

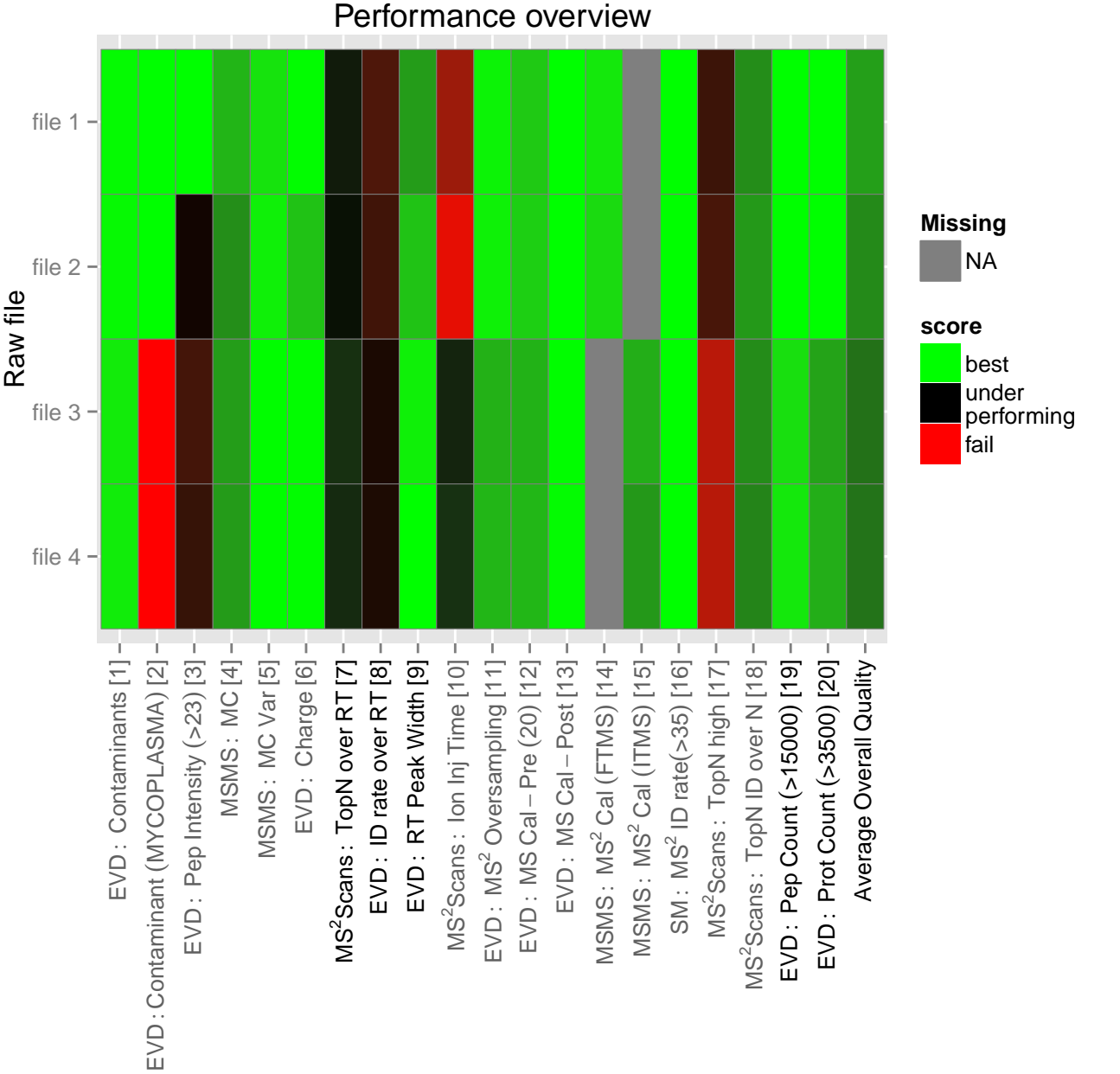
# PAR: parameters

Version	1.5.2.8	Min. peptide Length	7
User name	cbielow	Min. score for unmodified pe..	0
Machine name	CD02-WIN7	Min. score for modified pept..	40
Date of writing	08/10/2015 18:04:34	Min. delta score for unmodif..	0
Fixed modifications	Carbamidomethyl (C)	Min. delta score for modifie..	6
Decoy mode	revert	Min. unique peptides	0
Special AAs	KR	Min. razor peptides	1
Include contaminants	True	Min. peptides	1
MS/MS tol. (FTMS)	20 ppm	Use only unmodified peptides..	True
Top MS/MS peaks per 100 Da. ..	12	Modifications included in pr..	Acetyl (Protein N-term) Oxidation (M)
MS/MS deisotoping (FTMS)	True	Peptides used for protein qu..	Razor
MS/MS tol. (ITMS)	0.5 Da	Discard unmodified counterpa..	True
Top MS/MS peaks per 100 Da. ..	8	Min. ratio count	2
MS/MS deisotoping (ITMS)	False	Re-quantify	False
MS/MS tol. (TOF)	40 ppm	Use delta score	False
Top MS/MS peaks per 100 Da. ..	10	iBAQ	False
MS/MS deisotoping (TOF)	True	iBAQ log fit	False
MS/MS tol. (Unknown)	0.5 Da	Match between runs	False
Top MS/MS peaks per 100 Da. ..	8	Find dependent peptides	False
MS/MS deisotoping (Unknown)	False	Labeled amino acid filtering	True
PSM FDR	0.01	Site tables	Oxidation (M)Sites.txt
Protein FDR	0.01	RT shift	False
Site FDR	0.01	Advanced ratios	True
Use Normalized Ratios For Oc..	True	First pass AIF correlation	0.8

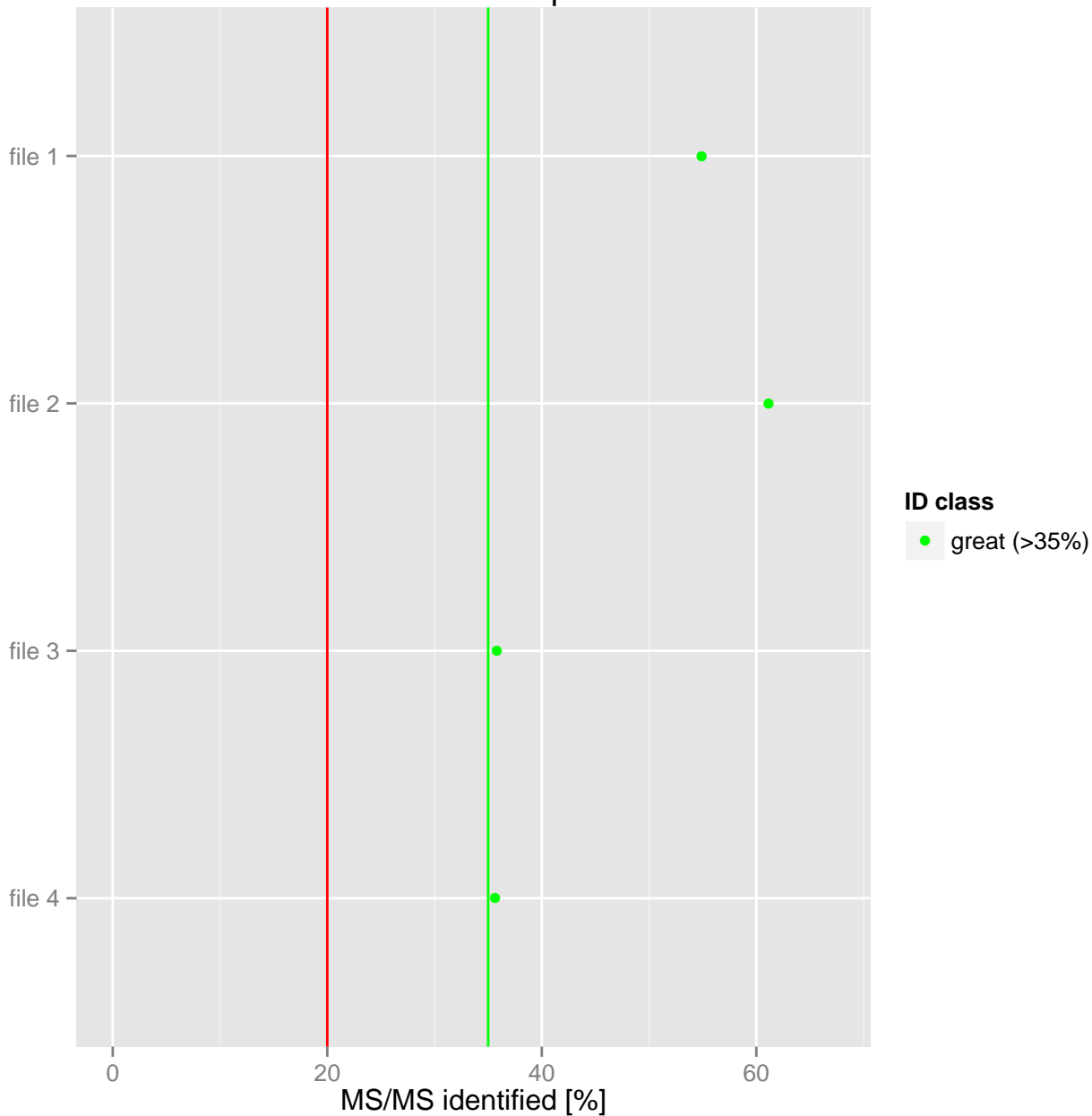
crap\_withMycoplasma.fasta  
uniprot\_human\_canonical\_and\_isoforms\_20130513.fasta

Mapping of Raw files to their short names  
Mapping source: automatic  
(automatic shortening of names was not sufficiently short – see 'best effort')

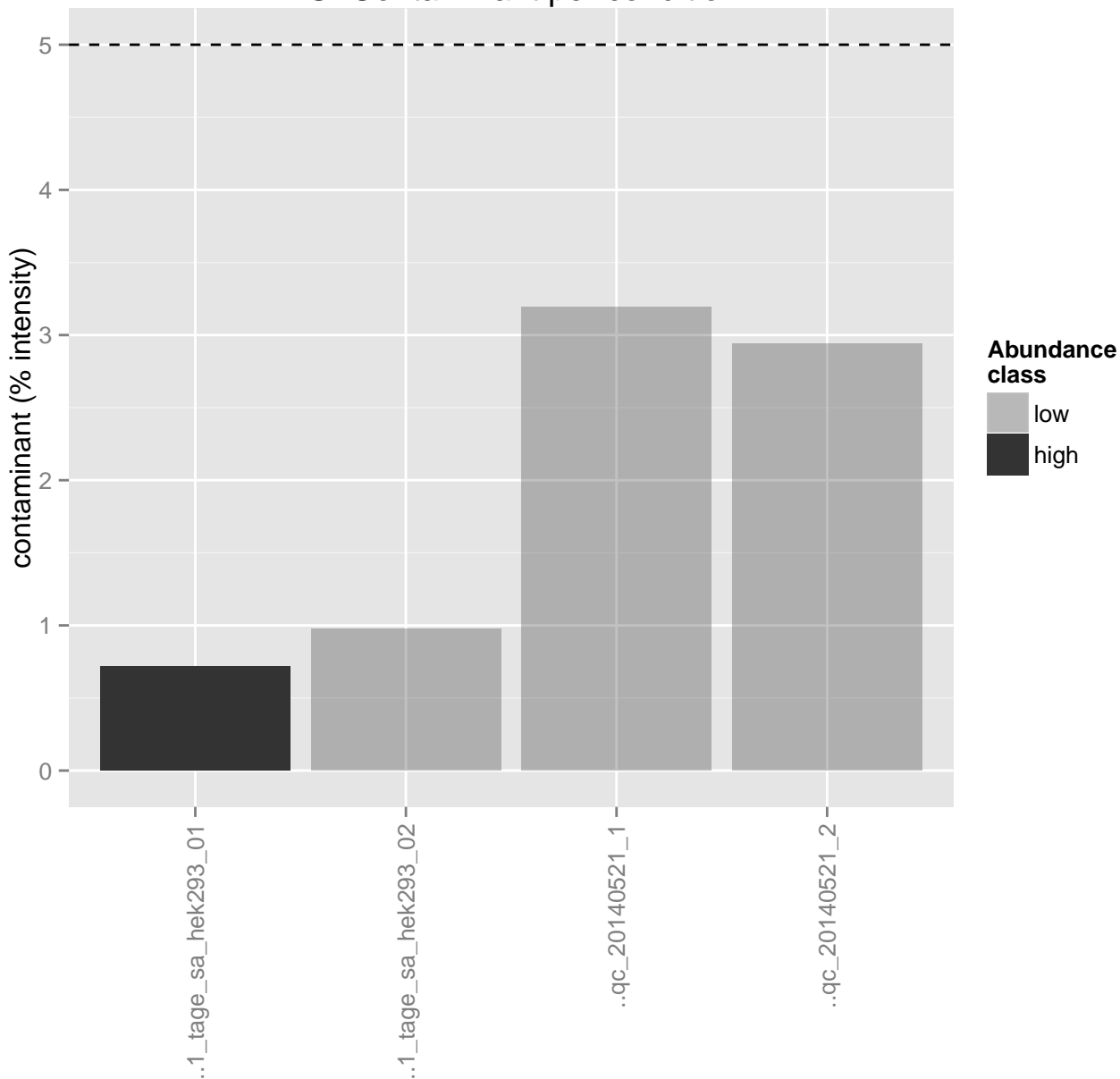
original	short name	best_effort
20101227_Velos1_TaGe_SA_HEK293_01	file 1	..20101227_Velos1_TaGe_SA_HEK293_01
20101227_Velos1_TaGe_SA_HEK293_02	file 2	..20101227_Velos1_TaGe_SA_HEK293_02
QC_20140521_1	file 3	..QC_20140521_1
QC_20140521_2	file 4	..QC_20140521_2



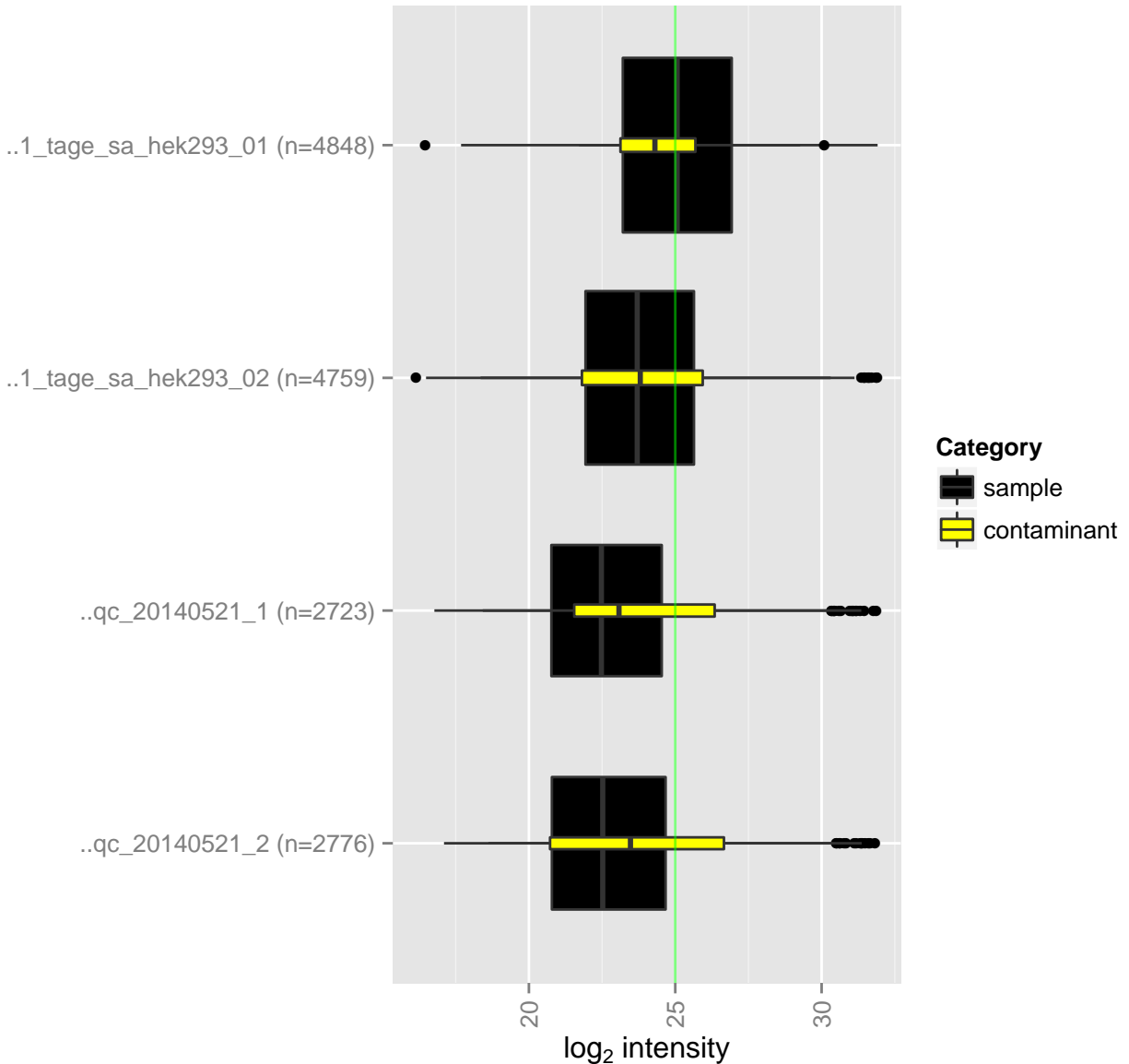
# SM: MS/MS identified per Raw file



## PG: Contaminant per condition

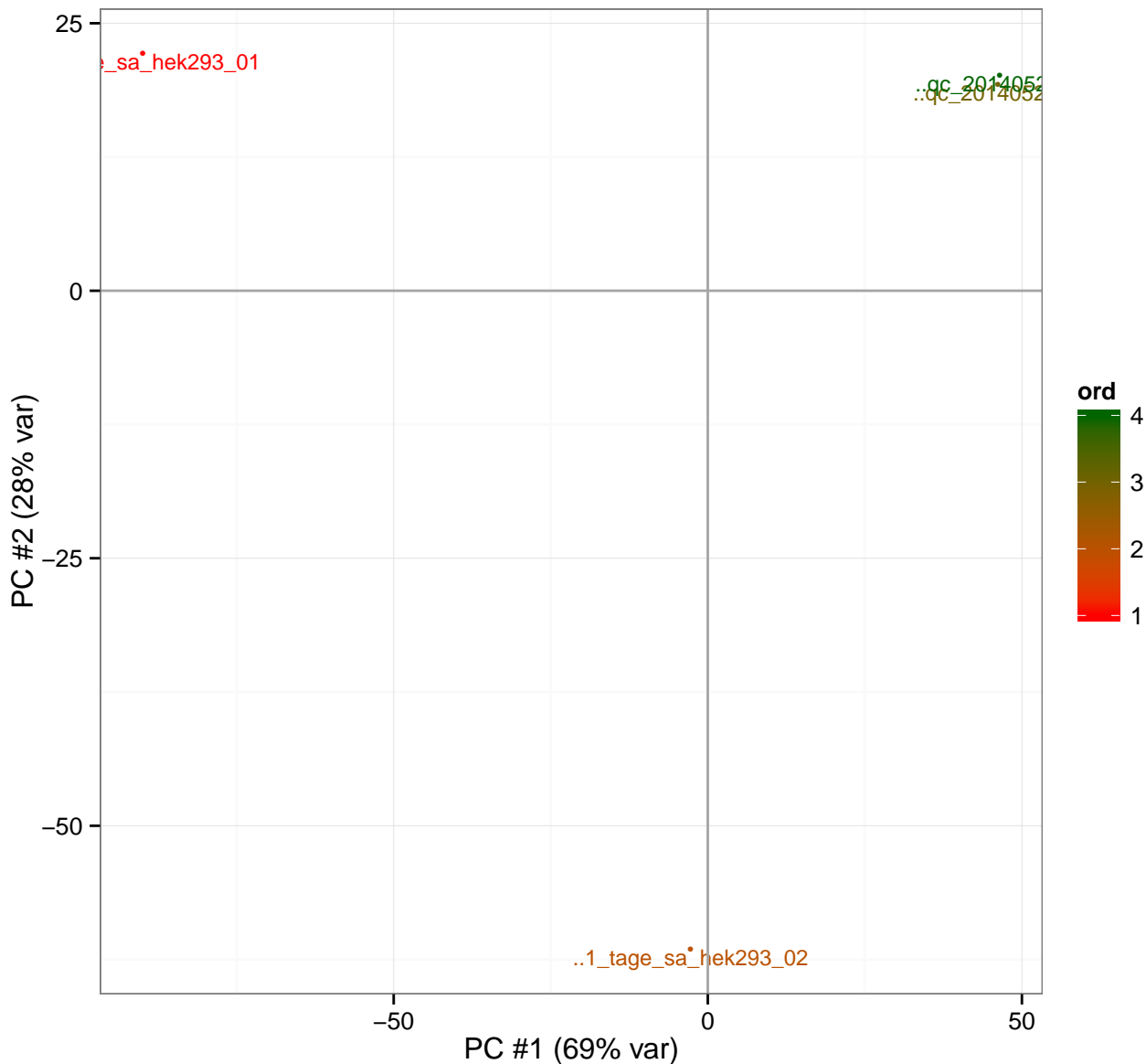


PG: intensity distribution  
RSD 5.2% (w/o zero mt.; expected < 5%)  
RSD 115.6% [high RSD --> few peptides]

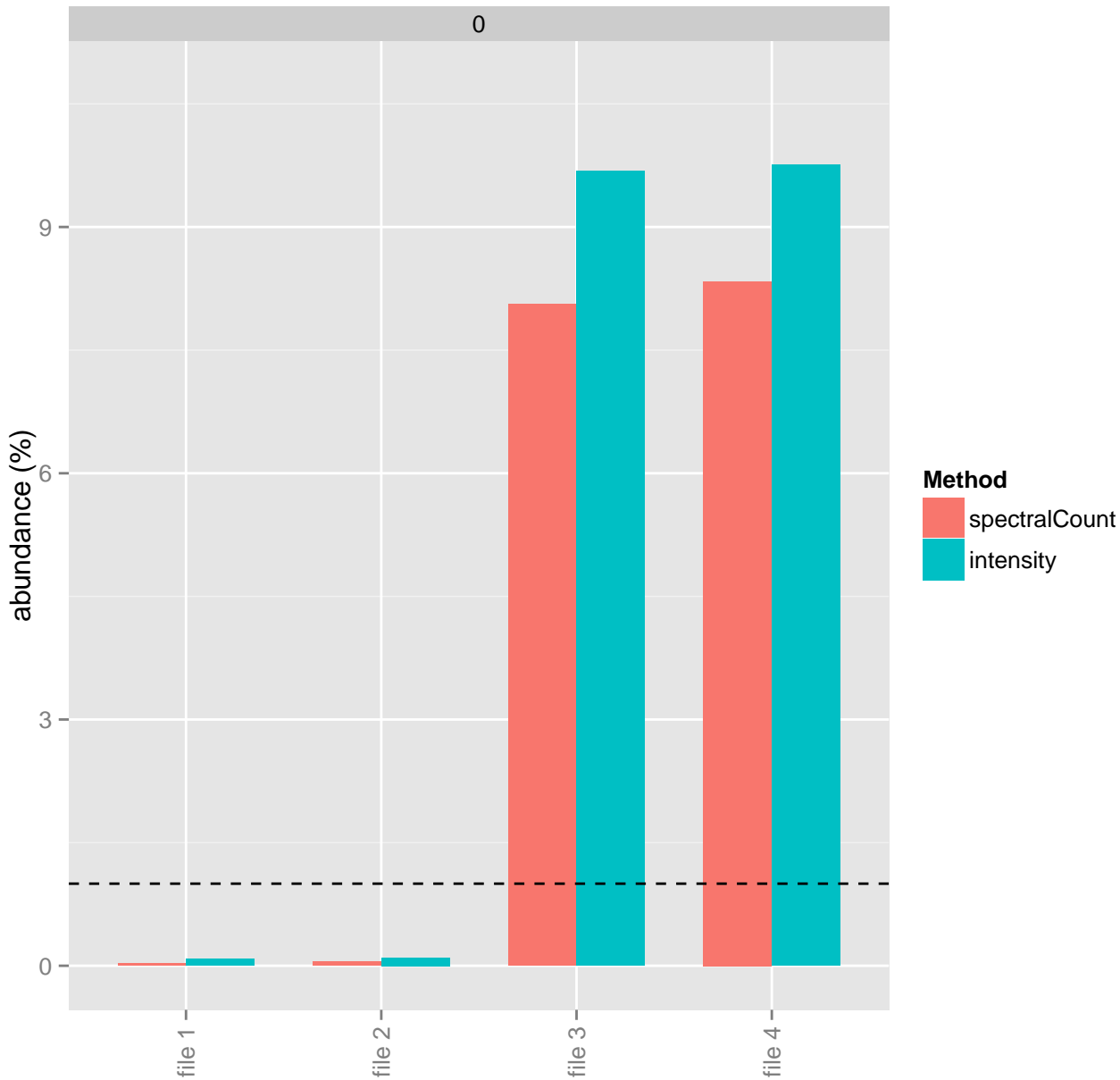


# PG: PCA of 'raw intensity'

(excludes contaminants)



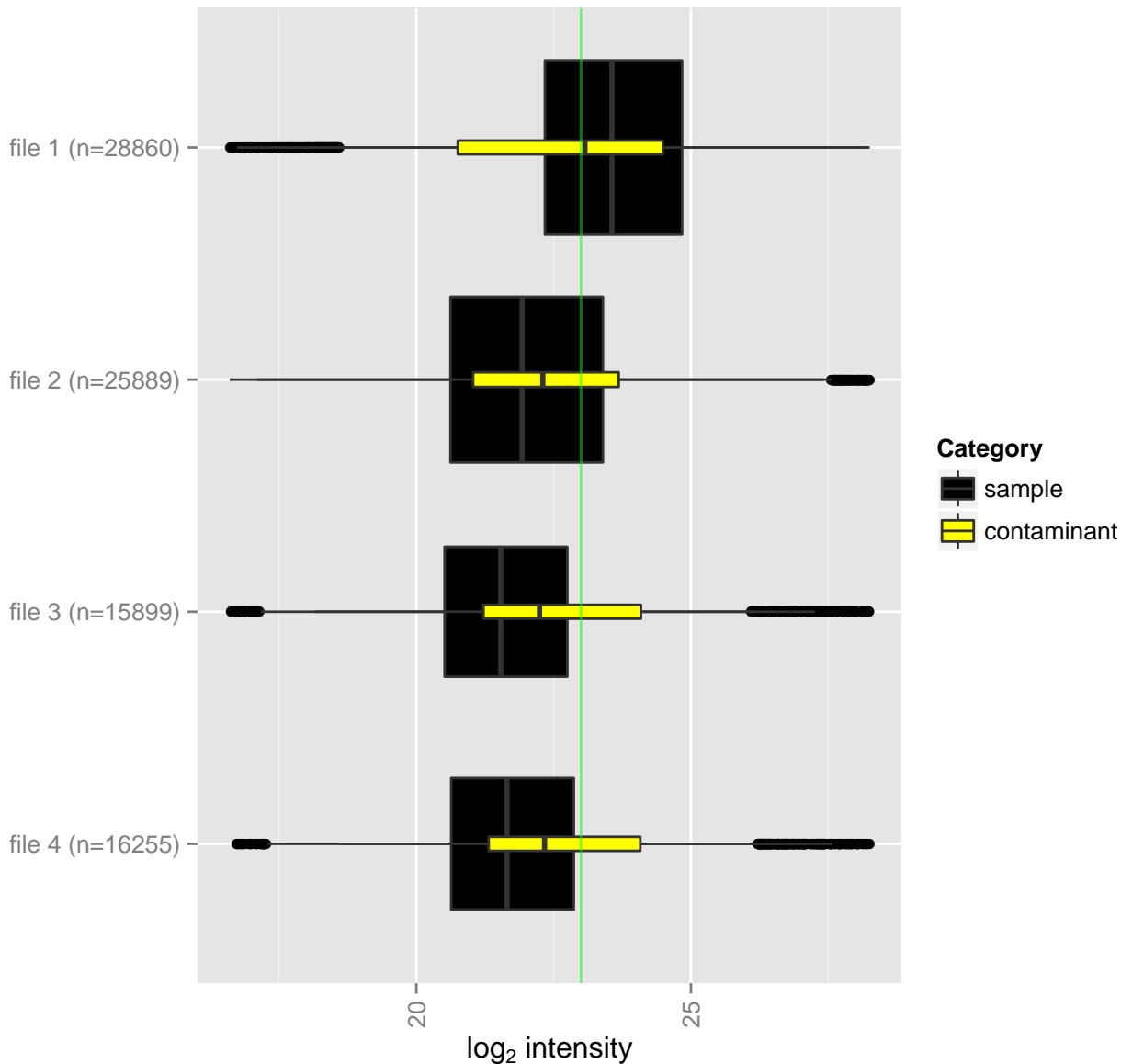
## EVD: Contaminant 'MYCOPLASMA'



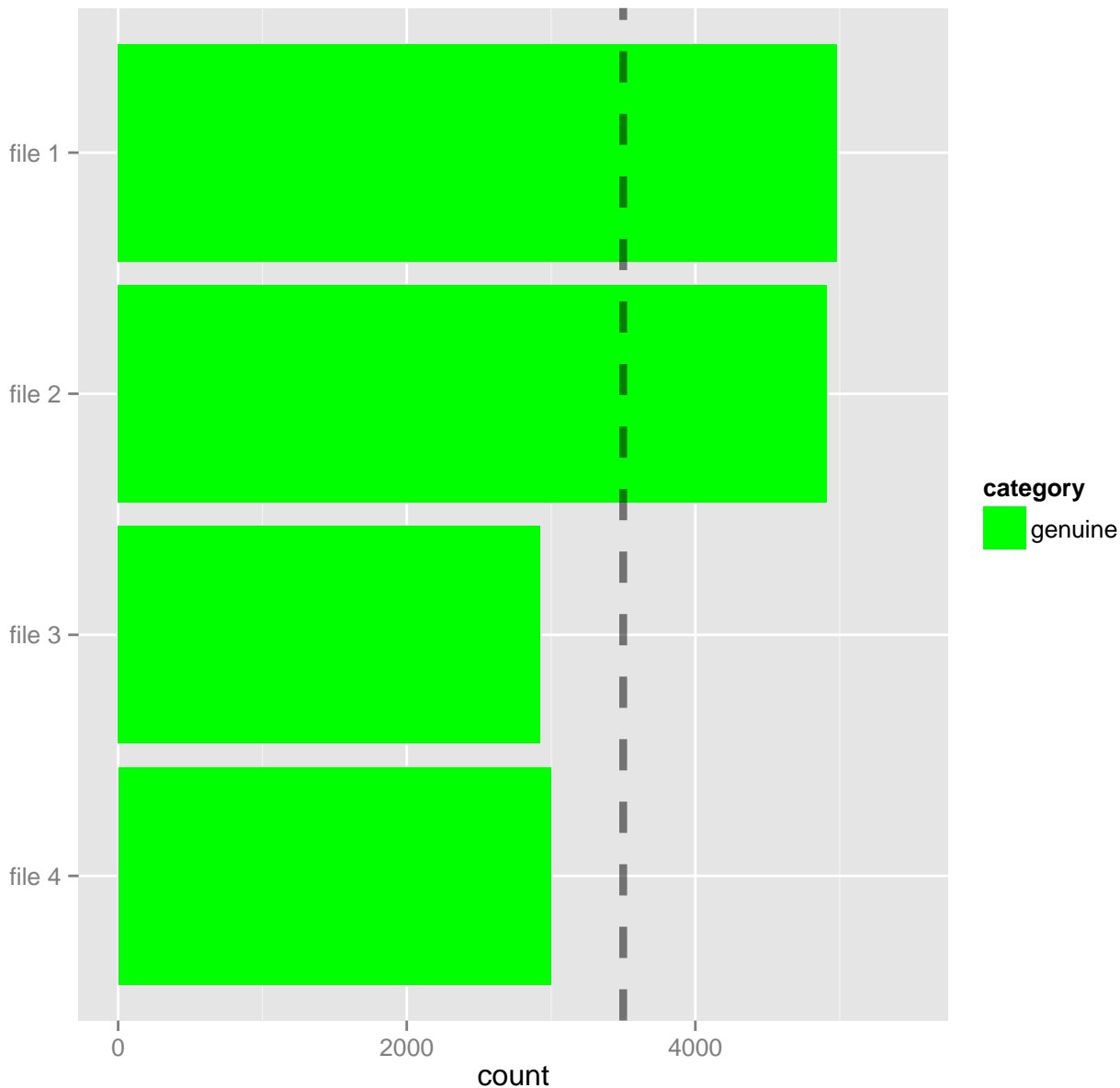


# EVD: peptide intensity distribution

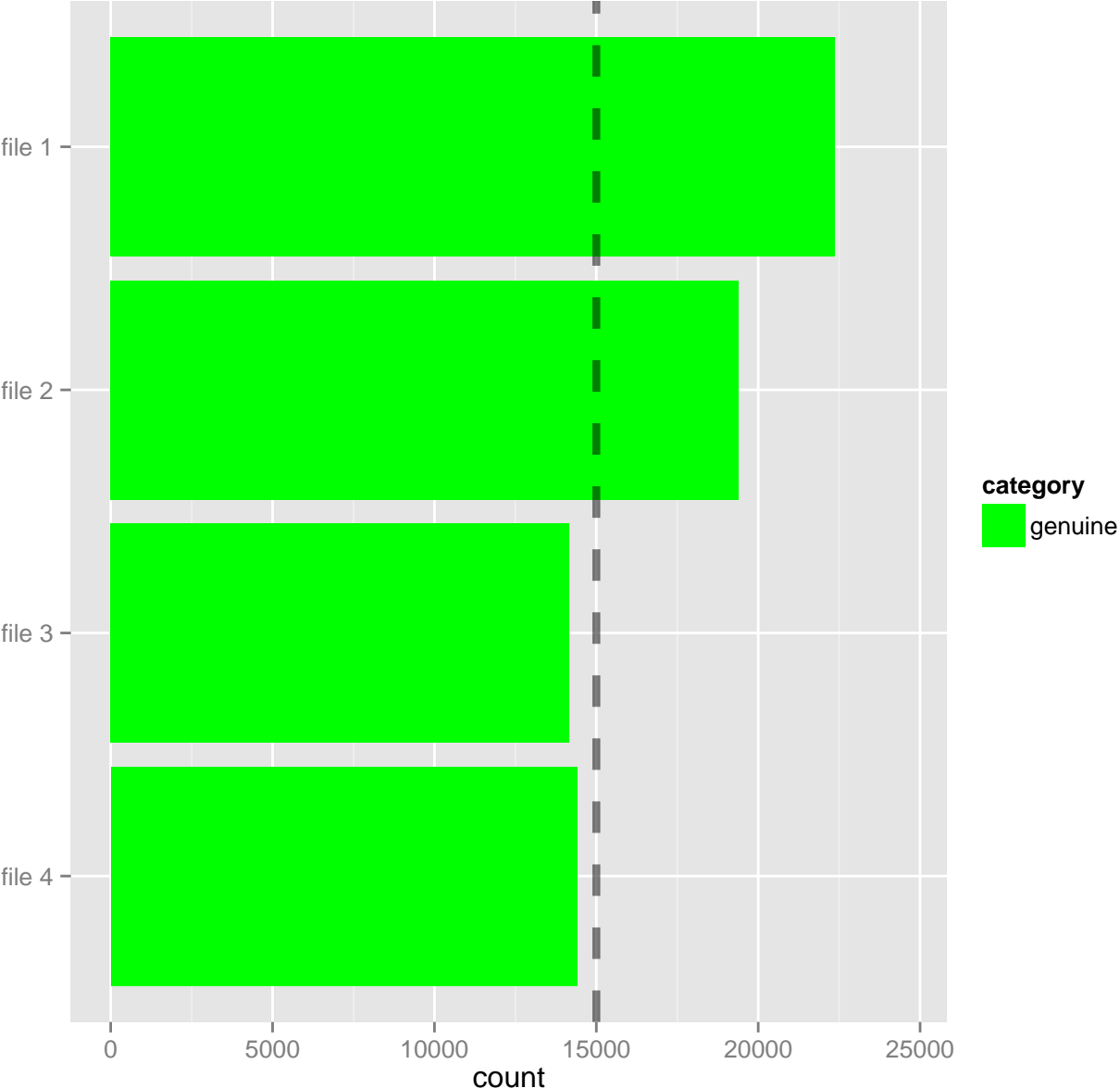
RSD 4.3% (expected < 5%)



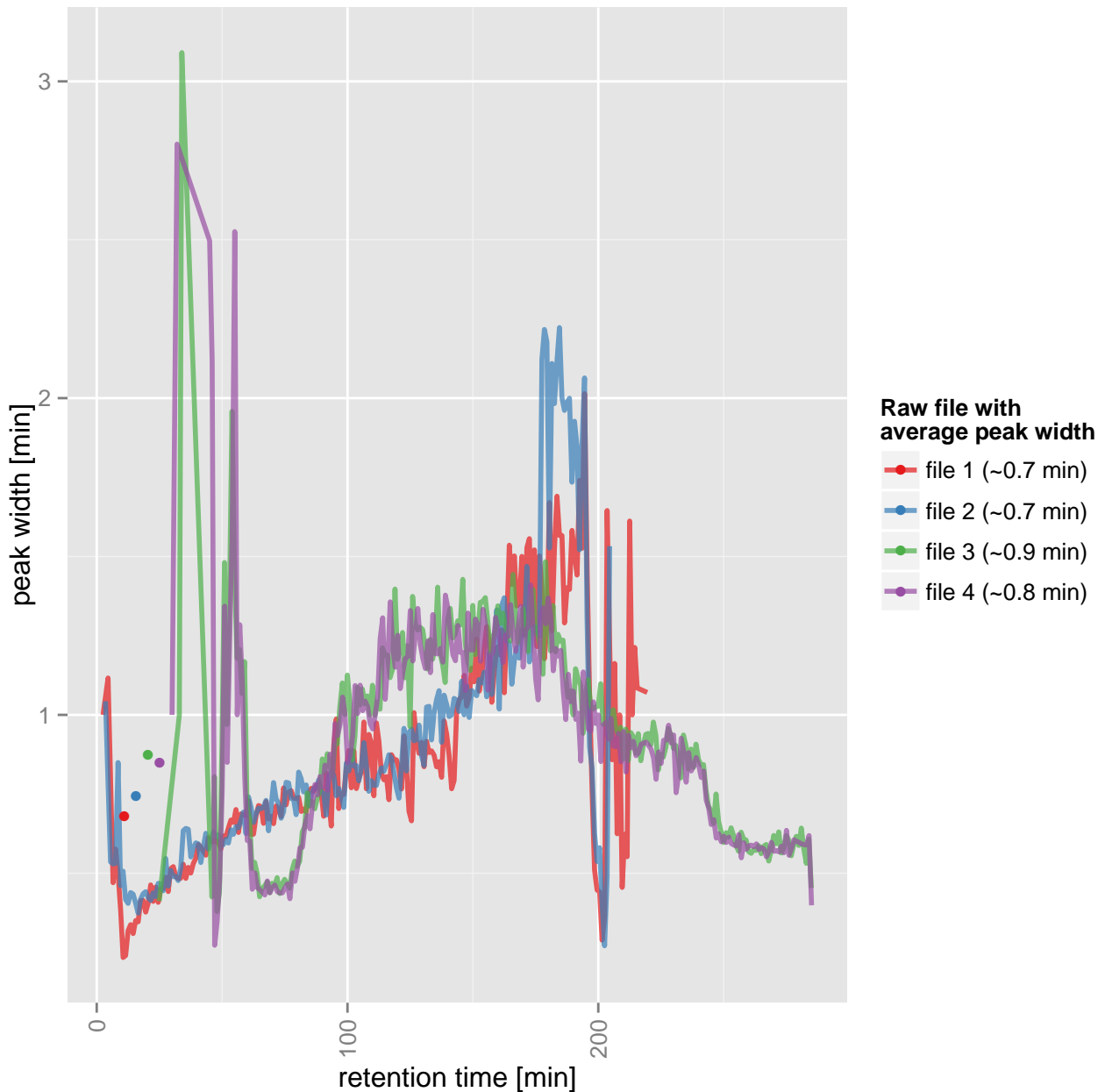
## EVD: ProteinGroups count



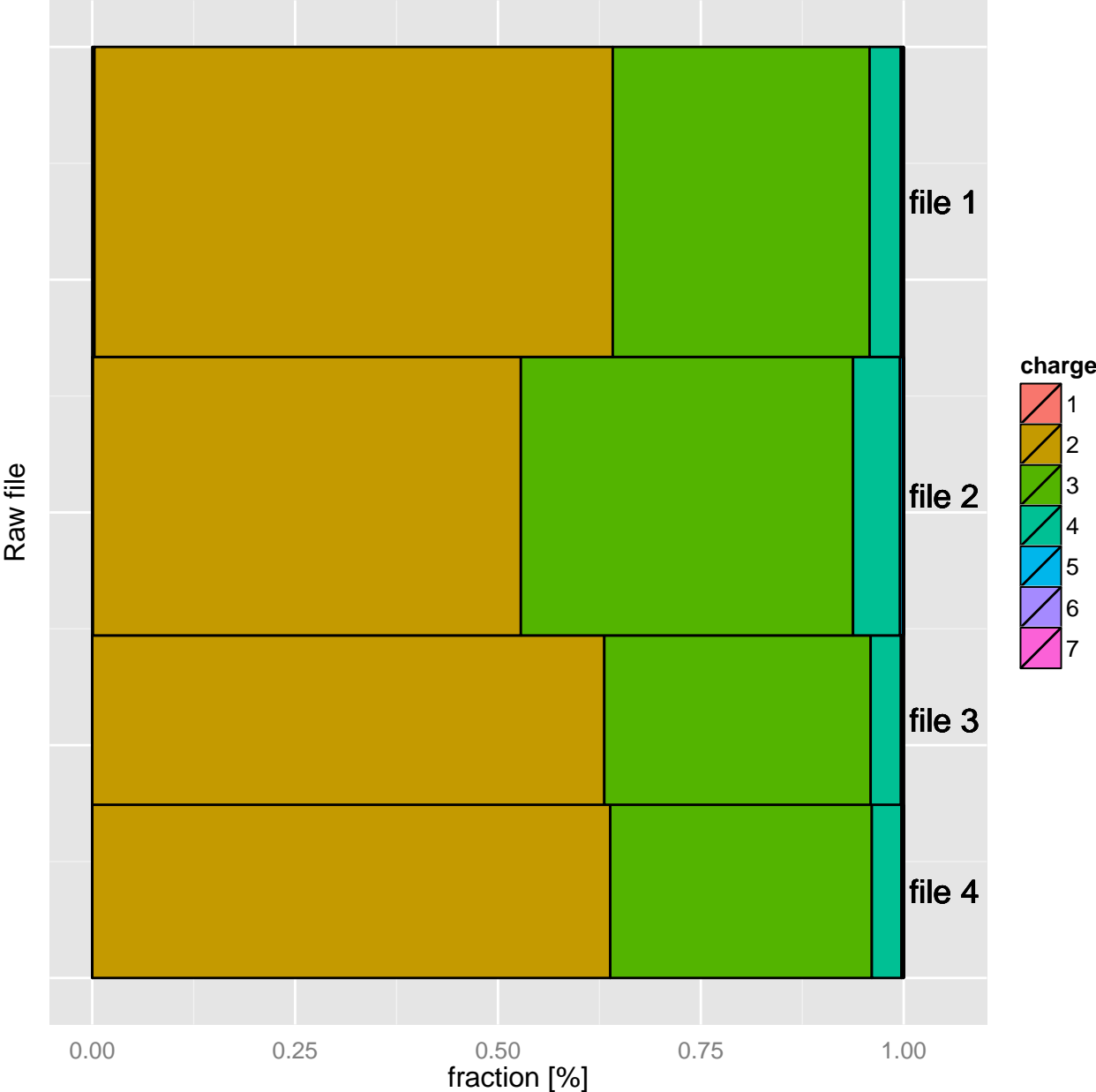
EVD: Peptide ID count



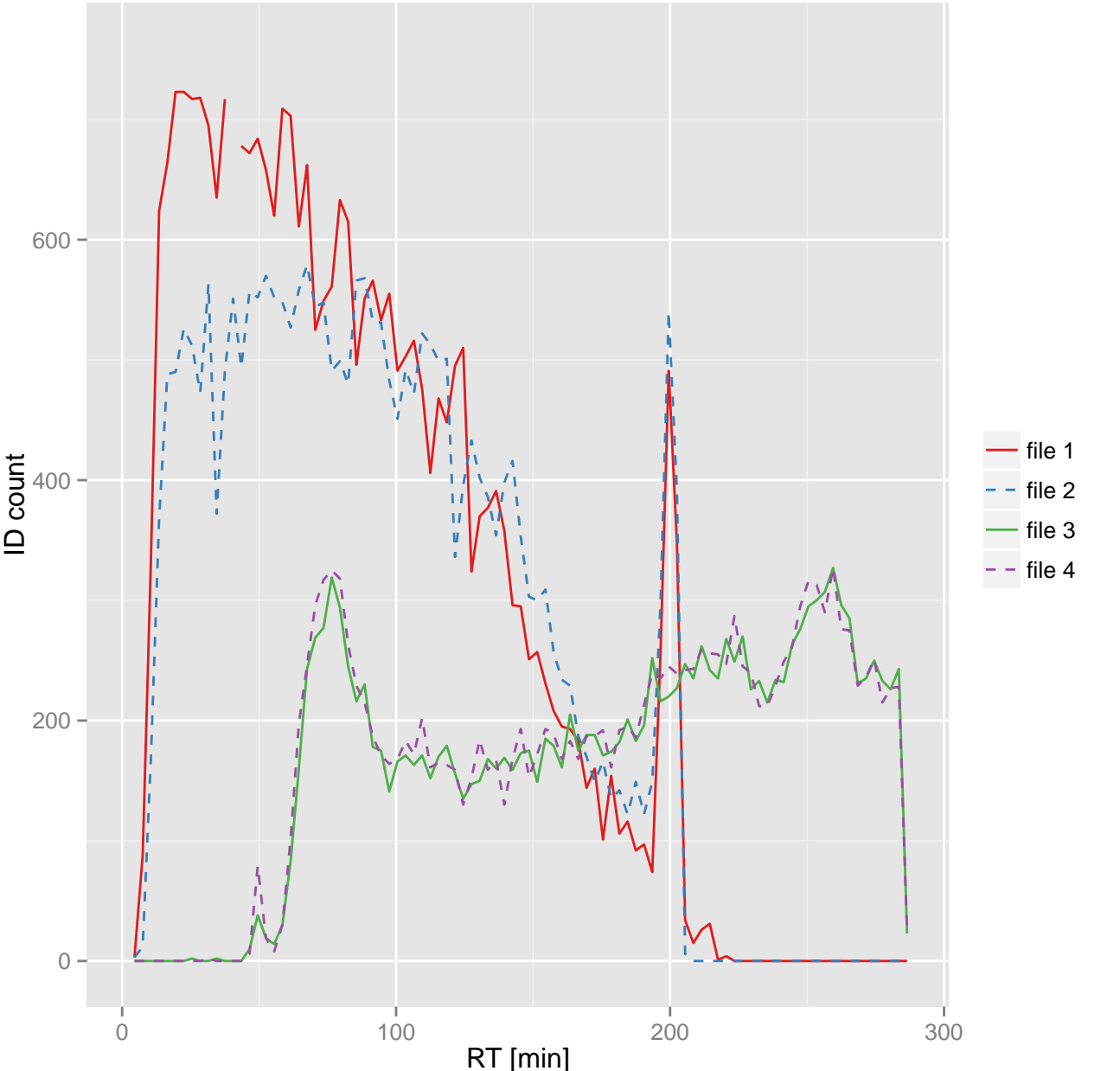
## EVD: Peak width over RT



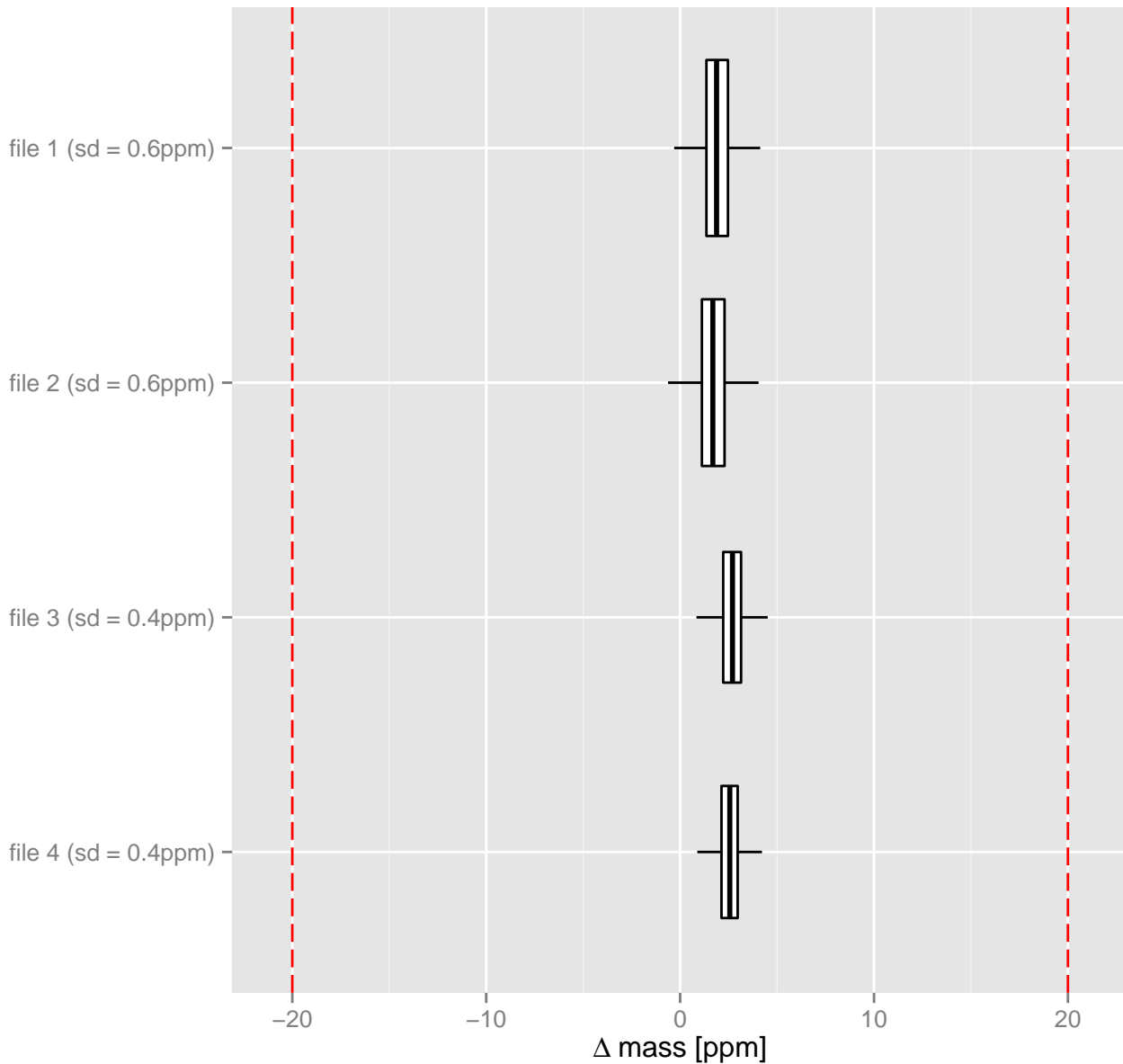
EVD: charge distribution



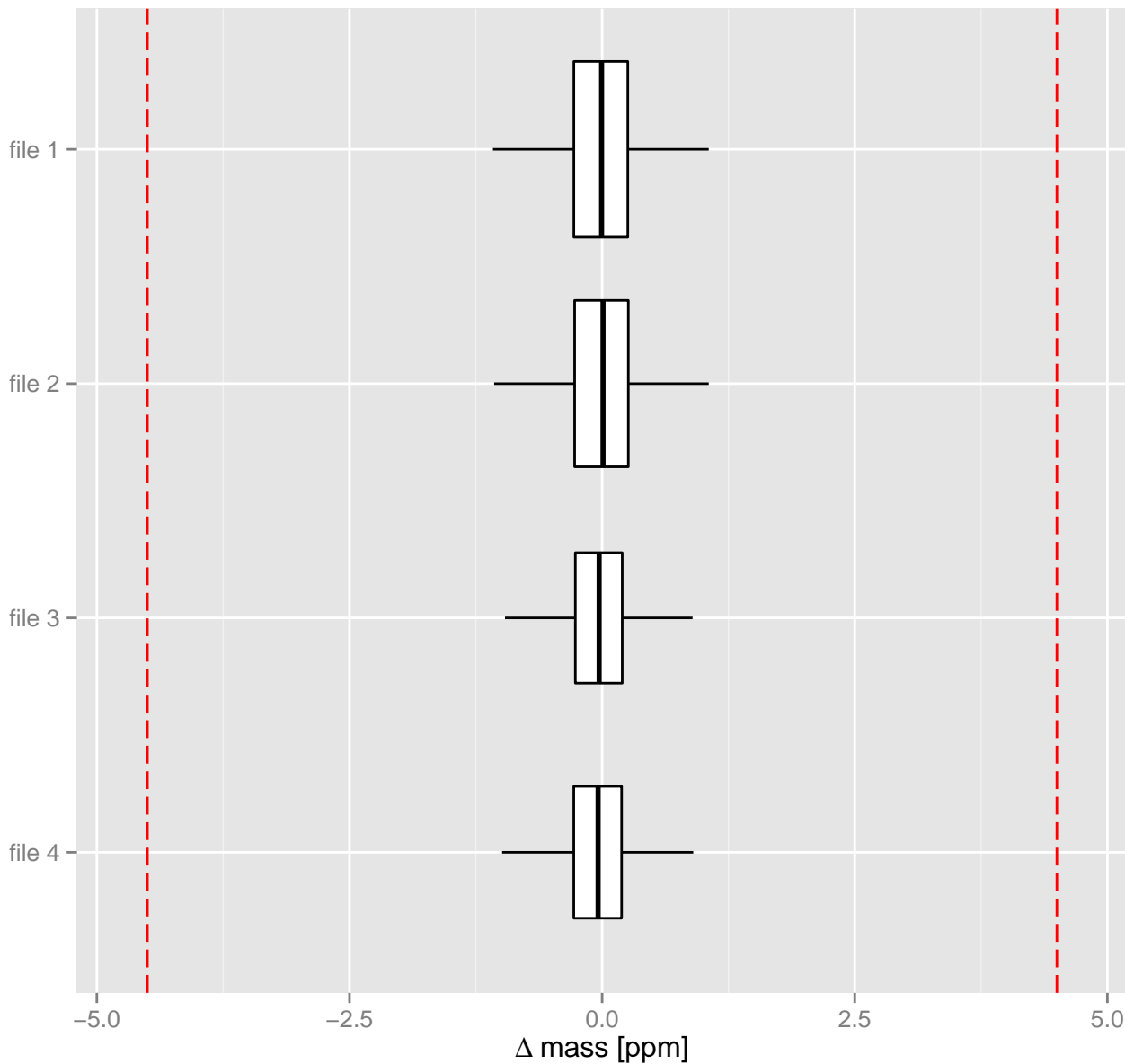
EVD: IDs over RT



# EVD: Uncalibrated mass error

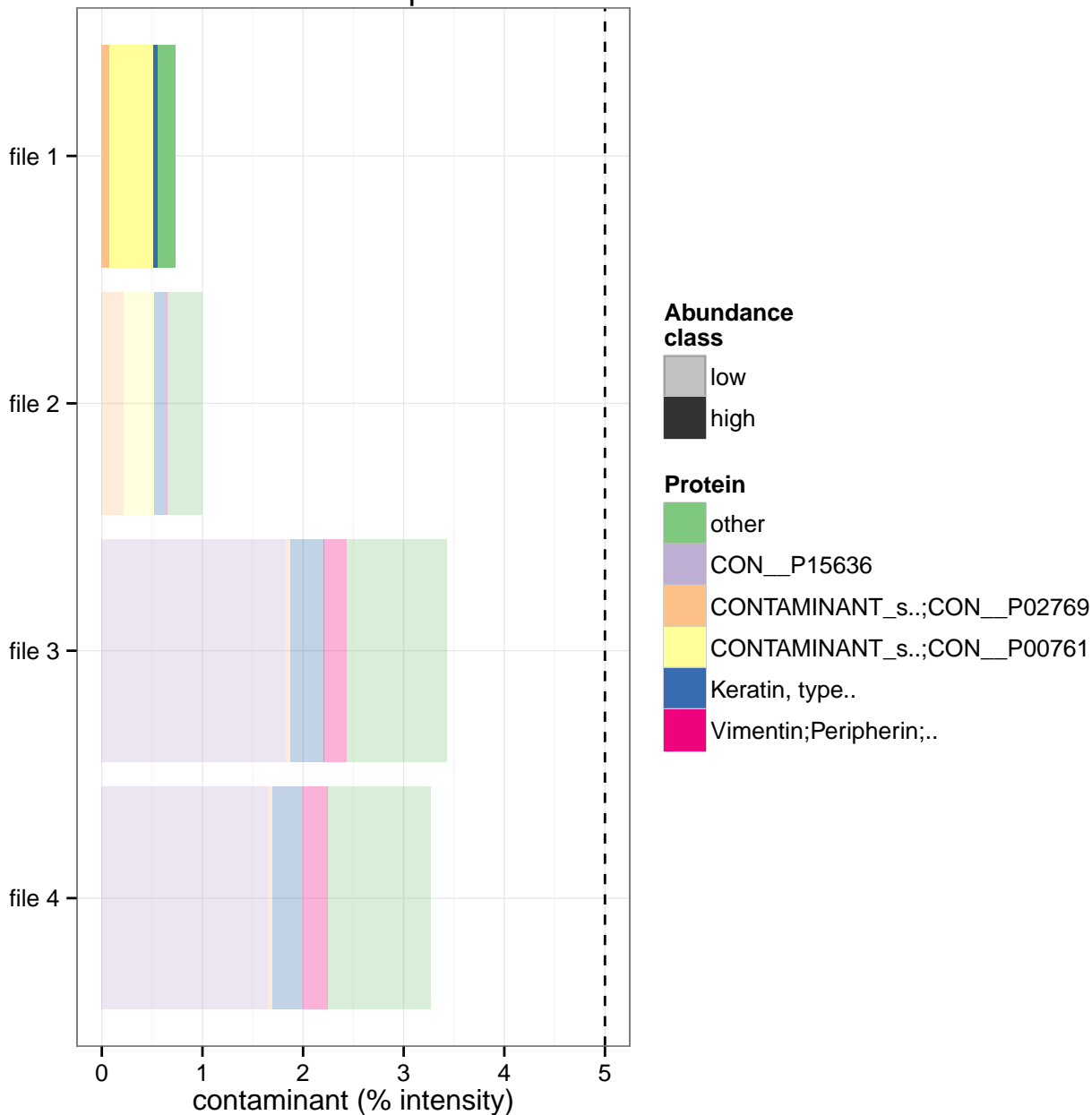


# EVD: Calibrated mass error

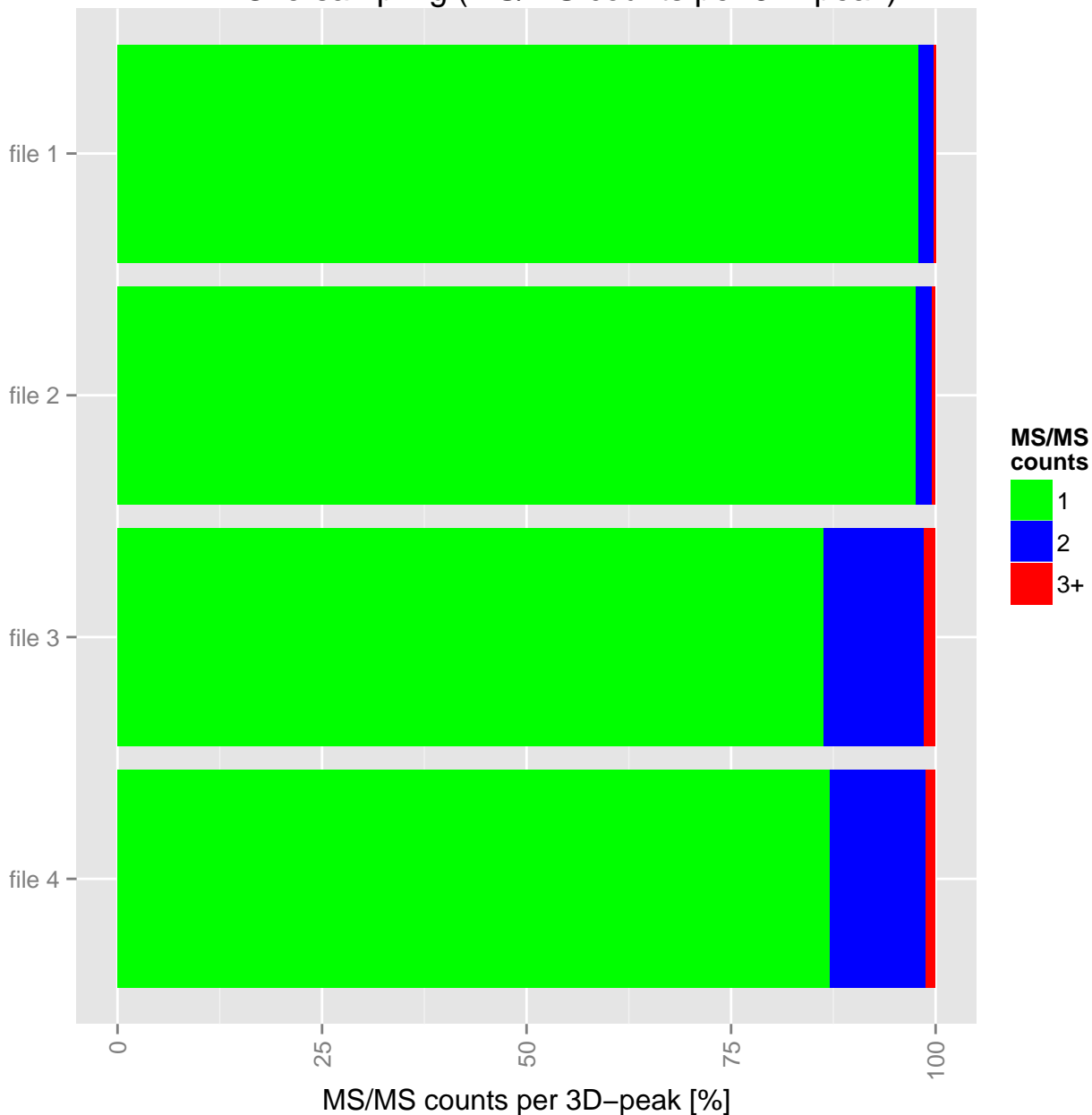




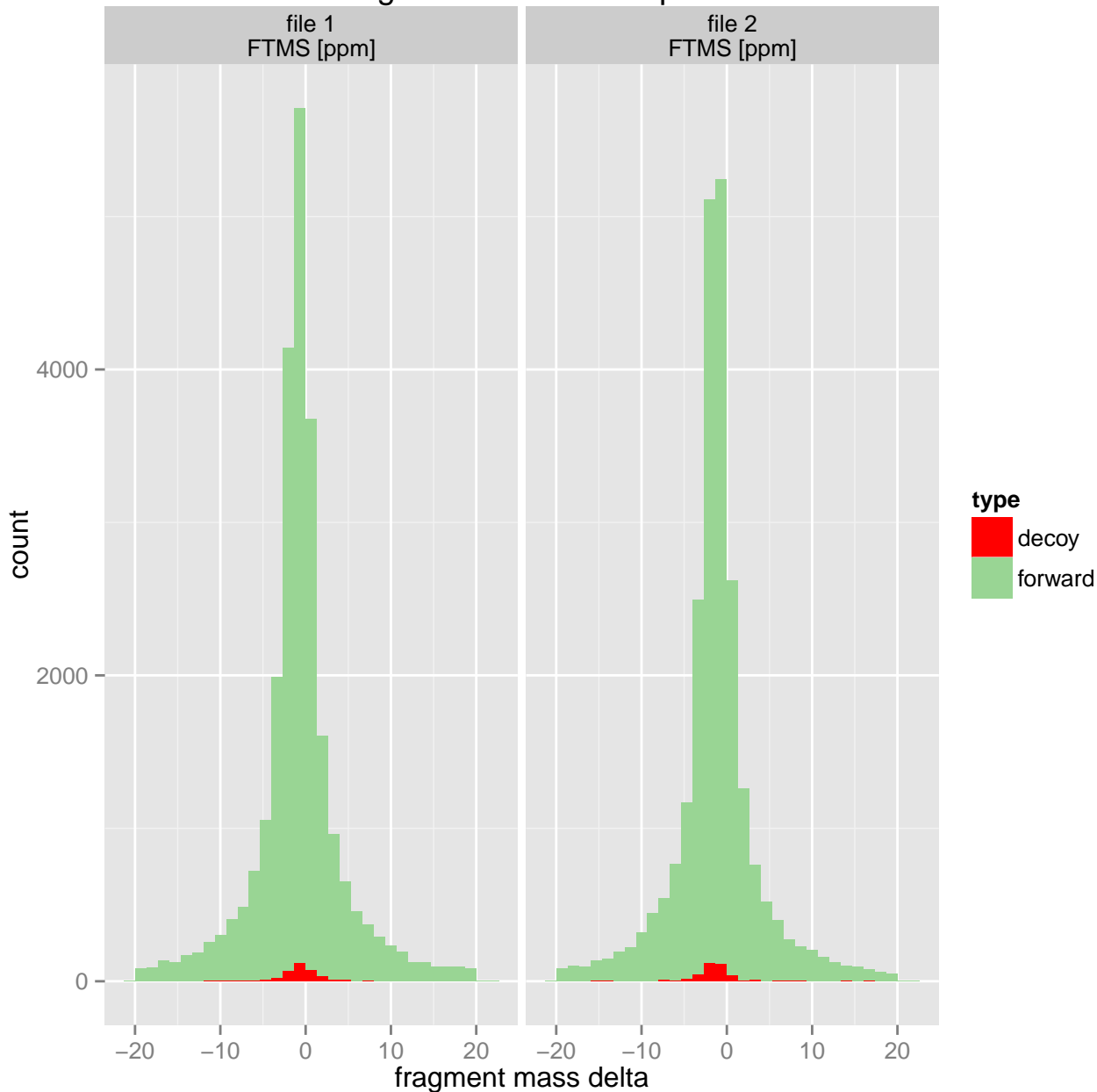
# EVD: Contaminant per Raw file



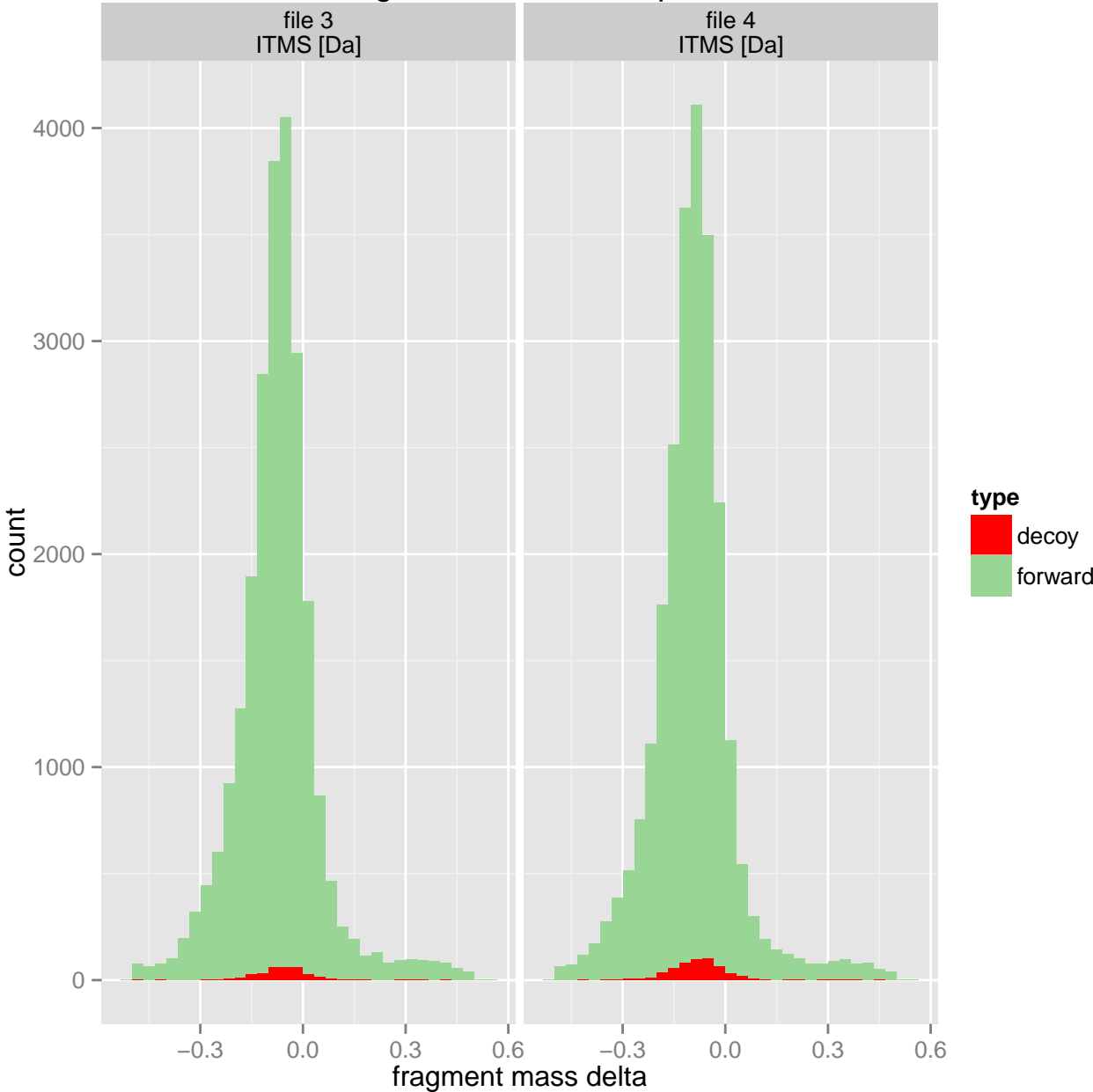
## EVD: Oversampling (MS/MS counts per 3D-peak)



# MSMS: Fragment mass errors per Raw file

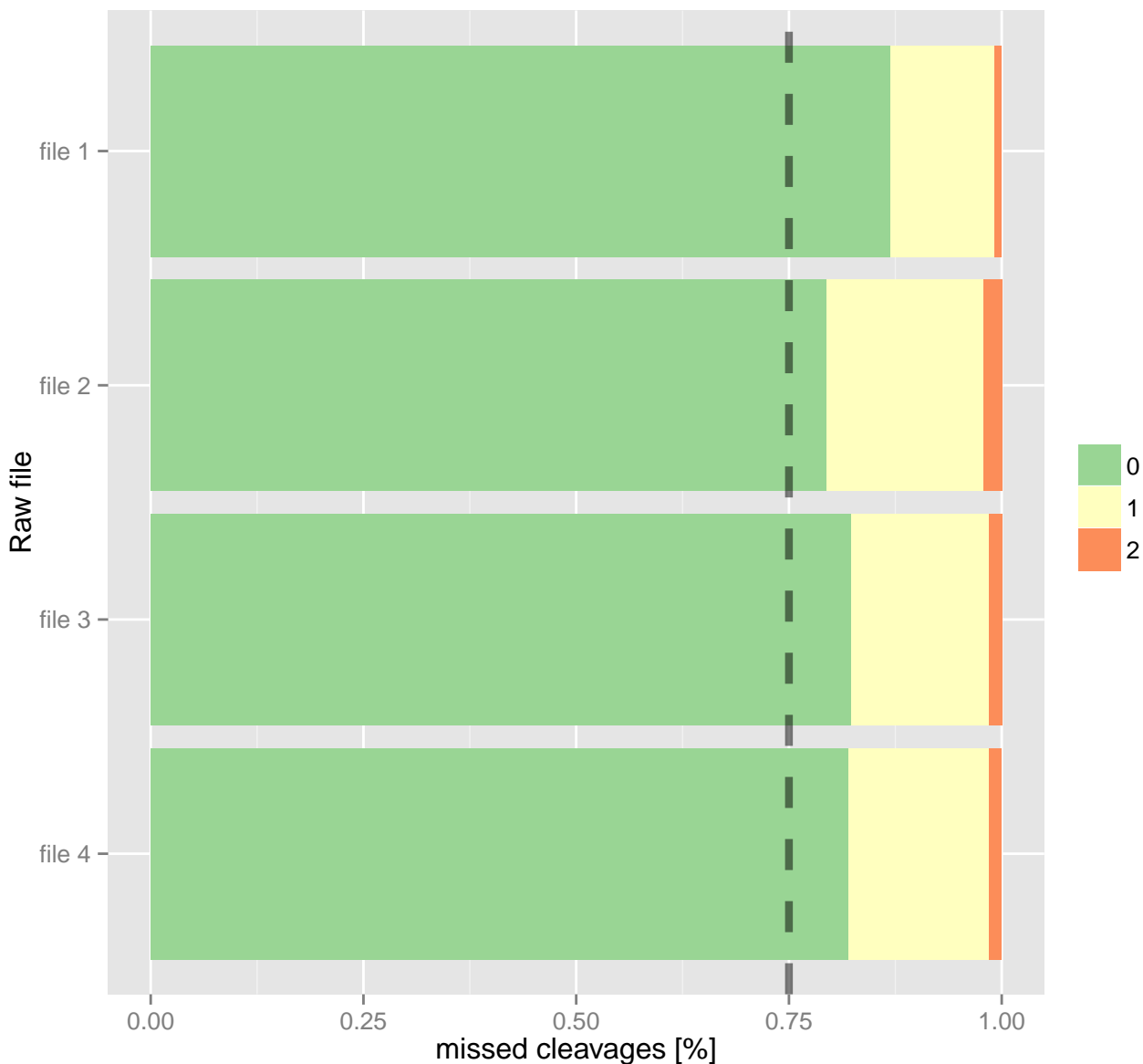


MSMS: Fragment mass errors per Raw file

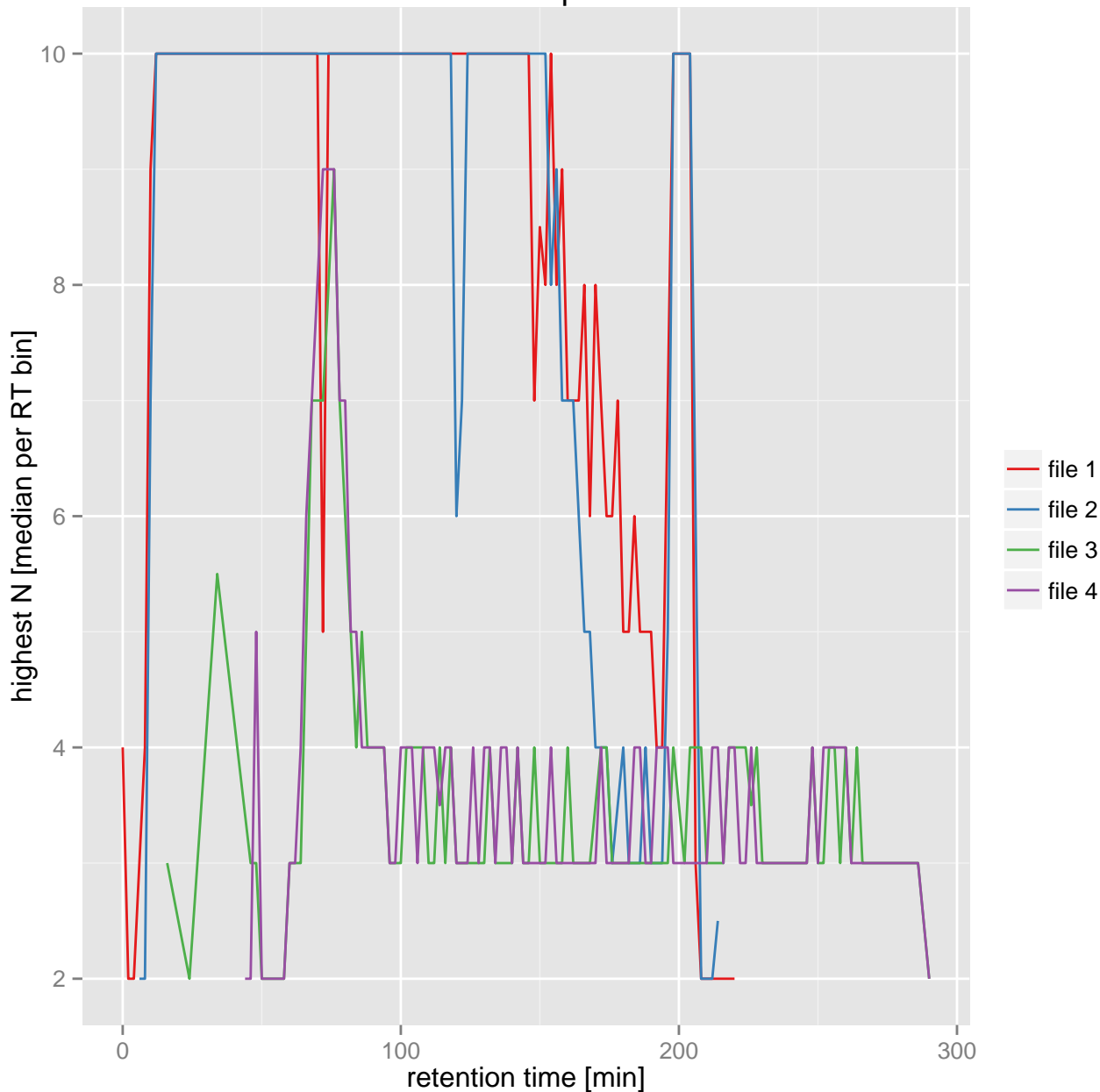


# MSMS: Missed cleavages per Raw file

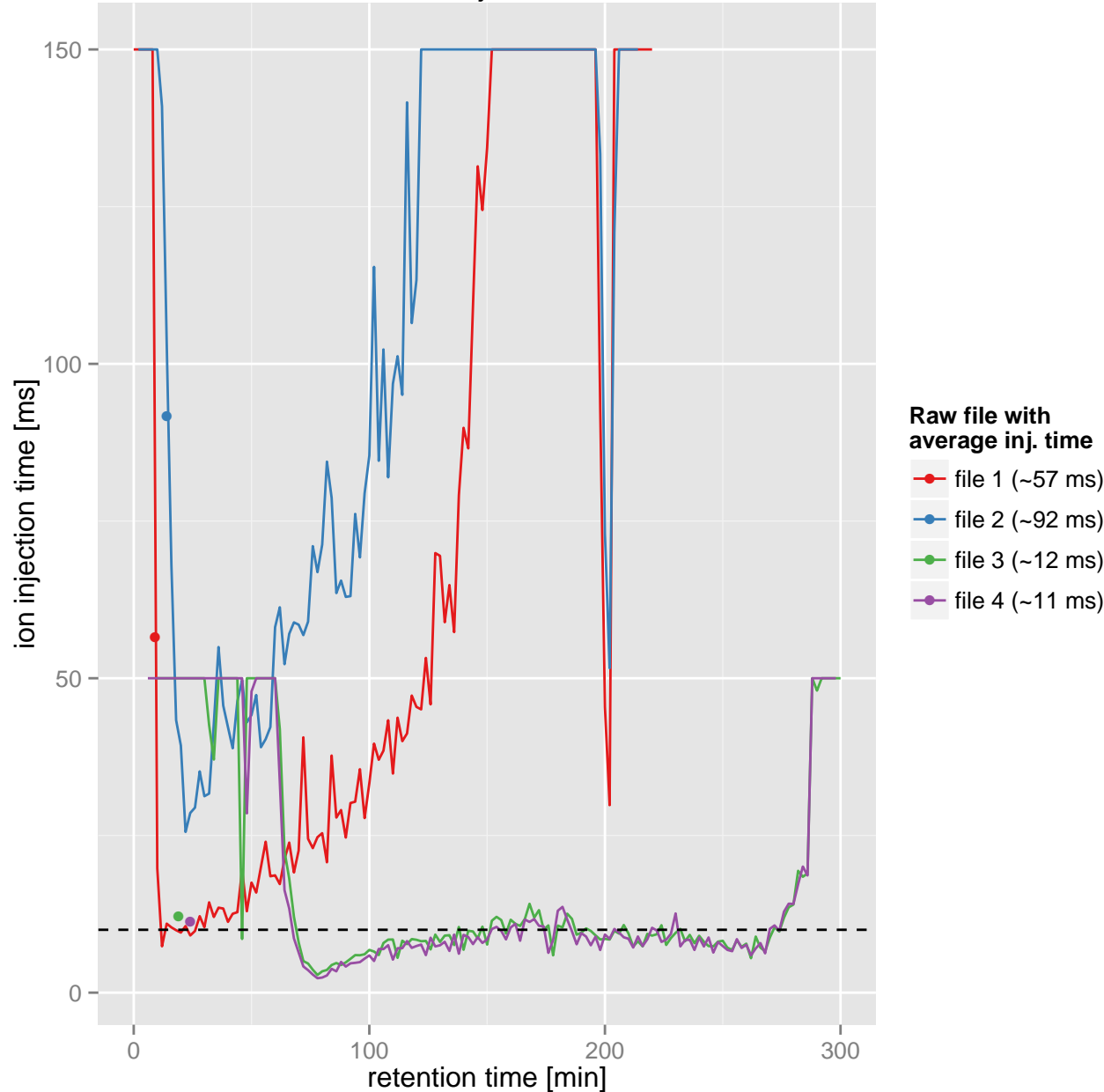
(excludes contaminants)



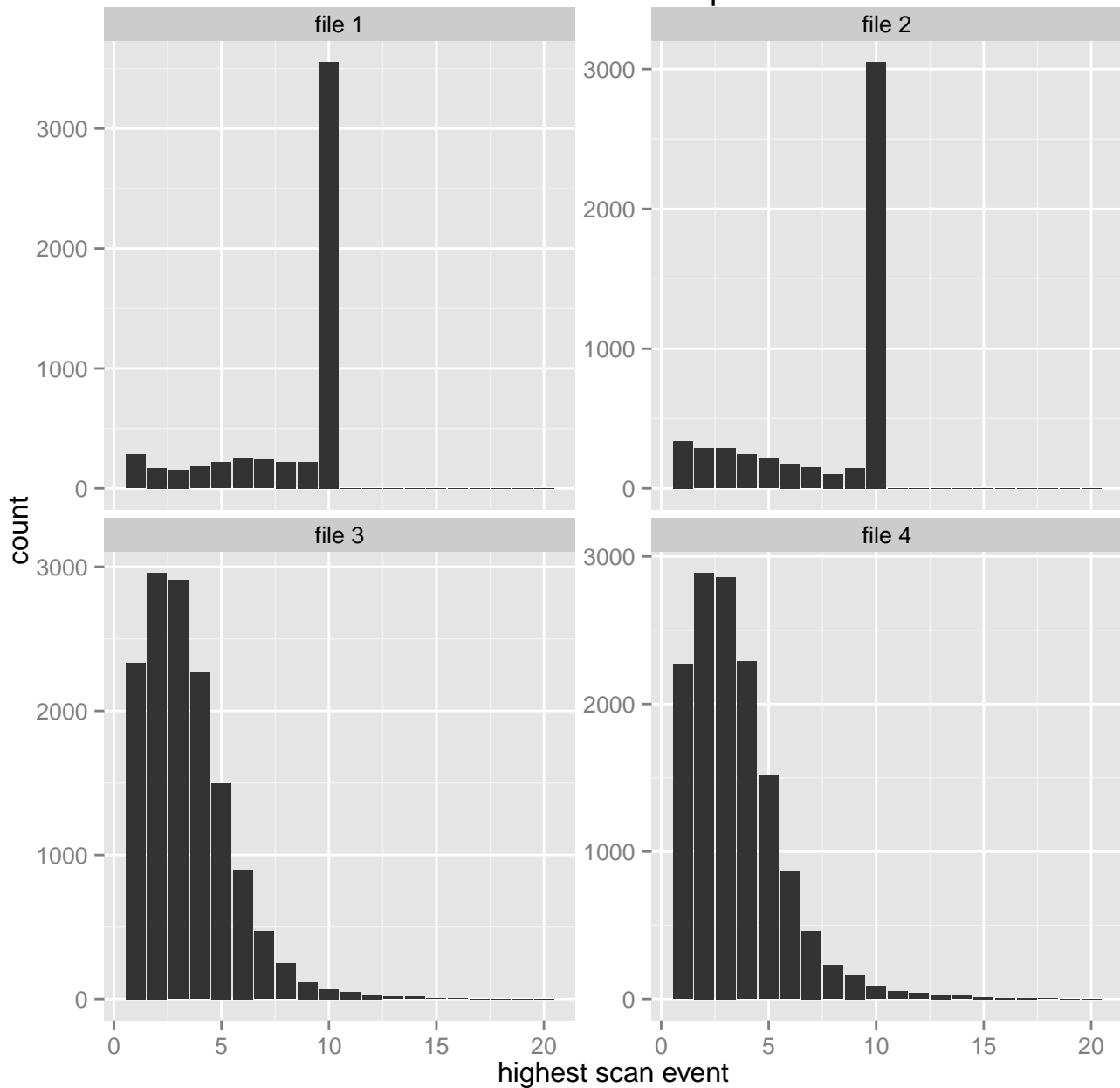
# MSMSscans: TopN over RT



# MSMSscans: Ion Injection Time over RT



# MSMSscans: TopN





# MSMScans: TopN % identified over N

