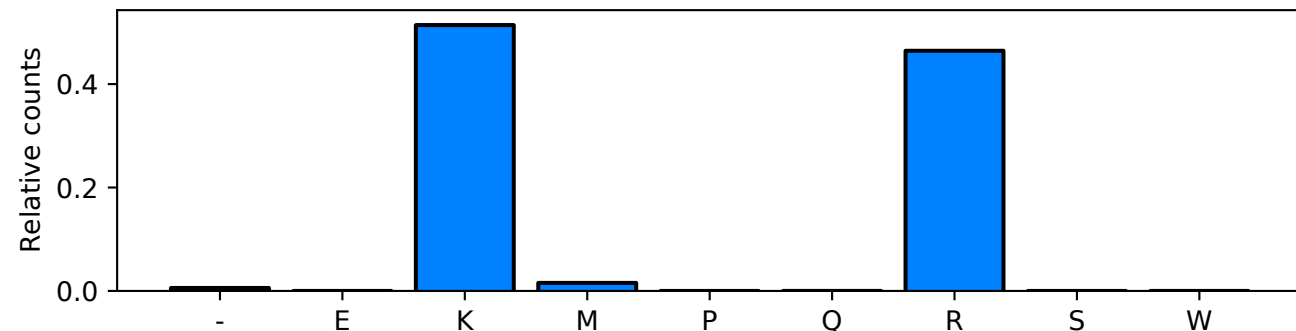
## Peptide charges



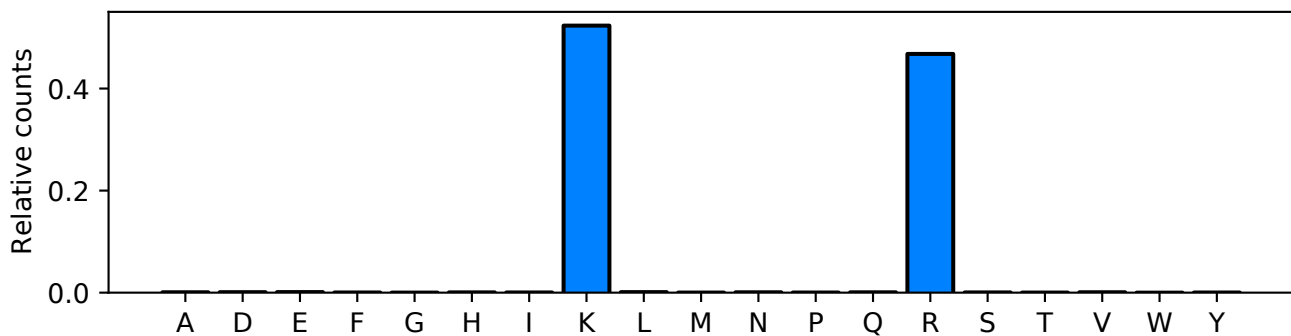
## Number of missed cleavages



## Amino acid before

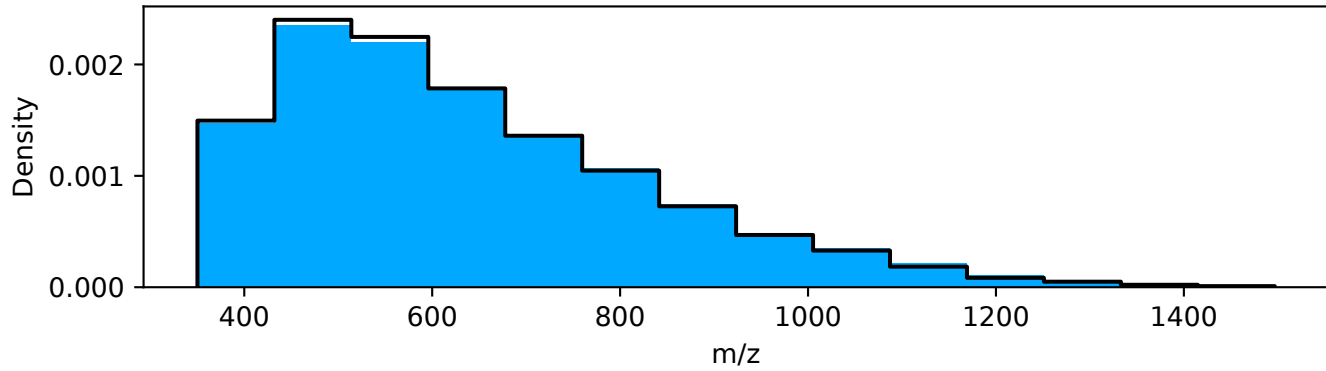


## Last amino acid

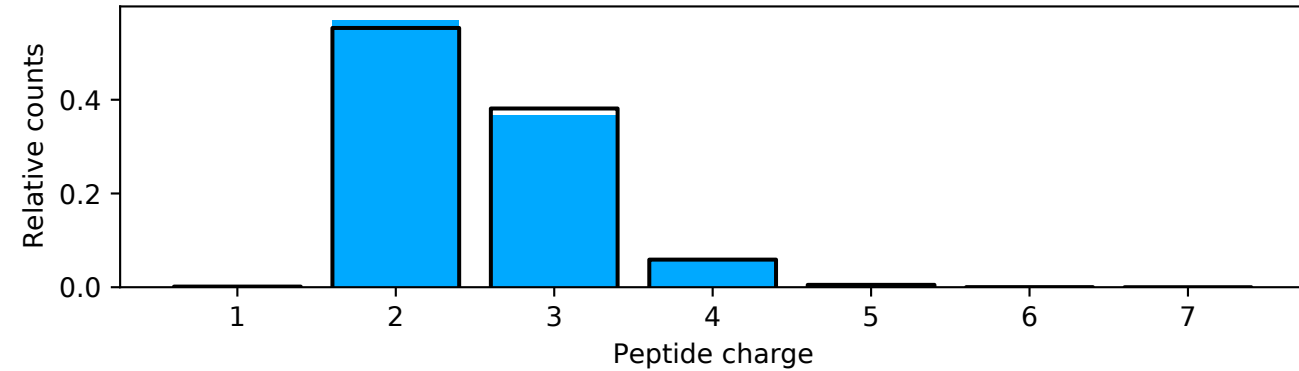


# H1975 unst Rep1 2

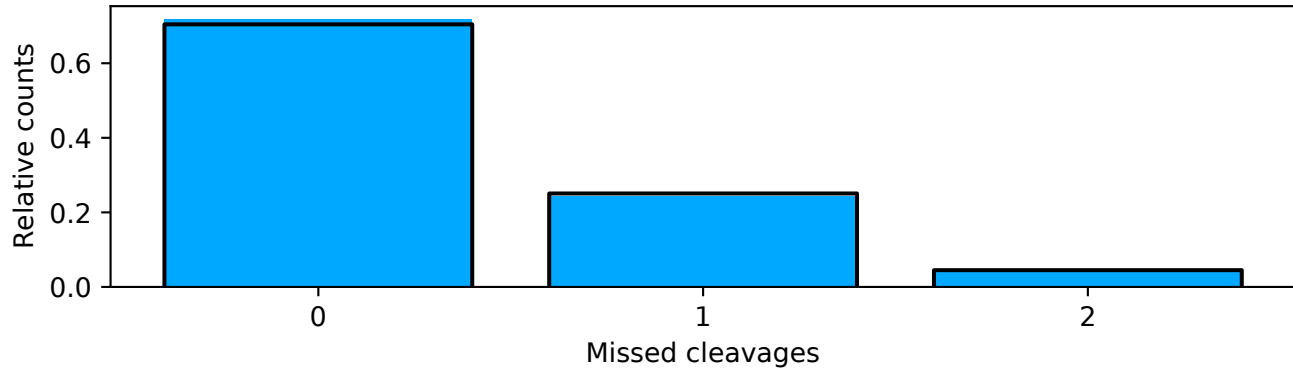
## Peptide m/z



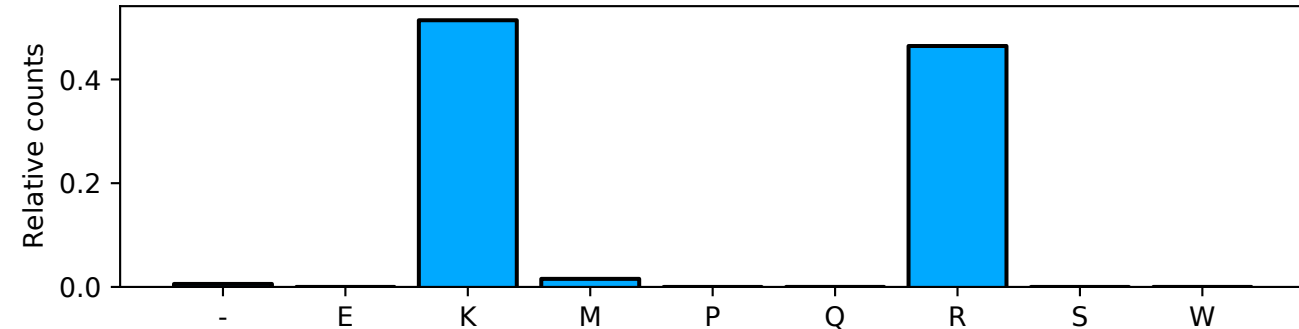
## Peptide charges



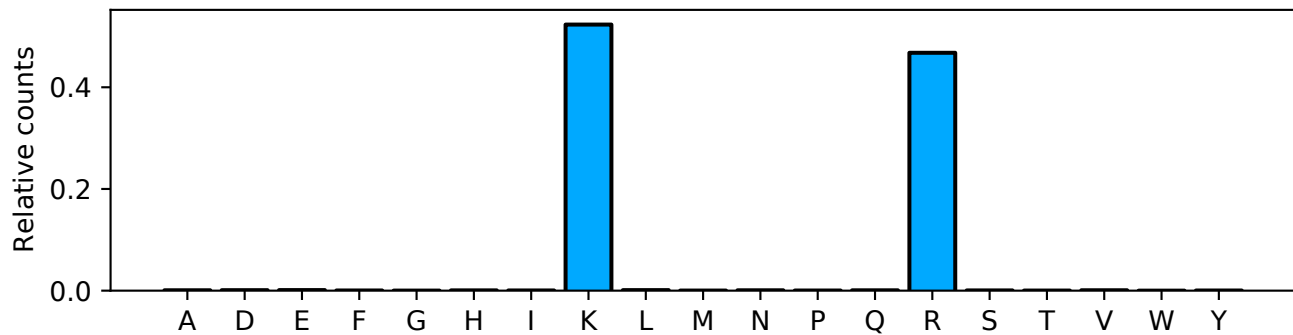
## Number of missed cleavages



## Amino acid before

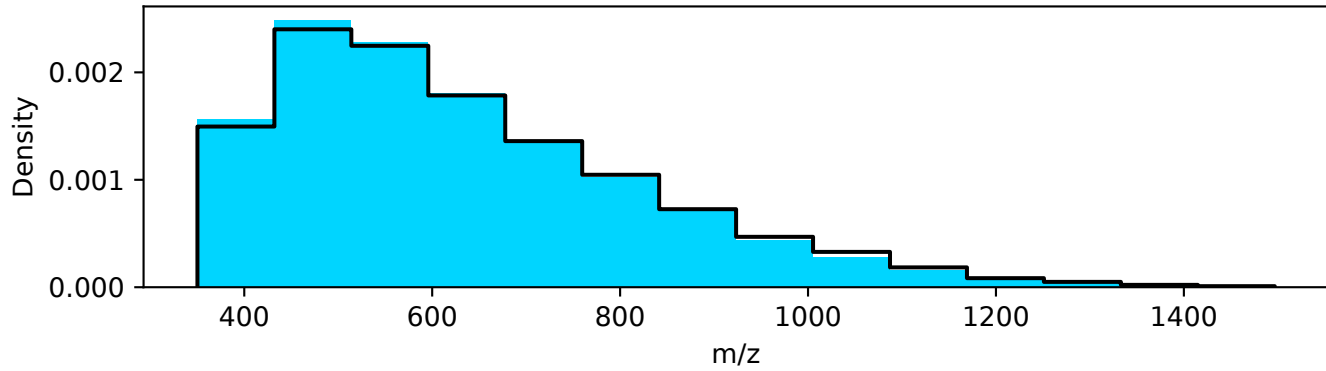


## Last amino acid

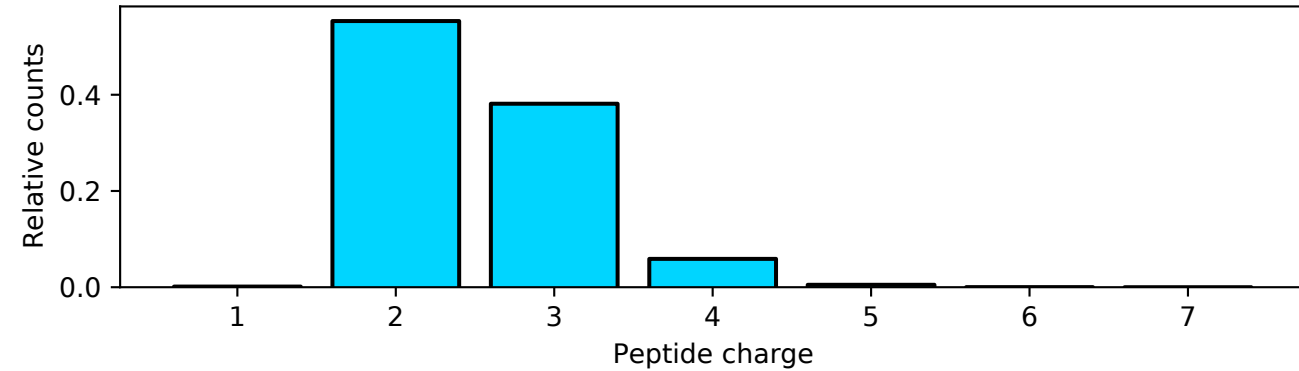


# H1975 unst Rep2 1

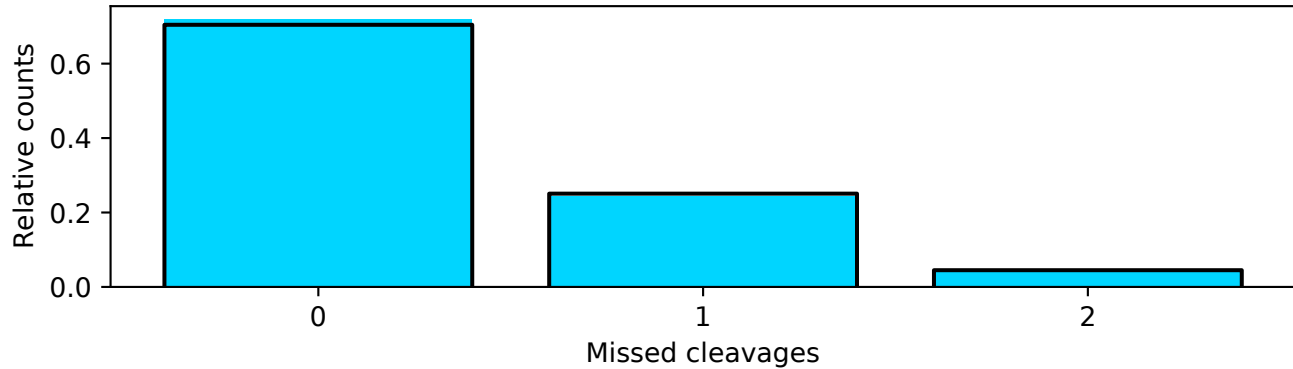
## Peptide m/z



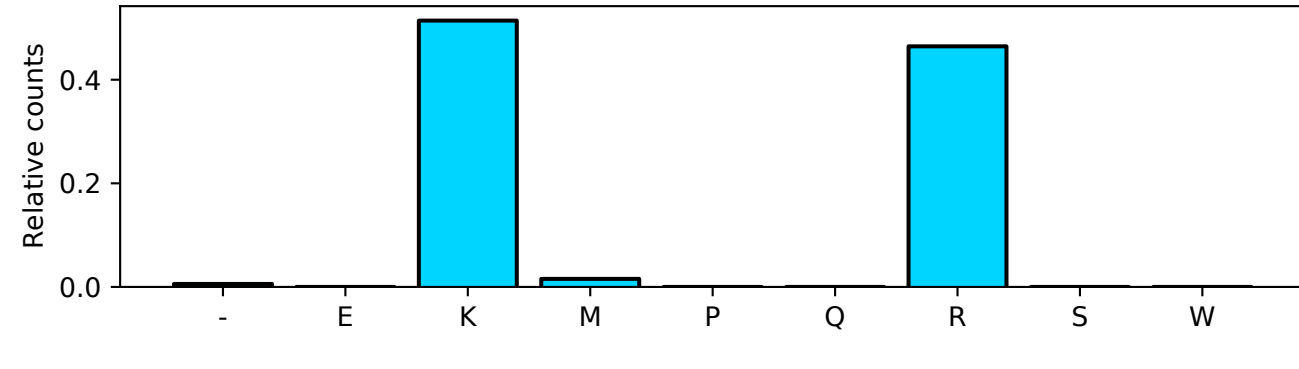
## Peptide charges



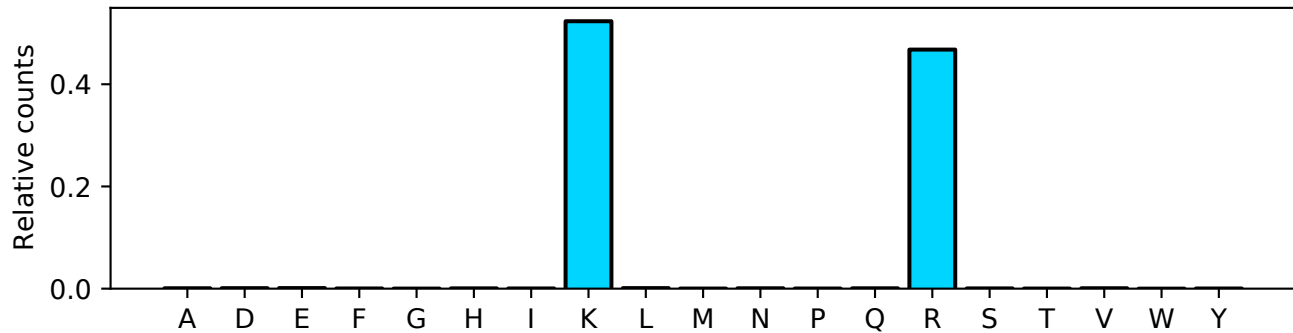
## Number of missed cleavages



## Amino acid before

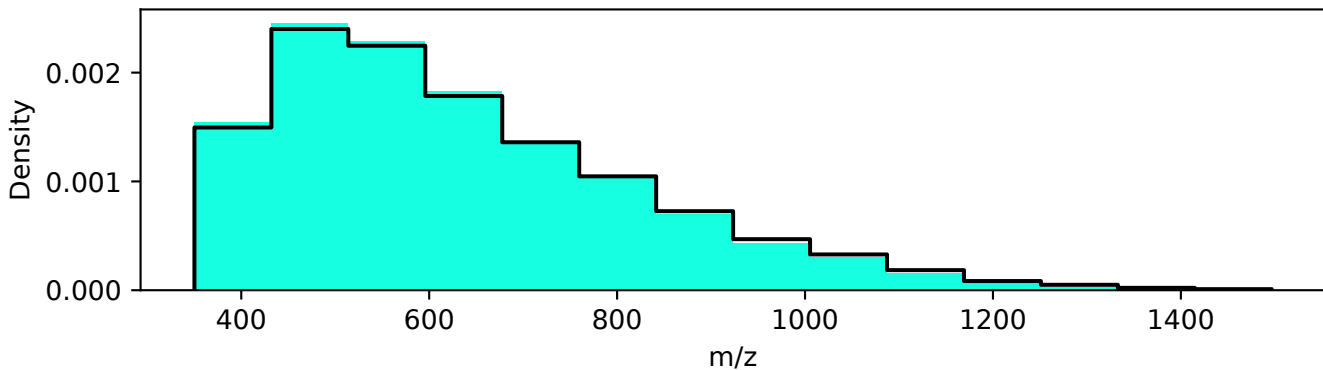


## Last amino acid

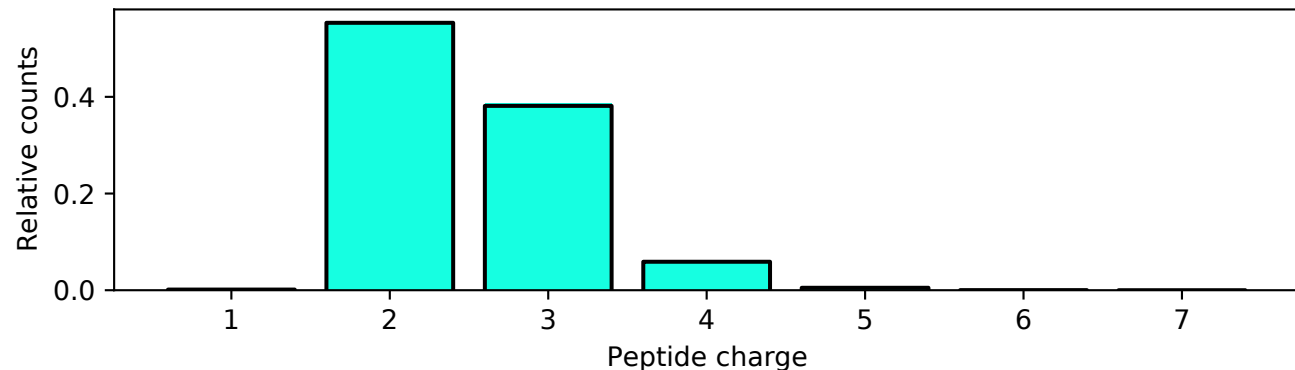


# H1975 unst Rep2 2

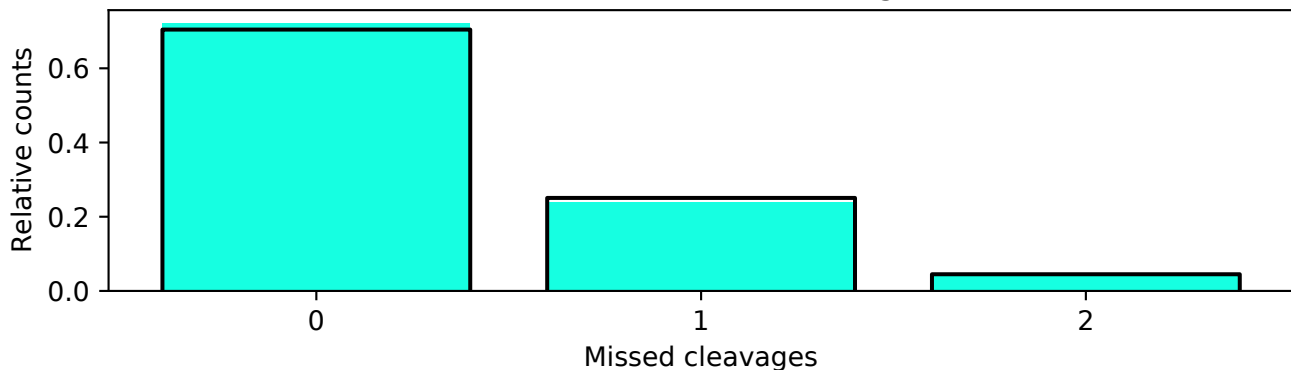
## Peptide m/z



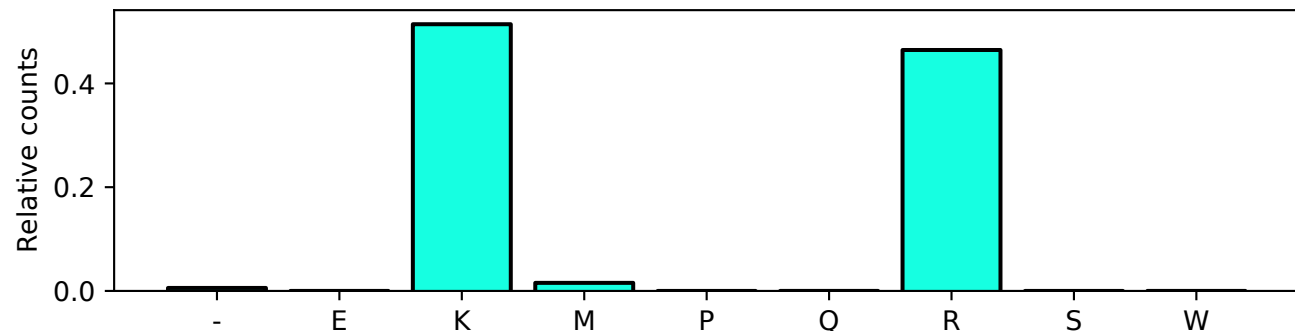
## Peptide charges



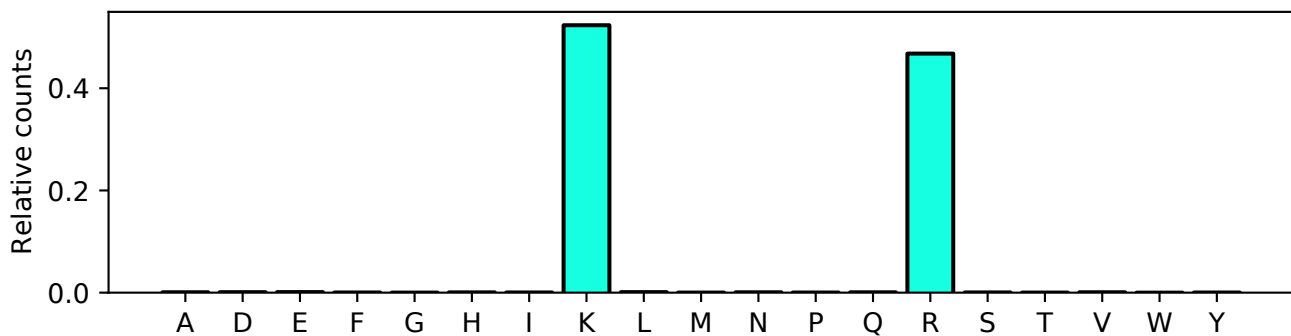
## Number of missed cleavages



## Amino acid before

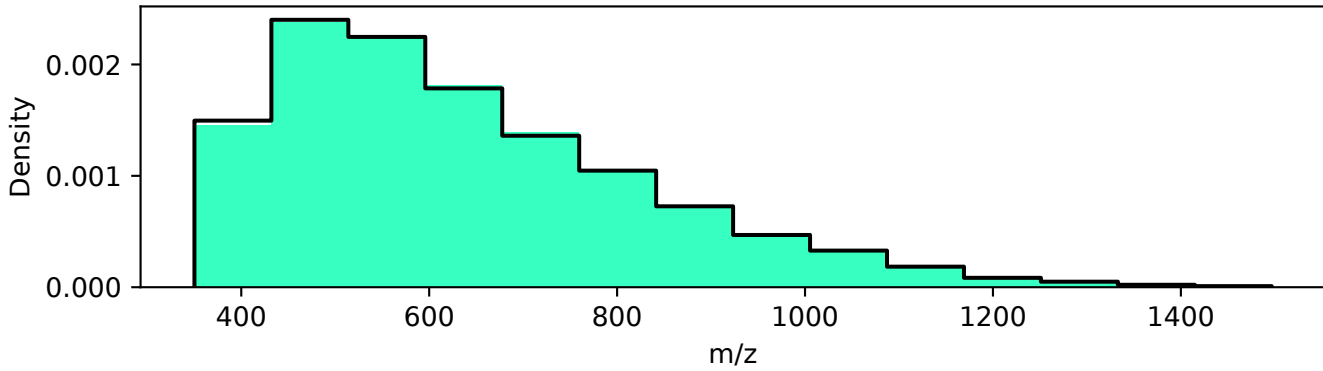


## Last amino acid

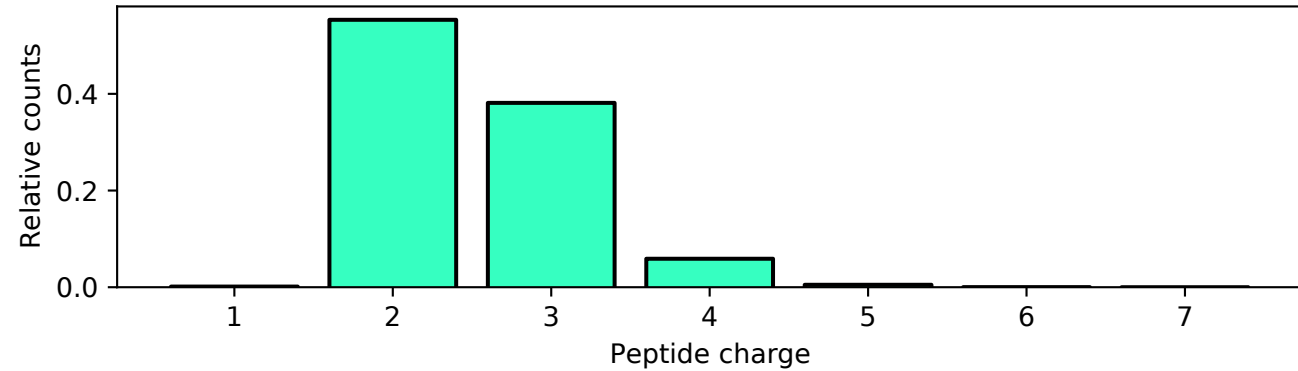


# H1975 unst Rep3 1

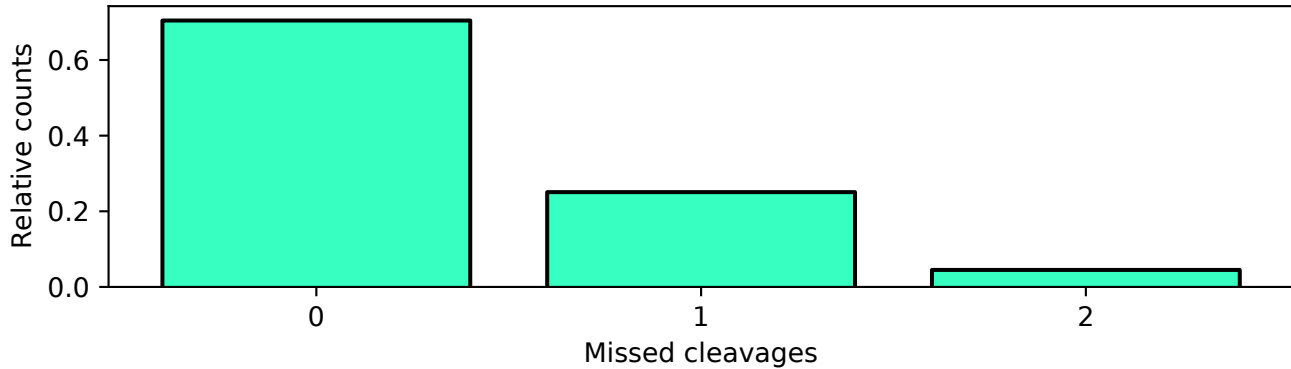
## Peptide m/z



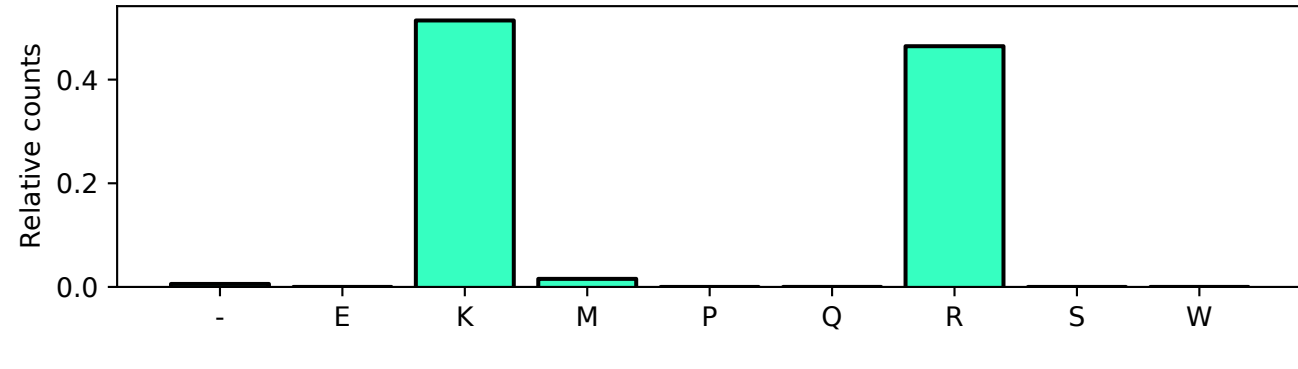
## Peptide charges



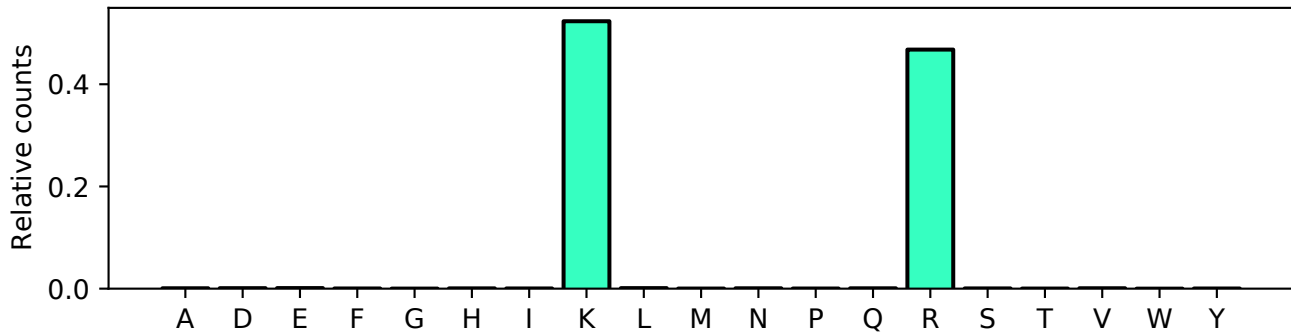
## Number of missed cleavages



## Amino acid before

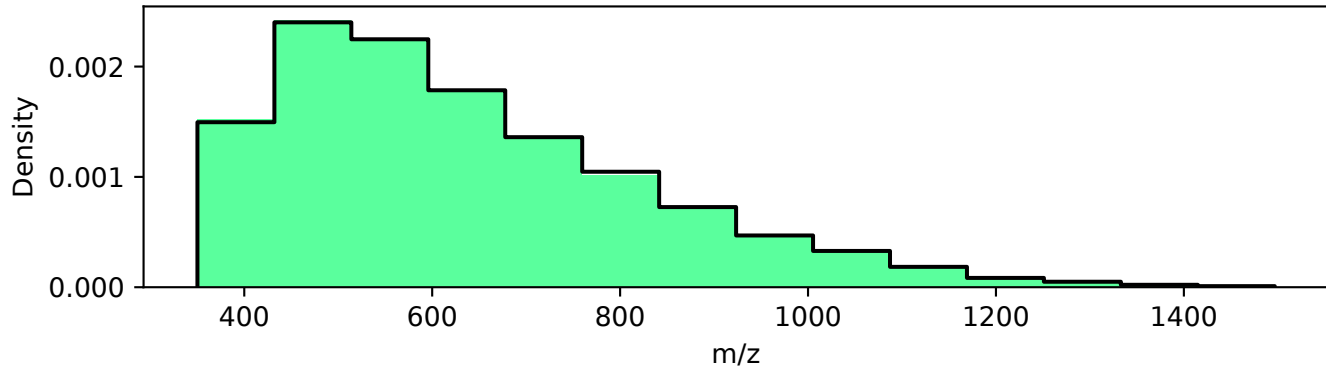


## Last amino acid

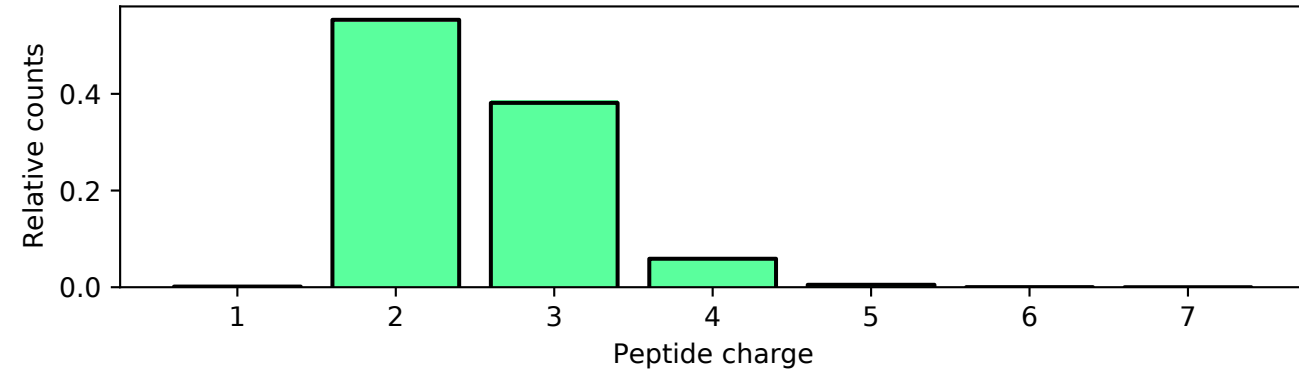


# H1975 unst Rep3 2

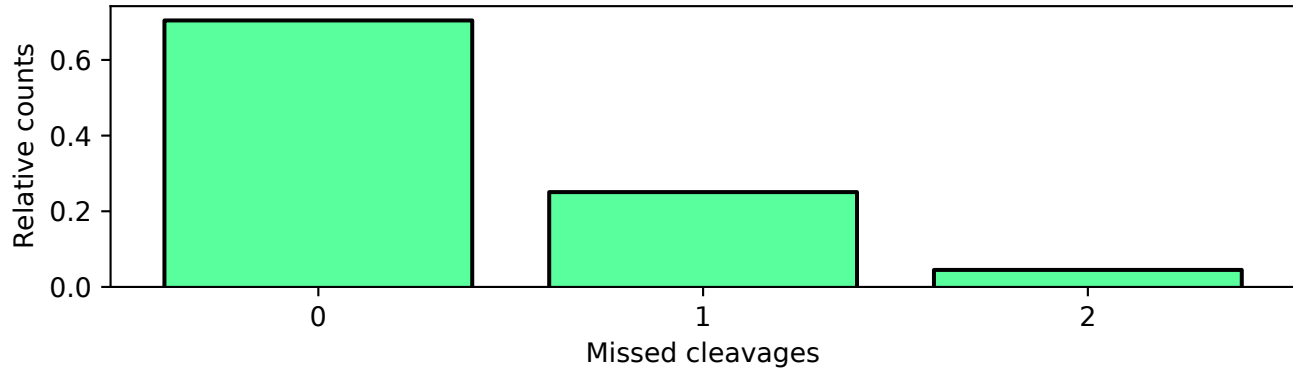
## Peptide m/z



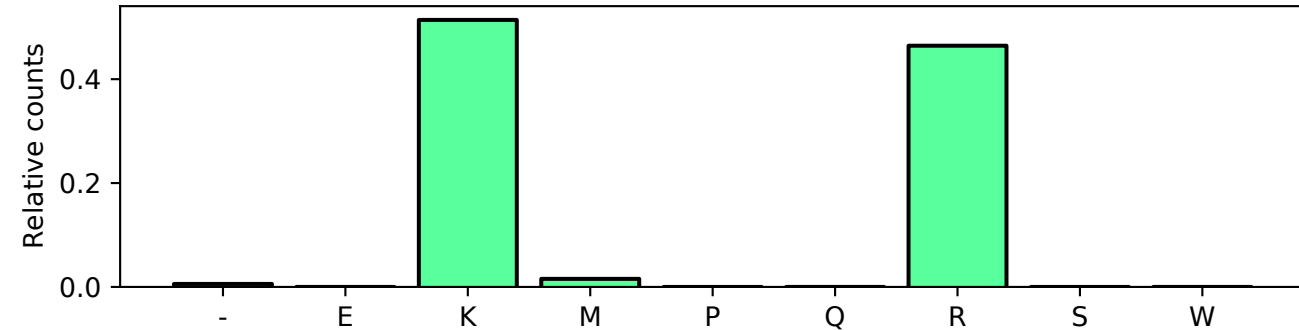
## Peptide charges



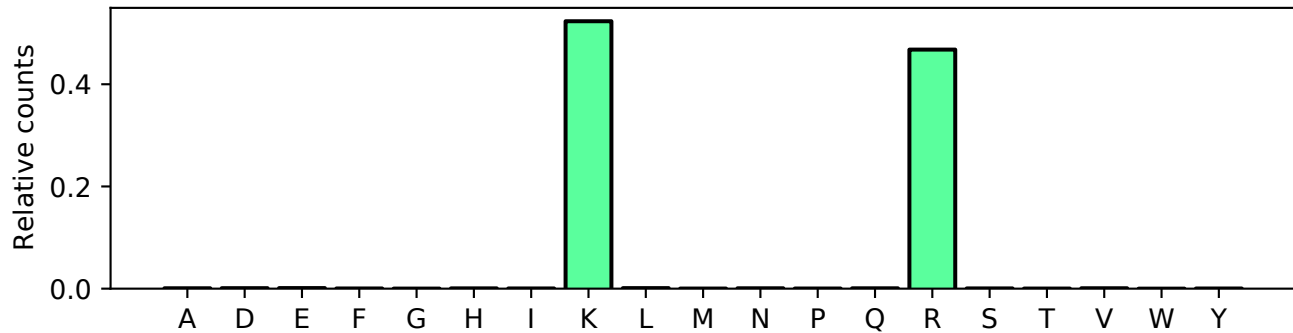
## Number of missed cleavages



## Amino acid before

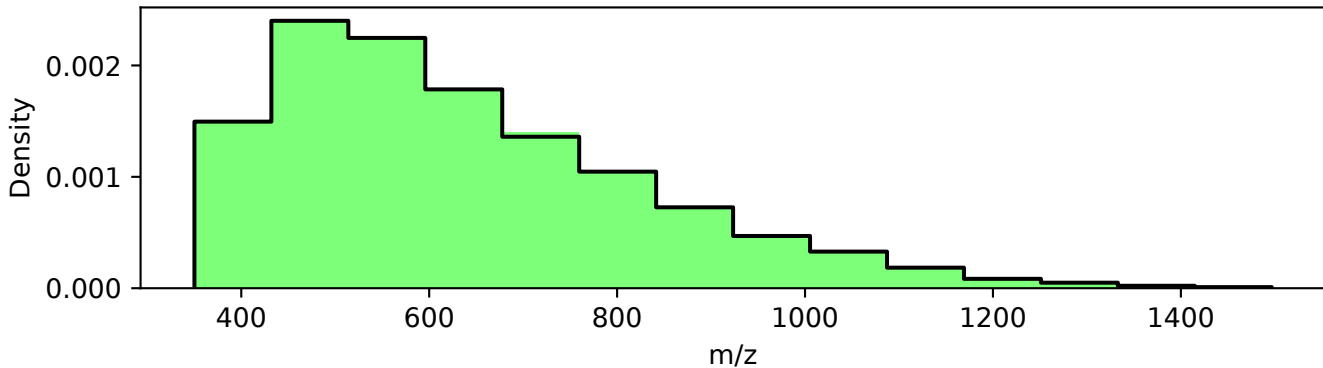


## Last amino acid

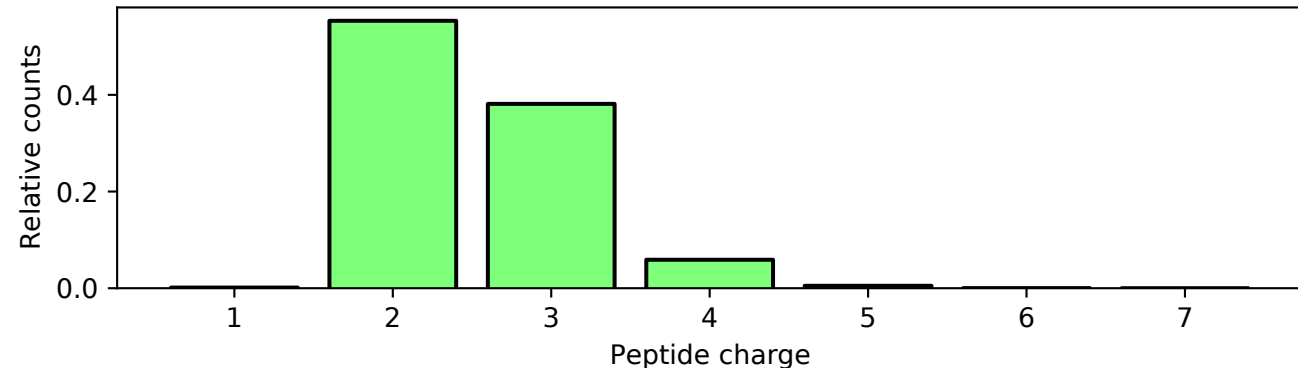


# H838 TGFb Rep1 1

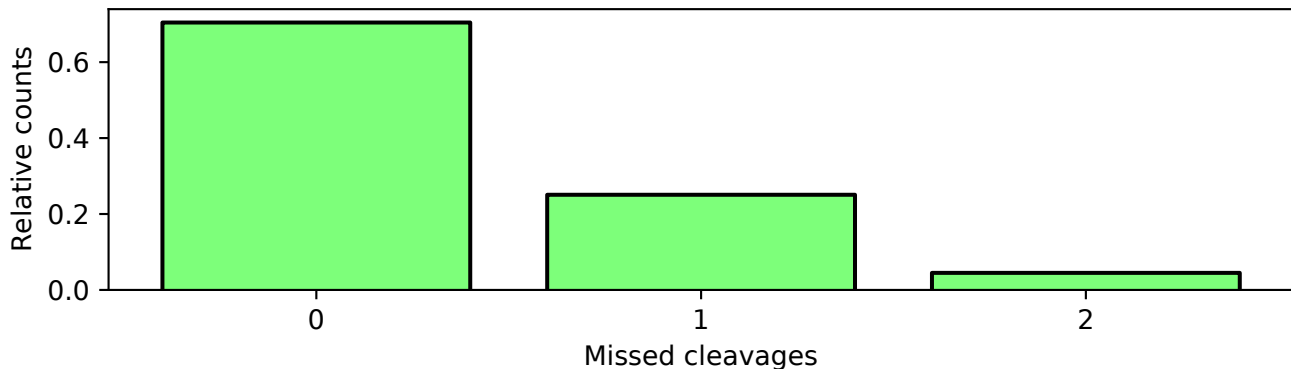
## Peptide m/z



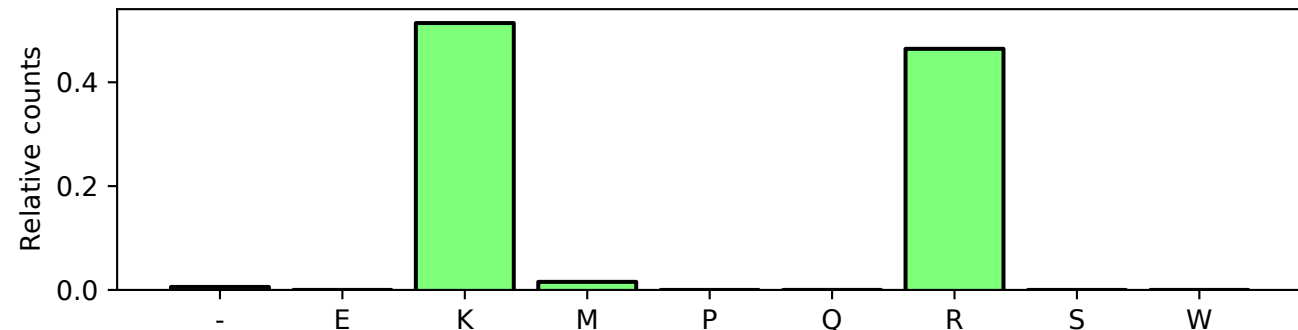
## Peptide charges



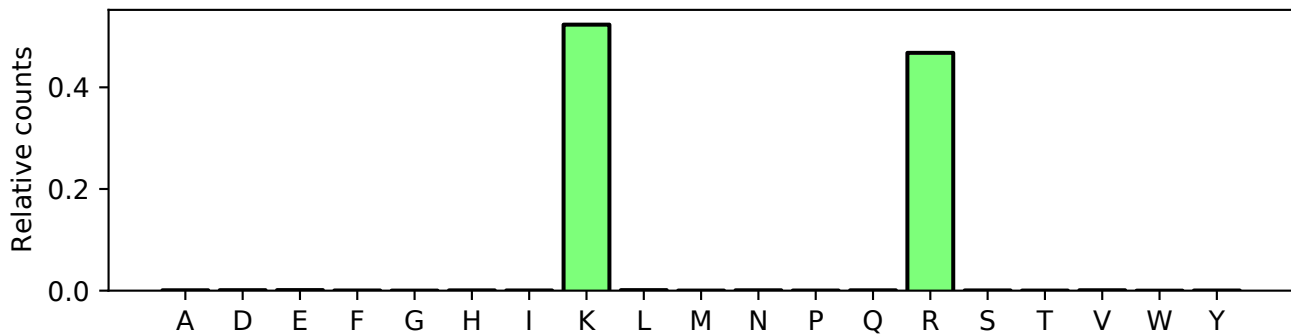
## Number of missed cleavages



## Amino acid before

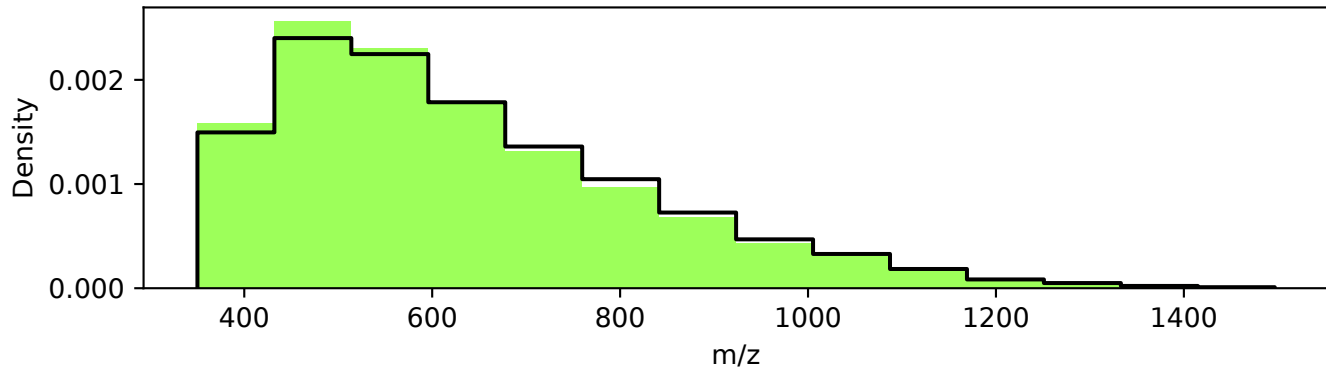


## Last amino acid

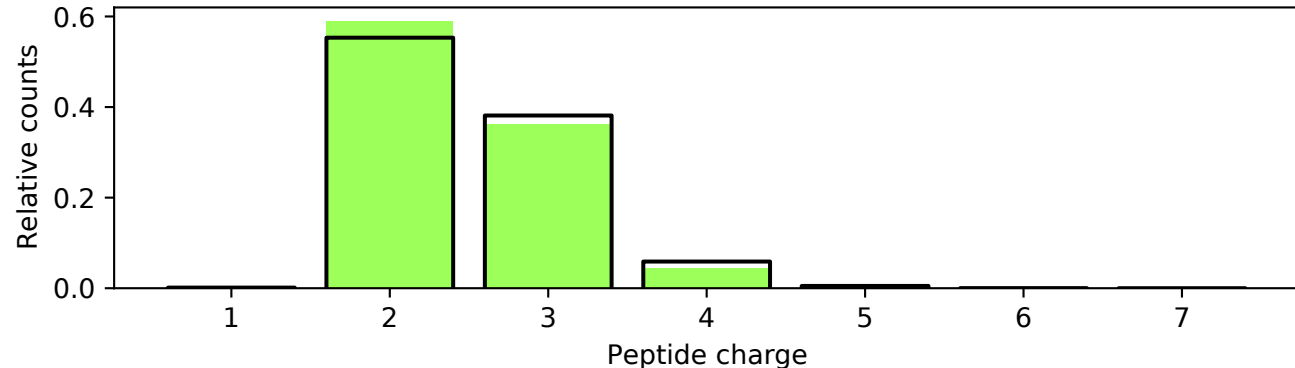


# H838 TGFb Rep1 2

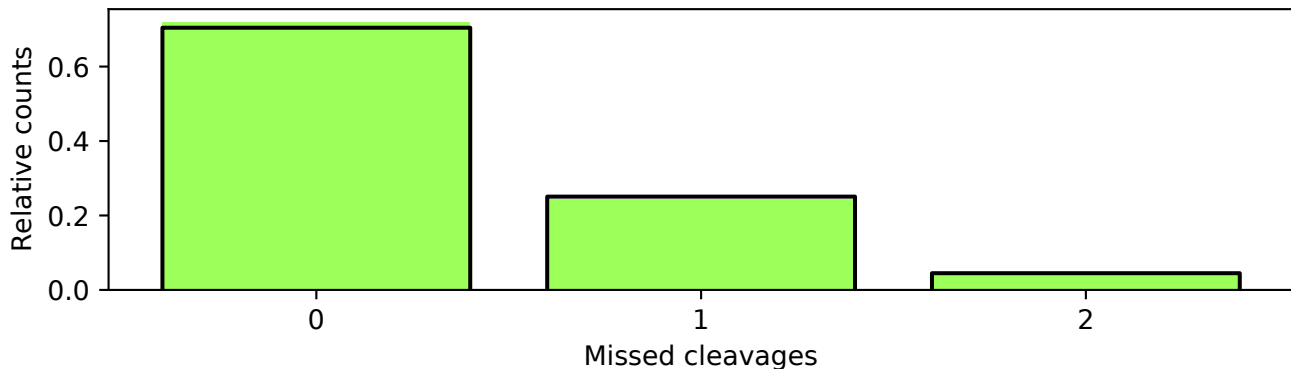
## Peptide m/z



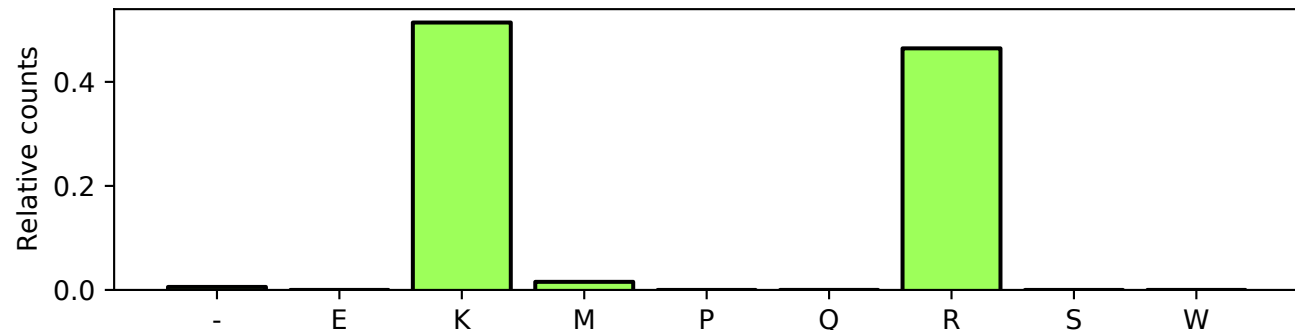
## Peptide charges



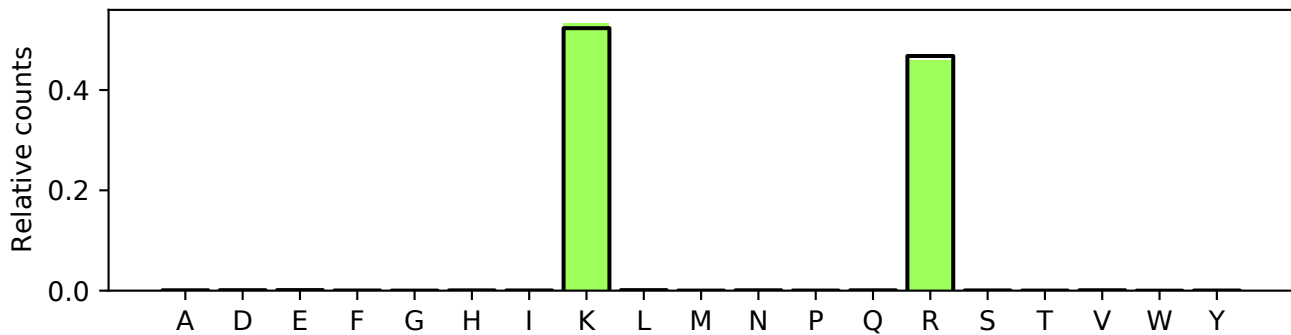
## Number of missed cleavages



## Amino acid before

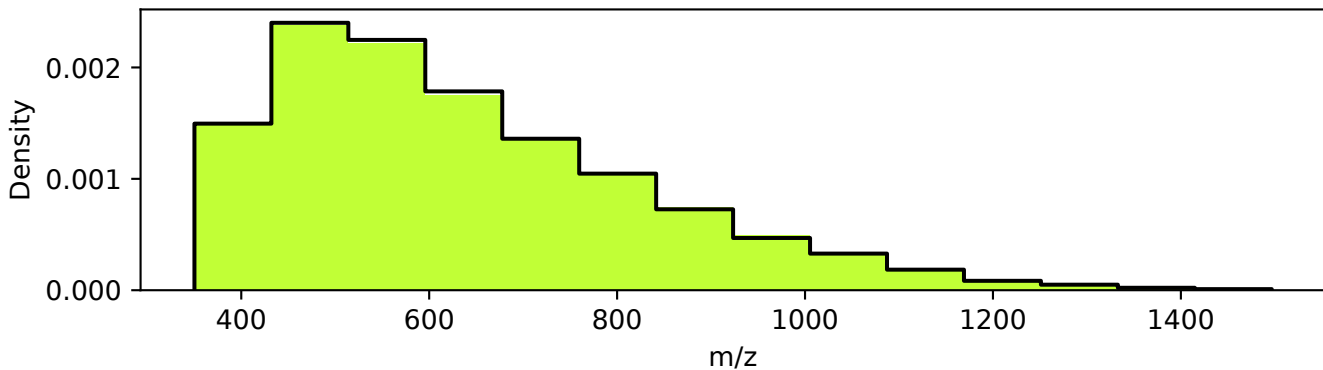


## Last amino acid

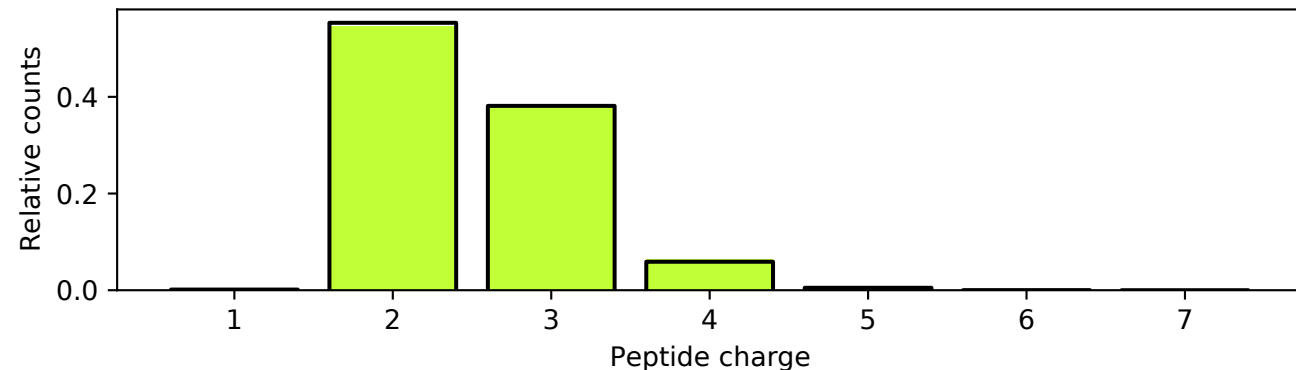


# H838 TGFb Rep2 1

## Peptide m/z



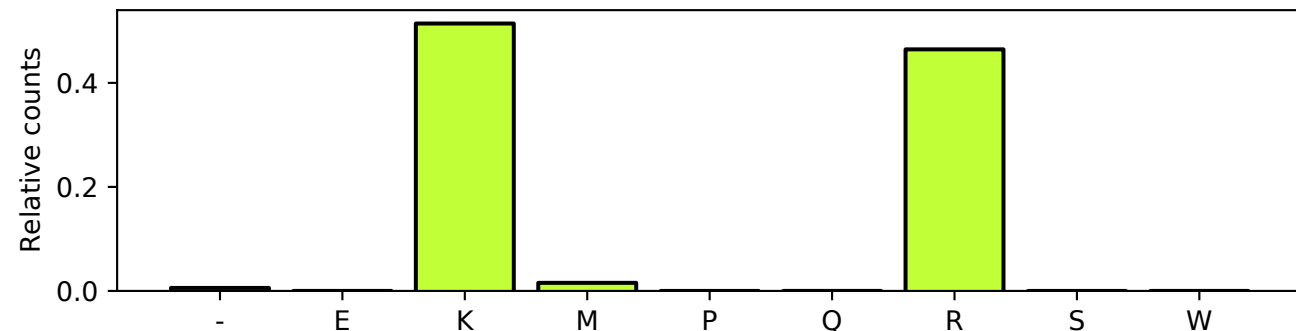
## Peptide charges



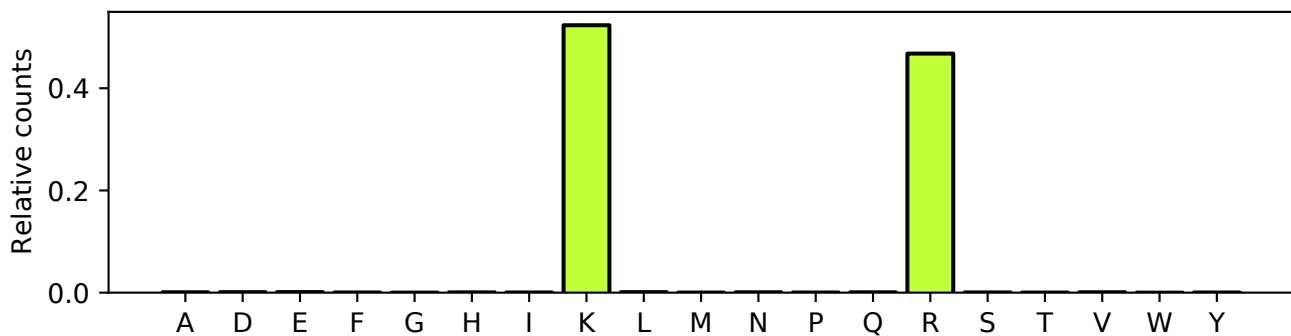
## Number of missed cleavages



## Amino acid before

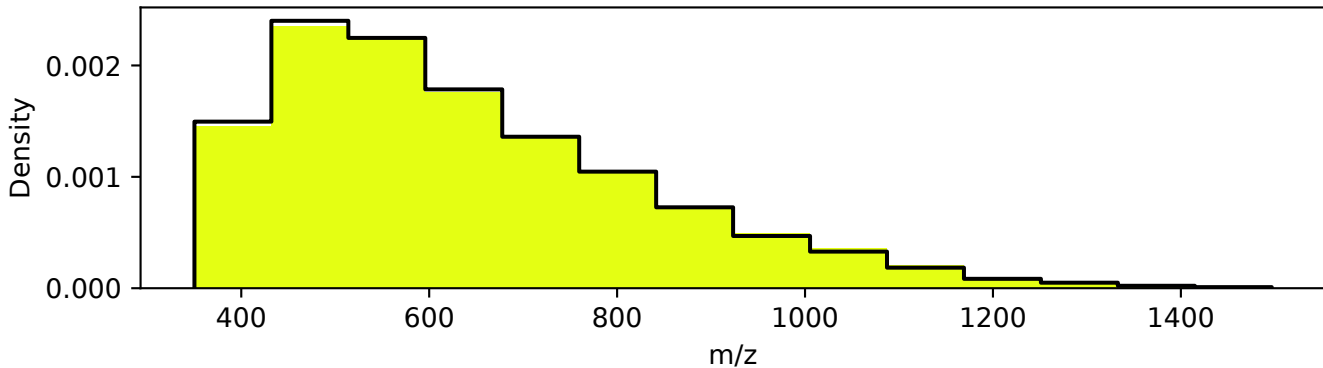


## Last amino acid

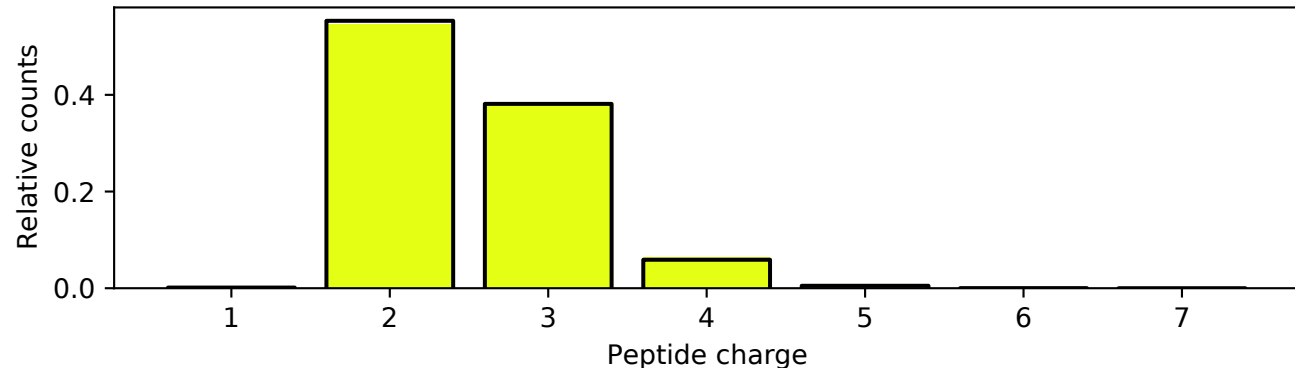


# H838 TGFb Rep2 2

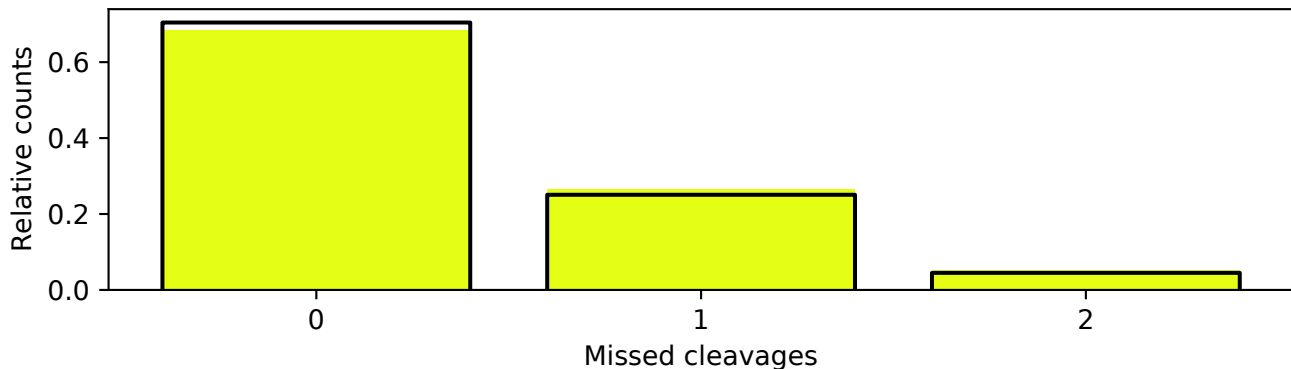
## Peptide m/z



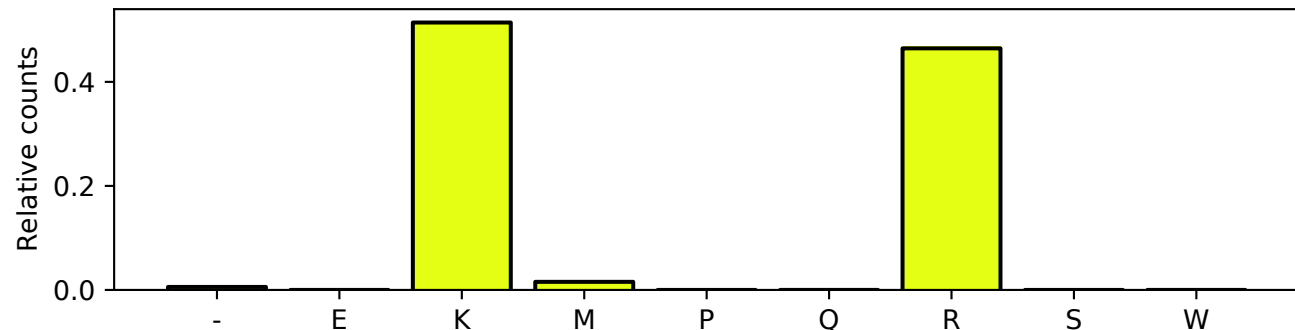
## Peptide charges



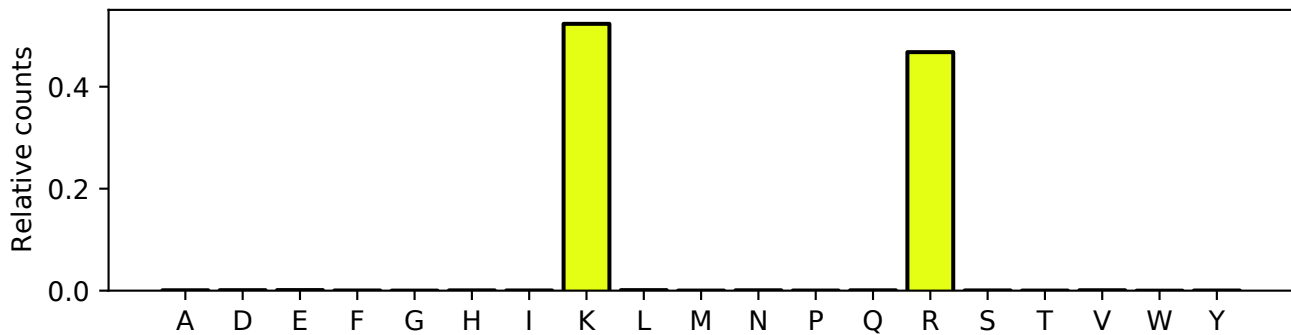
## Number of missed cleavages



## Amino acid before

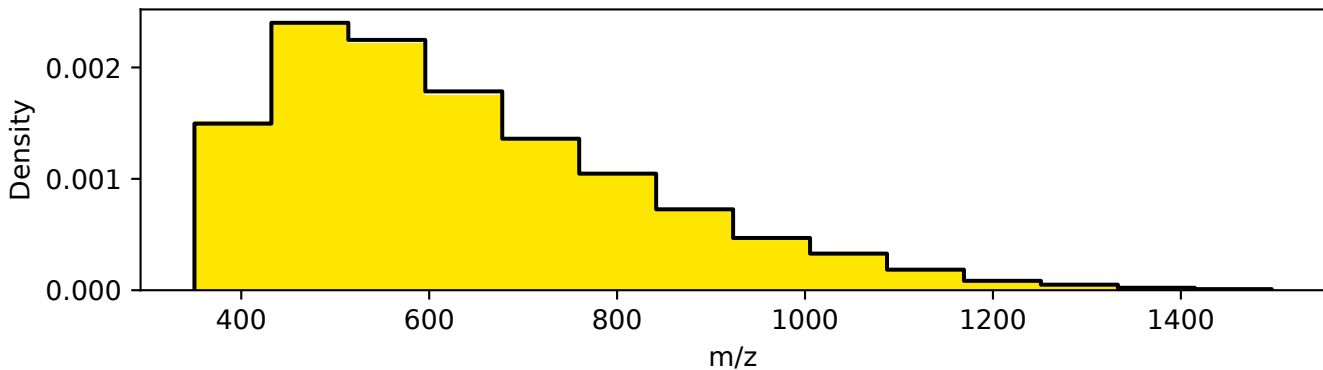


## Last amino acid

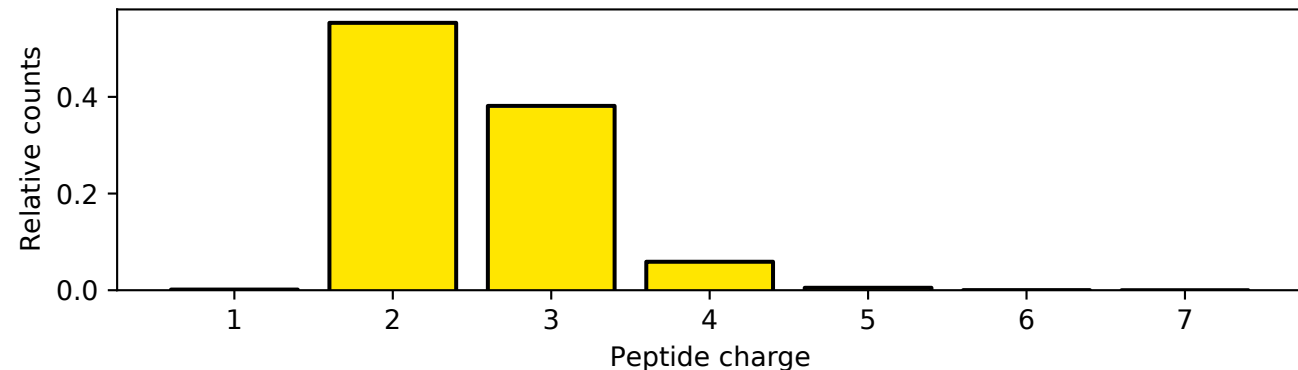


# H838 TGFb Rep3 1

## Peptide m/z



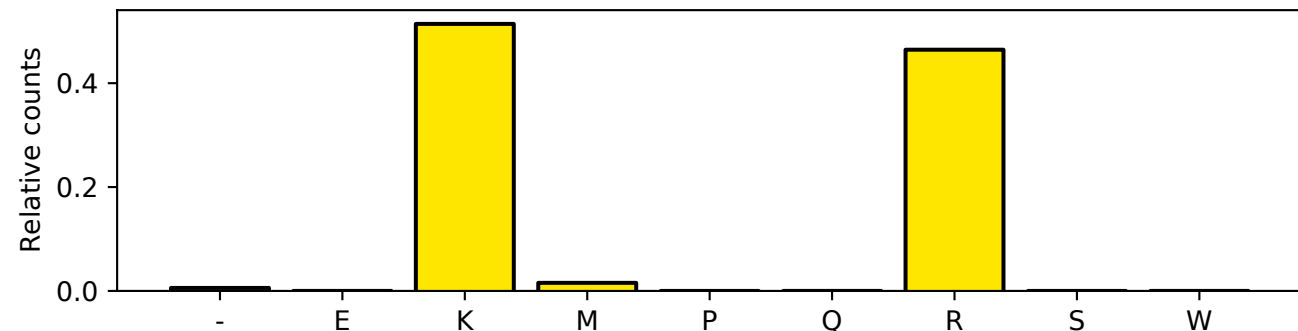
## Peptide charges



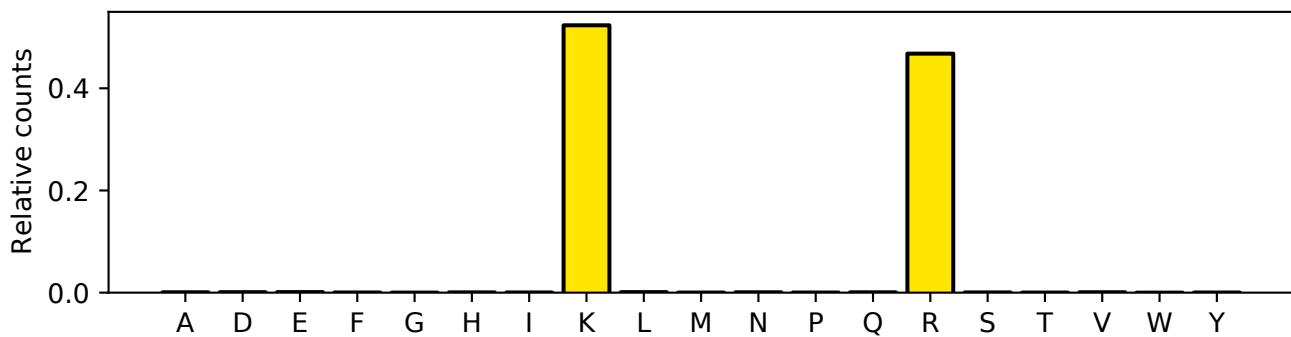
## Number of missed cleavages



## Amino acid before

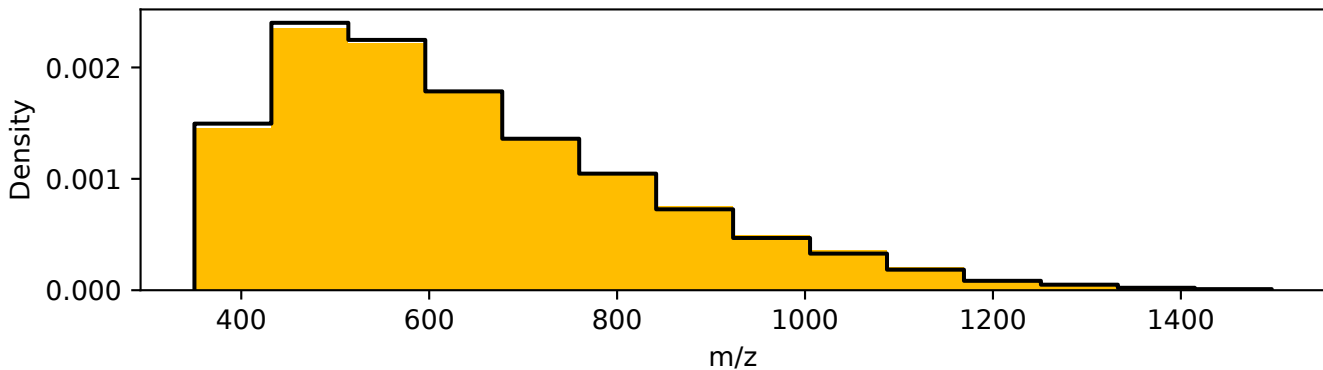


## Last amino acid

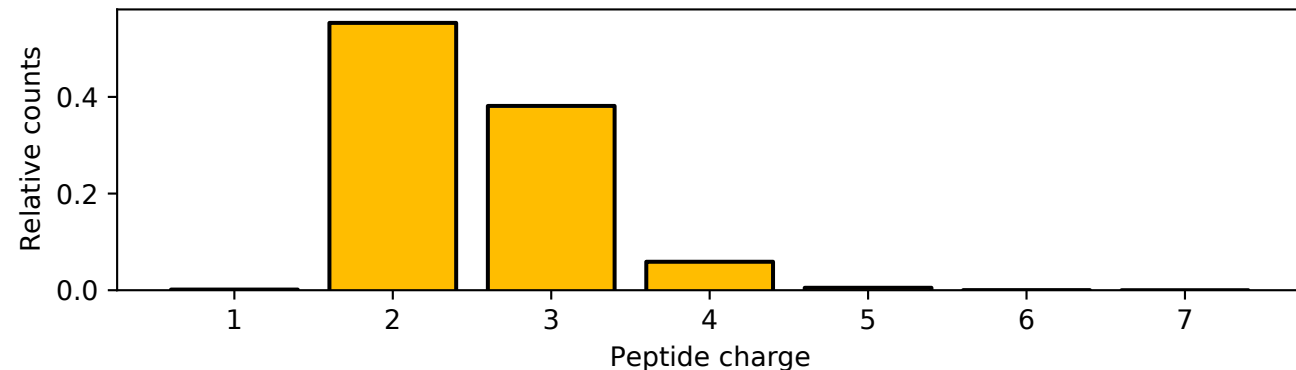


# H838 TGFb Rep3 2

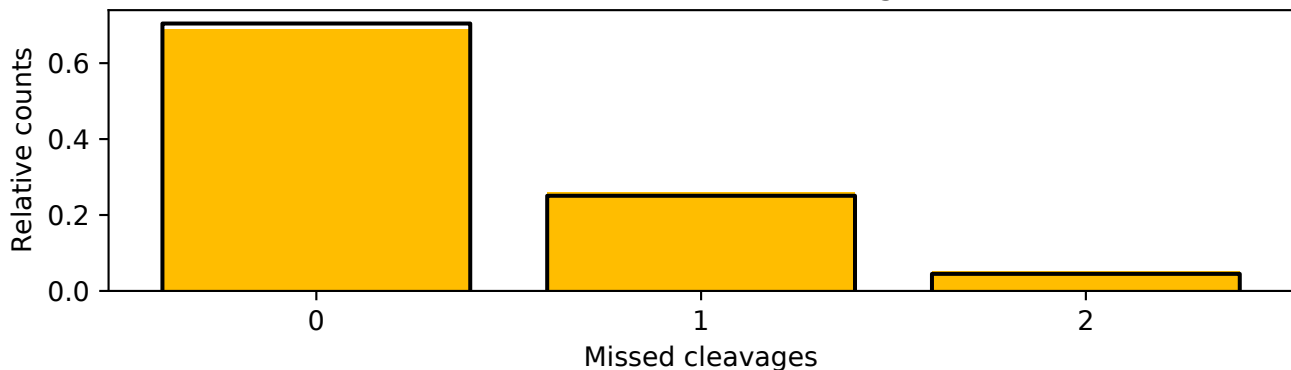
## Peptide m/z



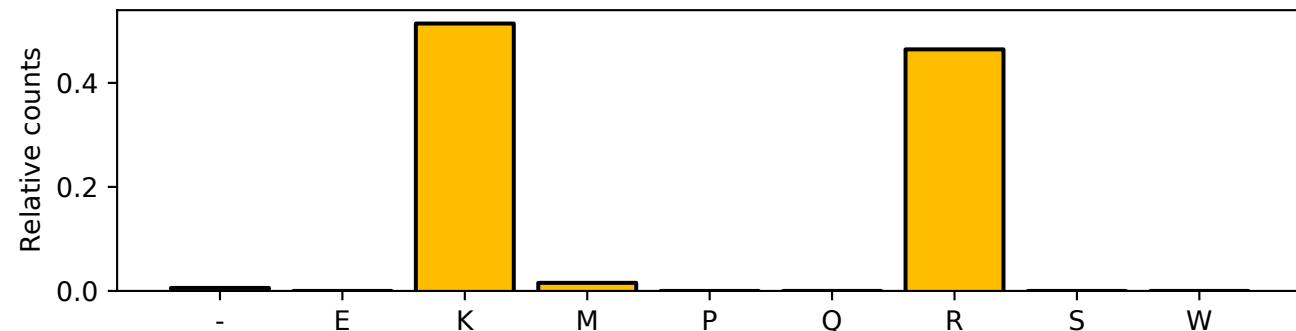
## Peptide charges



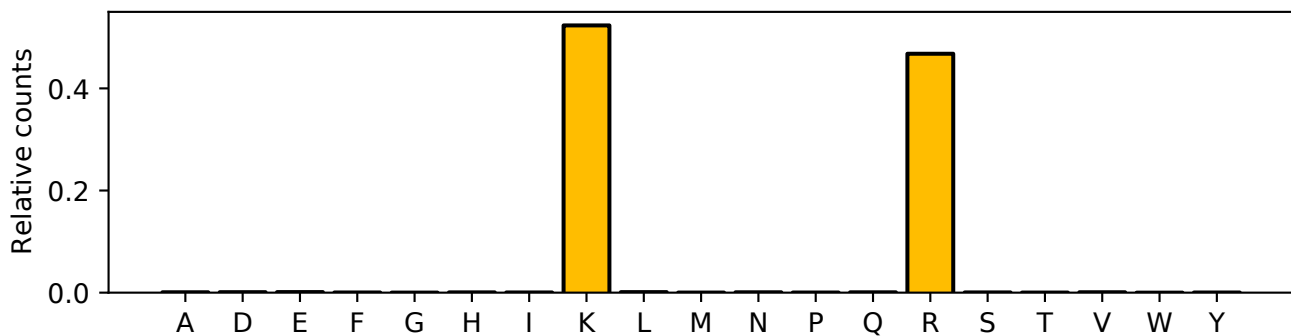
## Number of missed cleavages



## Amino acid before

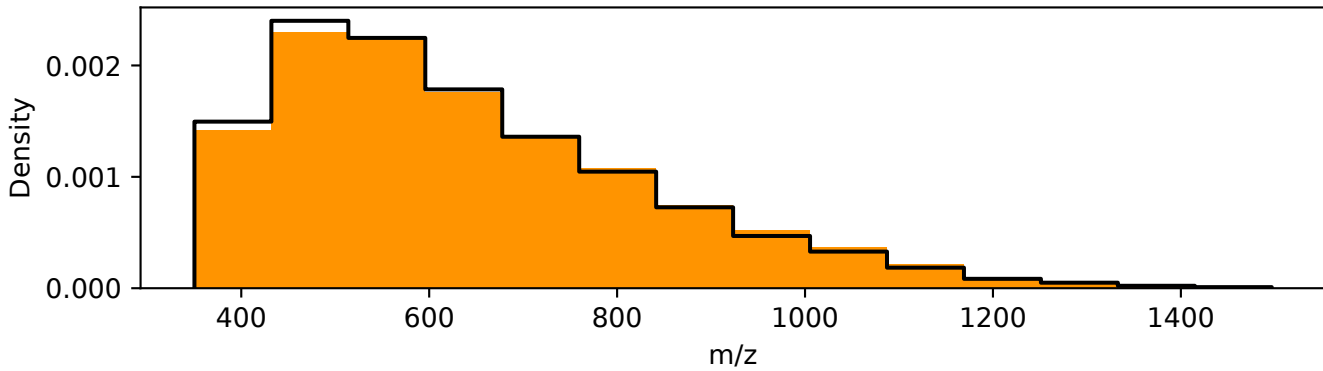


## Last amino acid

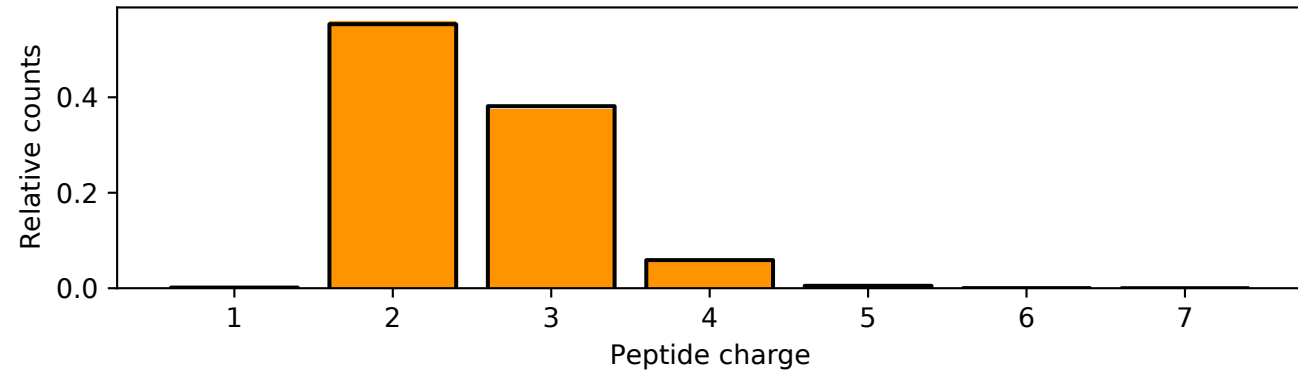


# H838 unst Rep1 1

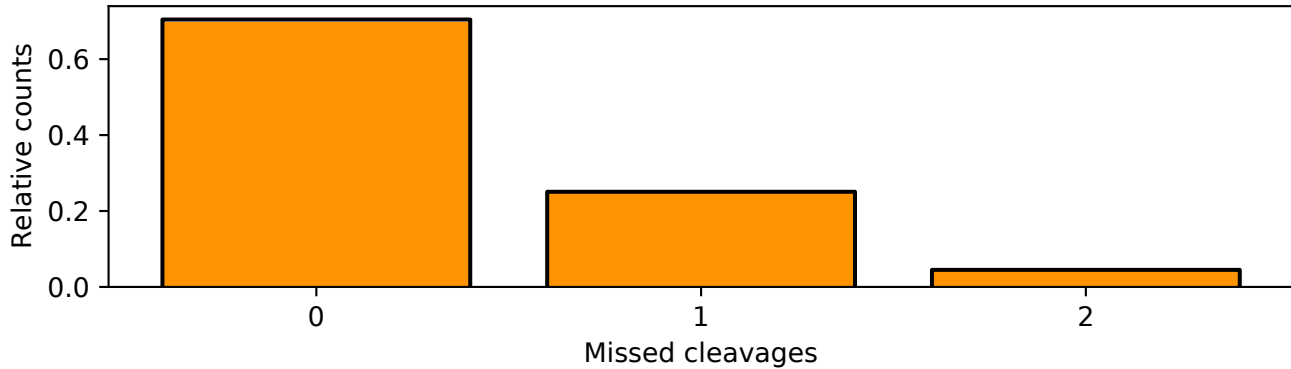
## Peptide m/z



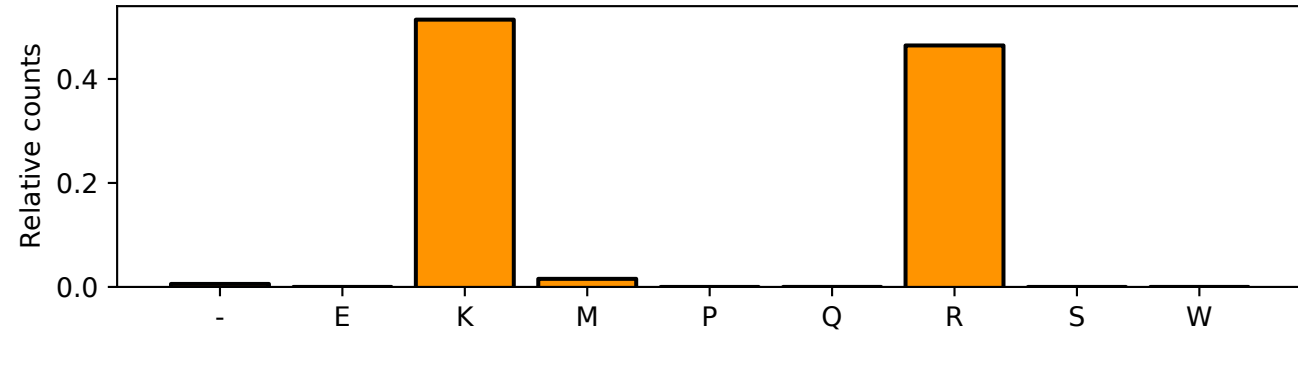
## Peptide charges



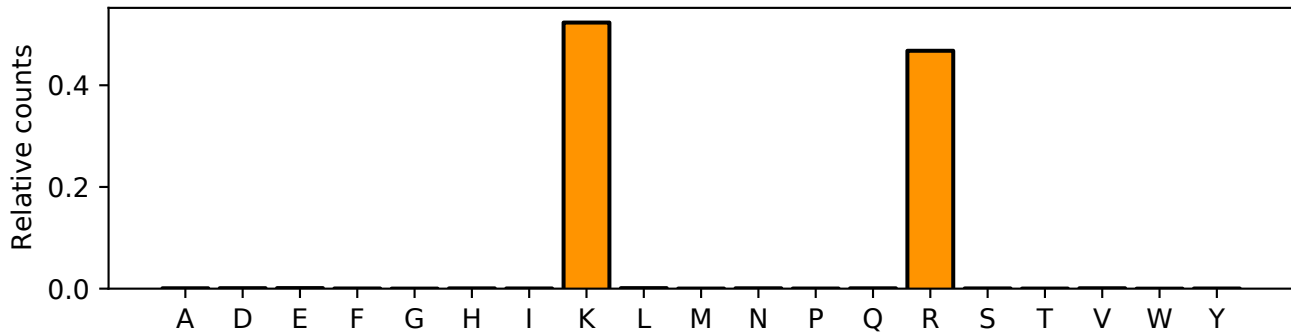
## Number of missed cleavages



## Amino acid before

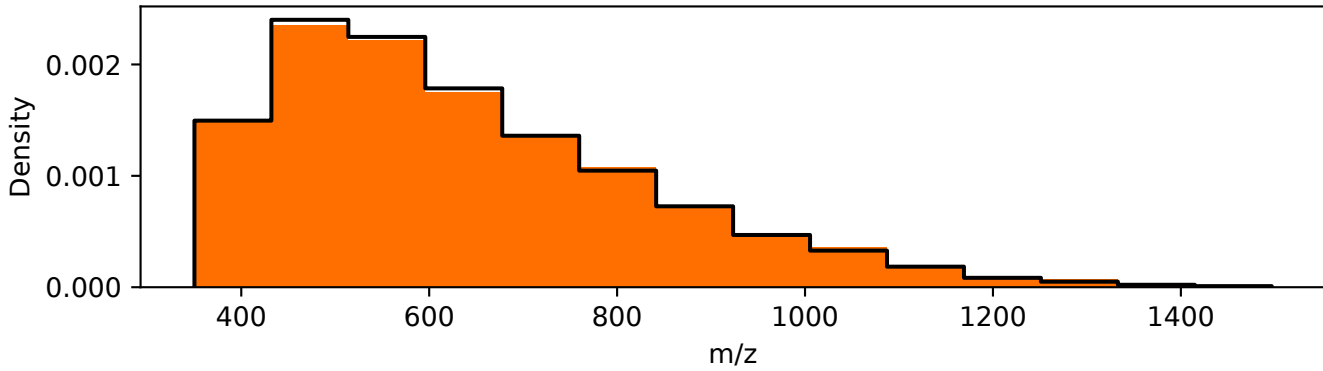


## Last amino acid

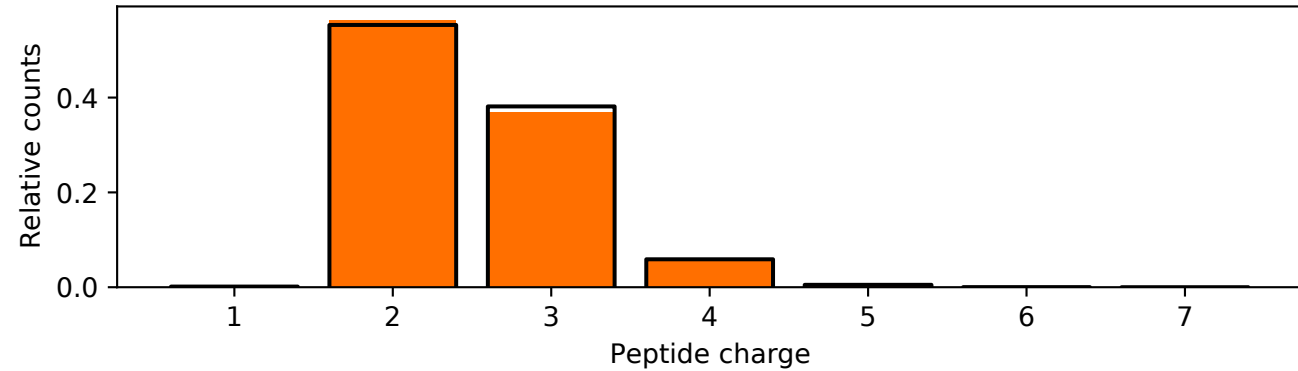


# H838 unst Rep1 2

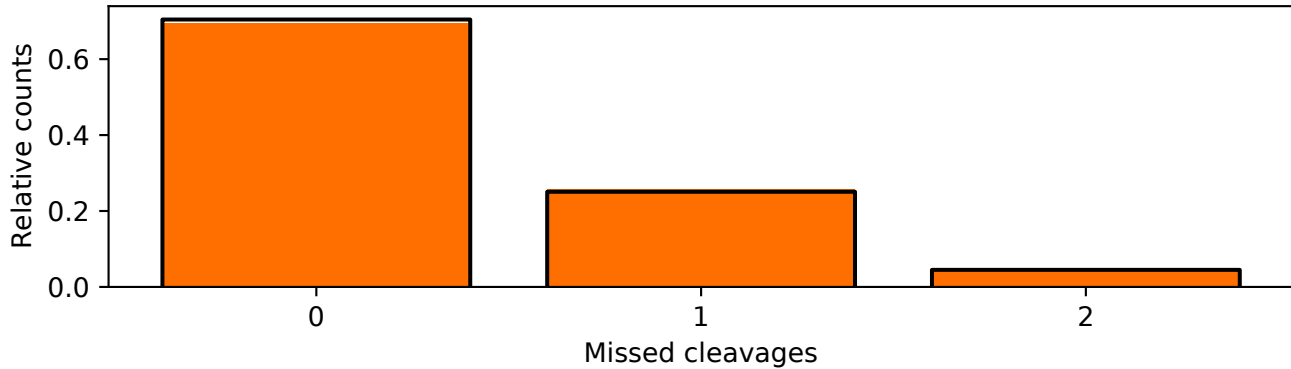
## Peptide m/z



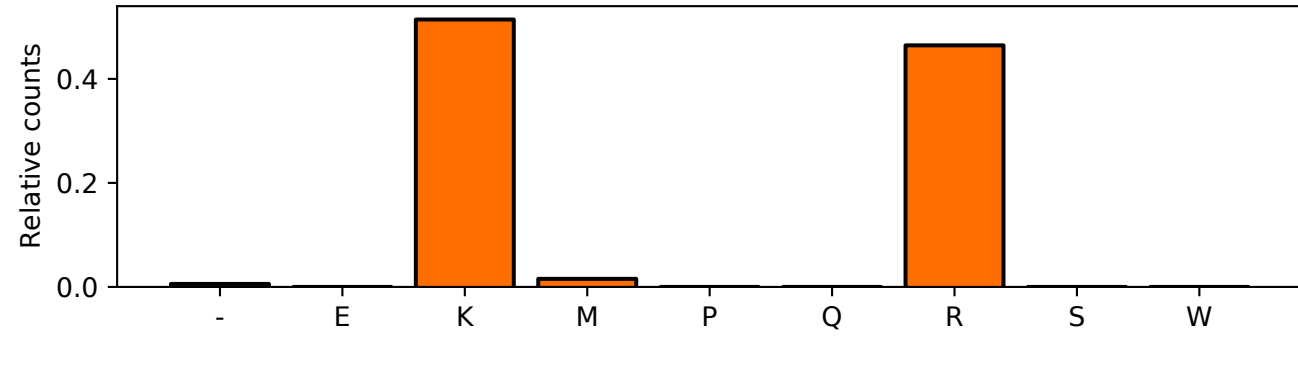
## Peptide charges



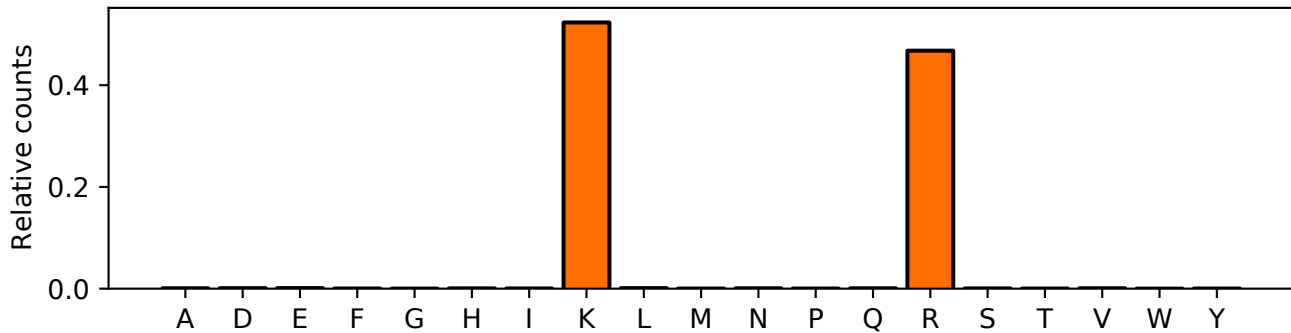
## Number of missed cleavages



## Amino acid before

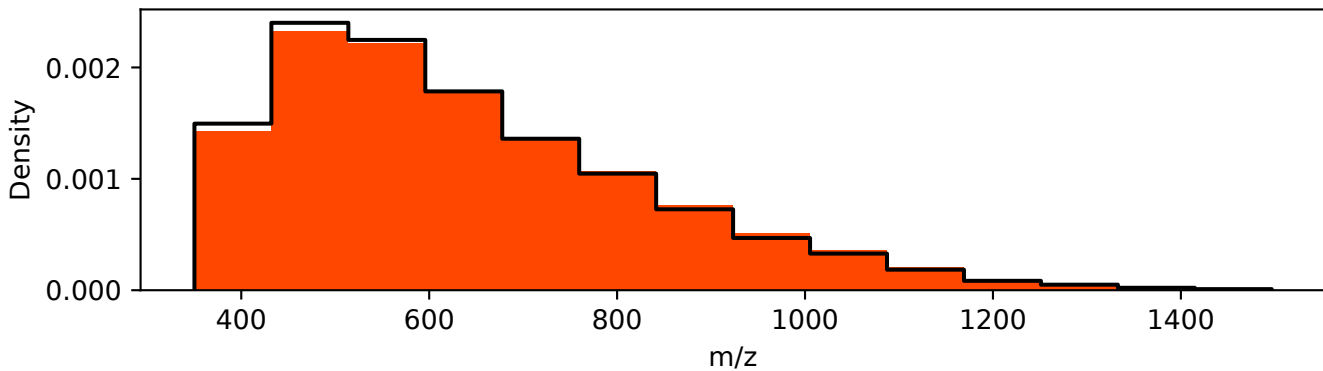


## Last amino acid

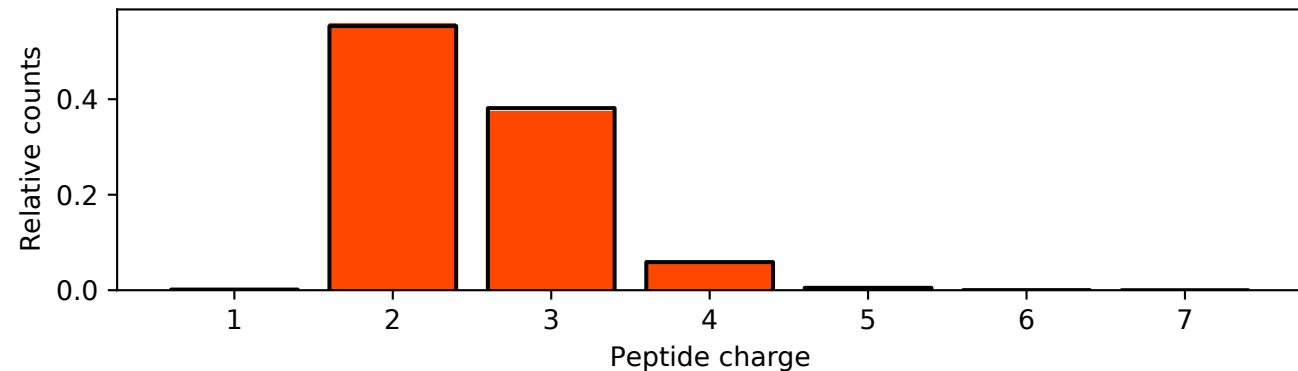


# H838 unst Rep2 1

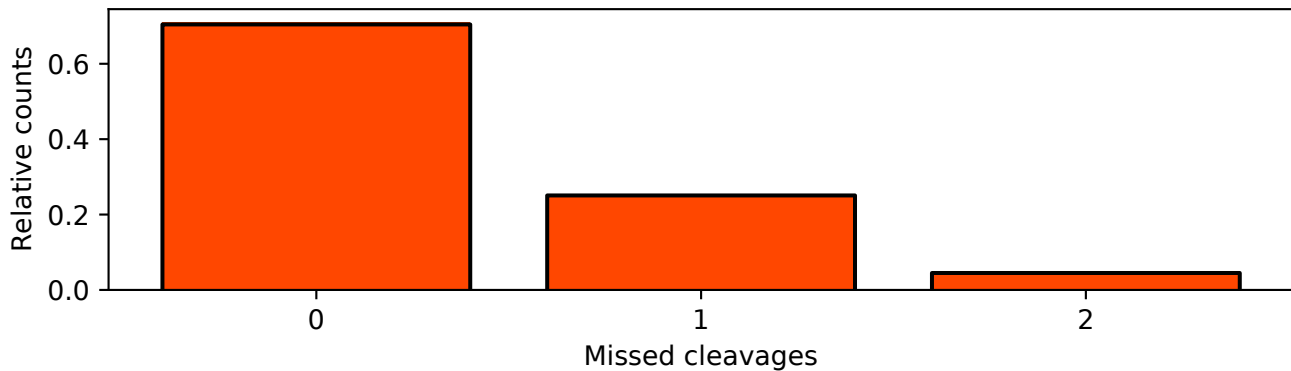
## Peptide m/z



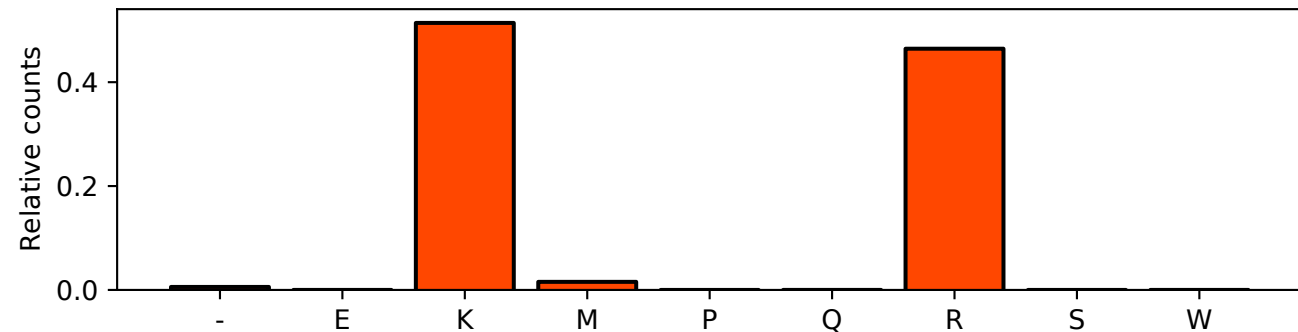
## Peptide charges



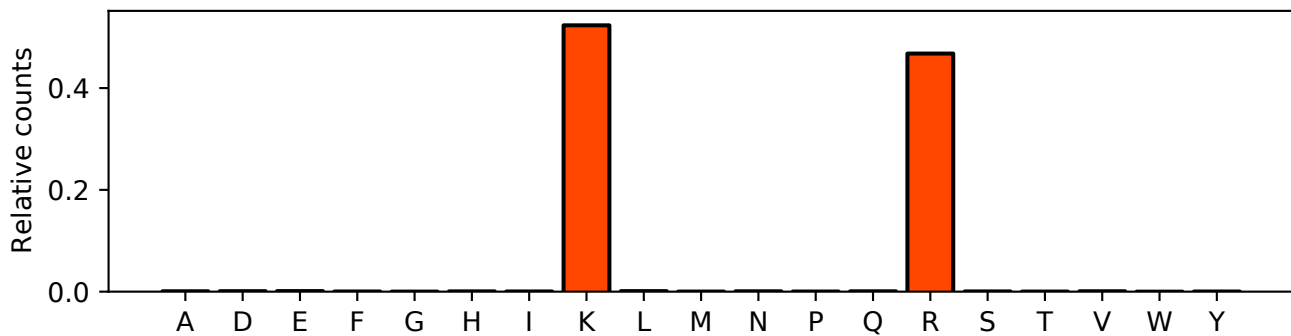
## Number of missed cleavages



## Amino acid before

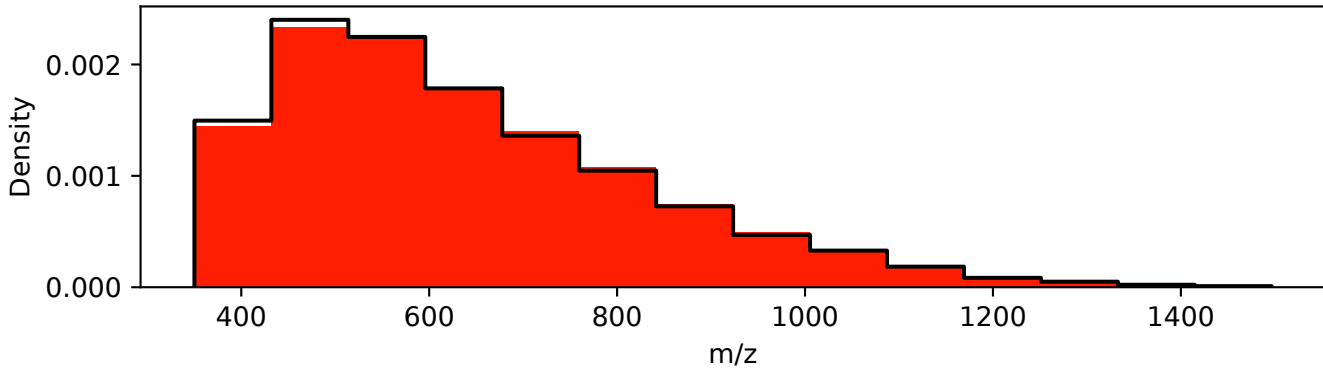


## Last amino acid

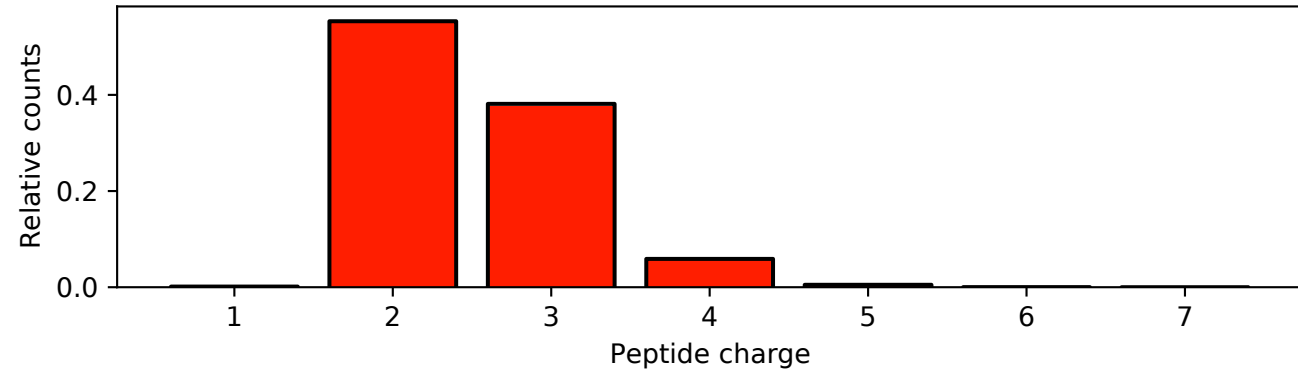


# H838 unst Rep2 2

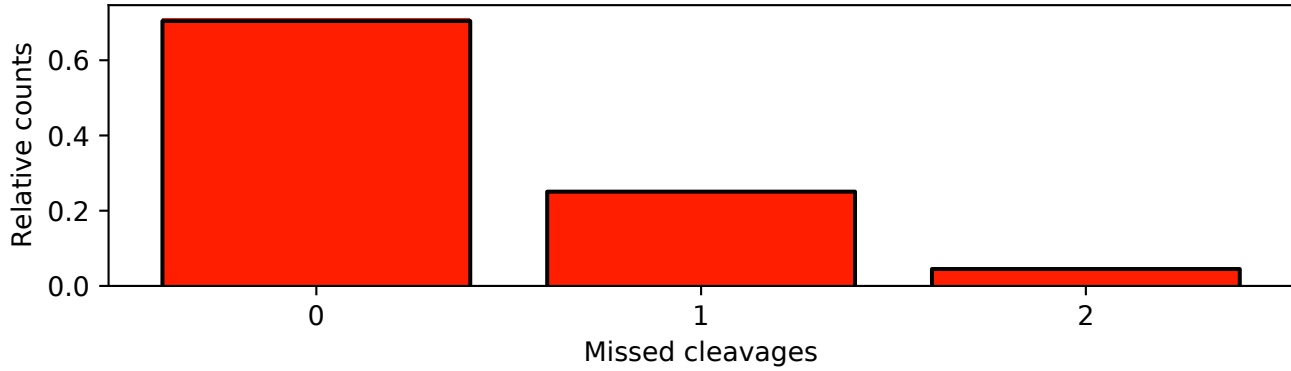
## Peptide m/z



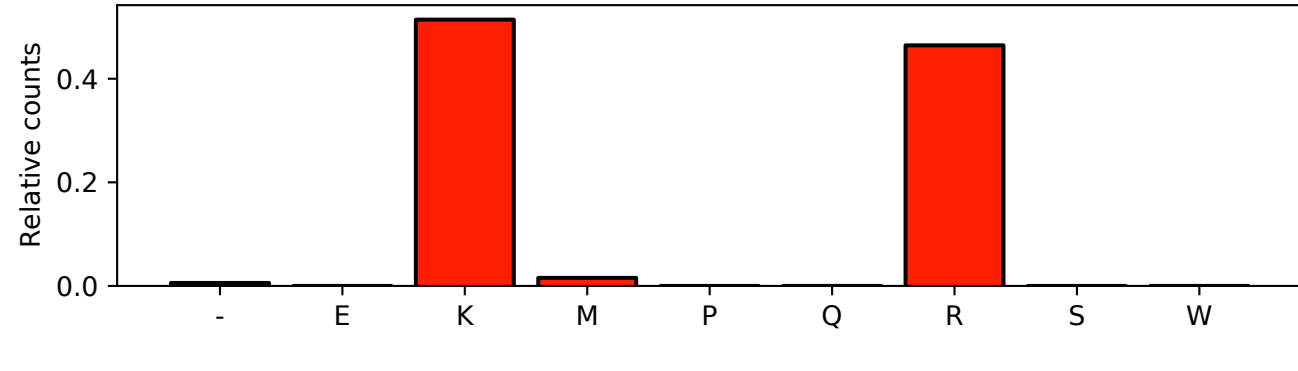
## Peptide charges



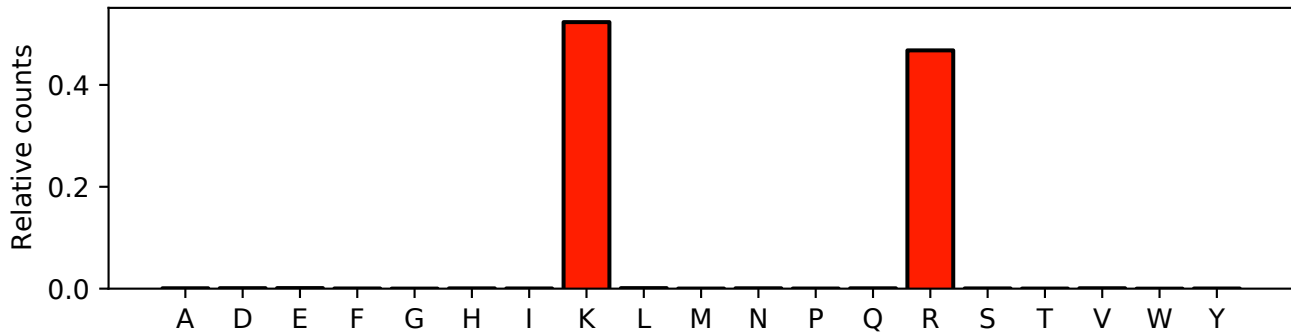
## Number of missed cleavages



## Amino acid before

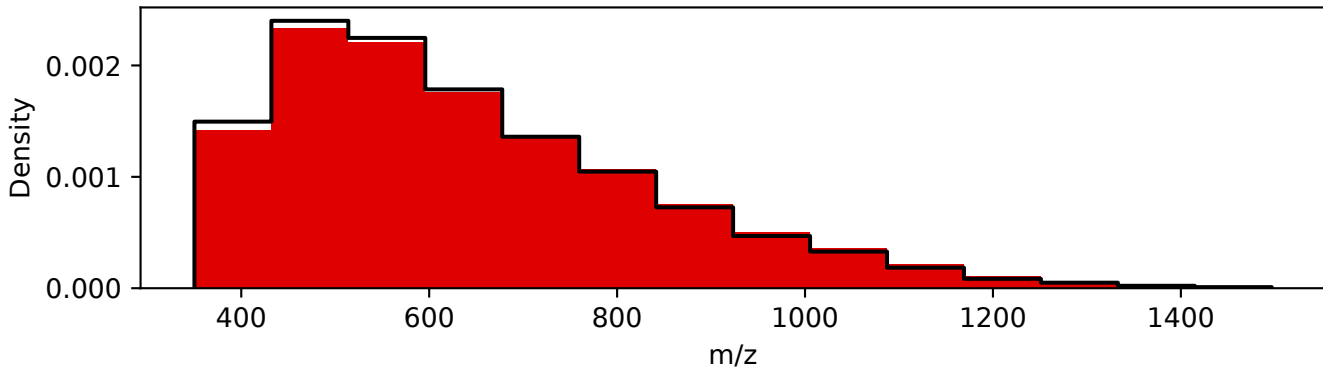


## Last amino acid

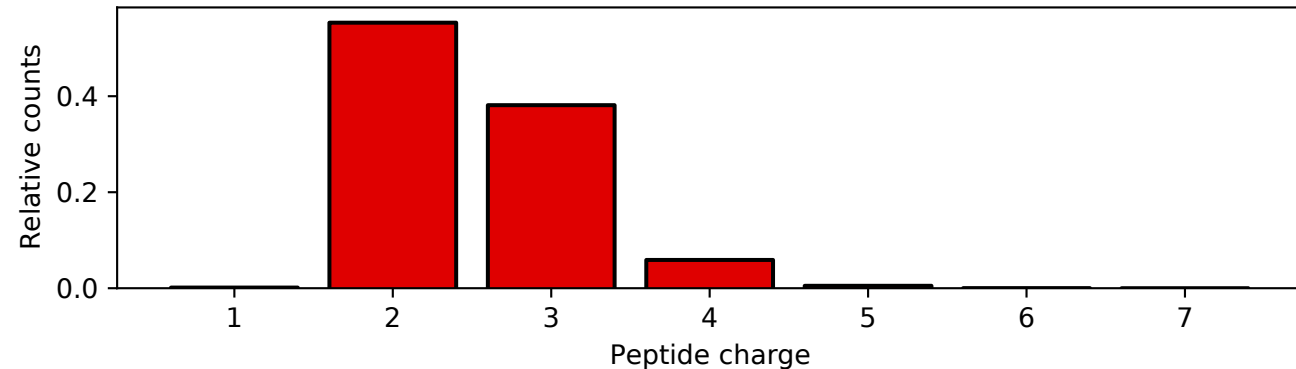


# H838 unst Rep3 1

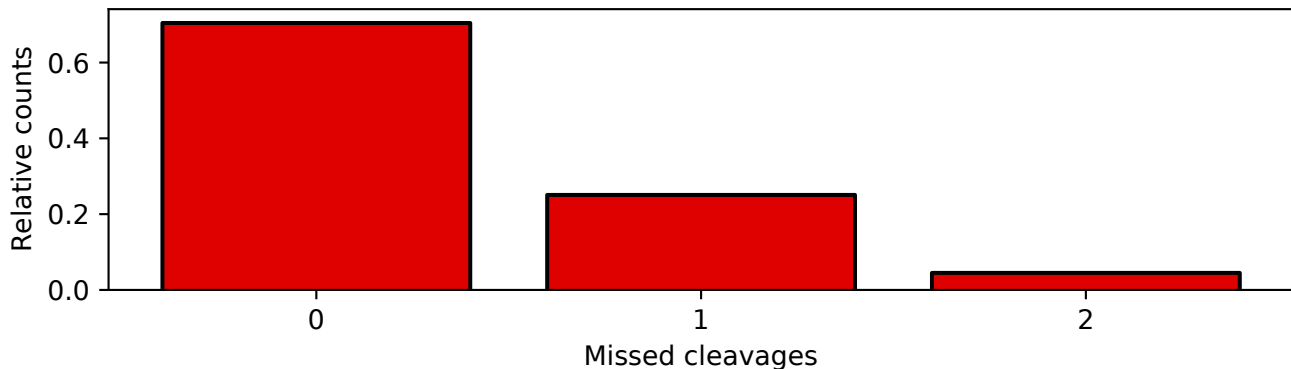
## Peptide m/z



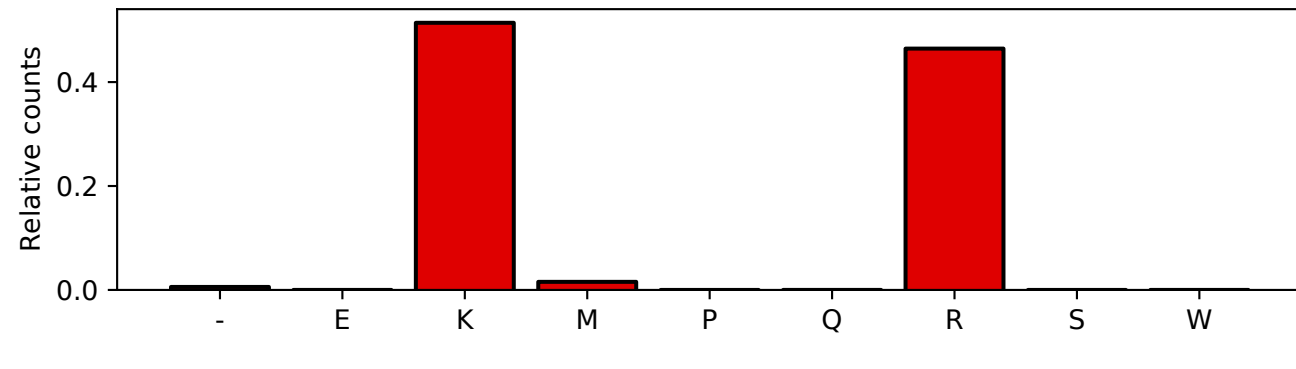
## Peptide charges



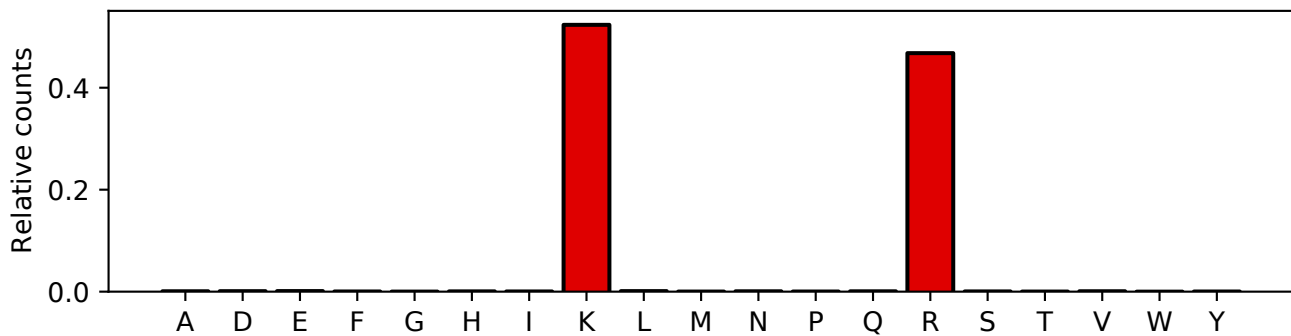
## Number of missed cleavages



## Amino acid before

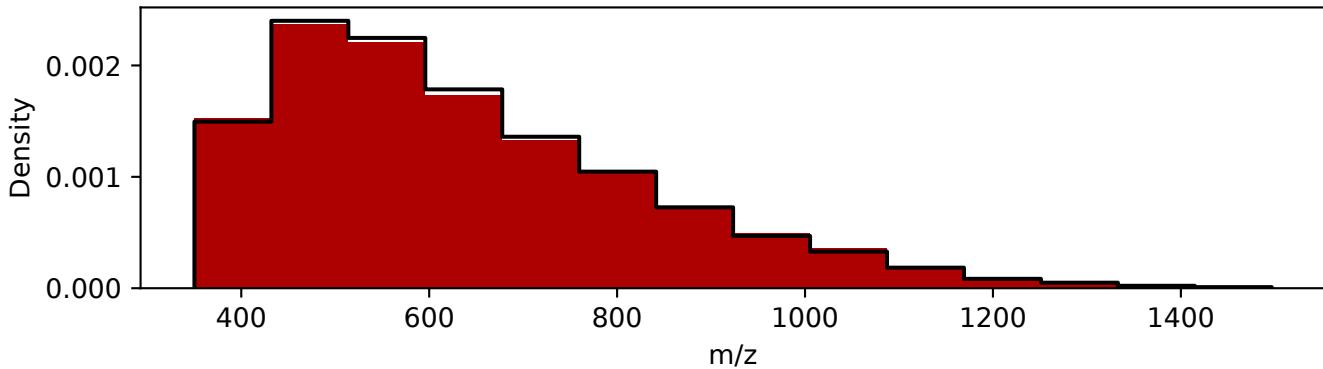


## Last amino acid

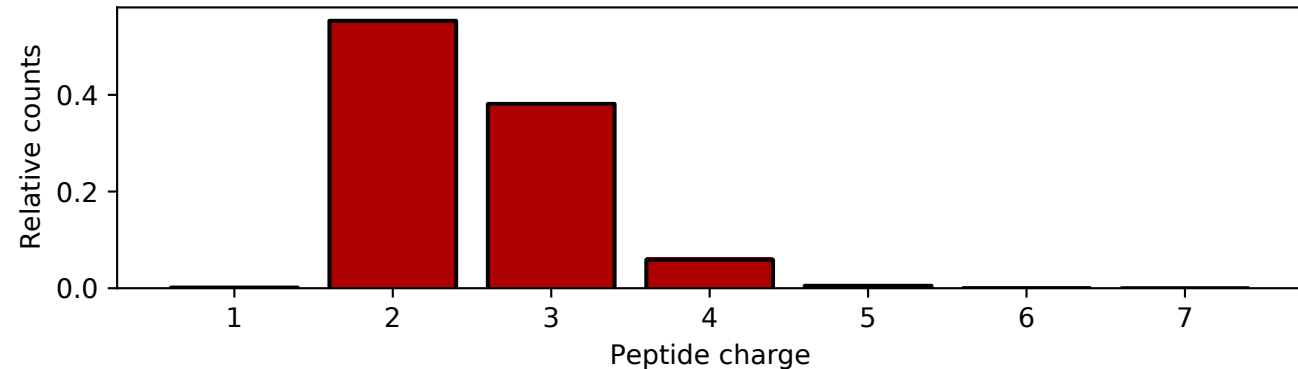


# H838 unst Rep3 2

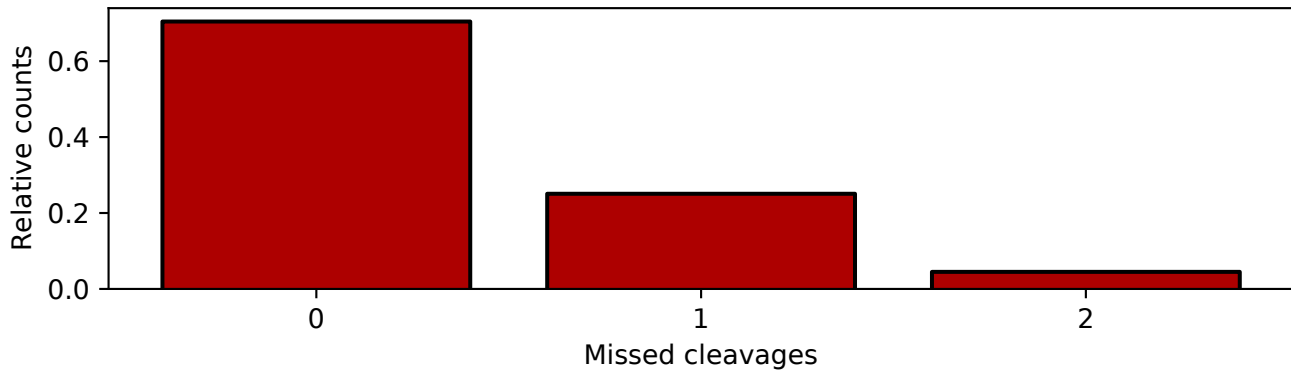
## Peptide m/z



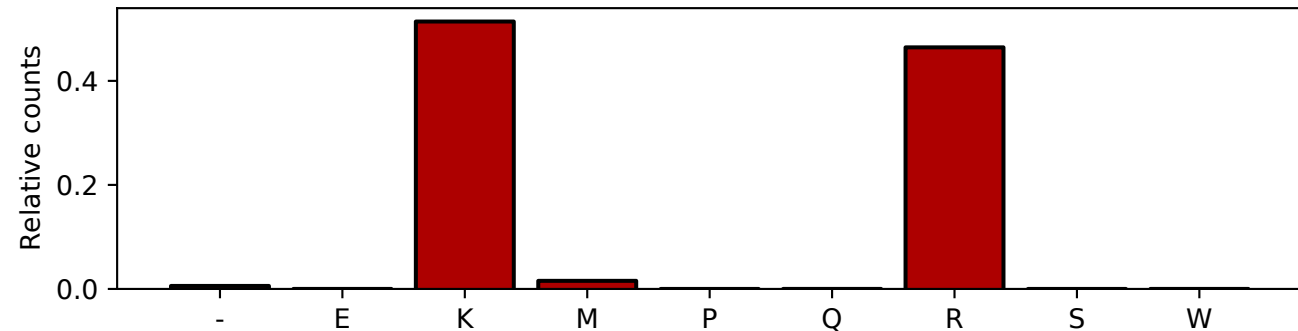
## Peptide charges



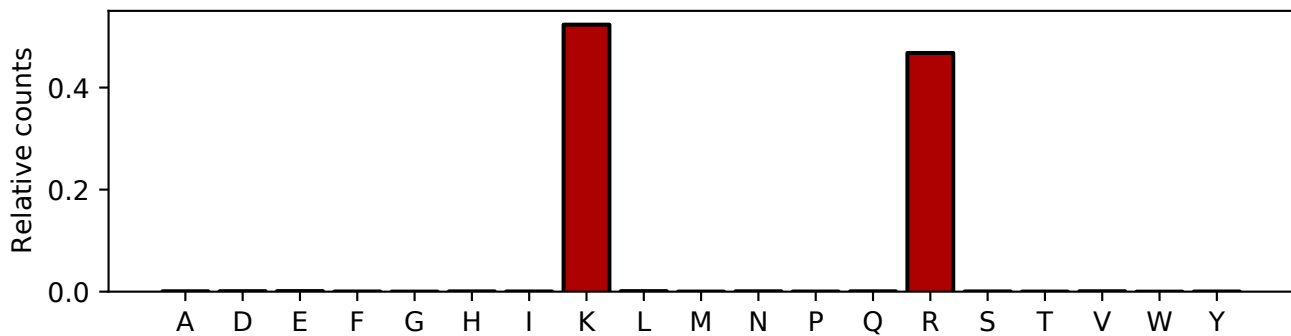
## Number of missed cleavages



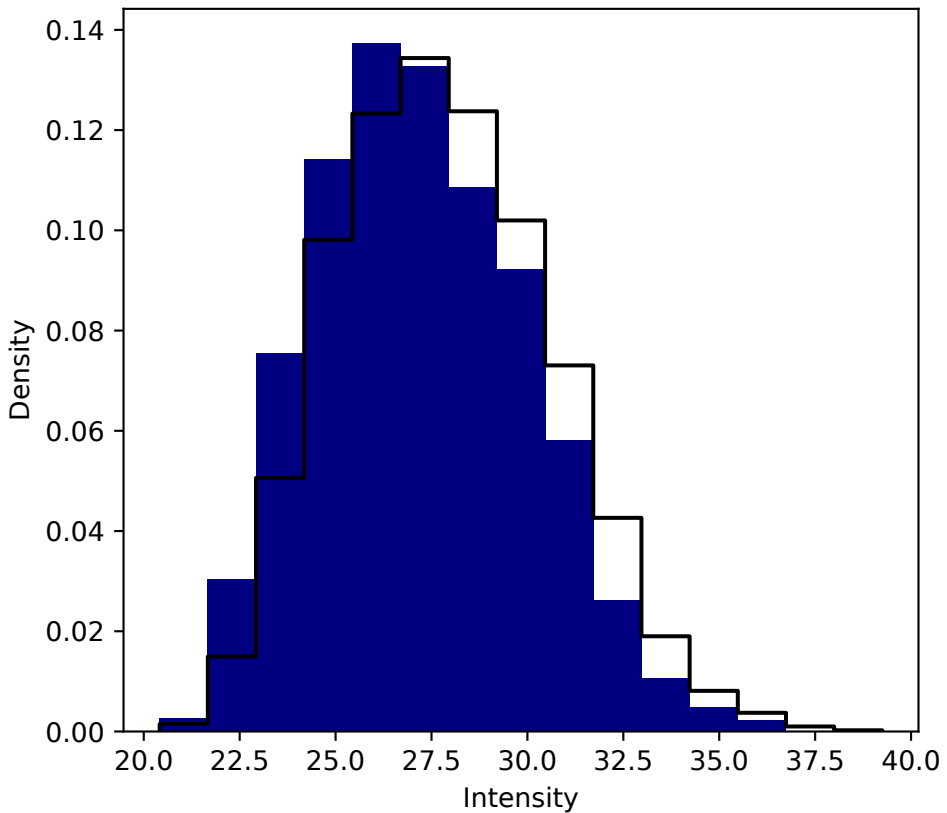
## Amino acid before



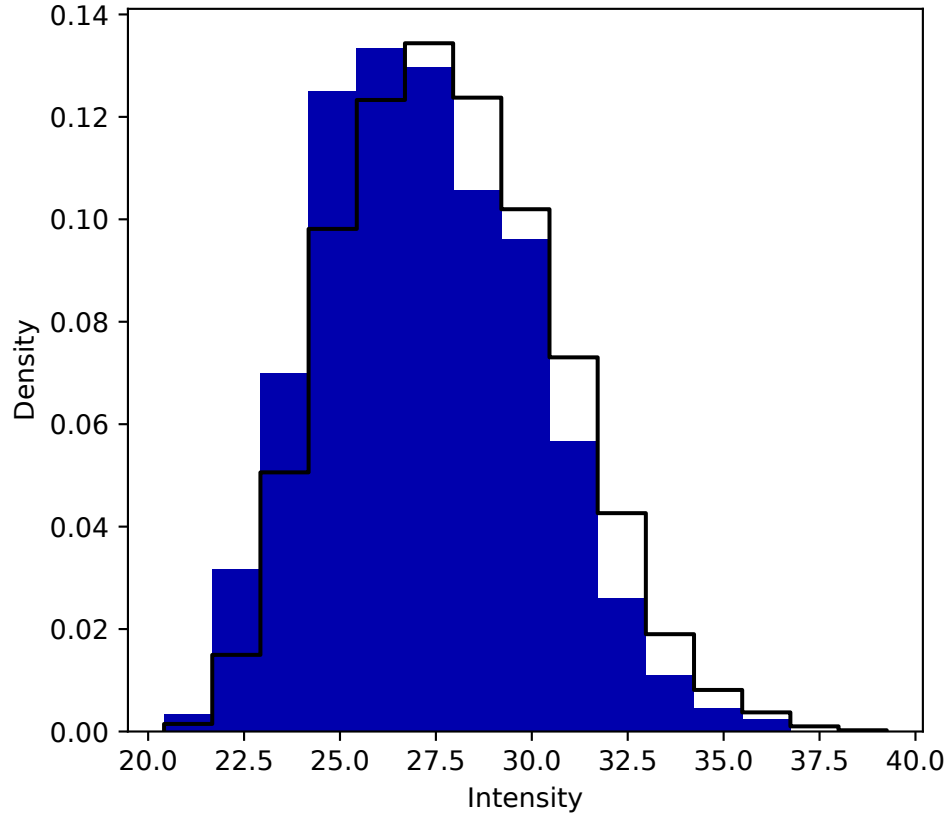
## Last amino acid



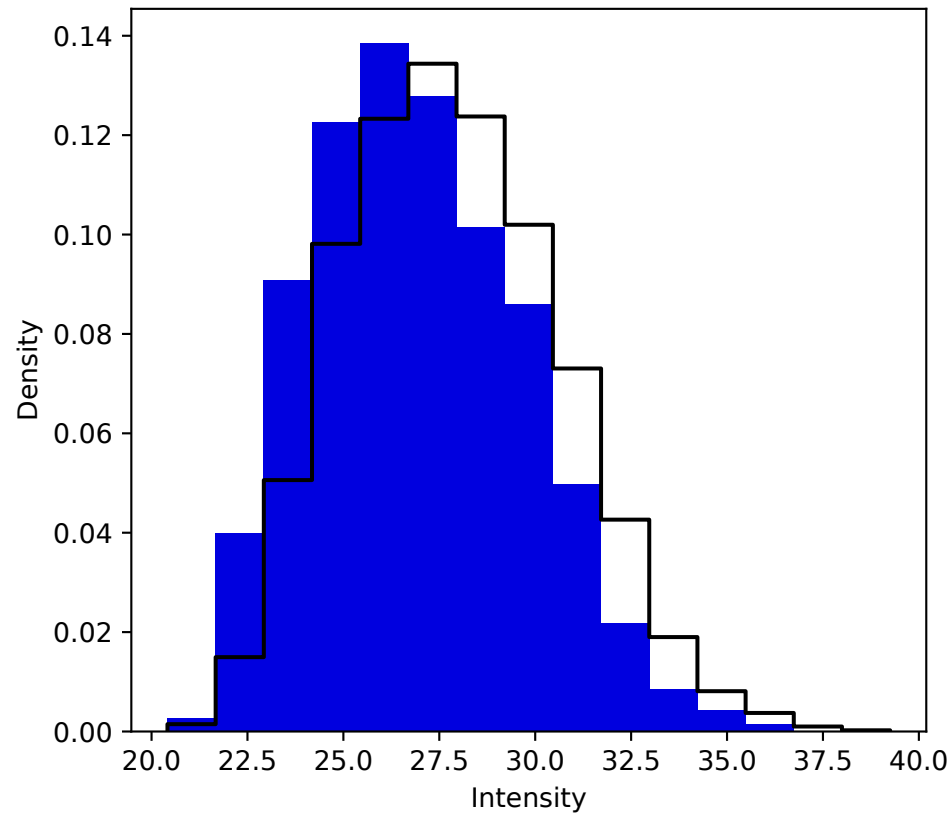
H1975 TGFb Rep1 1



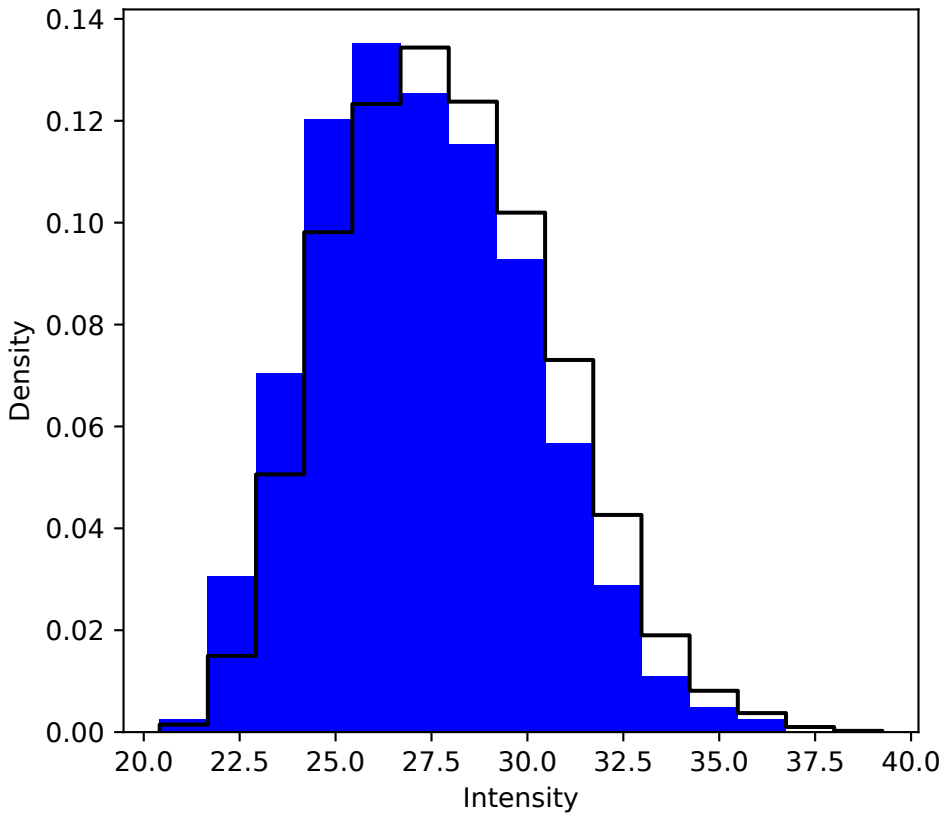
H1975 TGFb Rep1 2



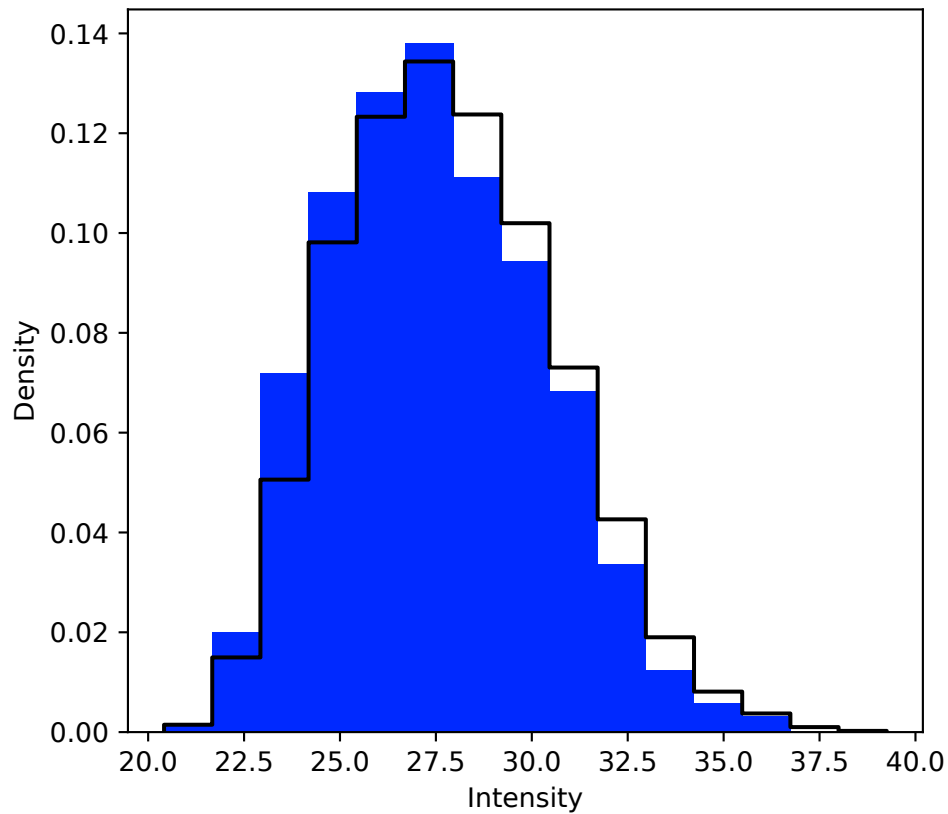
H1975 TGFb Rep2 1



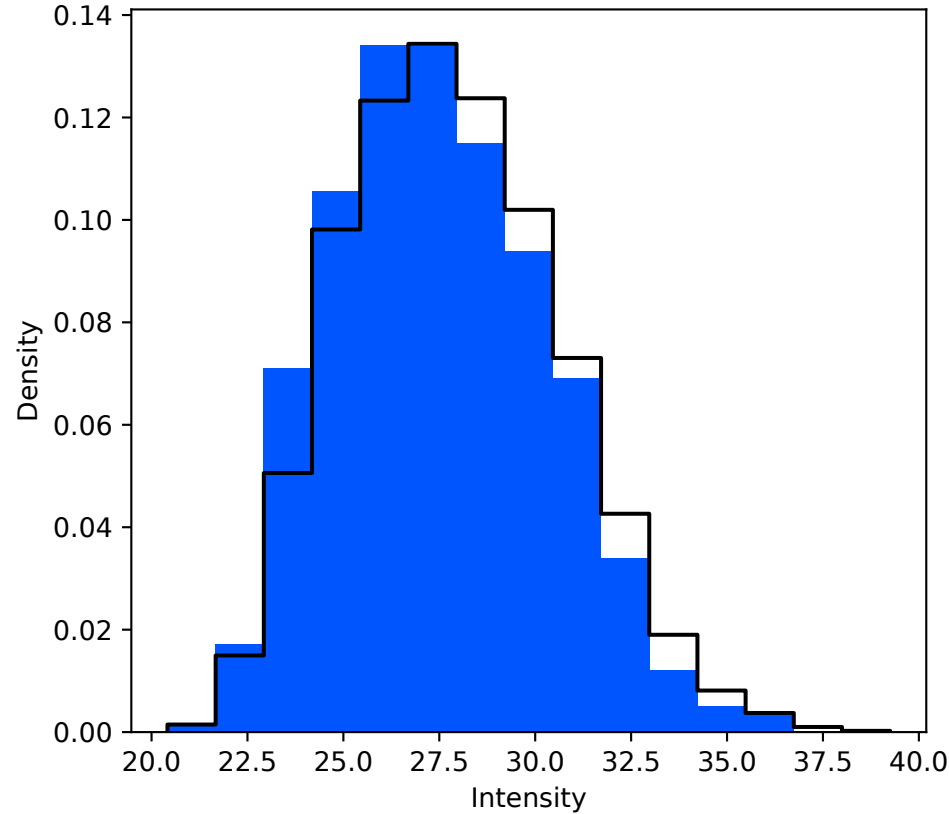
H1975 TGFb Rep2 2



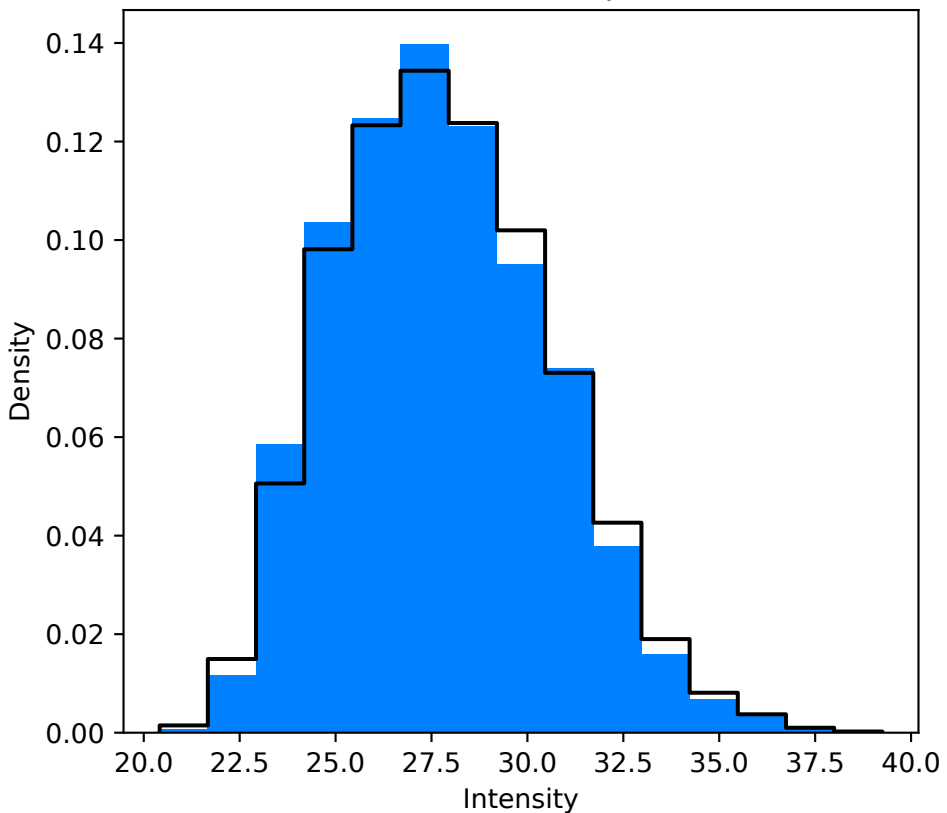
H1975 TGFb Rep3 1



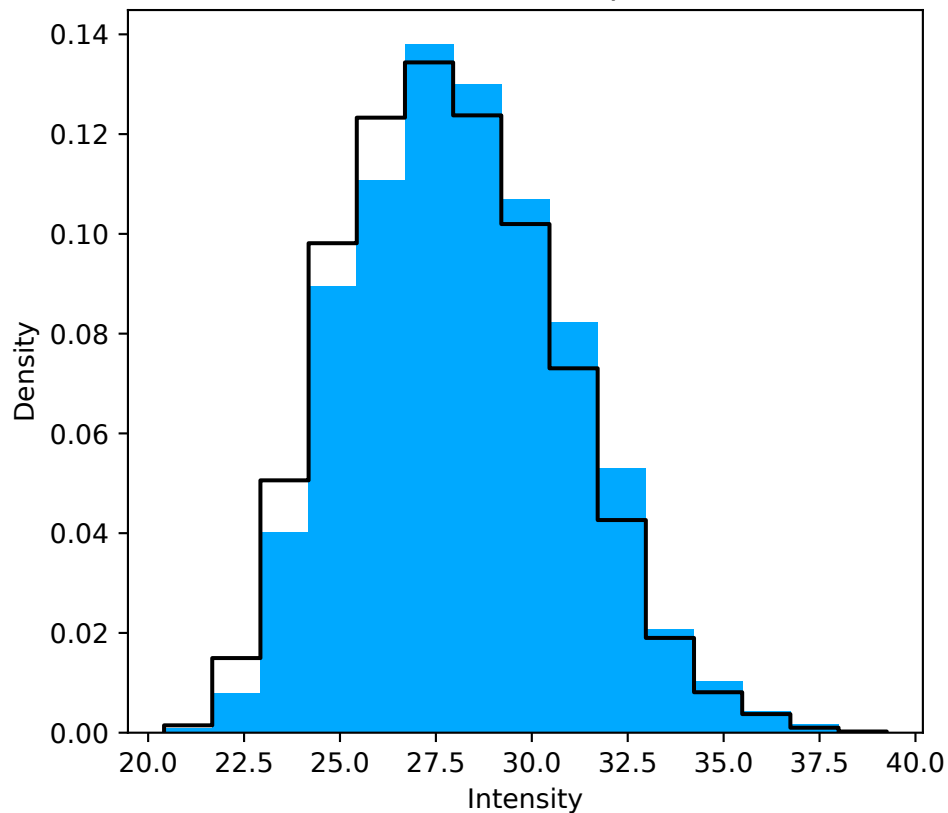
H1975 TGFb Rep3 2



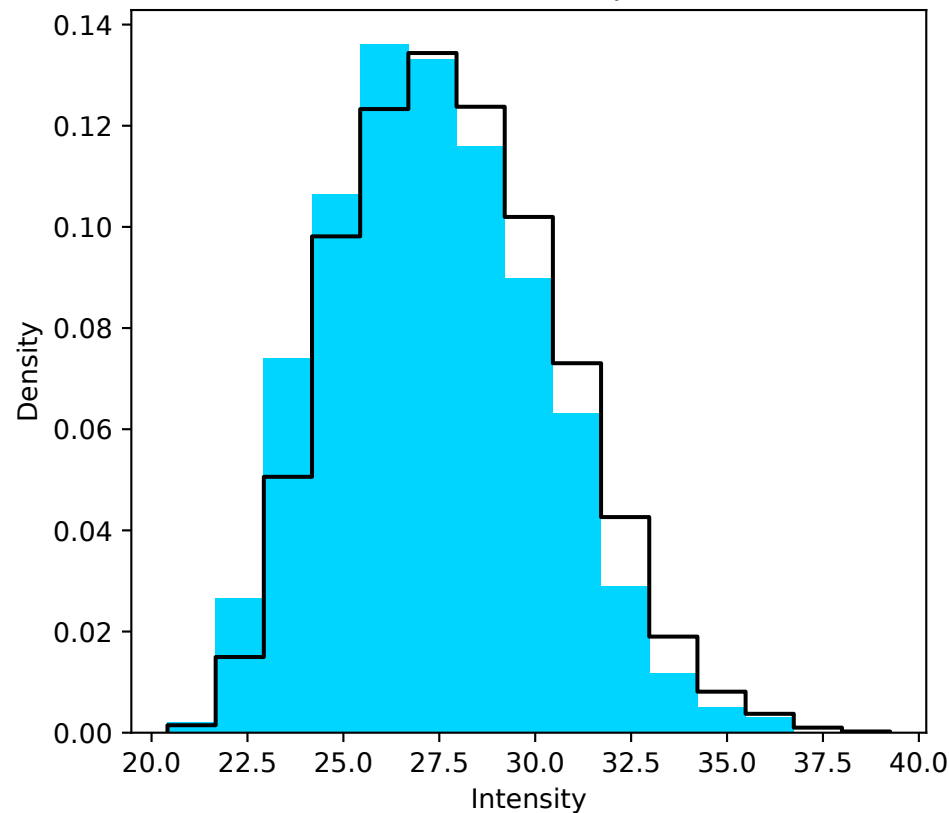
H1975 unst Rep1 1



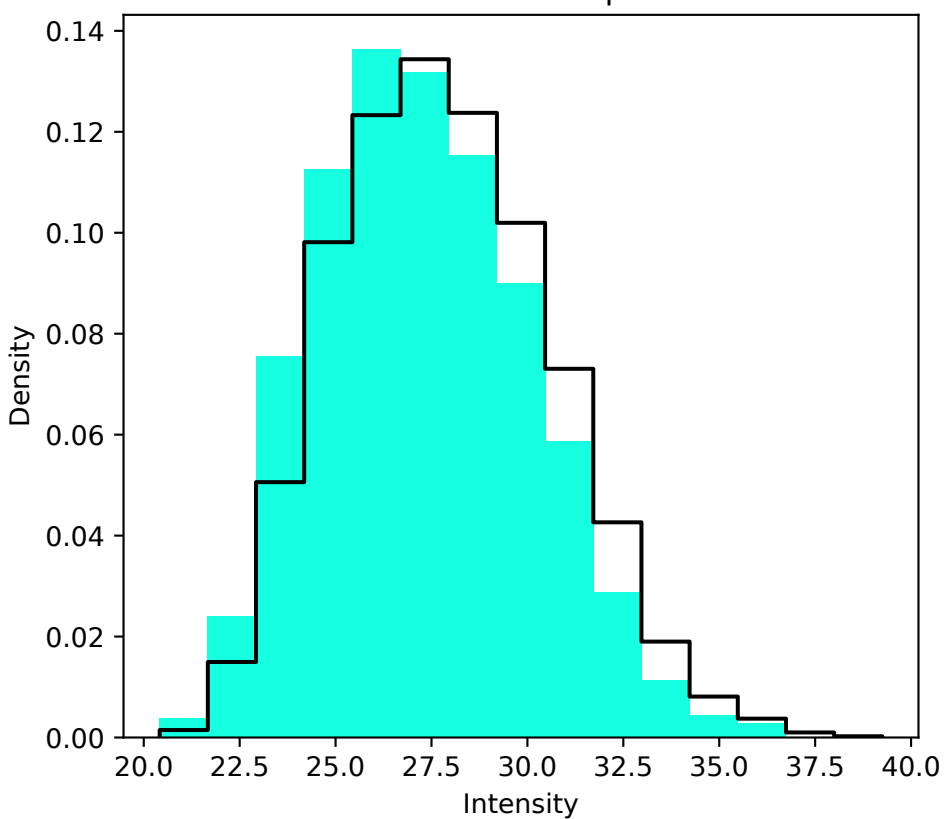
H1975 unst Rep1 2



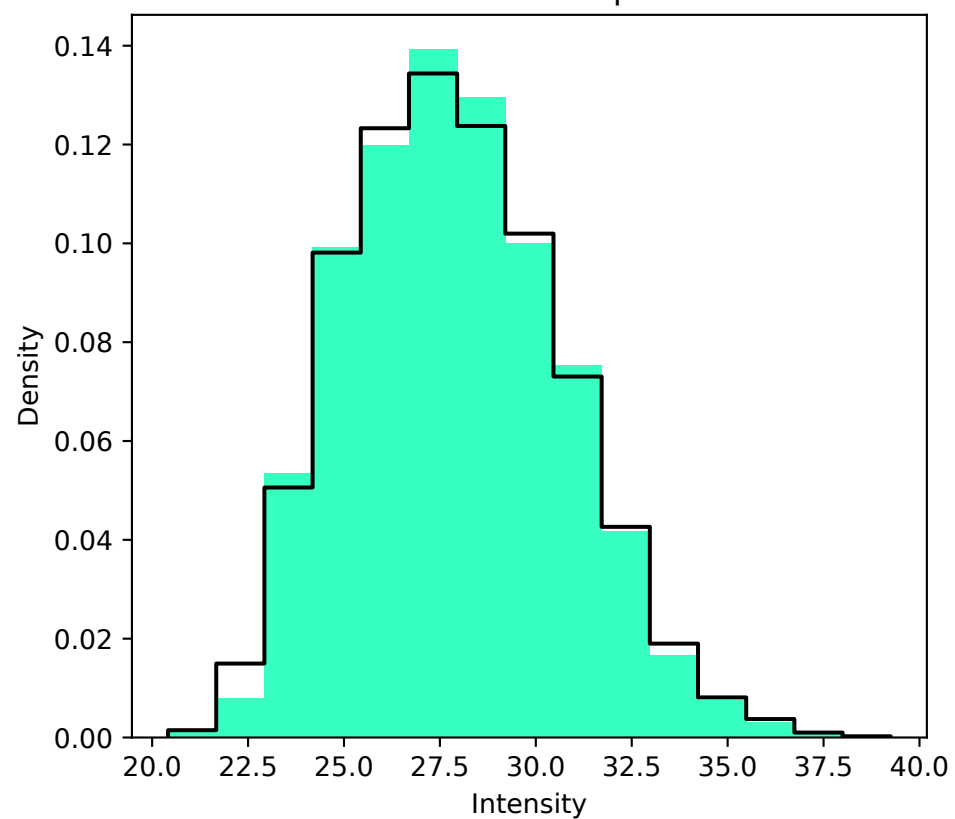
H1975 unst Rep2 1



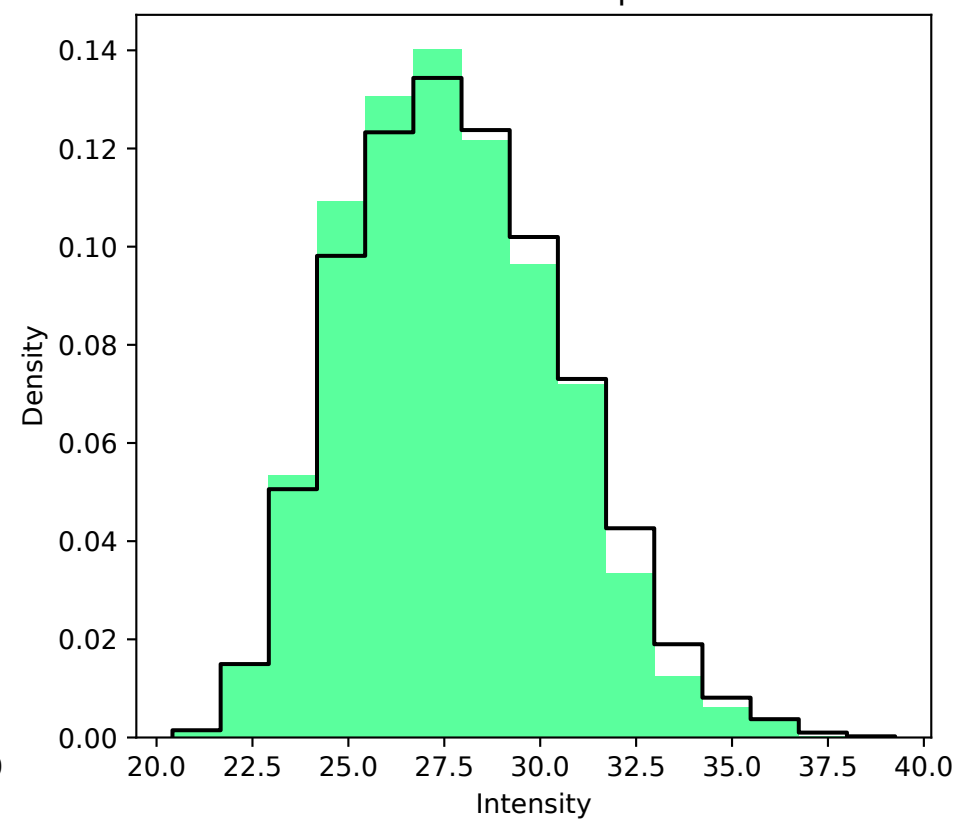
H1975 unst Rep2 2



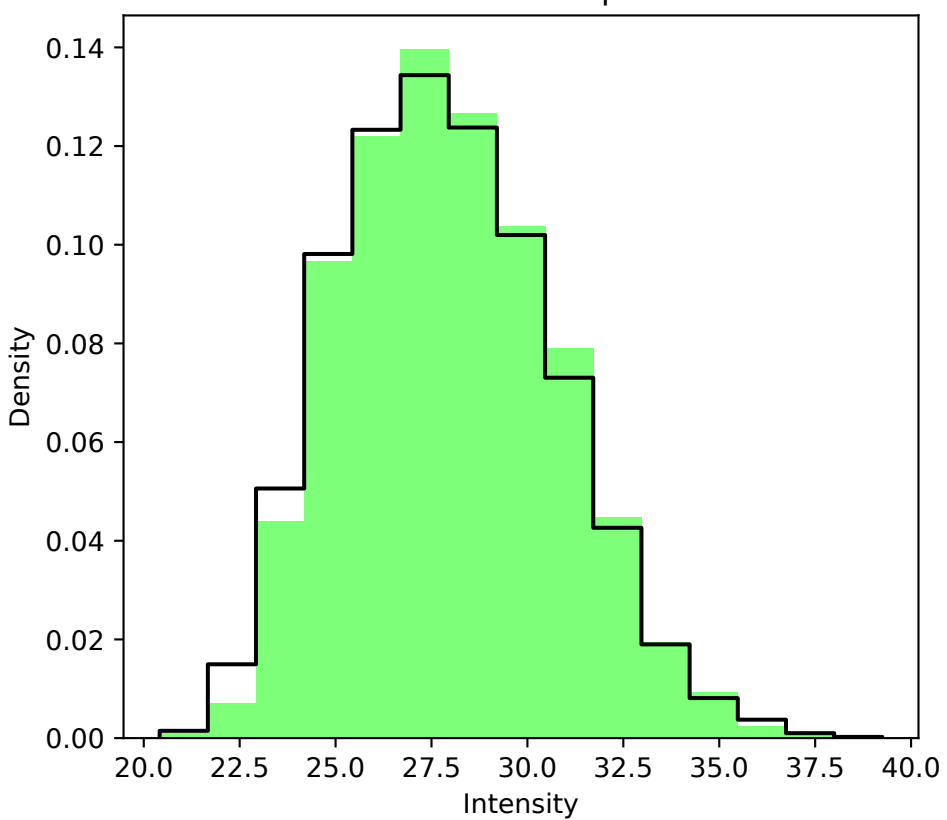
H1975 unst Rep3 1



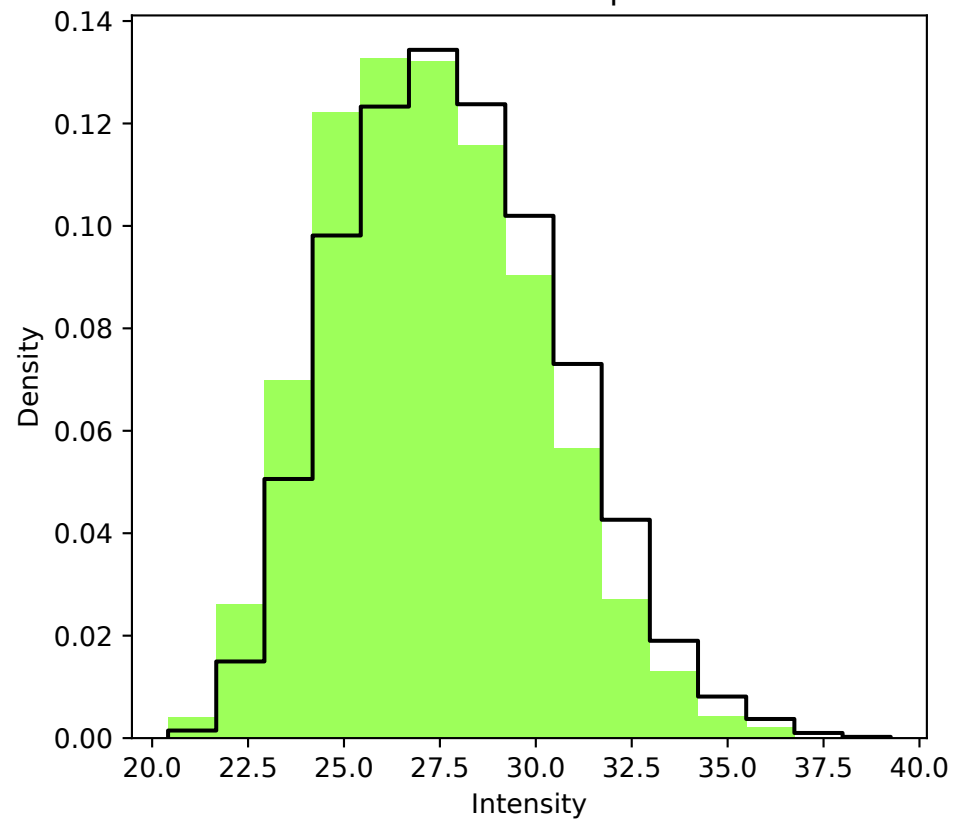
H1975 unst Rep3 2



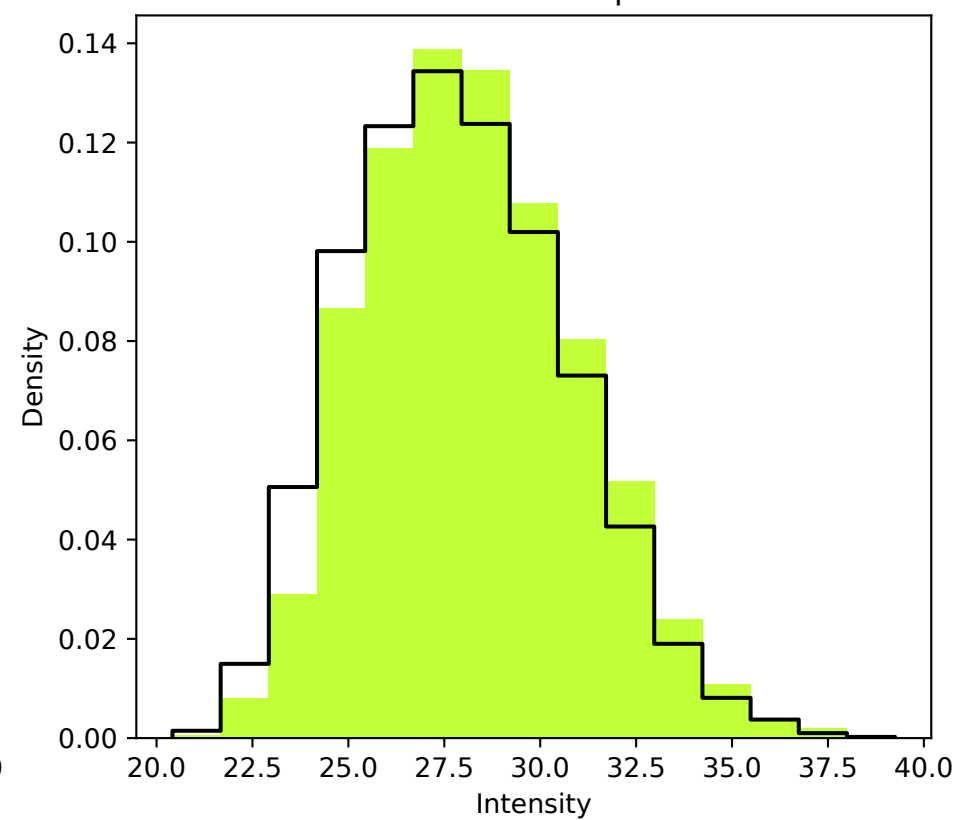
H838 TGFb Rep1 1



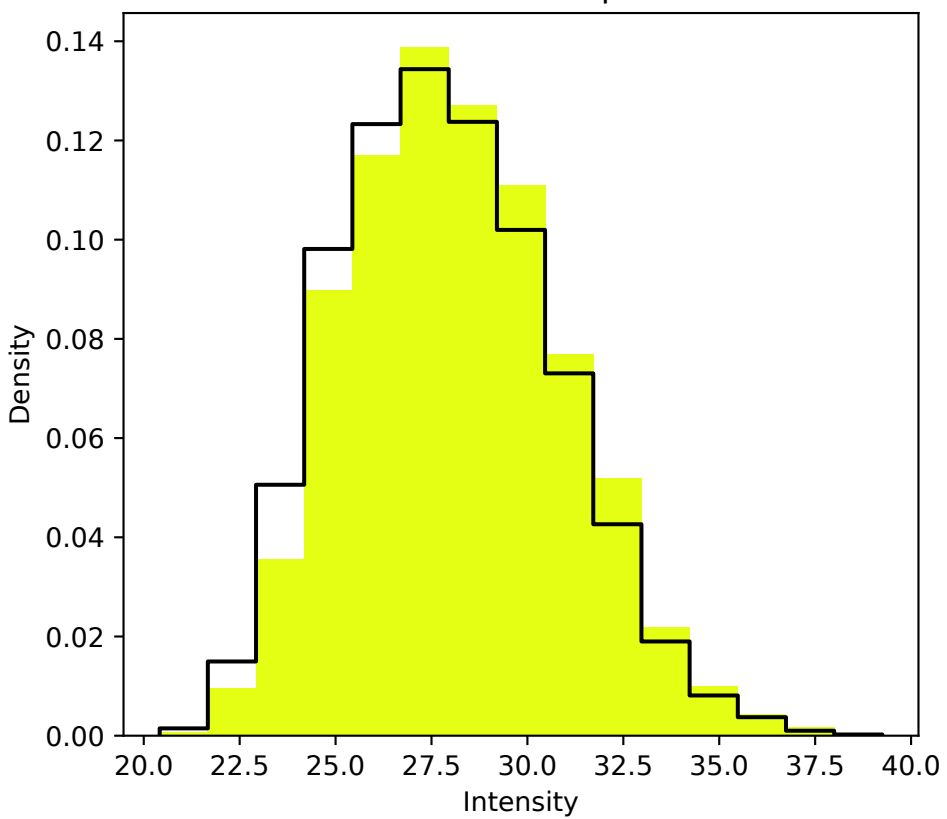
H838 TGFb Rep1 2



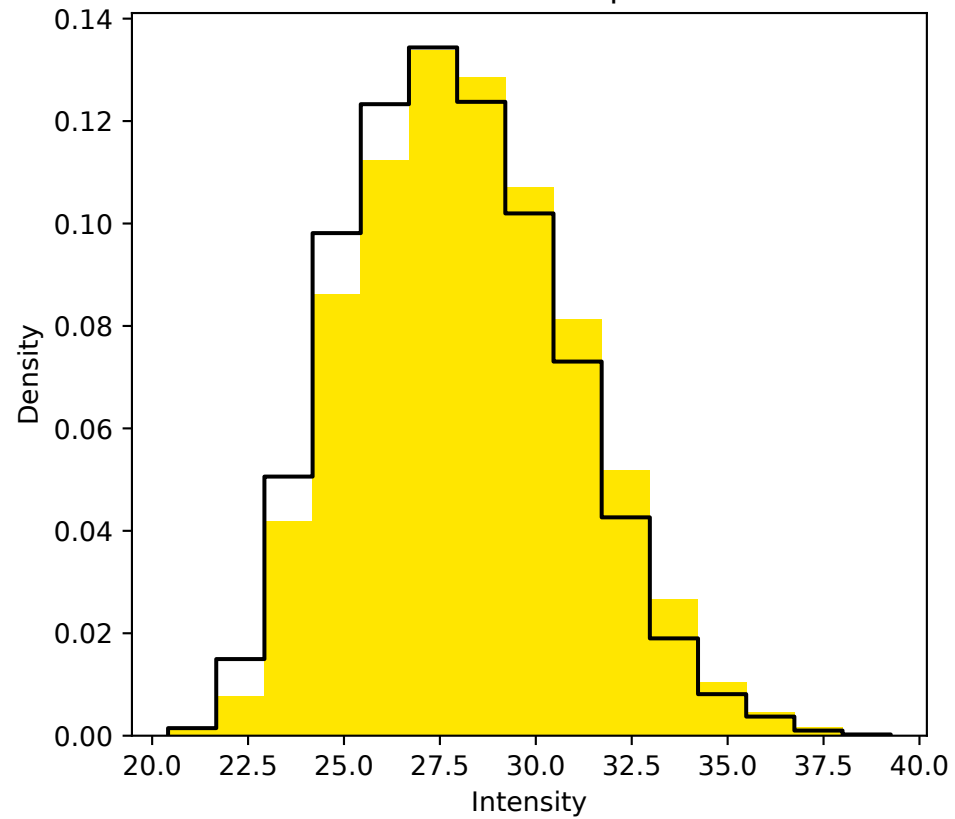
H838 TGFb Rep2 1



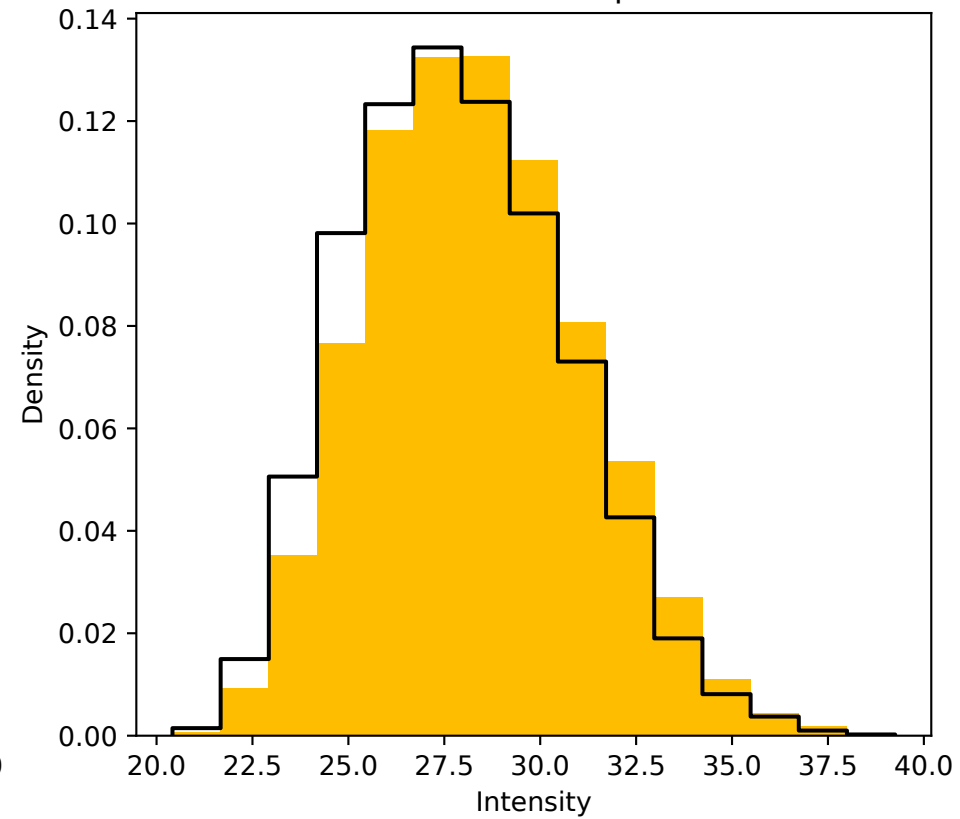
H838 TGFb Rep2 2



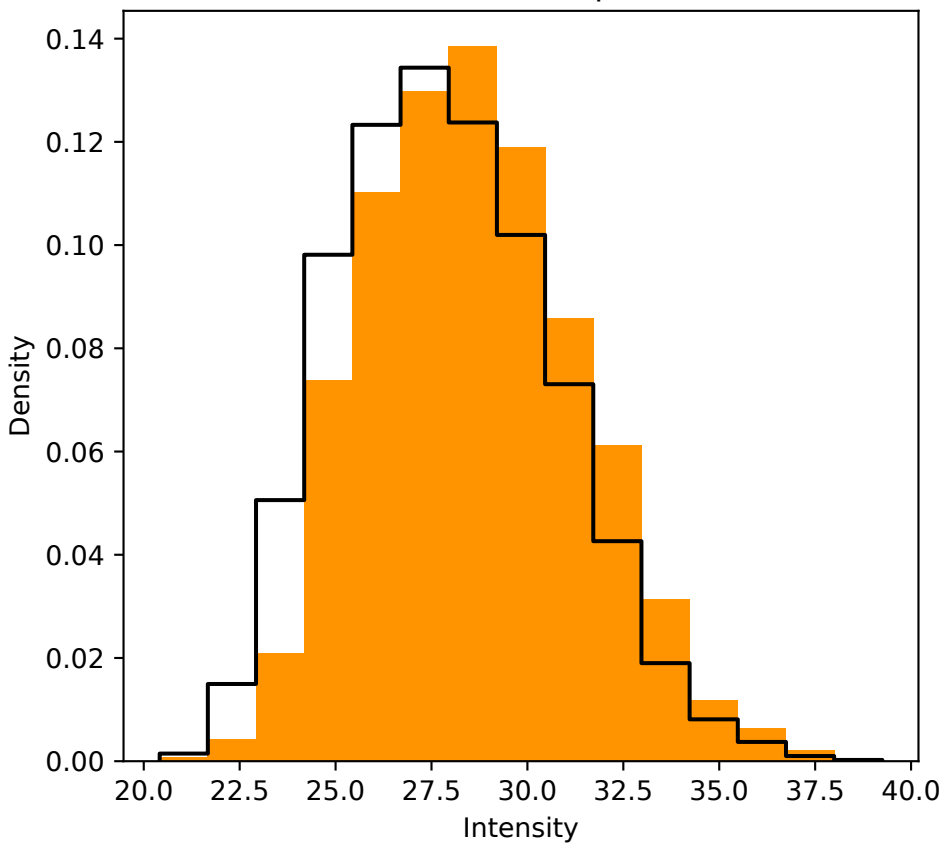
H838 TGFb Rep3 1



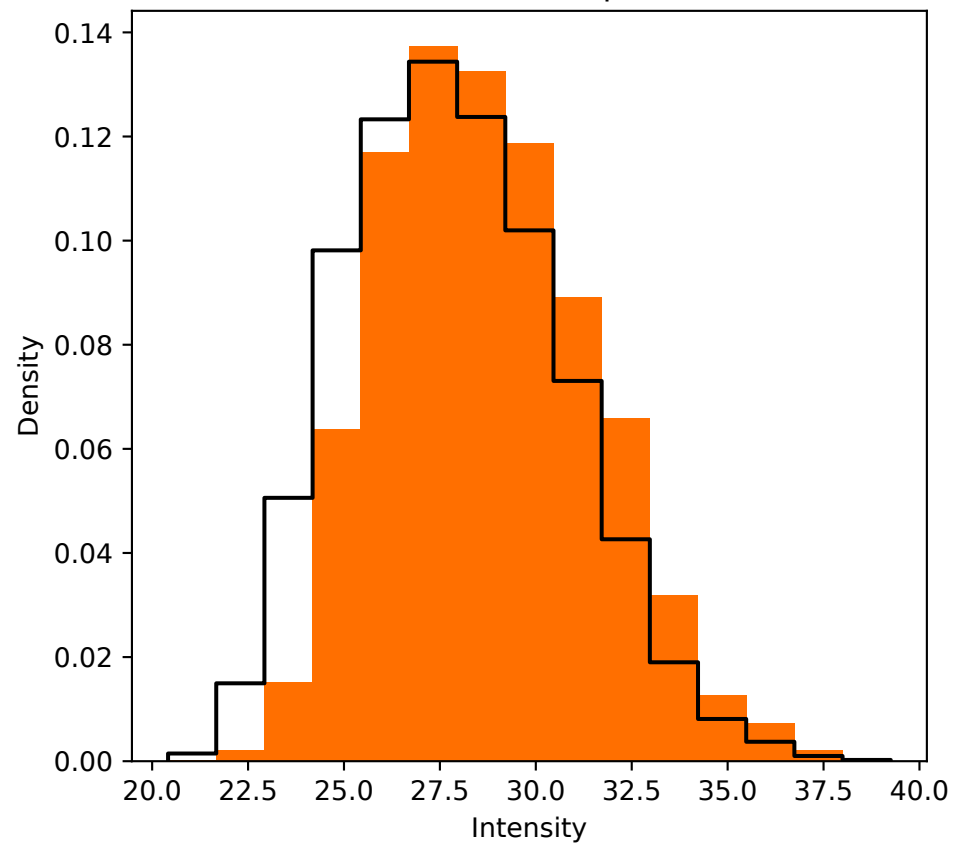
H838 TGFb Rep3 2



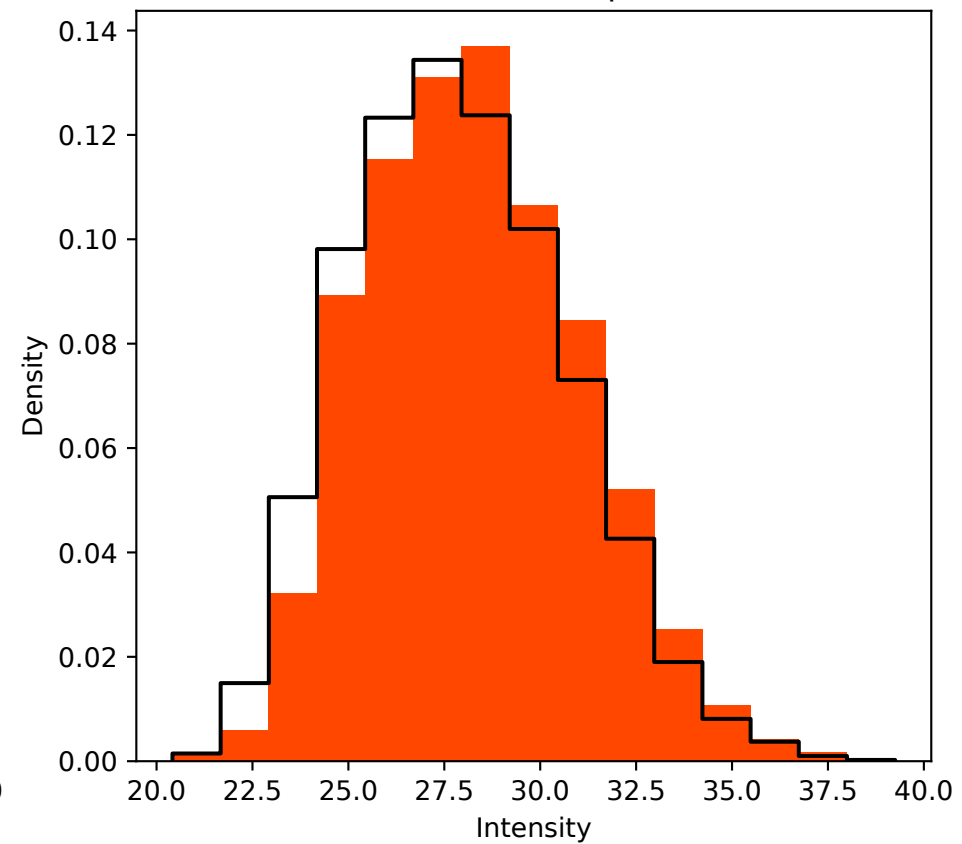
H838 unst Rep1 1



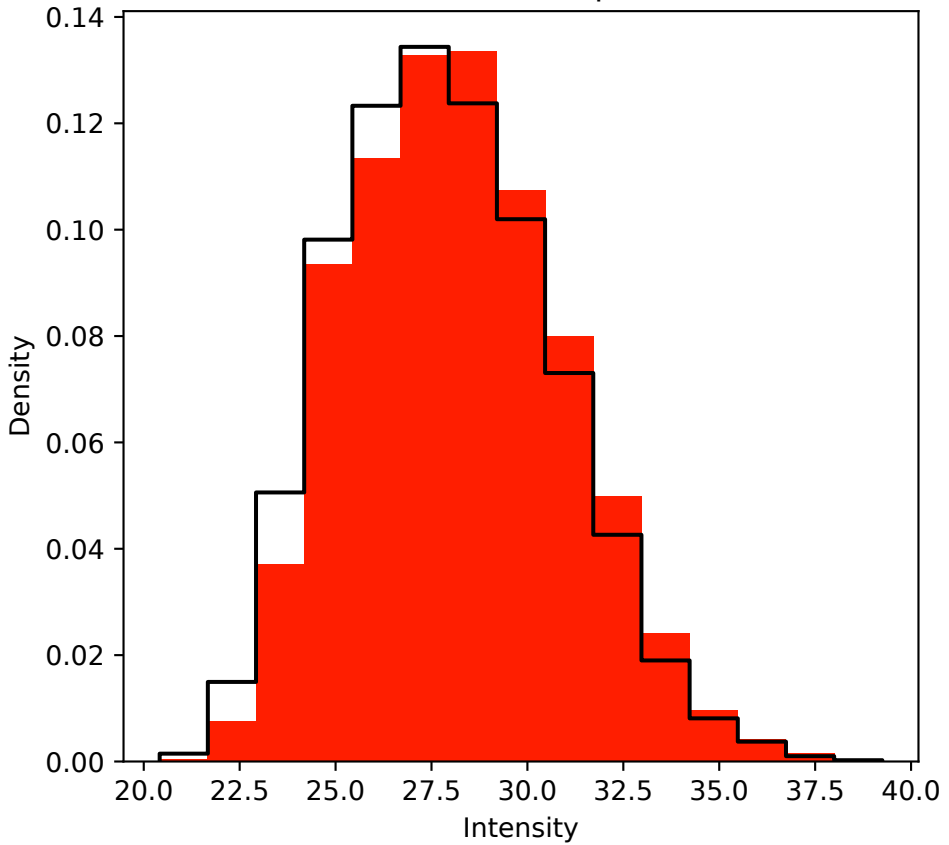
H838 unst Rep1 2



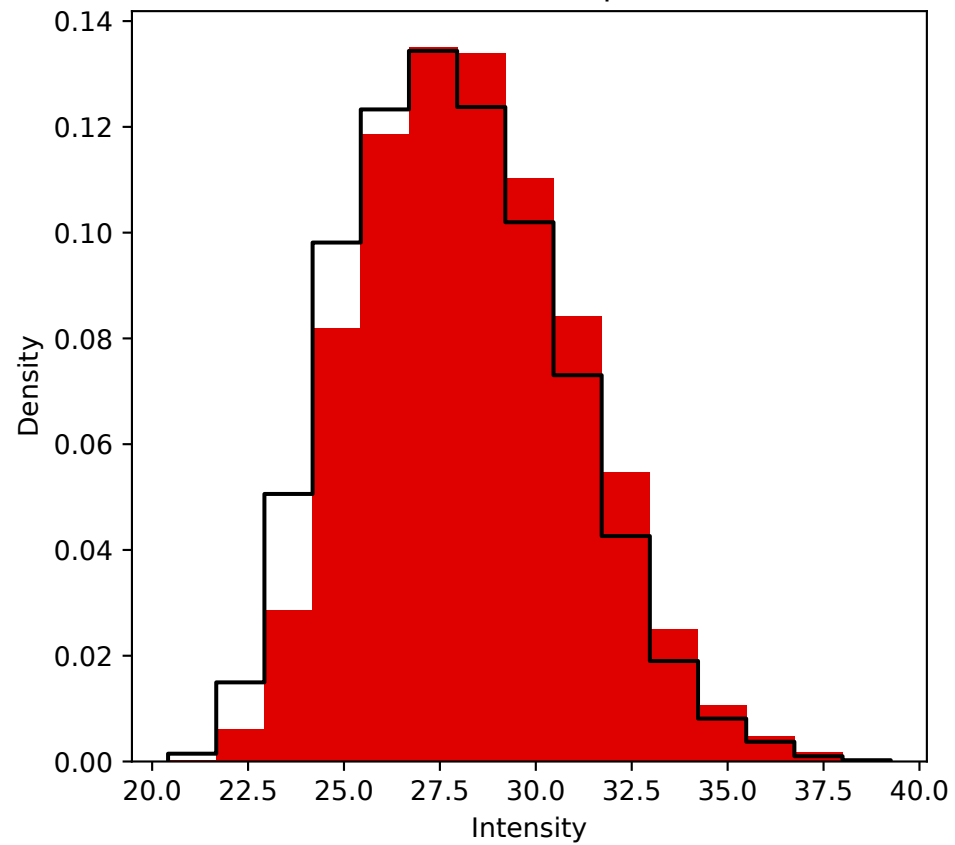
H838 unst Rep2 1



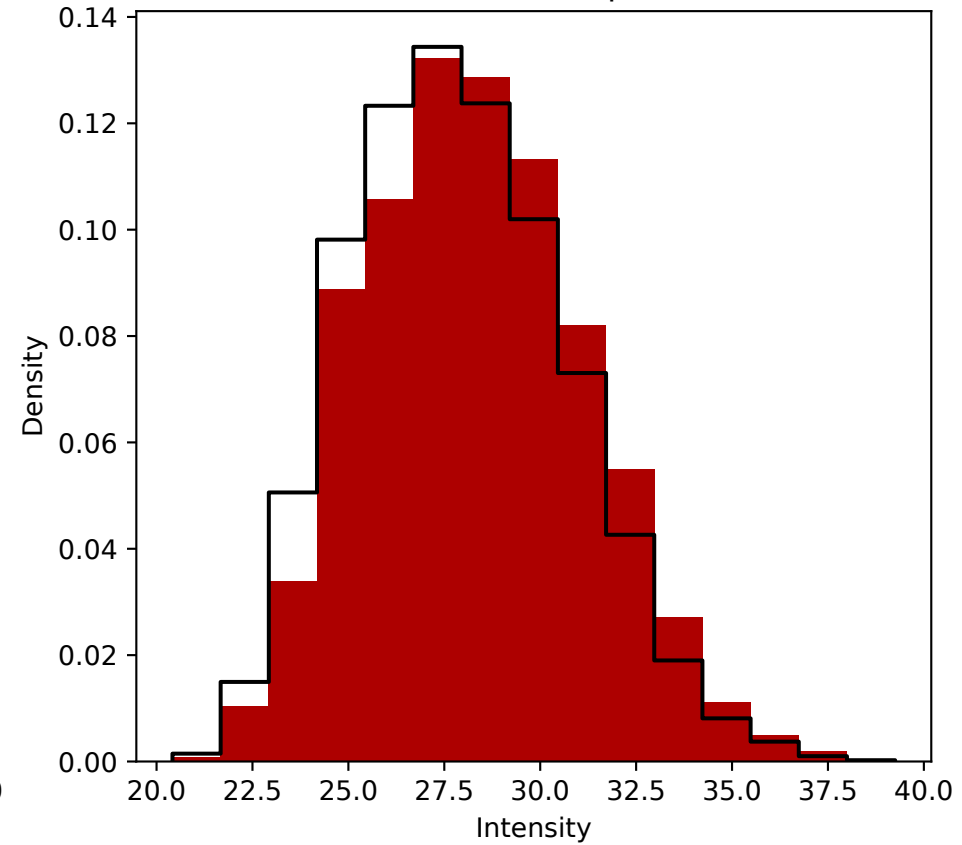
H838 unst Rep2 2



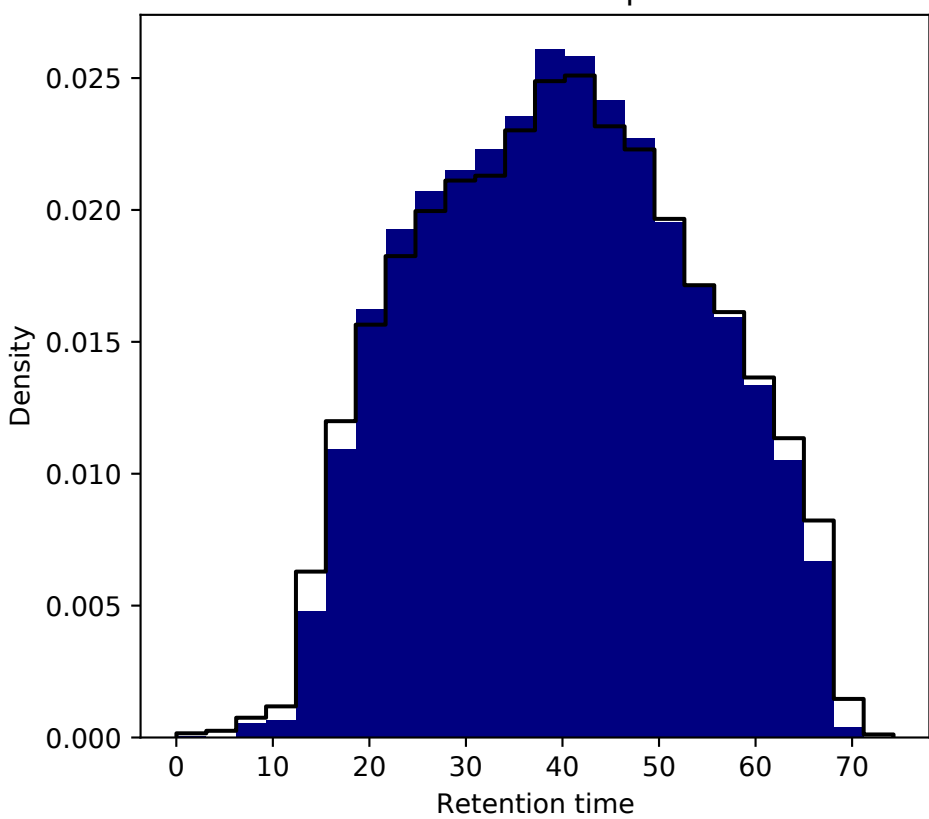
H838 unst Rep3 1



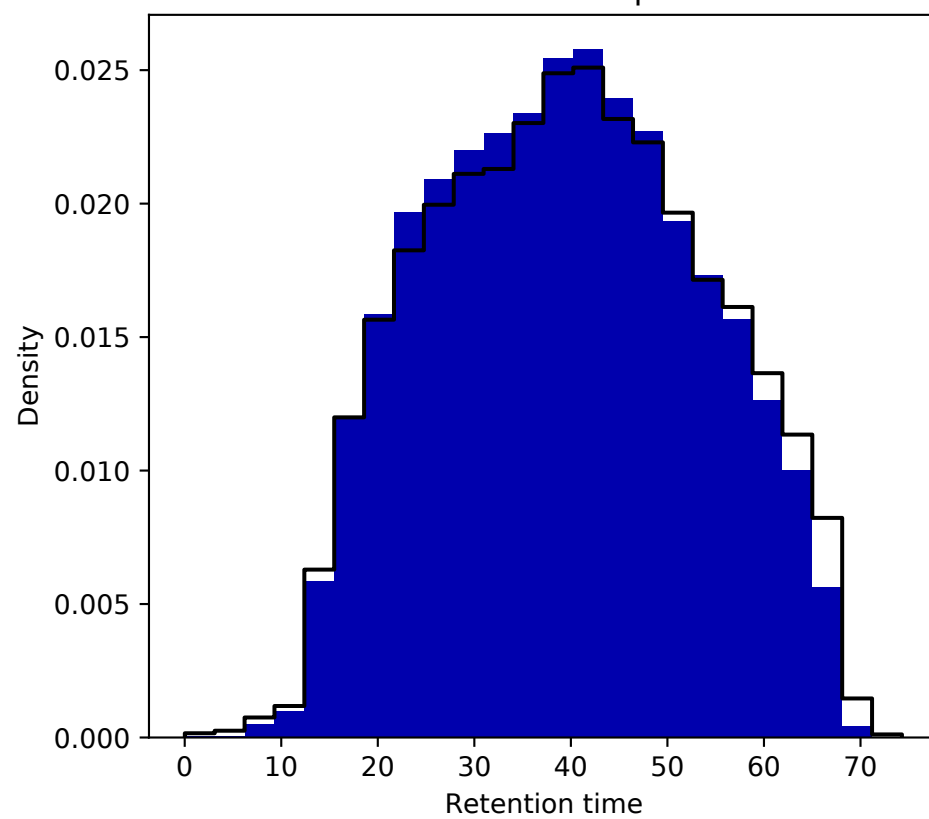
H838 unst Rep3 2



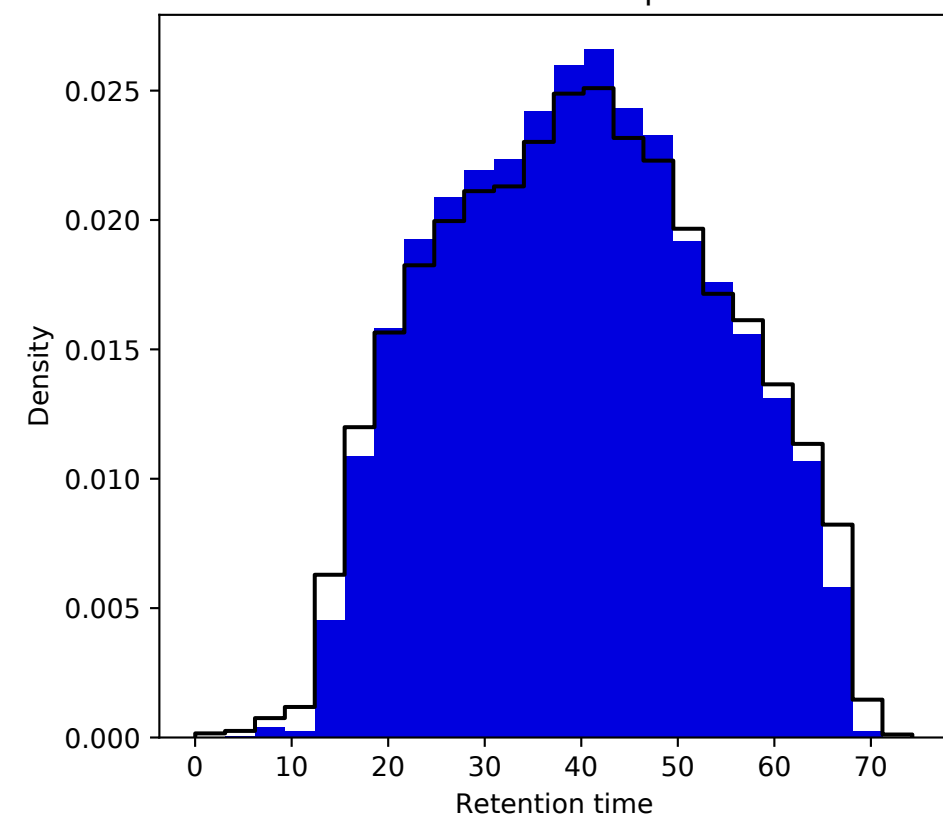
H1975 TGFb Rep1 1



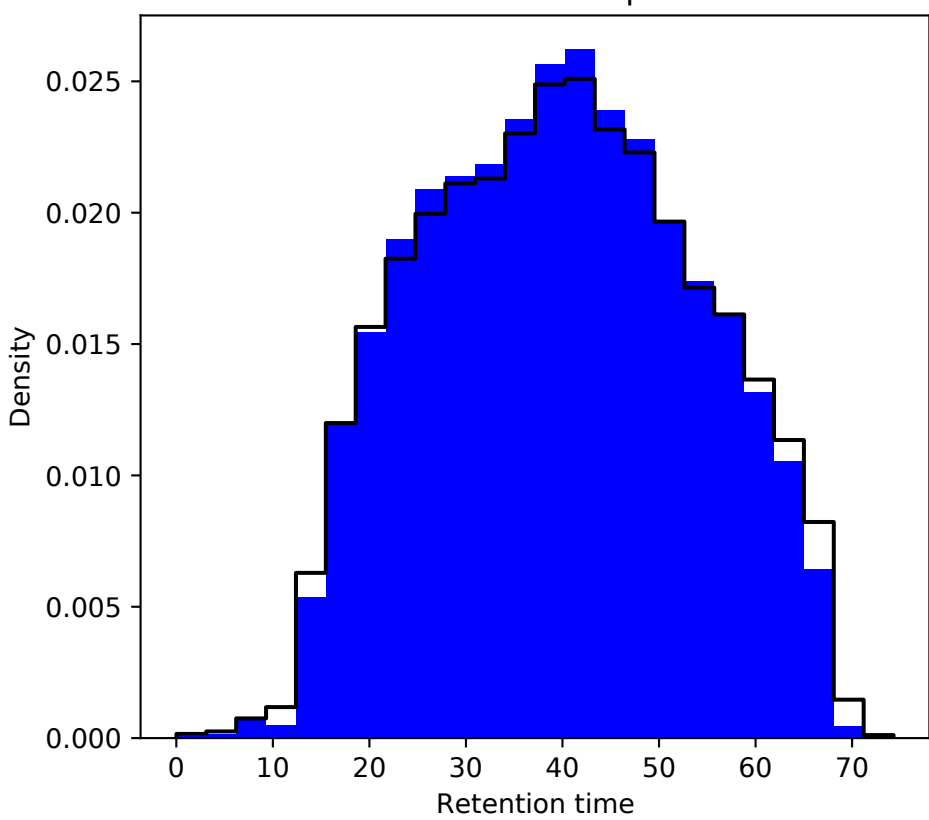
H1975 TGFb Rep1 2



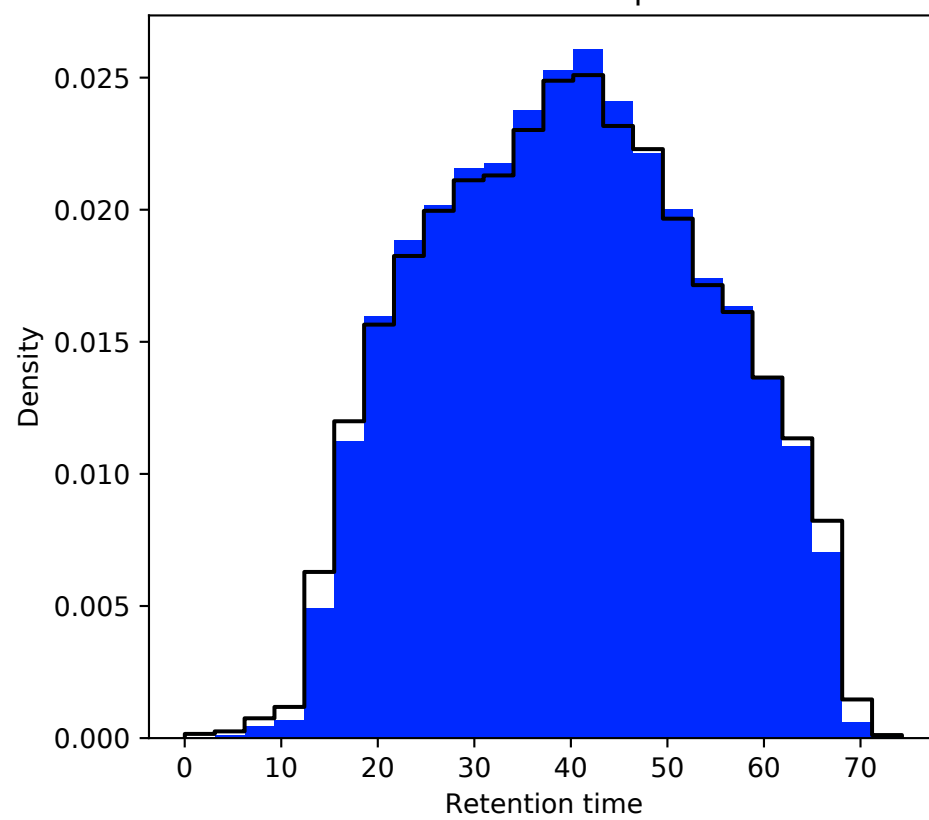
H1975 TGFb Rep2 1



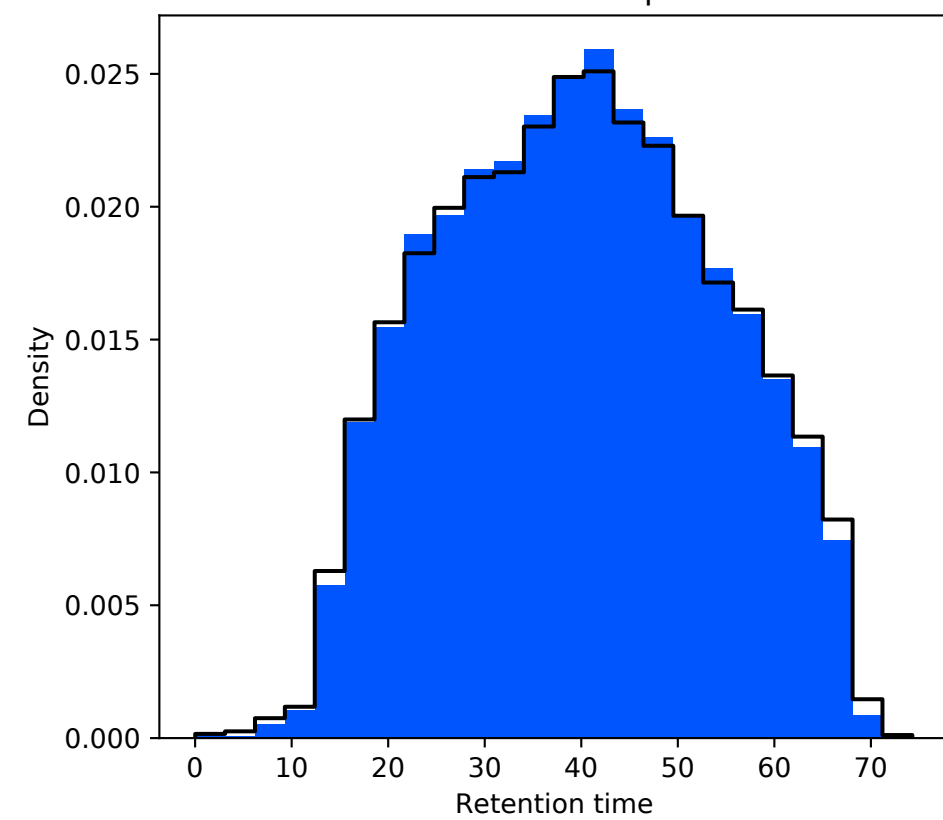
H1975 TGFb Rep2 2



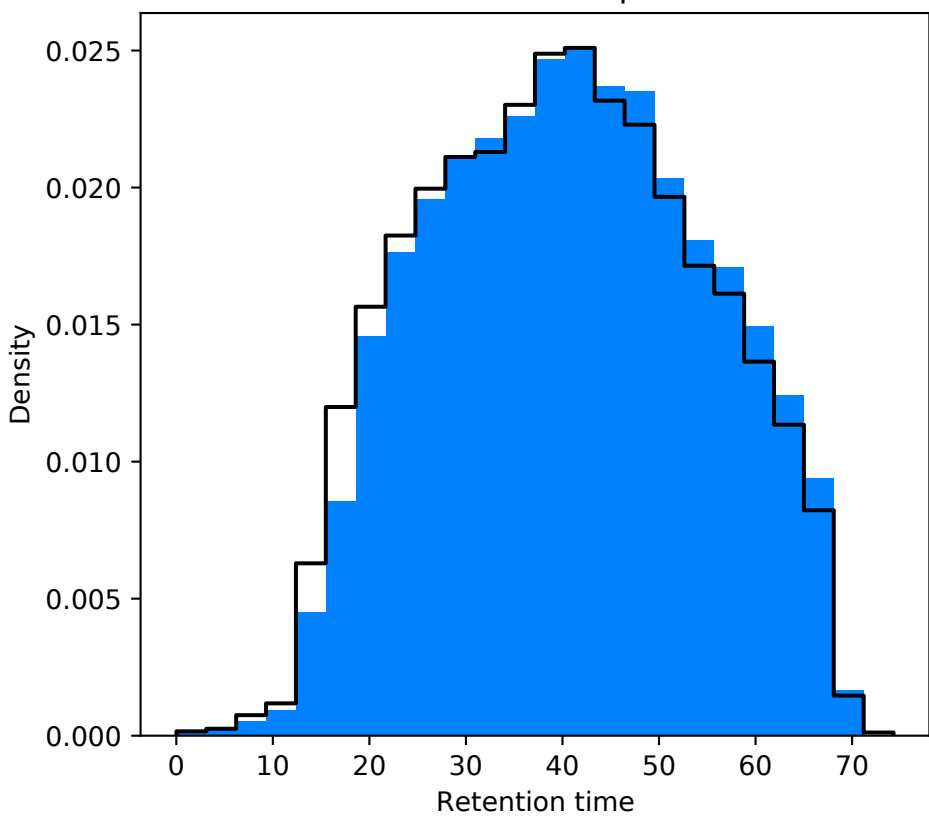
H1975 TGFb Rep3 1



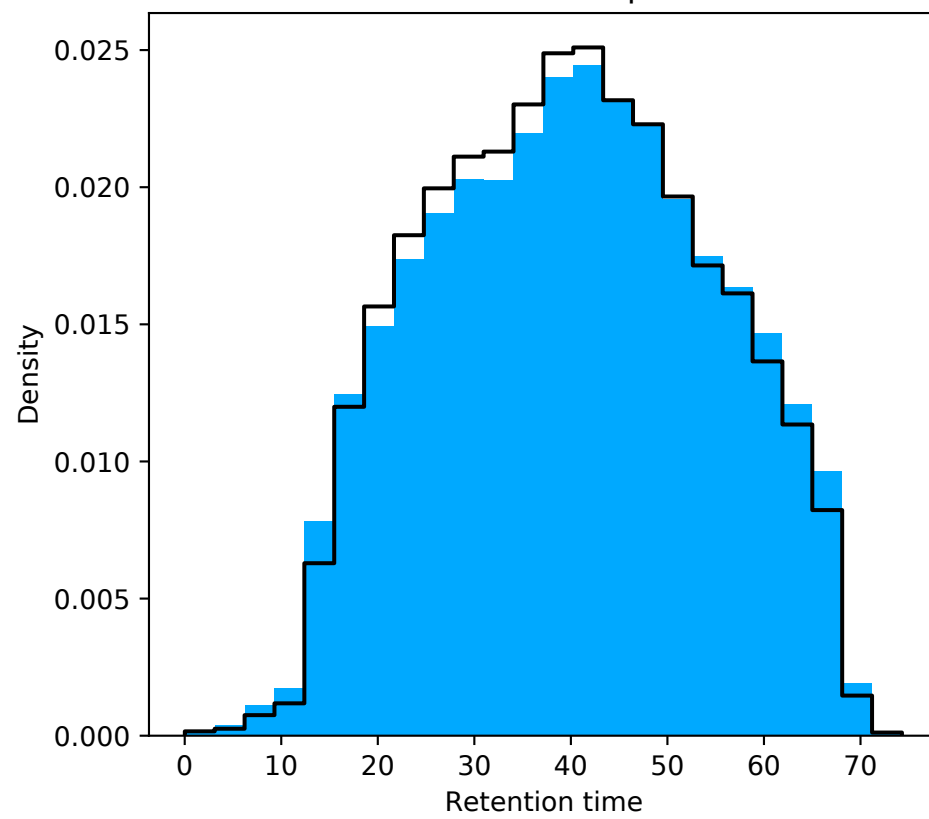
H1975 TGFb Rep3 2



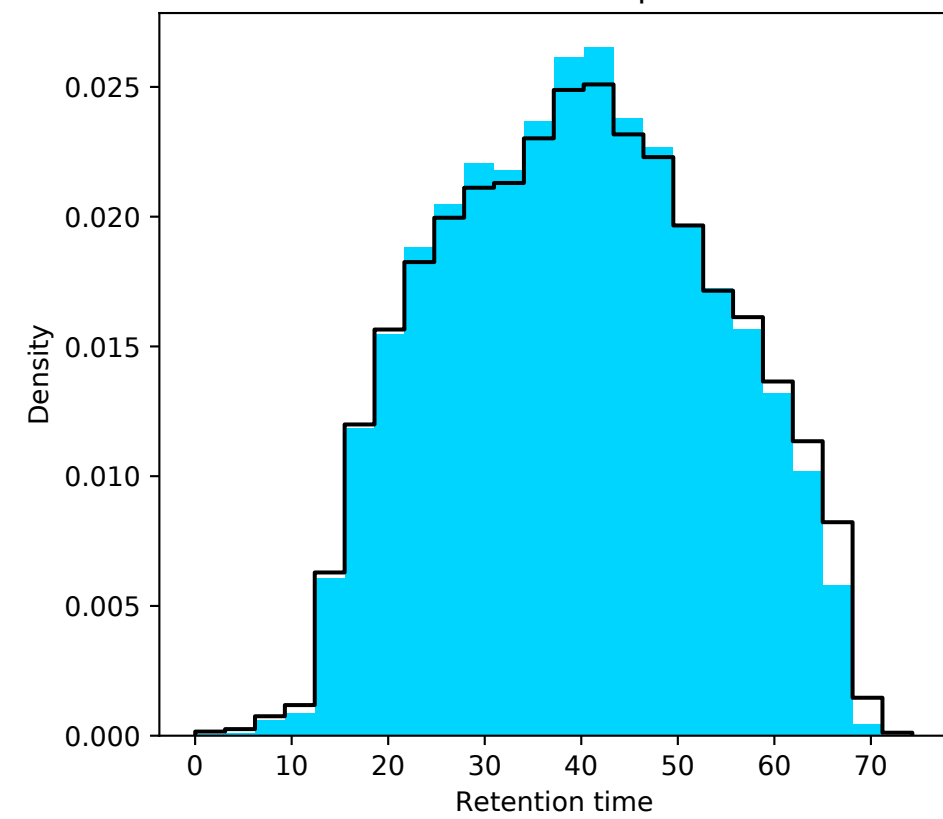
H1975 unst Rep1 1



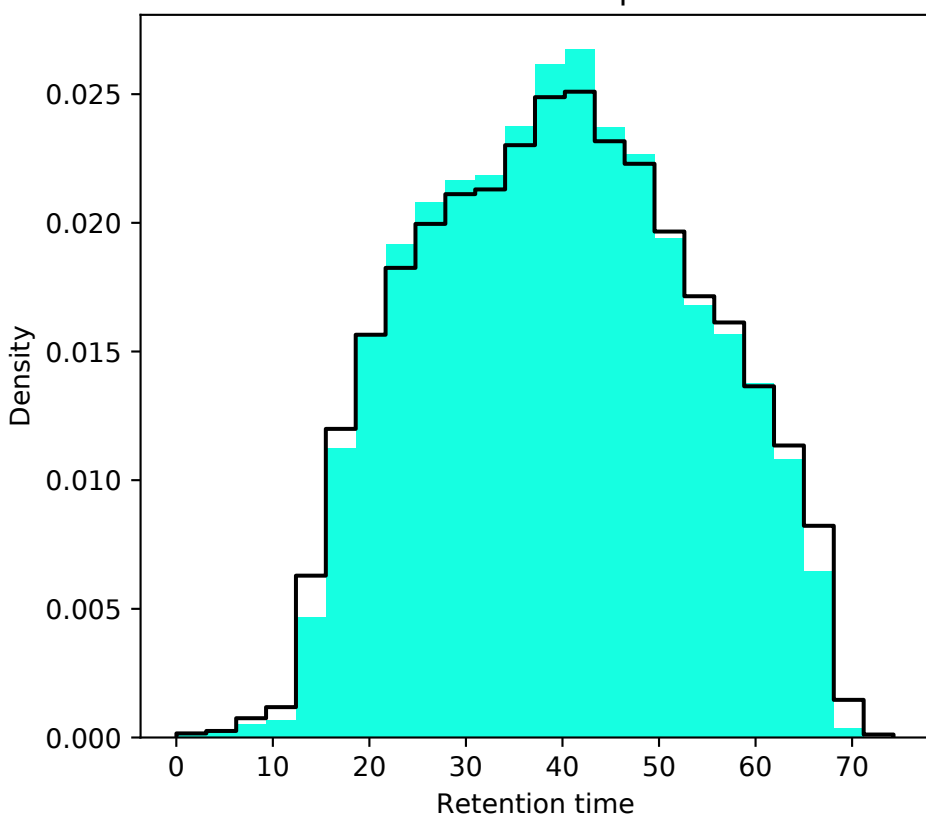
H1975 unst Rep1 2



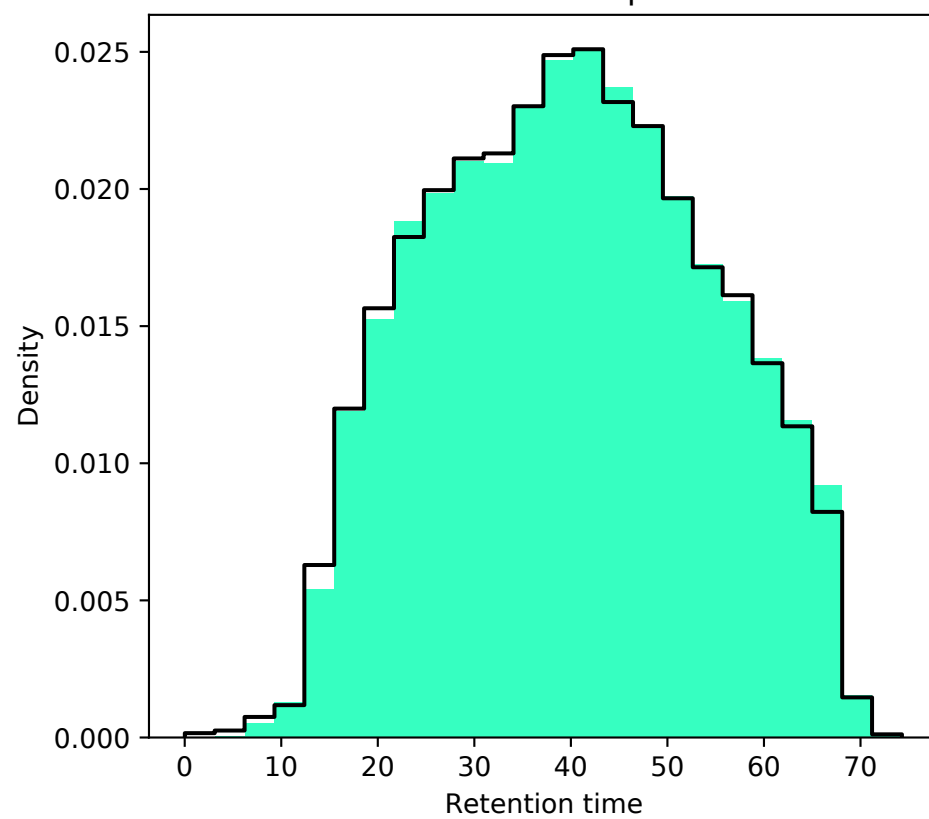
H1975 unst Rep2 1



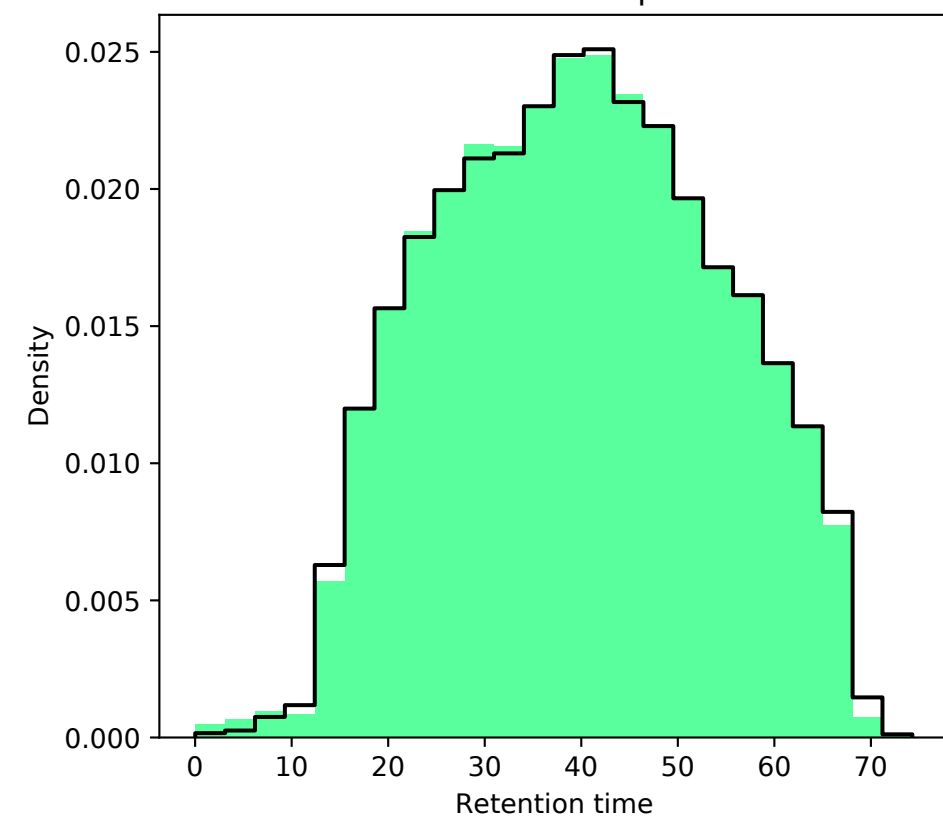
H1975 unst Rep2 2



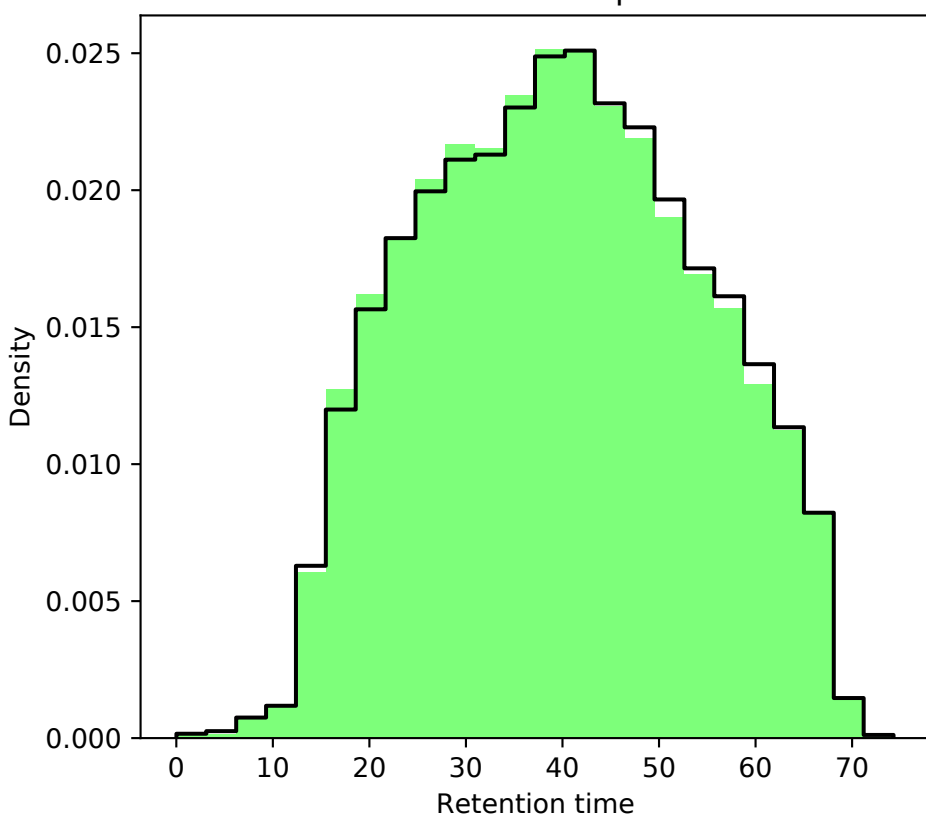
H1975 unst Rep3 1



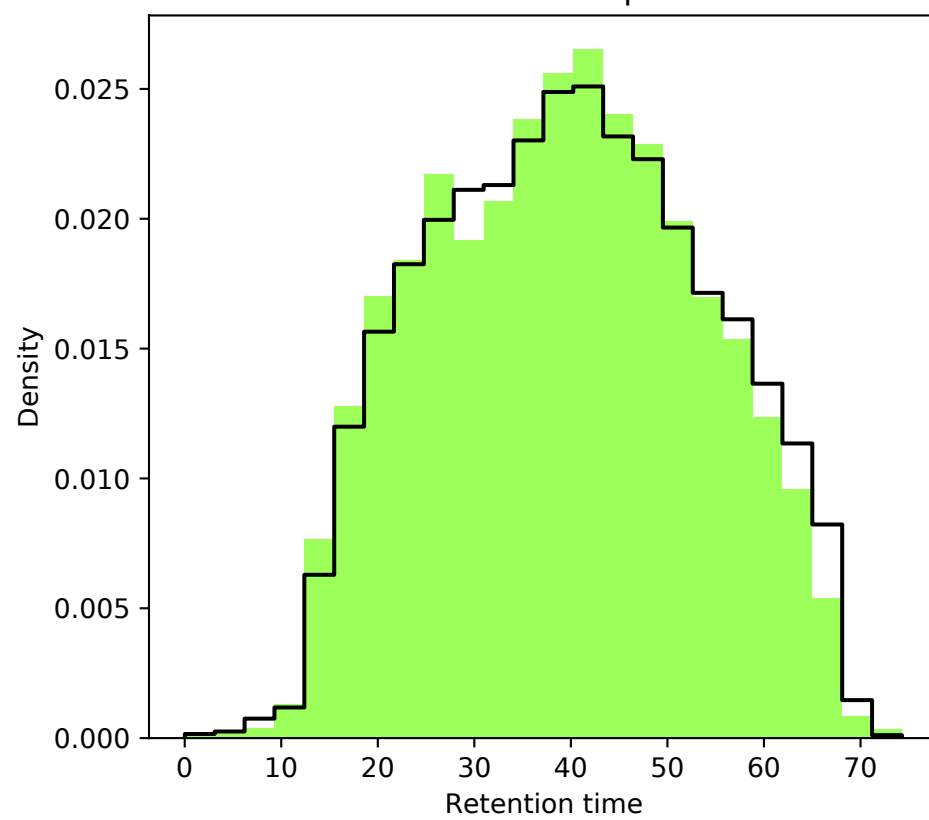
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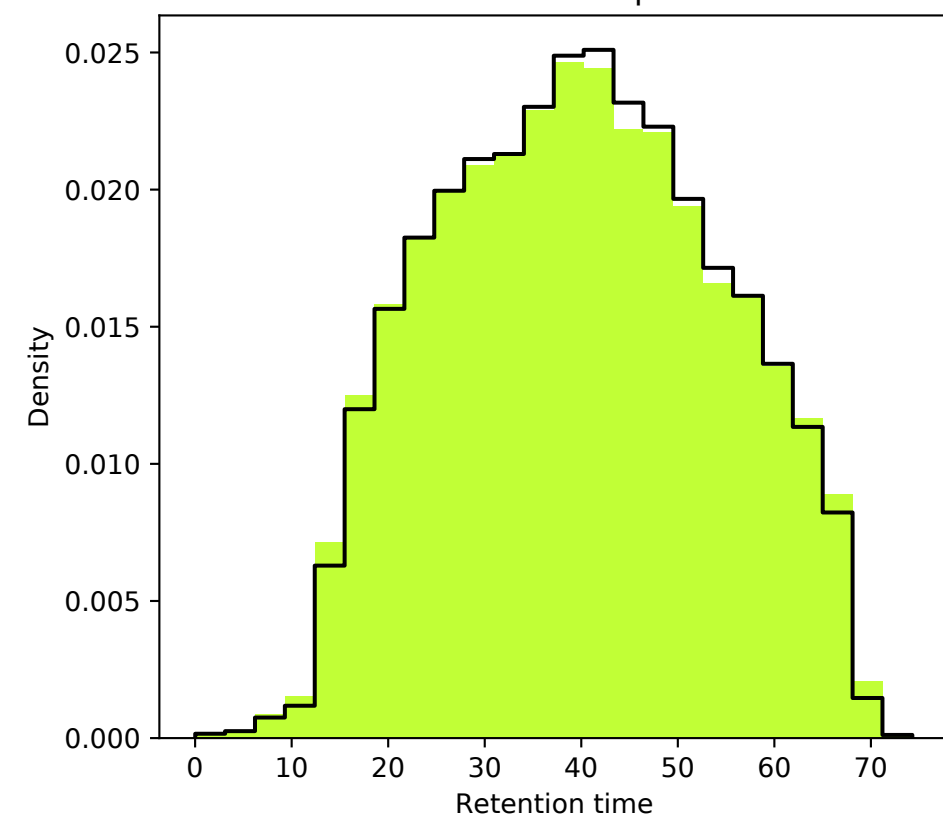
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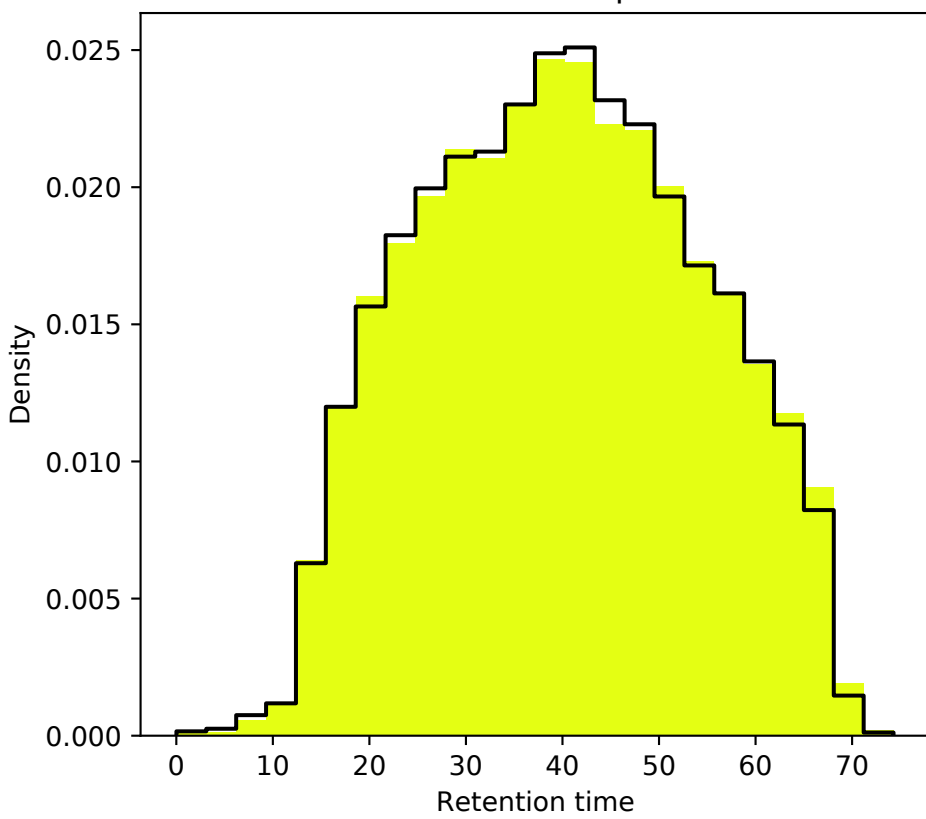
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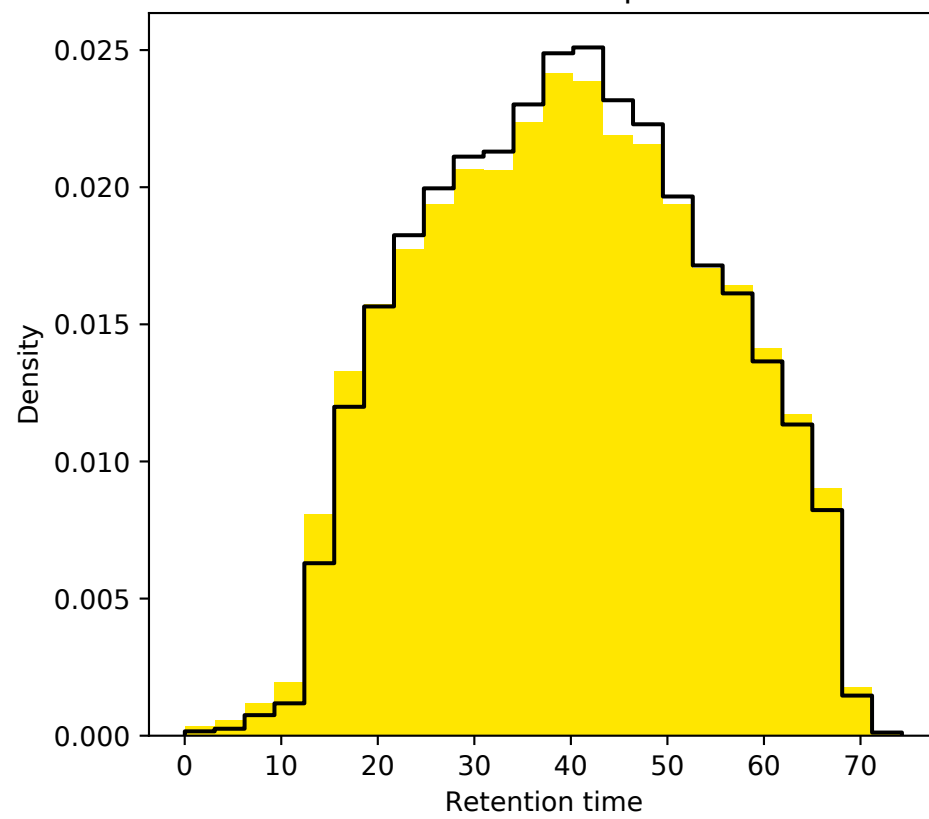
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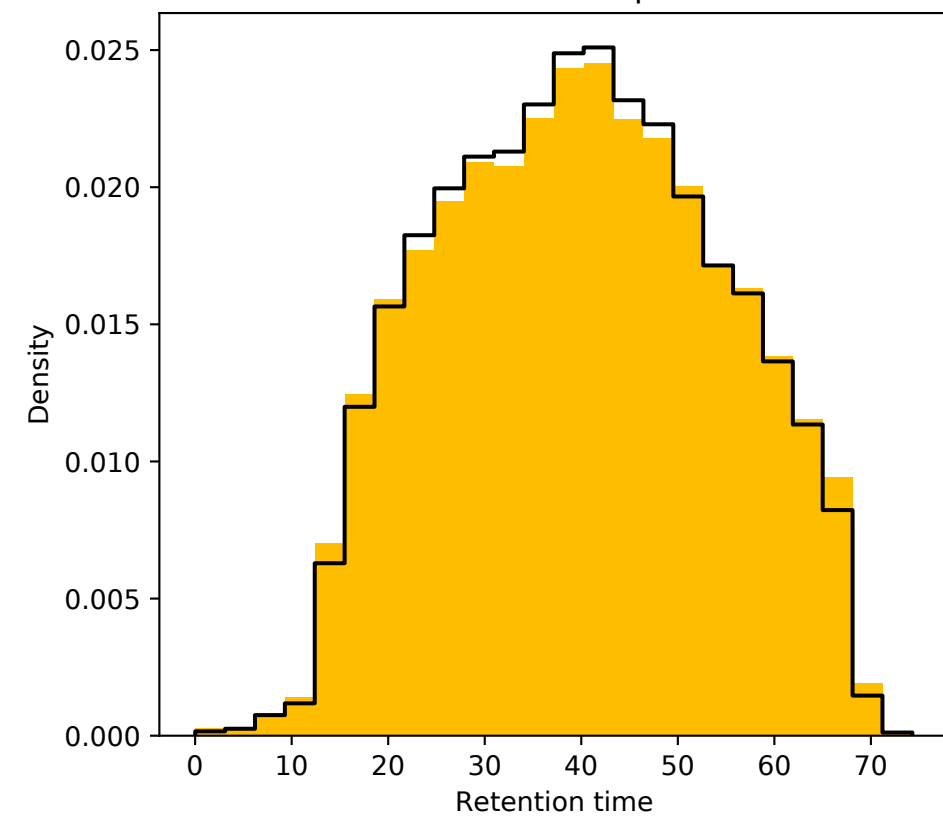
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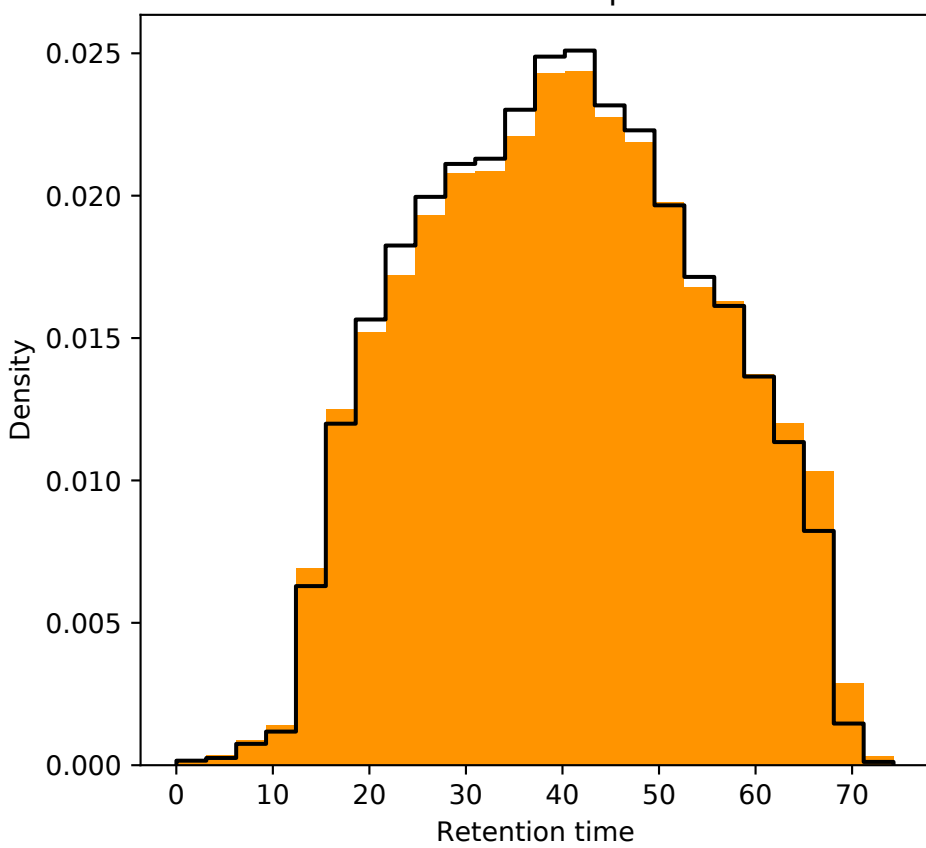
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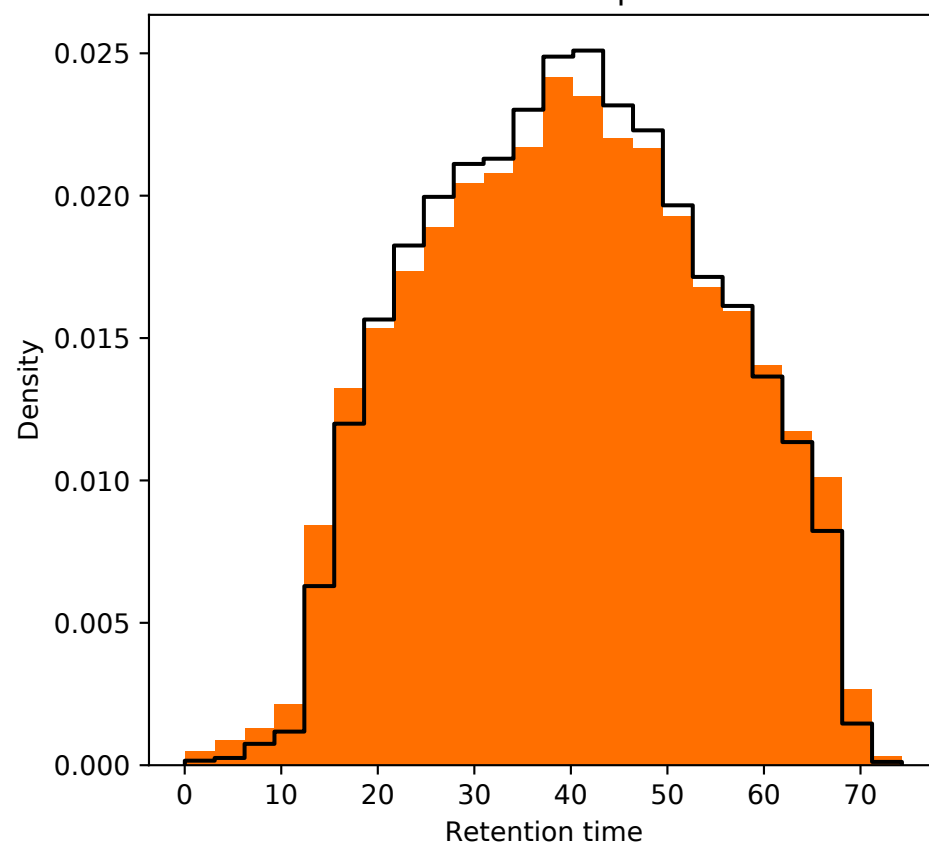
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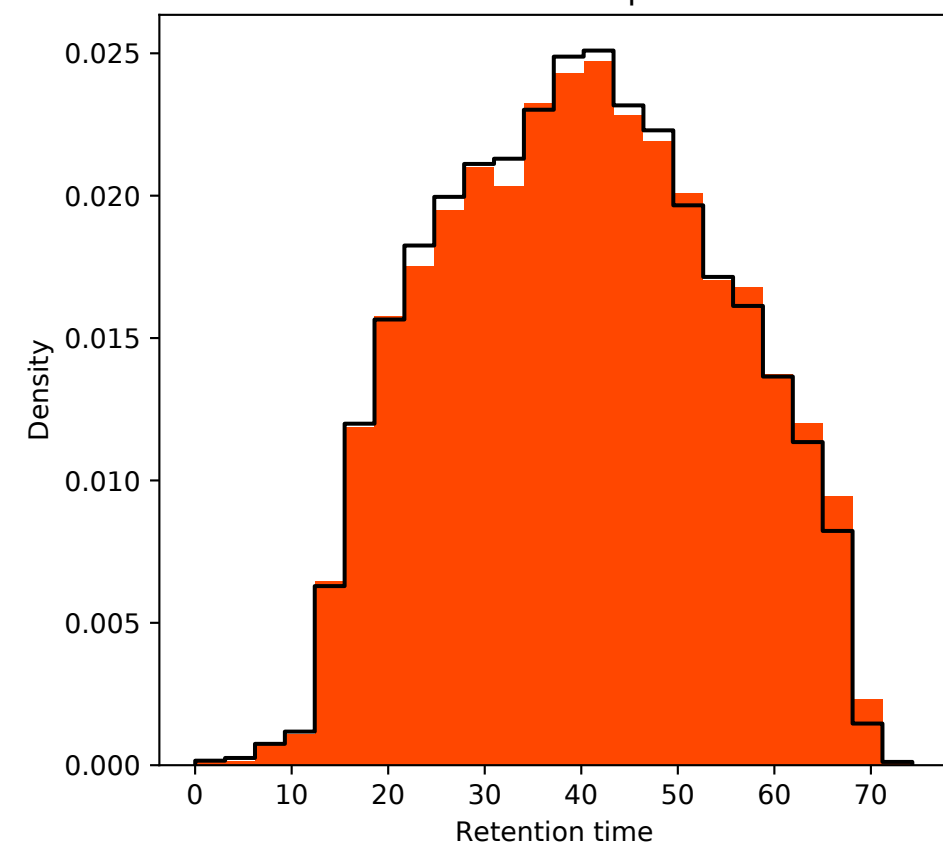
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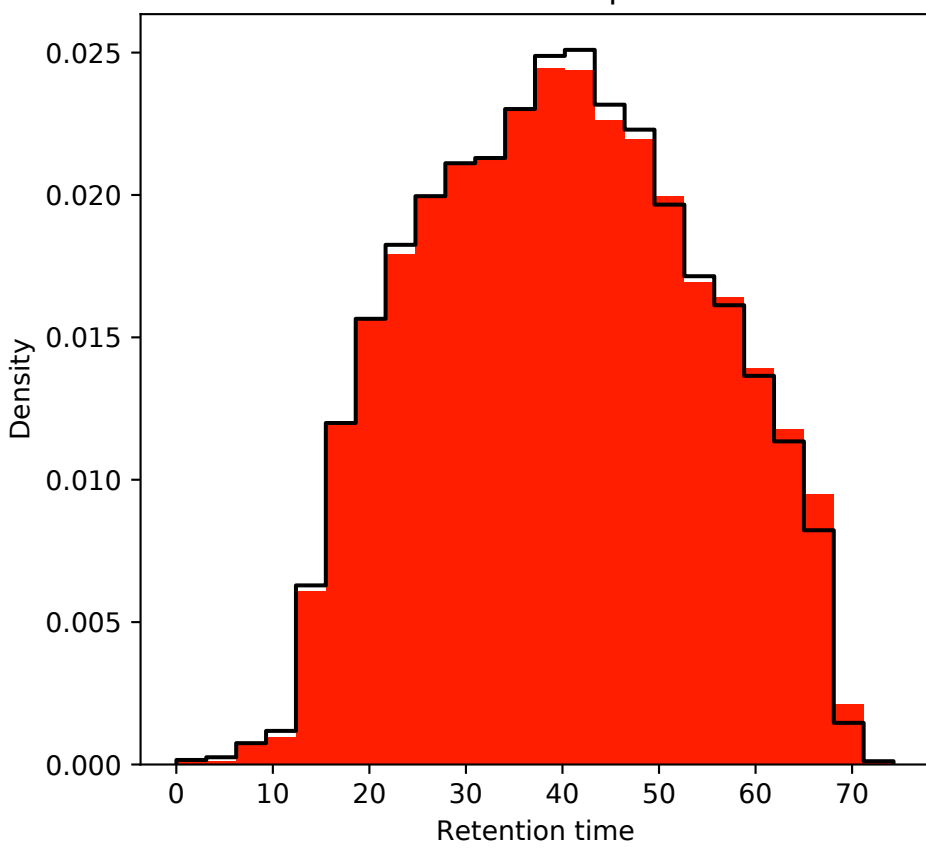
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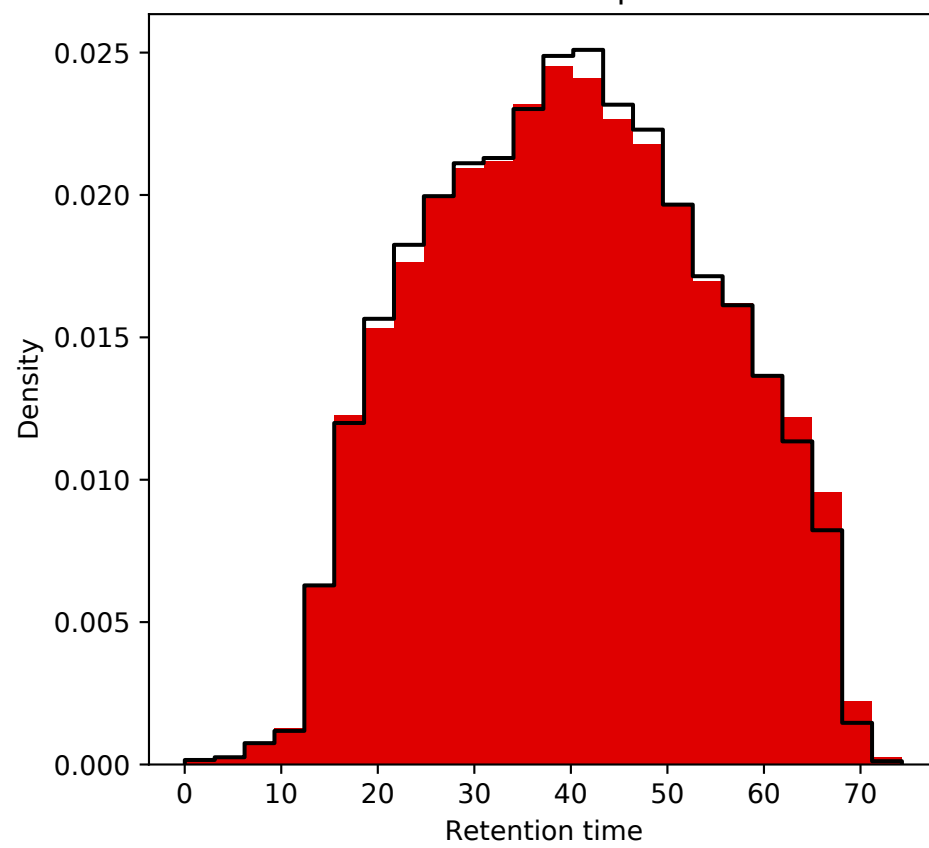
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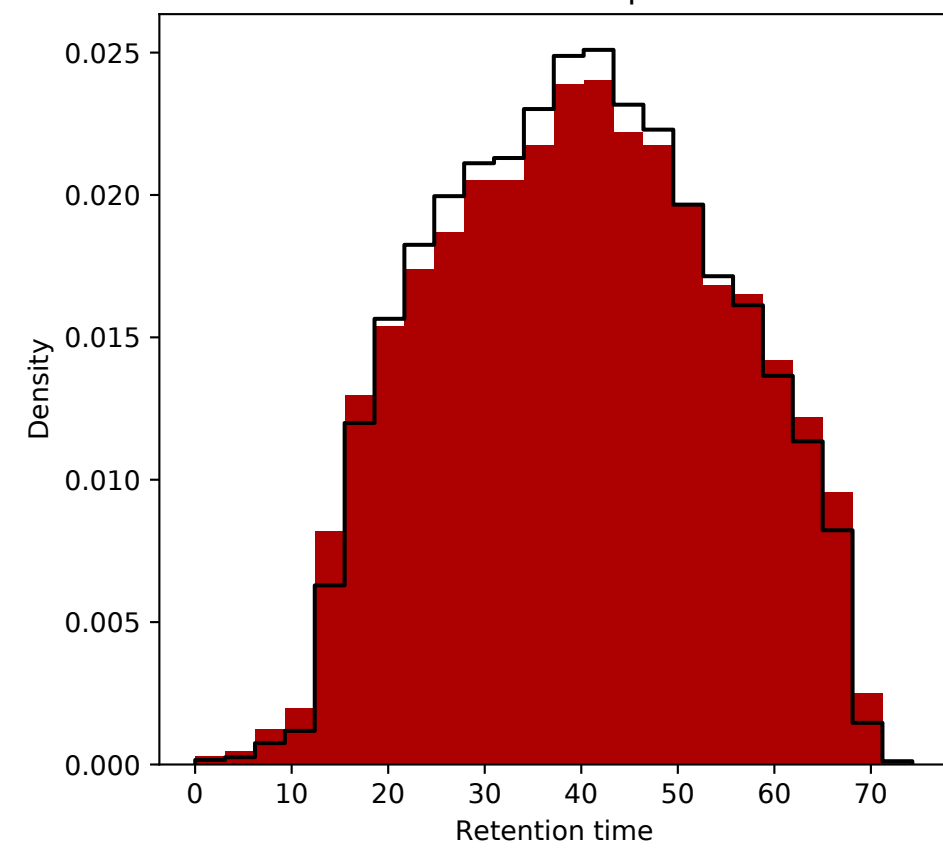
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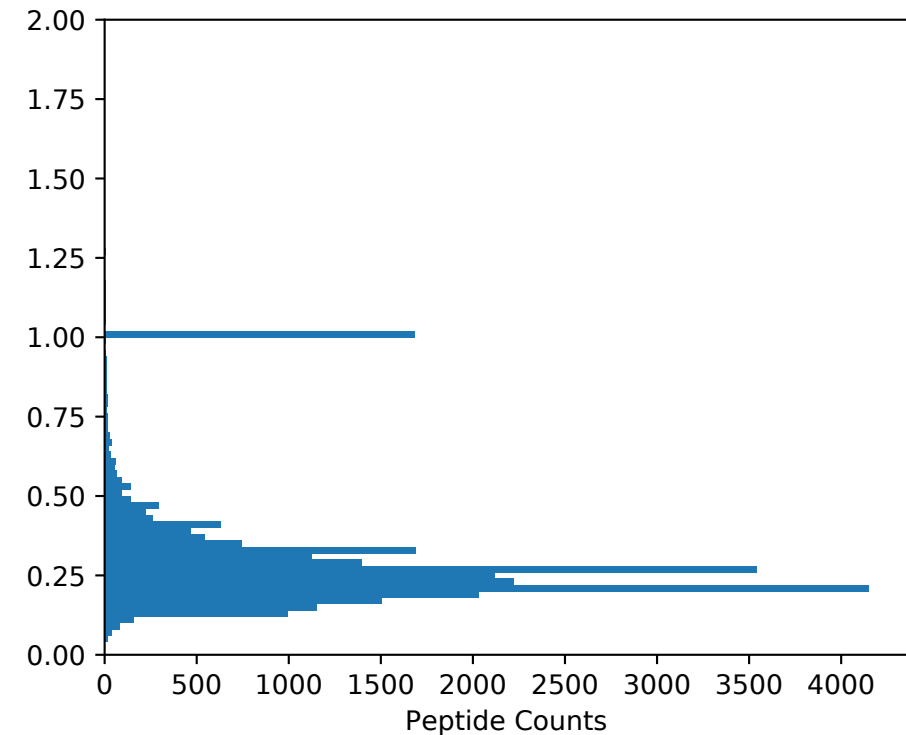
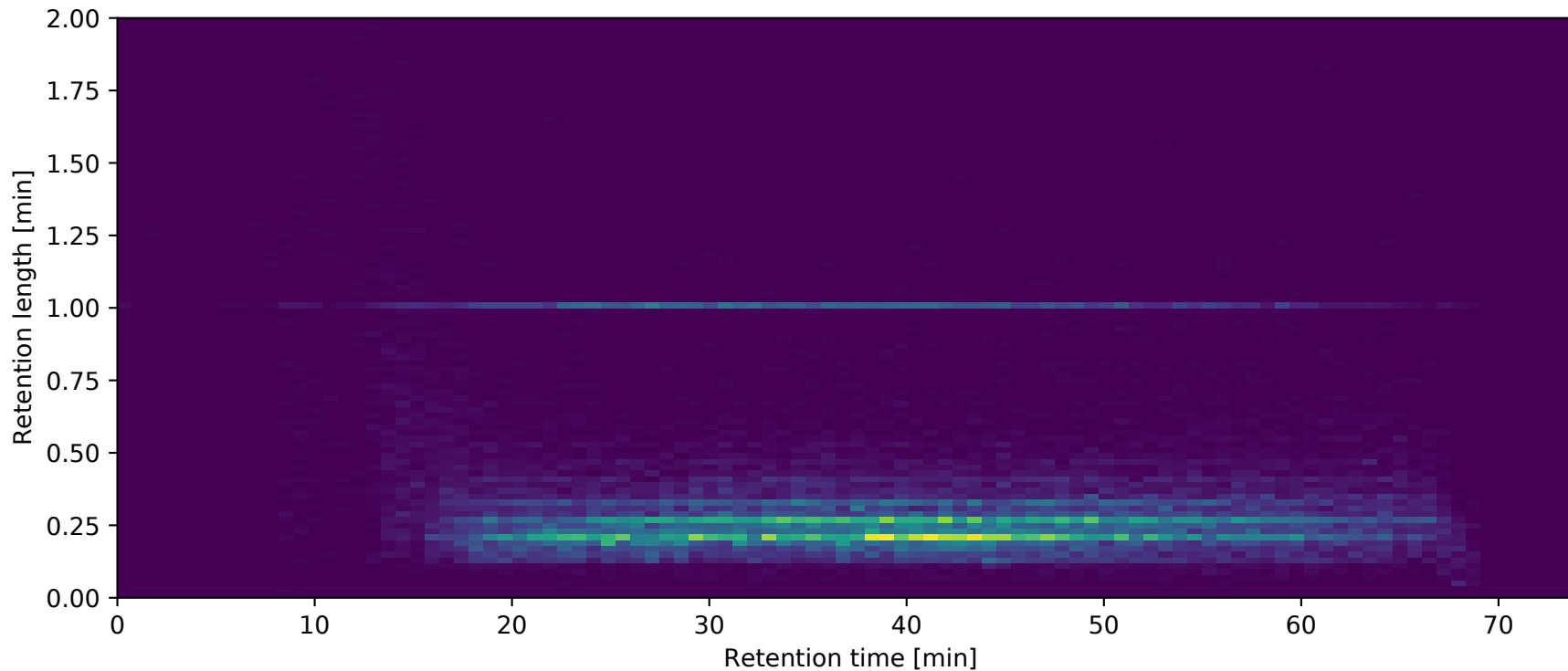
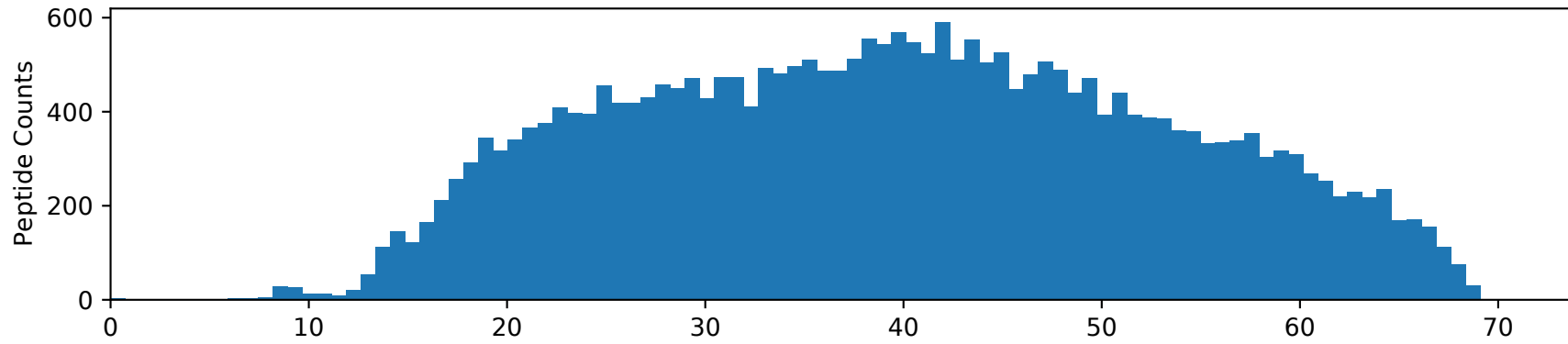
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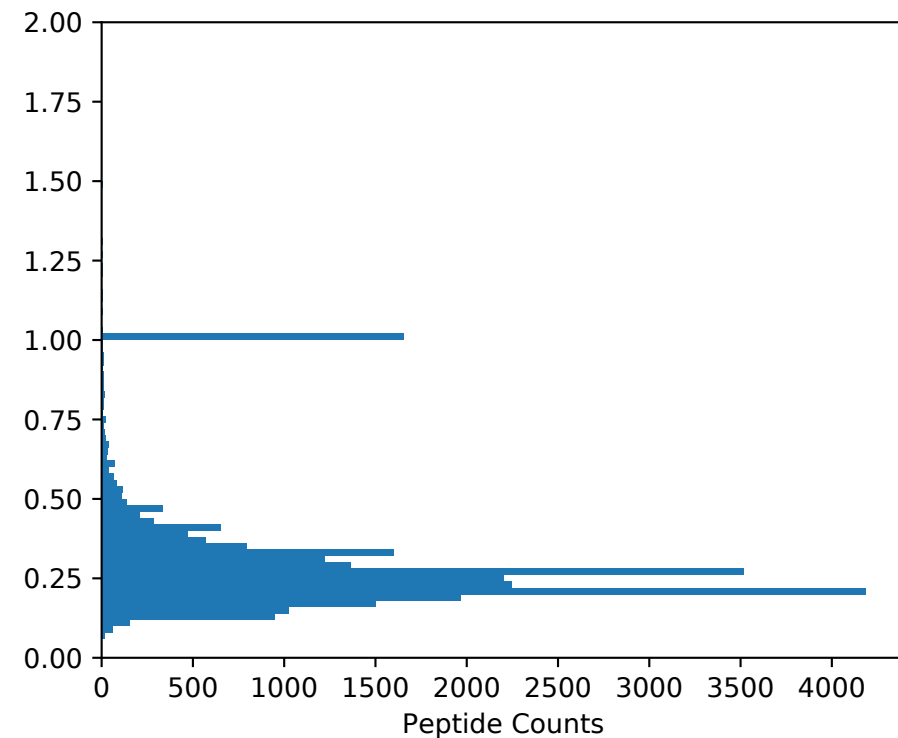
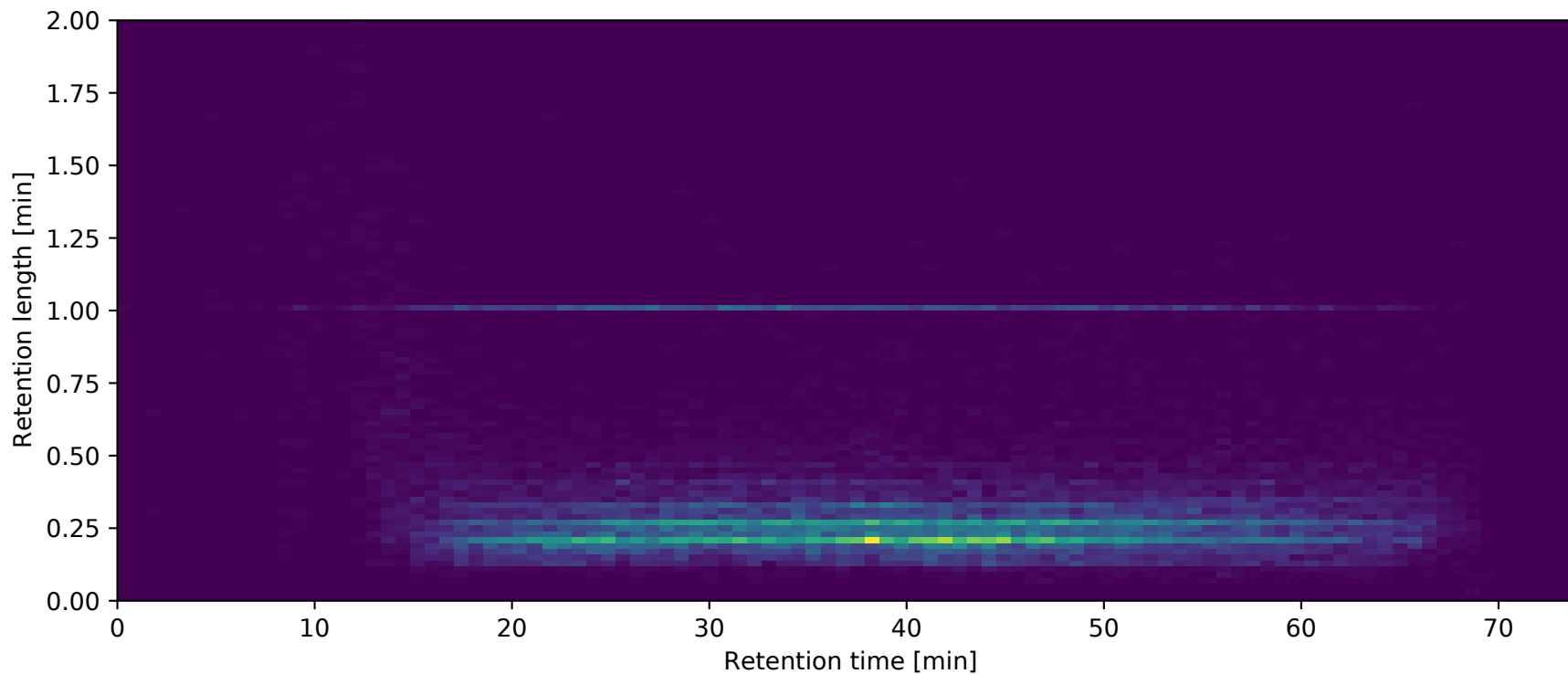
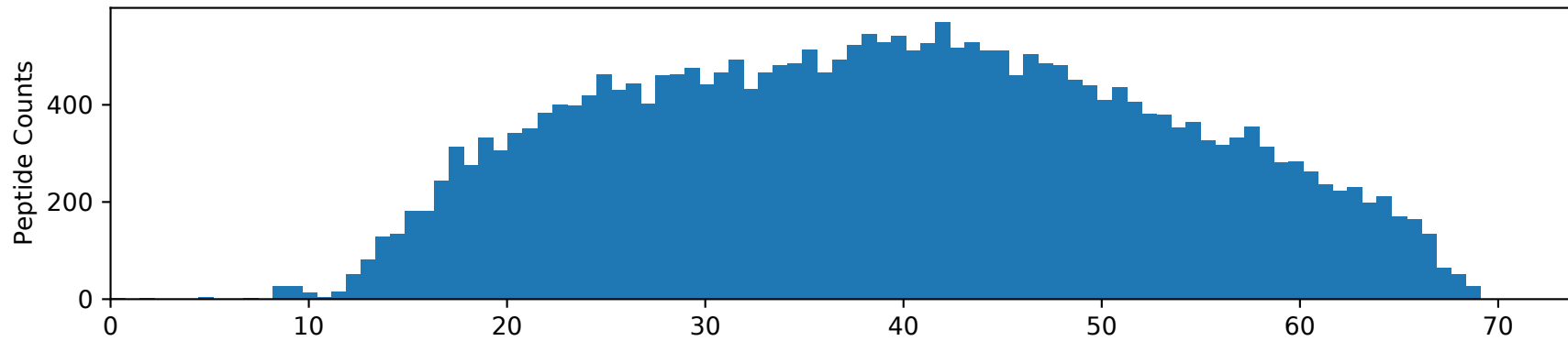
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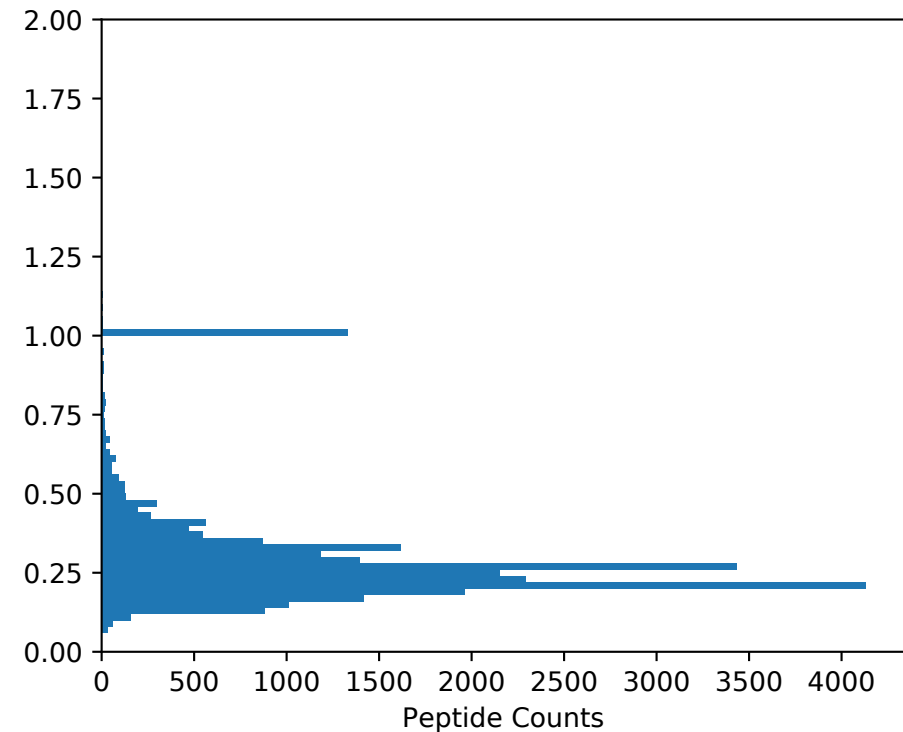
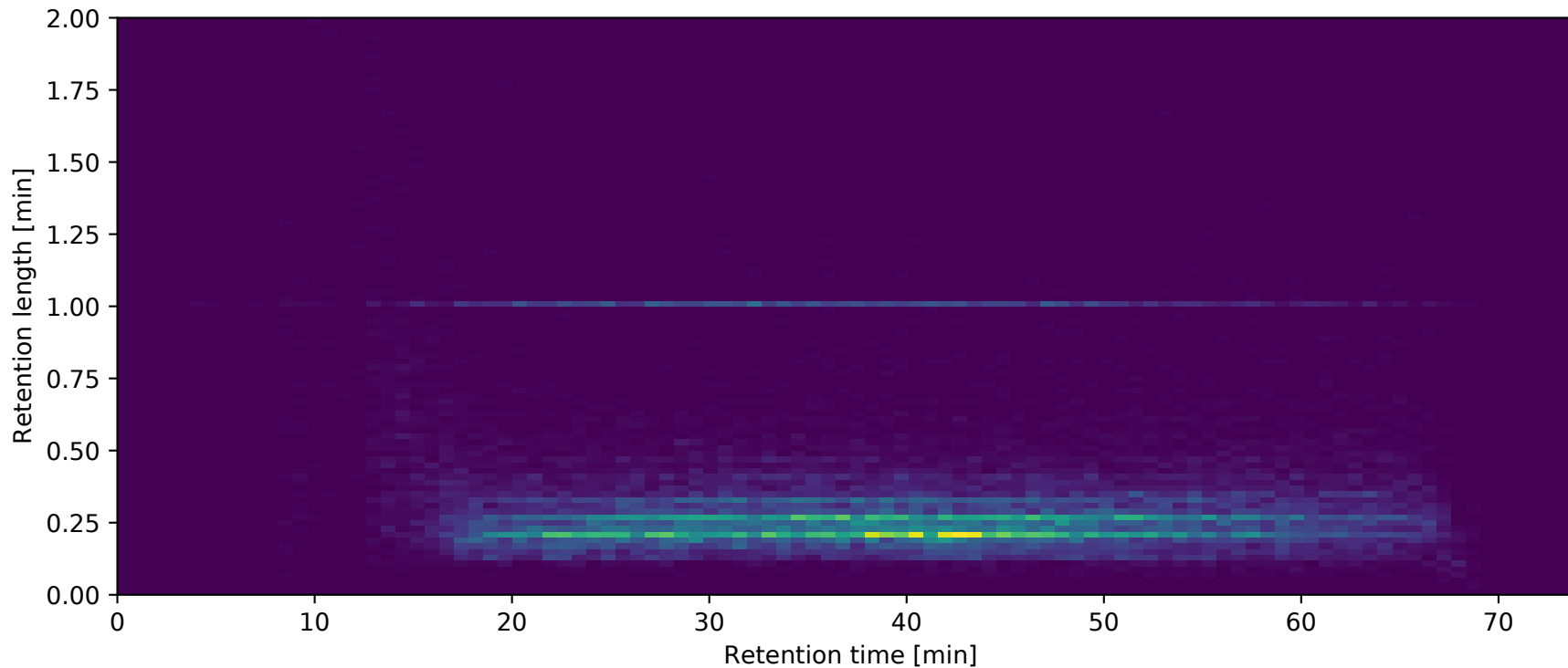
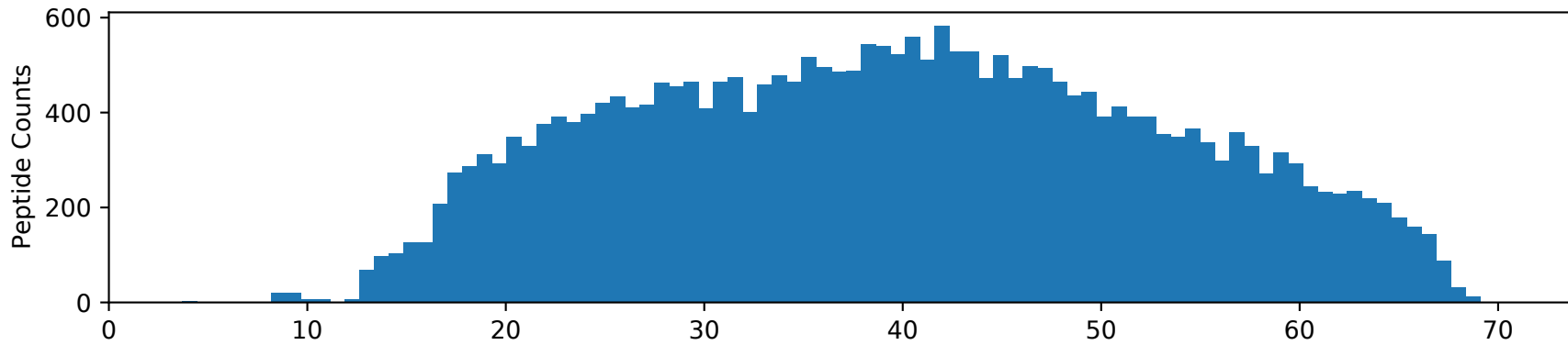
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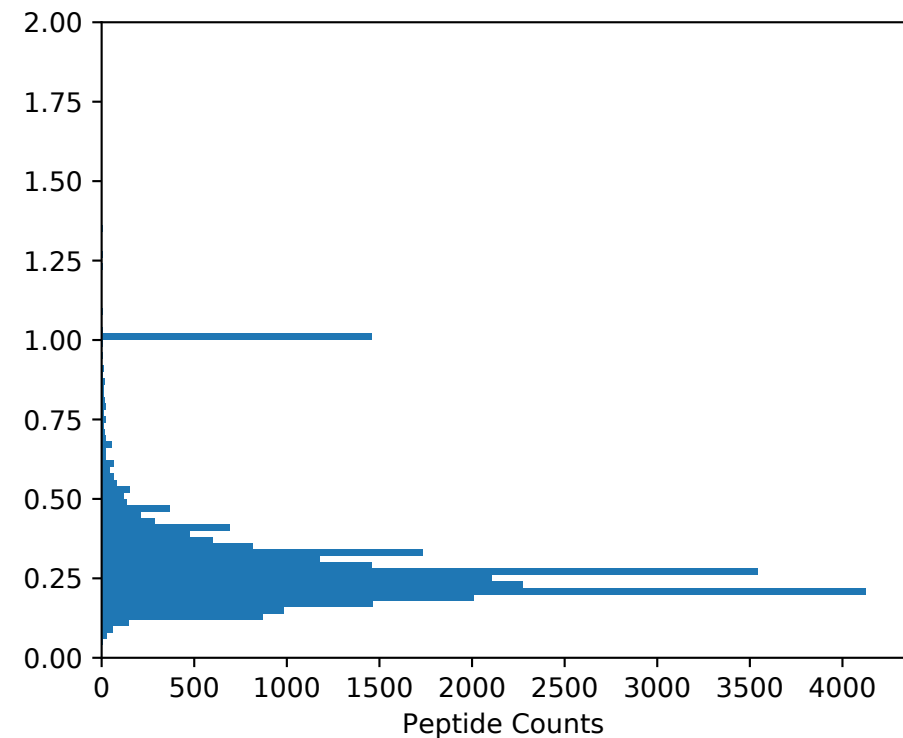
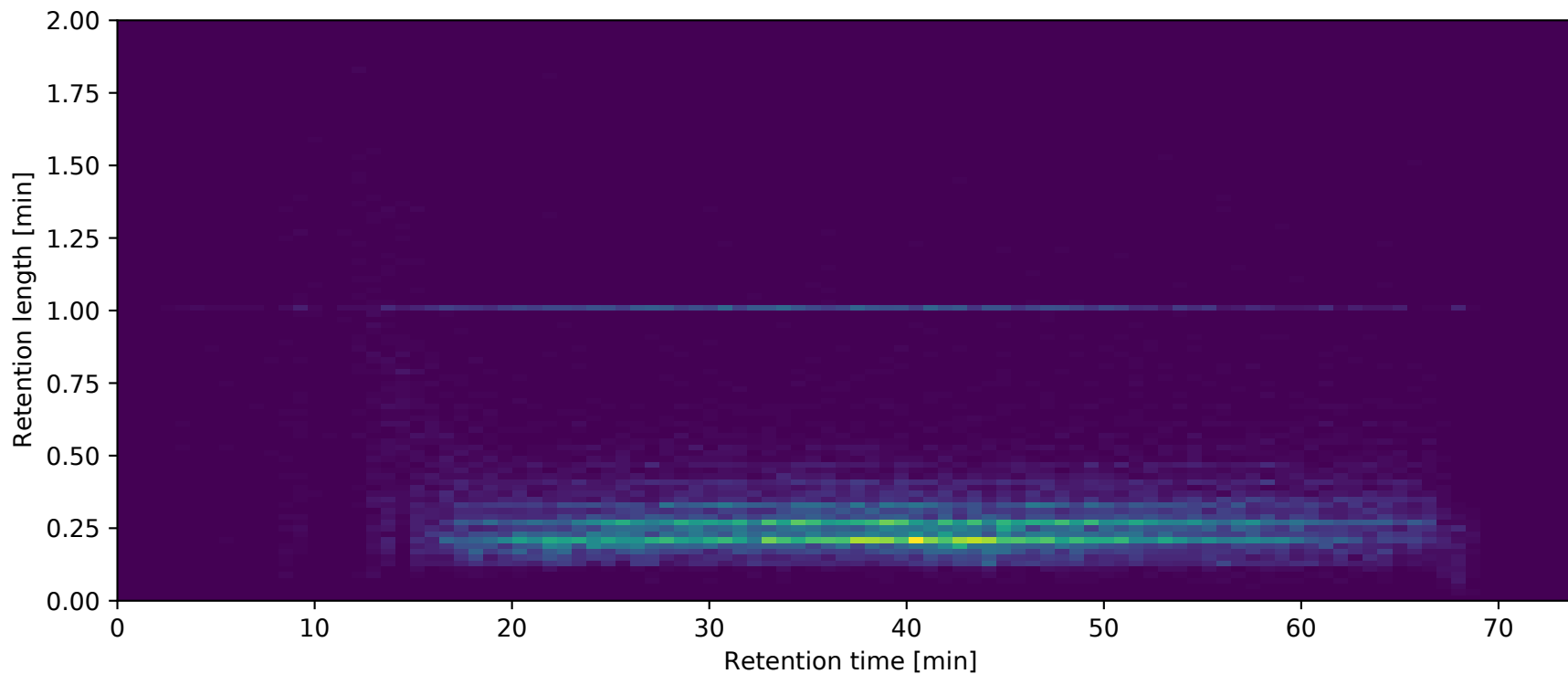
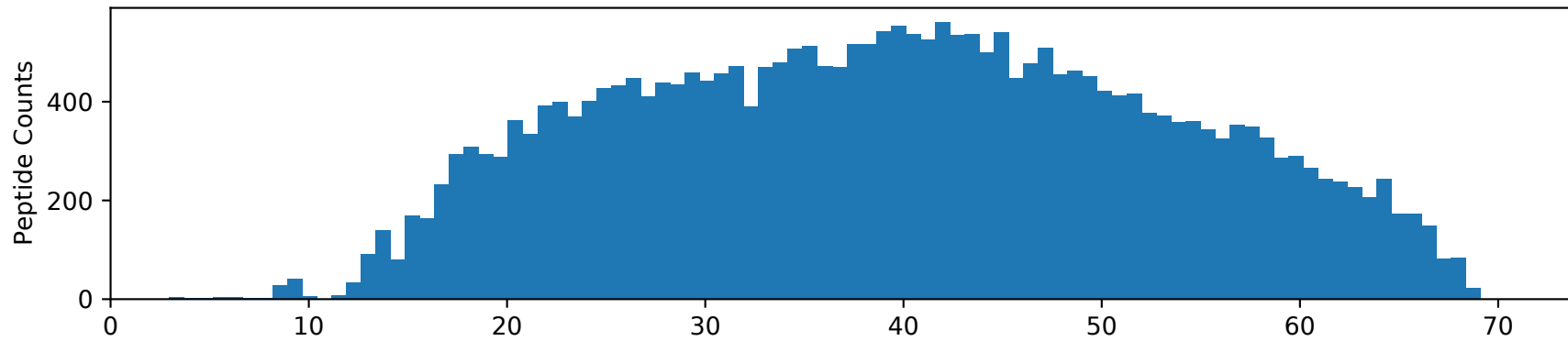
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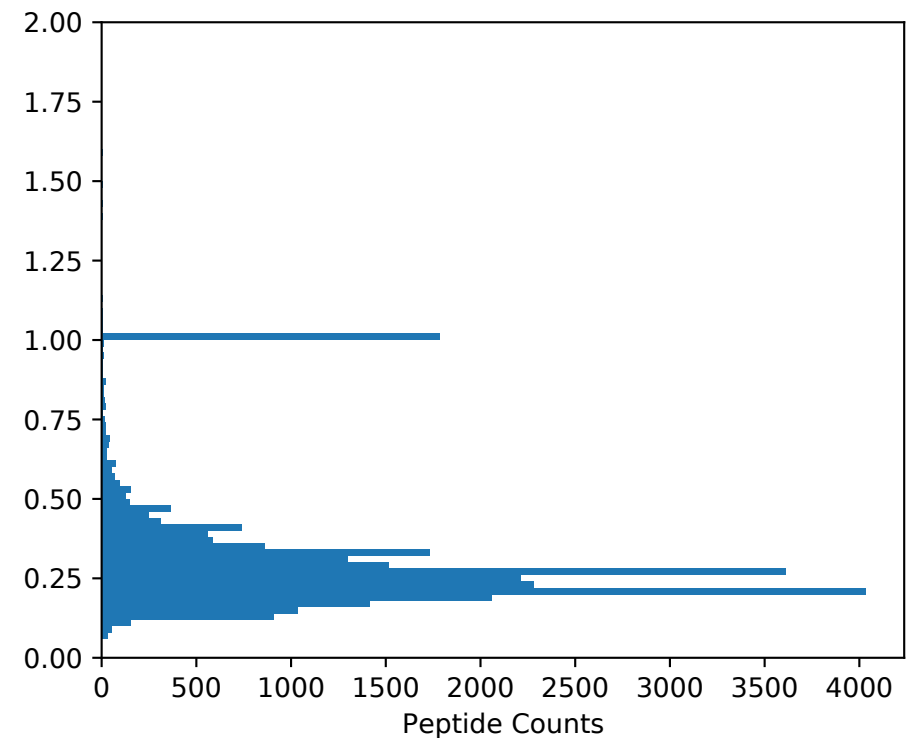
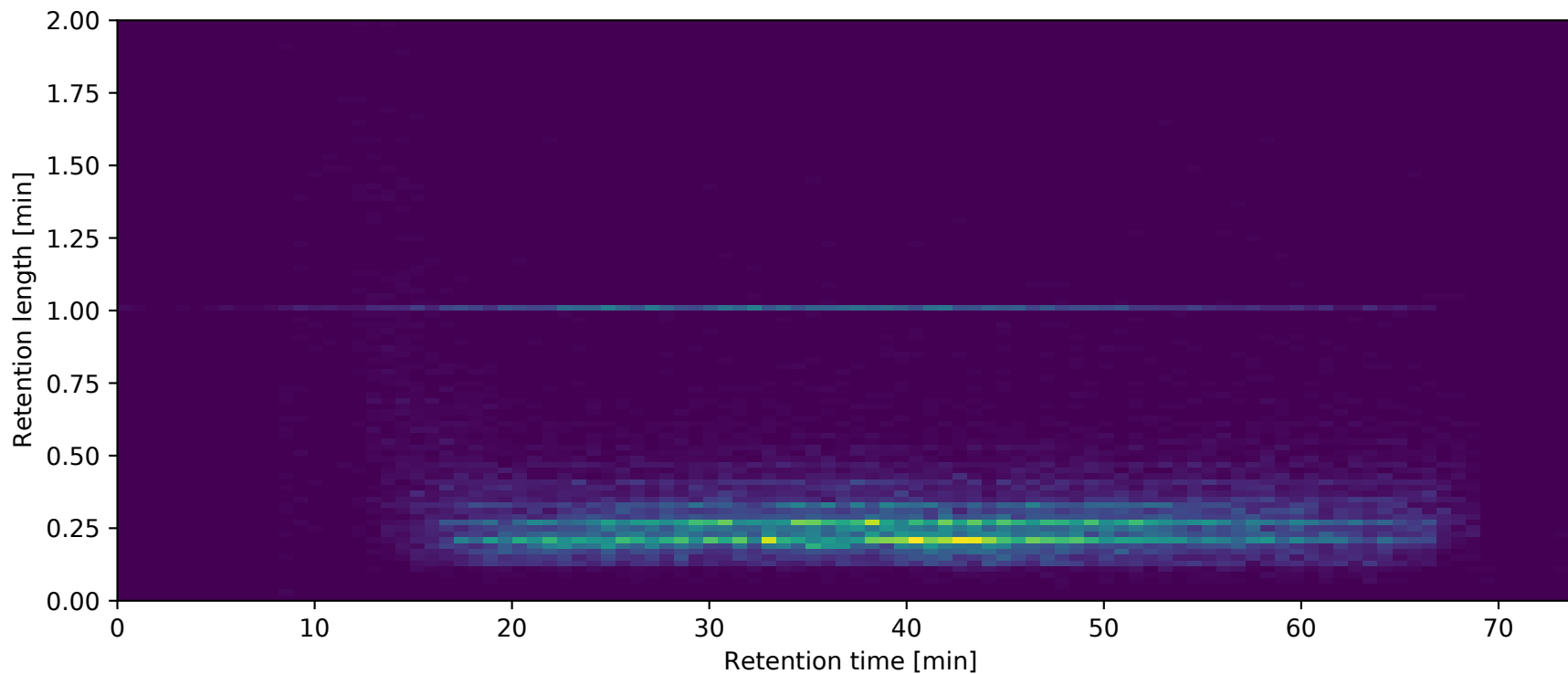
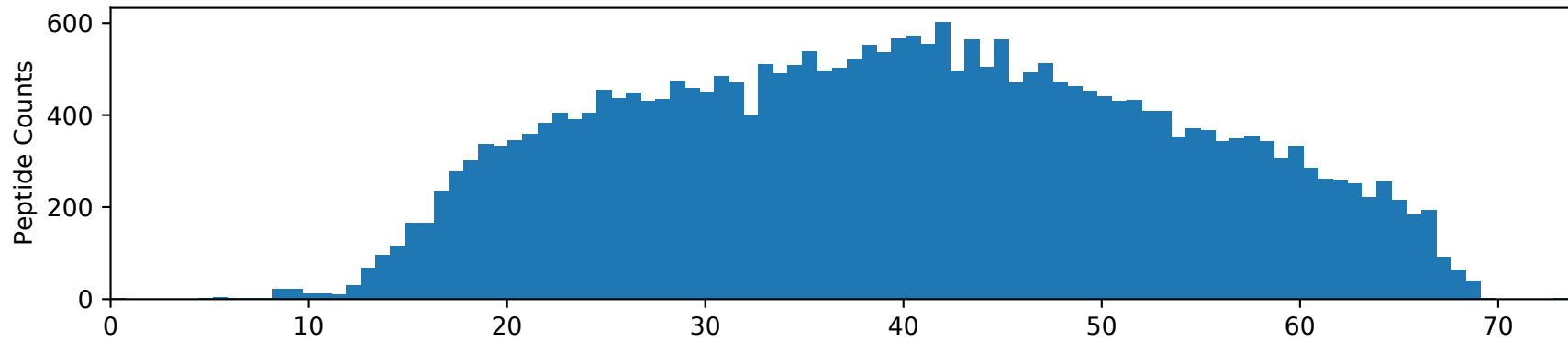
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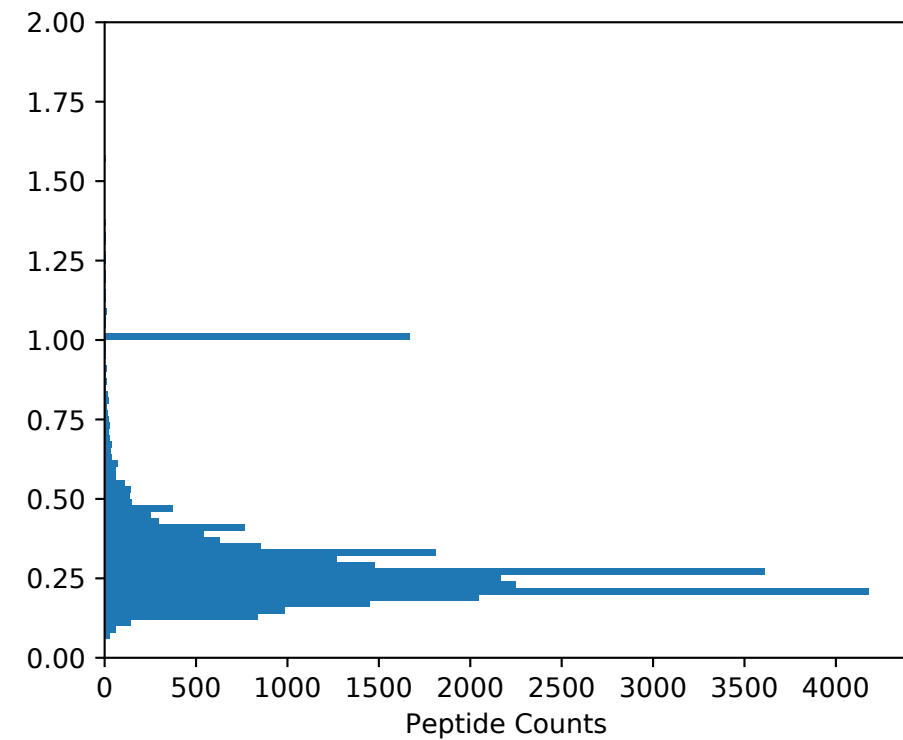
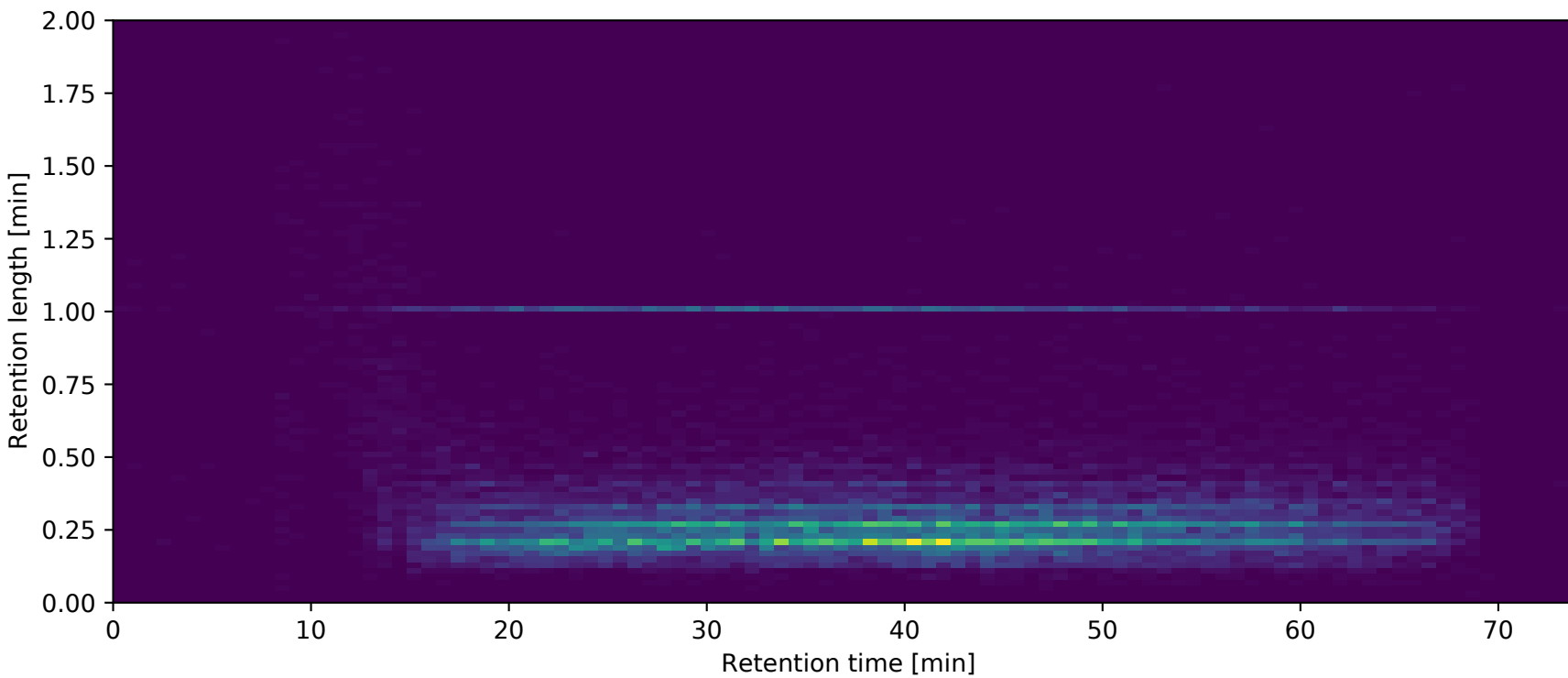
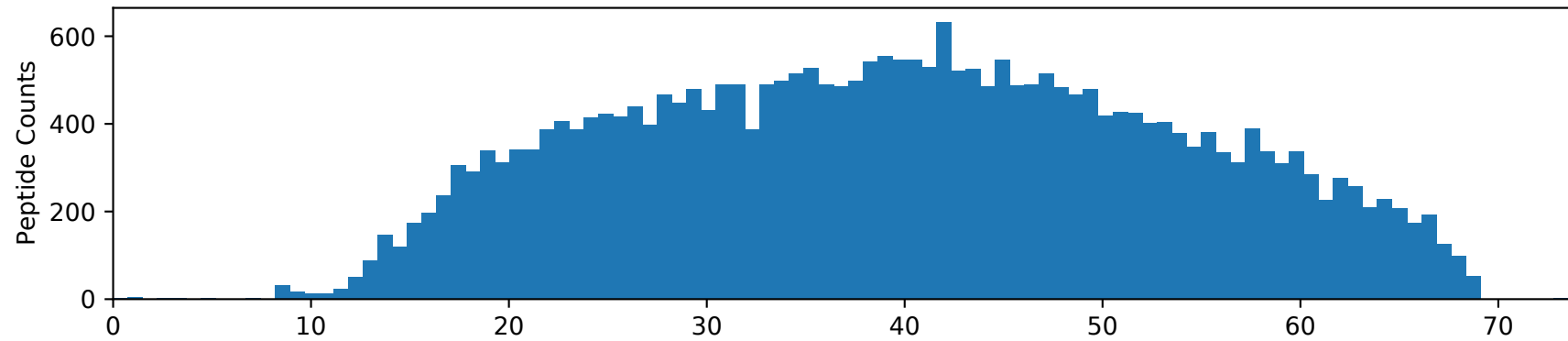
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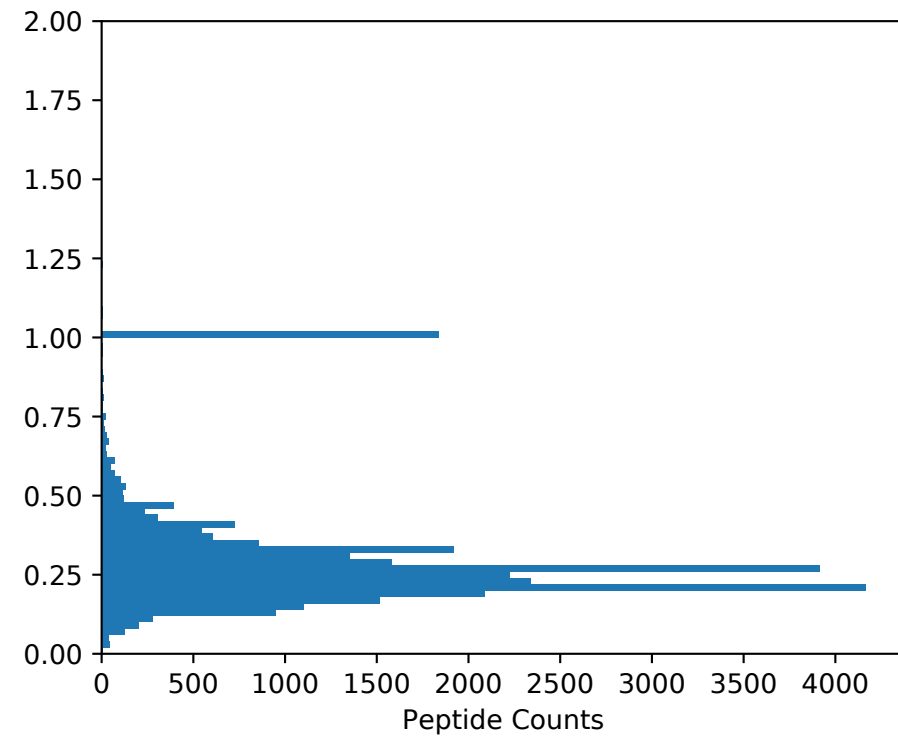
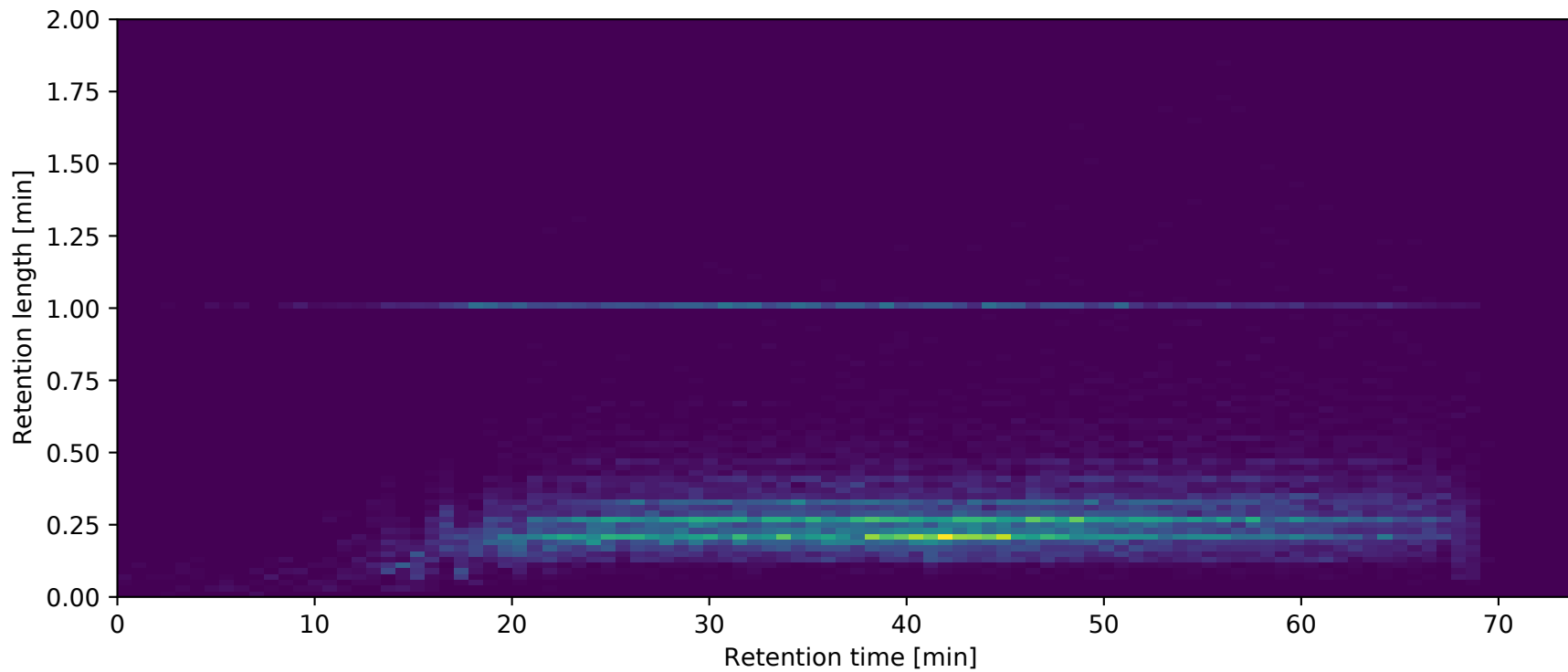
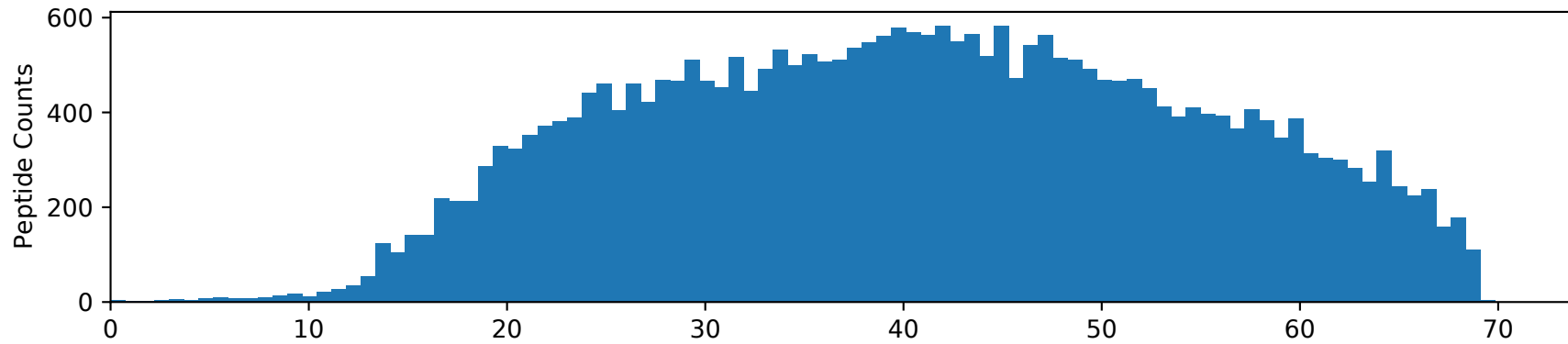
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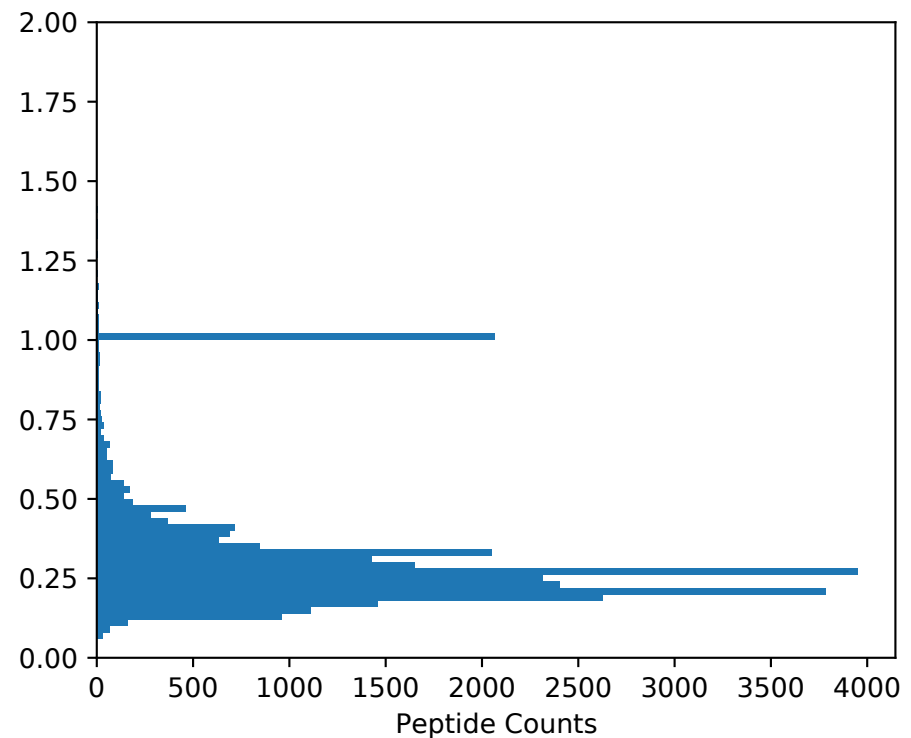
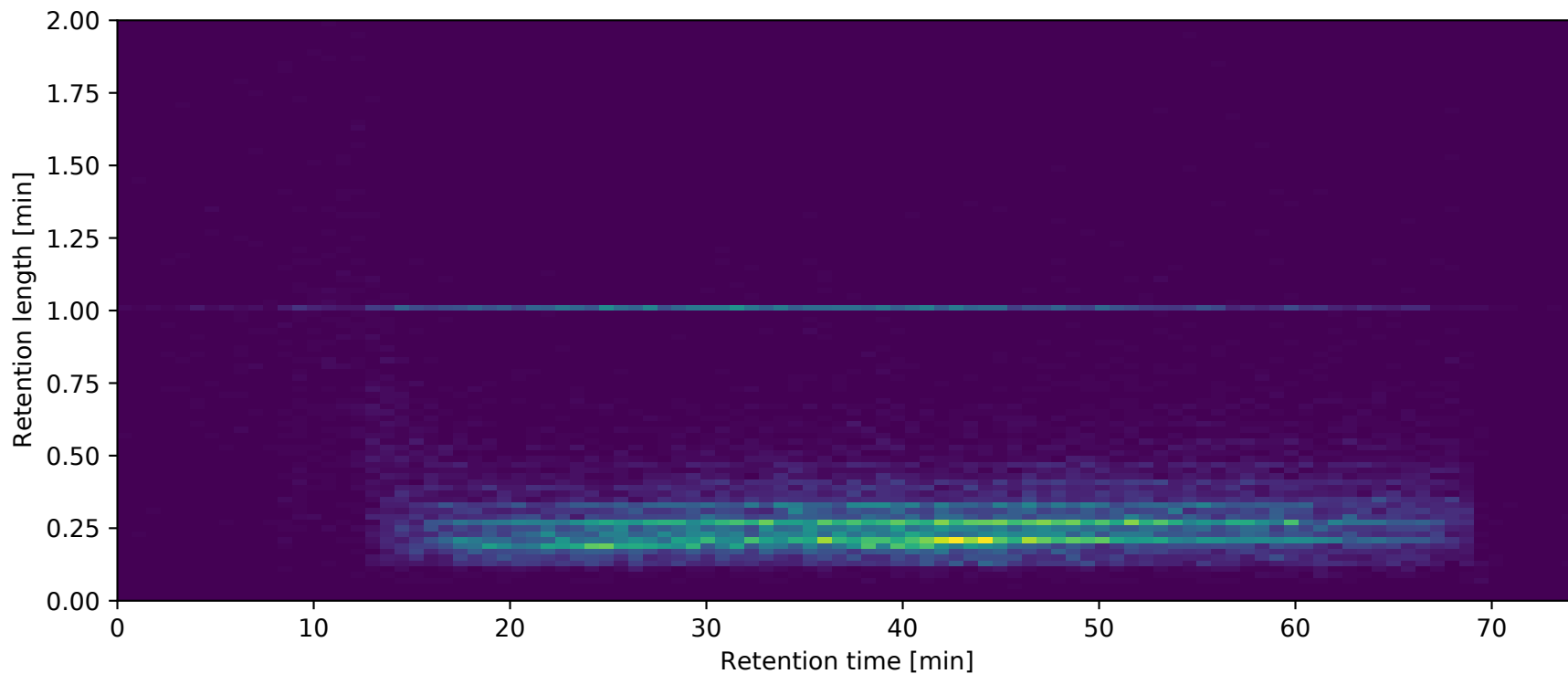
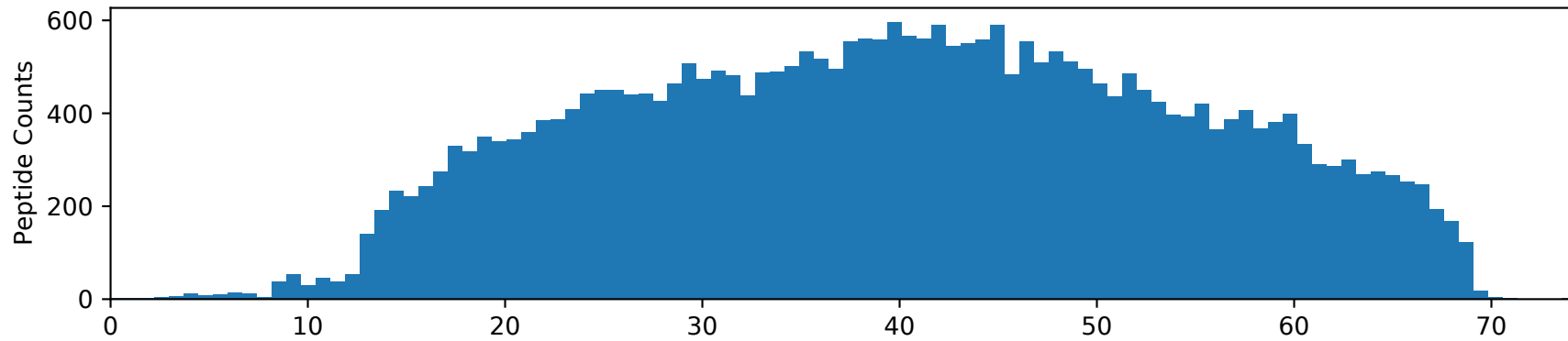
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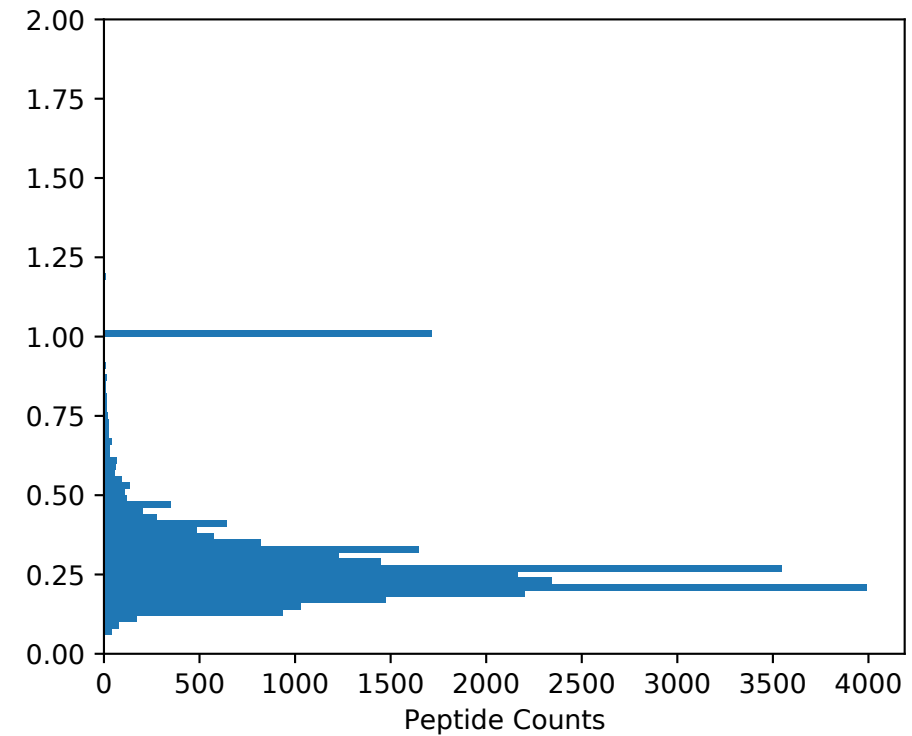
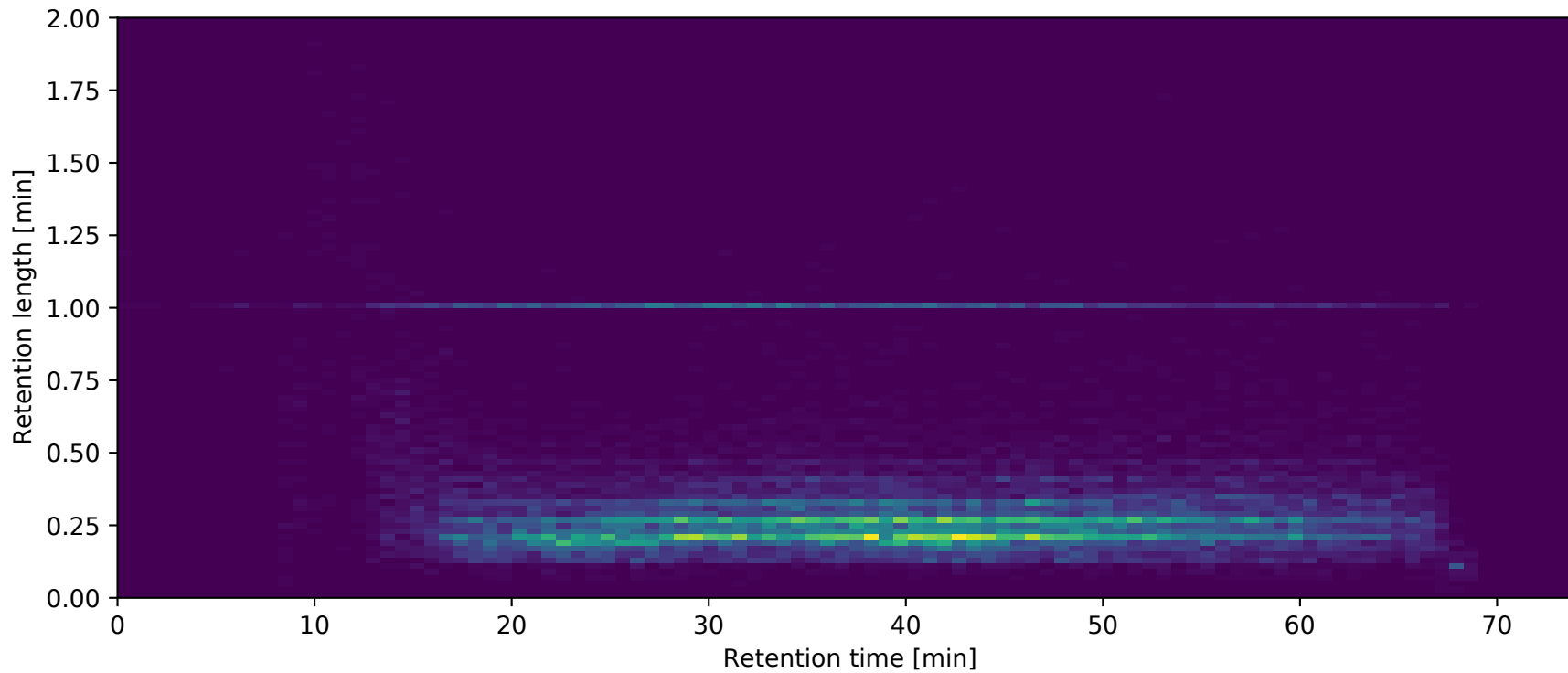
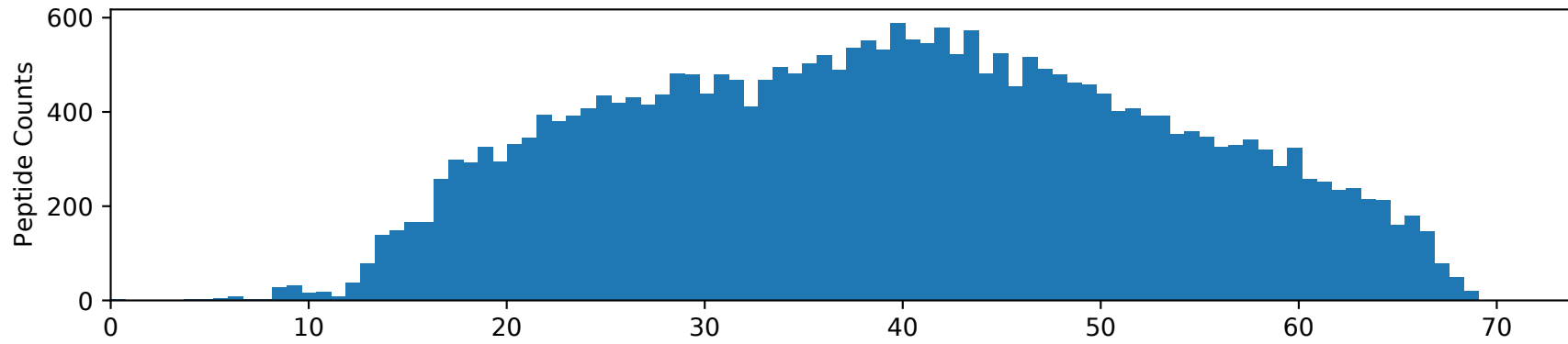
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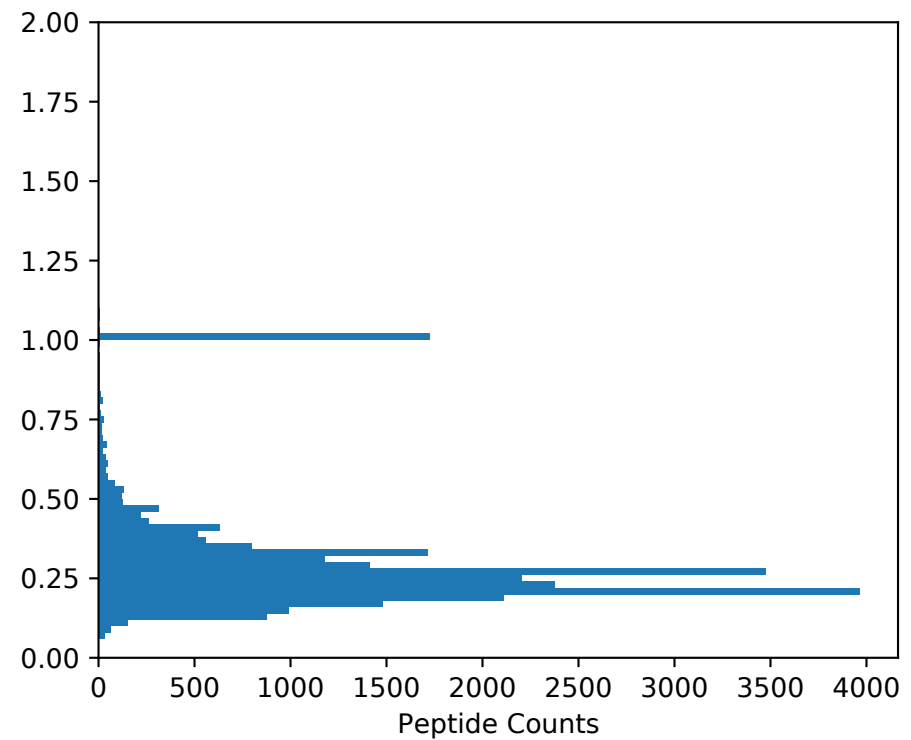
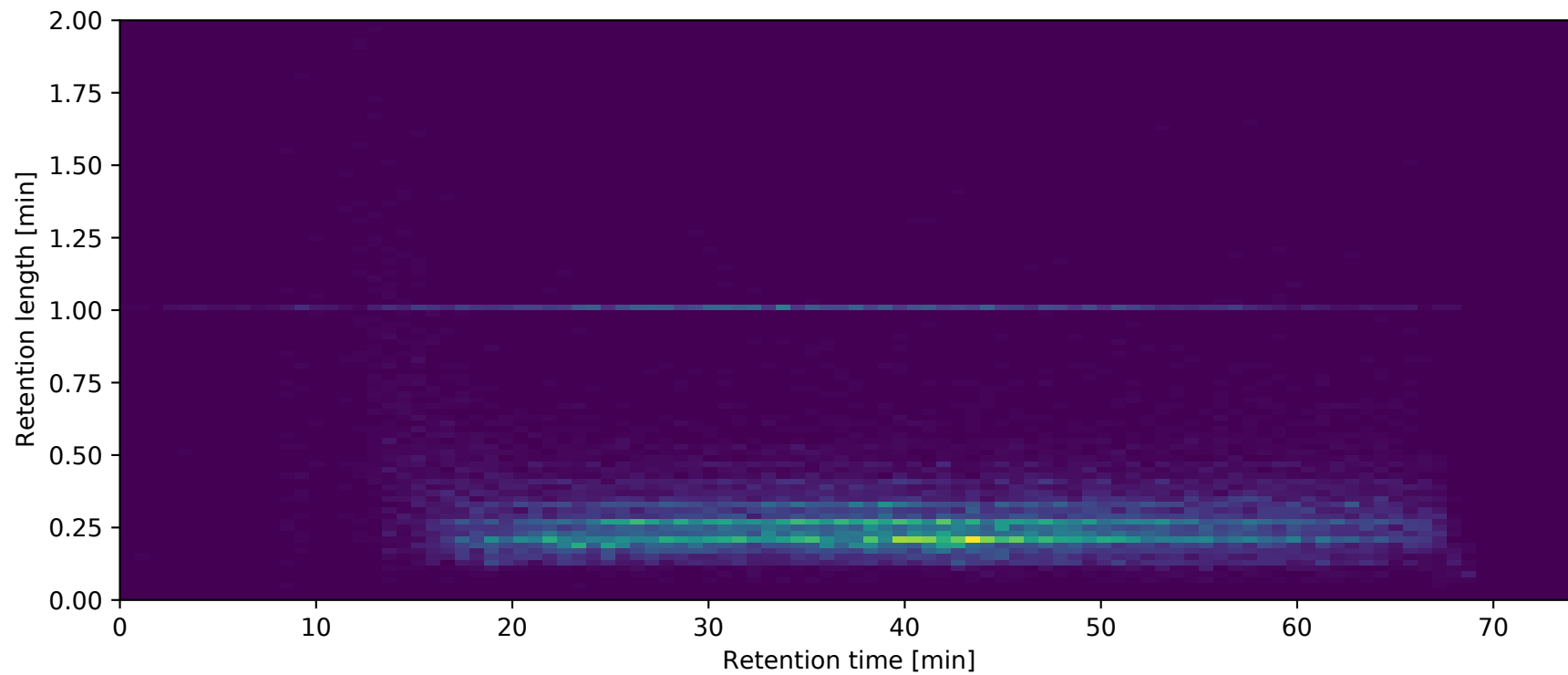
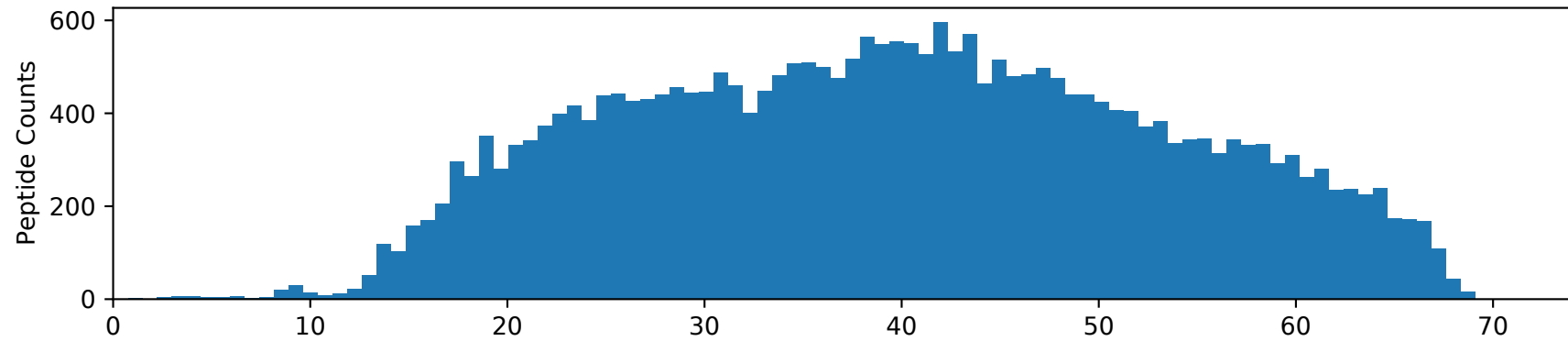
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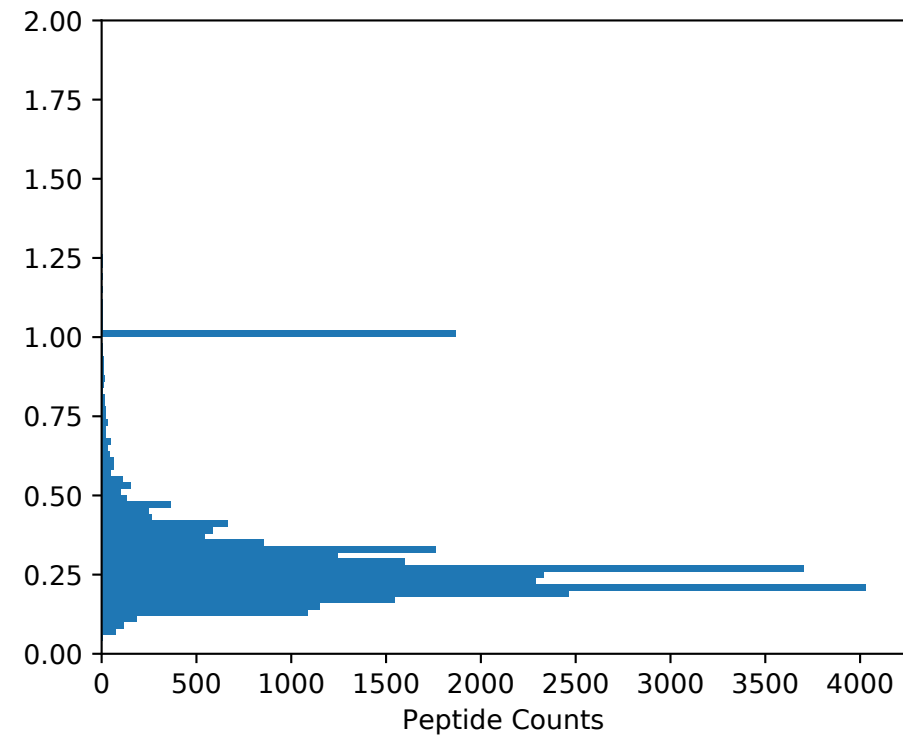
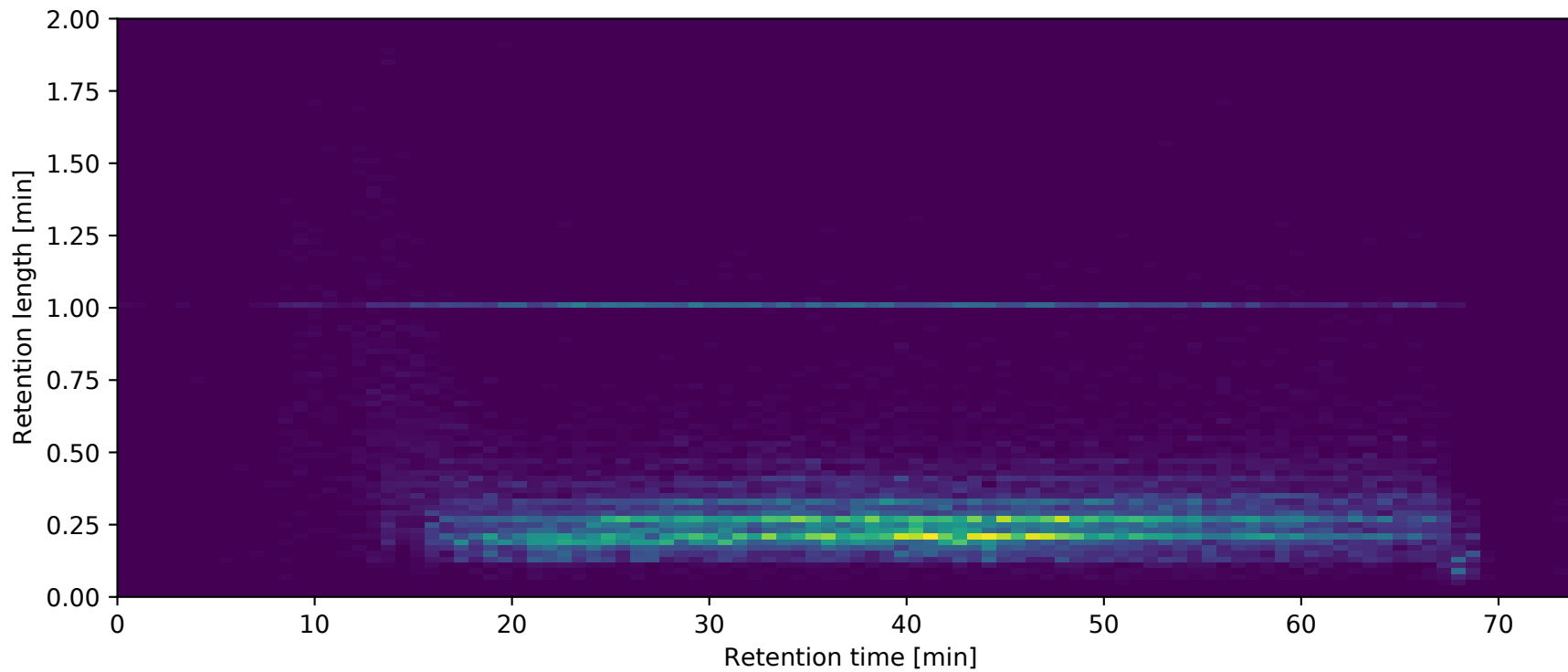
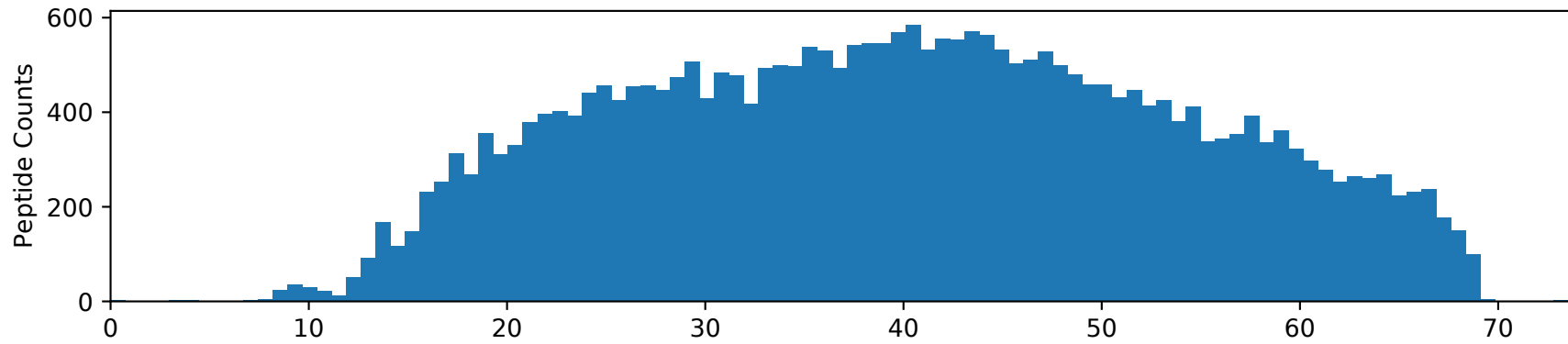
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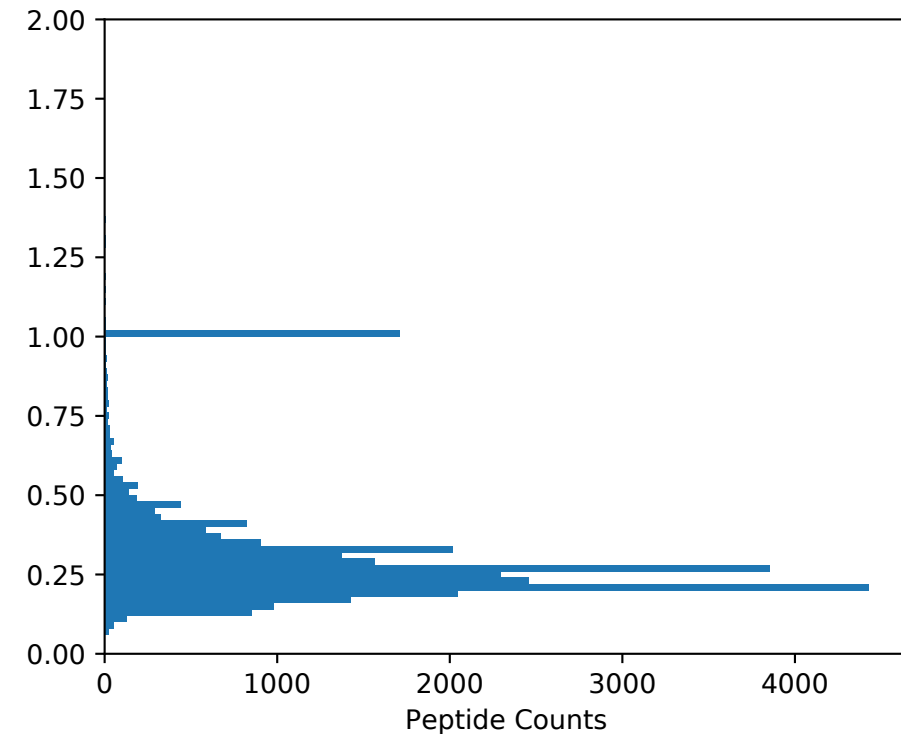
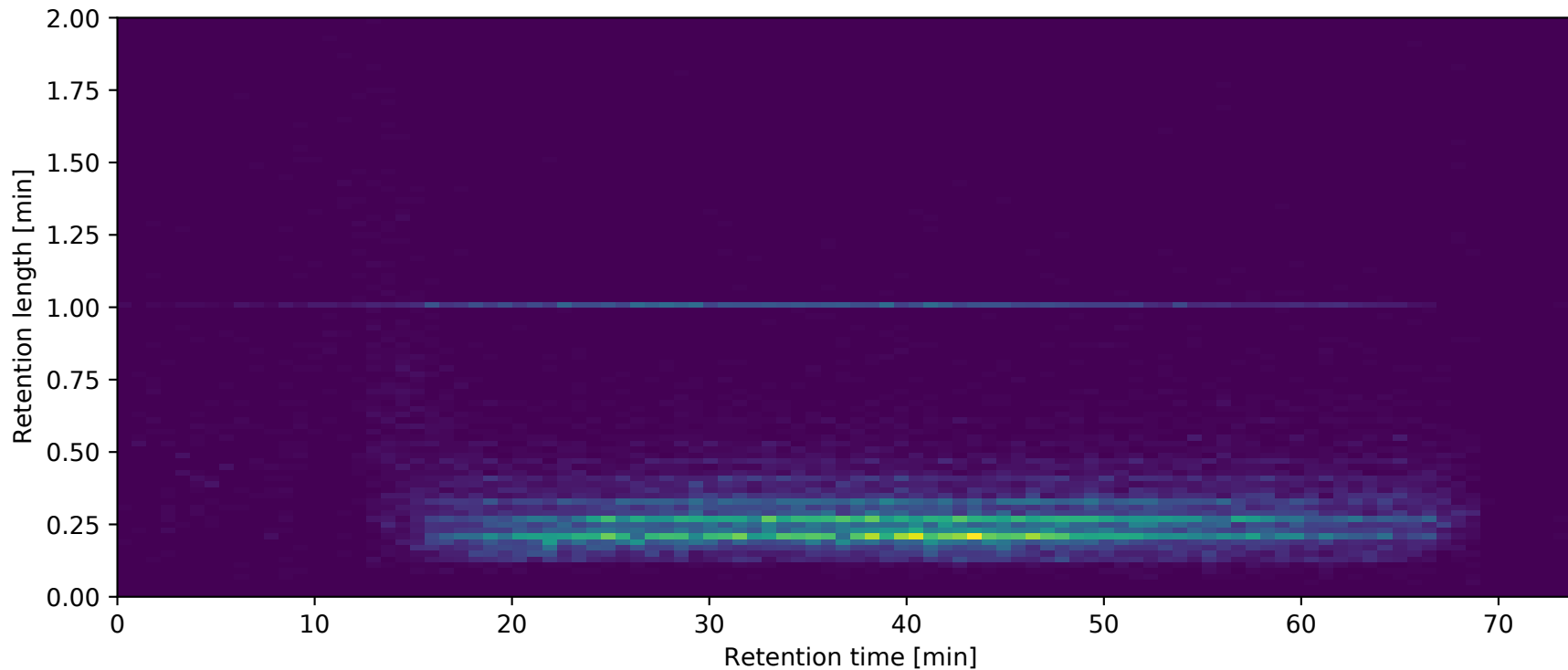
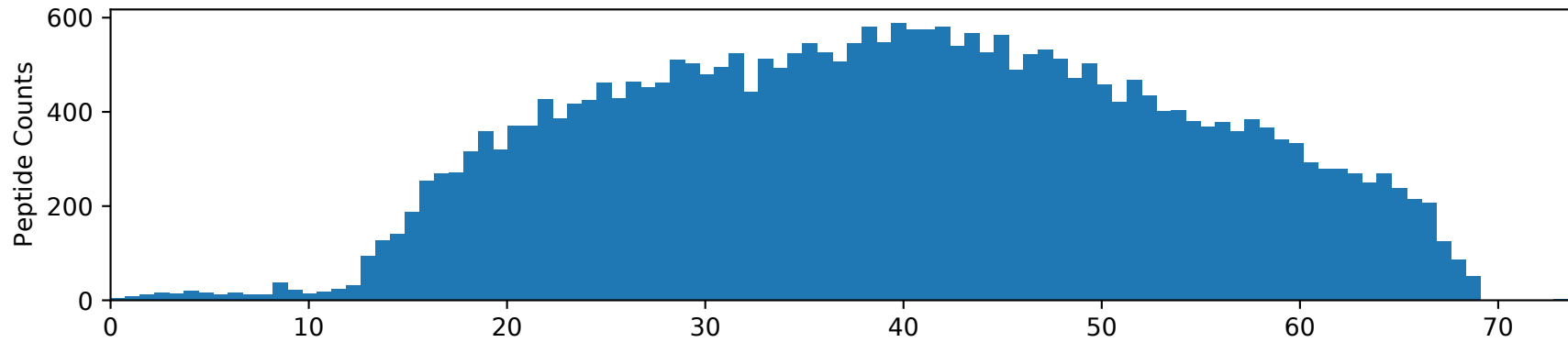
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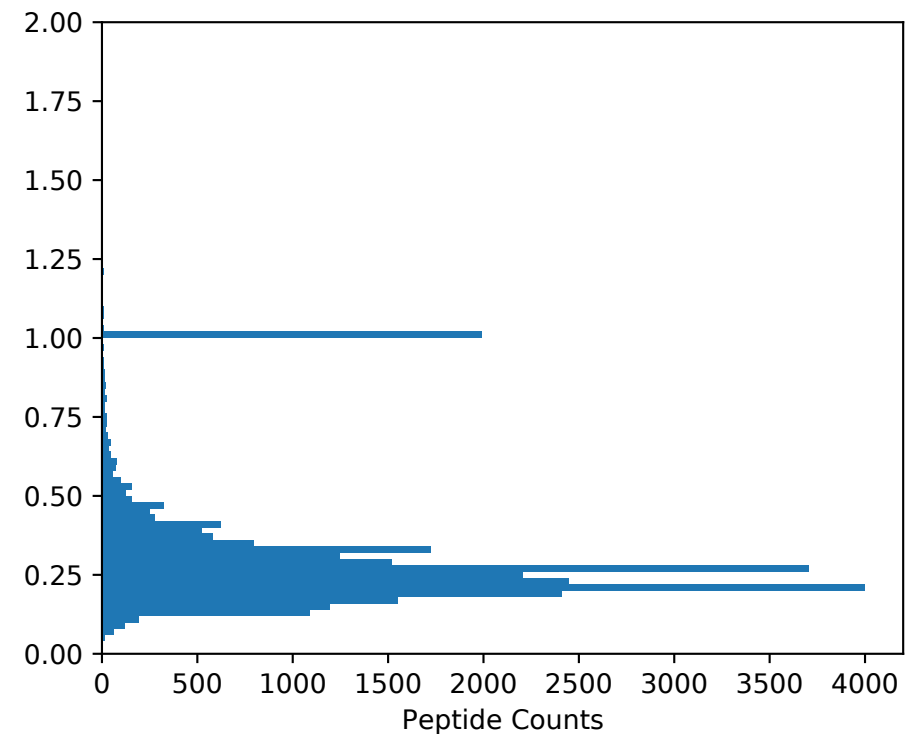
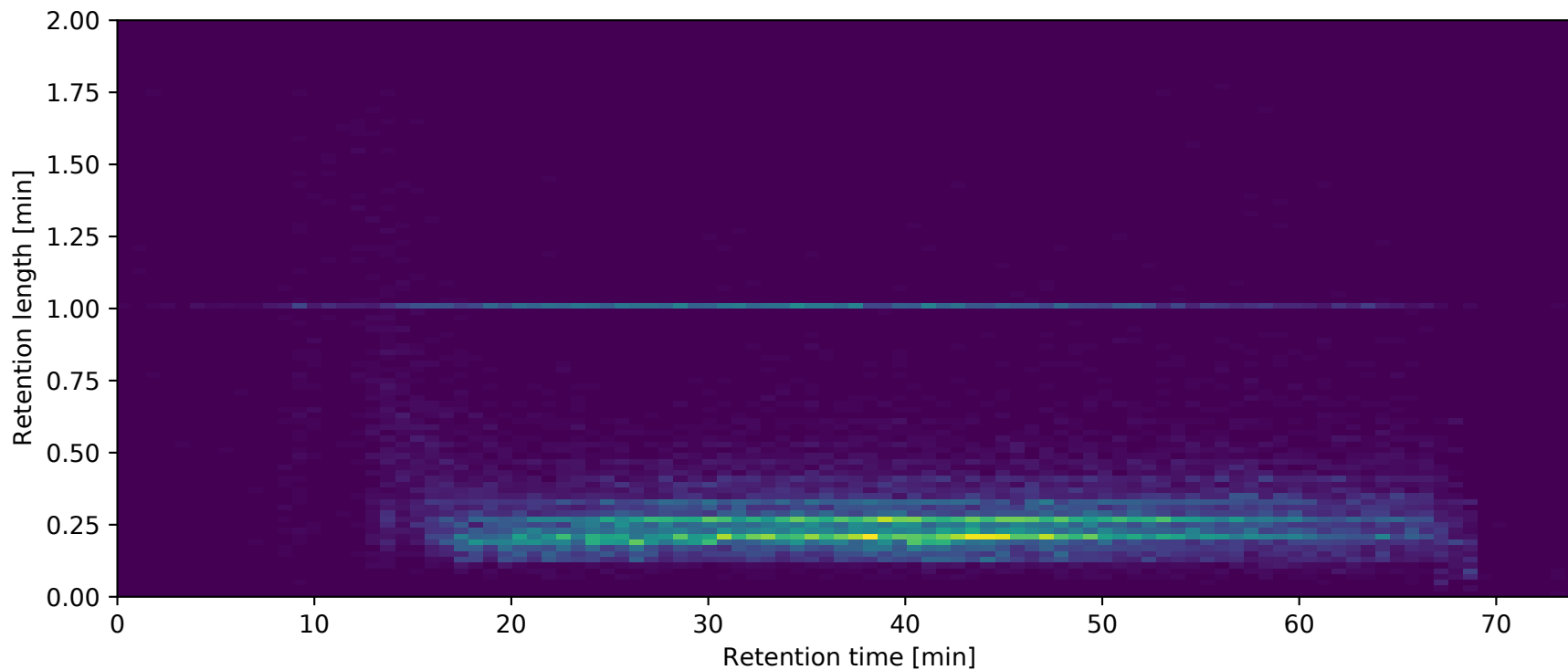
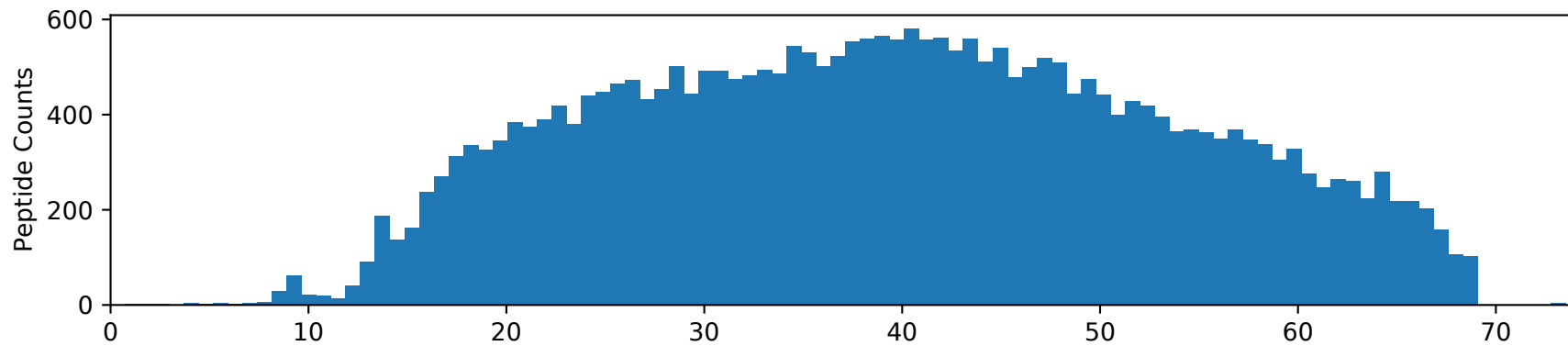
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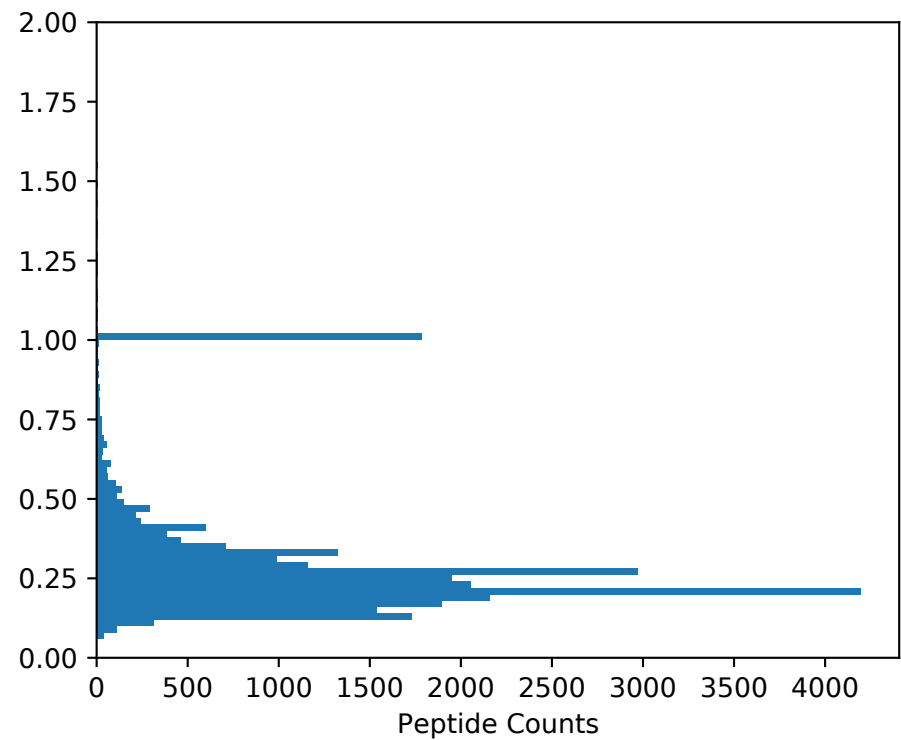
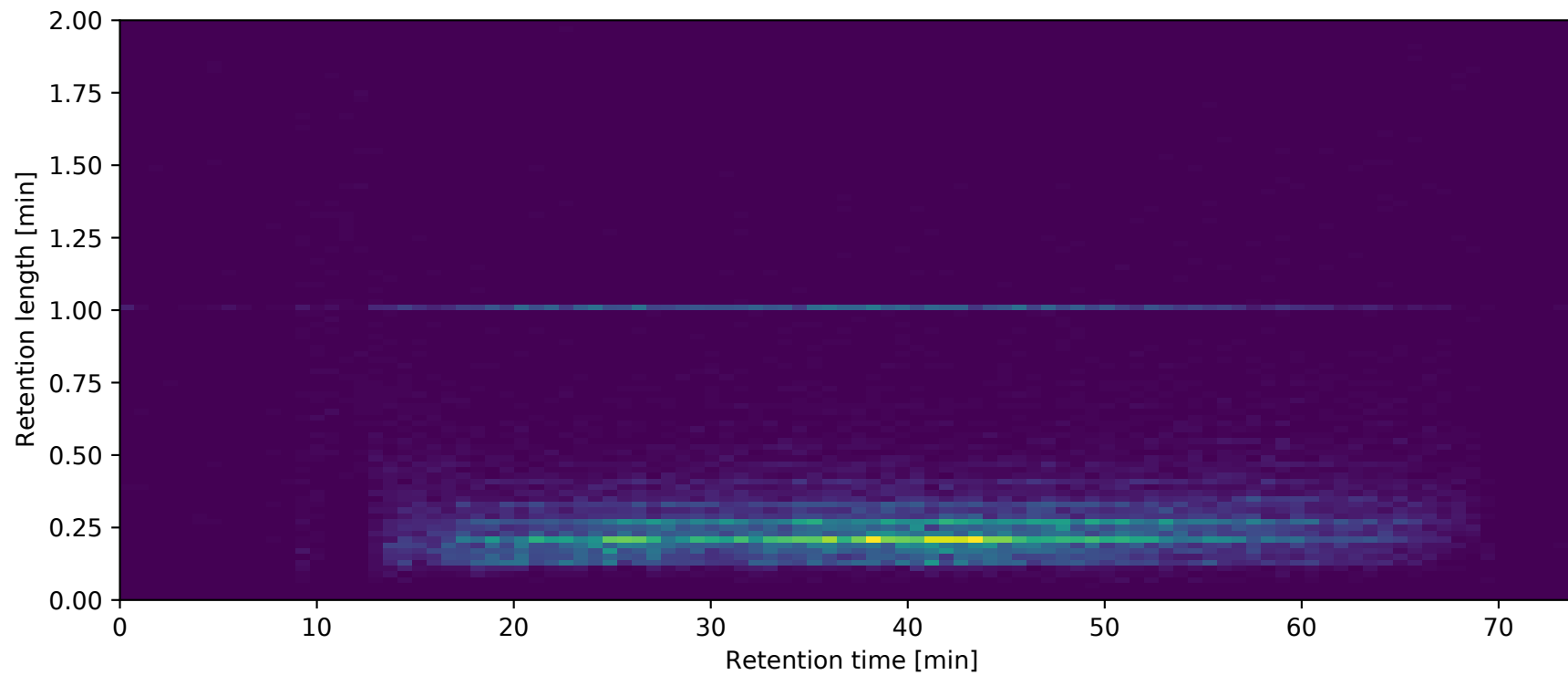
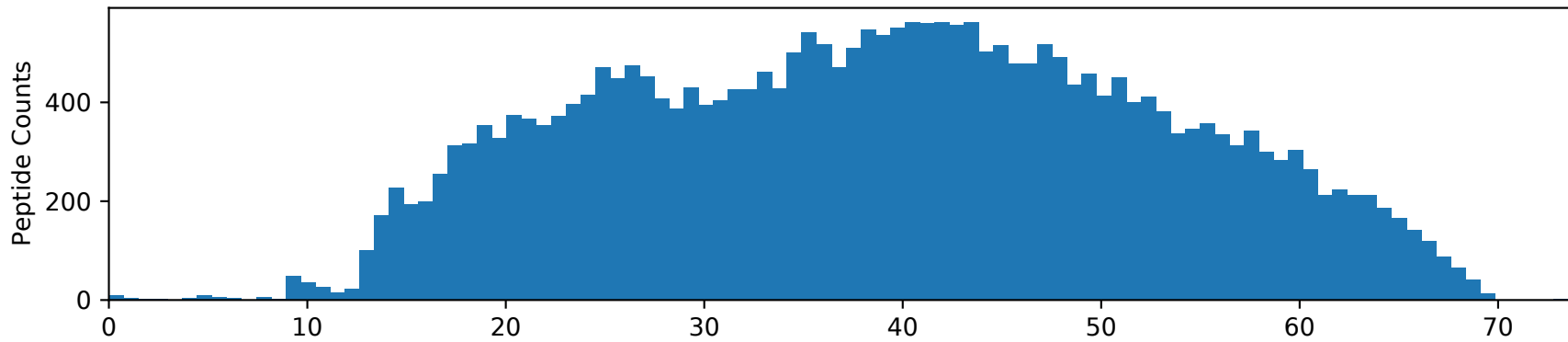
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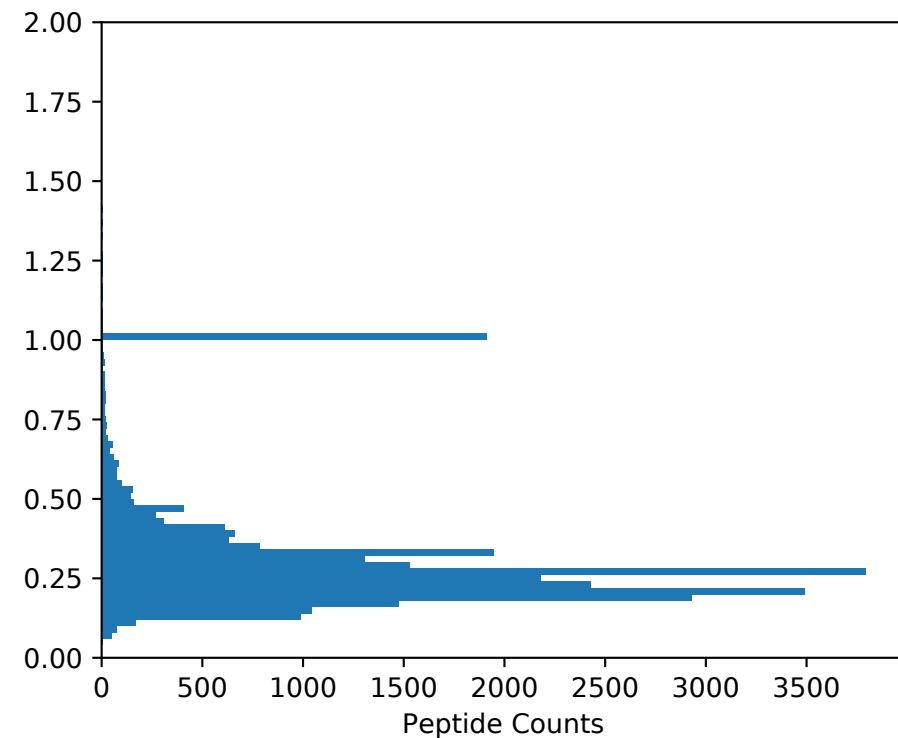
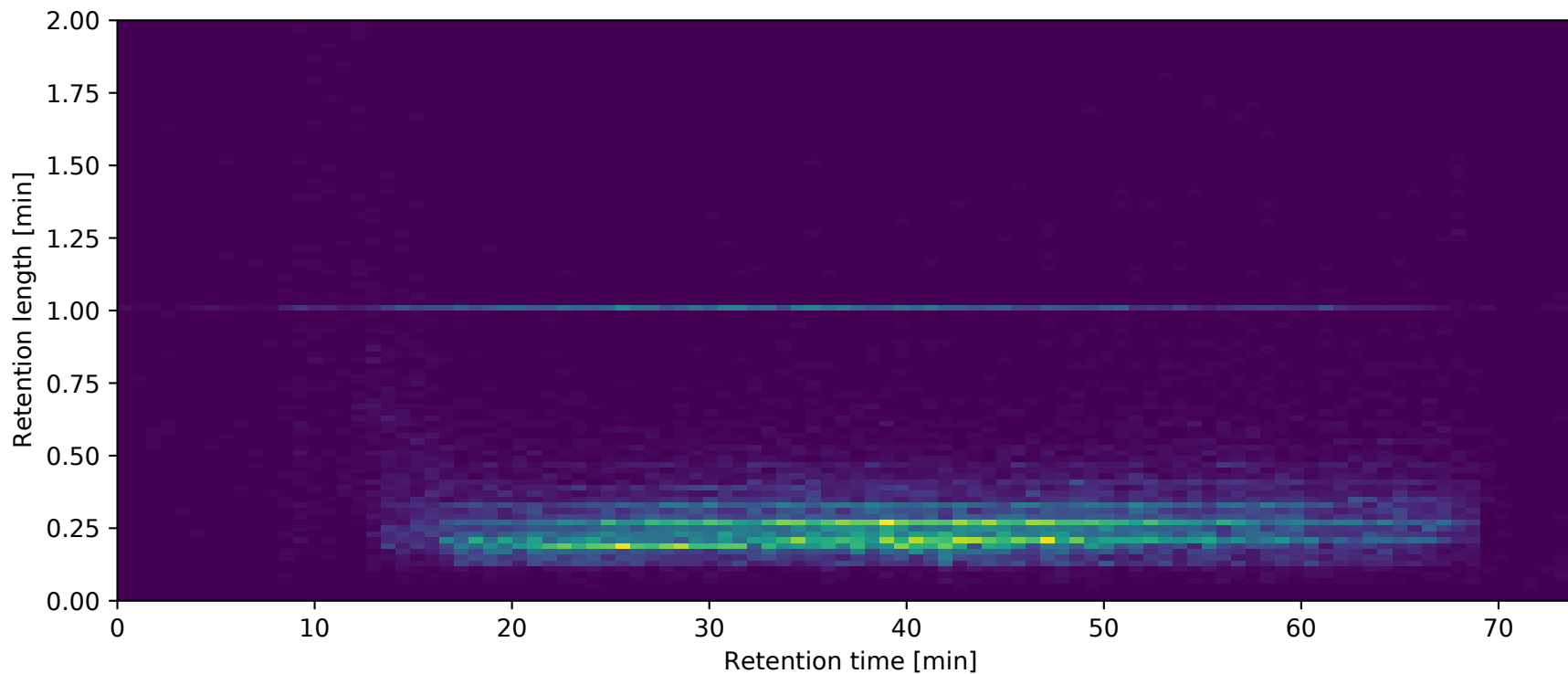
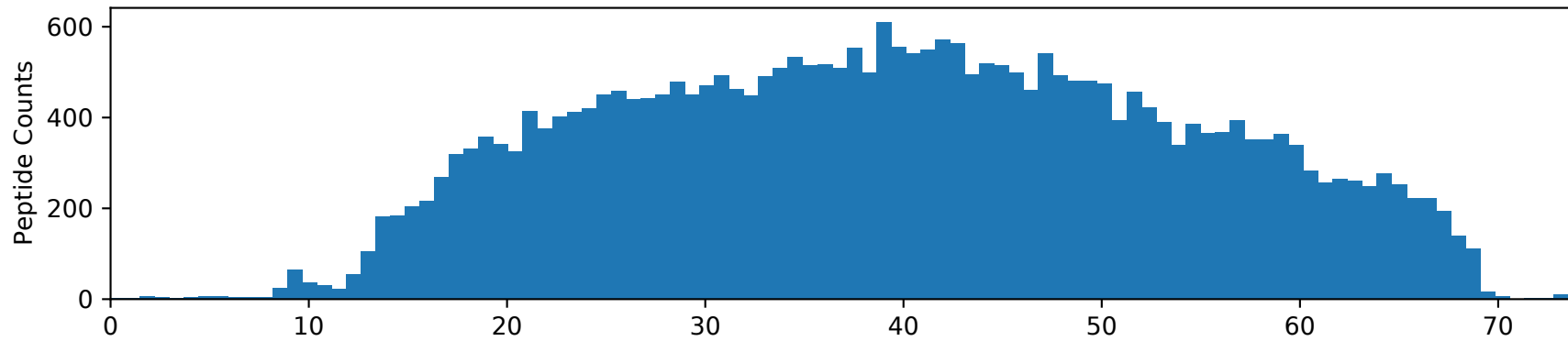
# H838 TGFb Rep1 1



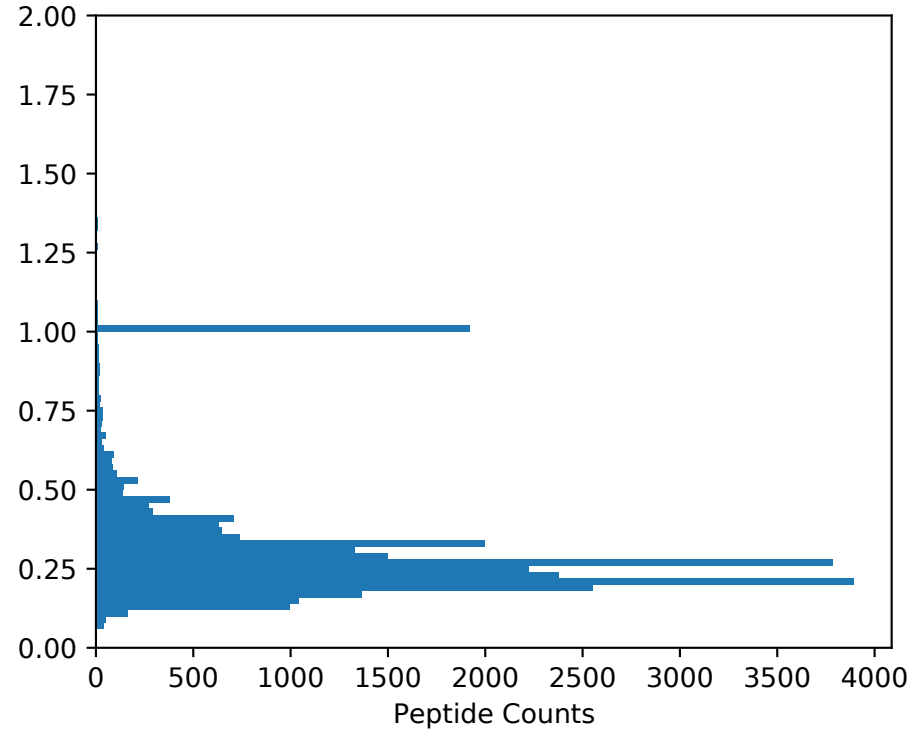
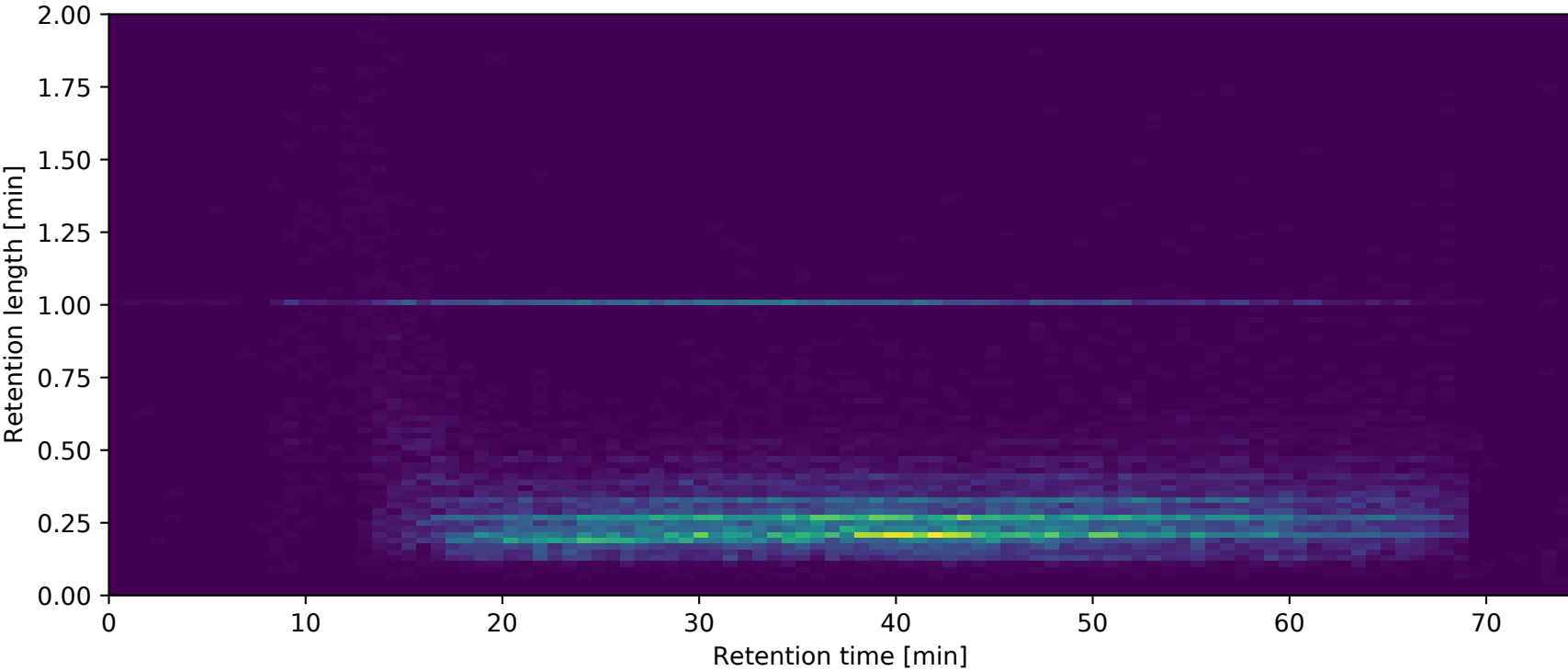
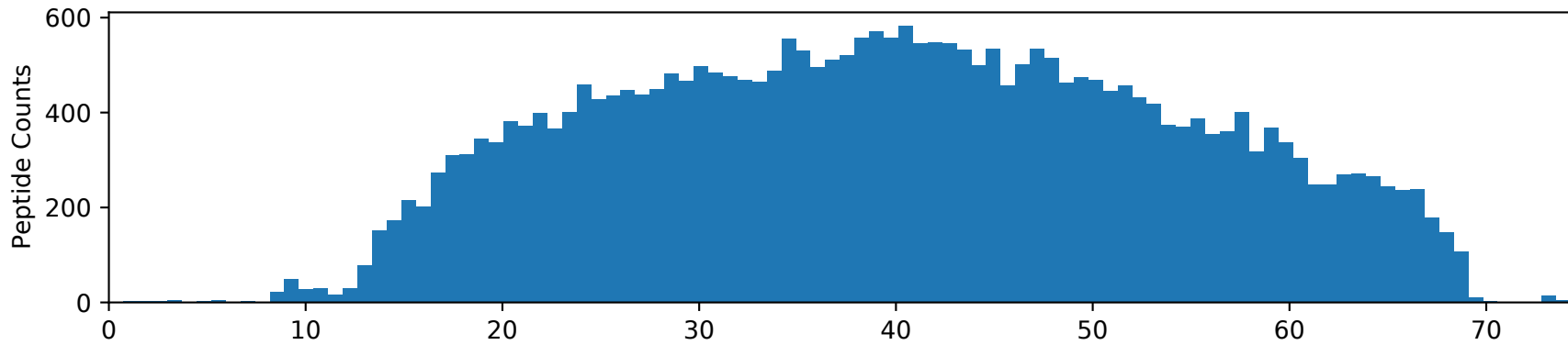
# H838 TGFb Rep1 2



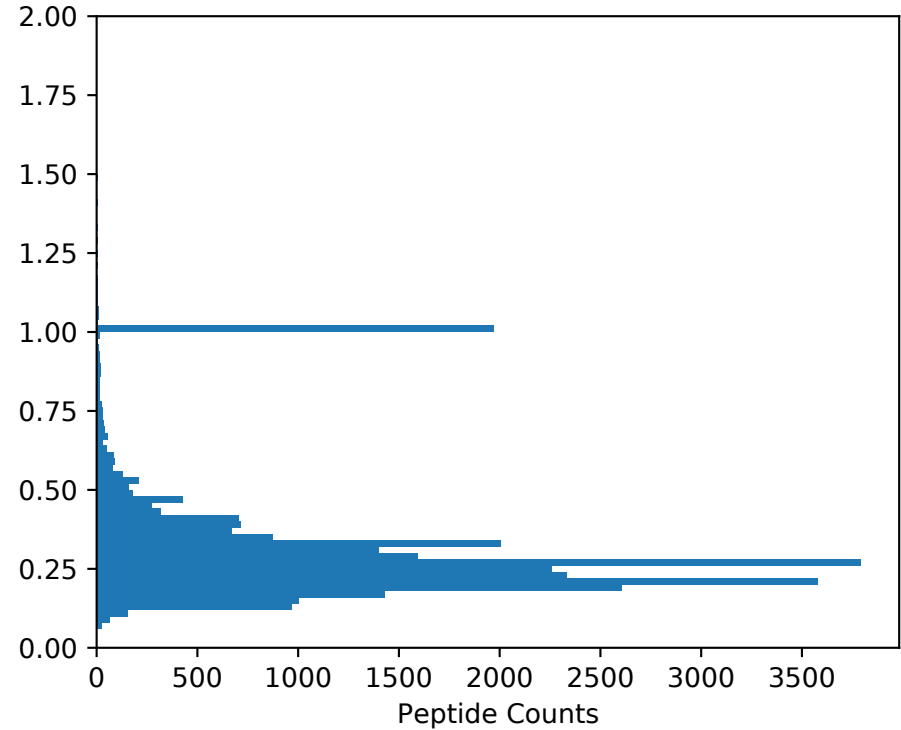
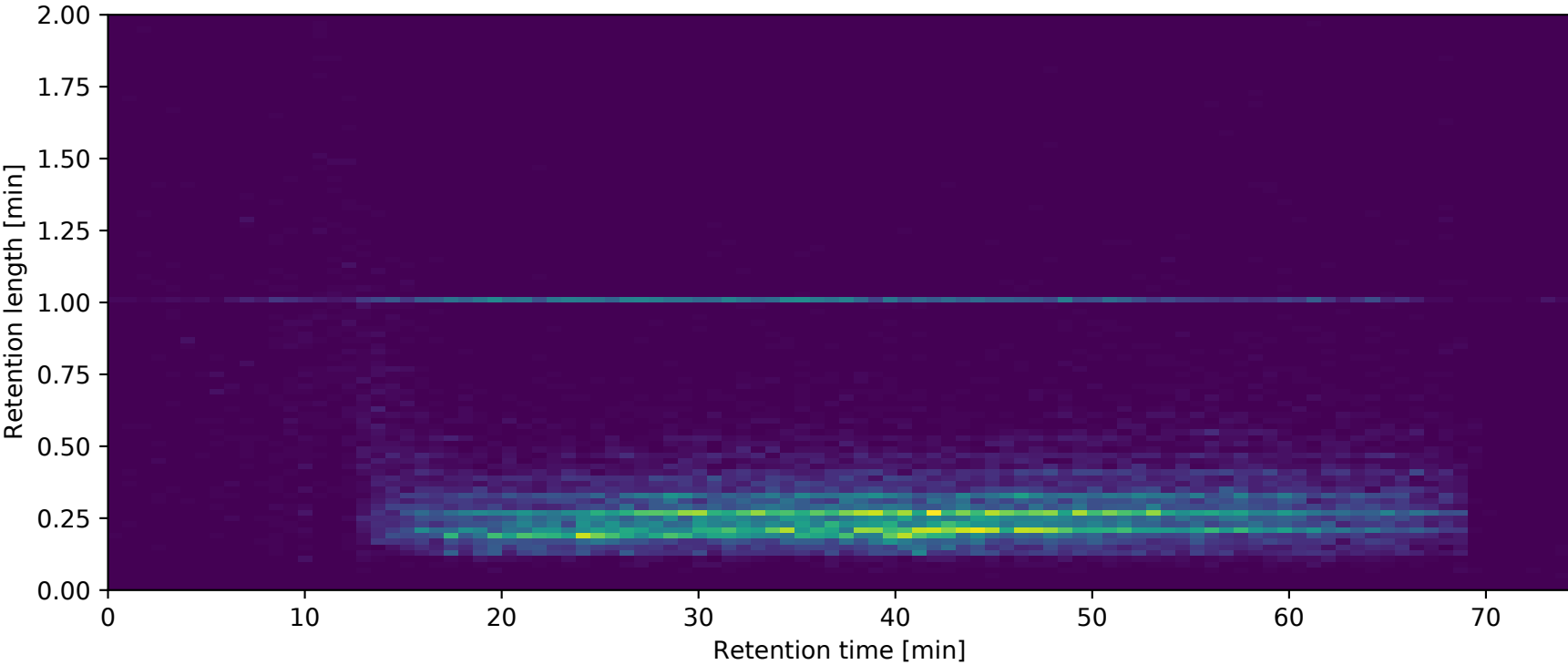
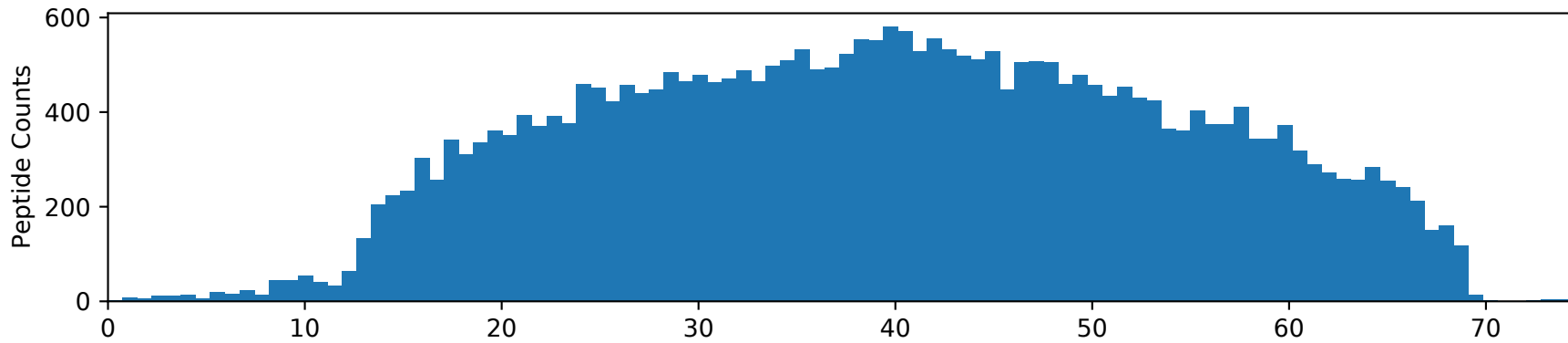
# H838 TGFb Rep2 1



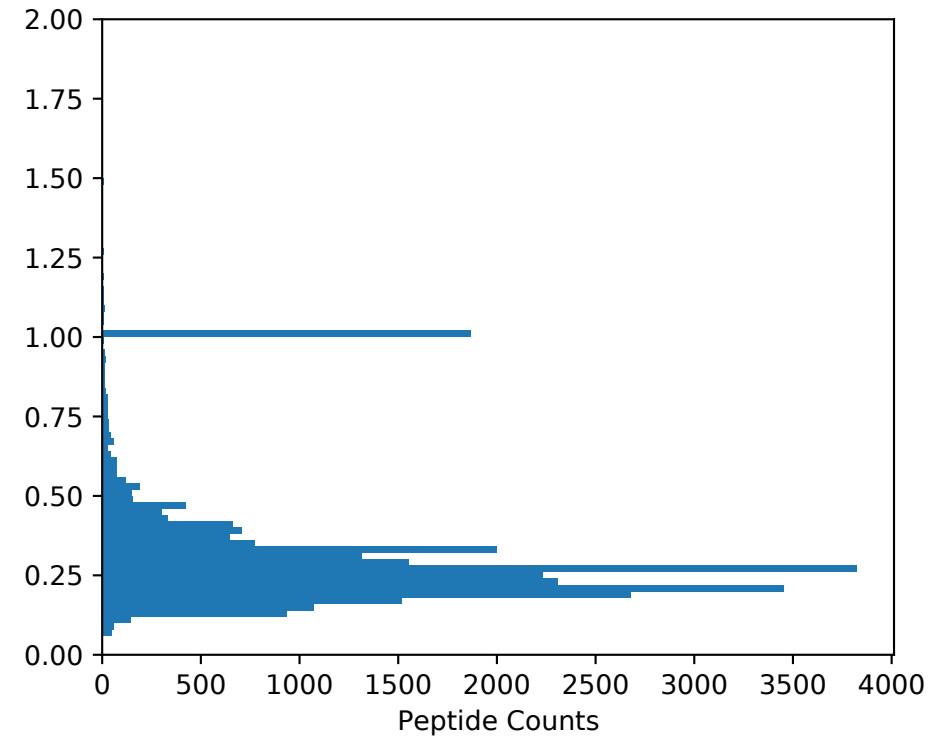
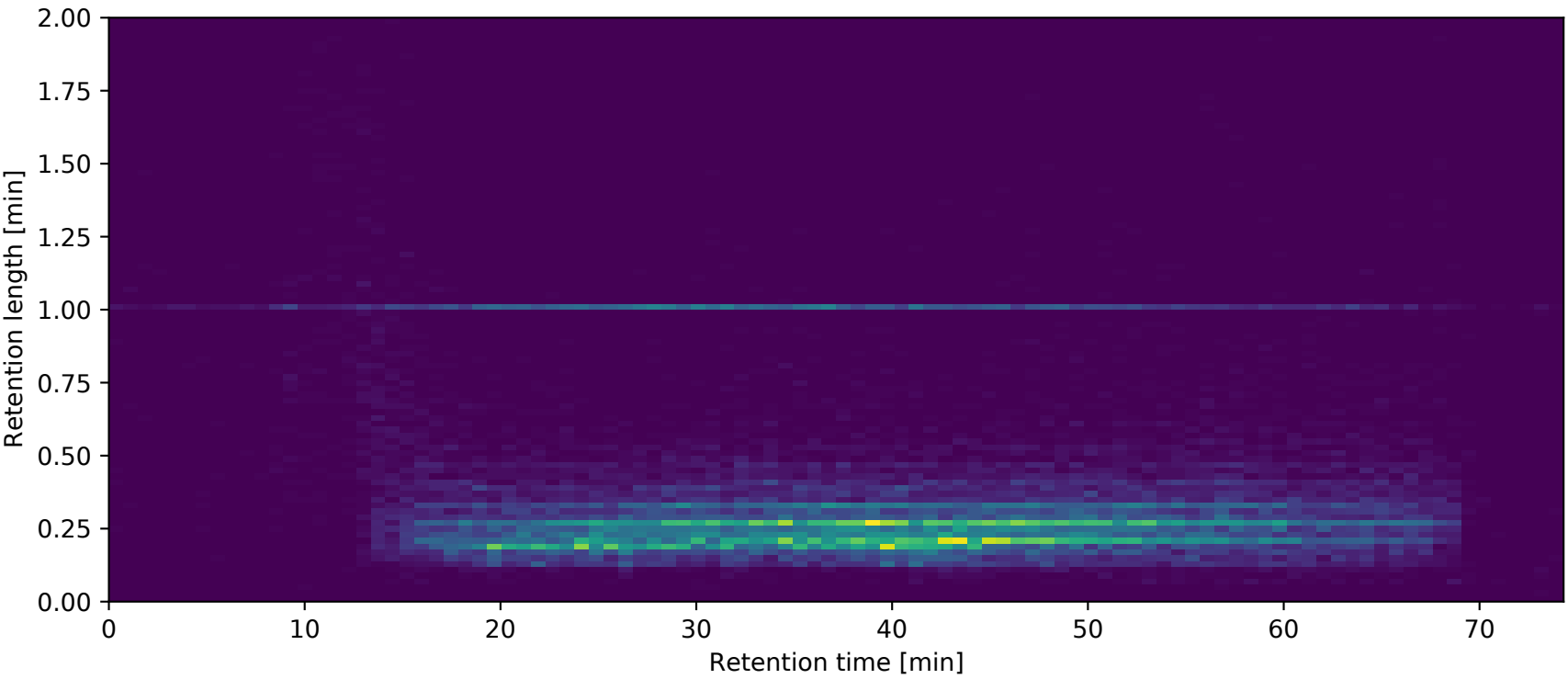
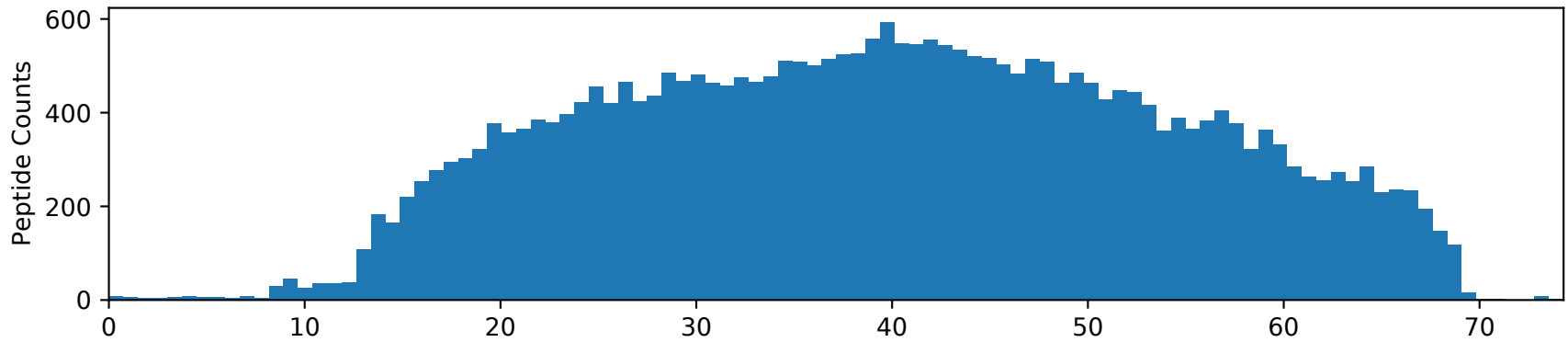
# H838 TGFb Rep2 2



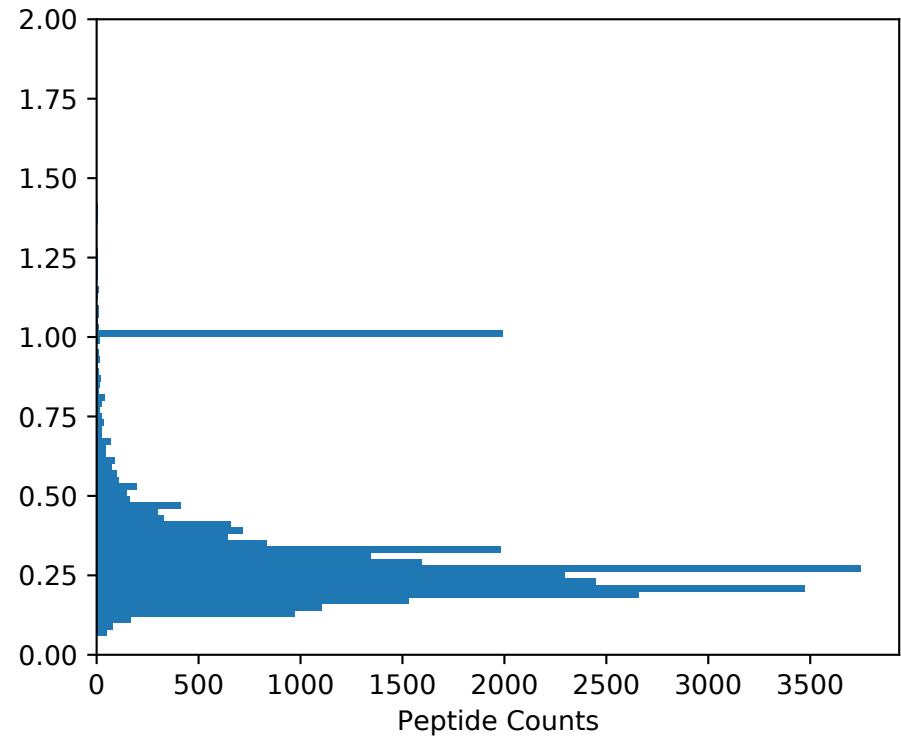
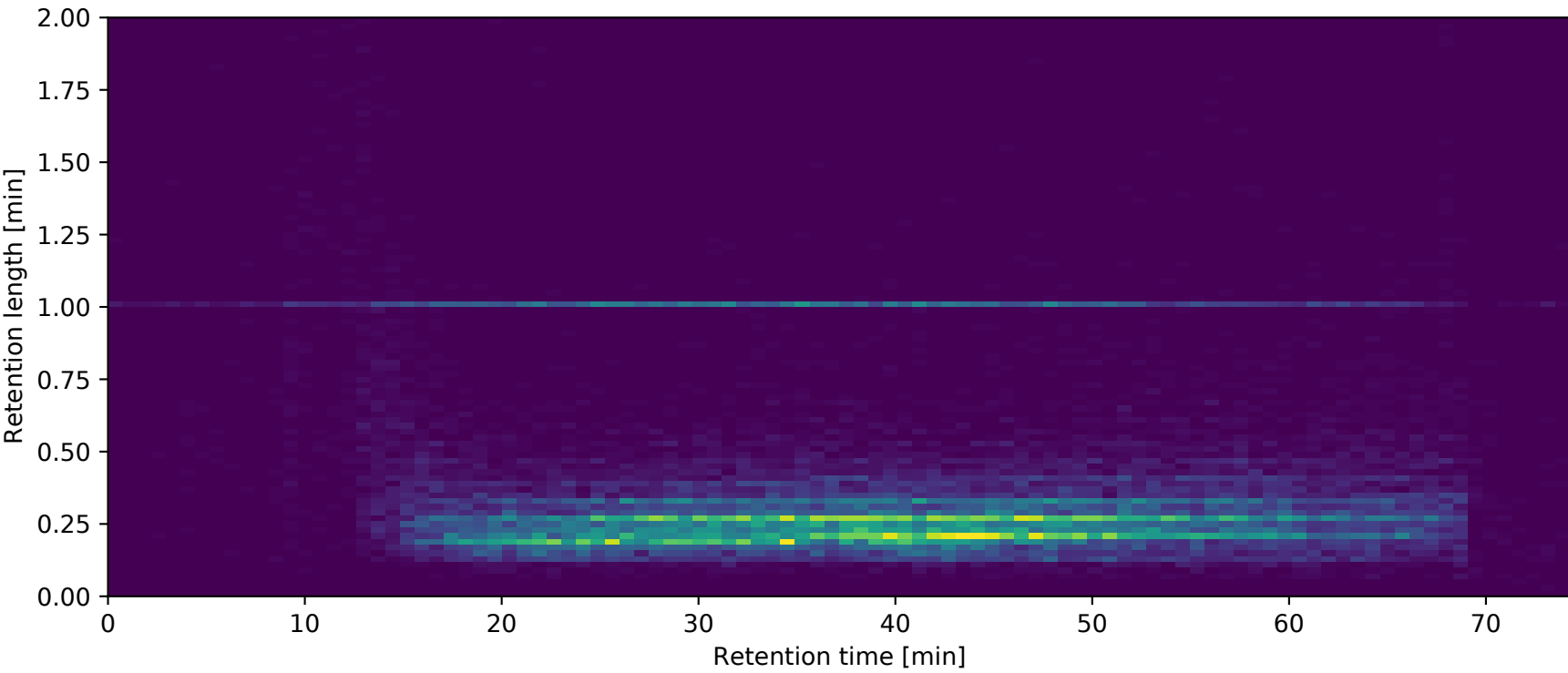
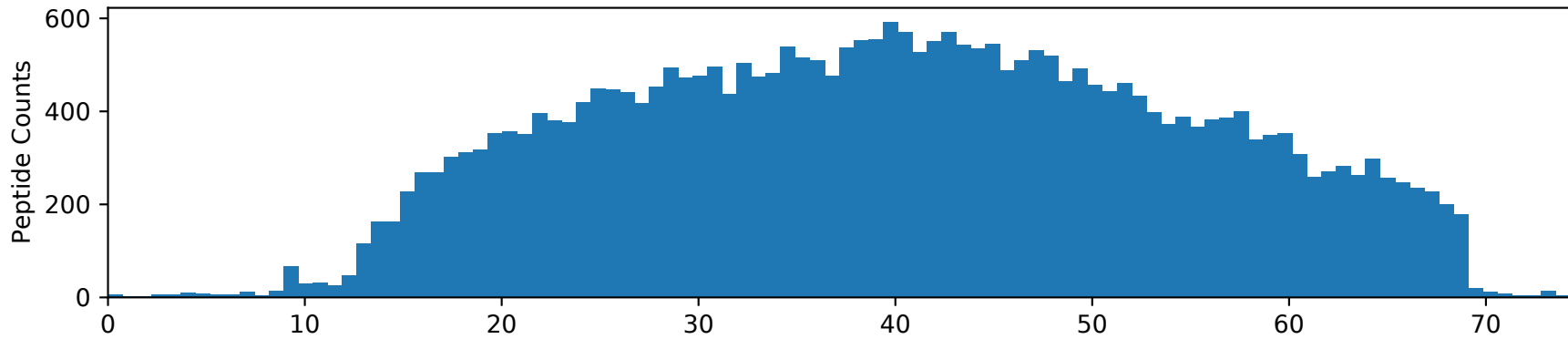
H838 TGFb Rep3 1



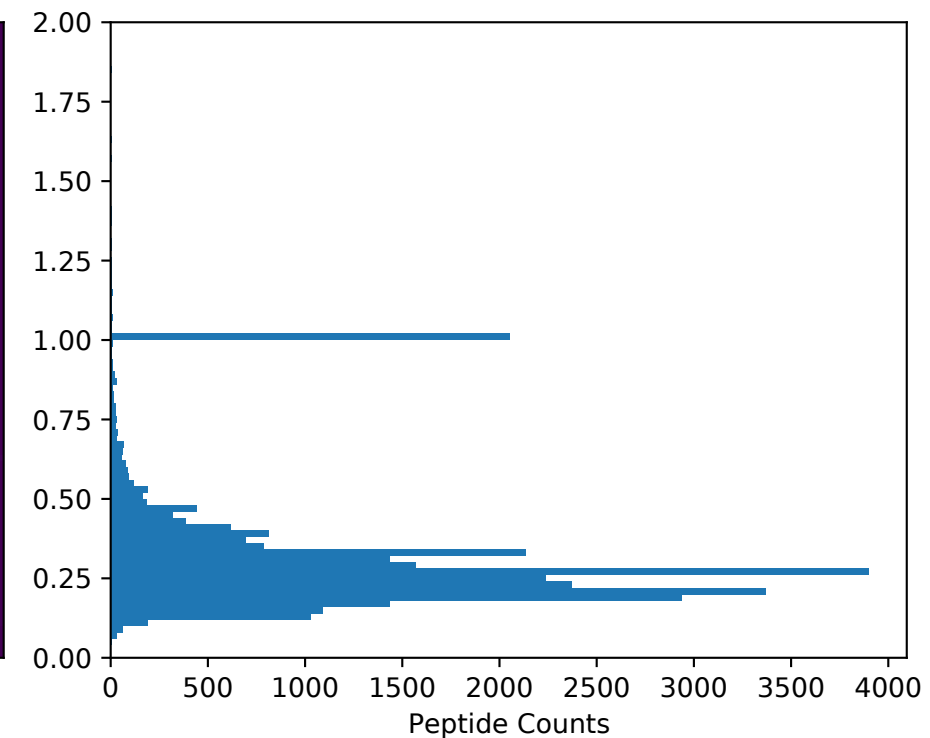
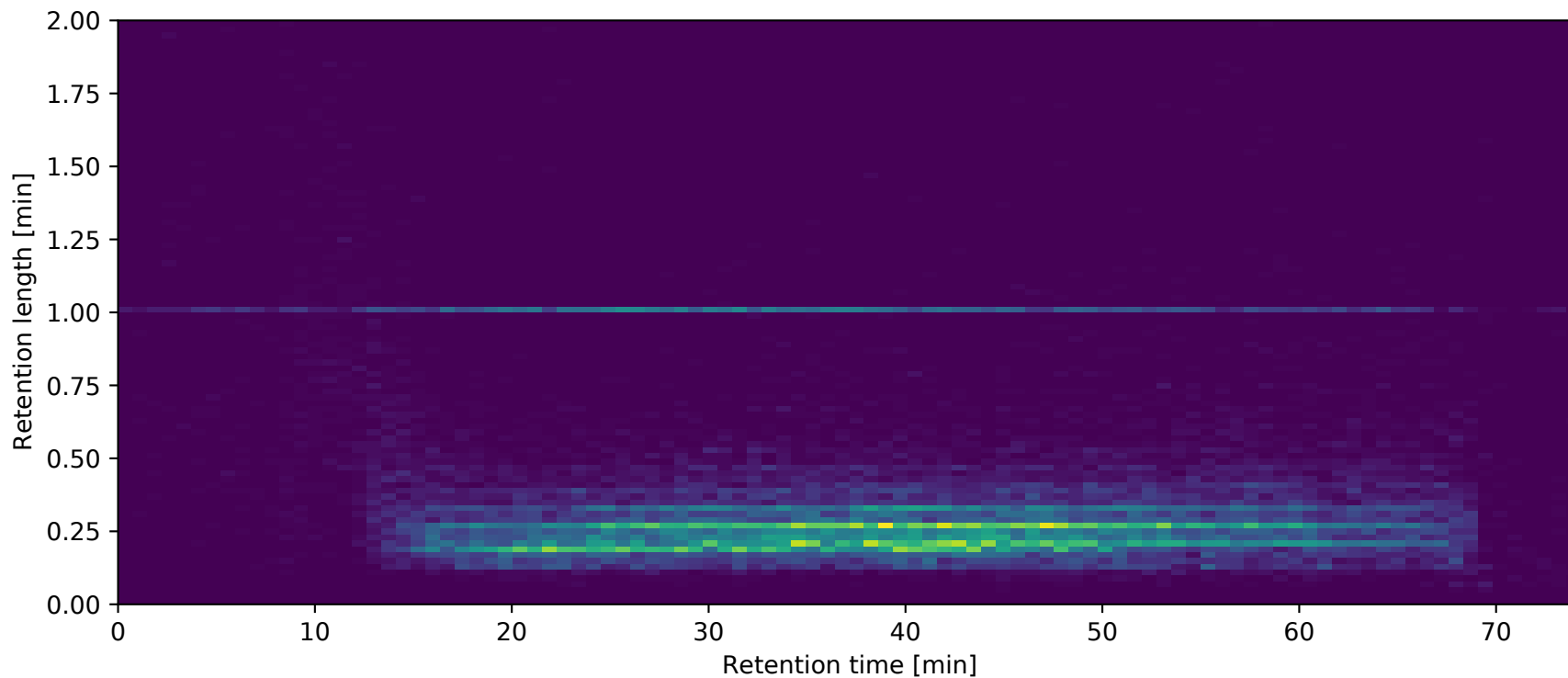
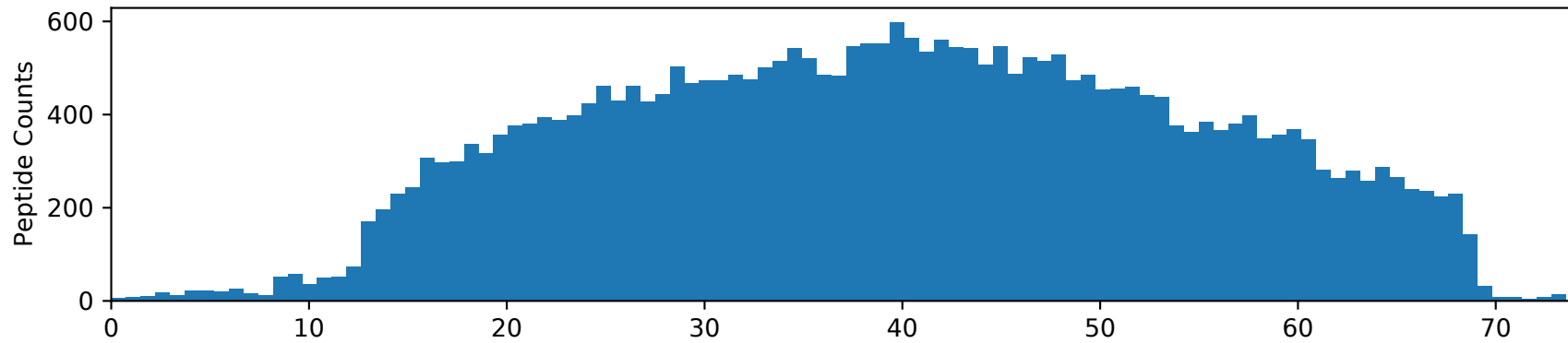
# H838 TGFb Rep3 2



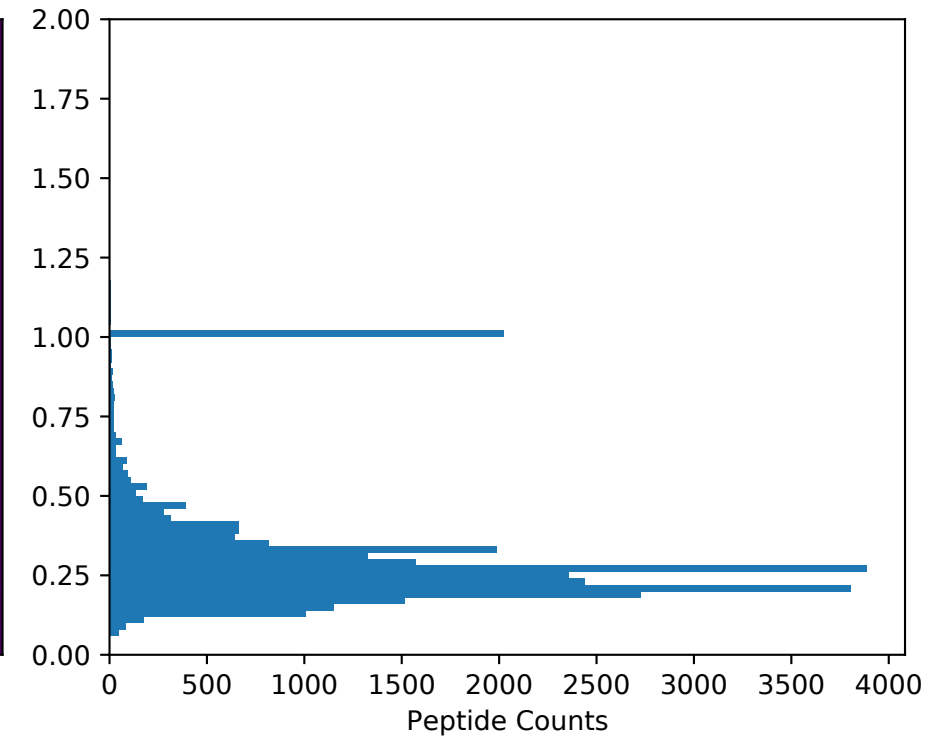
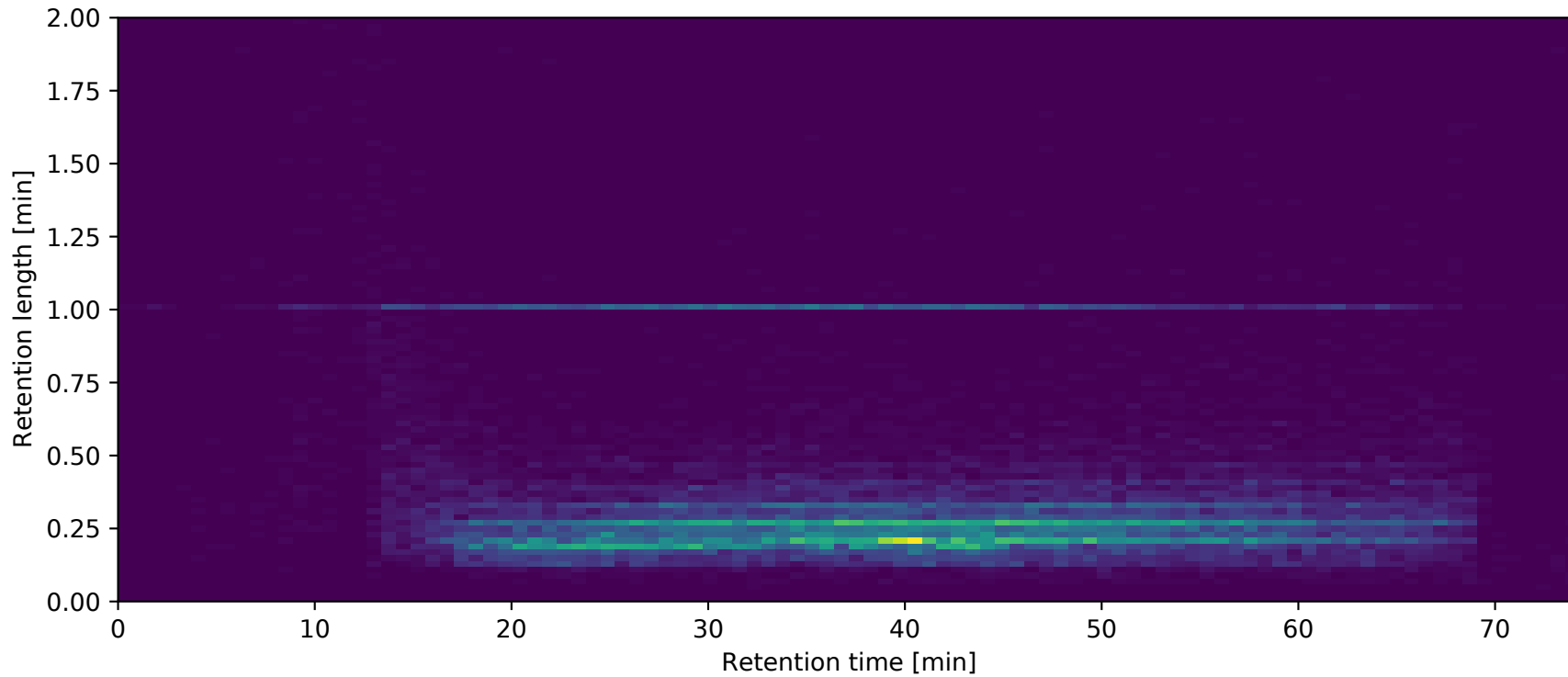
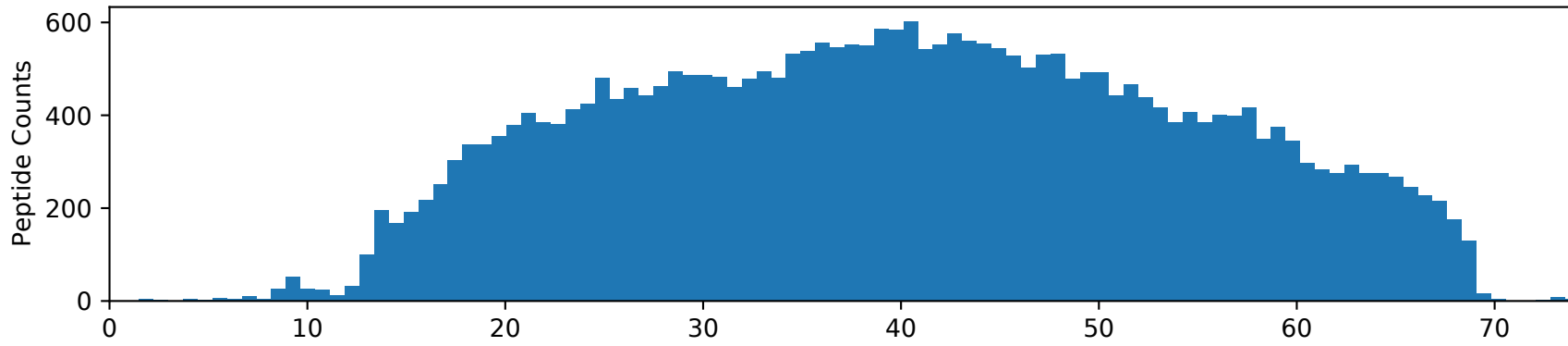
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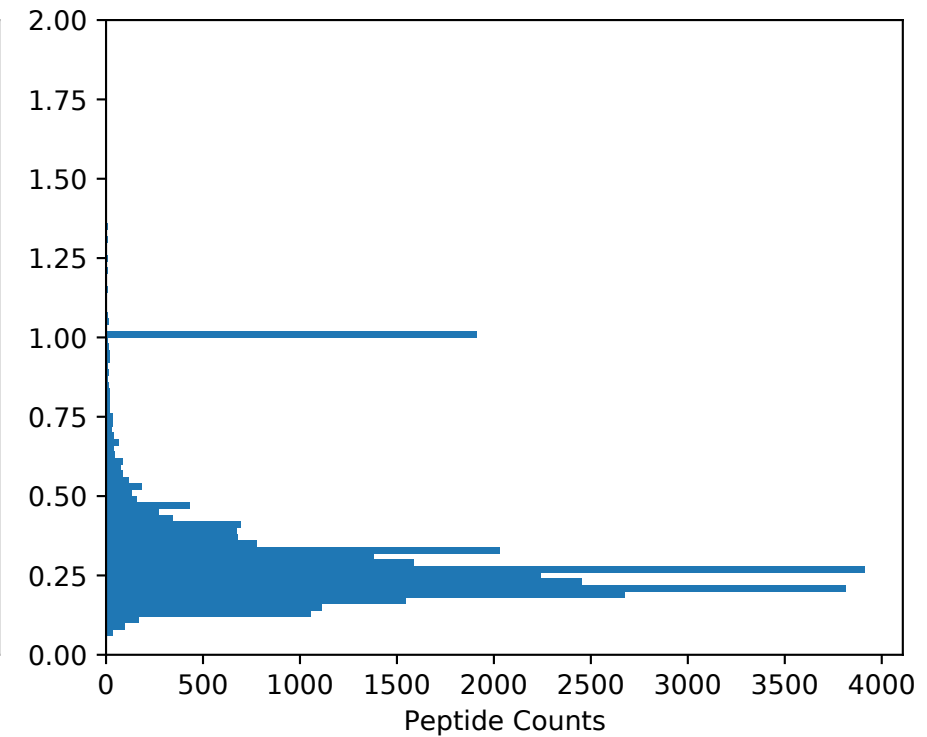
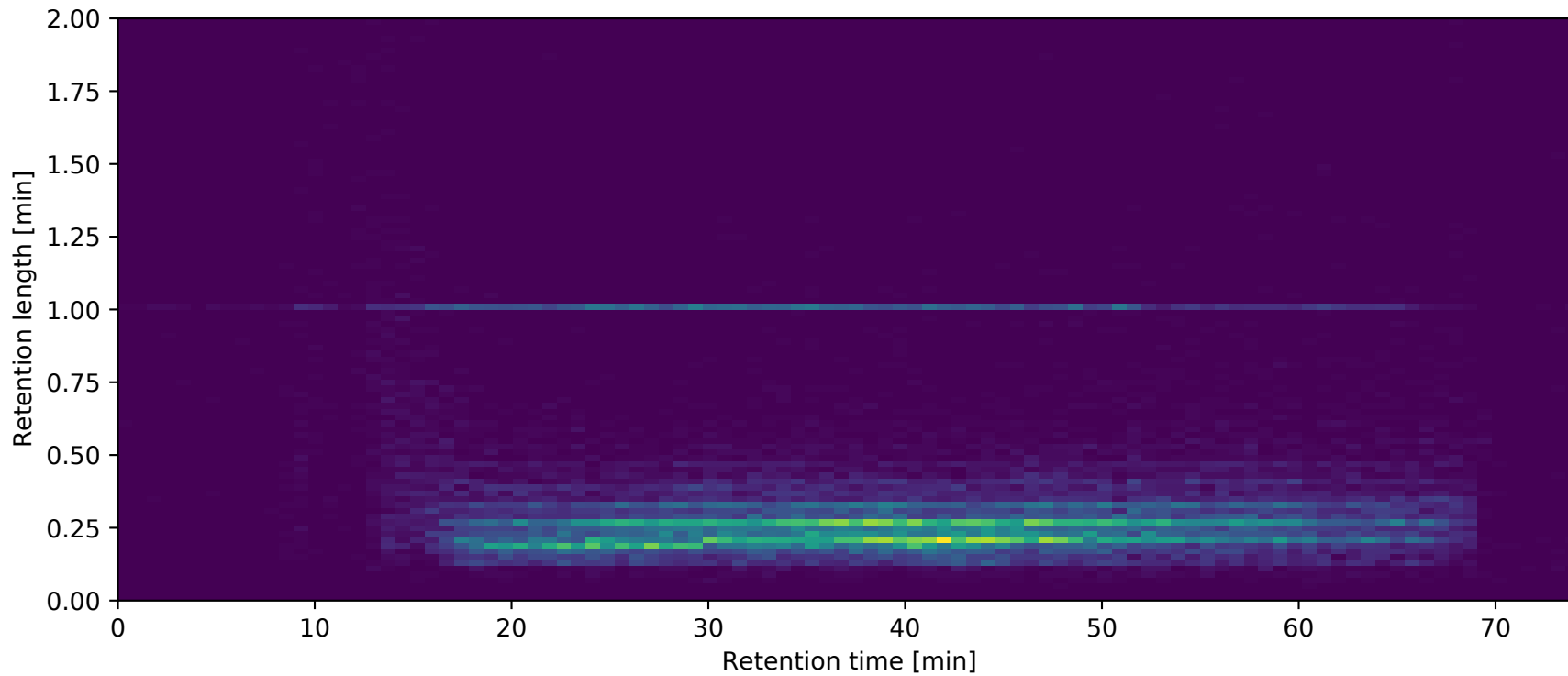
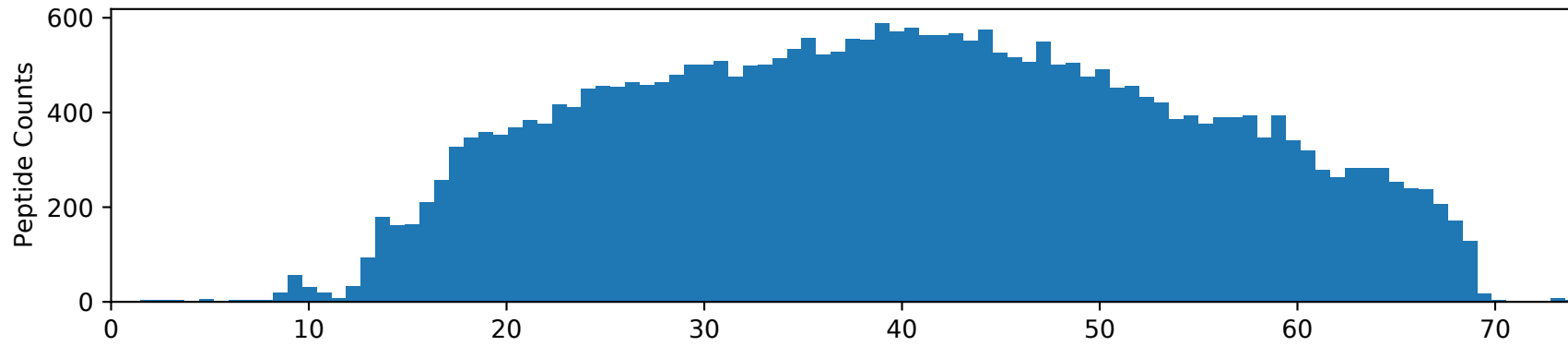
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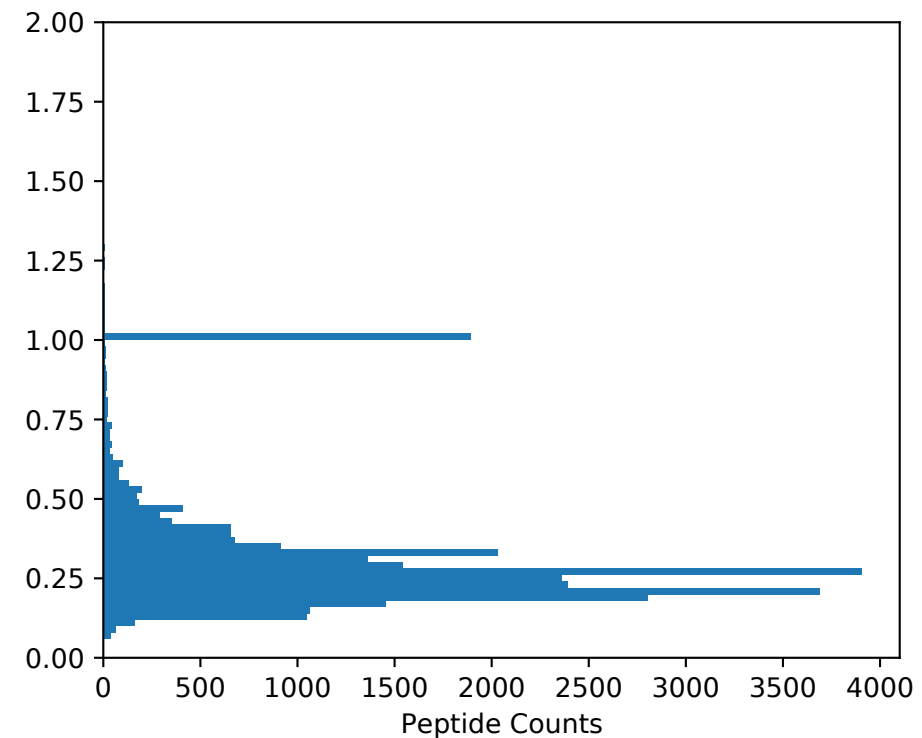
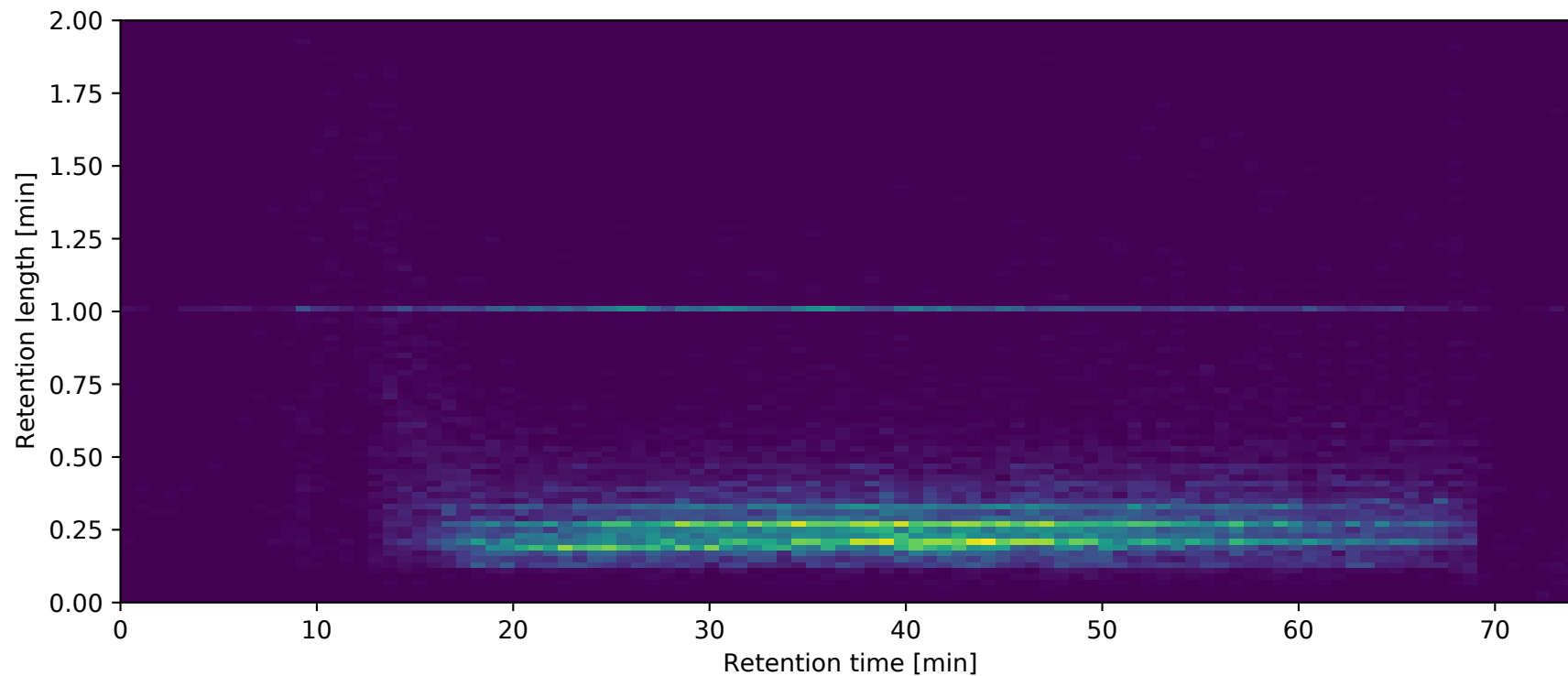
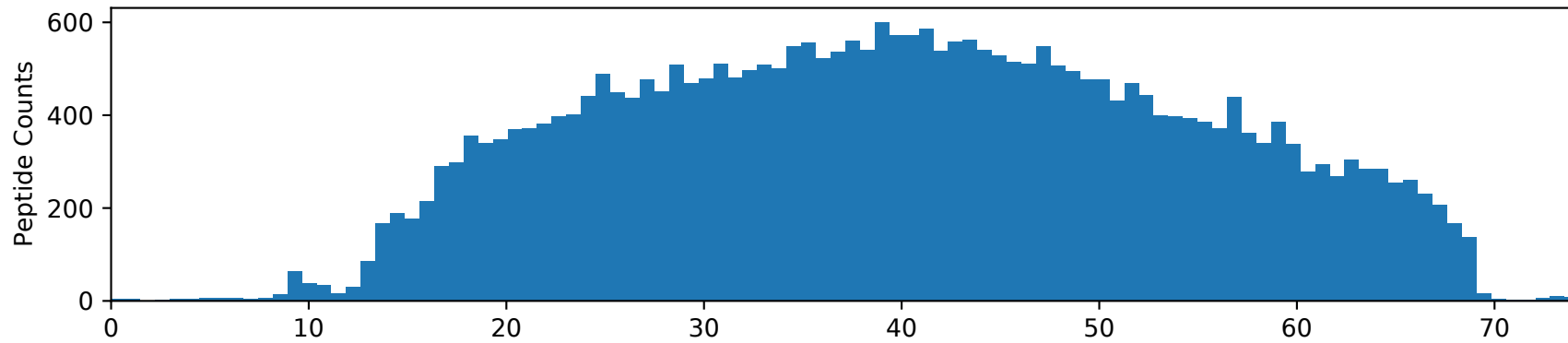
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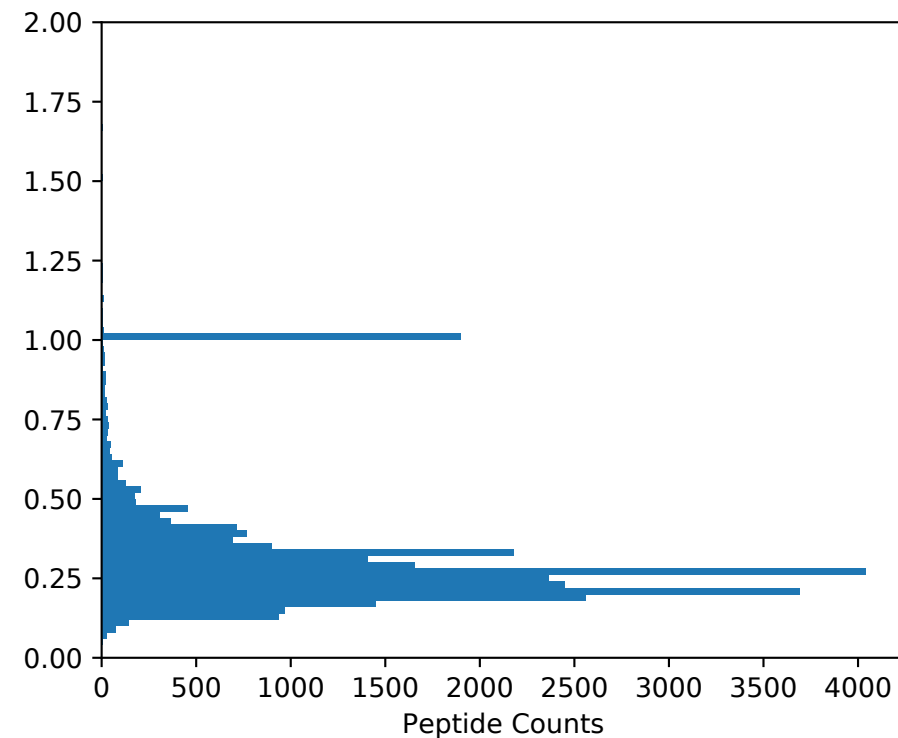
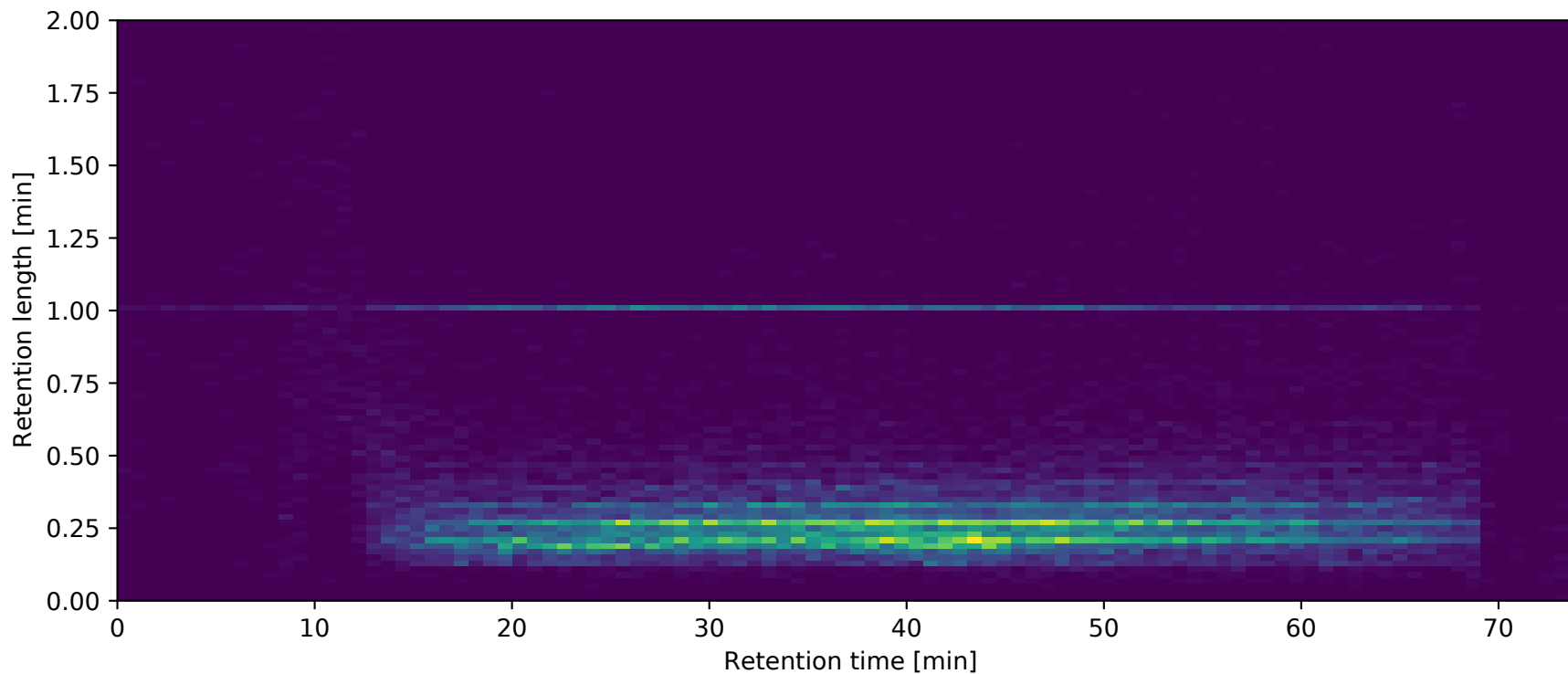
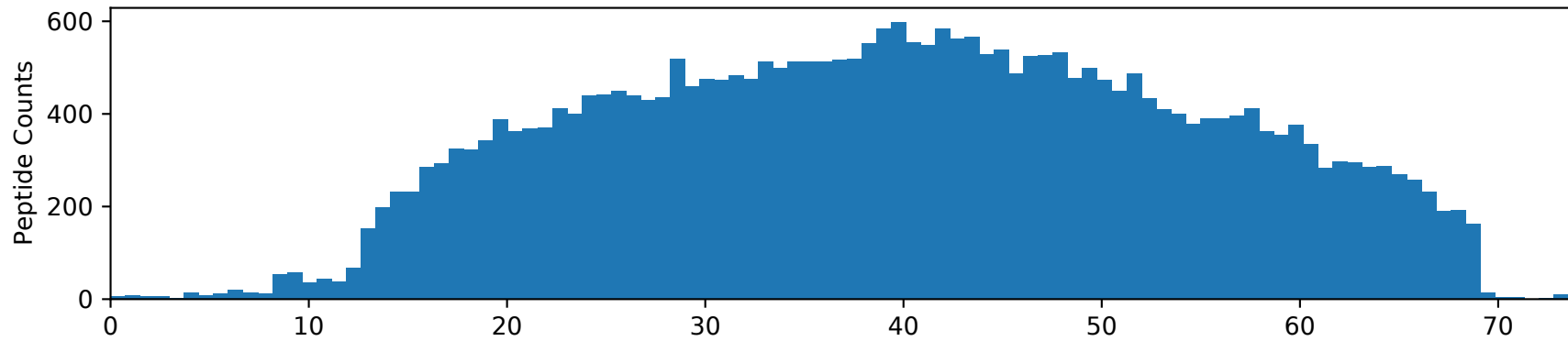
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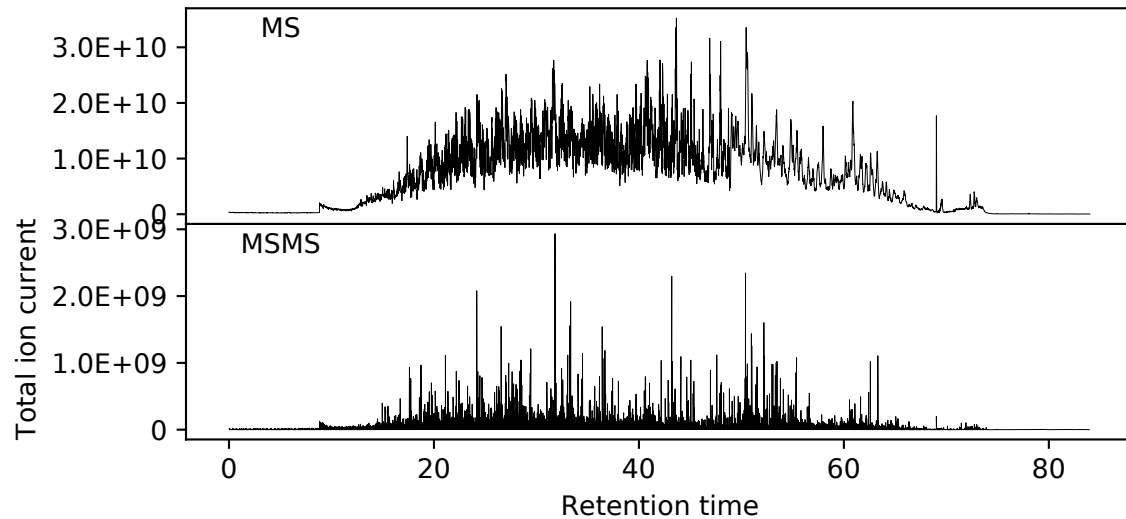
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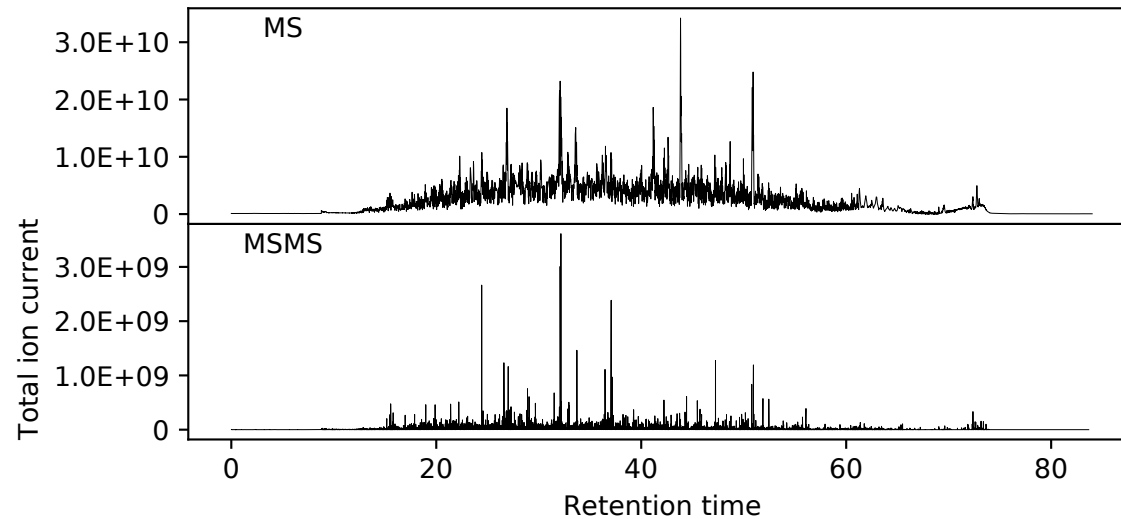
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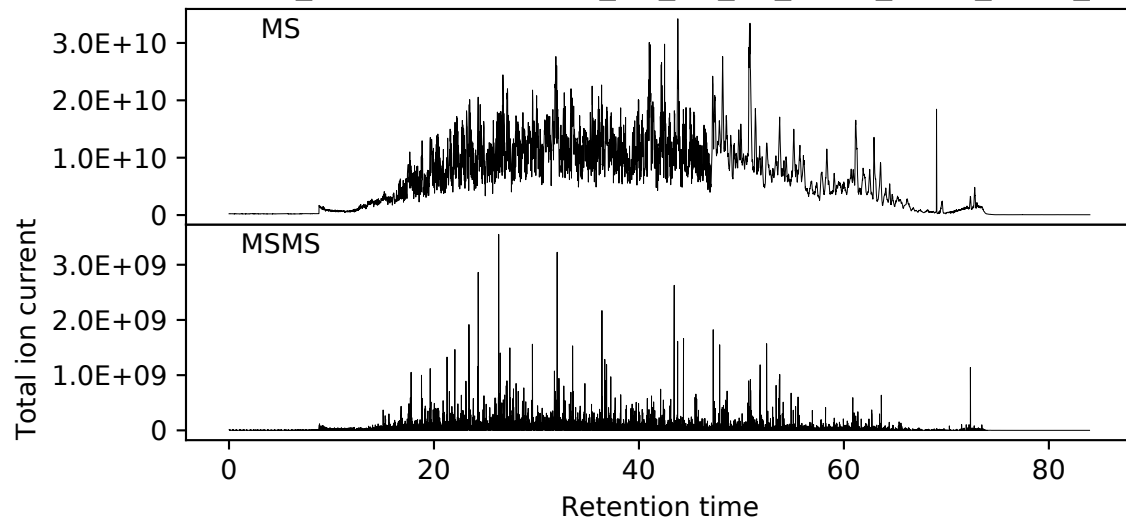
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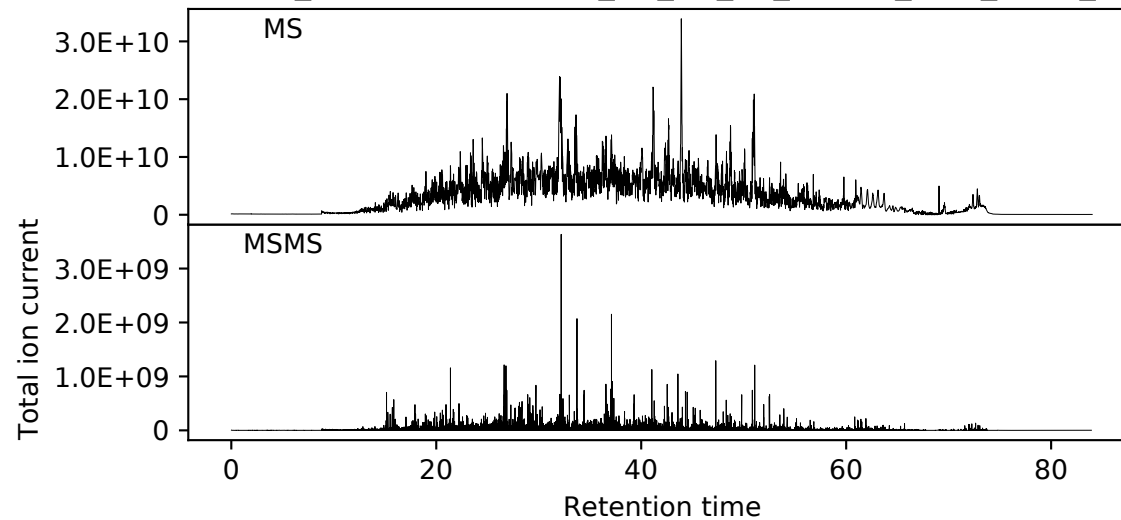
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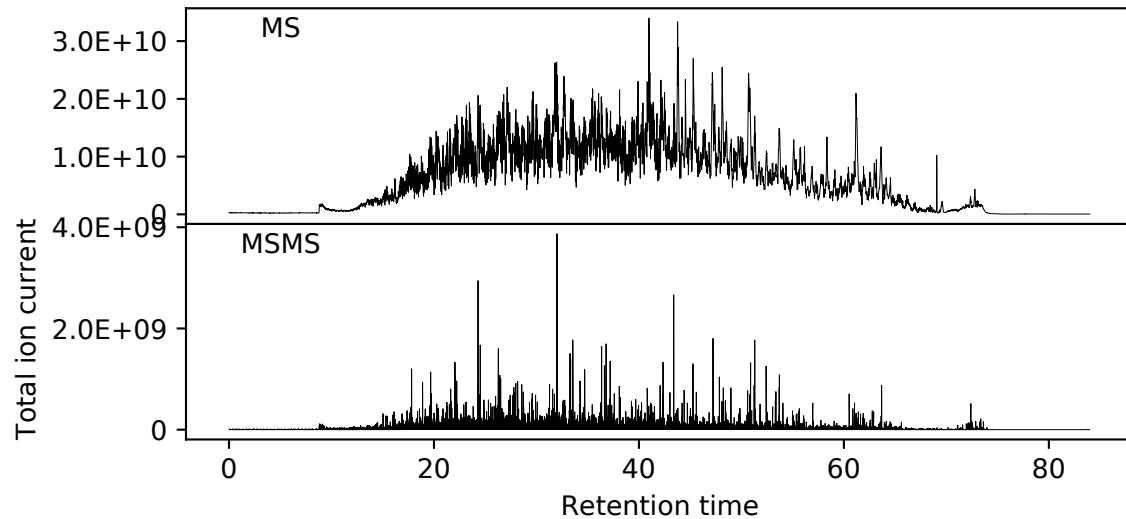
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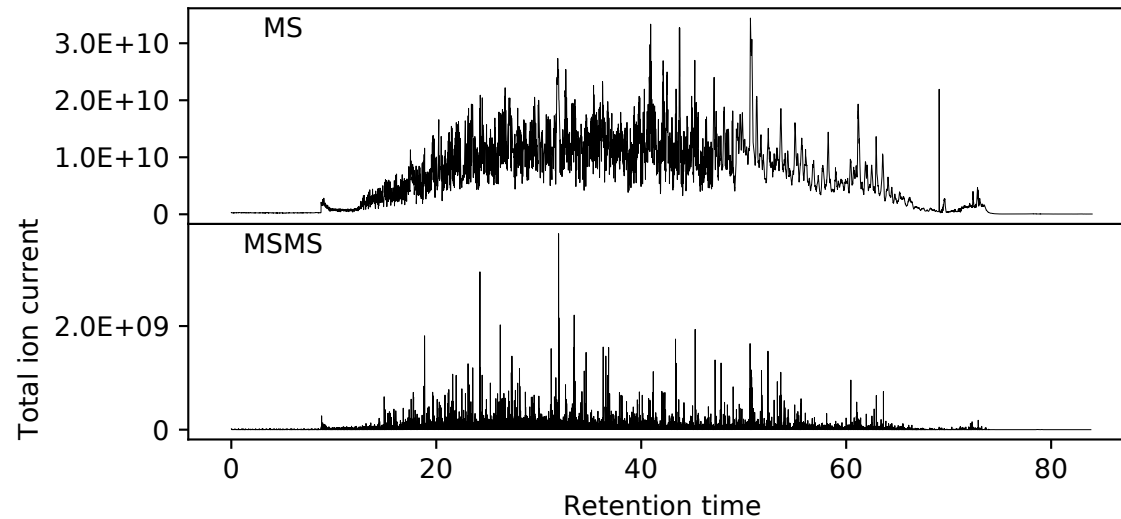
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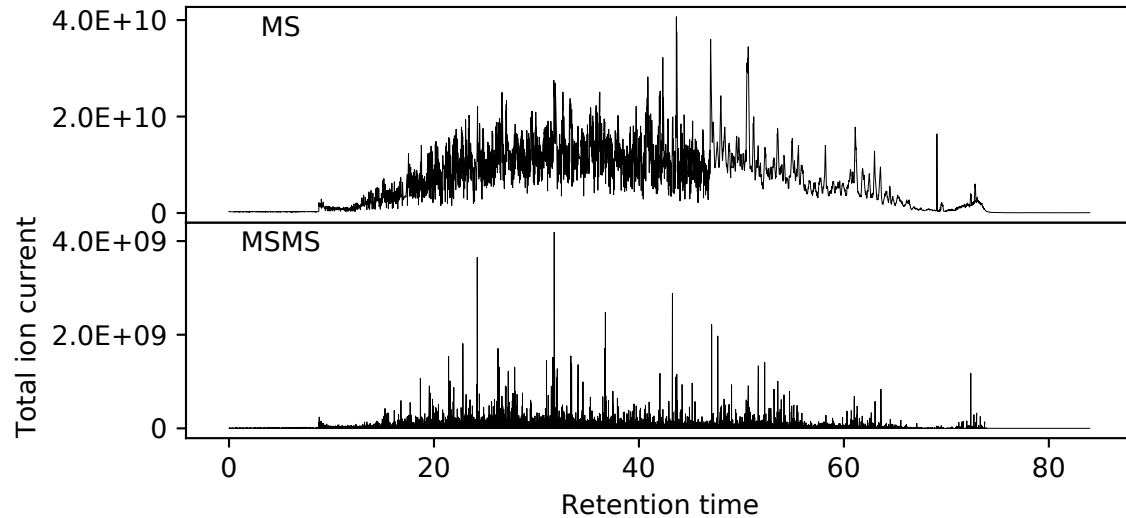
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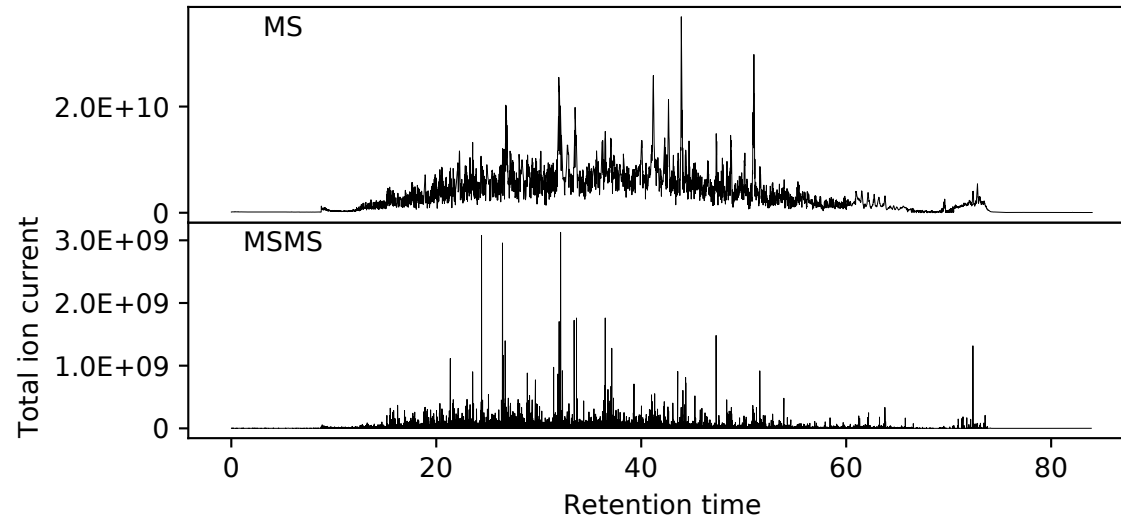
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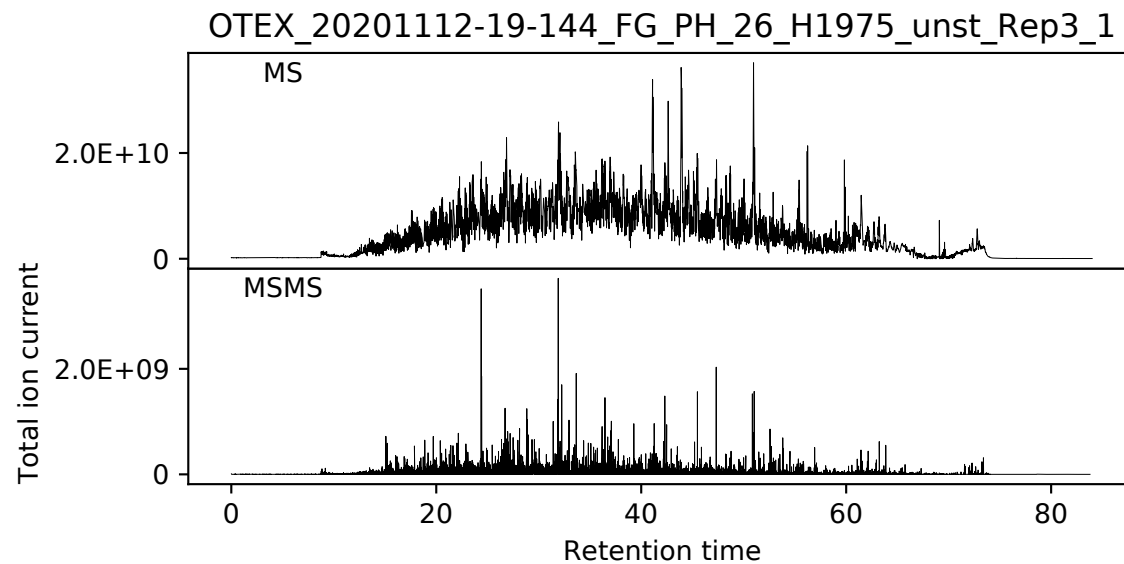
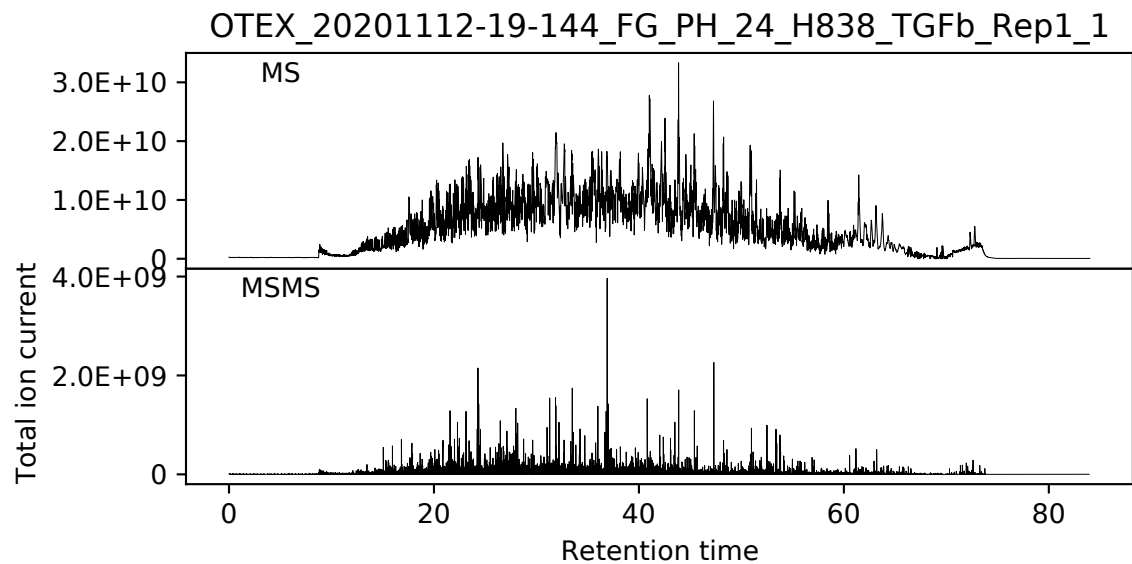
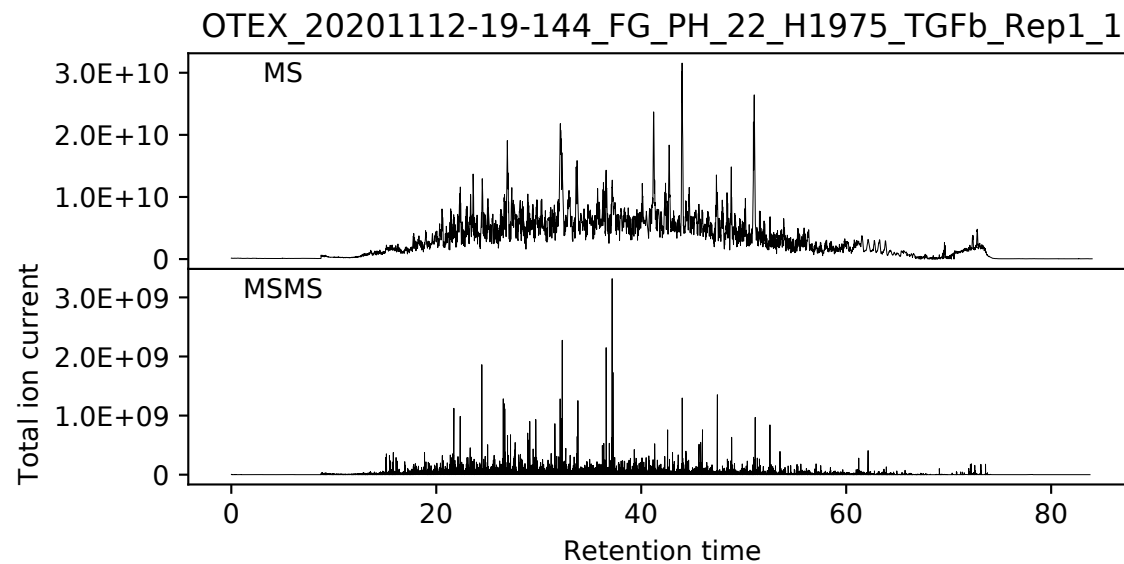
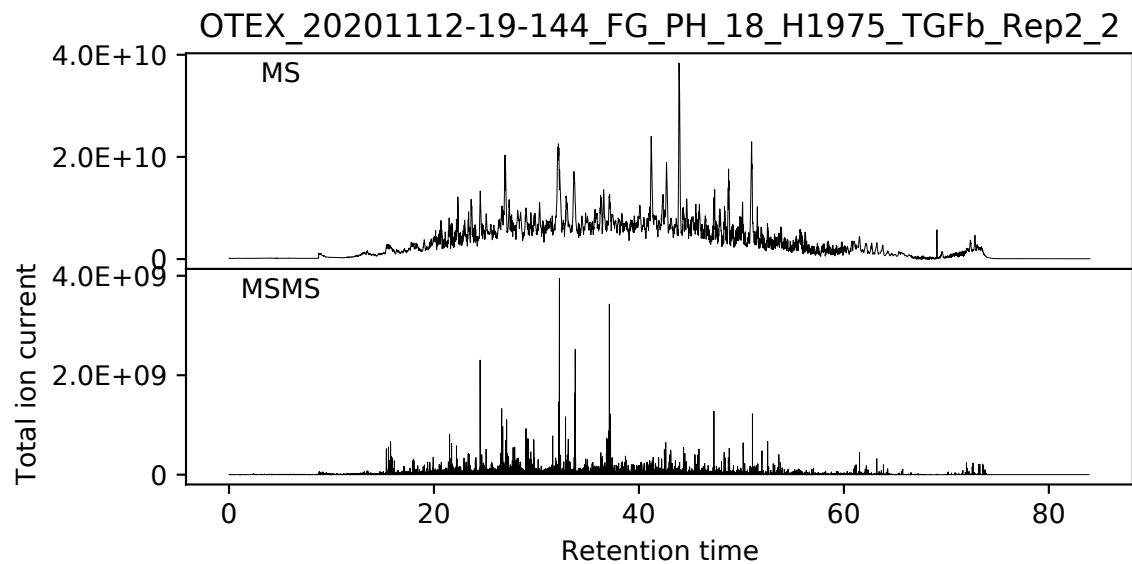


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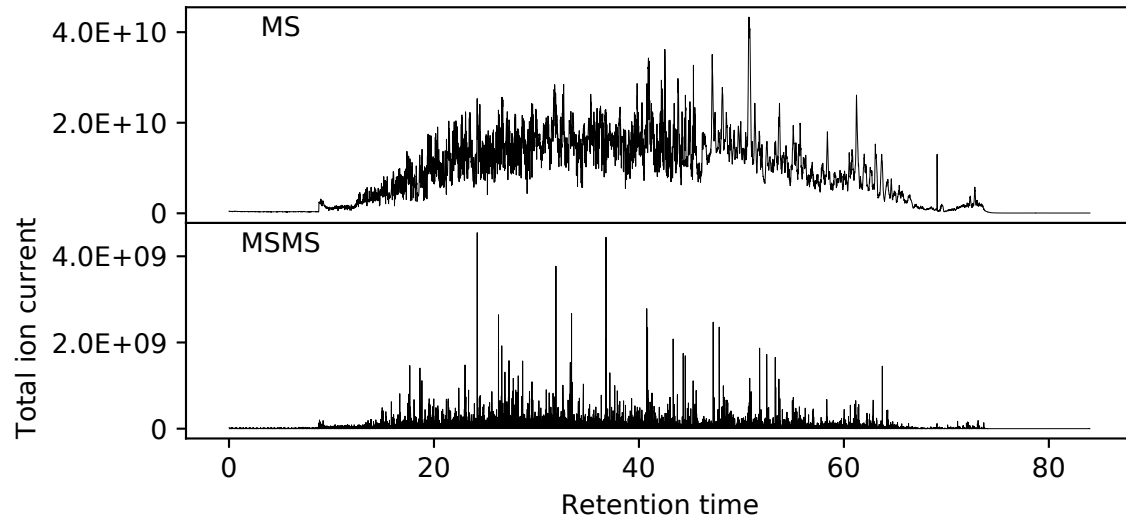


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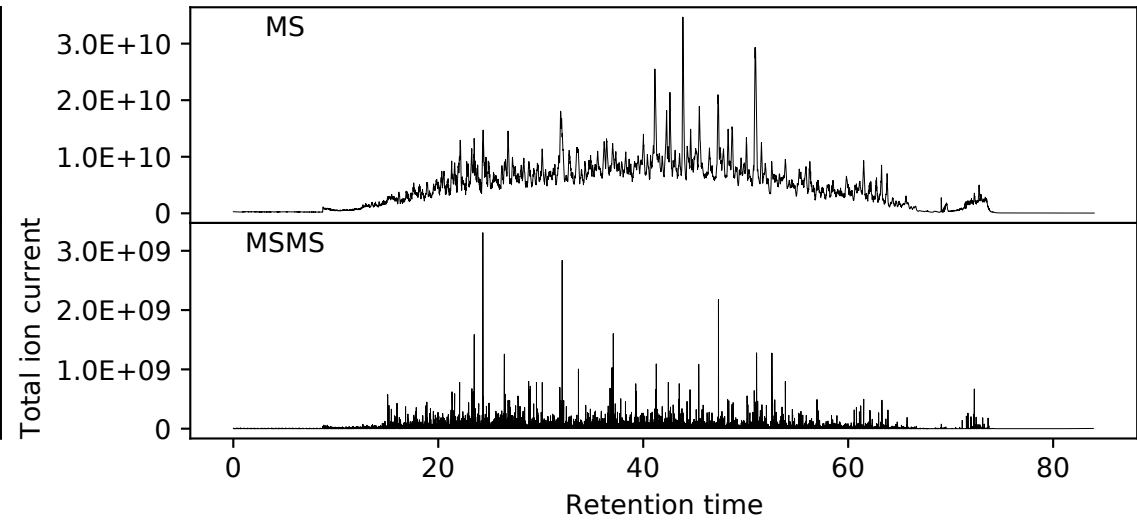




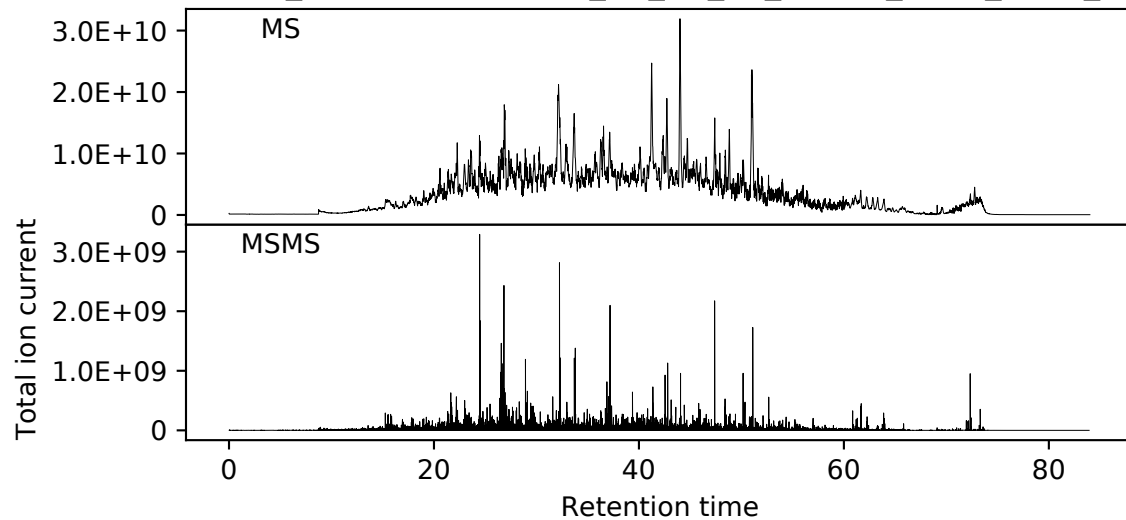
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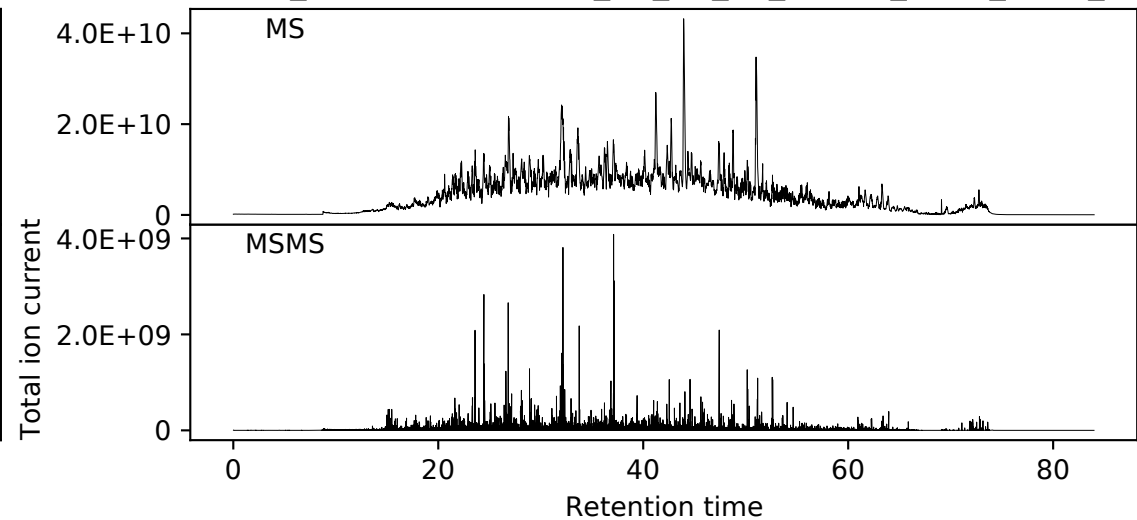
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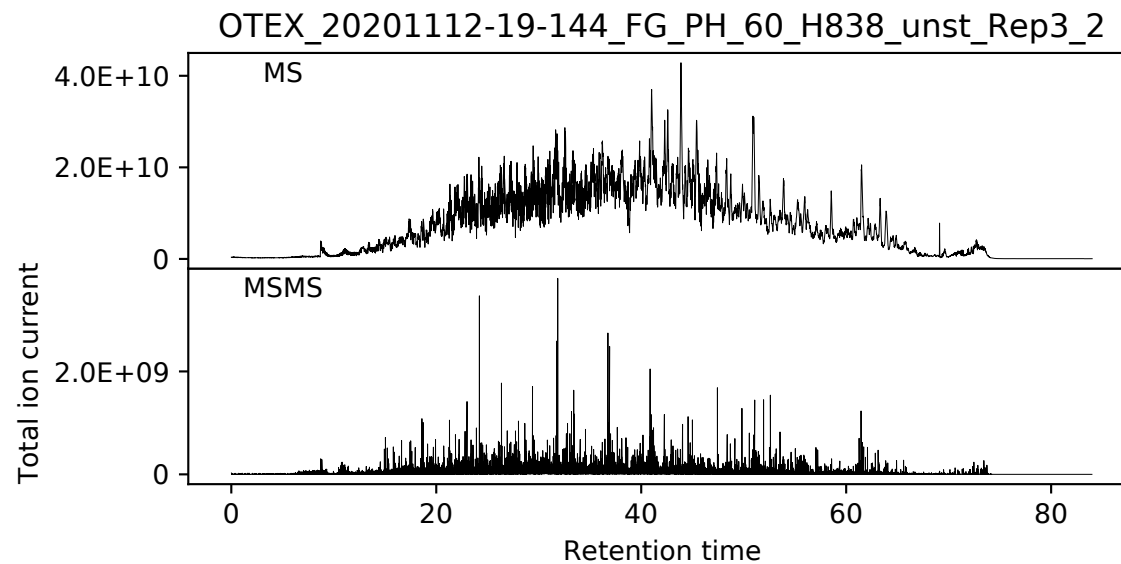
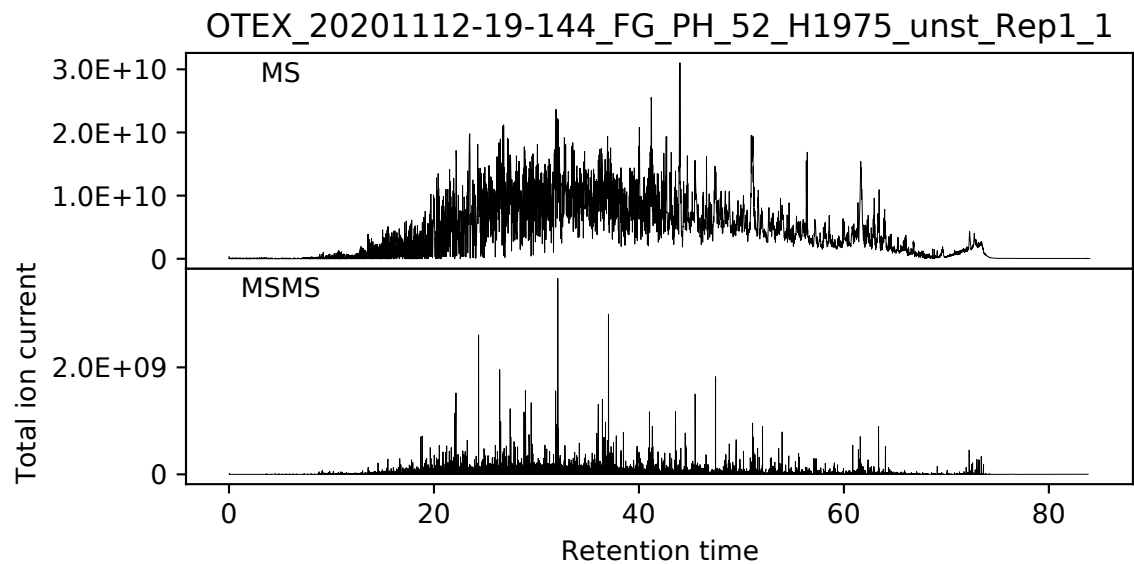
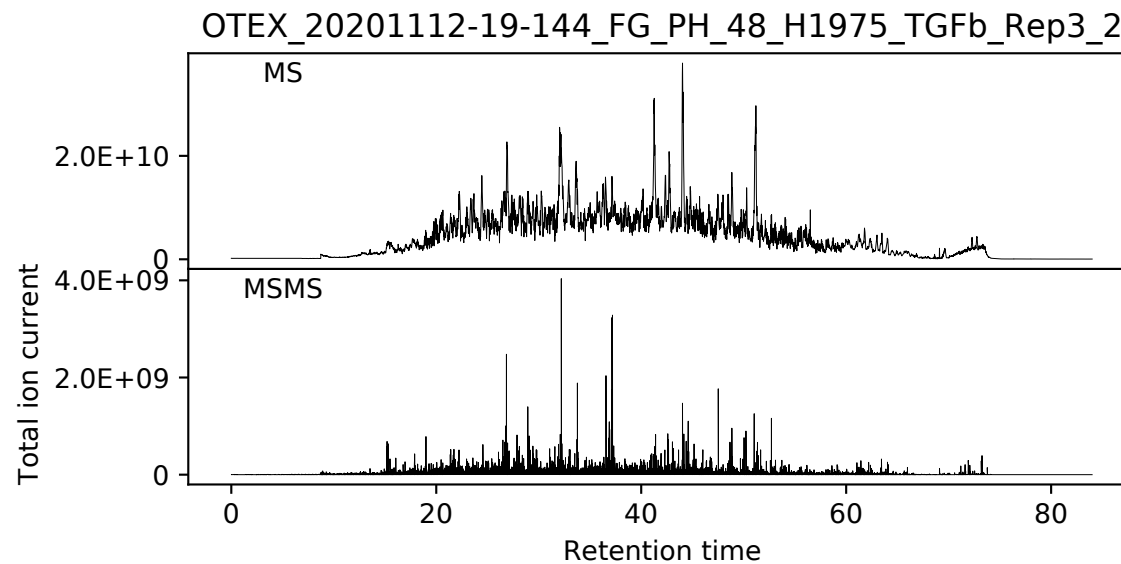
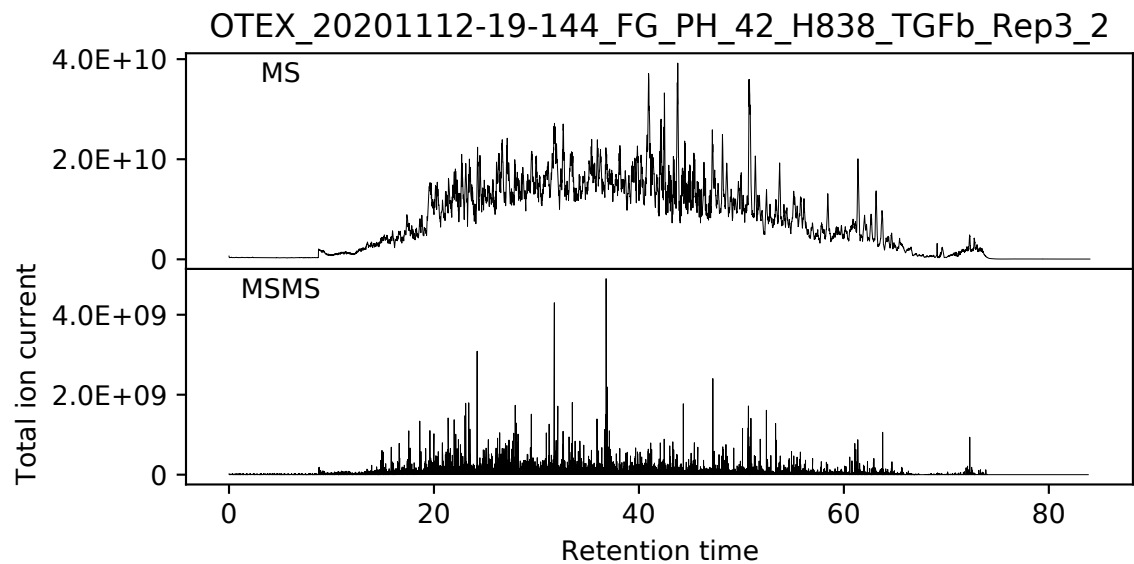


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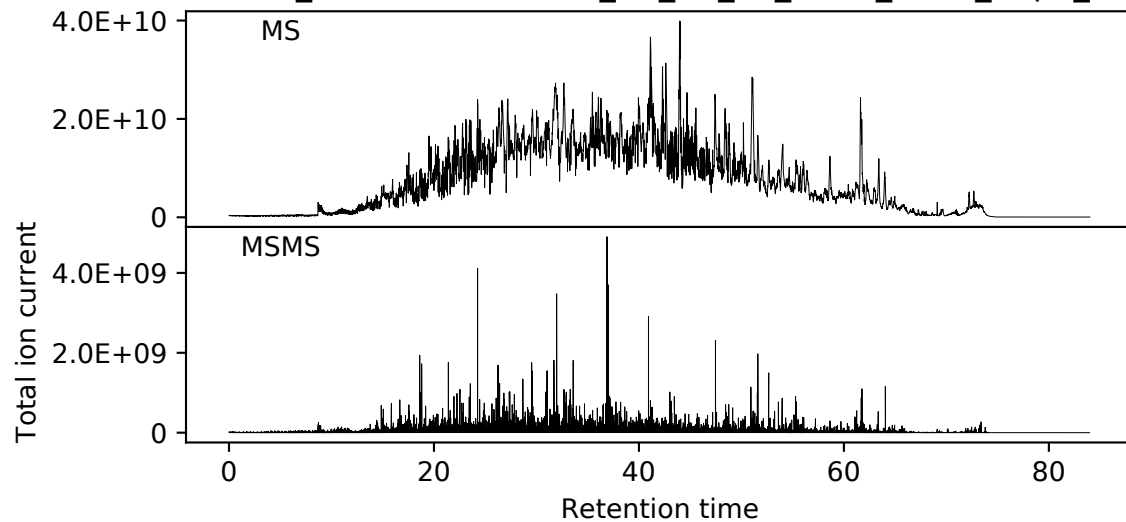


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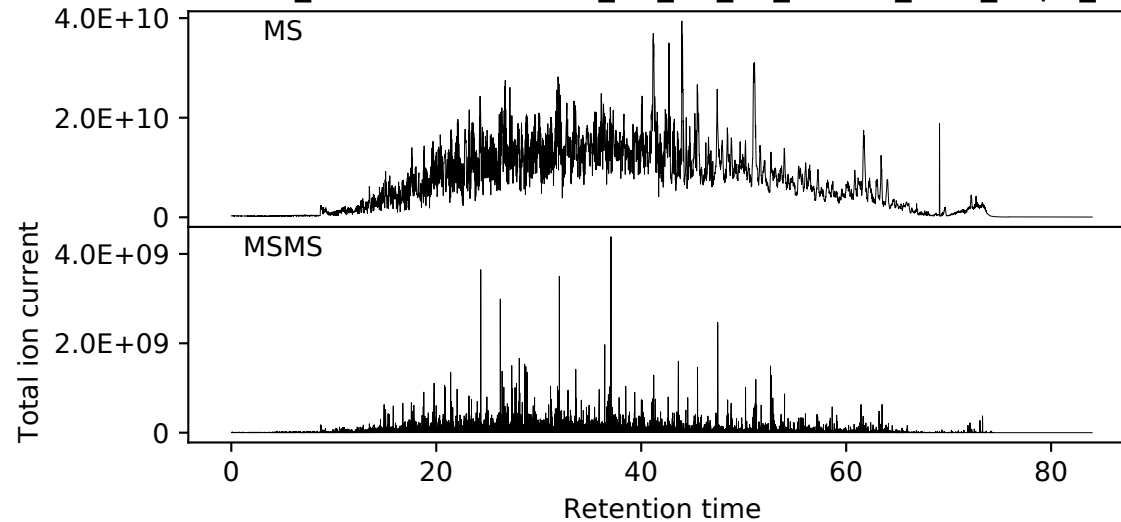




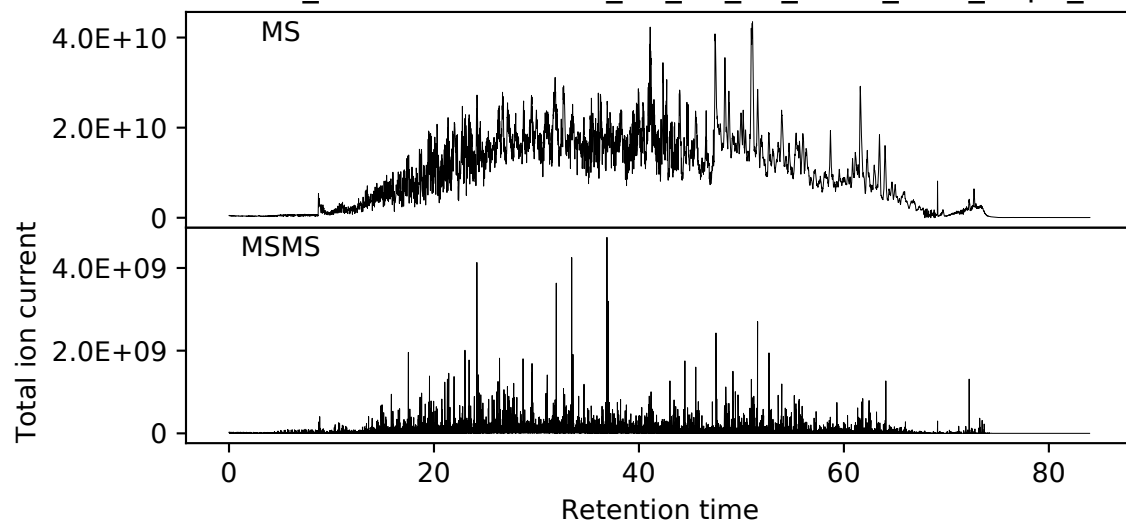
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OTEX\_20201112-19-144\_FG\_PH\_64\_H1975\_unst\_Rep1\_2



OTEX\_20201112-19-144\_FG\_PH\_66\_H838\_unst\_Rep1\_2



OTEX\_20201119-19-146\_FG\_PH\_78\_H838\_TGFb\_Rep1\_2

