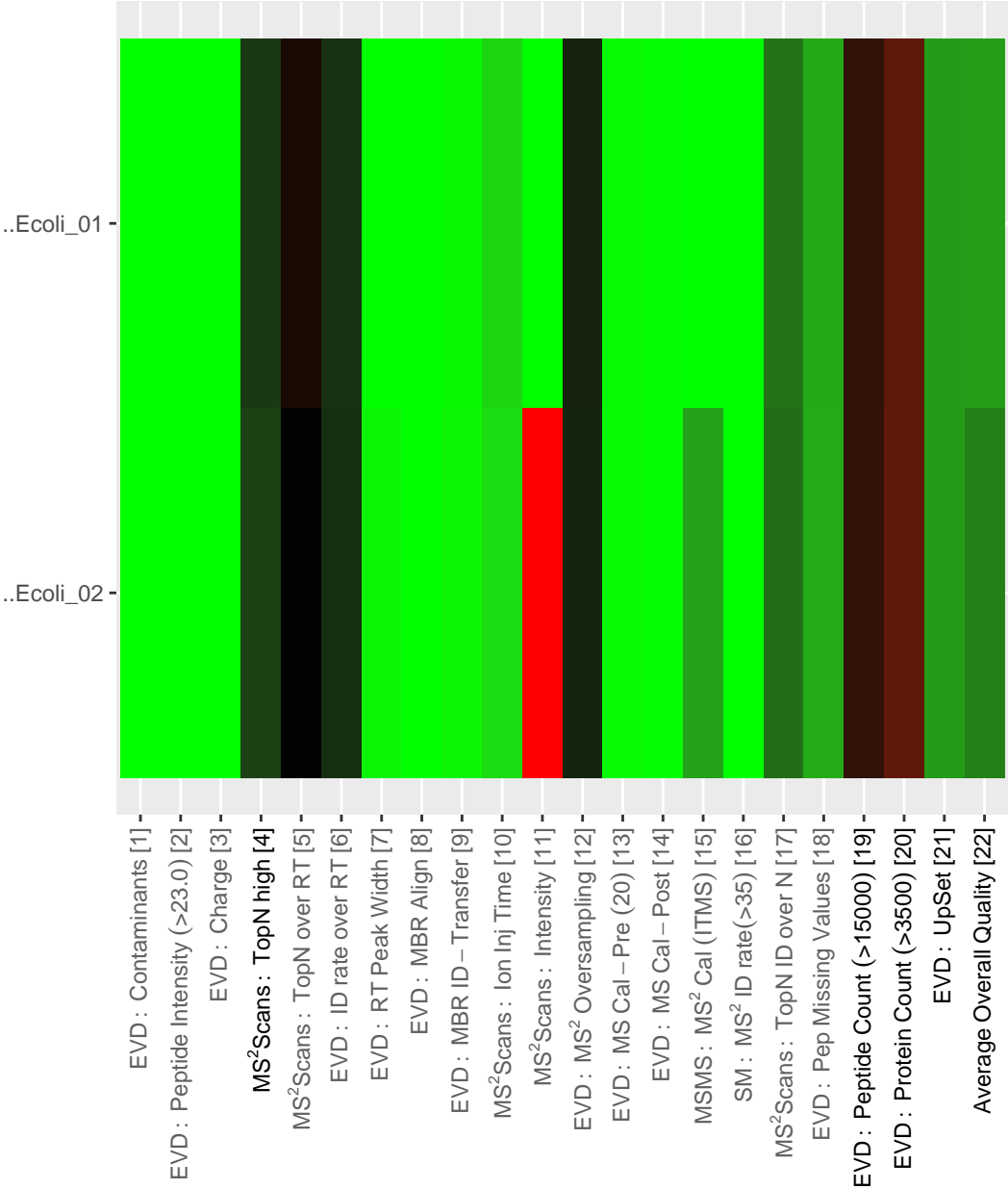


Performance overview

Raw file



score



Mapping of Raw files to their short names

Mapping source: automatic

	original	short name	best effort
	Toni_20120502_GM_Ecoli_01	..Ecoli_01	
	Toni_20120502_GM_Ecoli_02	..Ecoli_02	

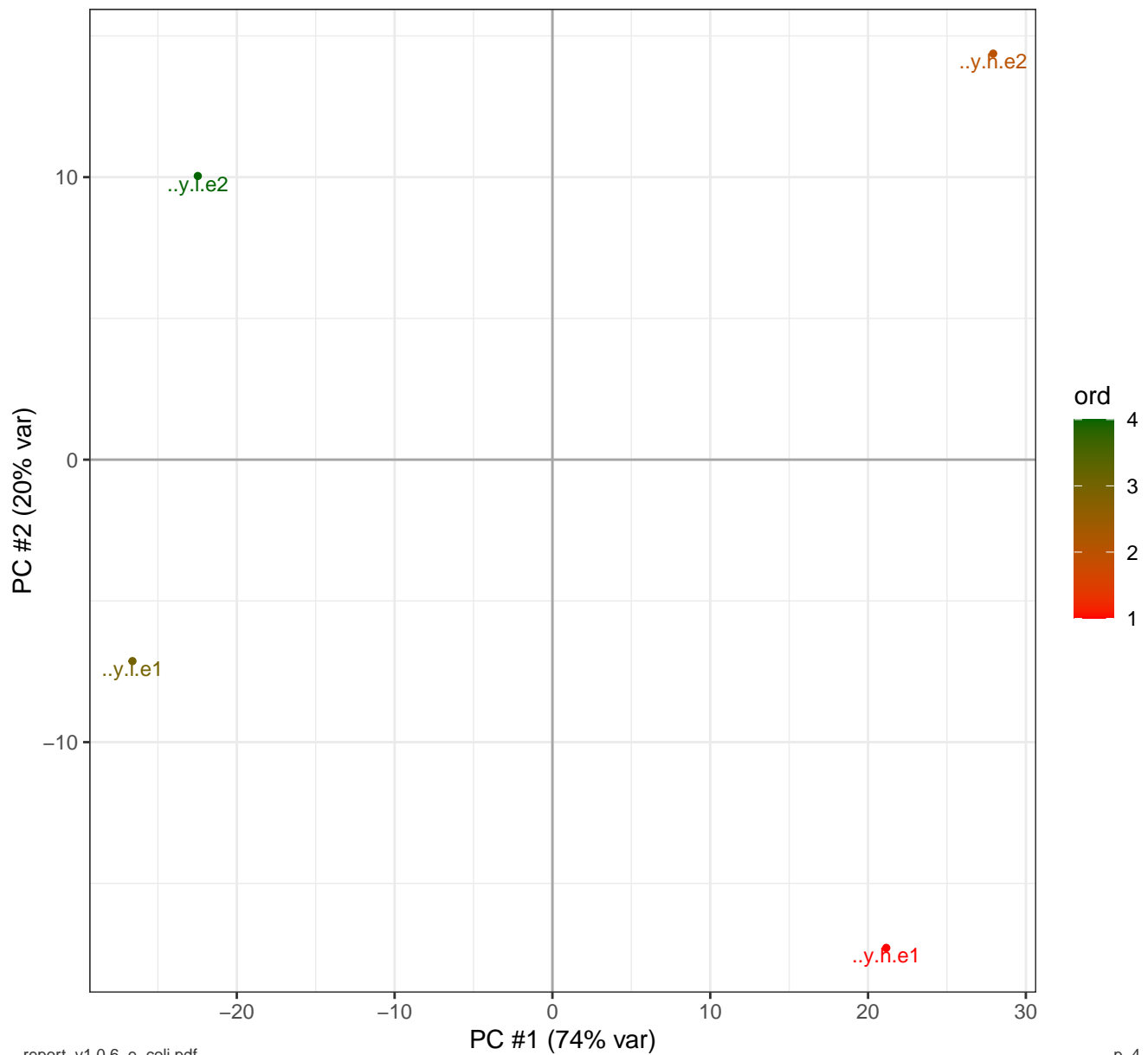
PAR: parameters

parameter	value	parameter	value
Advanced ratios	True	Min. score for modified pept..	40
Alignment time window [min]	20	Modifications included in pr..	Acetyl (Protein N-term) Oxidation (M)
Date of writing	11/13/2015 16:13:53	MS/MS tol. (FTMS)	20 ppm
Decoy mode	revert	MS/MS tol. (ITMS)	0.5 Da
Find dependent peptides	False	MS/MS tol. (TOF)	40 ppm
First pass AIF correlation	0.8	Peptides used for protein qu..	Razor
Fixed modifications	Carbamidomethyl (C)	Protein FDR	0.01
Machine name	CD02-WIN7	Site tables	Oxidation (M)Sites.txt
Matching time window [min]	0.7	Special AAs	KR
Min. delta score for modifie..	6	Top MS/MS peaks per 100 Da. ..	12
Min. delta score for unmodif..	0	Top MS/MS peaks per 100 Da. ..	8
Min. peptide Length	7	Top MS/MS peaks per 100 Da. ..	10
Min. peptides	1	User name	cbielow
Min. ratio count	2	Version	1.5.2.8

E_coli_k12.ASM584v1.16.pep.all.fasta

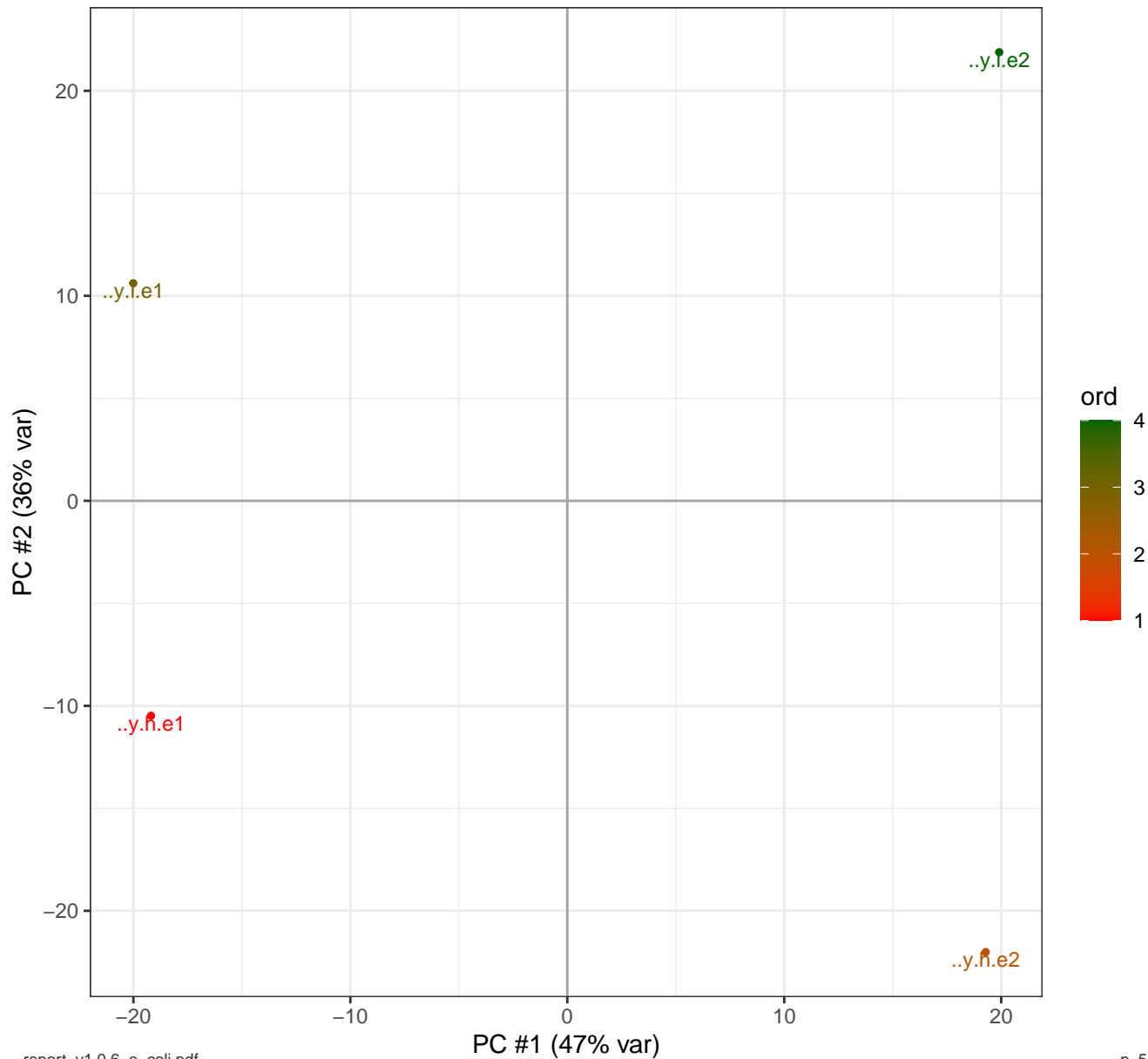
PG: PCA of 'raw intensity'

(excludes contaminants)

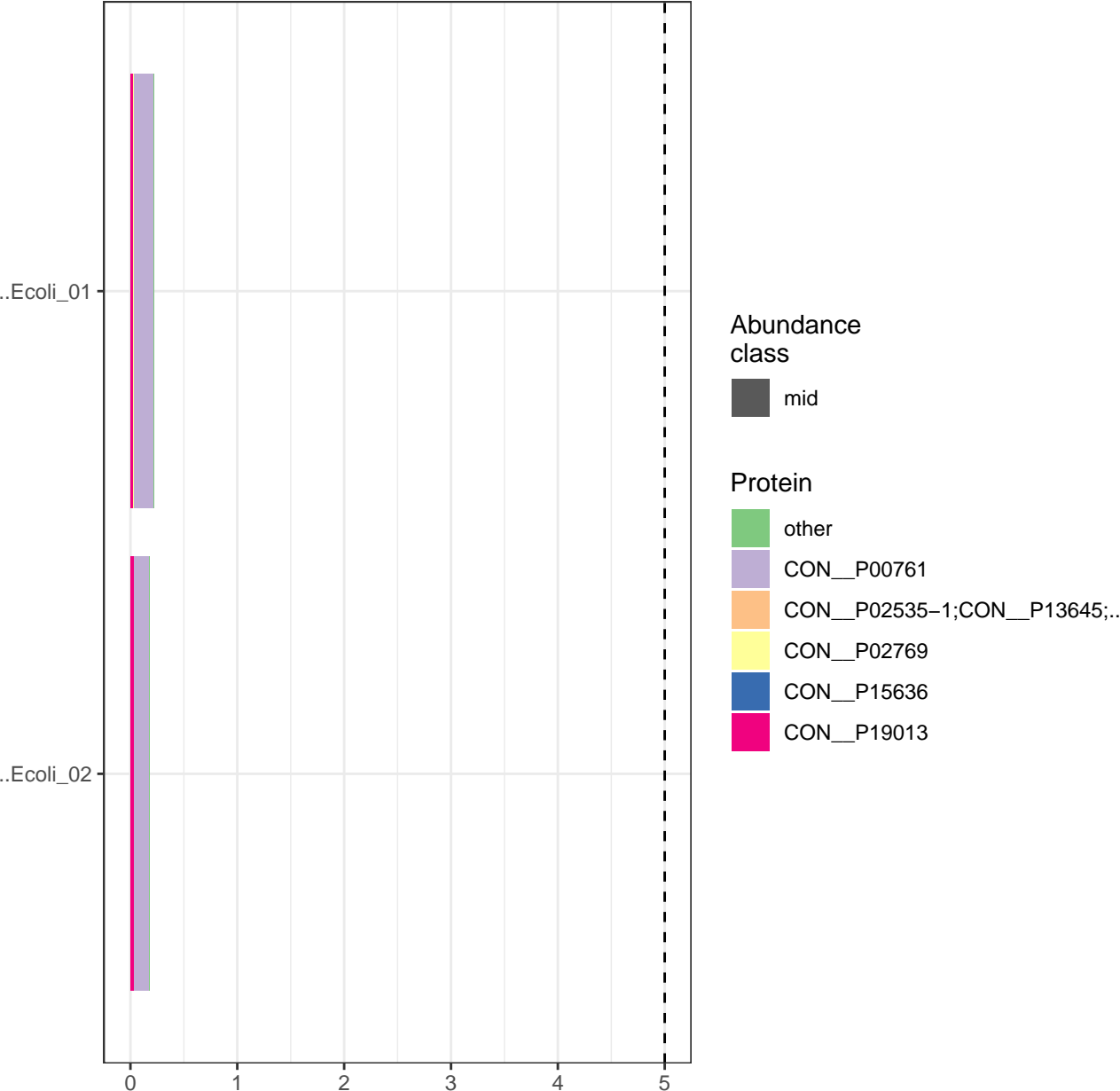


PG: PCA of 'lfq intensity'

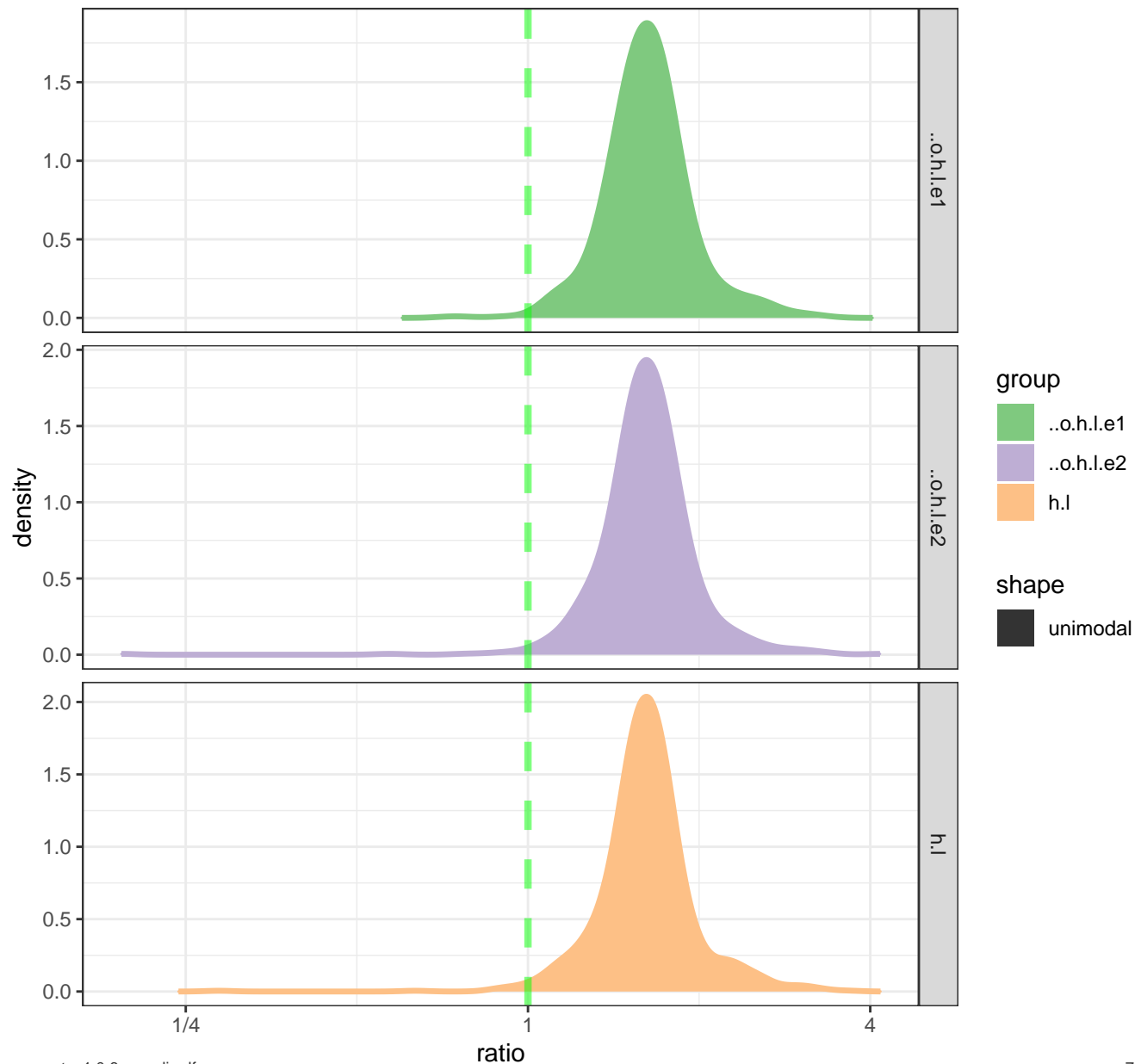
(excludes contaminants)



EVD: Top5 Contaminants per Raw file

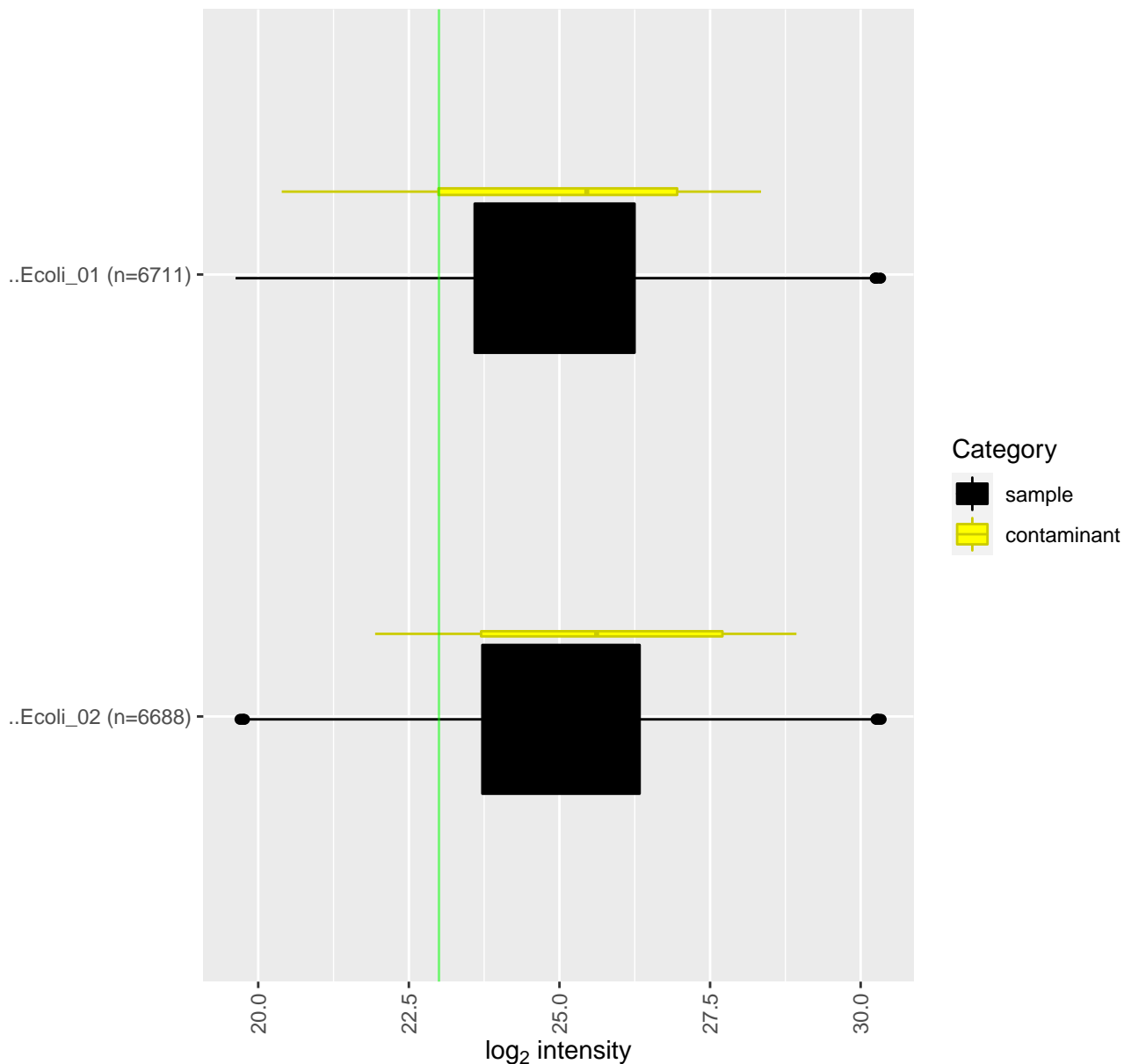


PG: ratio density (w/o contaminants)



EVD: peptide intensity distribution

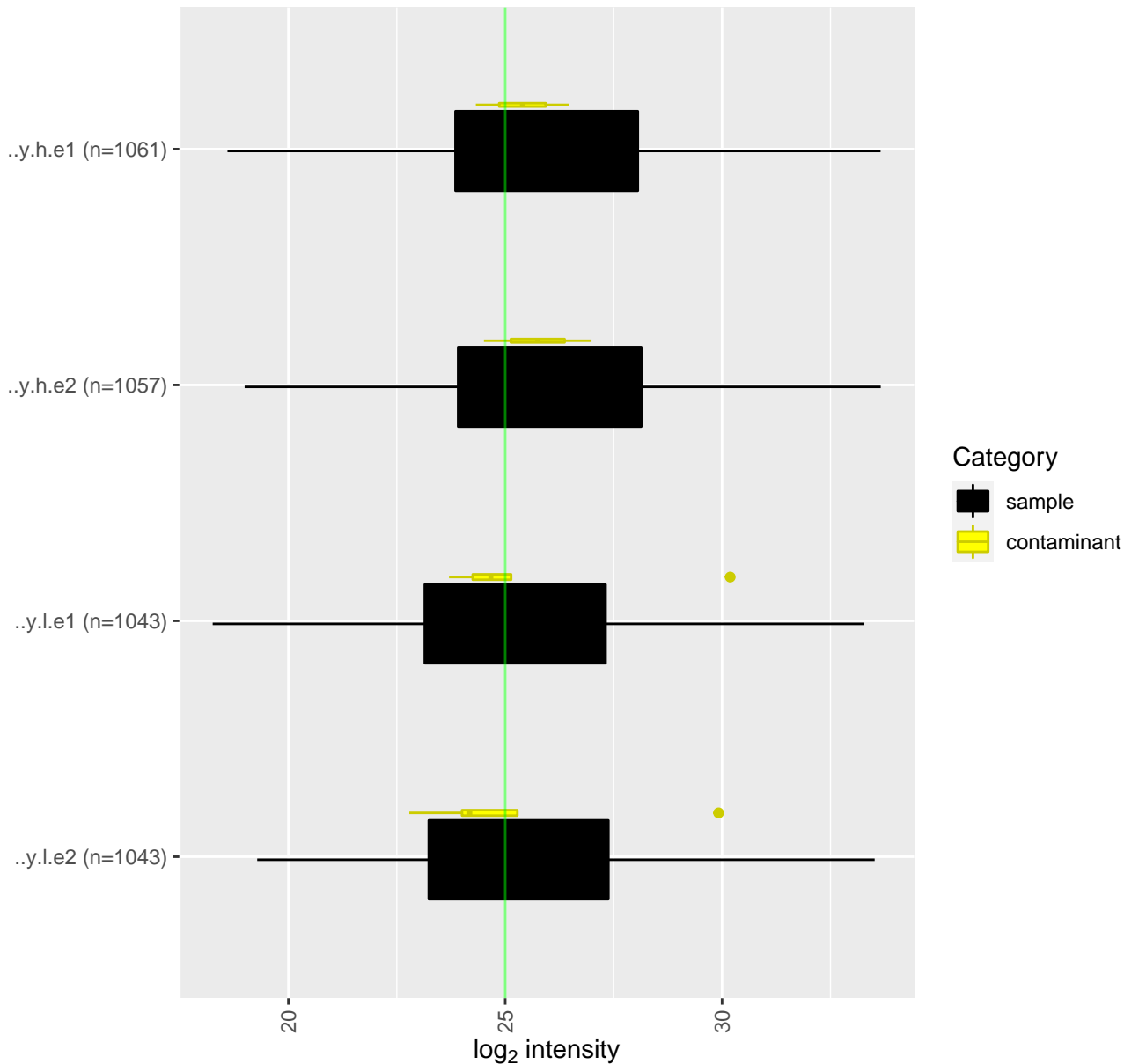
RSD 0.3% (expected < 5%)



PG: intensity distribution

RSD 1.8% (w/o zero int.; expected < 5%)

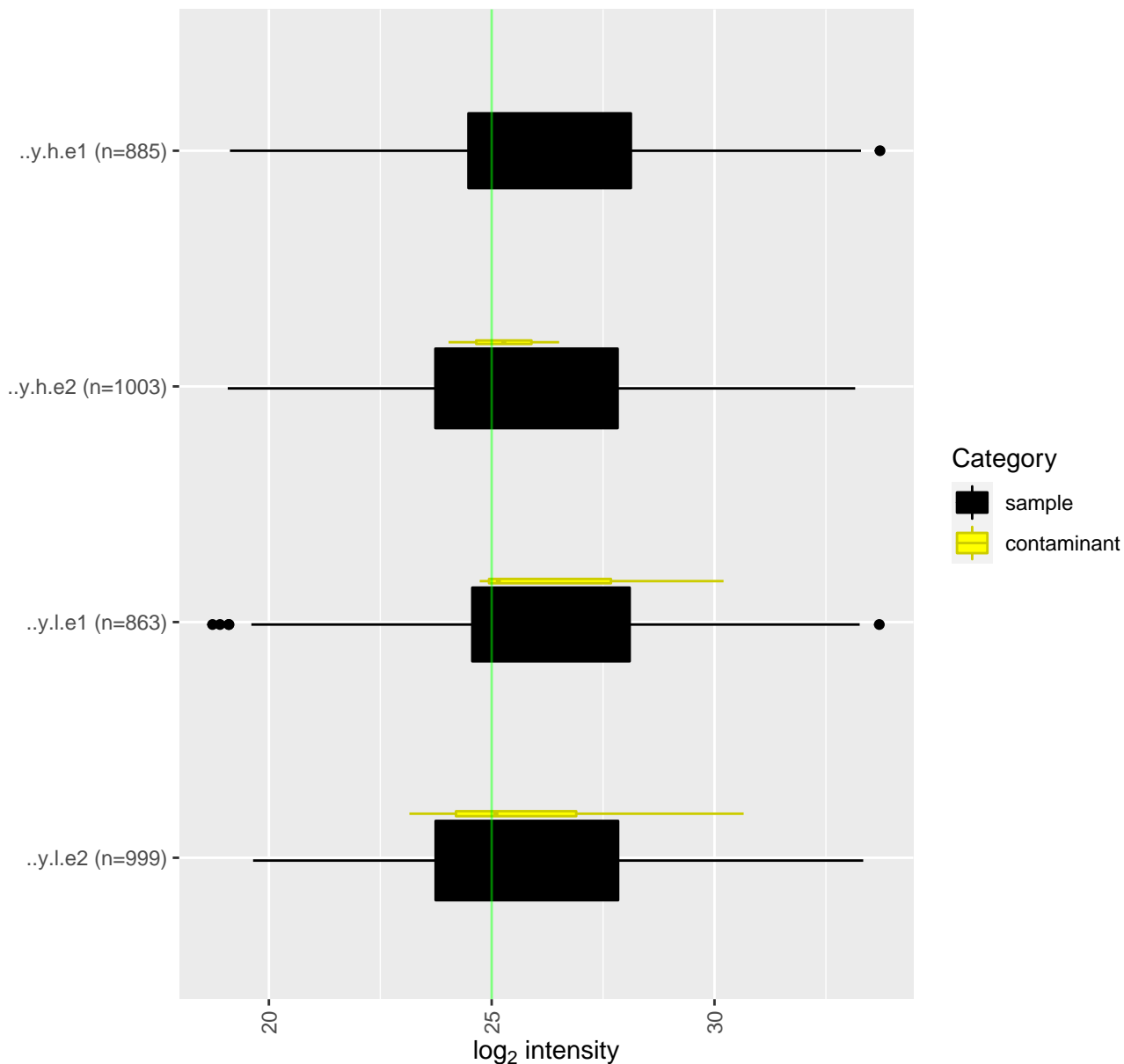
RSD 1.8% [high RSD --> few peptides])



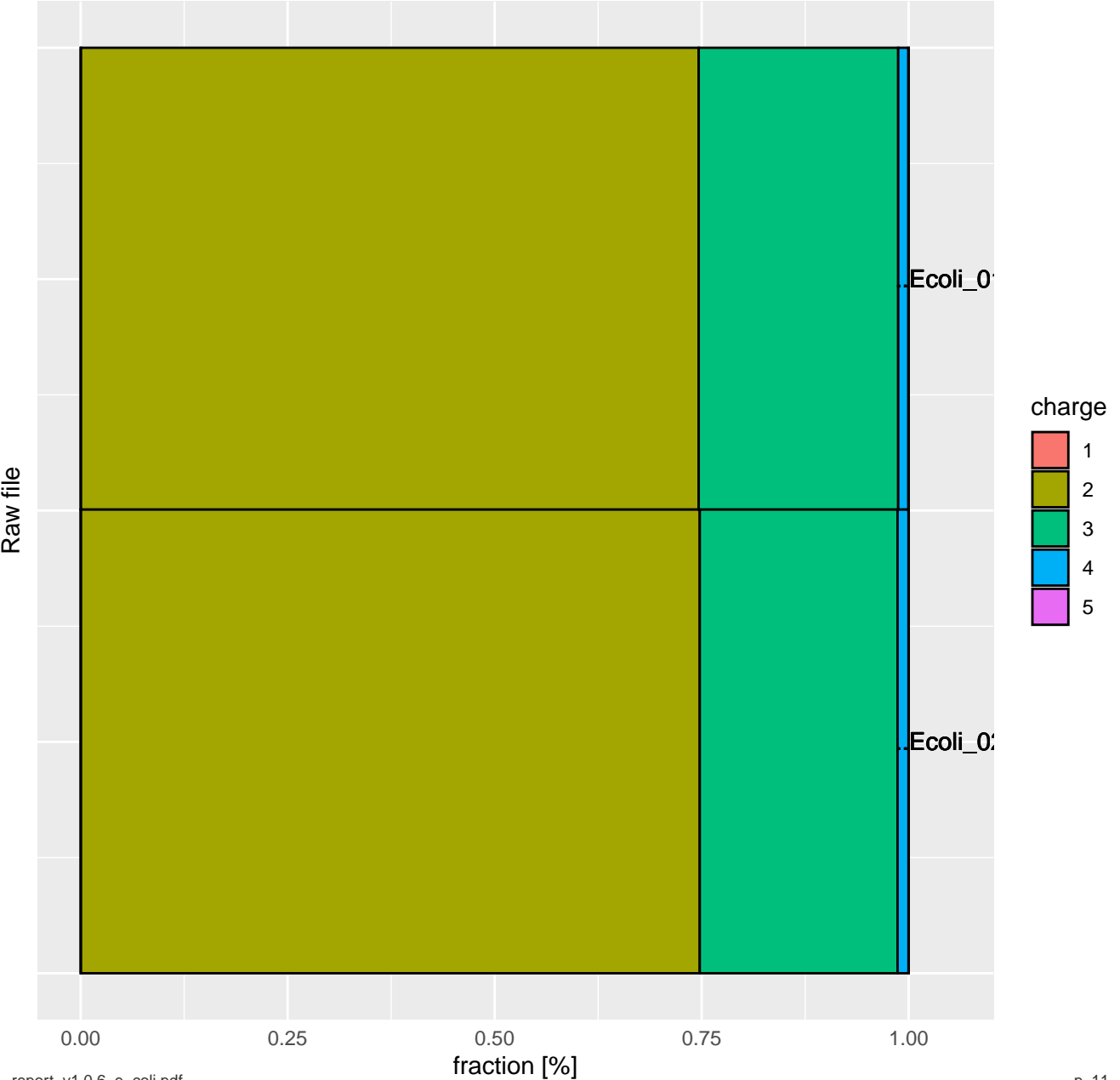
PG: LFQ intensity distribution

RSD 1.1% (w/o zero int.; expected < 5%)

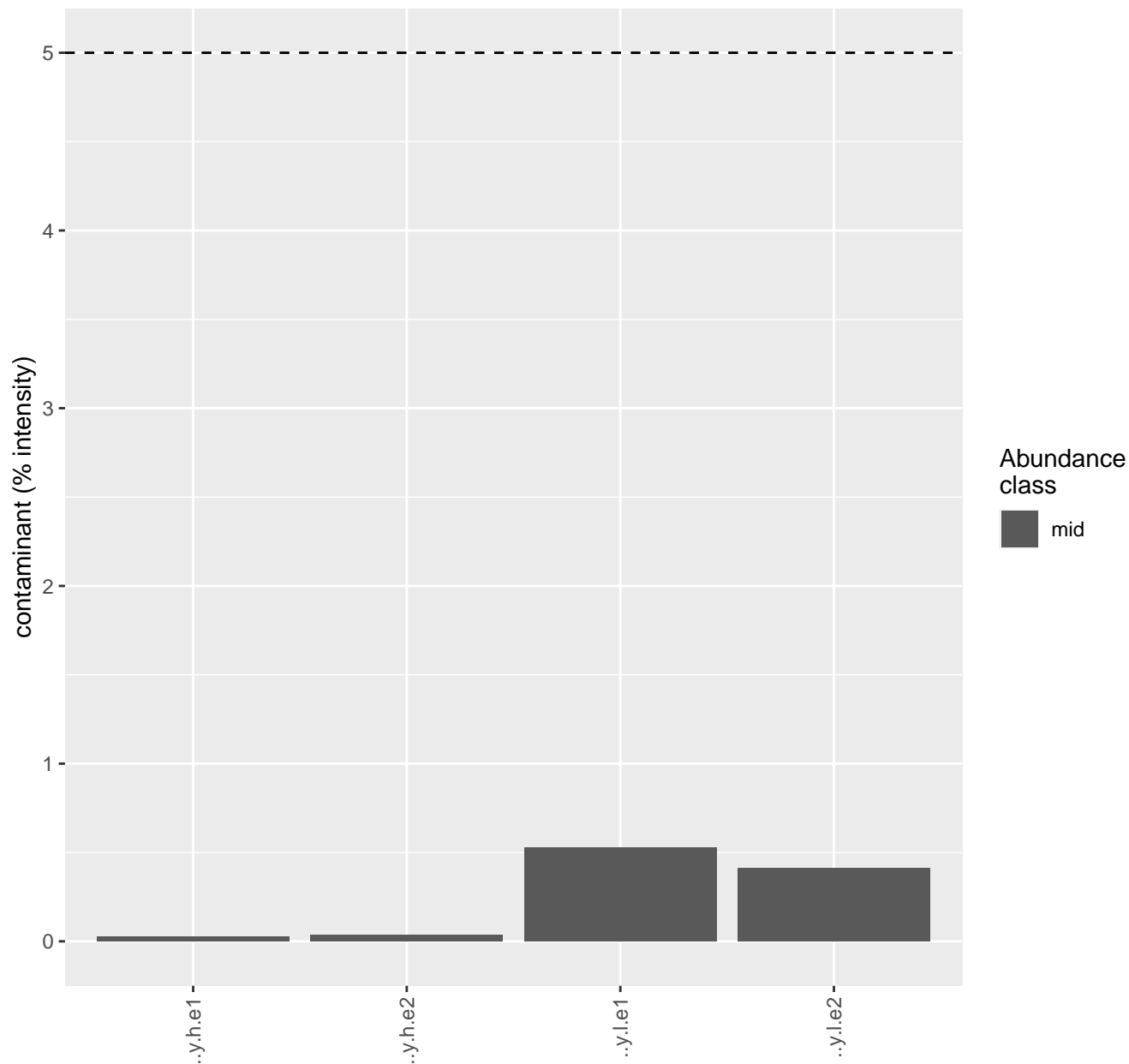
RSD 0.1% [high RSD --> few peptides]



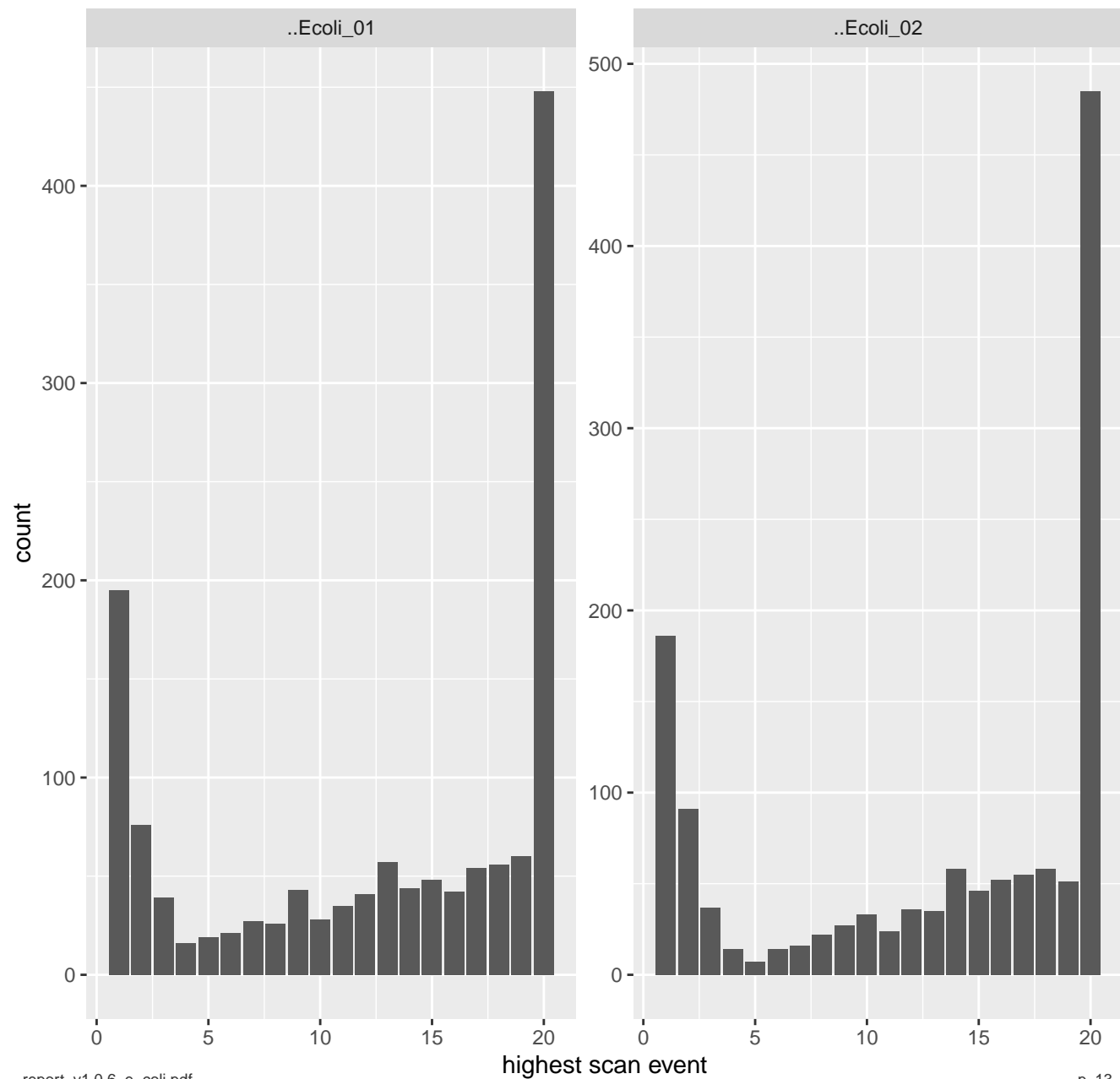
EVD: charge distribution



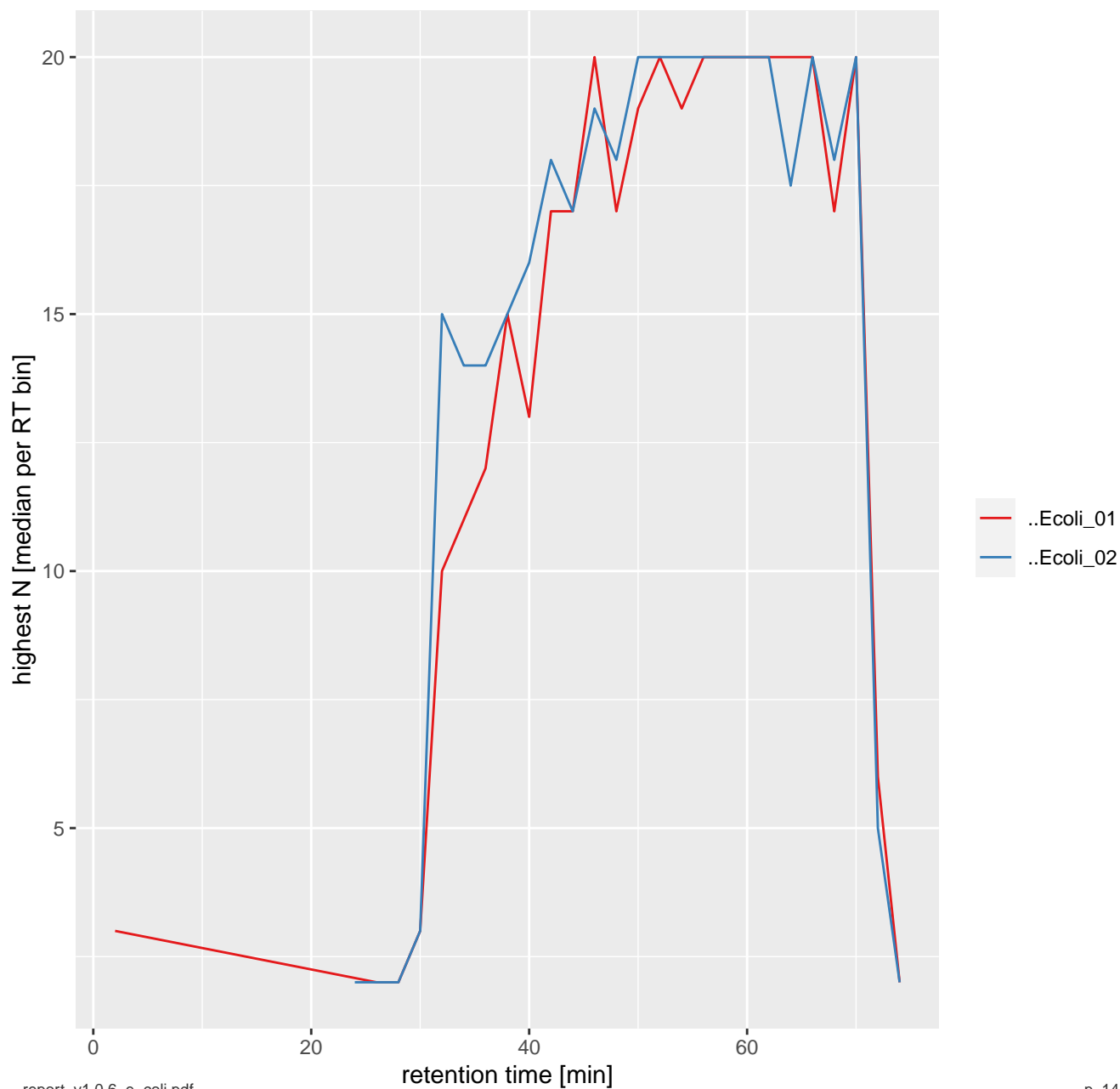
PG: Contaminant per condition



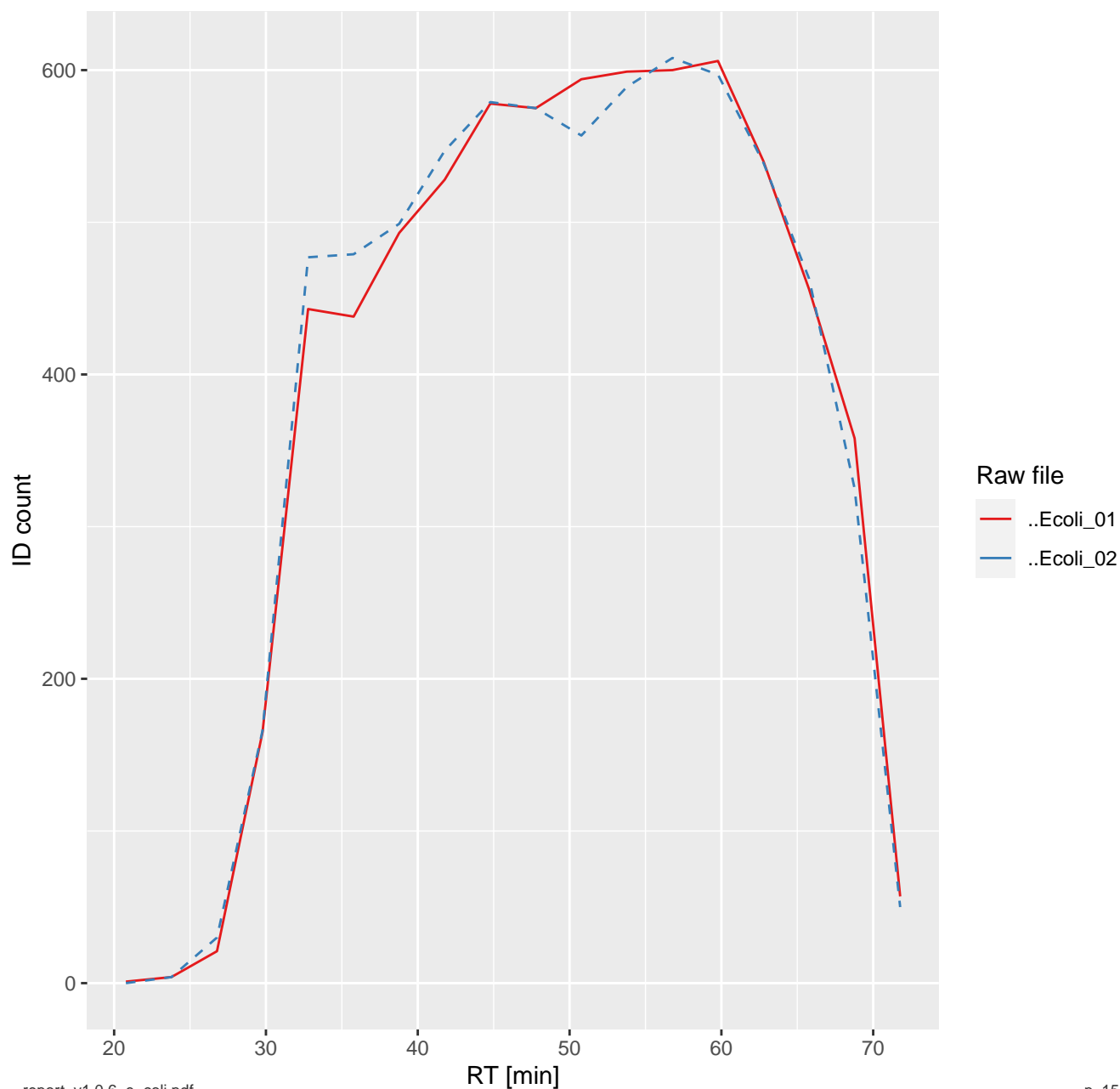
MSMSScans: TopN



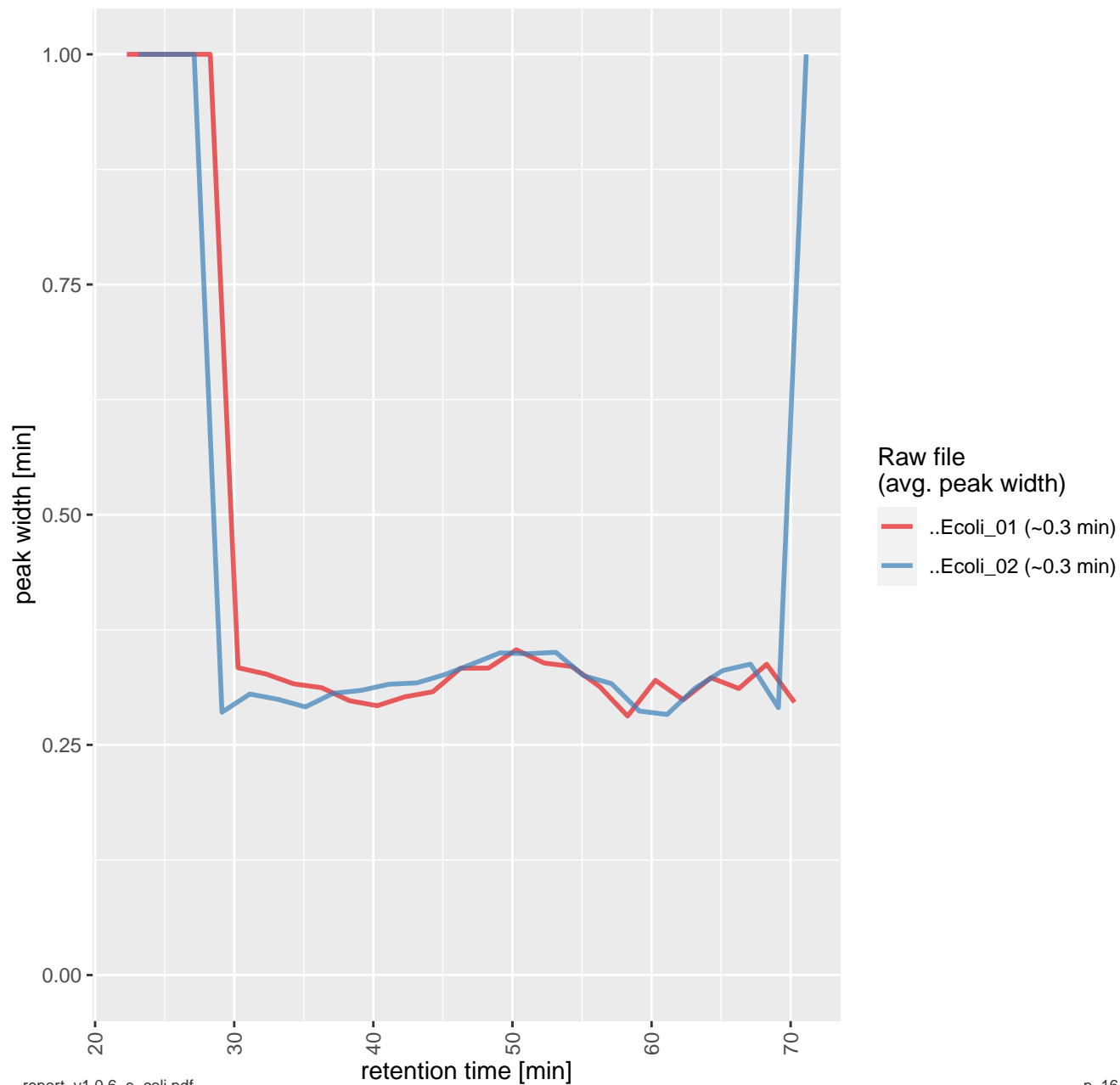
MSMSscans: TopN over RT



EVD: IDs over RT

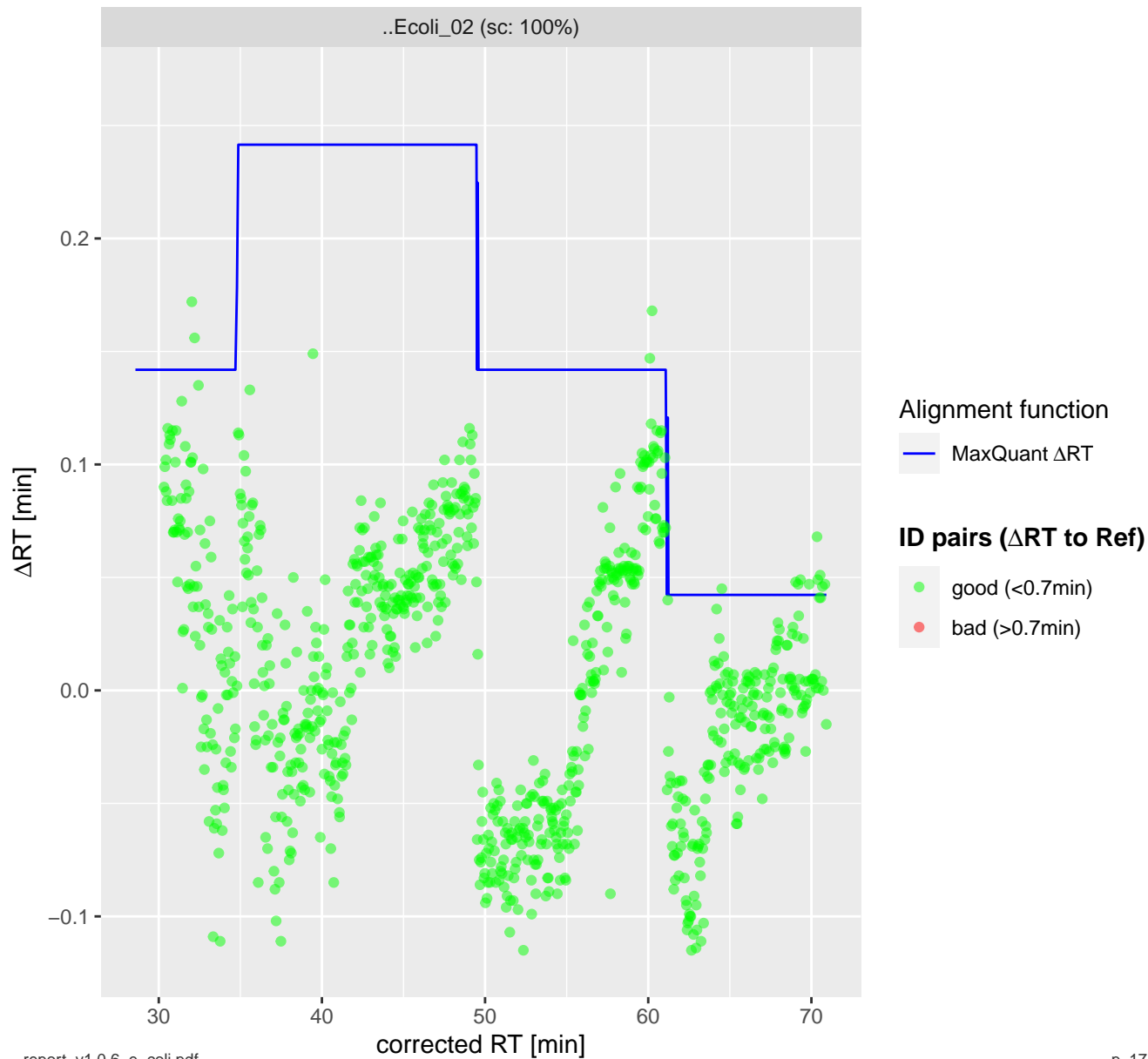


EVD: Peak width over RT

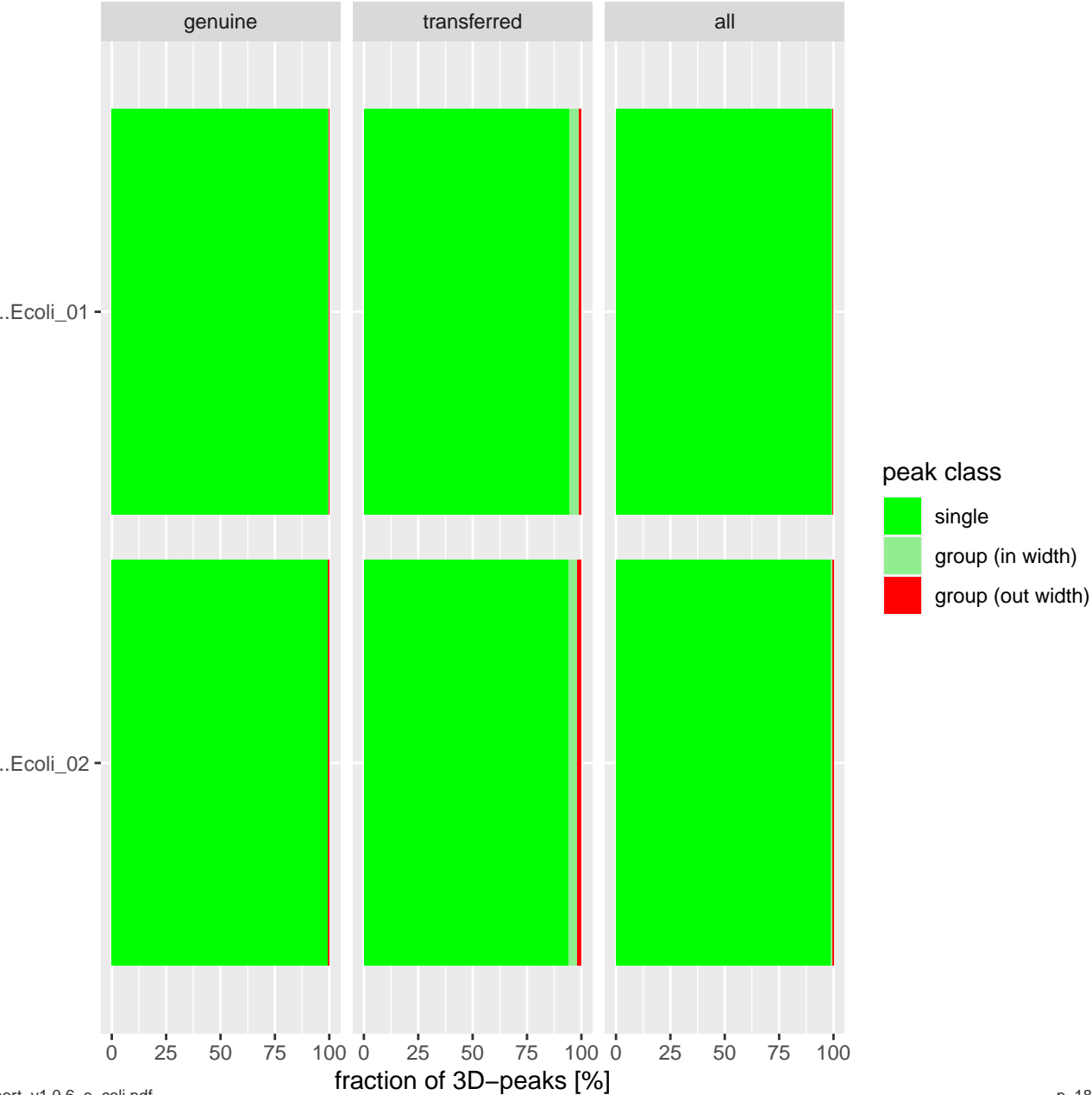


EVD: MBR – alignment

alignment reference: Toni_20120502_GM_Ecoli_01

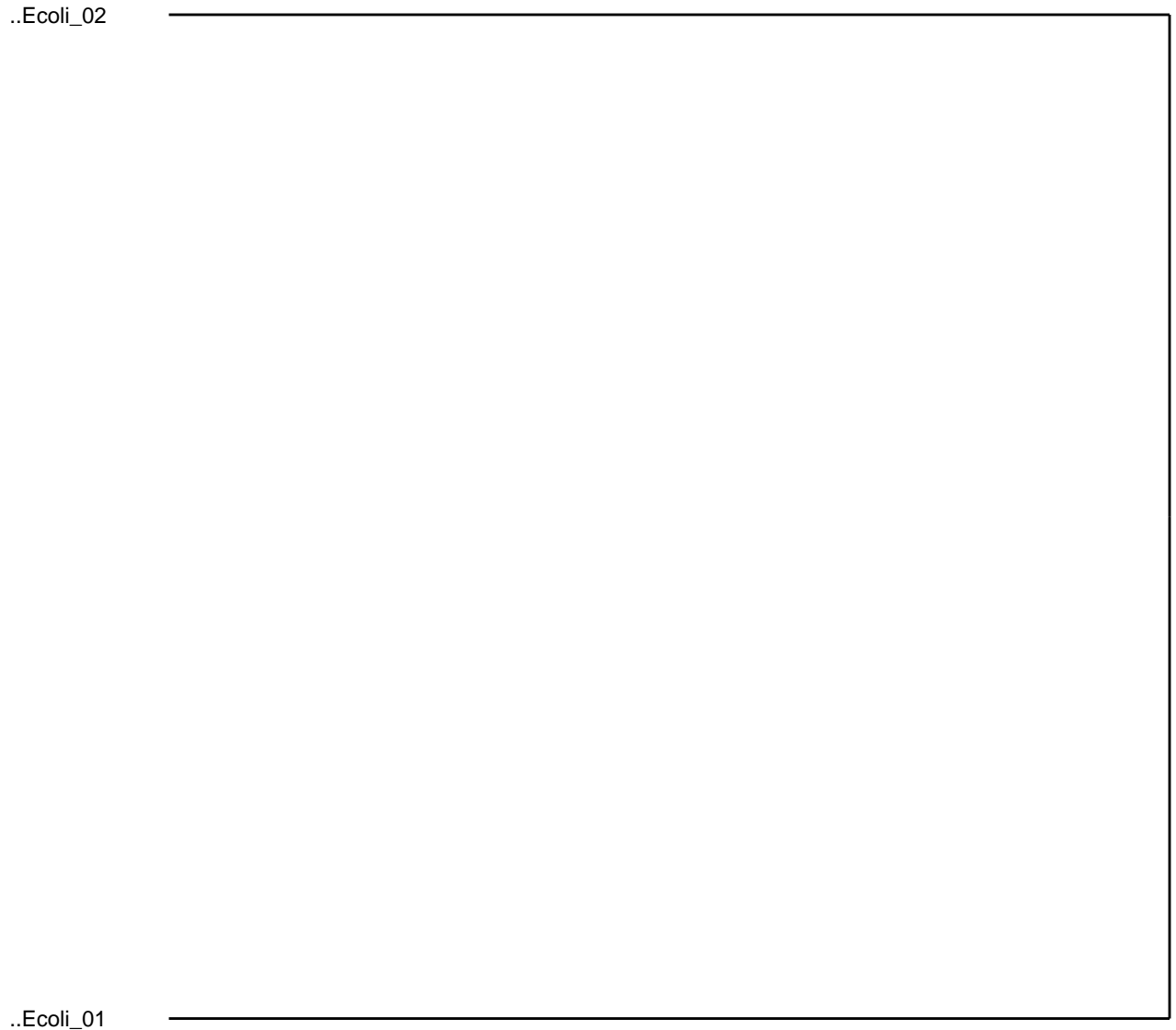


EVD: MBR – ID Transfer

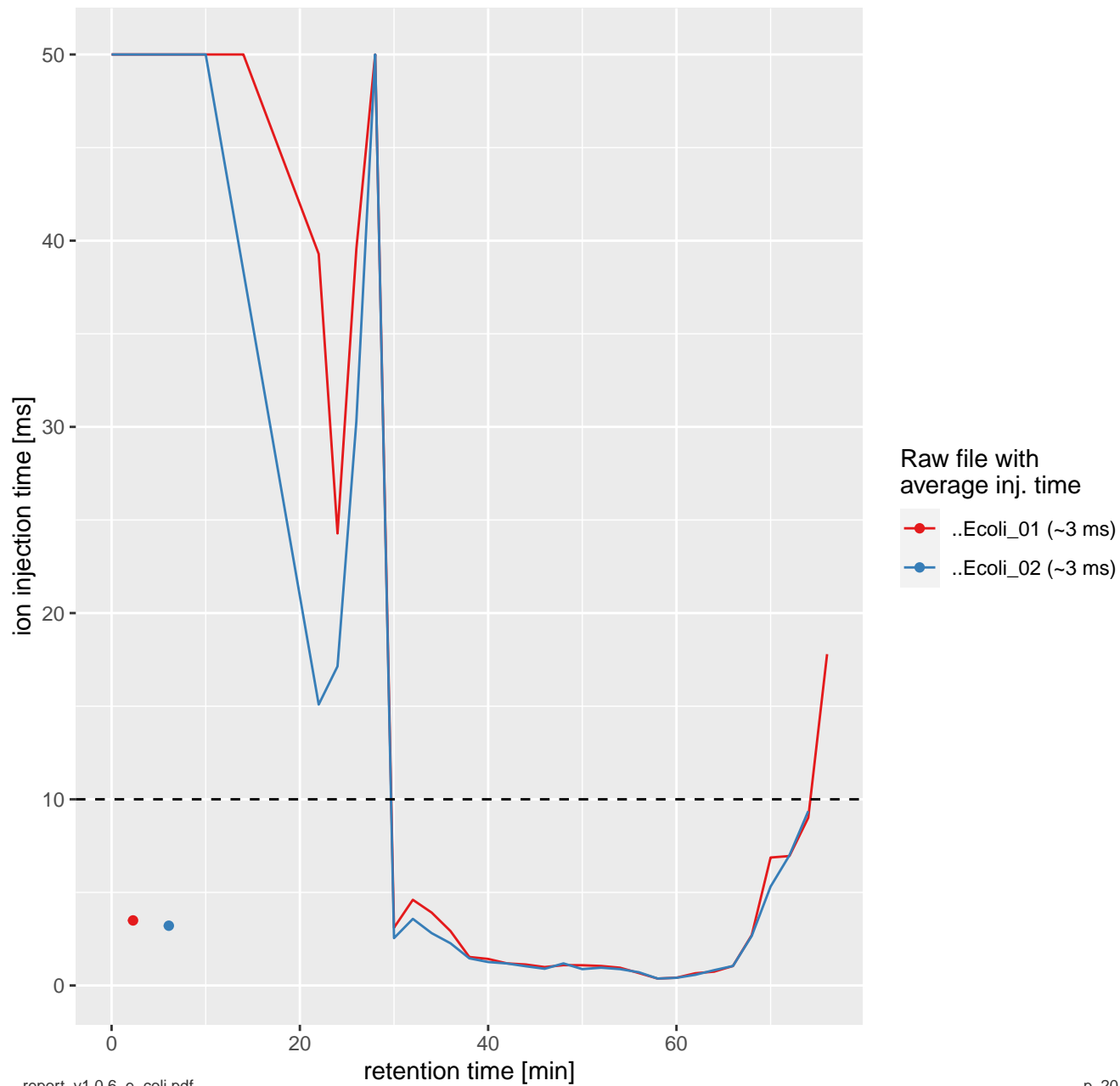


[experimental] EVD: Clustering Tree of Raw files

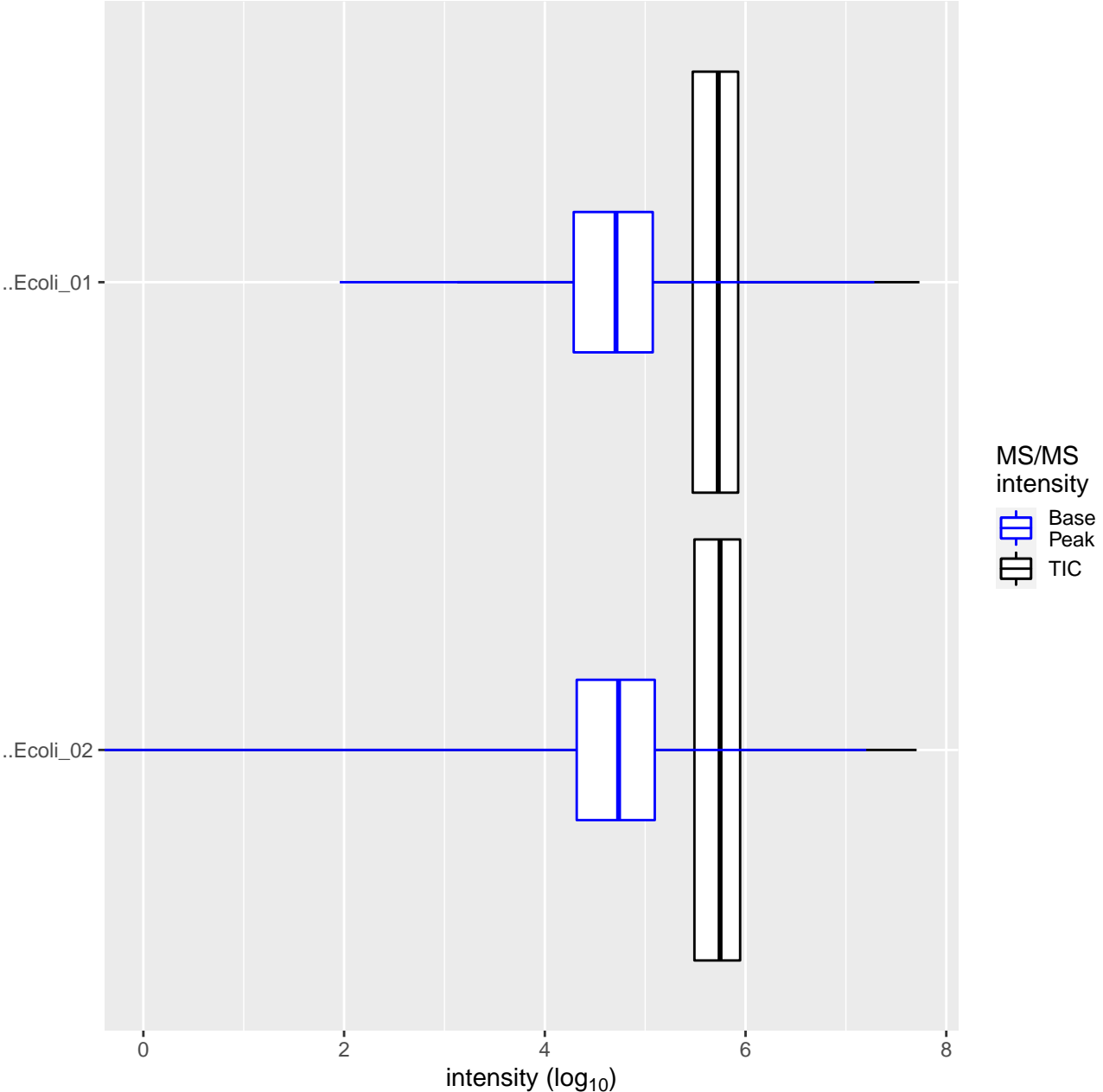
by Correlation of Corrected Retention Times



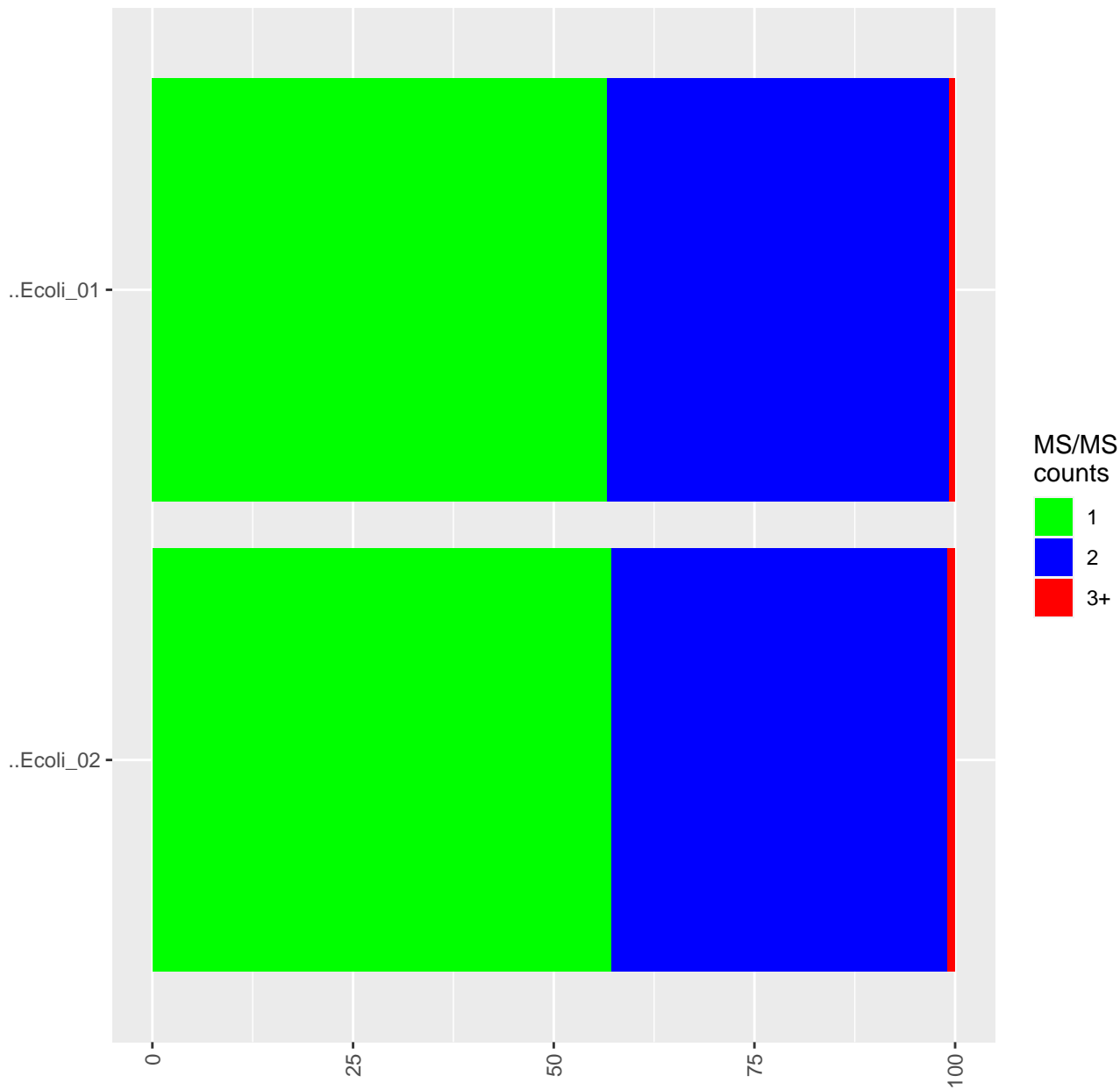
MSMSscans: Ion Injection Time over RT



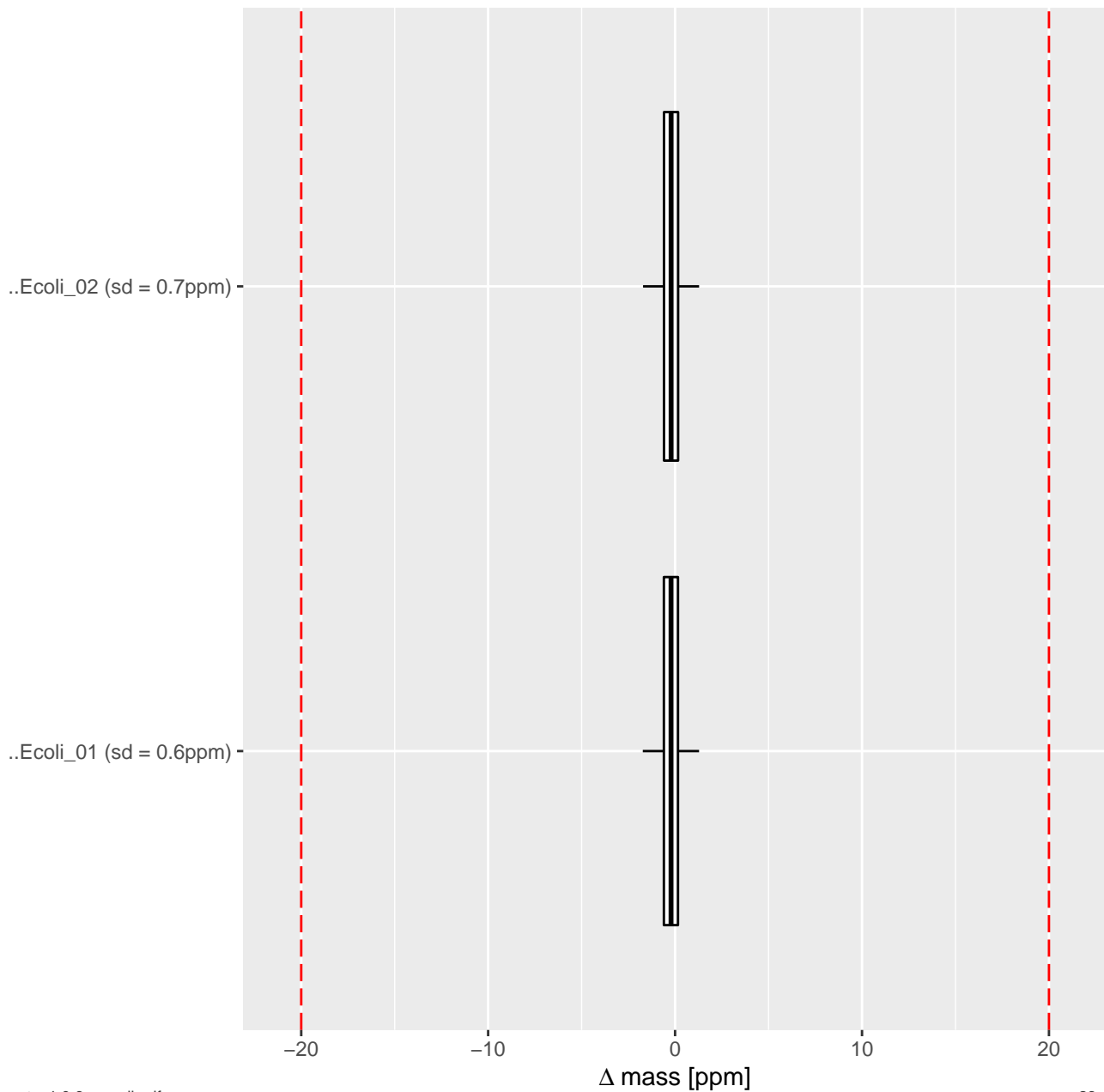
[experimental] MSMSscans: MS/MS intensity



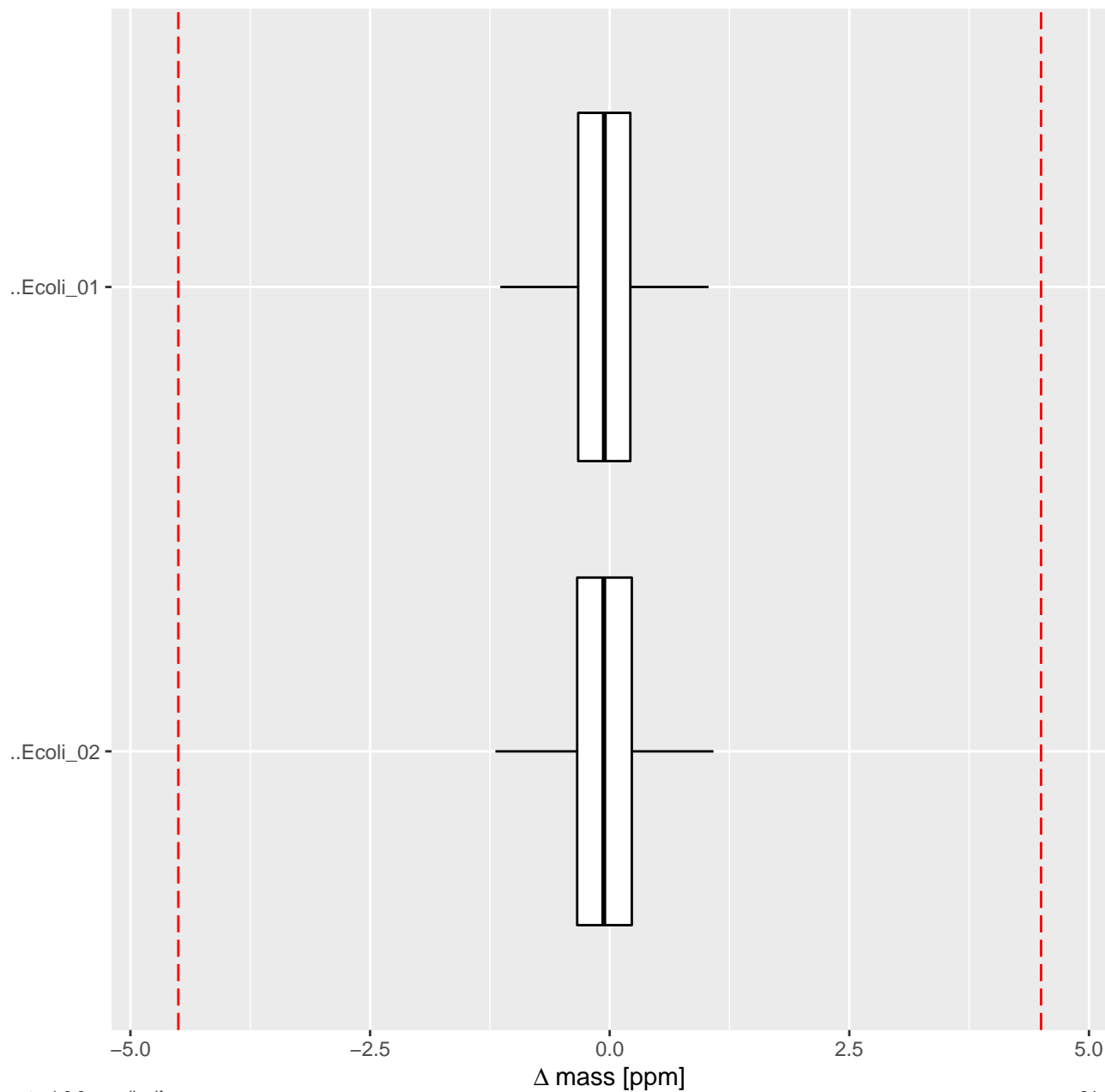
EVD: Oversampling (MS/MS counts per 3D-peak)



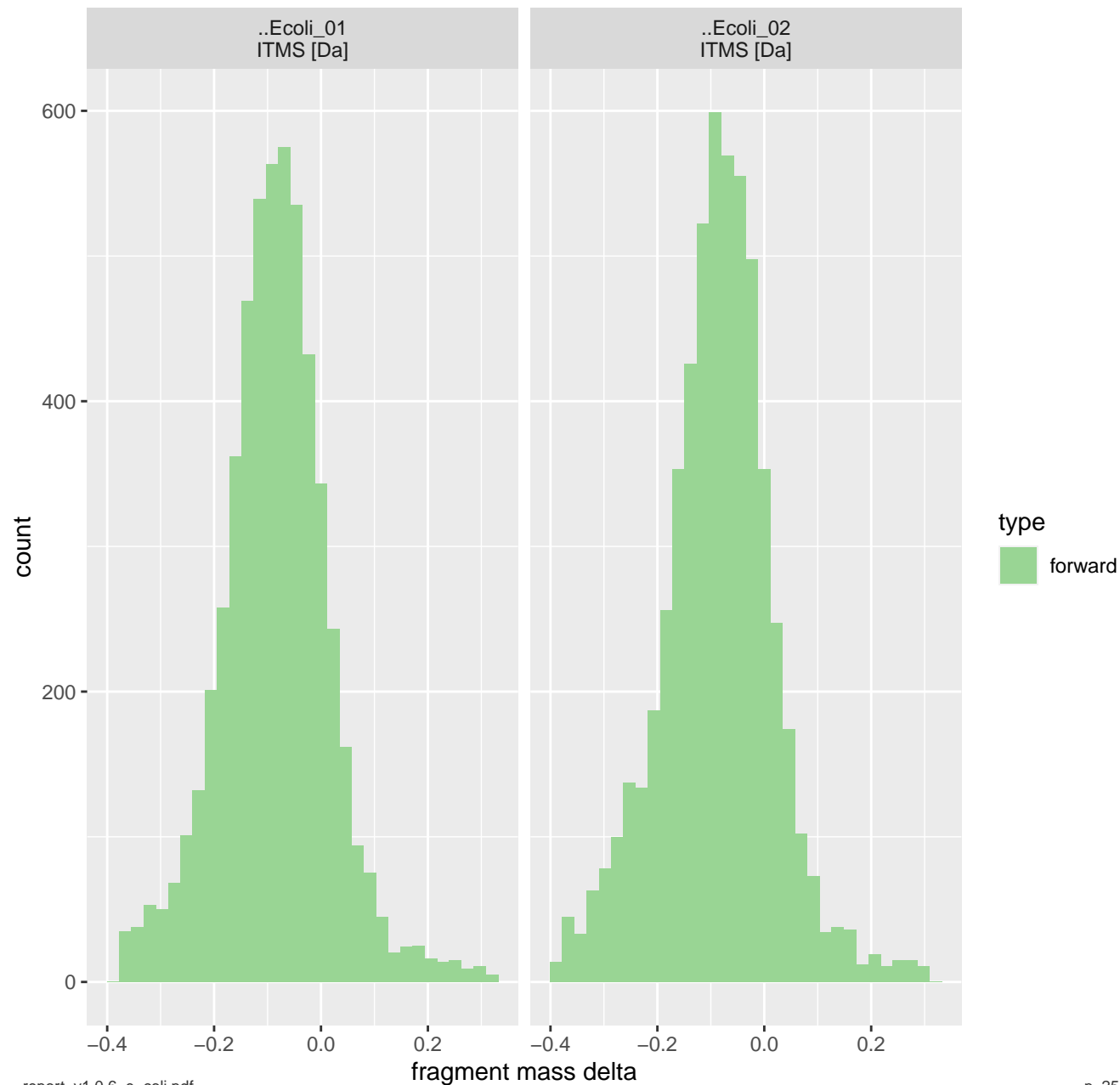
EVD: Uncalibrated mass error



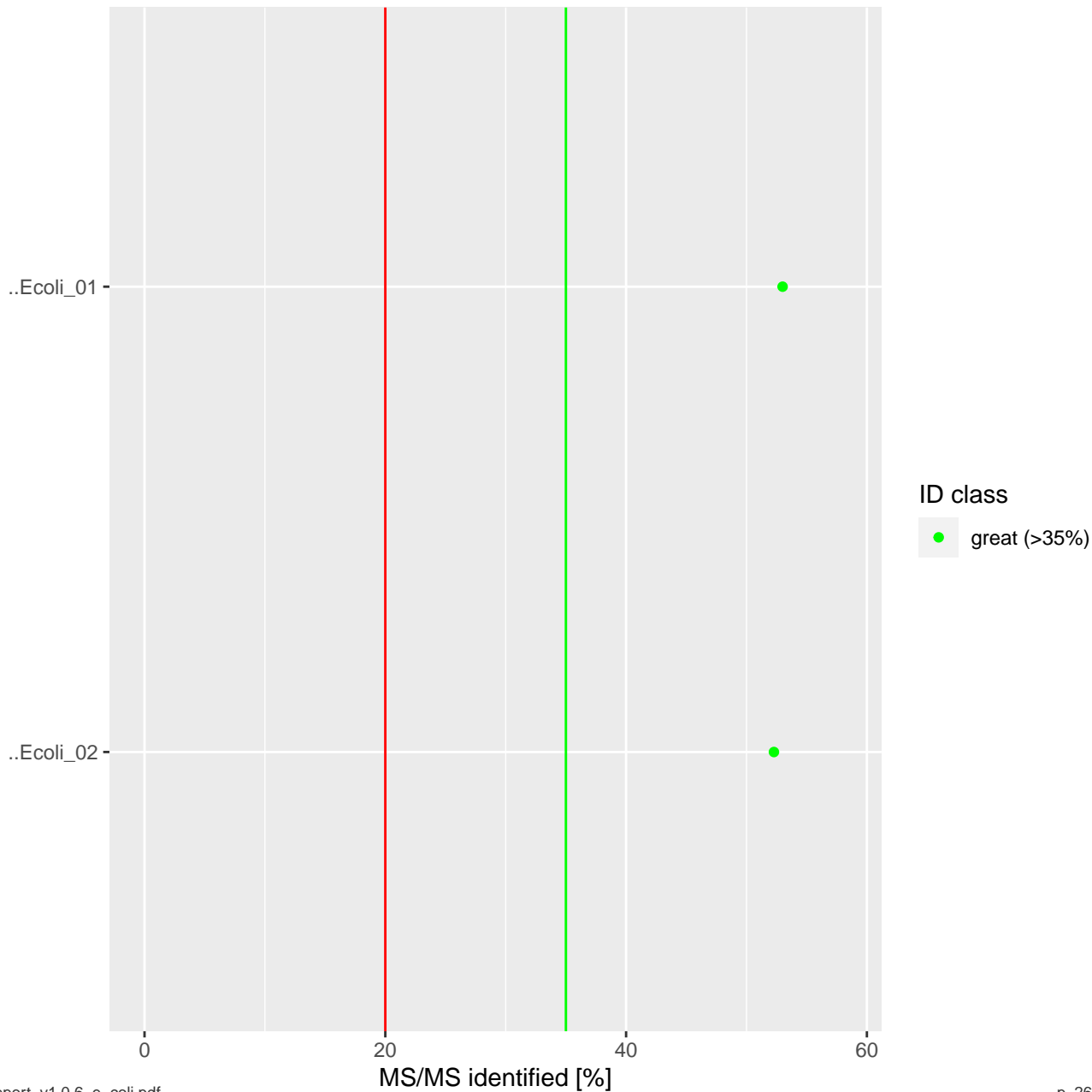
EVD: Calibrated mass error



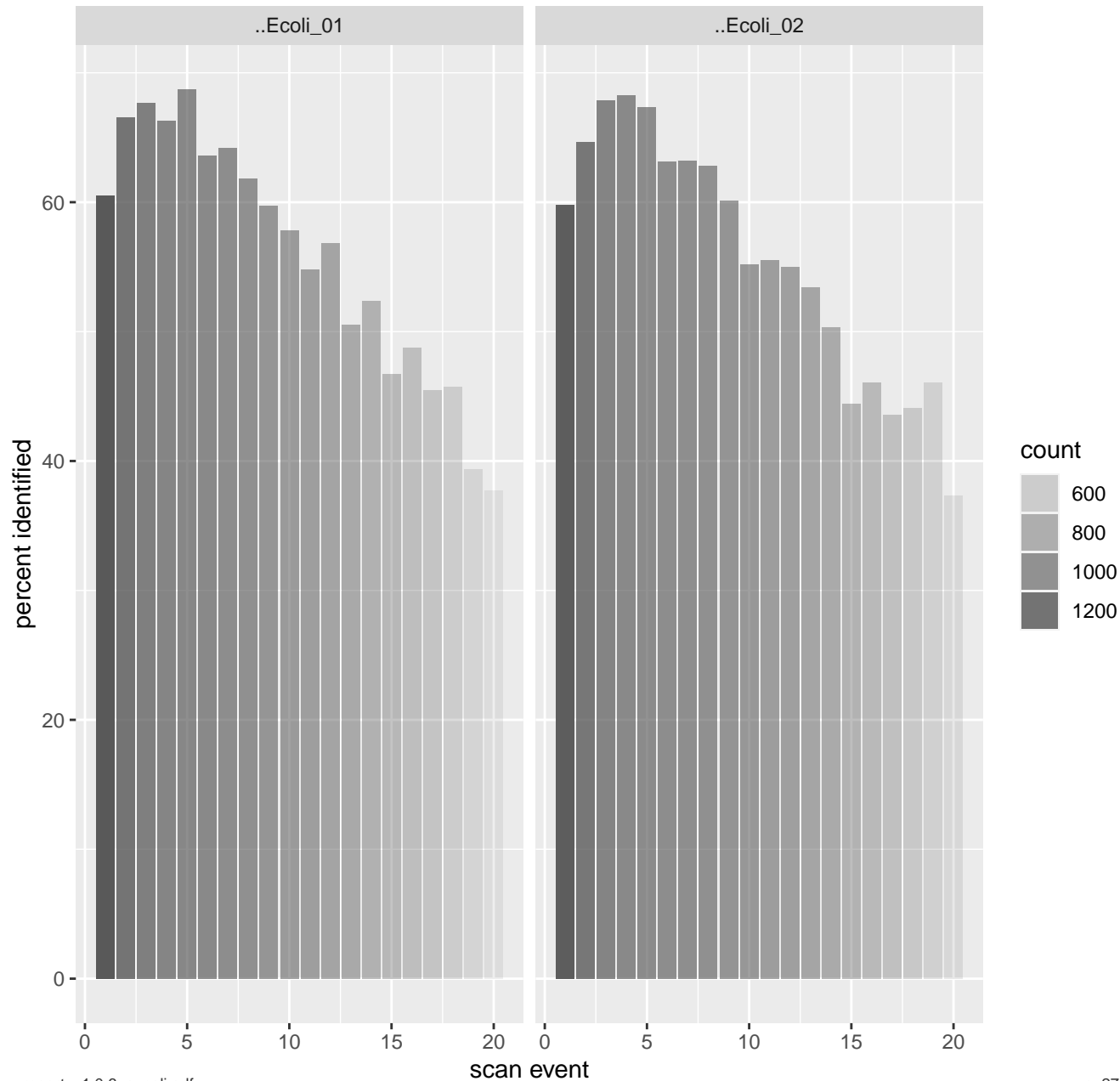
MSMS: Fragment mass errors per Raw file



SM: MS/MS identified per Raw file

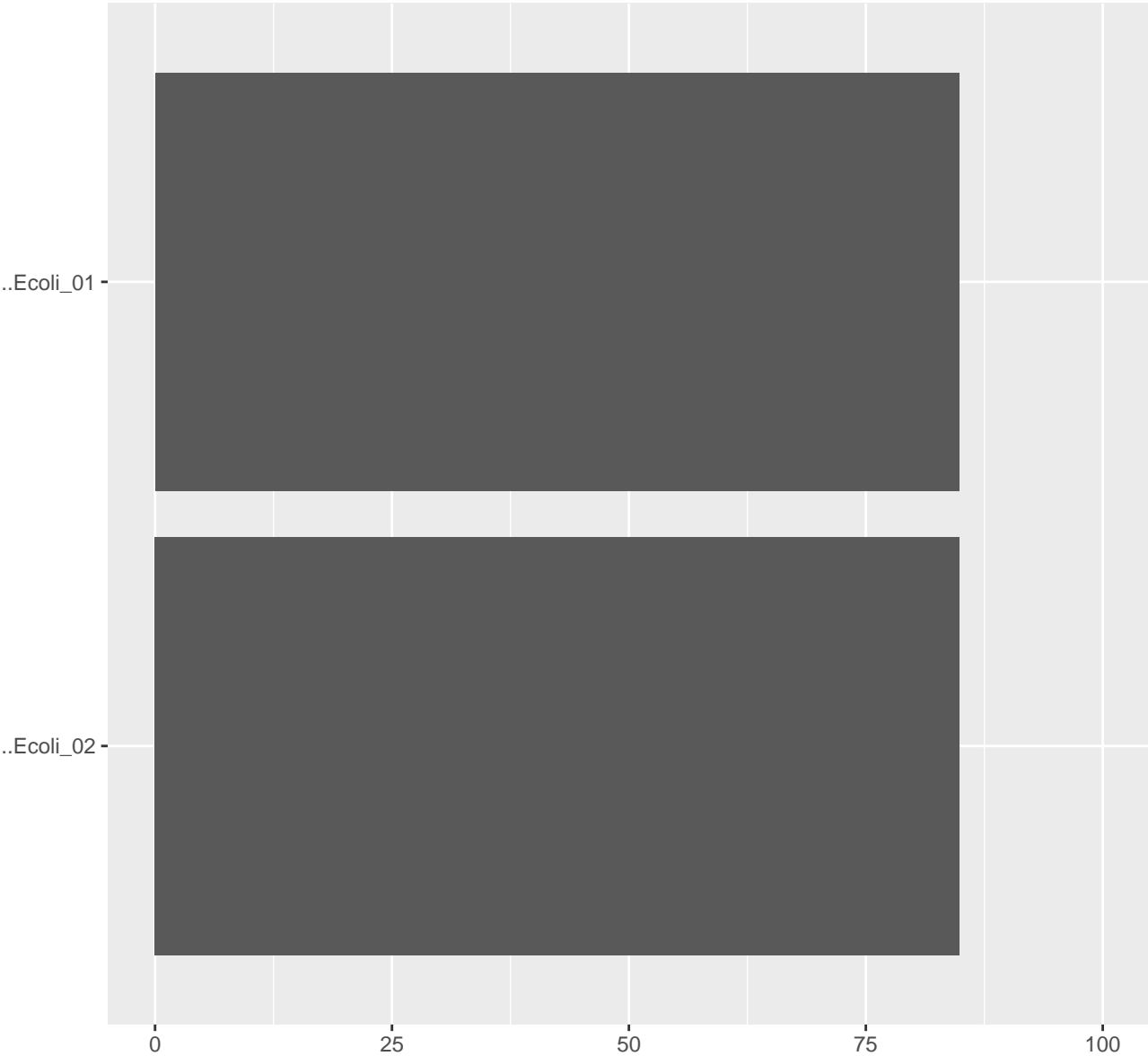


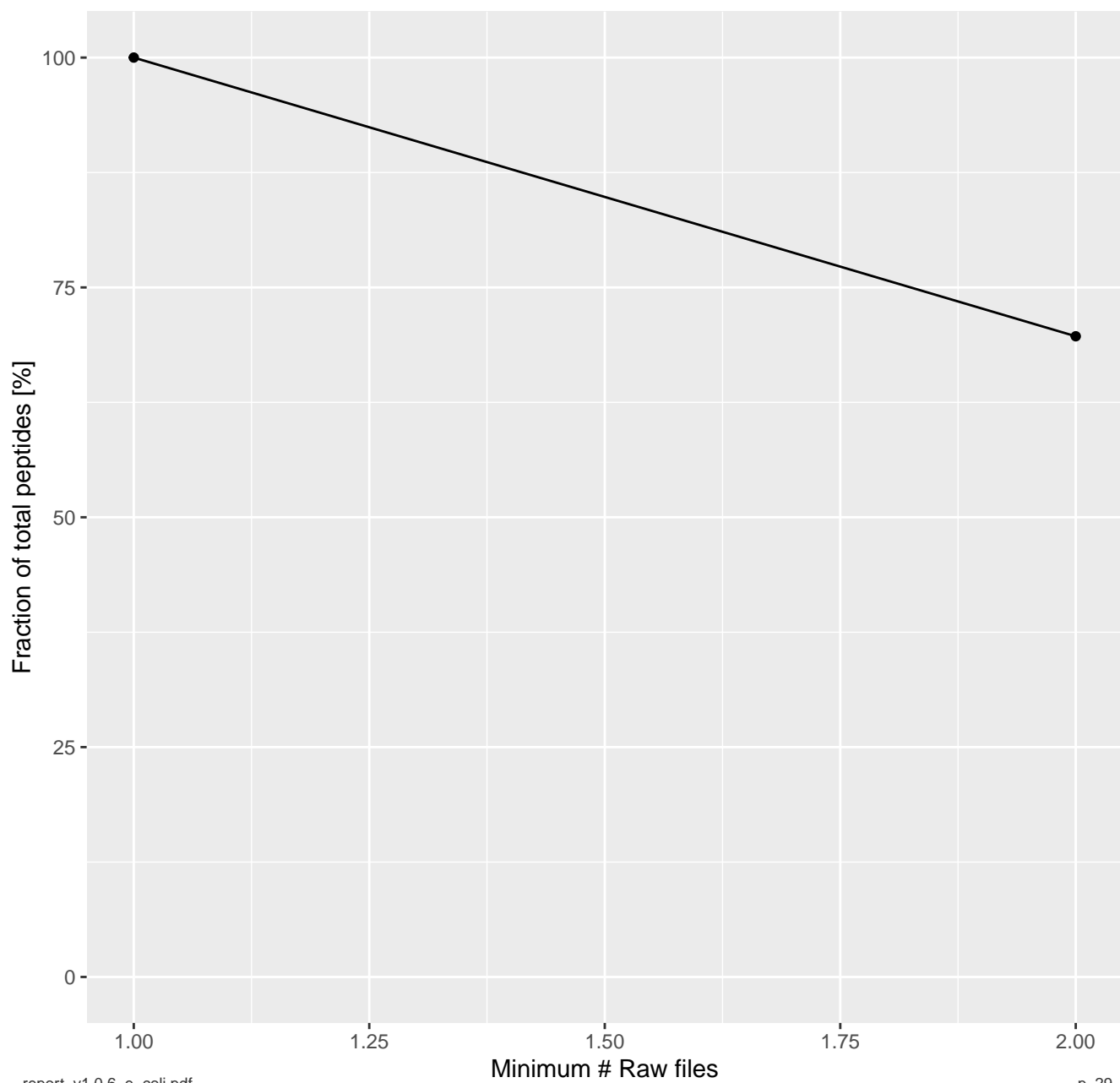
MSMSscans: TopN % identified over N



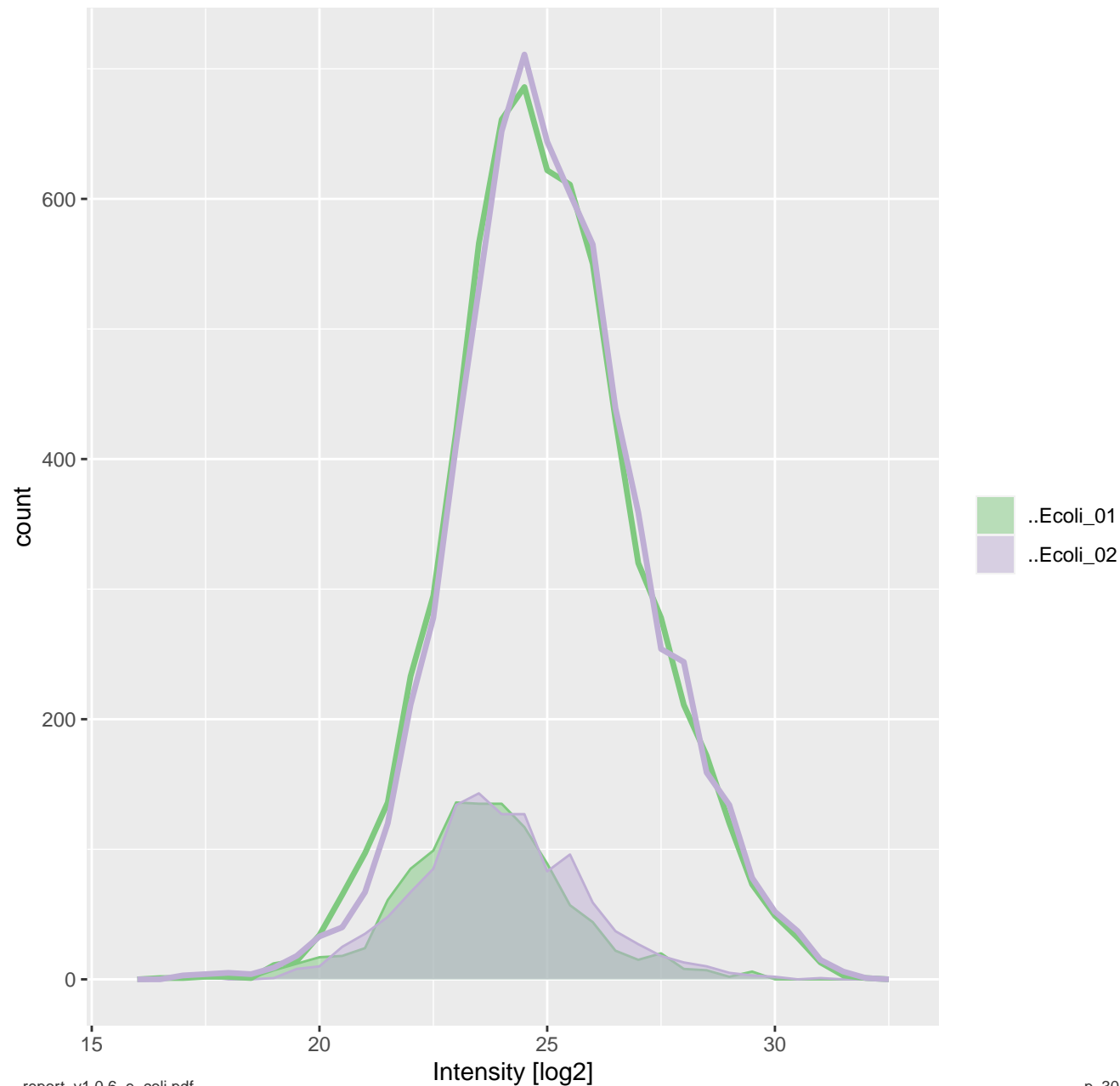
[experimental] EVD: Non-Missing Peptides

compared to all peptides seen in experiment

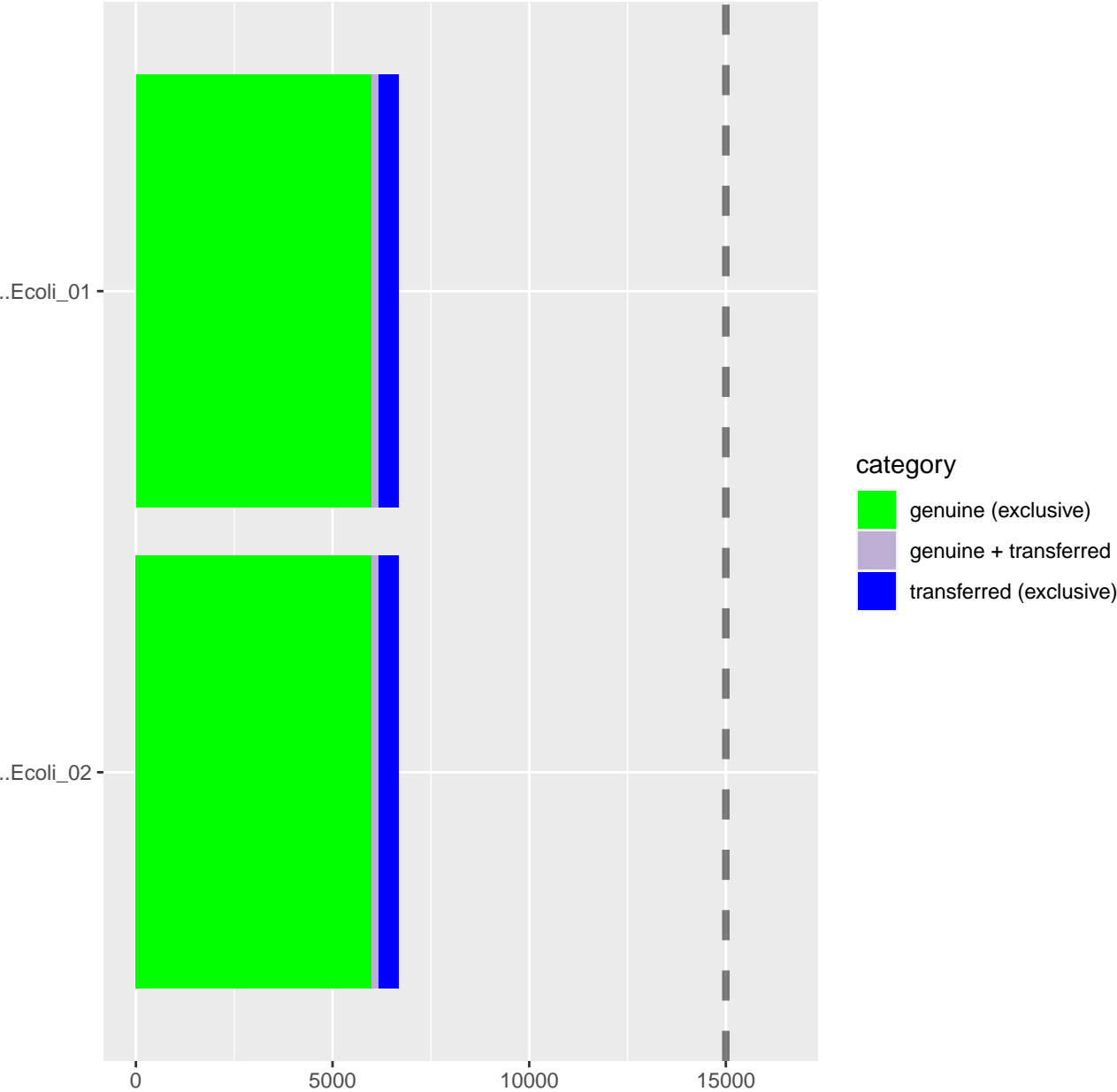




[experimental] EVD: Imputed Peptide Intensity Distribution of Missing Values



EVD: Peptide ID count



EVD: ProteinGroups count

MBR gain: +2%

