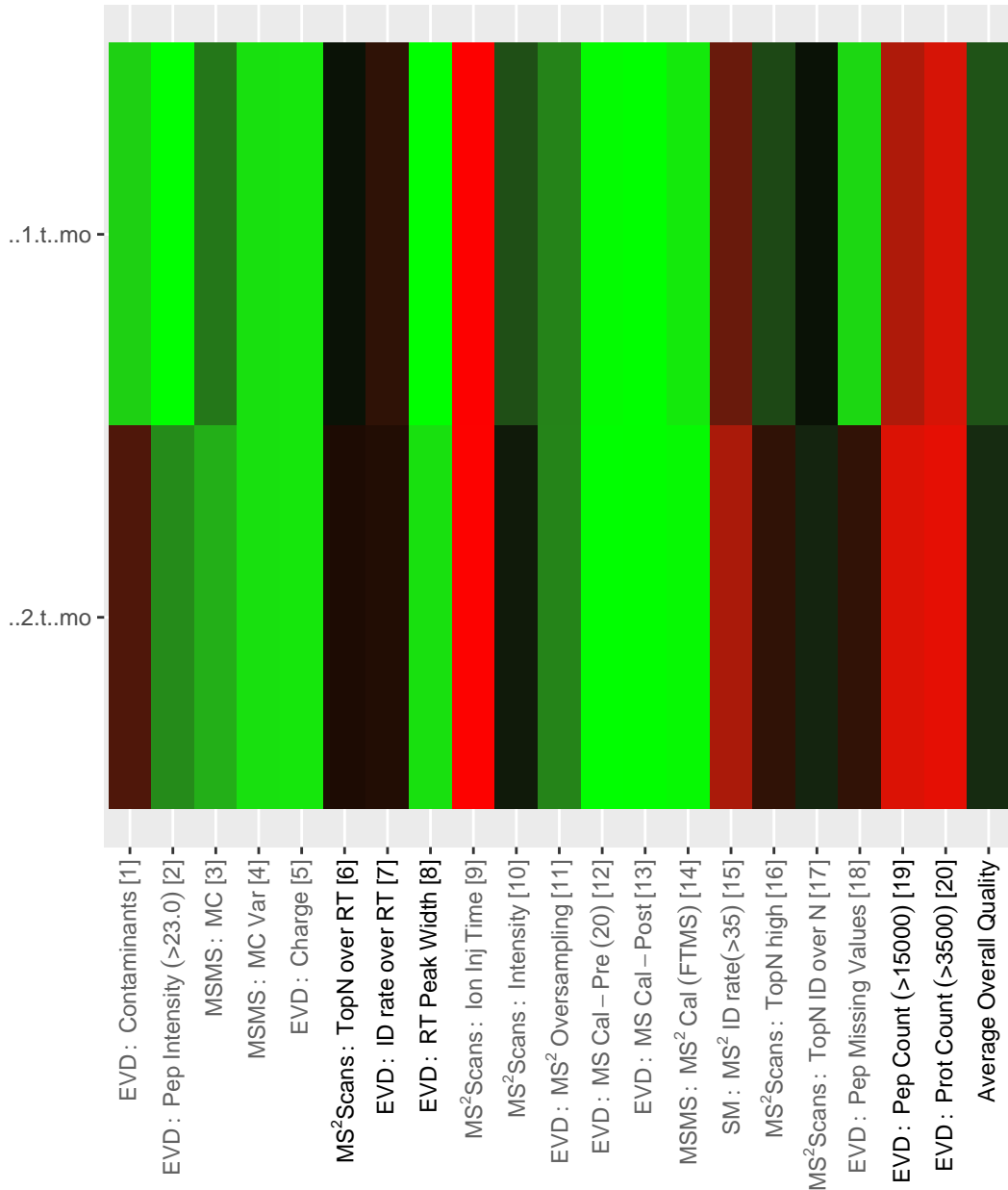
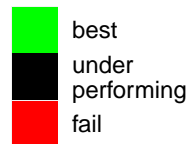


# Performance overview

Raw file



score



# Mapping of Raw files to their short names

Mapping source: automatic

original	short name	best effort
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sample1.thermo	..1.t.mo
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sample2.thermo	..2.t.mo
----------------	----------

## PAR: parameters

parameter	value	parameter	value
Advanced ratios	True	MS/MS deisotoping tolerance ..	7
Advanced site intensities	True	MS/MS deisotoping tolerance ..	ppm
Calculate peak properties	False	MS/MS dependent losses (FTMS..	True
Combined folder location		MS/MS dependent losses (ITMS..	True
Da interval. (FTMS)	100	MS/MS dependent losses (TOF)	True
Da interval. (ITMS)	100	MS/MS dependent losses (Unkn..	True
Da interval. (TOF)	100	MS/MS higher charges (FTMS)	True
Da interval. (Unknown)	100	MS/MS higher charges (ITMS)	True
Date of writing	04/27/2020 23:38:18	MS/MS higher charges (TOF)	True
Decoy mode	revert	MS/MS higher charges (Unknow..	True
Disable MD5	False	MS/MS recalibration (FTMS)	False
Discard unmodified counterpa..	True	MS/MS recalibration (ITMS)	False
Epsilon score for mutations		MS/MS recalibration (TOF)	False
Evaluate variant peptides se..	True	MS/MS recalibration (Unknown..	False
Find dependent peptides	False	MS/MS tol. (FTMS)	20 ppm
Fixed andromeda index folder		MS/MS tol. (ITMS)	0.5 Da
iBAQ	False	MS/MS tol. (TOF)	40 ppm
iBAQ log fit	False	MS/MS tol. (Unknown)	20 ppm
Include contaminants	True	MS/MS water loss (FTMS)	True
Label min. ratio count	2	MS/MS water loss (ITMS)	True
Machine name	vgcnbwc-compute-c20me-4652 .novalocal	MS/MS water loss (TOF)	True
Main search max. combination..	200	MS/MS water loss (Unknown)	True
Match between runs	False	Peptides used for protein qu..	Razor
Match unidentified features	False	Protein FDR	0.01
Max mods in site table	3	PSM FDR	0.01
Max. peptide length for unsp..	25	PSM FDR Crosslink	0.01

/data/dnb02/galaxy\_db/files/017/298/dataset\_17298078.dat

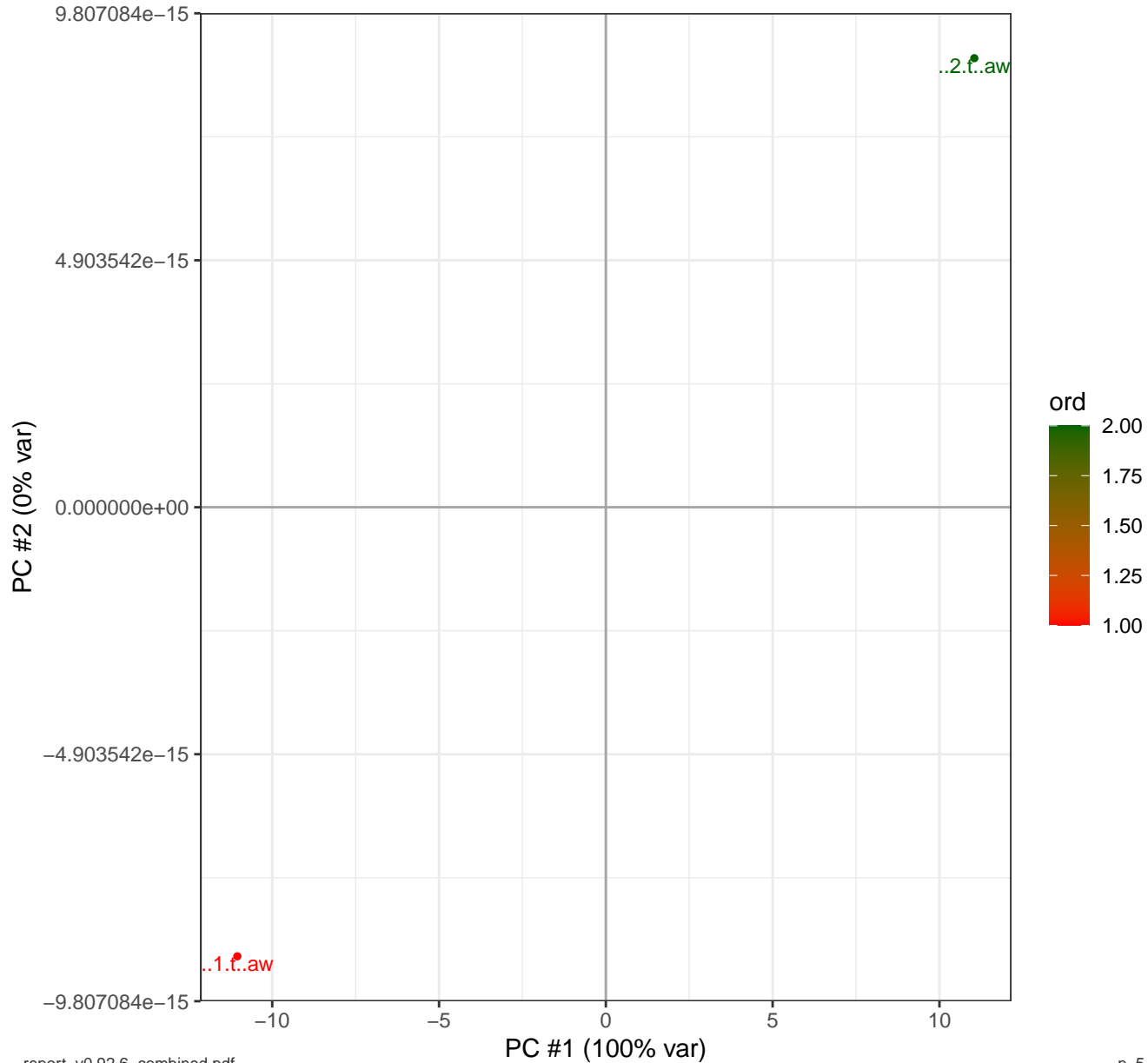
## PAR: parameters

parameter	value	parameter	value
Max. peptide mass [Da]	4600	Razor protein FDR	True
Min. delta score for modifie..	6	Require MS/MS for LFQ compar..	True
Min. delta score for unmodif..	0	Second peptides	True
Min. peptide Length	7	Separate LFQ in parameter gr..	False
Min. peptide length for unsp..	8	Site FDR	0.01
Min. peptides	1	Site tables	
Min. razor peptides	1	Stabilize large LFQ ratios	True
Min. score for modified pept..	40	Temporary folder	
Min. score for unmodified pe..	0	Top MS/MS peaks per Da inter..	12
Min. unique peptides	1	Top MS/MS peaks per Da inter..	8
Modifications included in pr..	Oxidation (M) Acetyl (Protein N-term)	Top MS/MS peaks per Da inter..	10
MS/MS ammonia loss (FTMS)	True	Top MS/MS peaks per Da inter..	12
MS/MS ammonia loss (ITMS)	True	Use delta score	False
MS/MS ammonia loss (TOF)	True	Use Normalized Ratios For Oc..	True
MS/MS ammonia loss (Unknown)	True	Use only unmodified peptides..	True
MS/MS deisotoping (FTMS)	True	User name	galaxy
MS/MS deisotoping (ITMS)	False	Variation mode	None
MS/MS deisotoping (TOF)	True	Version	1.6.10.43
MS/MS deisotoping (Unknown)	True	Write accumulatedPasefMsmsSc.	True
MS/MS deisotoping tolerance ..	7	Write allPeptides table	True
MS/MS deisotoping tolerance ..	ppm	Write ms3Scans table	True
MS/MS deisotoping tolerance ..	0.15	Write msmsScans table	True
MS/MS deisotoping tolerance ..	Da	Write msScans table	False
MS/MS deisotoping tolerance ..	0.01	Write mzRange table	True
MS/MS deisotoping tolerance ..	Da	Write pasefMsmsScans table	True

/data/dnb02/galaxy\_db/files/017/298/dataset\_17298078.dat

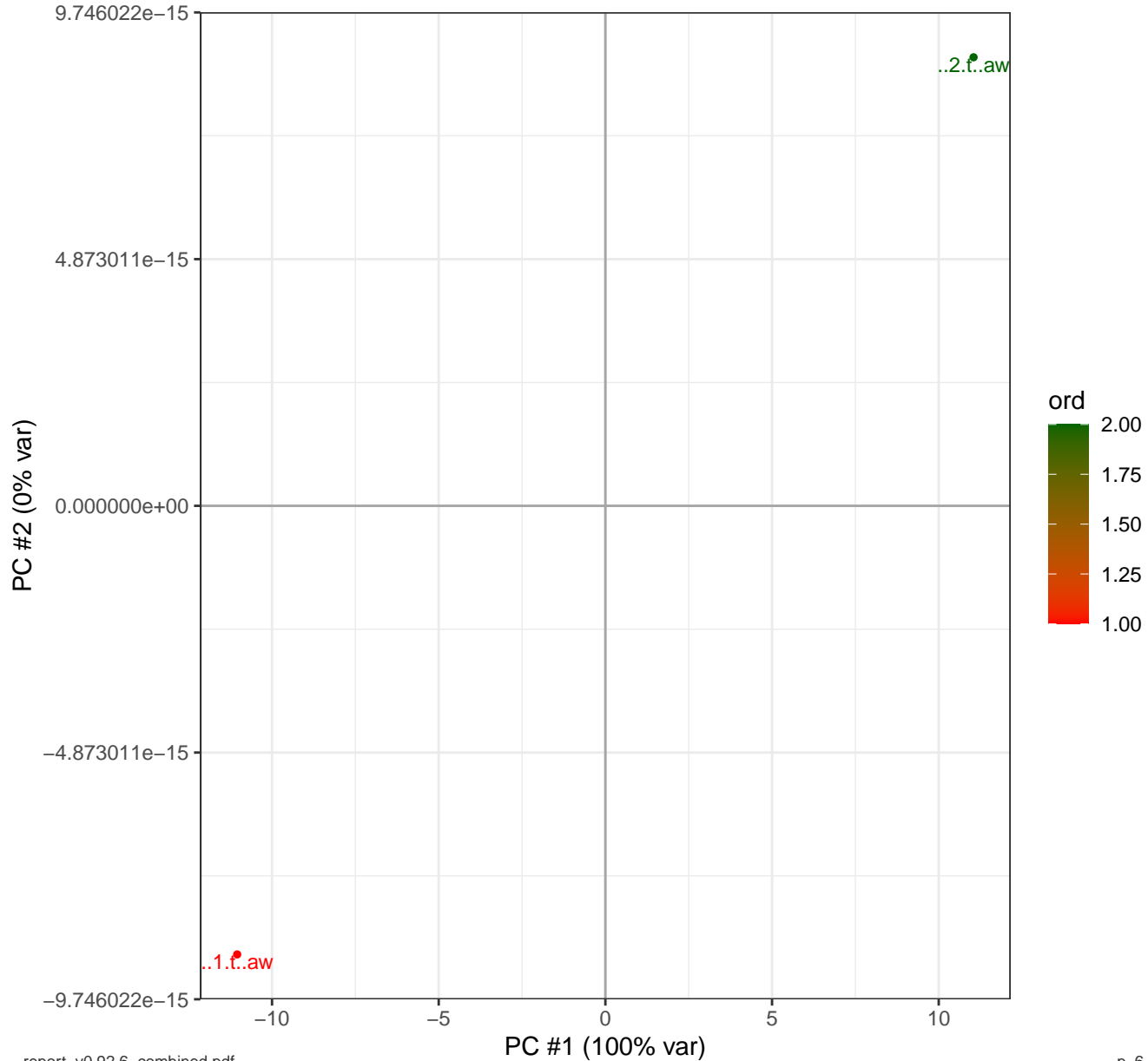
# PG: PCA of 'raw intensity'

(excludes contaminants)

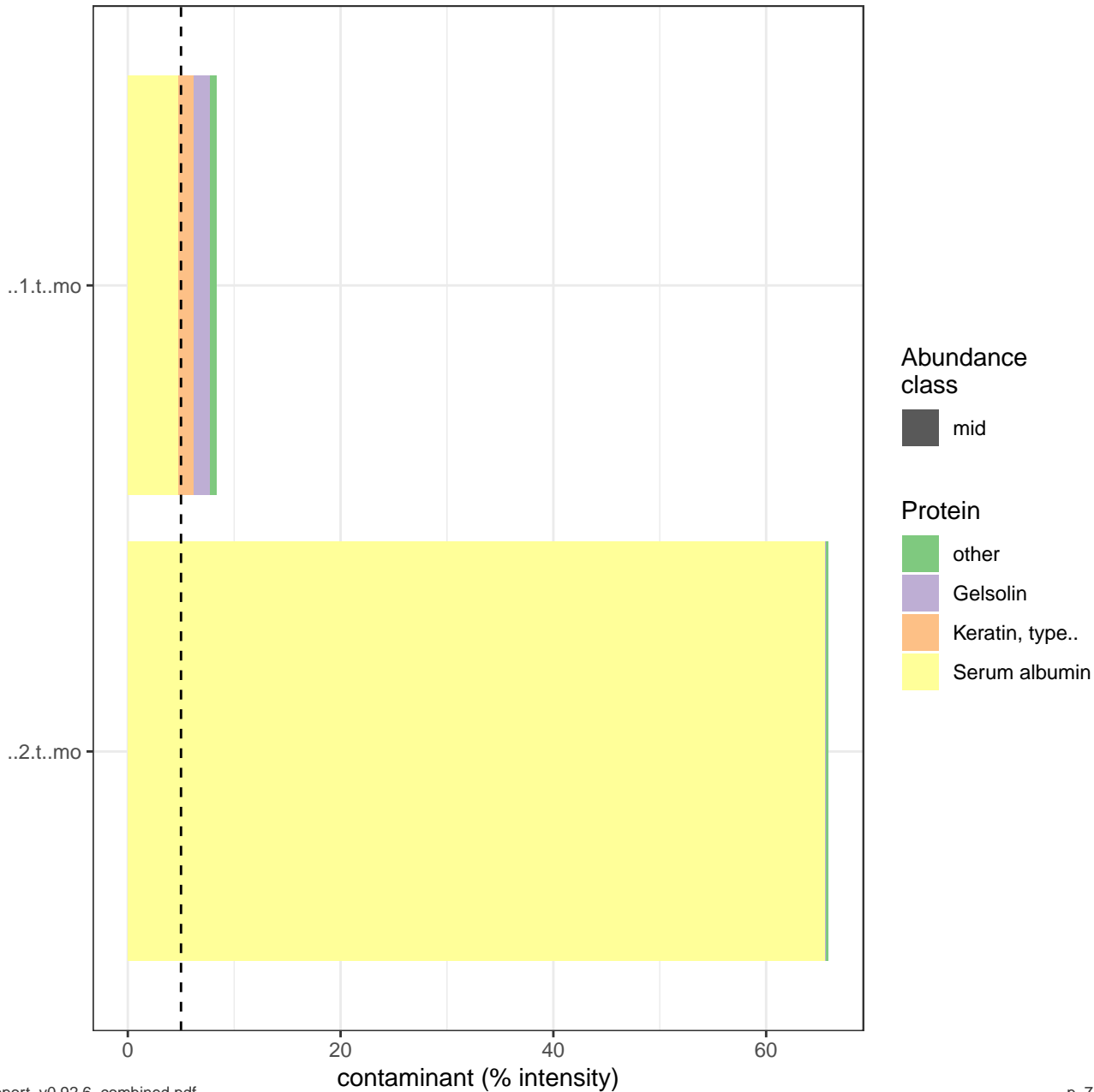


# PG: PCA of 'lfq intensity'

(excludes contaminants)



# EVD: Top5 Contaminants per Raw file



## EVD: Contaminants

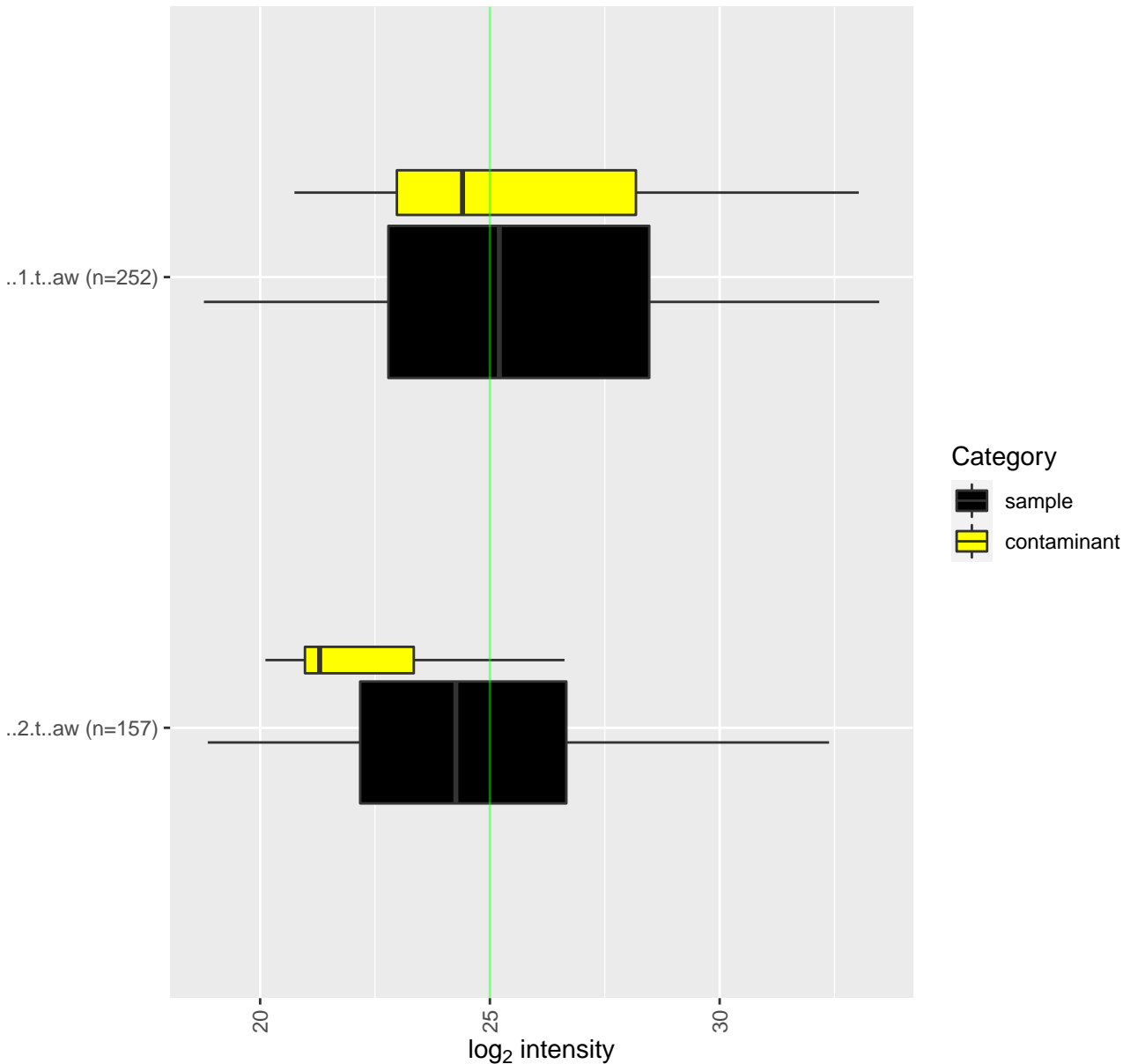
Contaminant 'MYCOPLASMA' was not found in any sample.

Did you use the correct database?





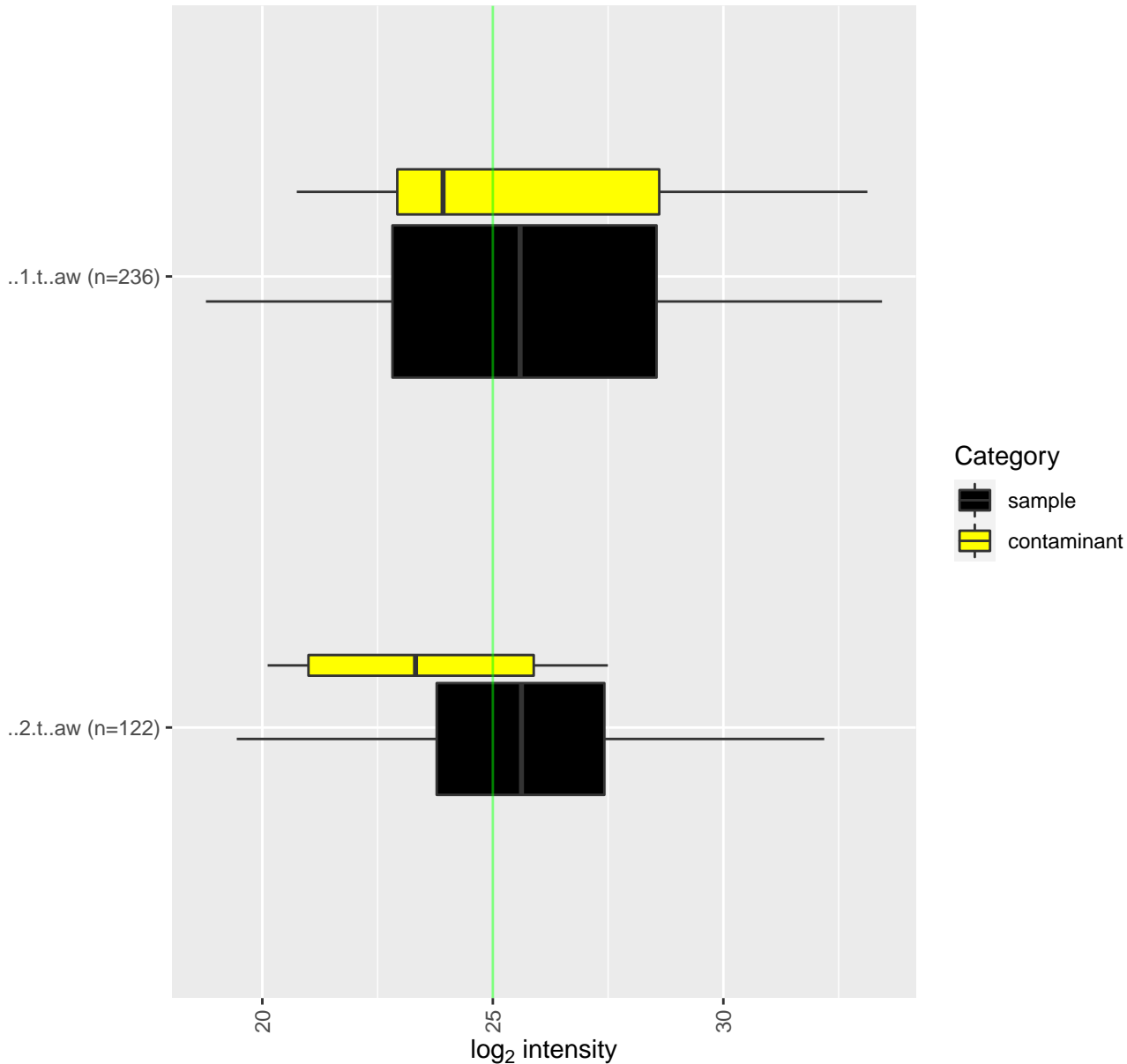
PG: intensity distribution  
RSD 2.5% (w/o zero int.; expected < 5%)  
RSD 10.5% [high RSD --> few peptides]



# PG: LFQ intensity distribution

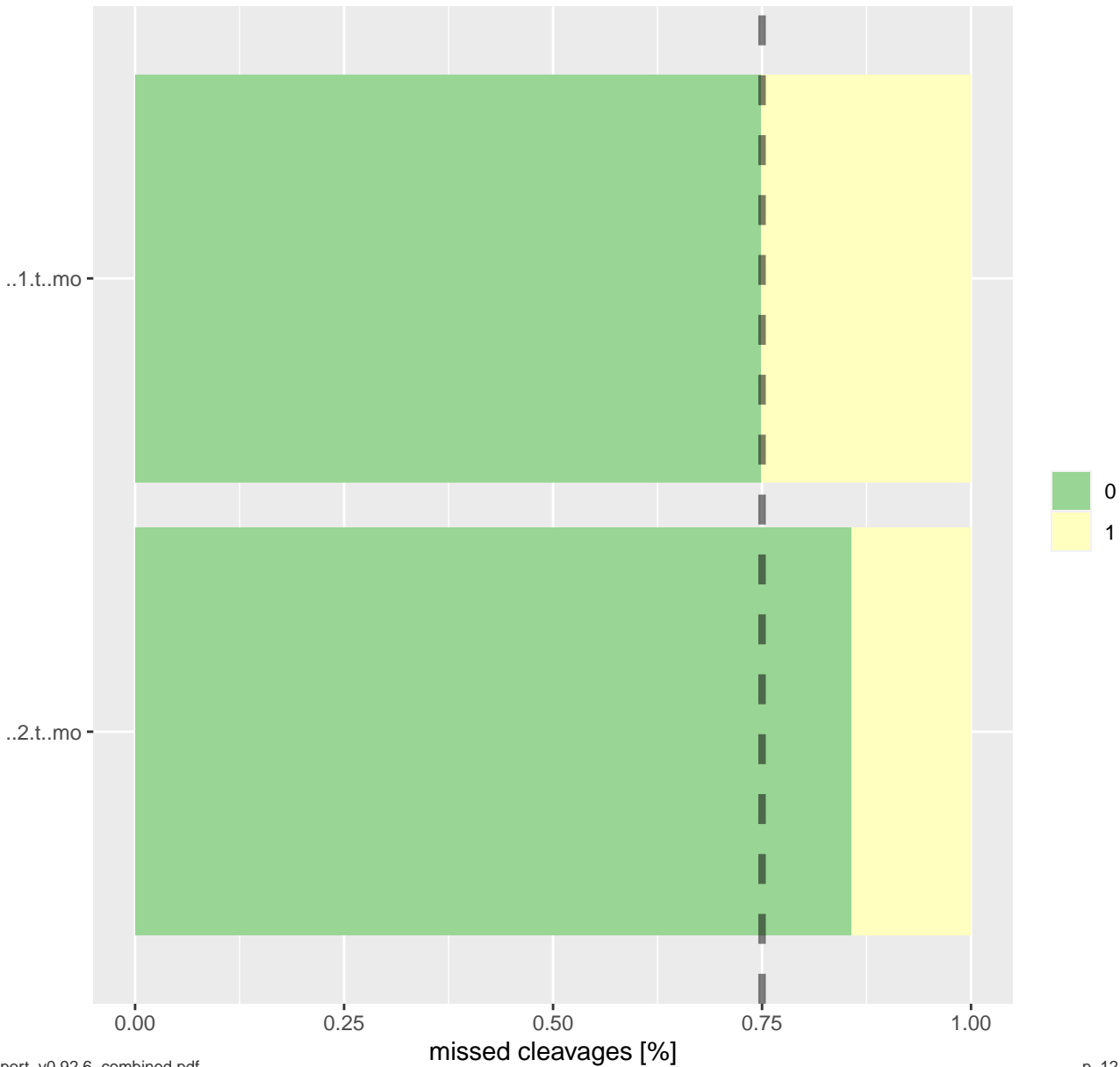
RSD 0.3% (w/o zero int.; expected < 5%)

RSD 141.4% [high RSD --> few peptides]

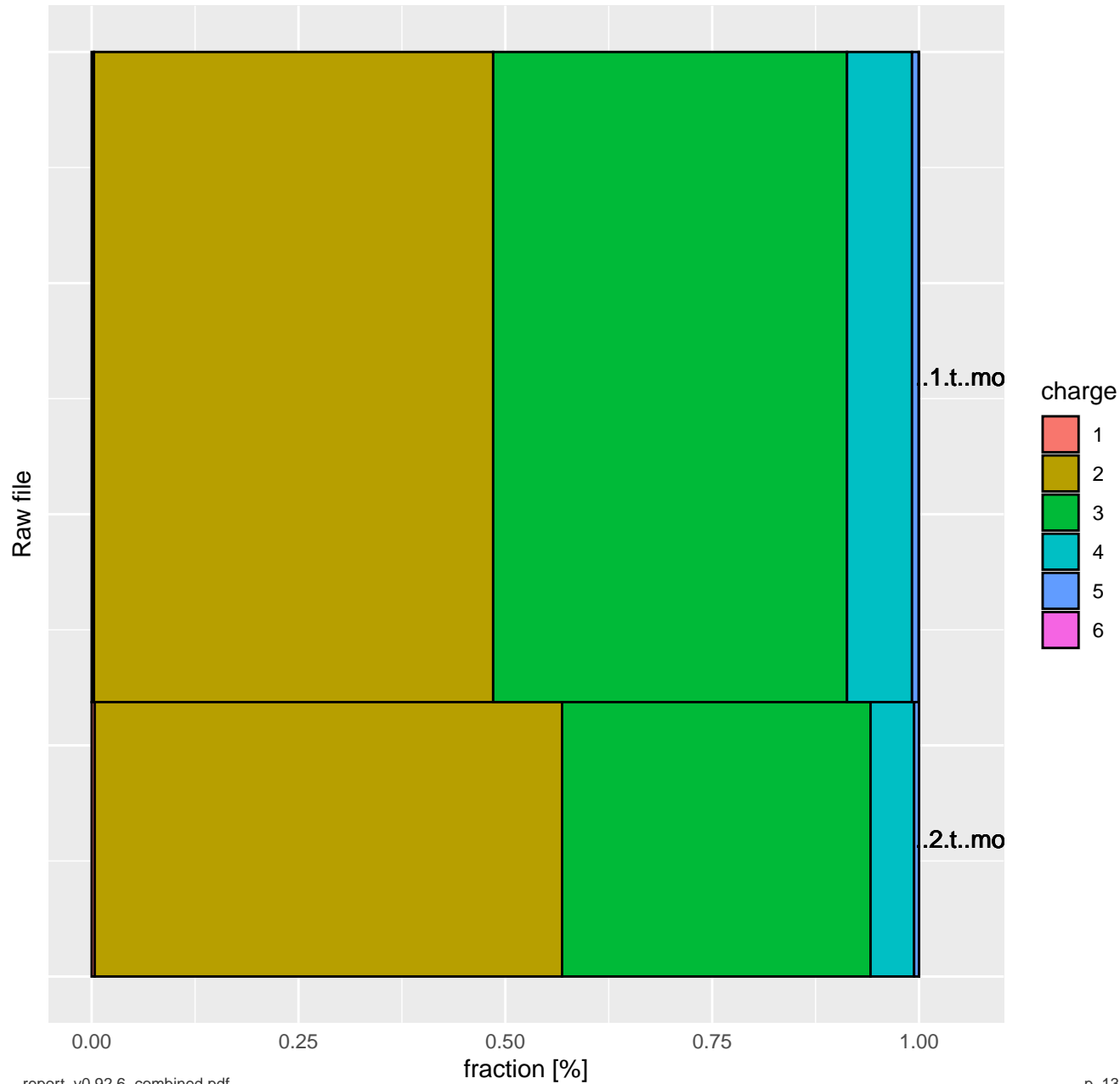


# MSMS: Missed cleavages per Raw file

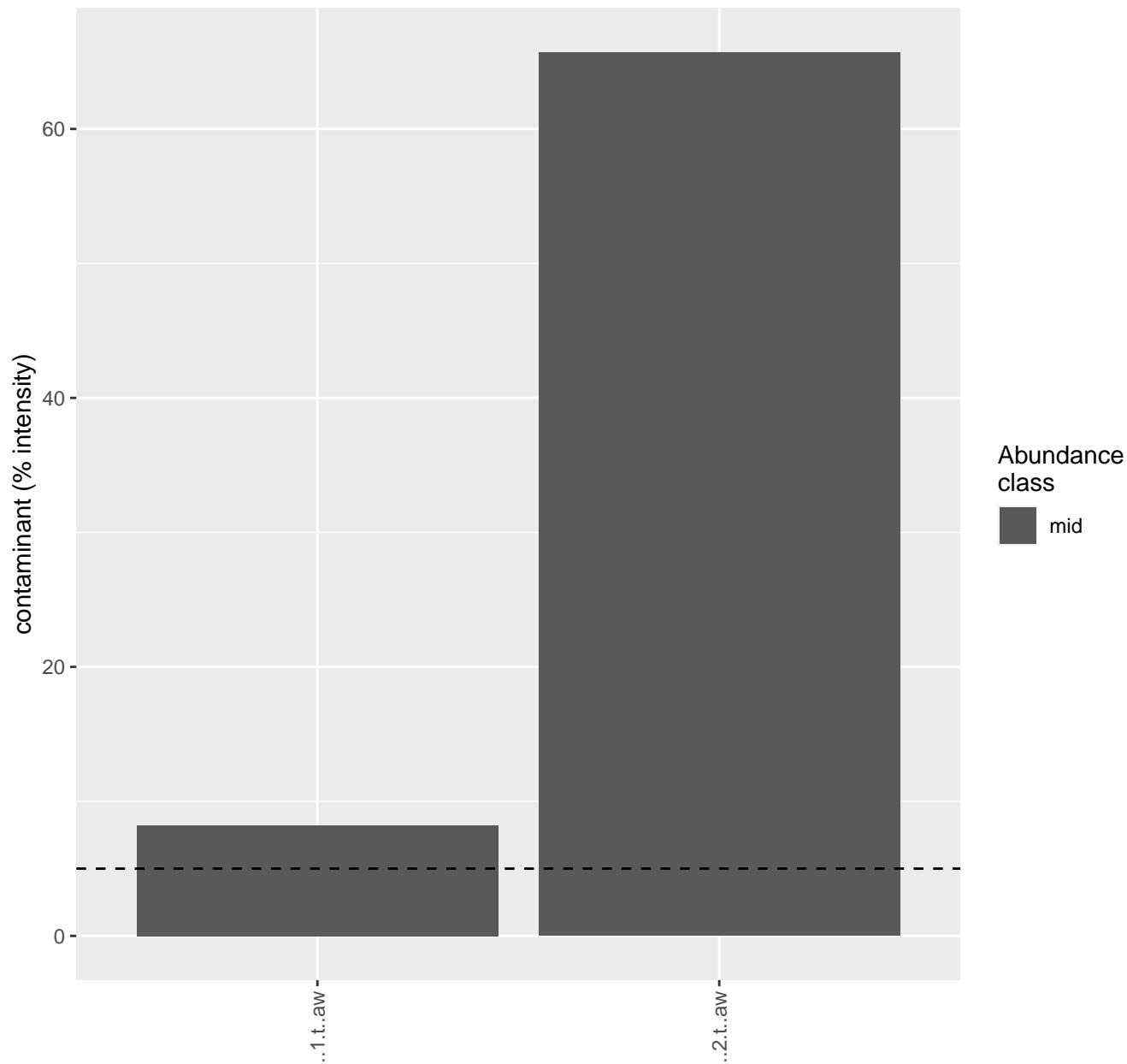
(excludes contaminants)



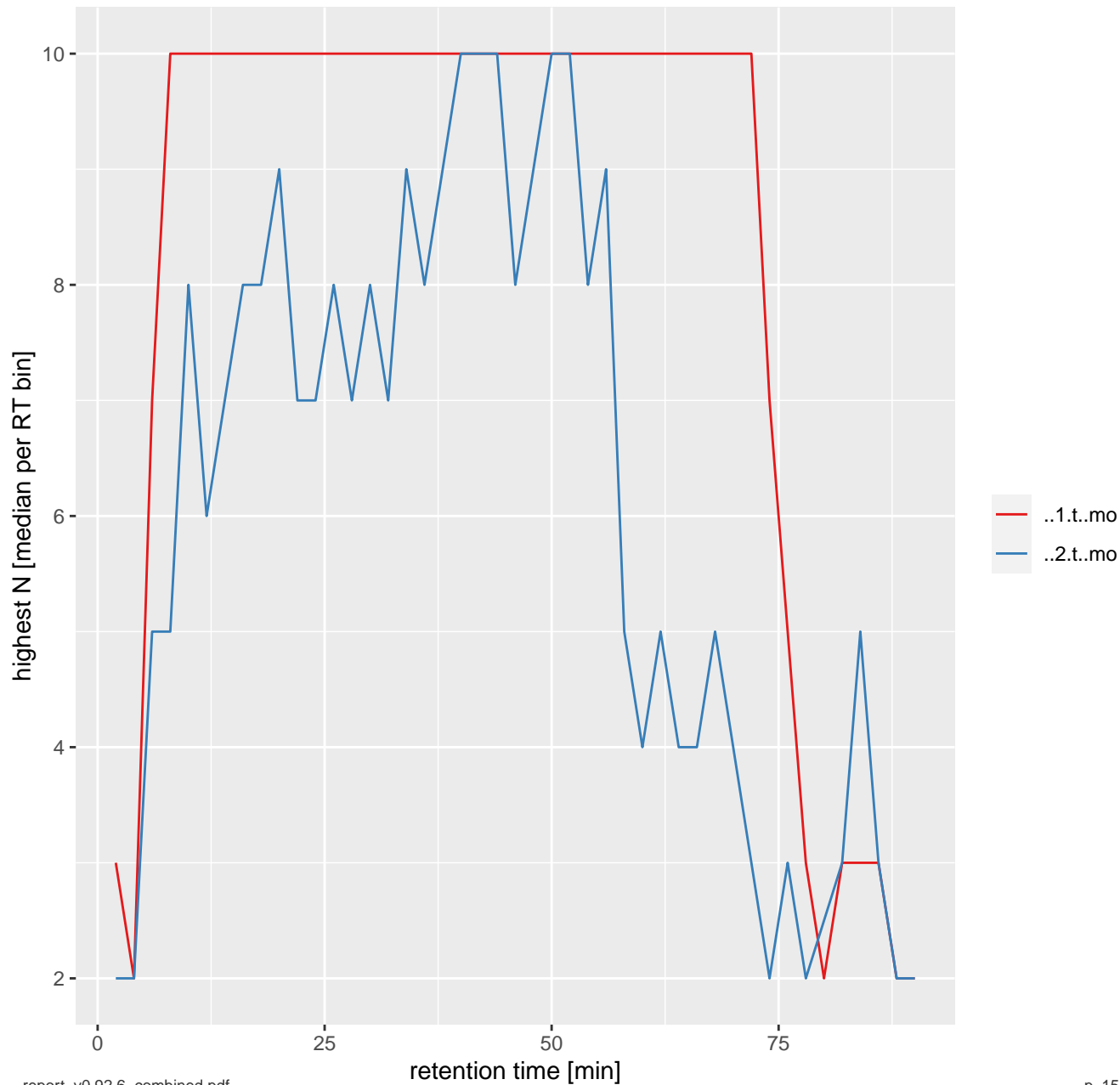
# EVD: charge distribution



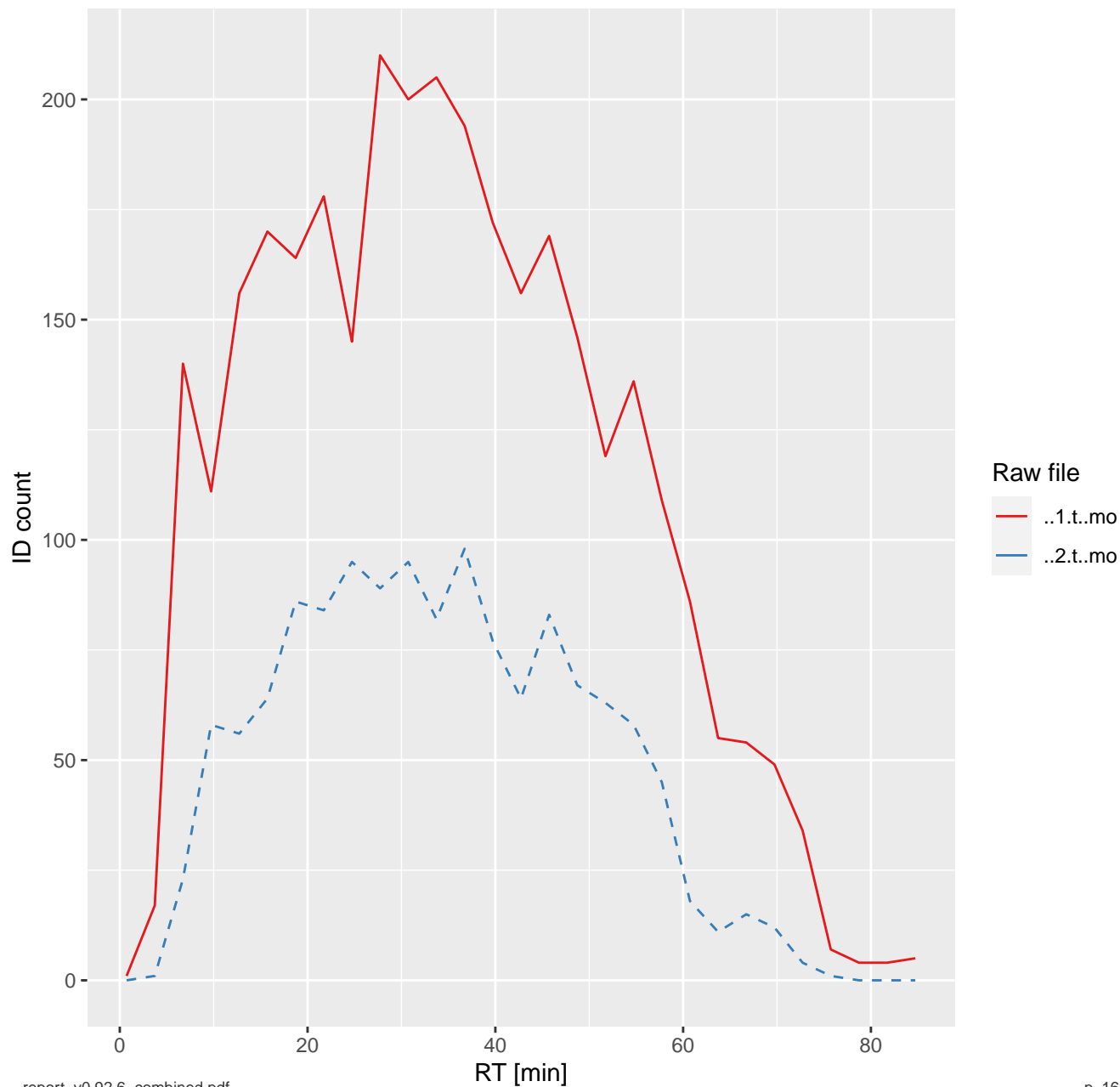
# PG: Contaminant per condition



# MSMSscans: TopN over RT

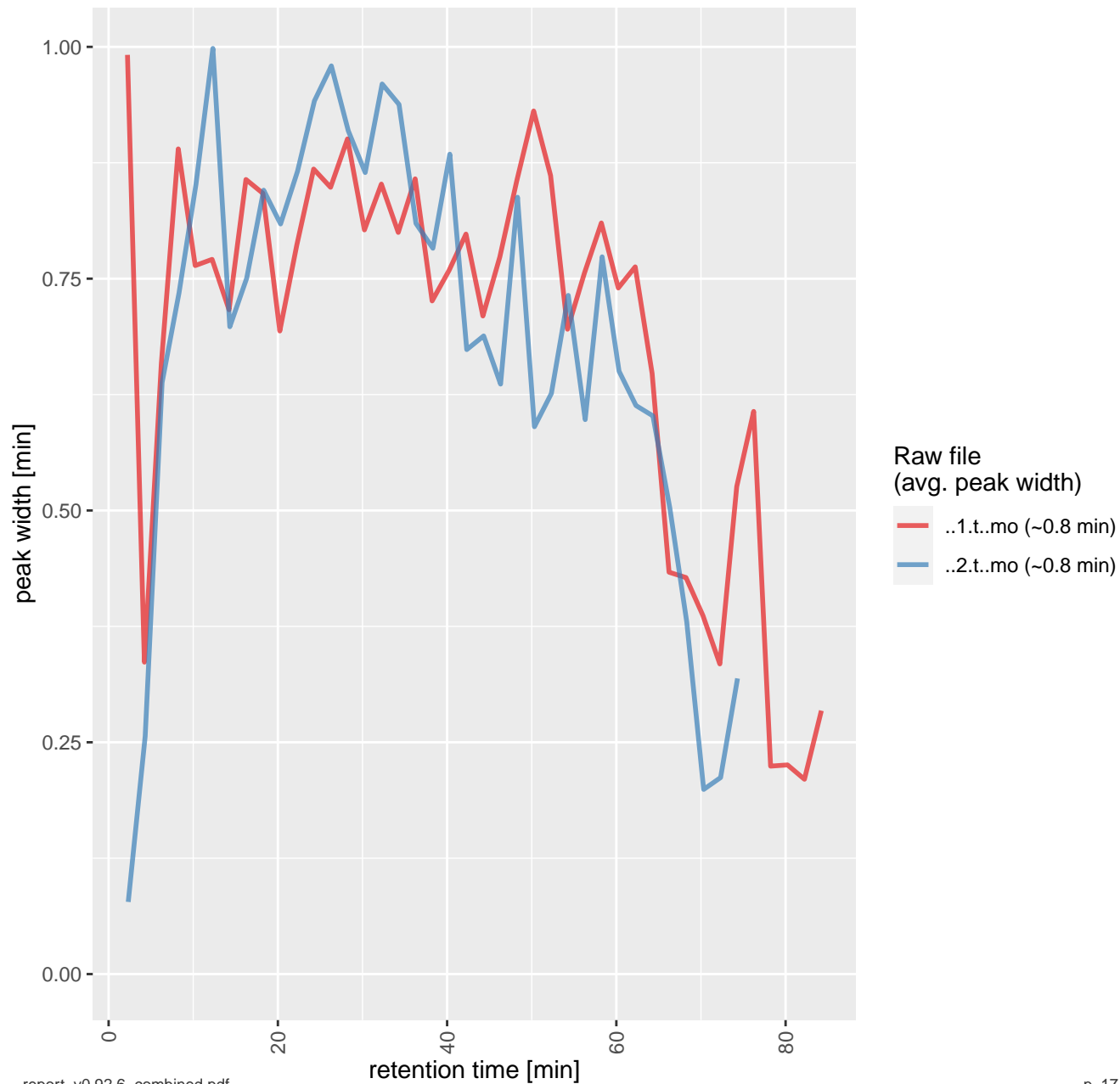


# EVD: IDs over RT

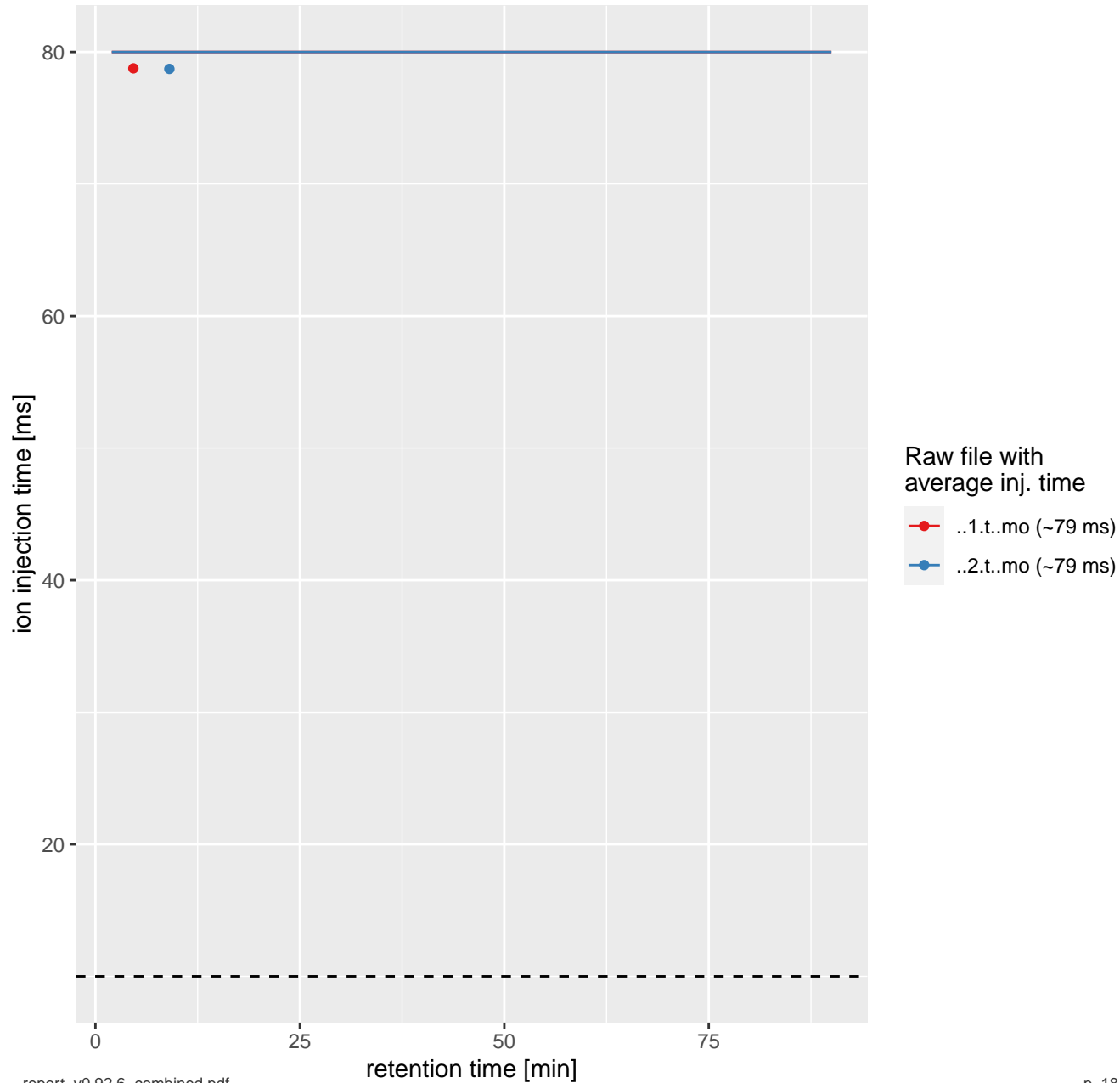




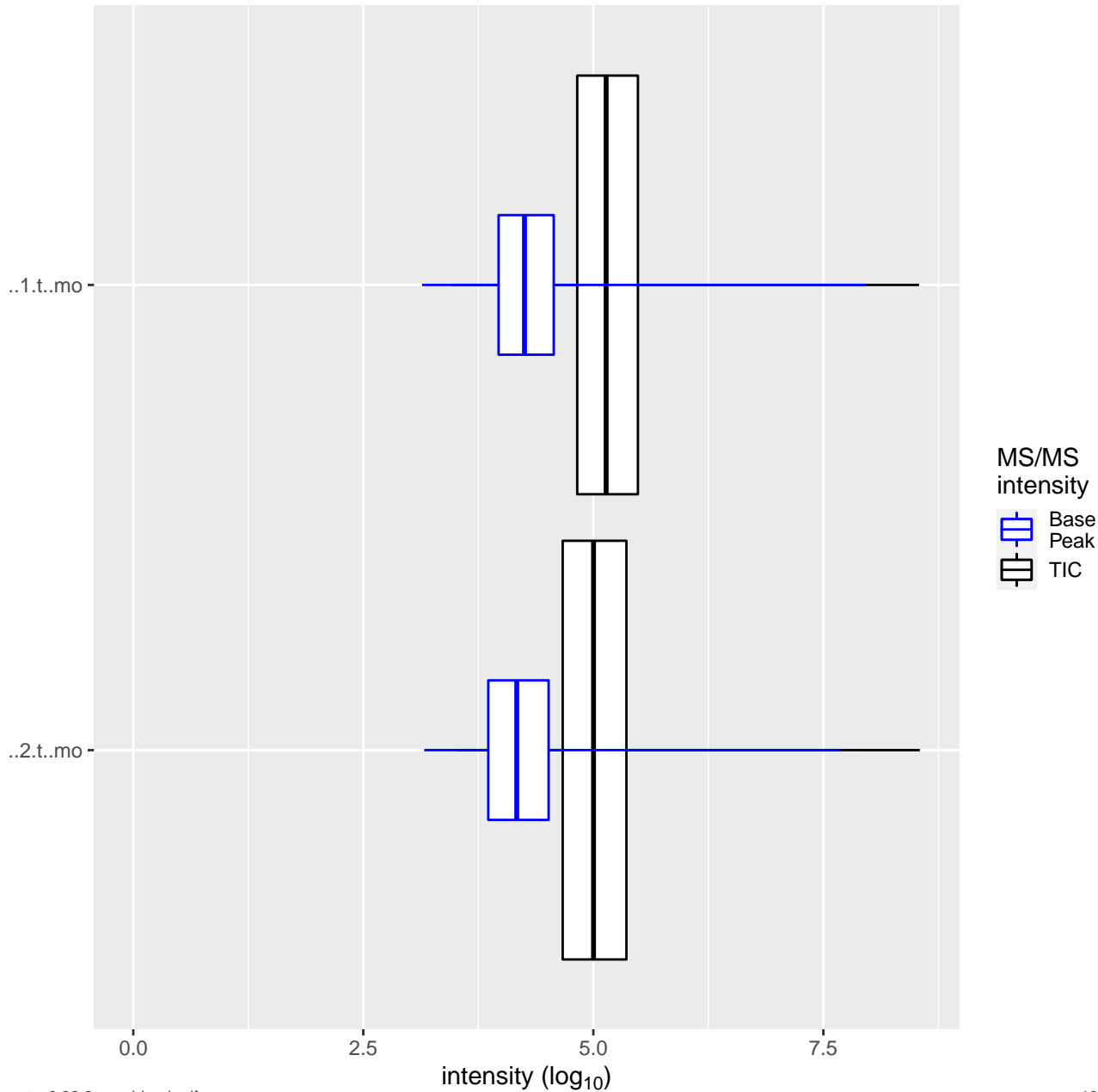
# EVD: Peak width over RT



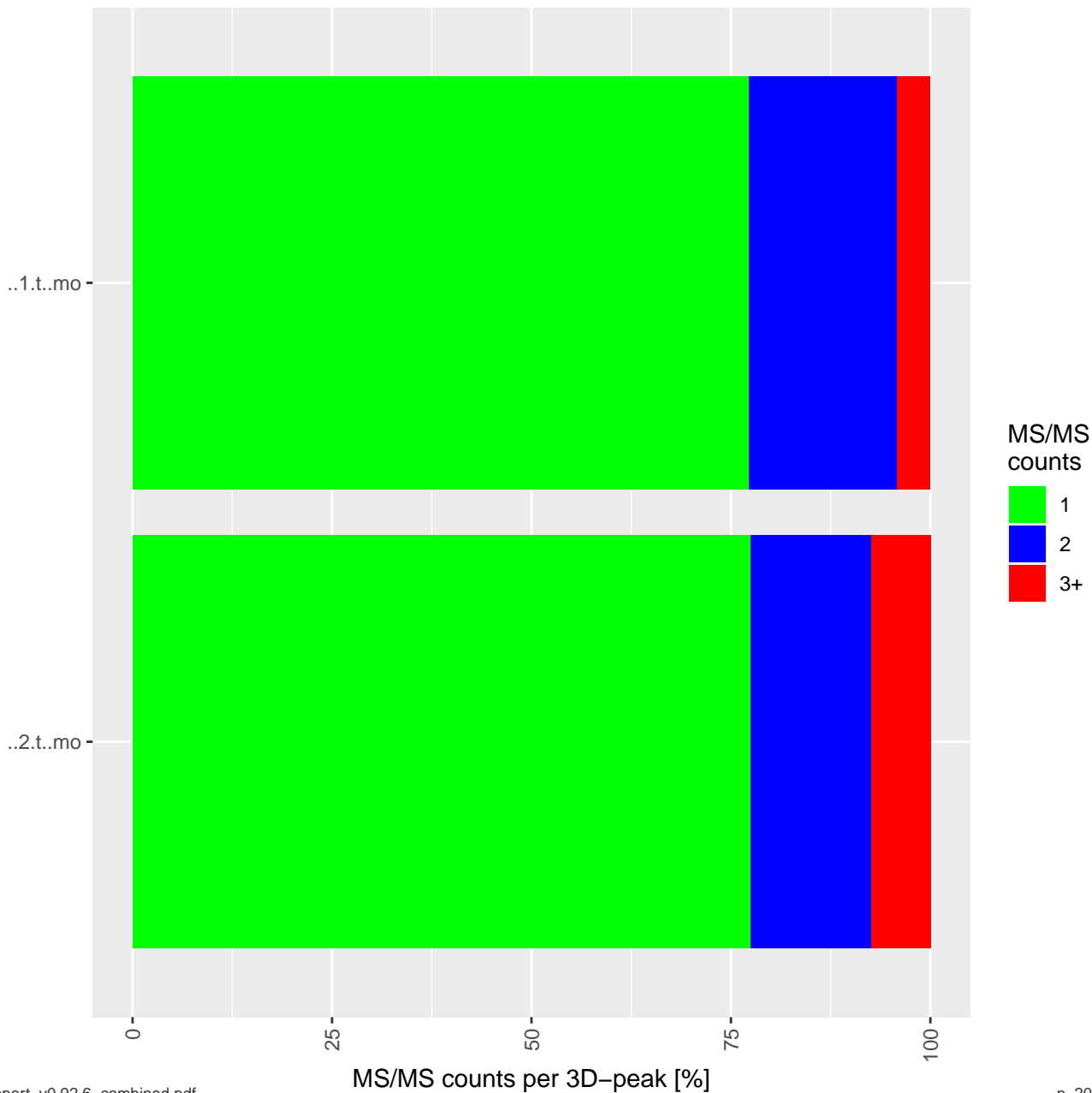
# MSMSscans: Ion Injection Time over RT



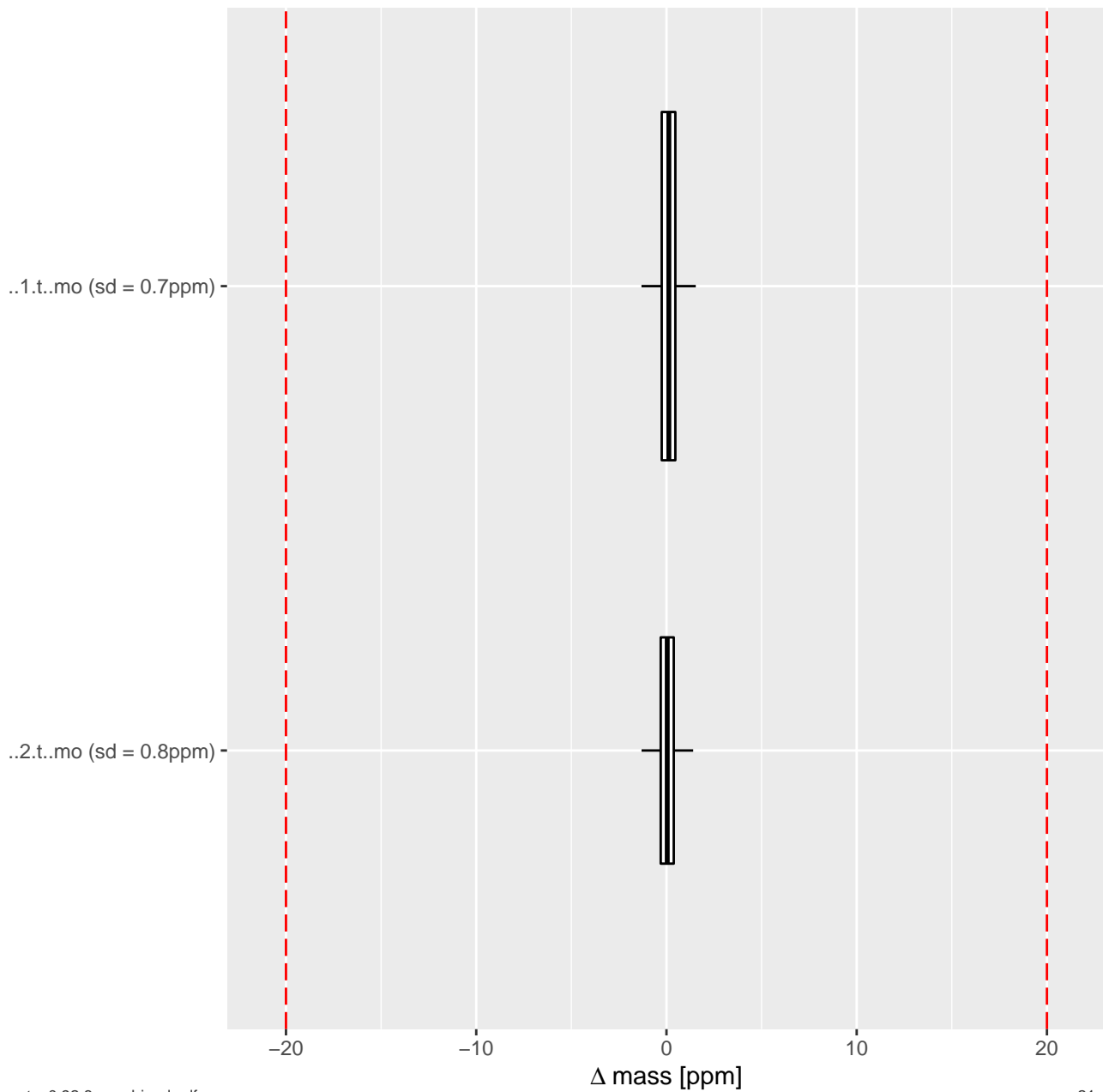
# [experimental] MSMSscans: MS/MS intensity



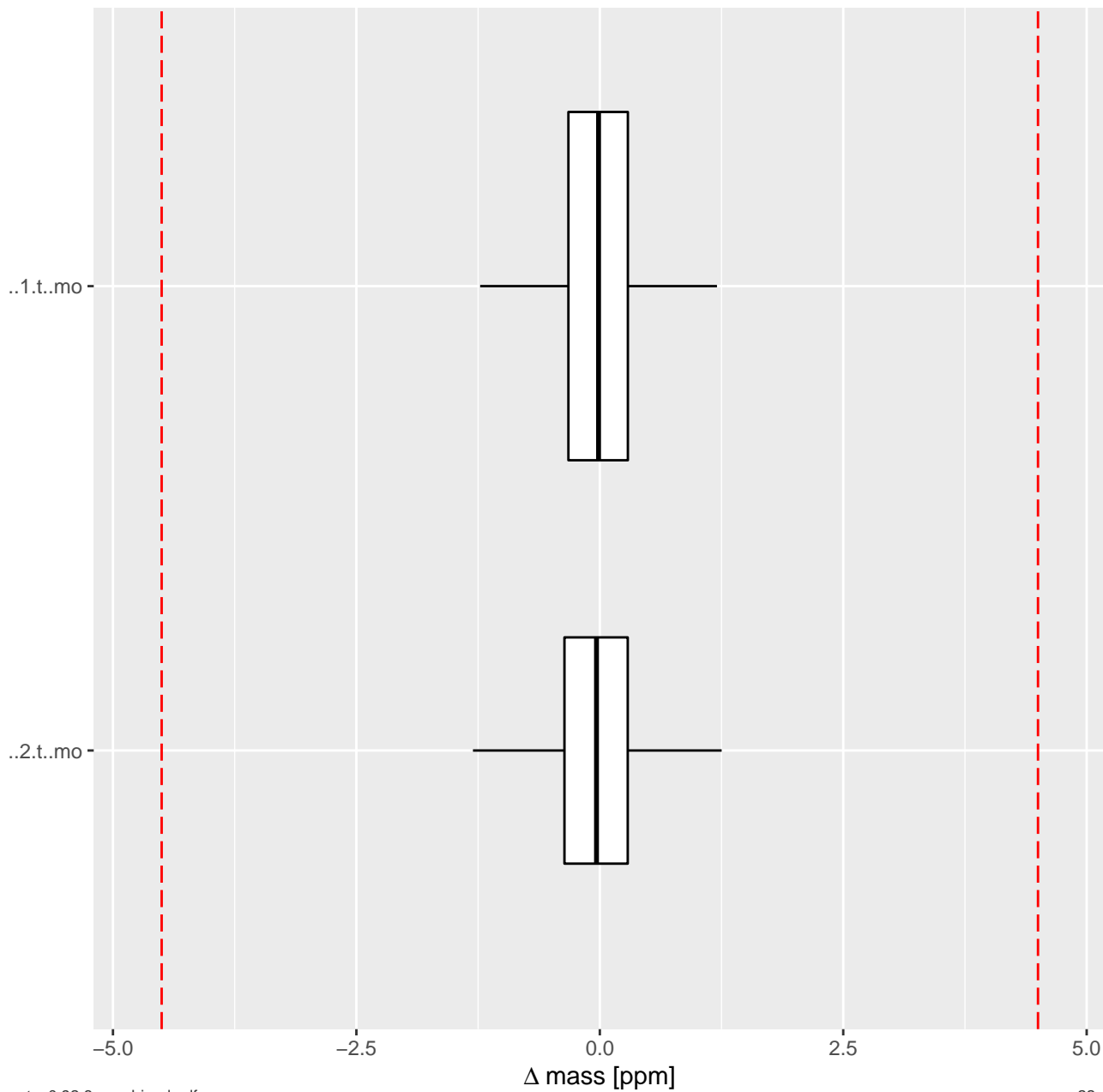
# EVD: Oversampling (MS/MS counts per 3D-peak)



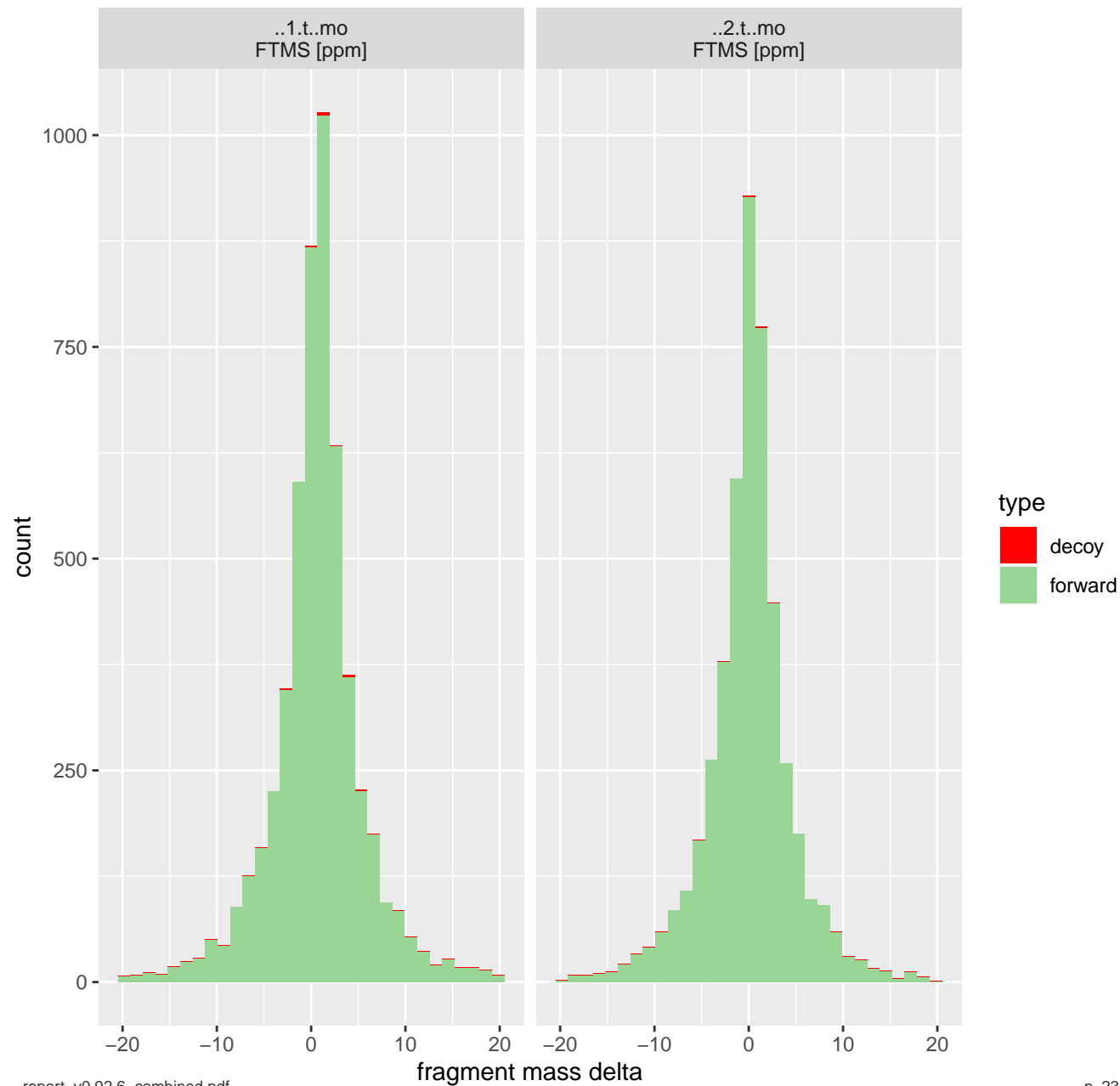
# EVD: Uncalibrated mass error



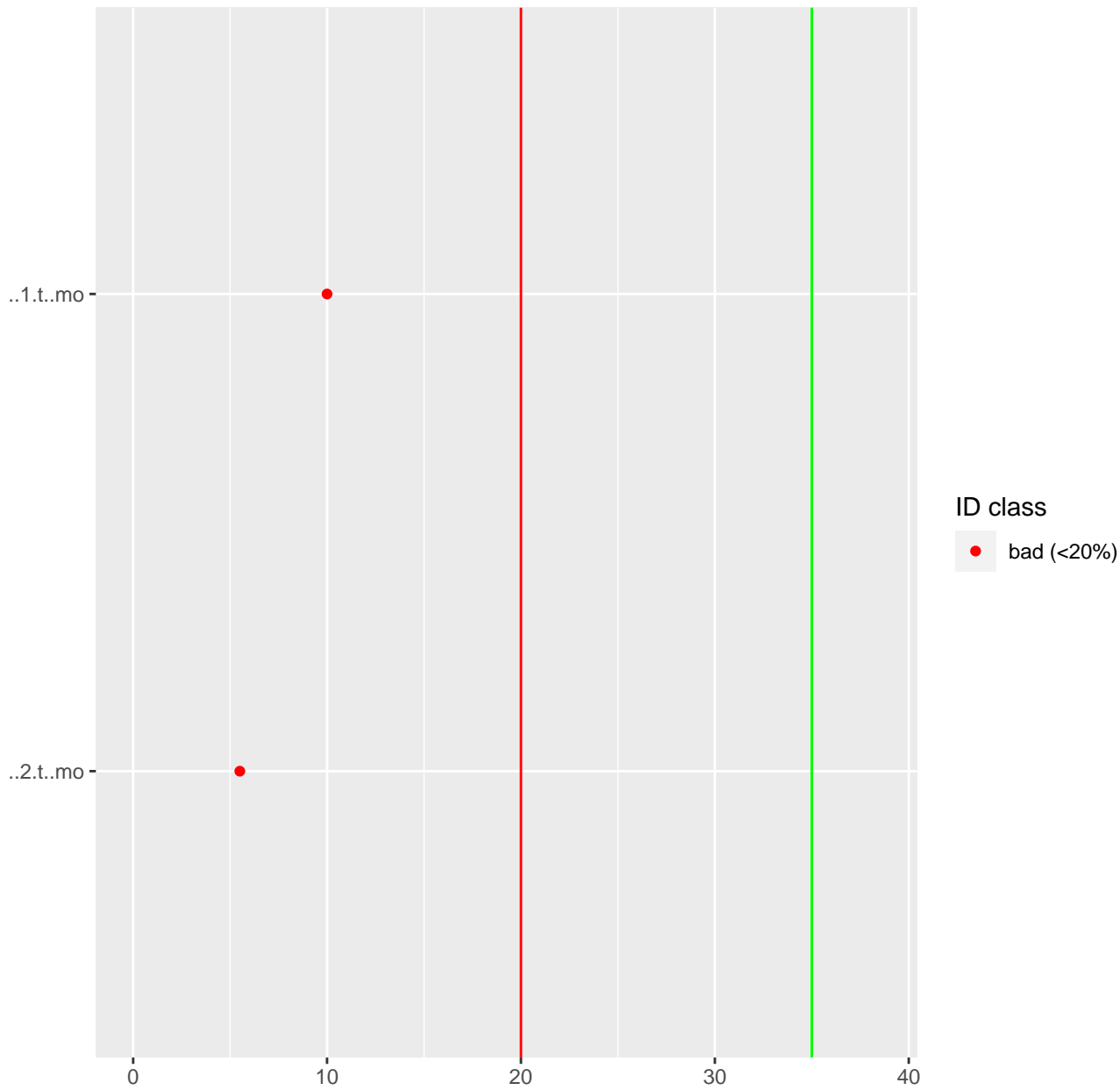
# EVD: Calibrated mass error



# MSMS: Fragment mass errors per Raw file



# SM: MS/MS identified per Raw file



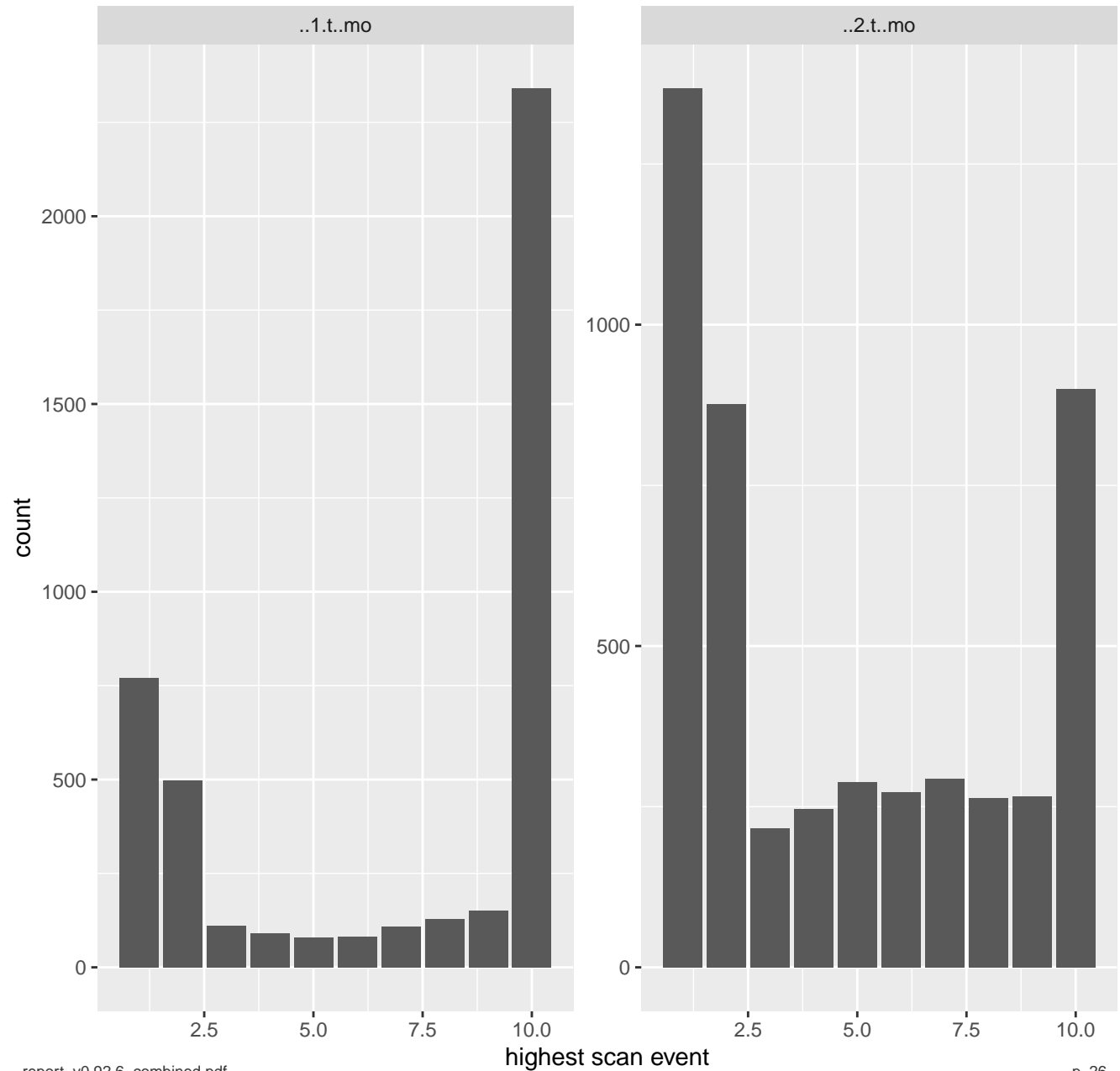


## SM: Files with 'red' ID rate

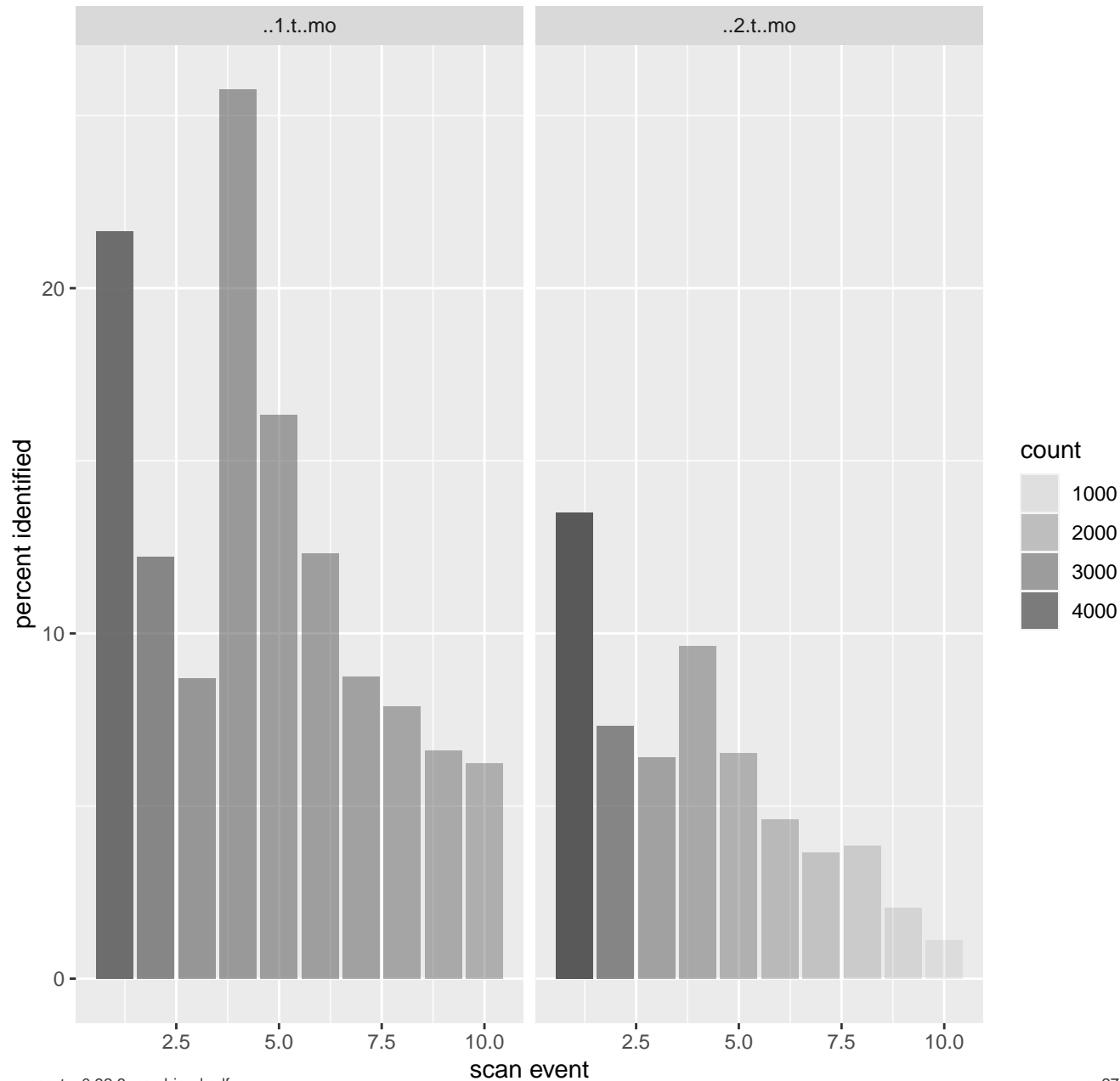
Raw file	% identified
sample1.thermo	10.0
sample2.thermo	5.5

100% of samples)

# MSMSscans: TopN

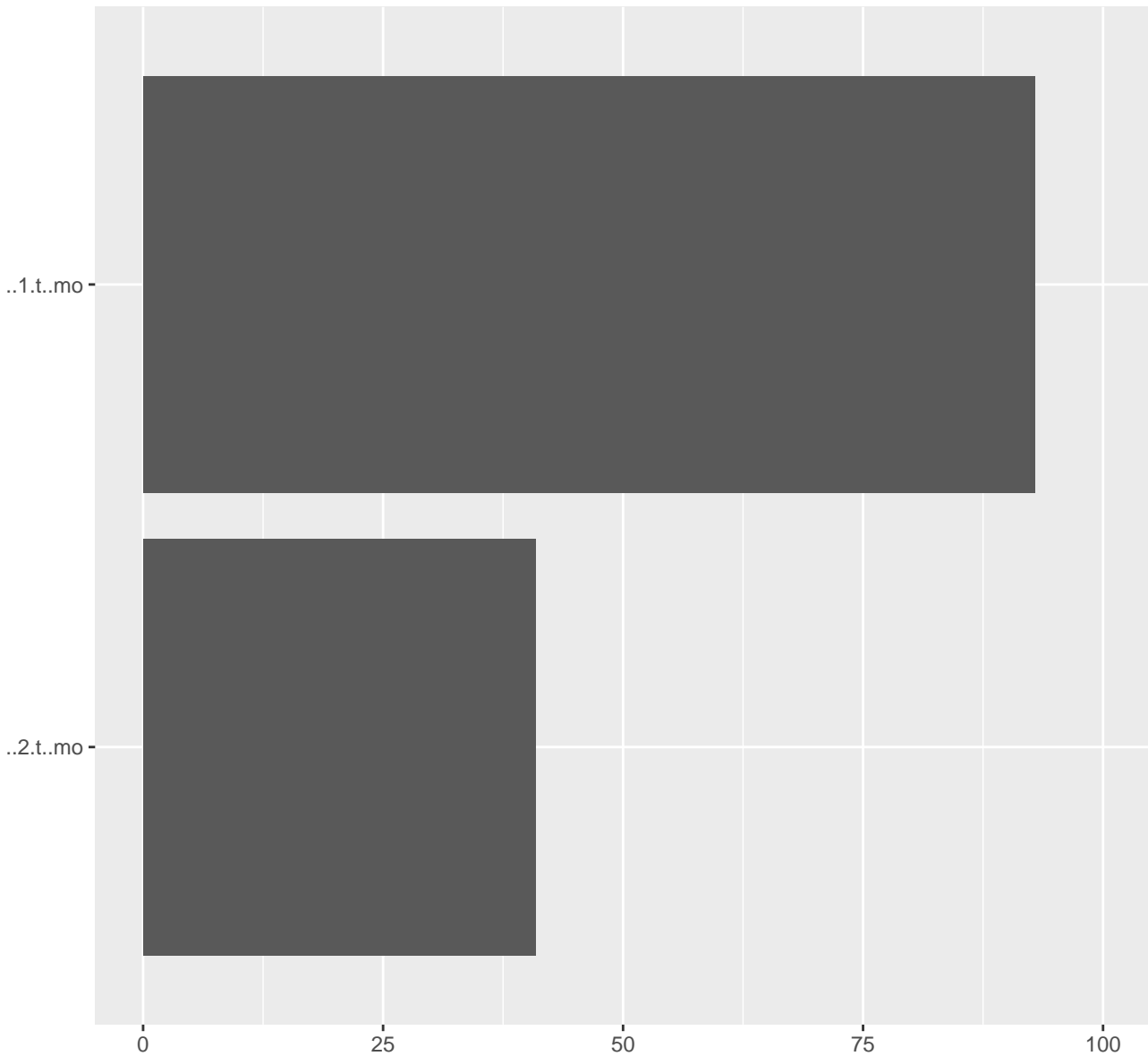


# MSMSscans: TopN % identified over N

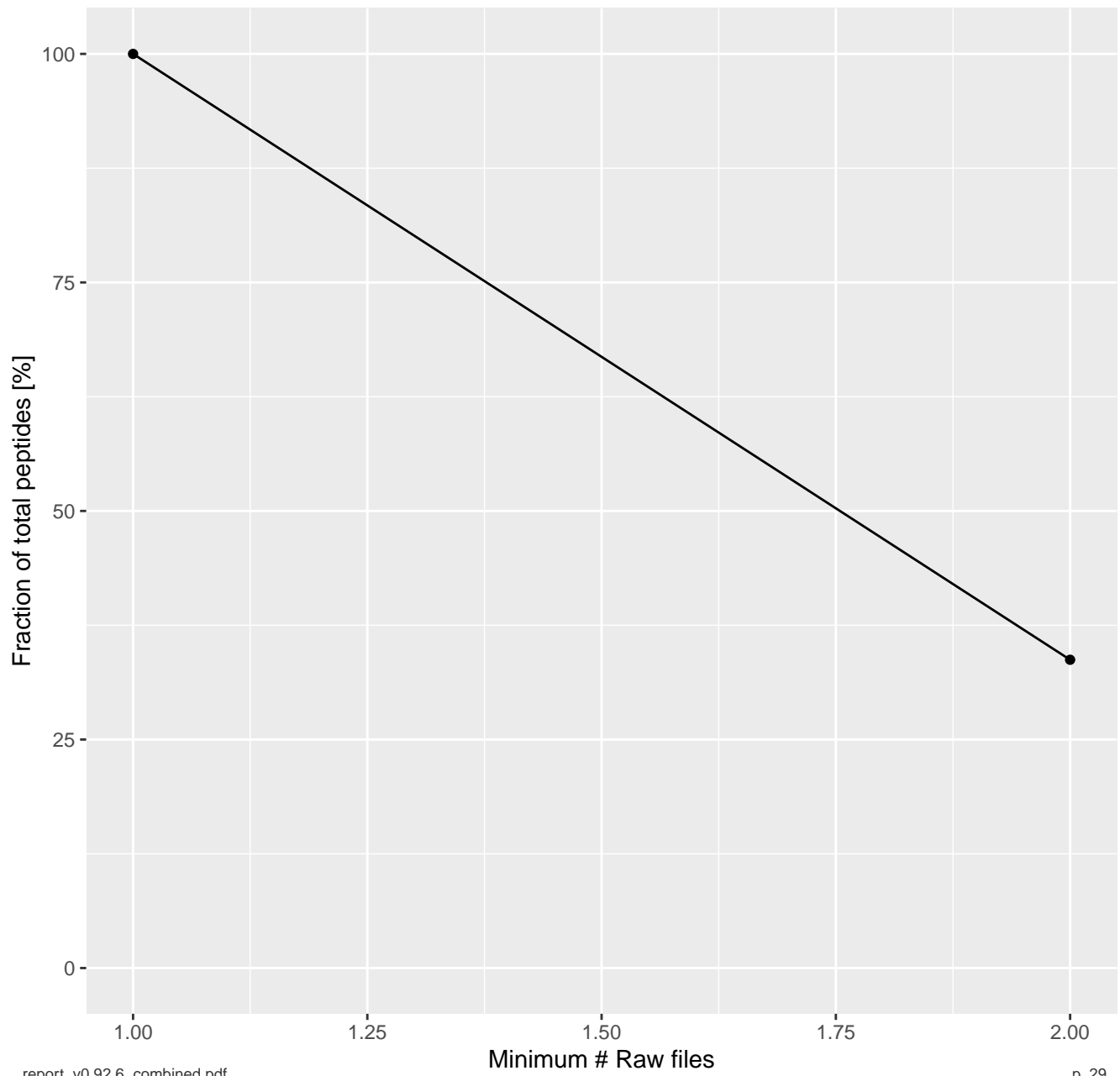


# [experimental] EVD: Non-Missing Peptides

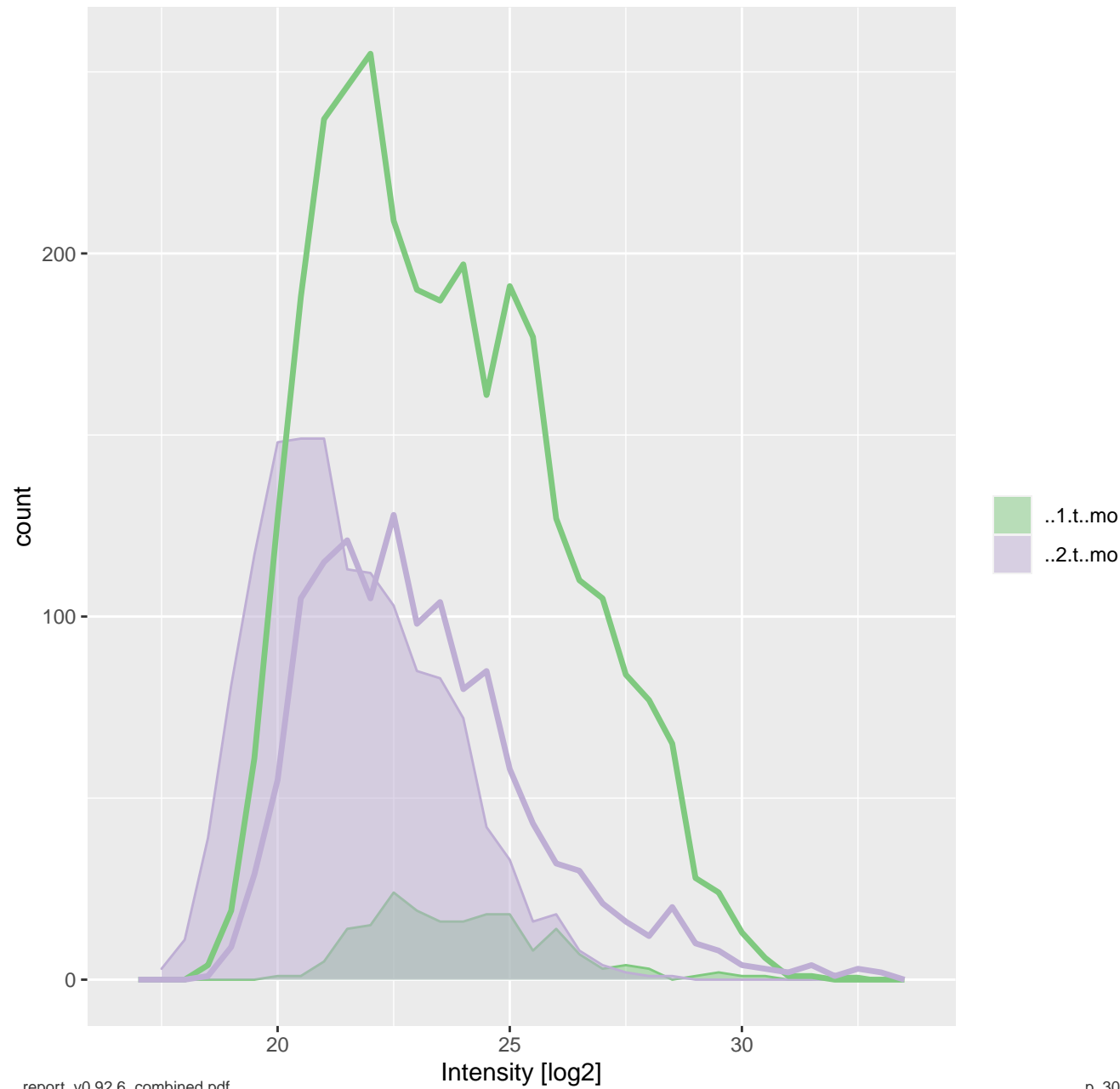
compared to all peptides seen in experiment



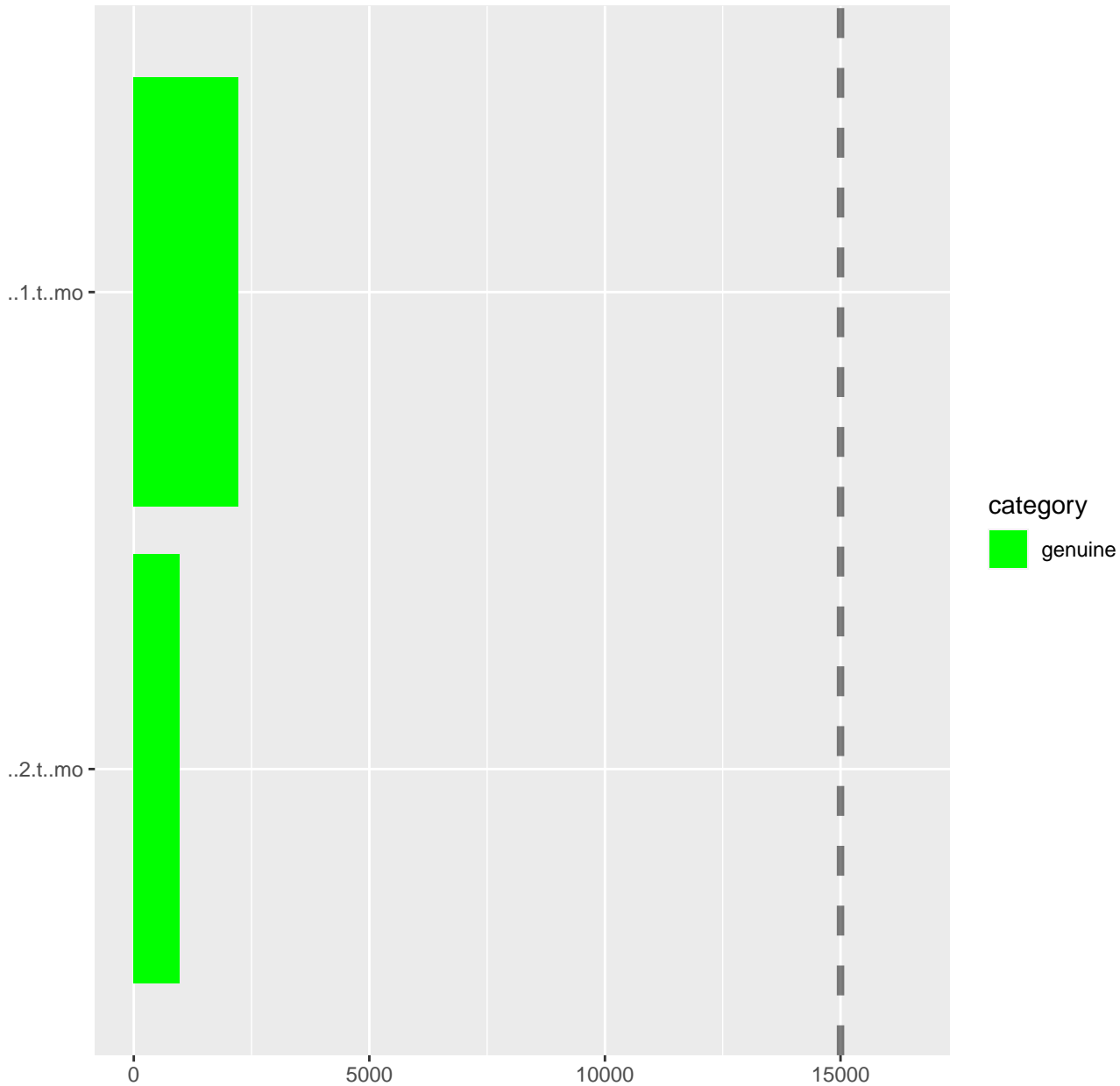
# [experimental] EVD: Non-missing by set



# [experimental] EVD: Imputed Peptide Intensity Distribution of Missing Values



# EVD: Peptide ID count



# EVD: ProteinGroups count

