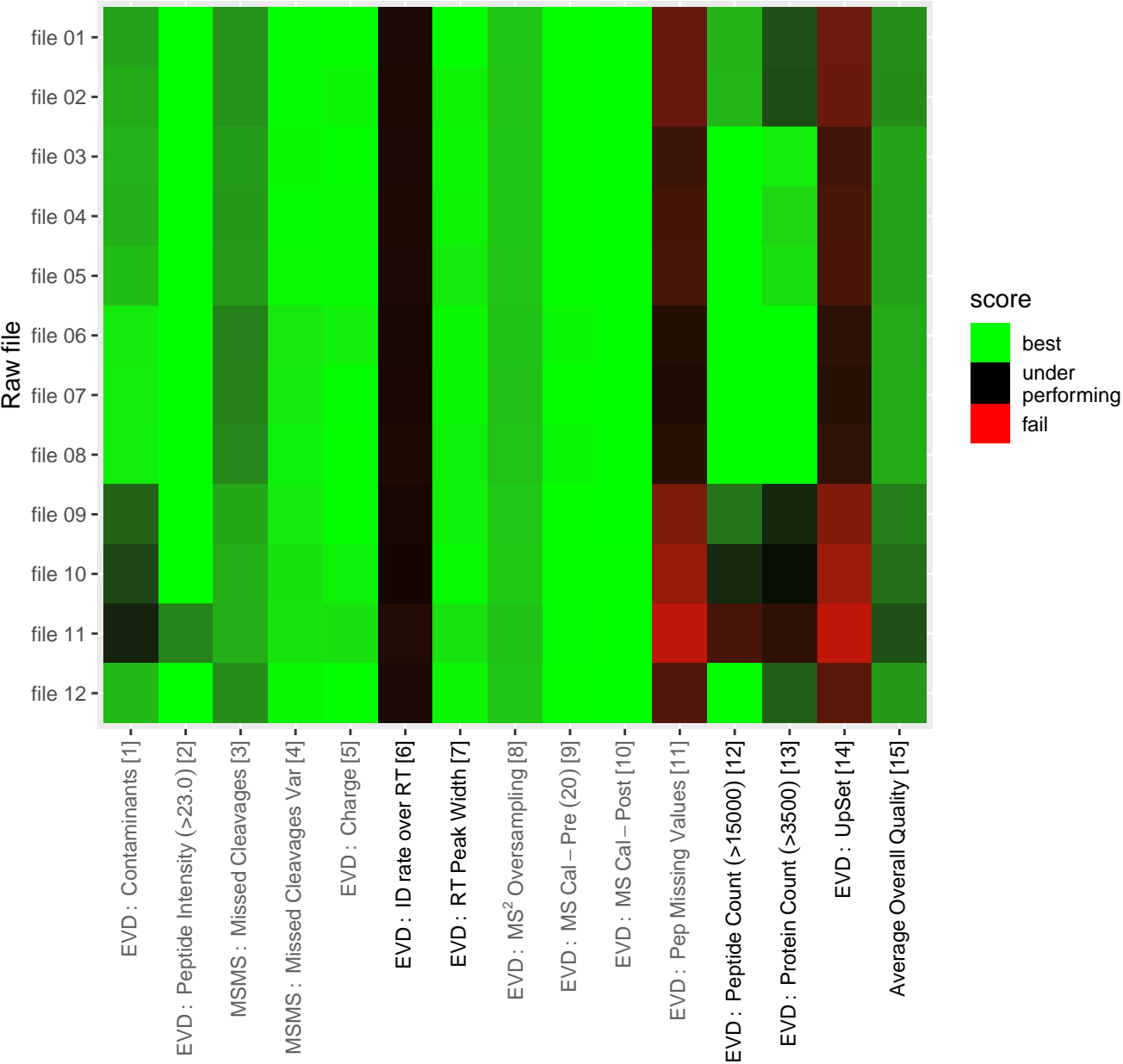


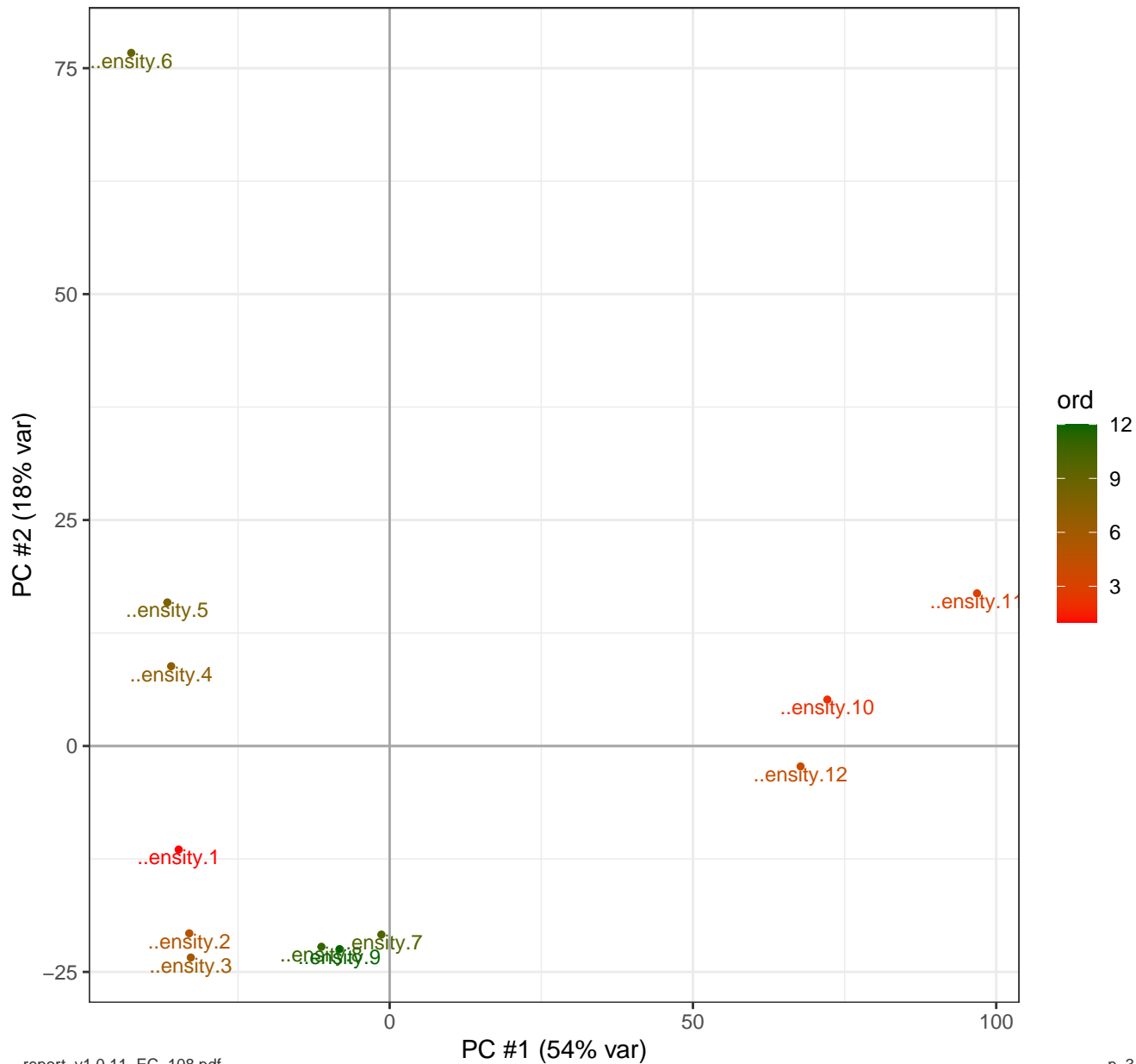
Performance overview



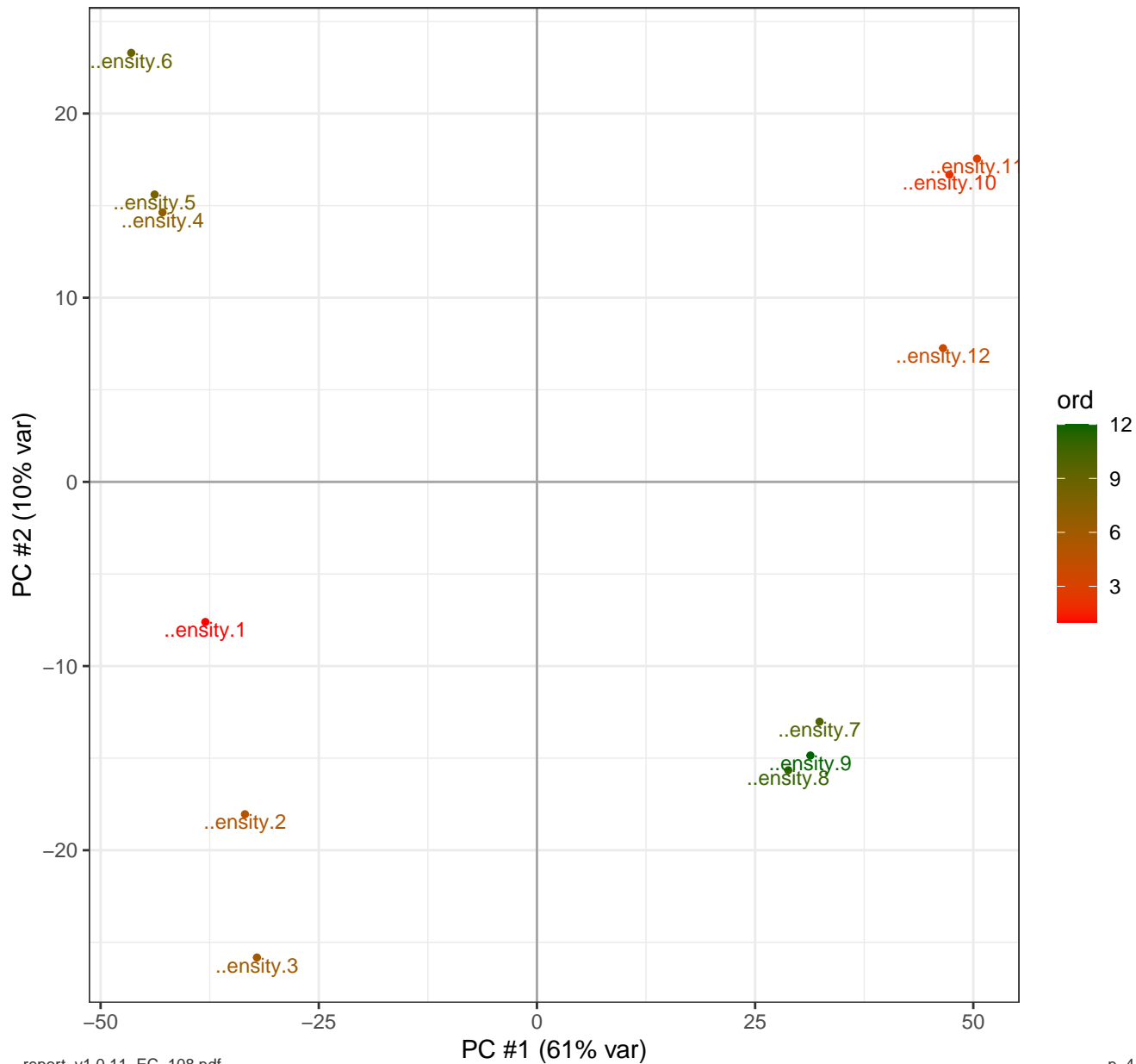
Mapping of Raw files to their short names
Mapping source: automatic
(automatic shortening of names was not sufficient – see 'best effort')

original	short name	best effort
EC_118-M990-A04-P11909-1	file 01	..A04-P..1909-1
EC_118-M990-A05-P11910-1	file 02	..A05-P..1910-1
EC_118-M990-A07-P11912-1	file 03	..A07-P..1912-1
EC_118-M990-A08-P11913-1	file 04	..A08-P..1913-1
EC_118-M990-B01-P11914-1	file 05	..B01-P..1914-1
EC_118-M990-B02-P11915-1	file 06	..B02-P..1915-1
EC_118-M990-B03-P11916-1	file 07	..B03-P..1916-1
EC_118-M990-B04-P11917-1	file 08	..B04-P..1917-1
EC_118-M990-A01-P11906-1	file 09	..A01-P..1906-1
EC_118-M990-A02-P11907-1	file 10	..A02-P..1907-1
EC_118-M990-A03-P11908-1	file 11	..A03-P..1908-1
EC_118-M990-A06-P11911-1	file 12	..A06-P..1911-1

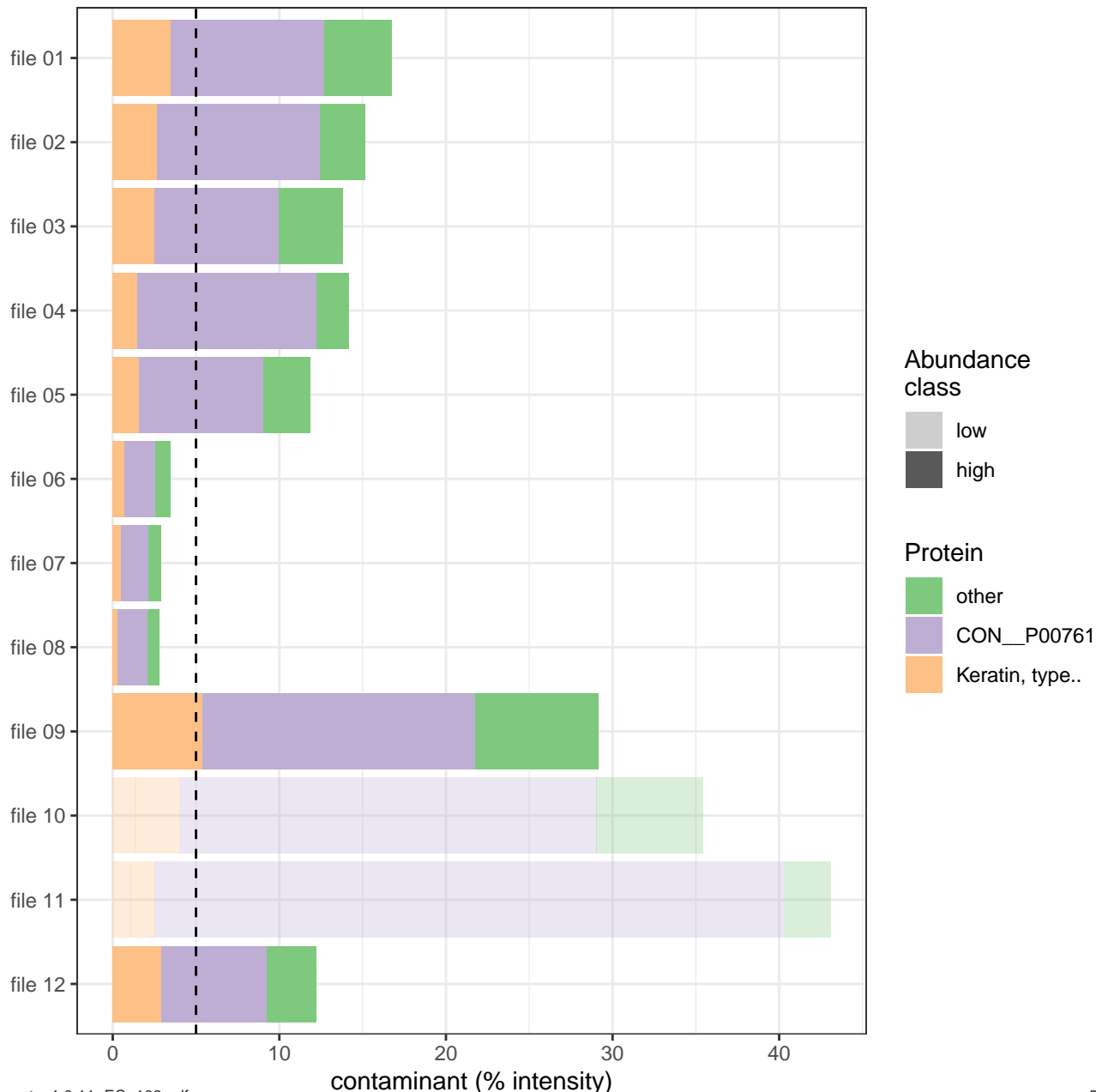
PG: PCA of 'raw intensity'
(excludes contaminants)



PG: PCA of 'lfq intensity'
(excludes contaminants)

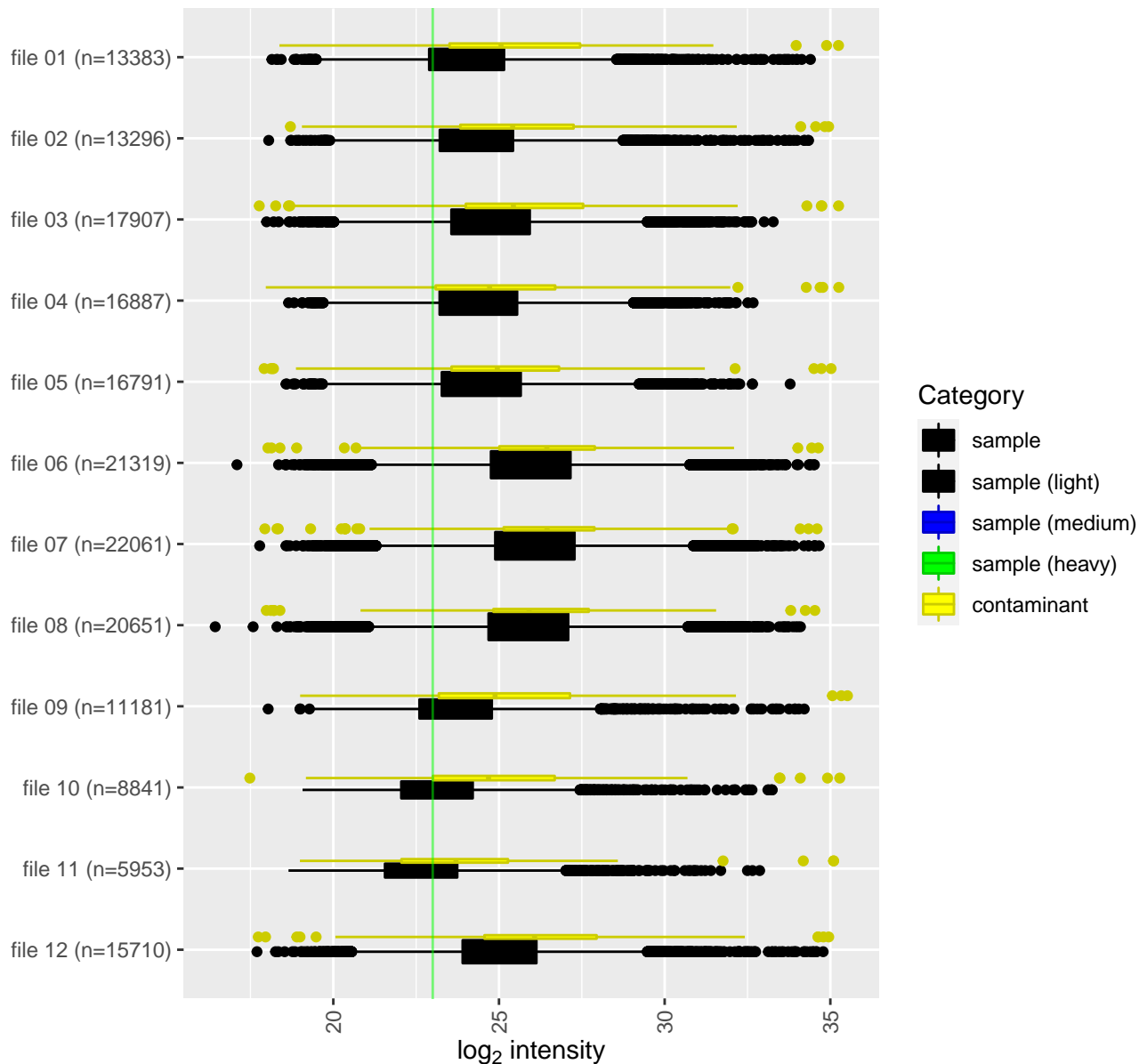


EVD: Top5 Contaminants per Raw file



EVD: peptide intensity distribution

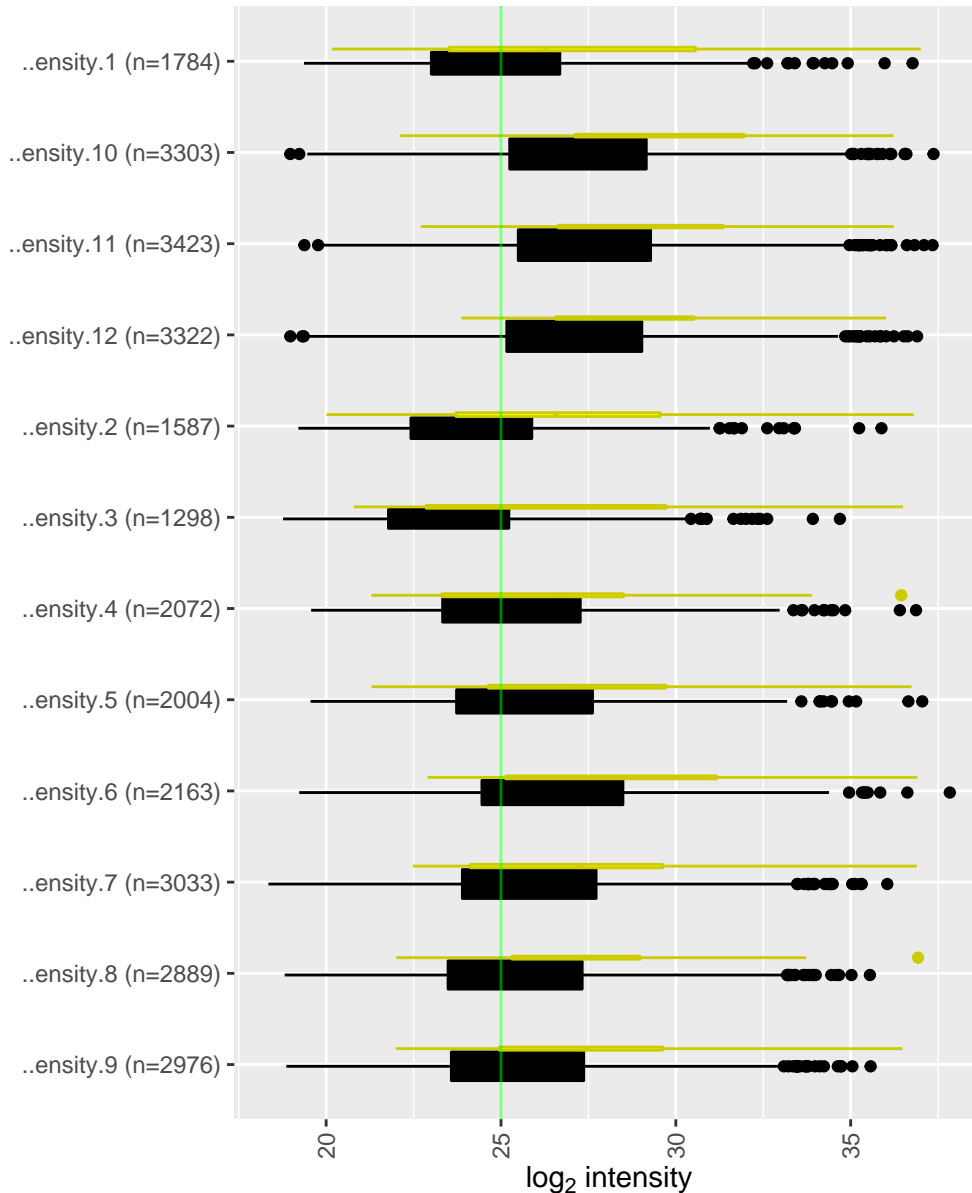
RSD 4.4% (expected < 5%)



PG: intensity distribution

RSD 4.5% (w/o zero int.; expected < 5%)

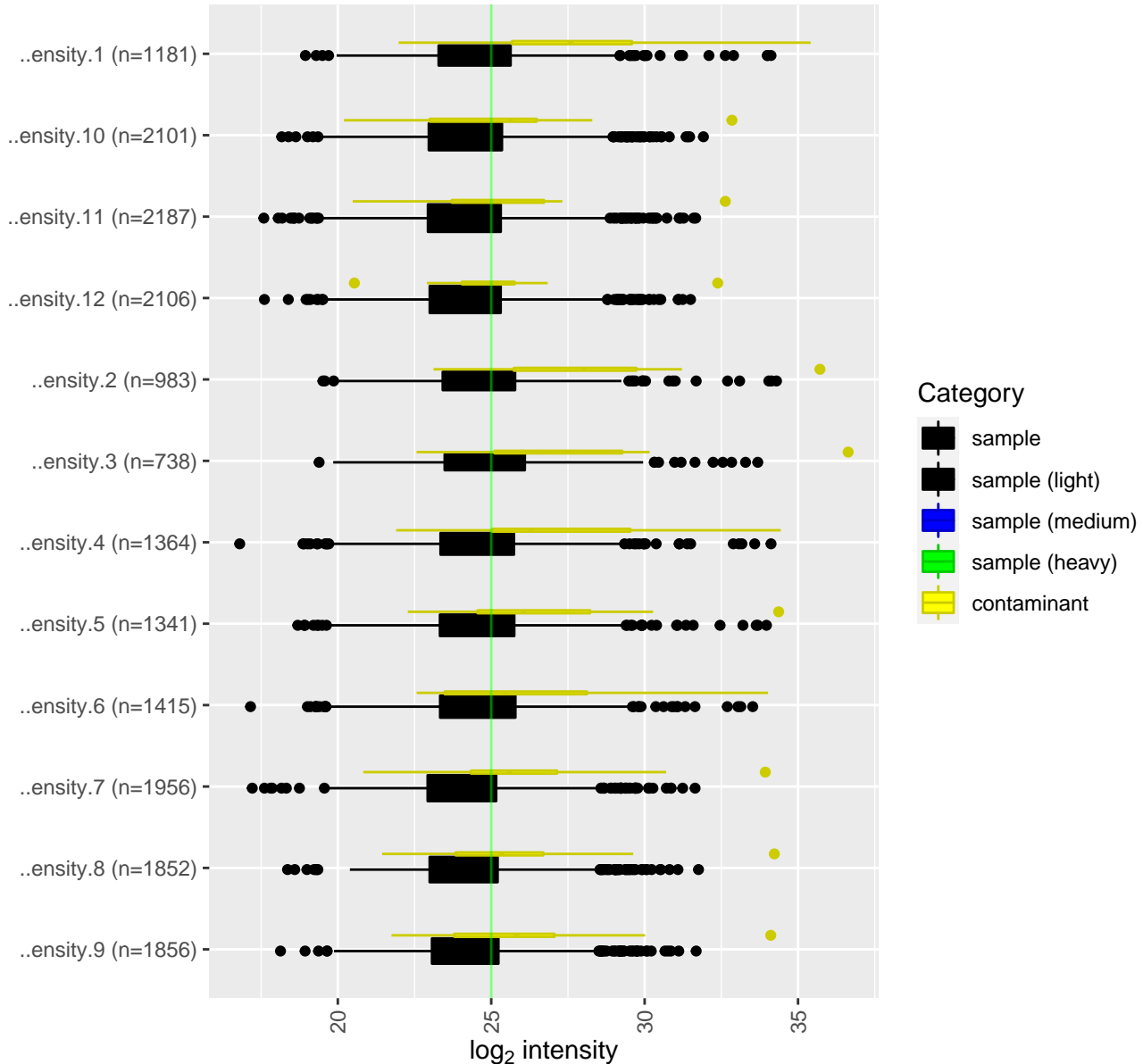
RSD 104.7% [high RSD --> few peptides]



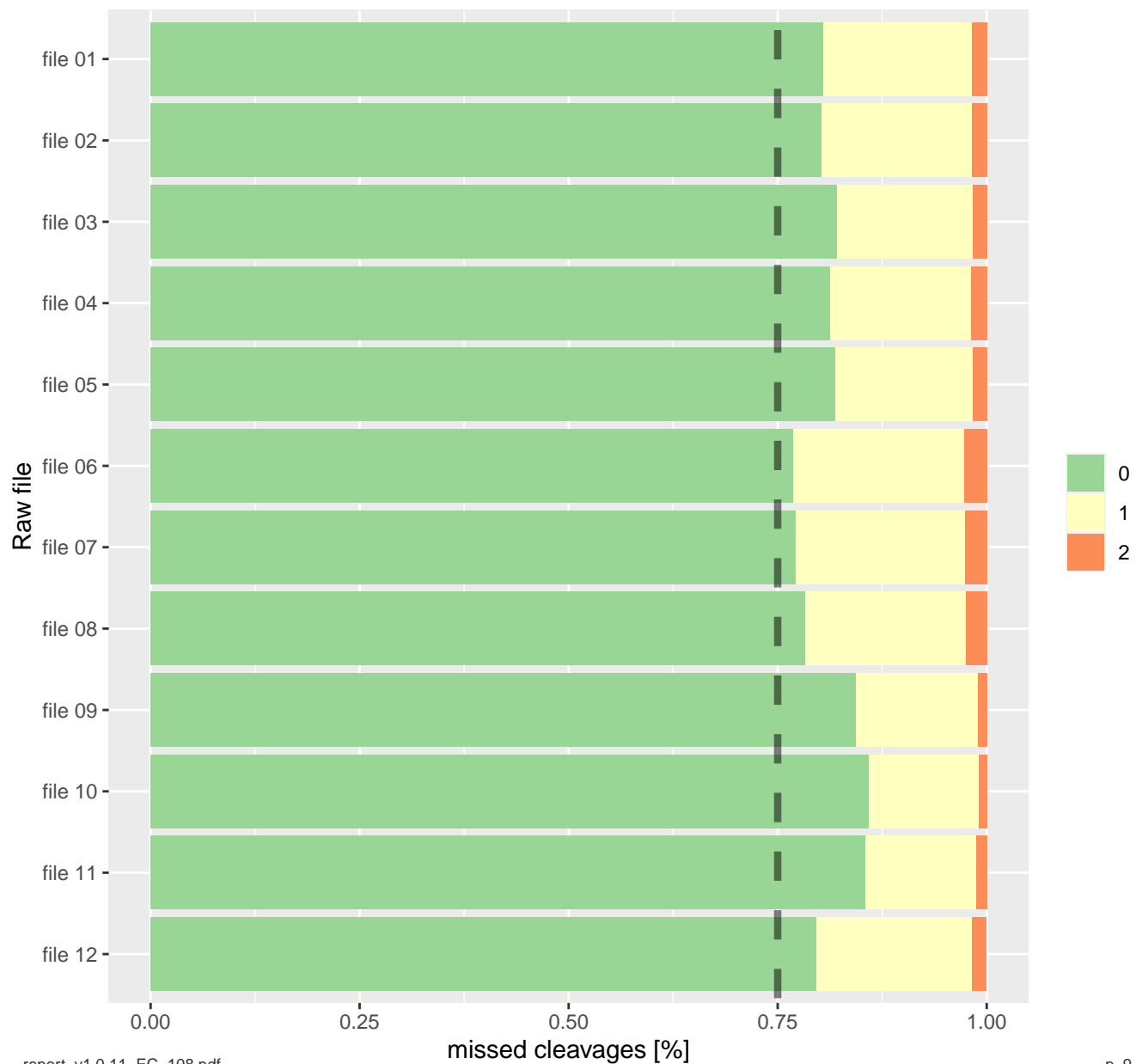
PG: LFQ intensity distribution

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

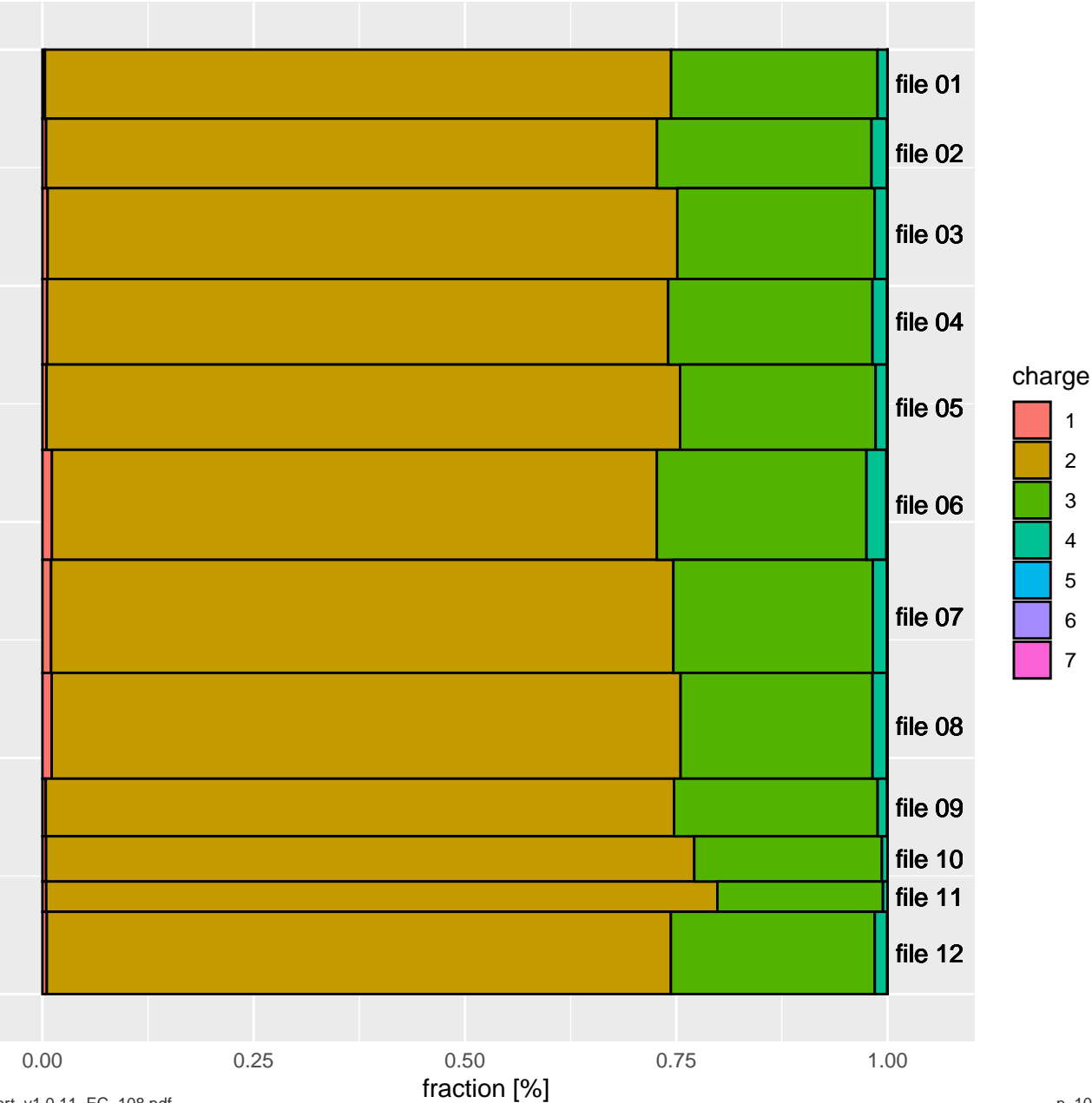
RSD NaN% [high RSD --> few peptides]



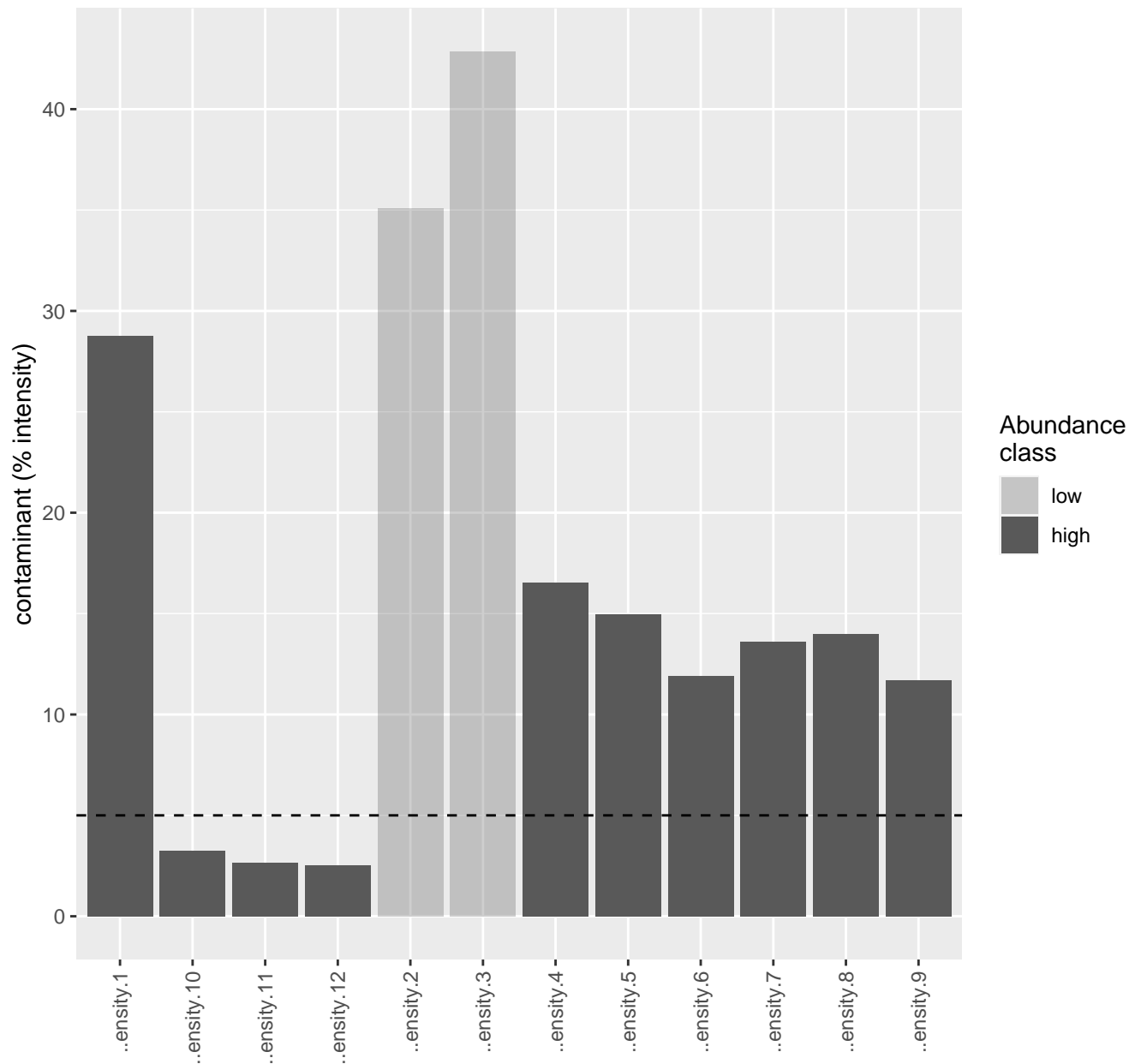
MSMS: Missed cleavages per Raw file (excludes contaminants)



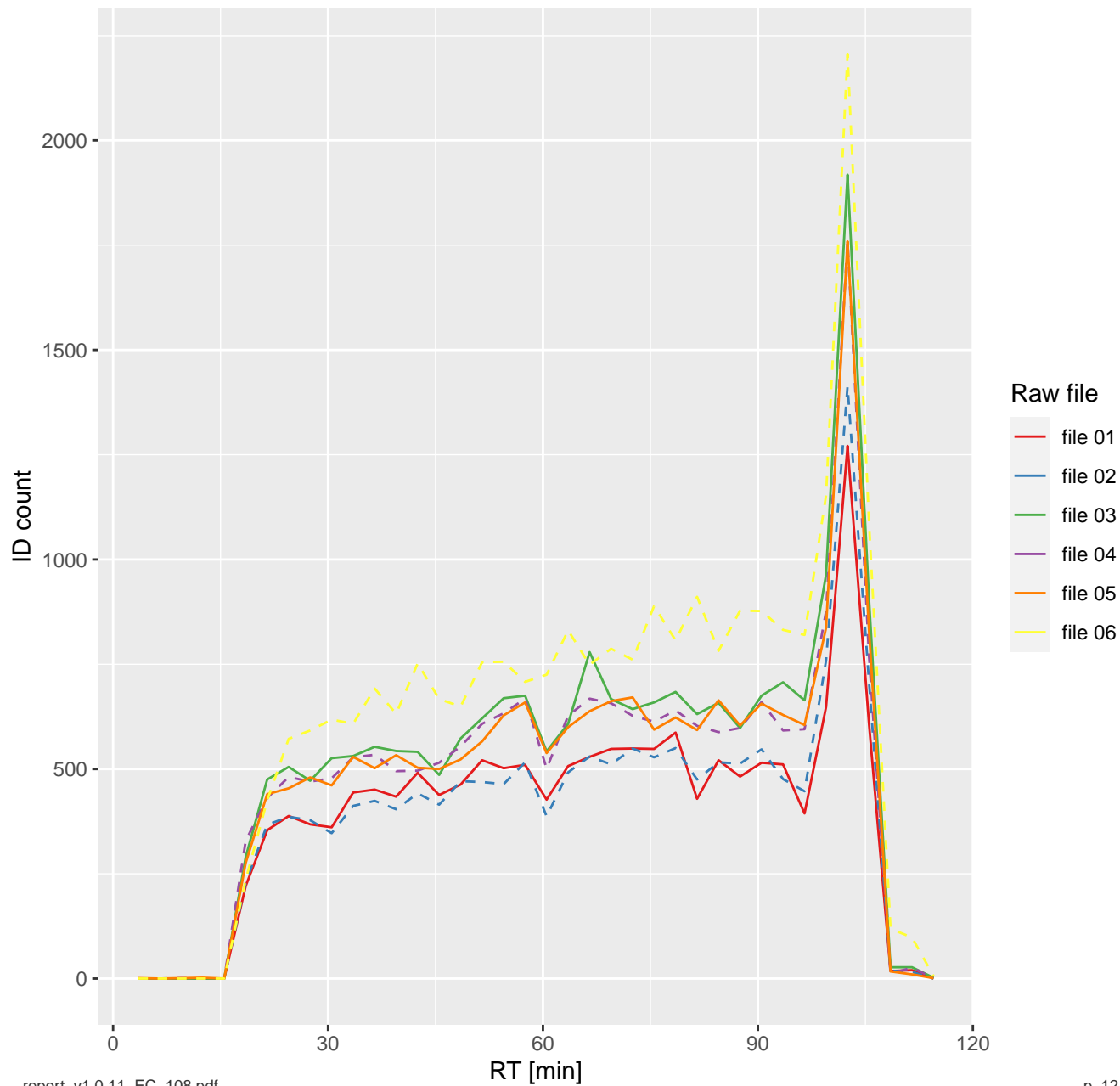
EVD: charge distribution



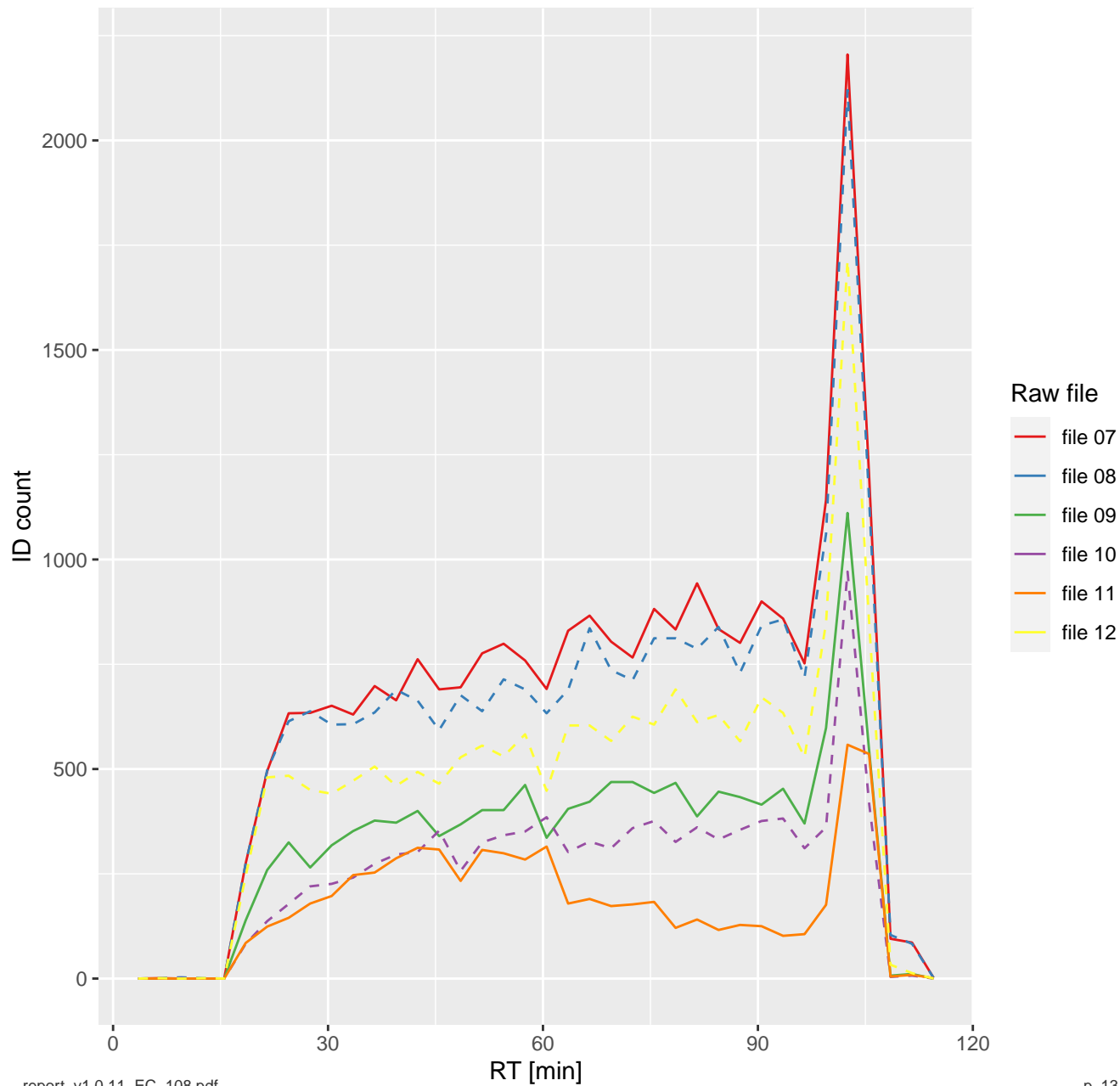
PG: Contaminant per condition



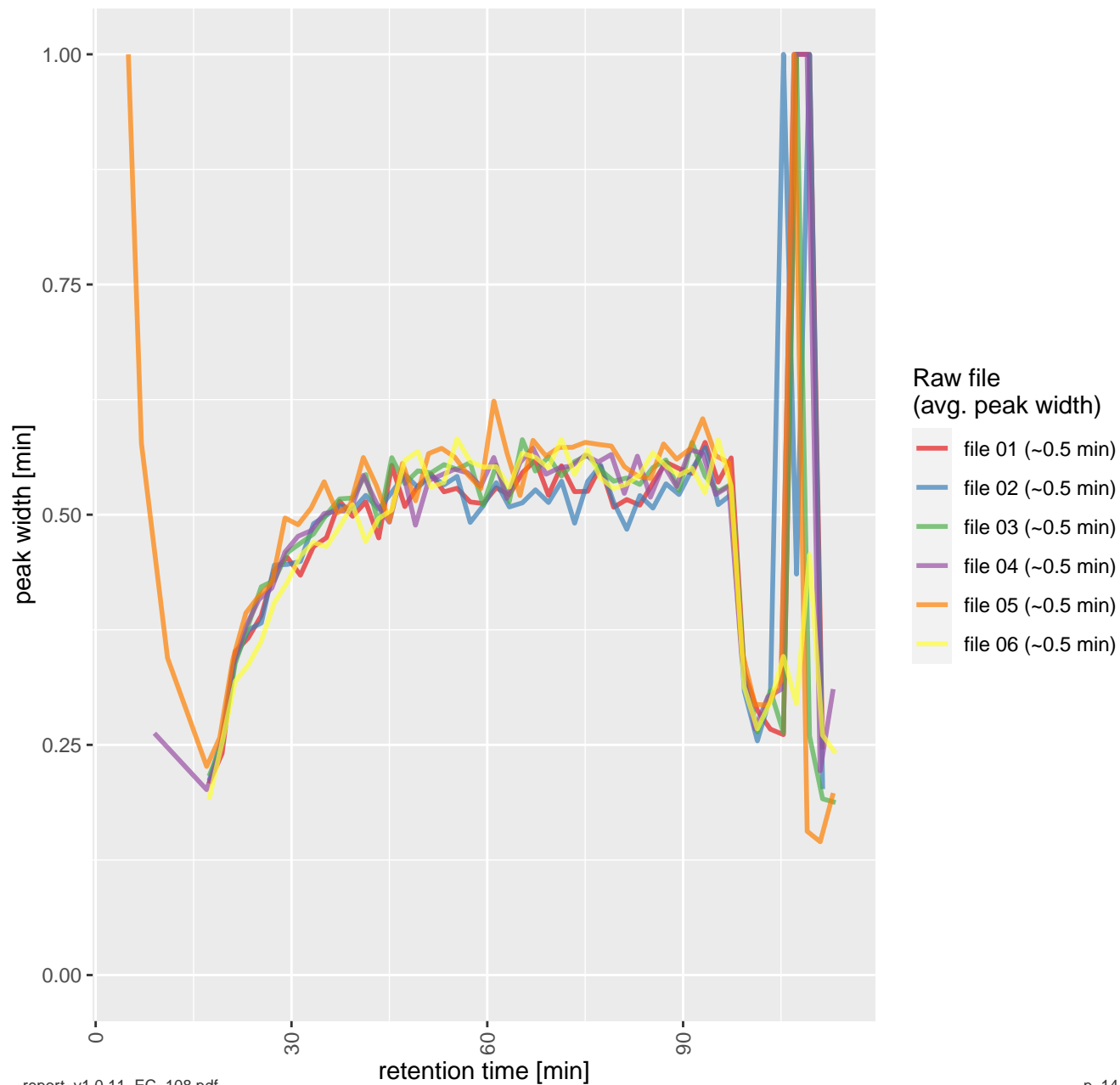
EVD: IDs over RT



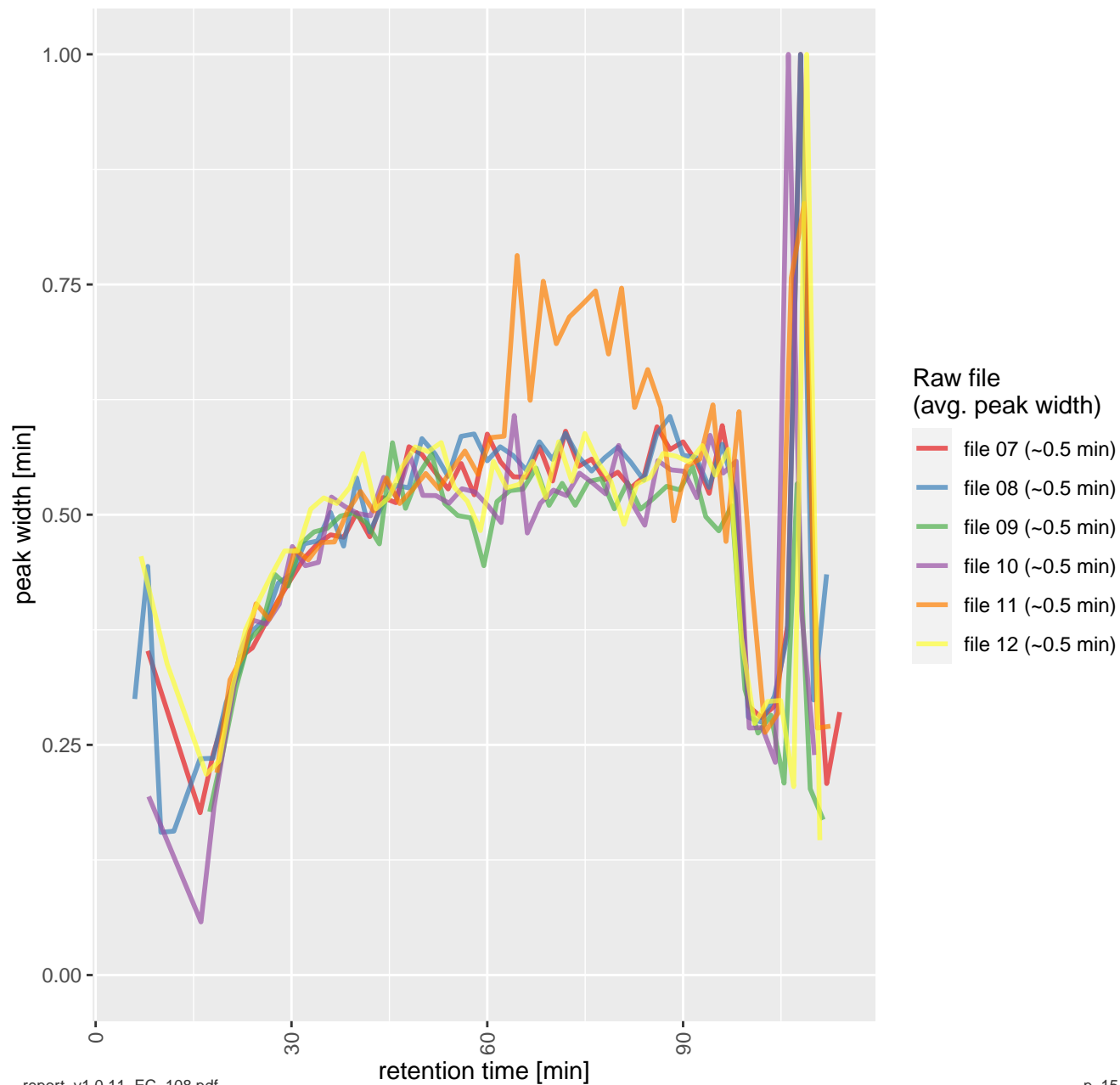
EVD: IDs over RT



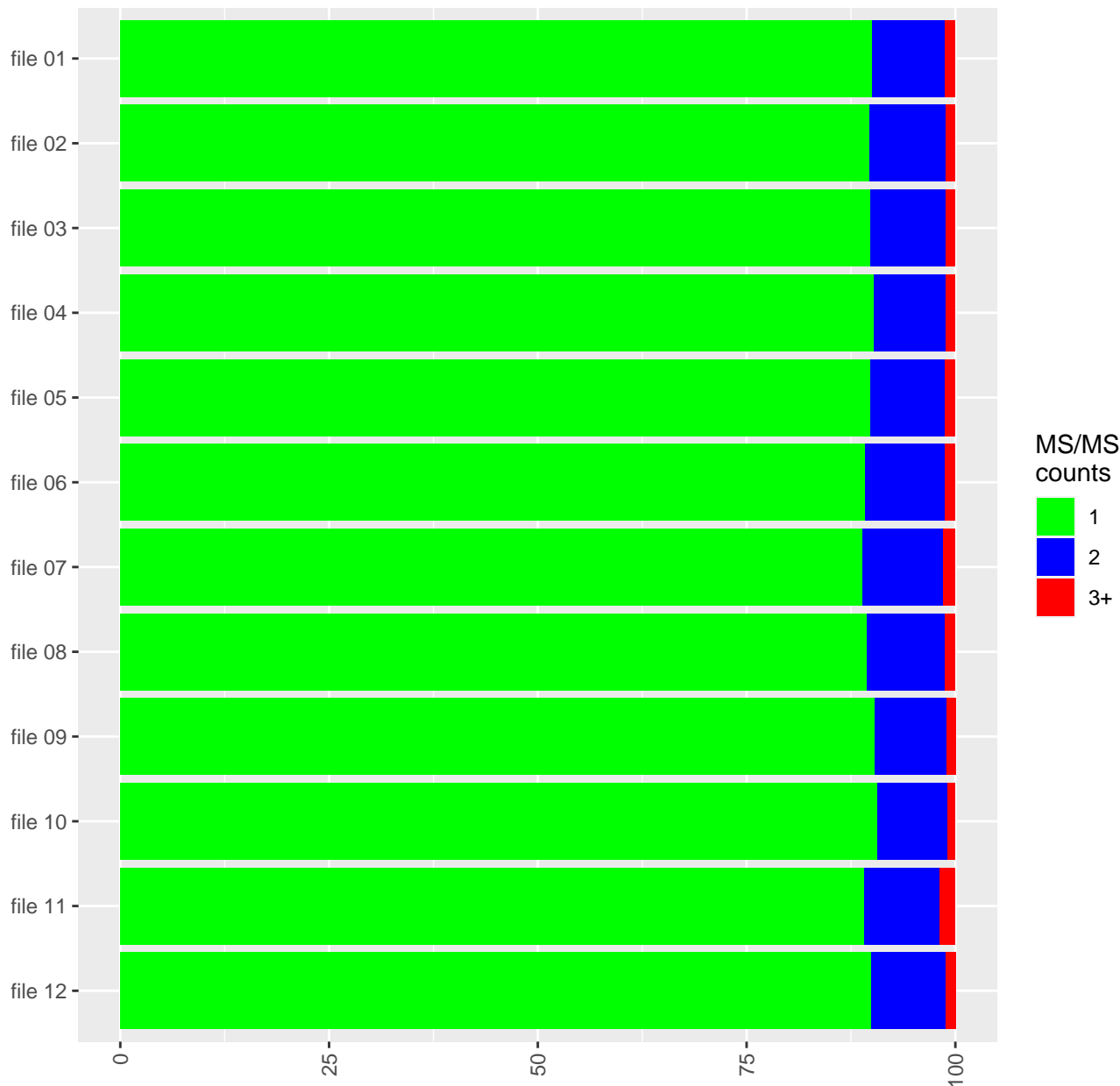
EVD: Peak width over RT



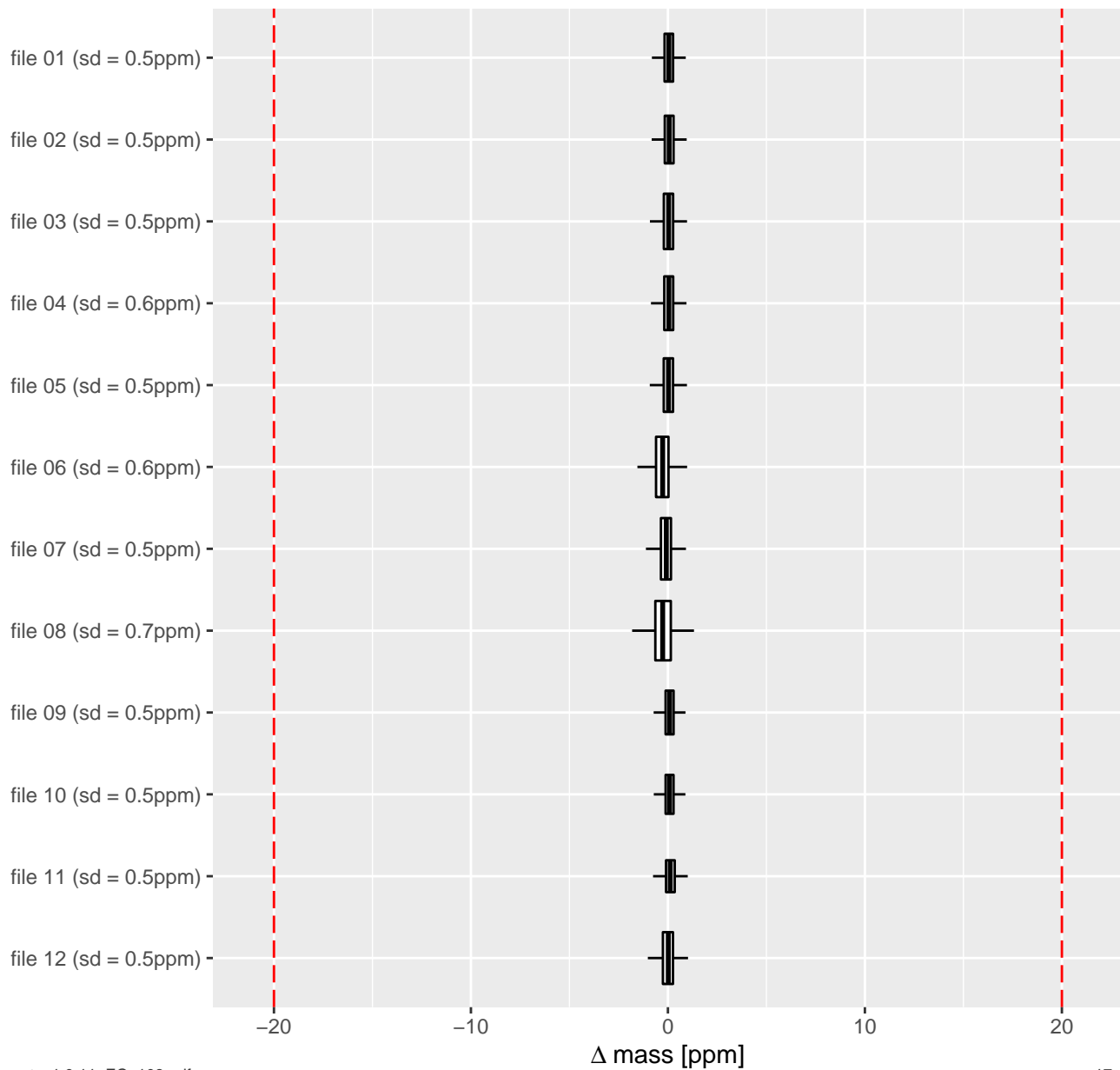
EVD: Peak width over RT



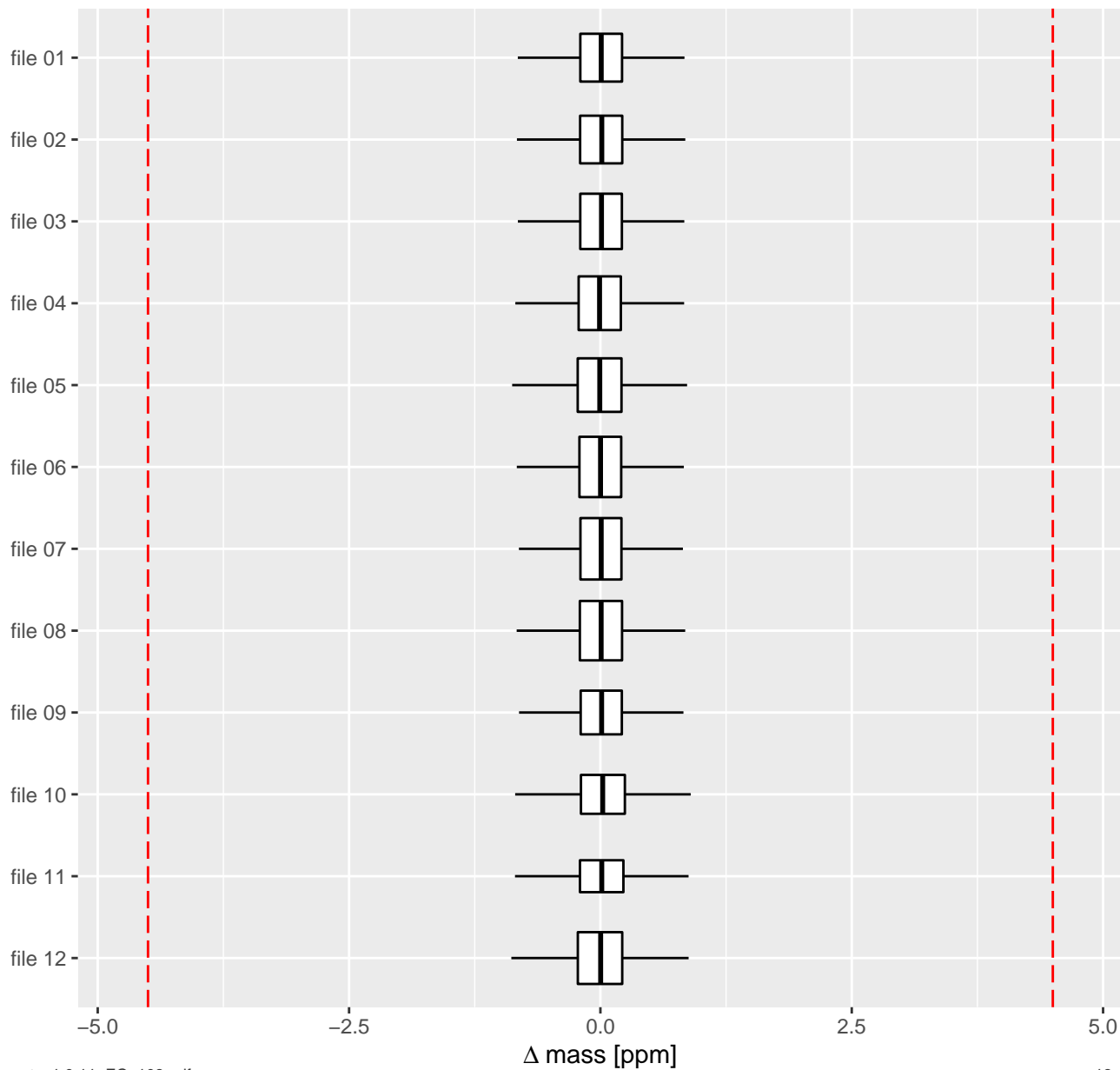
EVD: Oversampling (MS/MS counts per 3D-peak)



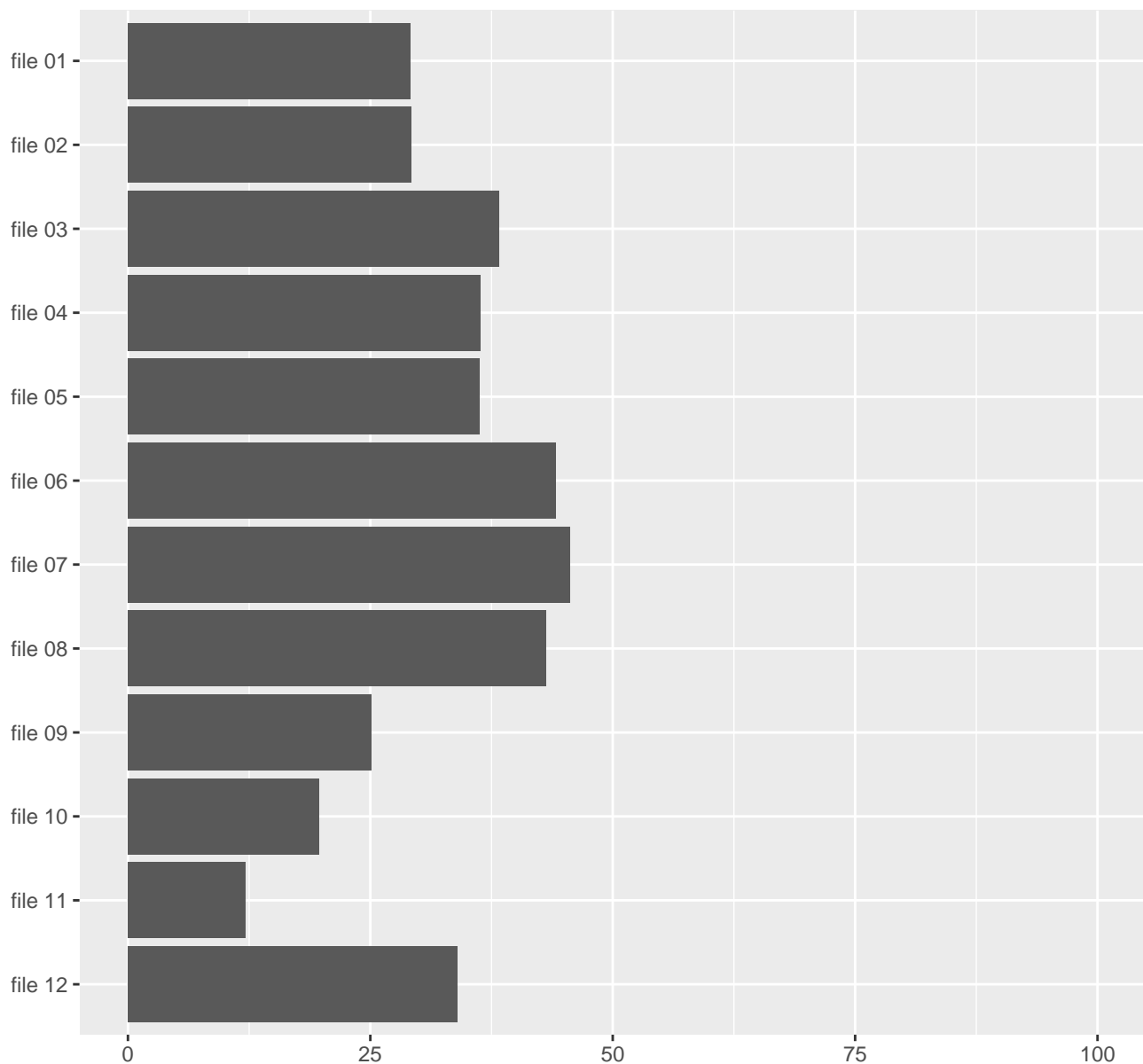
EVD: Uncalibrated mass error

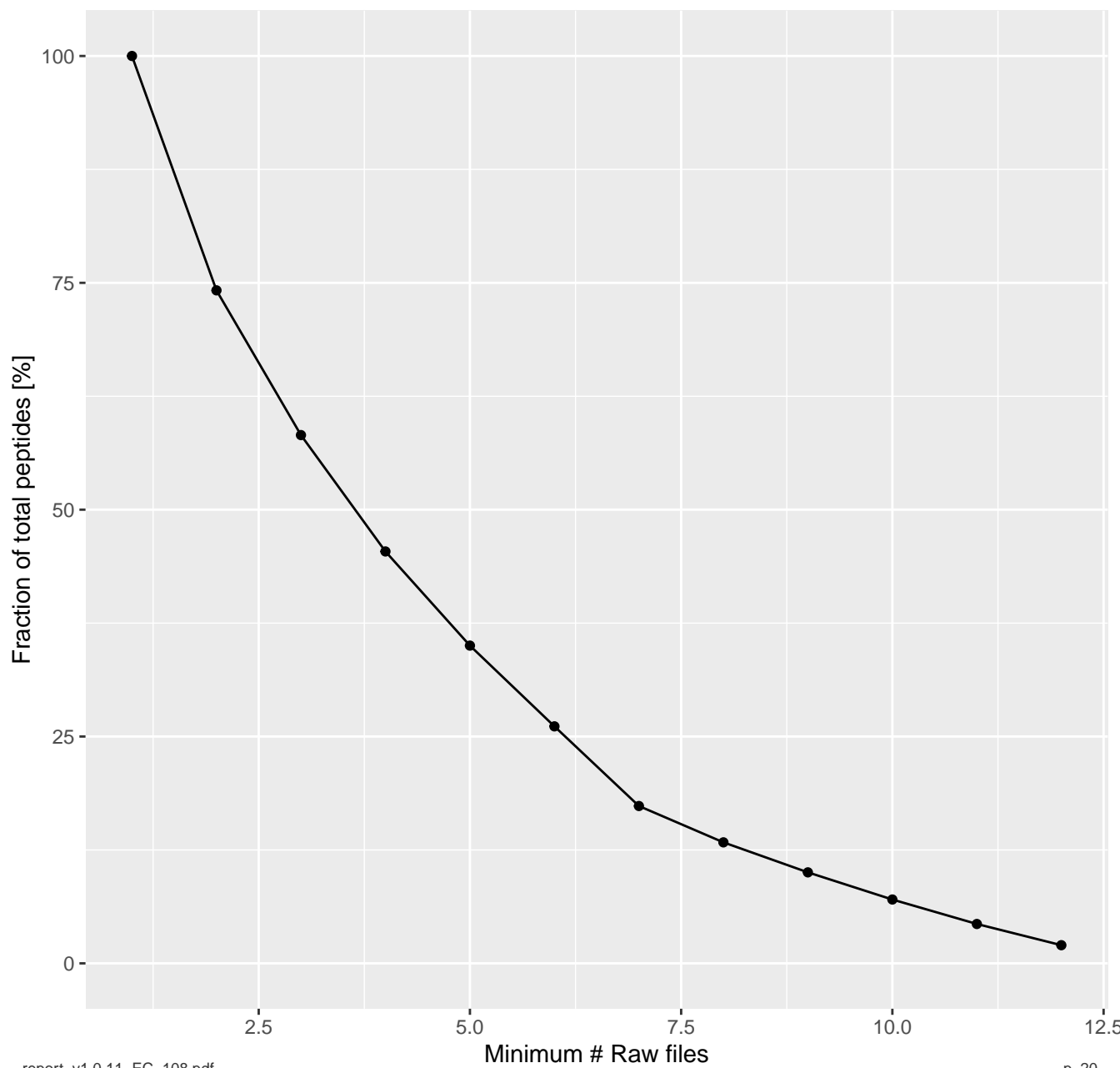


EVD: Calibrated mass error

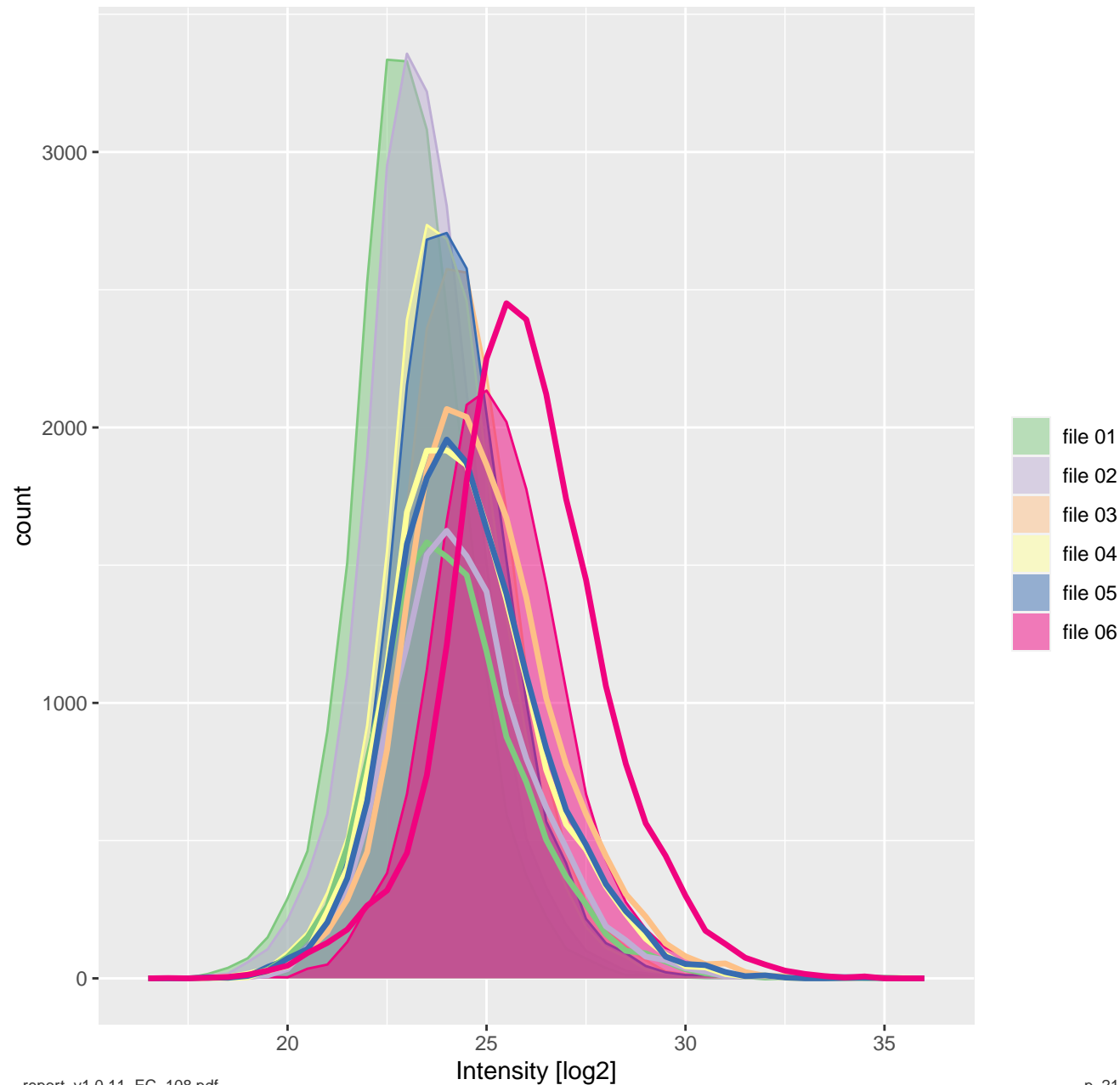


[experimental] EVD: Non-Missing Peptides
compared to all peptides seen in experiment

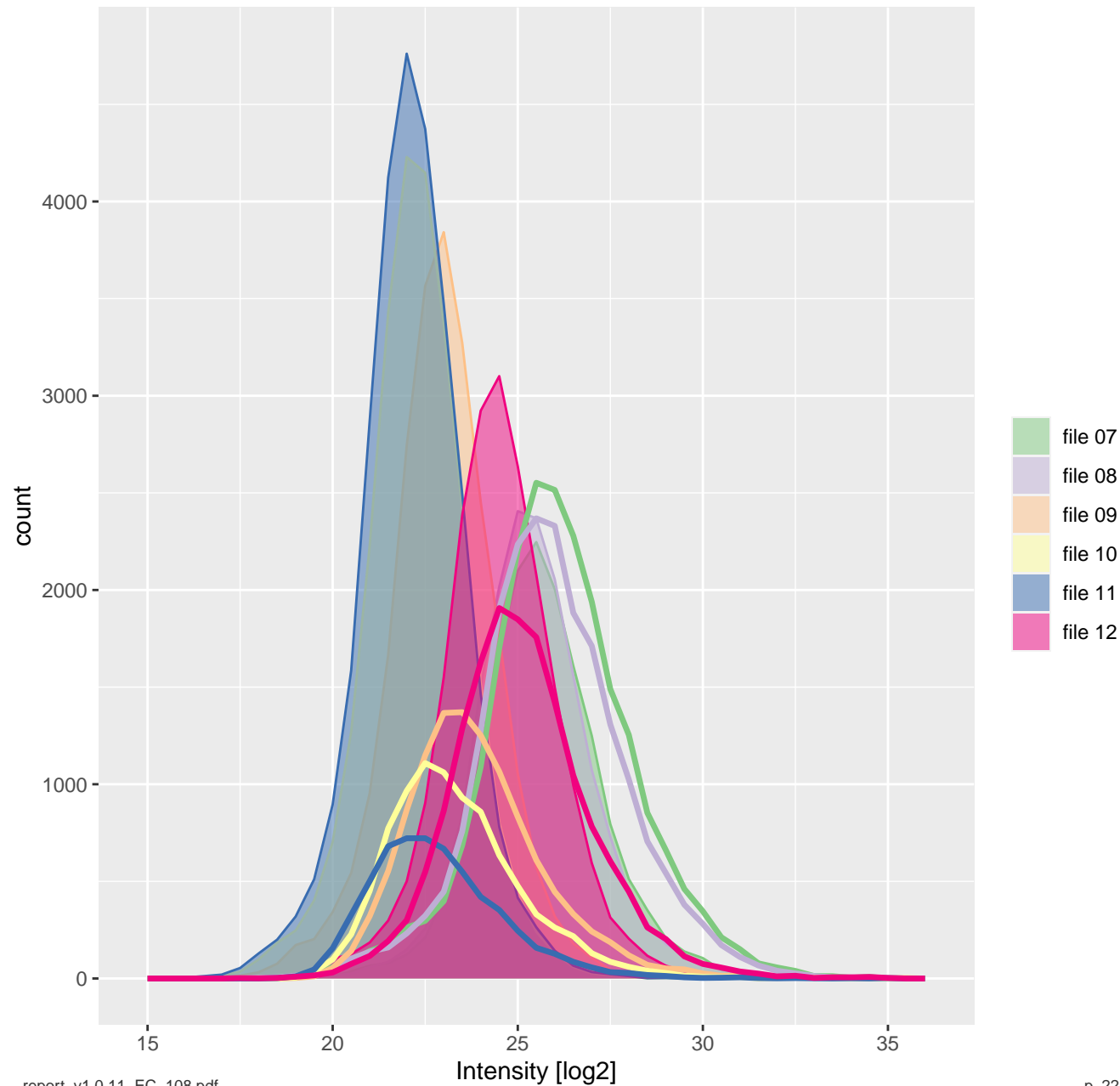




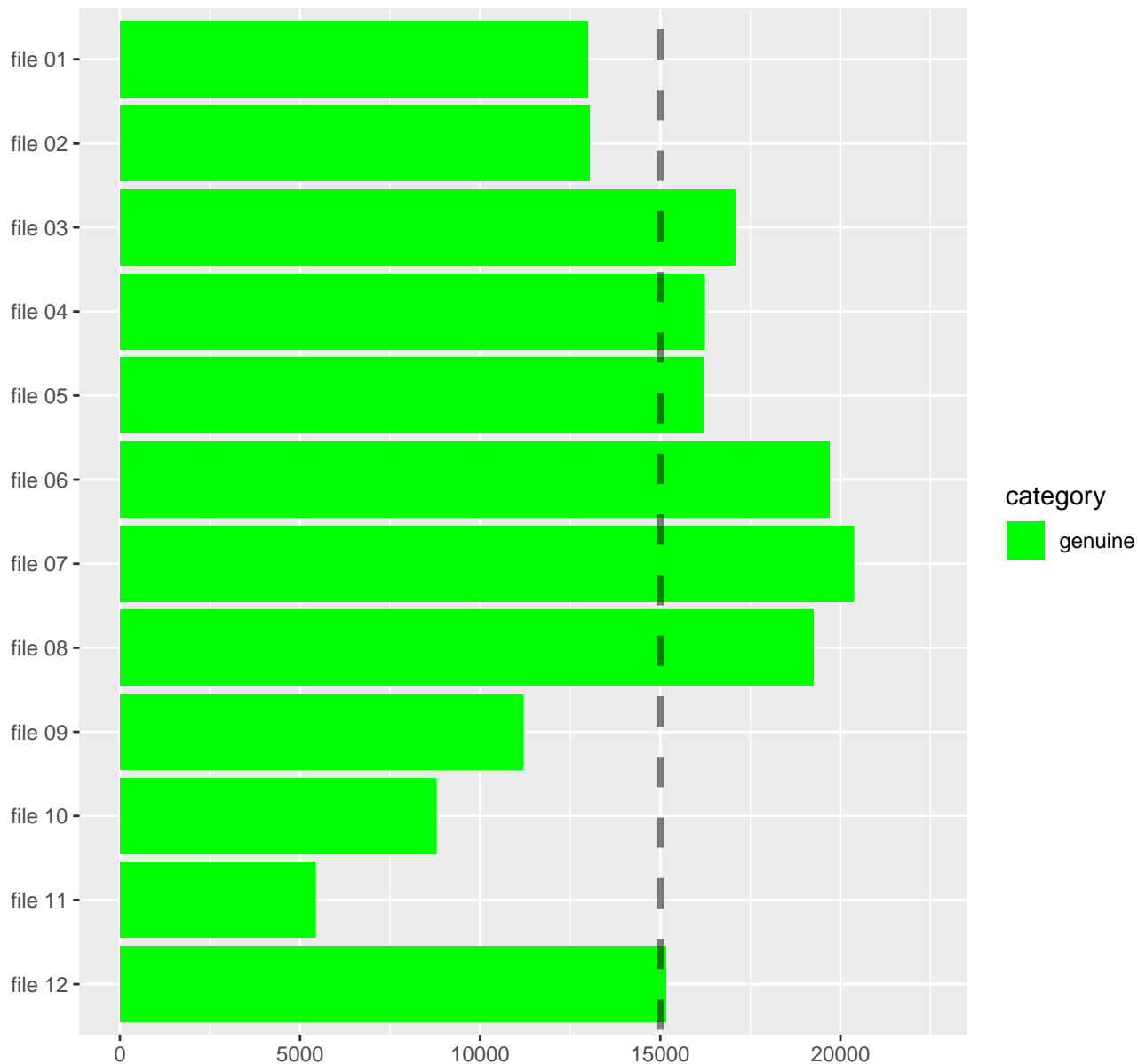
[experimental] EVD: Imputed Peptide Intensity Distribution of Missing Values



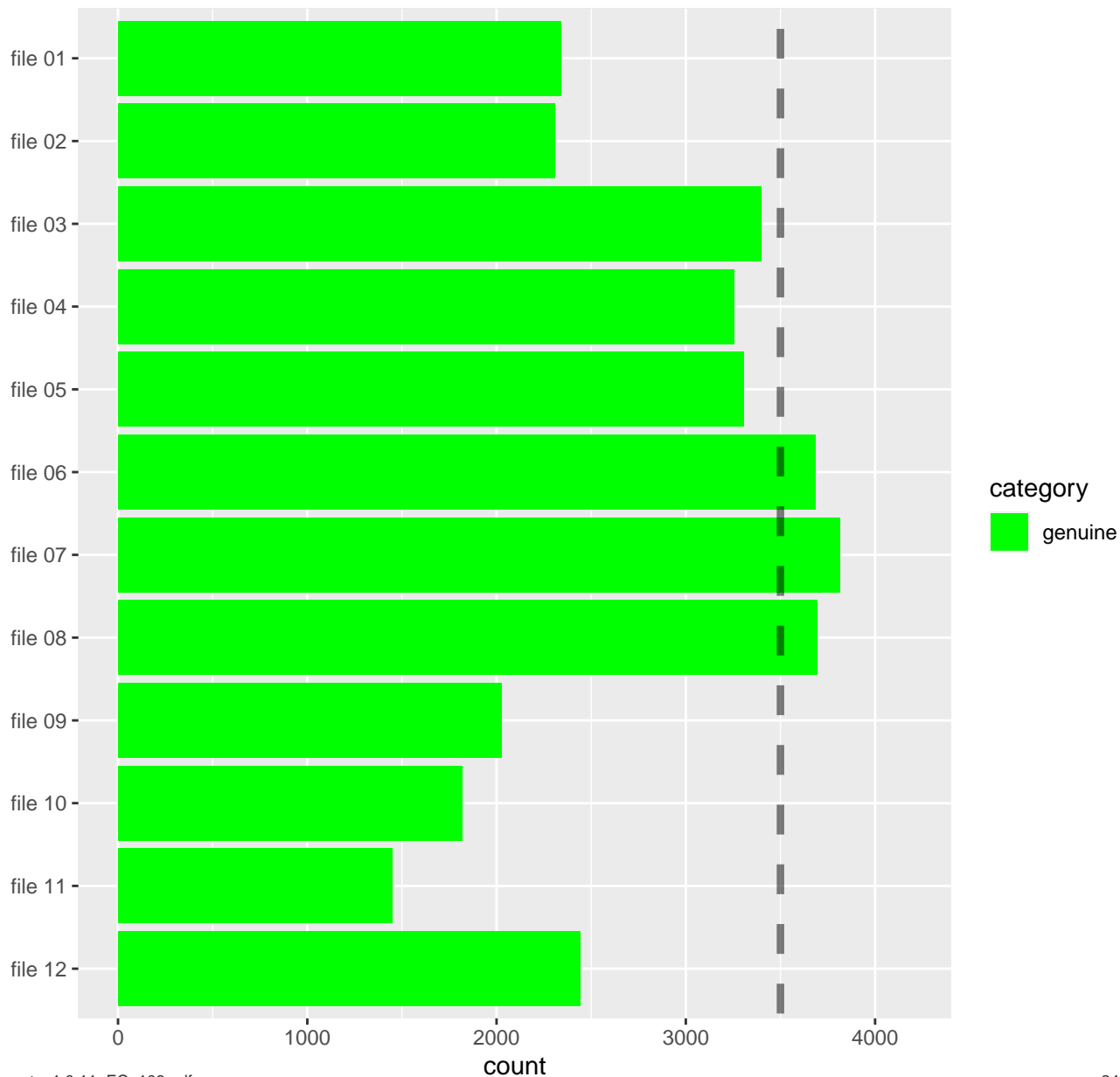
[experimental] EVD: Imputed Peptide Intensity Distribution of Missing Values



EVD: Peptide ID count

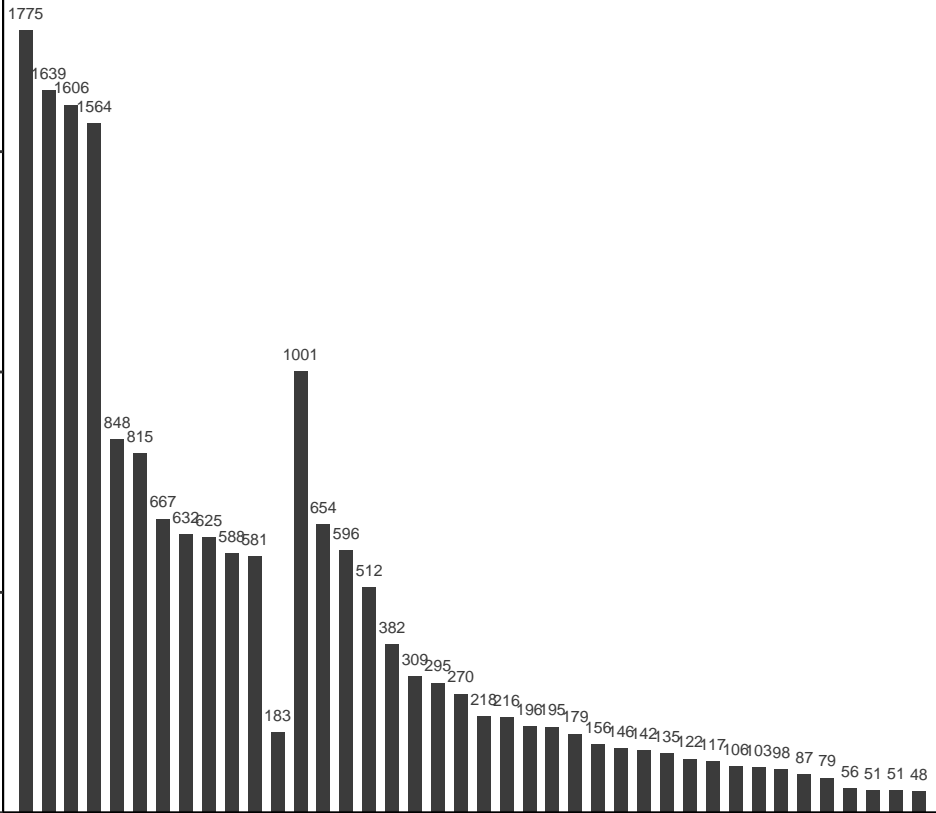


EVD: ProteinGroups count



distinct size

2000
1500
1000
500
0



file 11
file 10
file 09
file 01
file 02
file 12
file 05
file 04
file 03
file 08
file 06
file 07

