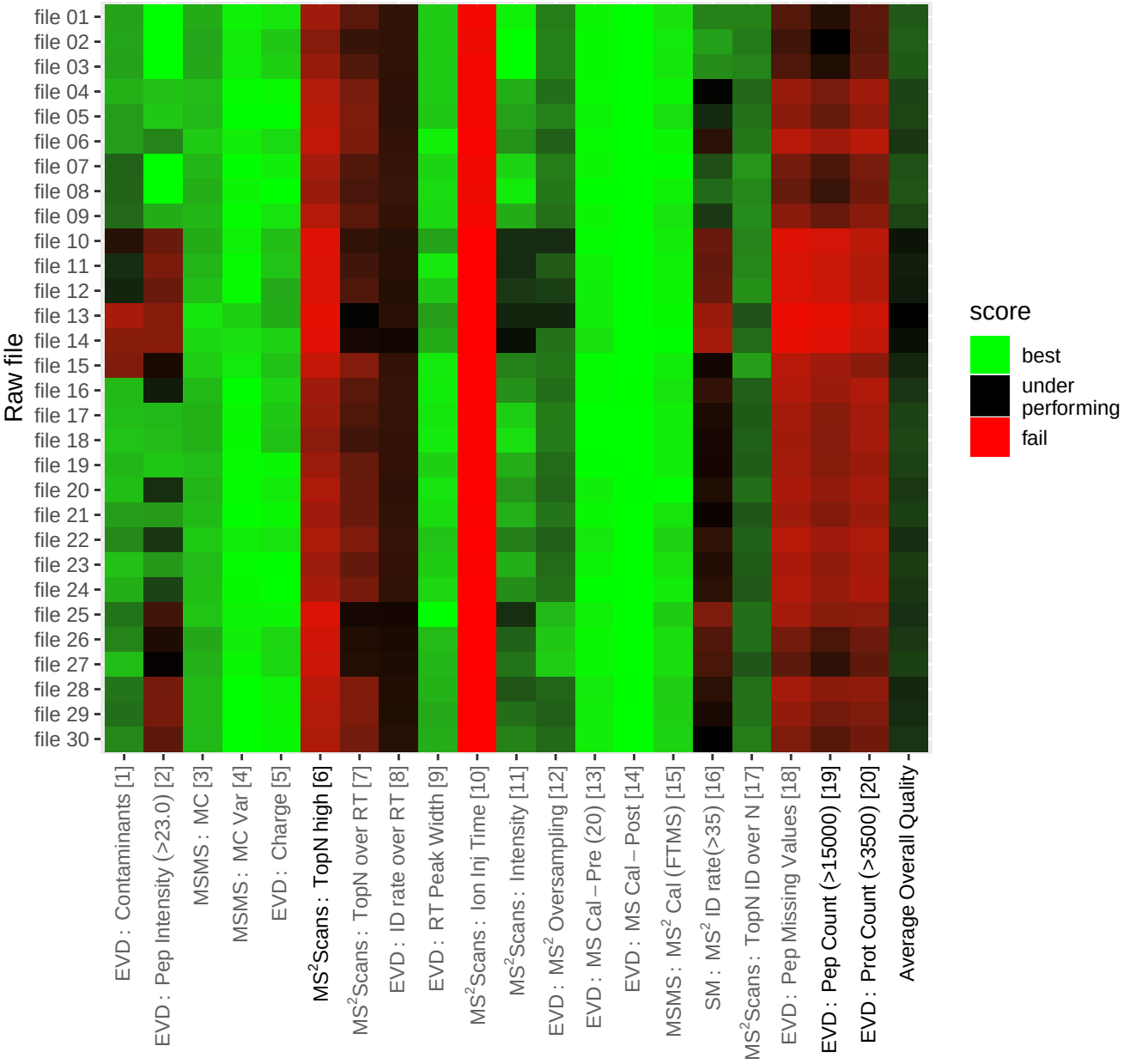
# Performance overview



# 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 |
|---|---|---|
| 20170427_144T_1a_170427152838 | file 01 | ..20170427_144T_1a_170427152838 |
| 20170427_144T_1b | file 02 | ..20170427_144T_1b |
| 20170427_144T_1c | file 03 | ..20170427_144T_1c |
| 20170427_144T_2a | file 04 | ..20170427_144T_2a |
| 20170427_144T_2b | file 05 | ..20170427_144T_2b |
| 20170427_144T_2c | file 06 | ..20170427_144T_2c |
| 20170427_159N_5a | file 07 | ..20170427_159N_5a |
| 20170427_159N_5b | file 08 | ..20170427_159N_5b |
| 20170427_159N_5c | file 09 | ..20170427_159N_5c |
| 20170427_159T_3a | file 10 | ..20170427_159T_3a |
| 20170427_159T_3b | file 11 | ..20170427_159T_3b |
| 20170427_159T_3c | file 12 | ..20170427_159T_3c |
| 20170427_159T_4a | file 13 | ..20170427_159T_4a |
| 20170427_159T_4b | file 14 | ..20170427_159T_4b |
| 20170427_159T_4c | file 15 | ..20170427_159T_4c |

# 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 |
|---|---|---|
| 20170427_163N_8a | file 16 | ..20170427_163N_8a |
| 20170427_163N_8b | file 17 | ..20170427_163N_8b |
| 20170427_163N_8c | file 18 | ..20170427_163N_8c |
| 20170427_163T_6a | file 19 | ..20170427_163T_6a |
| 20170427_163T_6b | file 20 | ..20170427_163T_6b |
| 20170427_163T_6c | file 21 | ..20170427_163T_6c |
| 20170427_163T_7a | file 22 | ..20170427_163T_7a |
| 20170427_163T_7b | file 23 | ..20170427_163T_7b |
| 20170427_163T_7c | file 24 | ..20170427_163T_7c |
| 144T_mIgG1 | file 25 | ..144T_mIgG1 |
| 144T_mIgG2 | file 26 | ..144T_mIgG2 |
| 144T_mIgG3 | file 27 | ..144T_mIgG3 |
| 144T_Orf1_1 | file 28 | ..144T_Orf1_1 |
| 144T_Orf1_2 | file 29 | ..144T_Orf1_2 |
| 144T_Orf1_3 | file 30 | ..144T_Orf1_3 |

# PAR: parameters

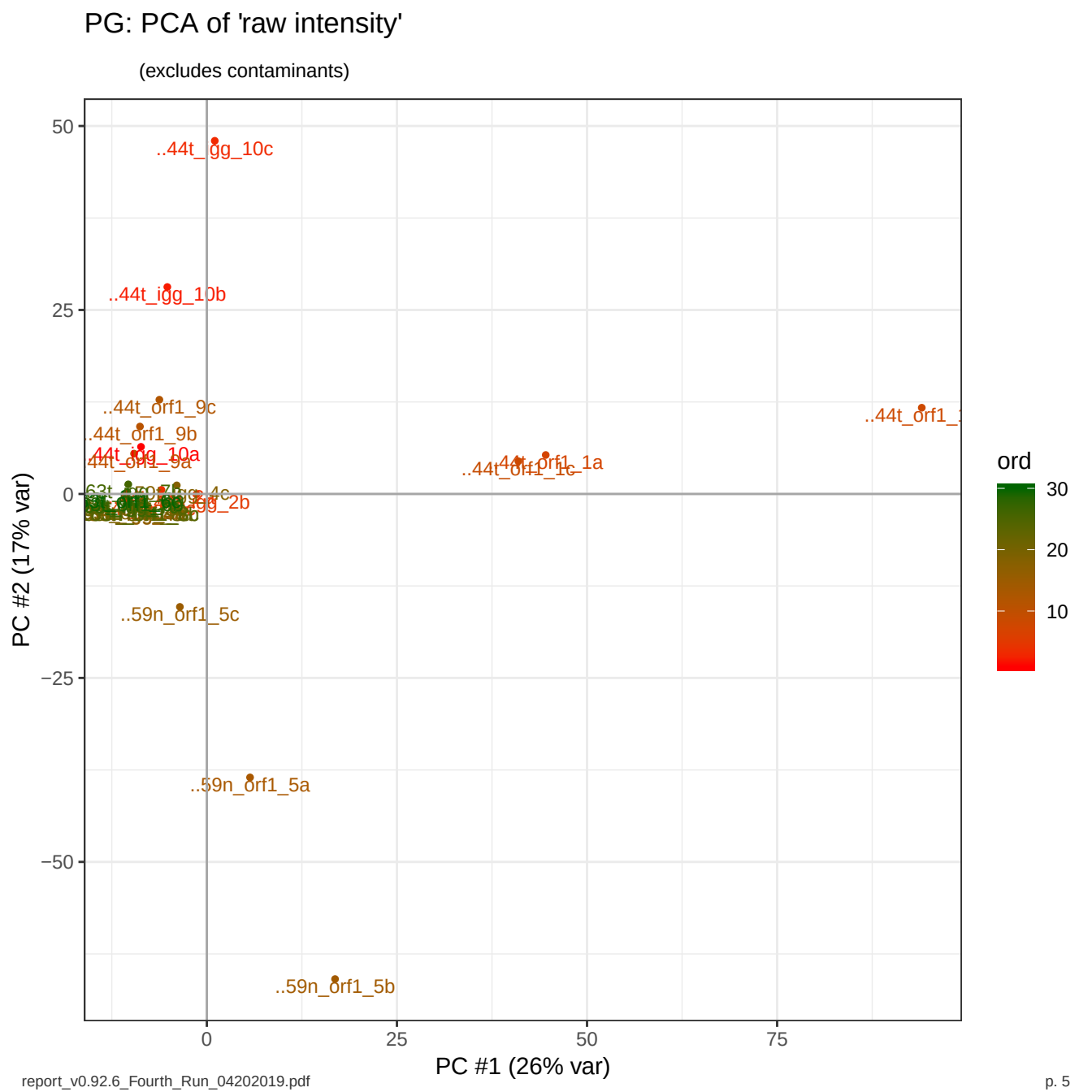
| parameter | value | parameter | value |
|---|---|---|---|
| Advanced ratios | False | MS/MS deisotoping tolerance .. | 0.01 |
| Advanced site intensities | True | MS/MS deisotoping tolerance .. | Da |
| Alignment ion mobility windo.. | 0 | MS/MS deisotoping tolerance .. | 0.15 |
| Alignment time window [min] | 20 | MS/MS deisotoping tolerance .. | Da |
| Calculate peak properties | False | MS/MS dependent losses (FTMS.. | True |
| Combined folder location | G:\LaCava\CRC_v4 | 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 | 04/15/2019 08:59:48 | 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 | G:\LaCava\CRC_v4 | 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 | C:\Users\ProteHomics\Desktop\MaxQuant\Andromeda_Index | MS/MS tol. (ITMS) | 0.5 Da |
| iBAQ | True | MS/MS tol. (TOF) | 40 ppm |
| iBAQ log fit | False | MS/MS tol. (Unknown) | 0.5 Da |
| Include contaminants | True | MS/MS water loss (FTMS) | True |
| Label min. ratio count | 2 | MS/MS water loss (ITMS) | True |
| Machine name | DESKTOP−RHO63DE | MS/MS water loss (TOF) | True |
| Main search max. combination.. | 200 | MS/MS water loss (Unknown) | True |
| Match between runs | True | Peptides used for protein qu.. | Razor |
| Match ion mobility window [i.. | 0 | Protein FDR | 0.01 |
| Match unidentified features | False | PSM FDR | 0.01 |

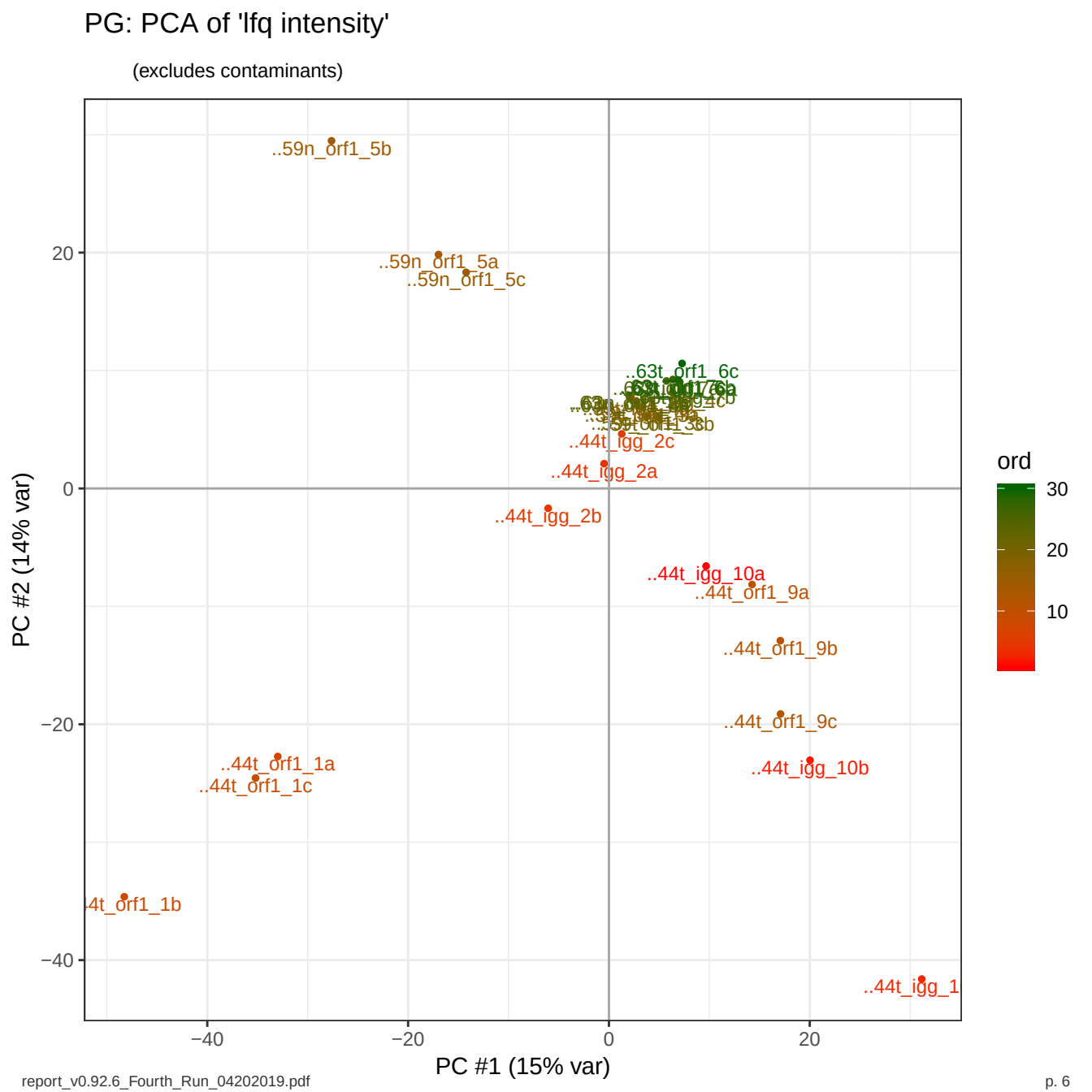
ortho_orf1.fasta

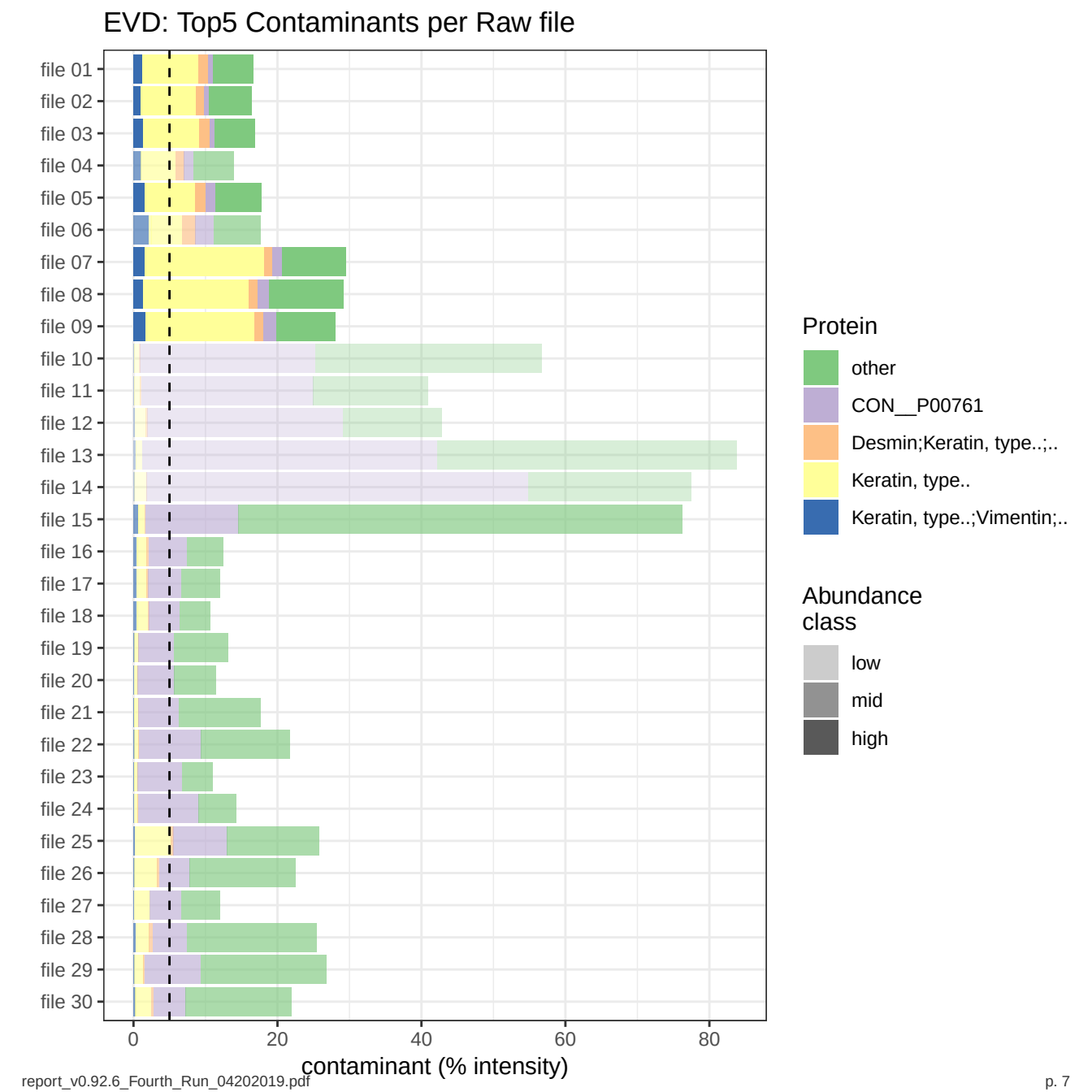
# PAR: parameters

| parameter | value | parameter | value |
|---|---|---|---|
| Matching time window [min] | 0.7 | PSM FDR Crosslink | 0.01 |
| Max mods in site table | 3 | Razor protein FDR | True |
| Max. peptide length for unsp.. | 25 | Require MS/MS for LFQ compar.. | True |
| Max. peptide mass [Da] | 4600 | Second peptides | True |
| Min. delta score for modifie.. | 6 | Separate LFQ in parameter gr.. | False |
| Min. delta score for unmodif.. | 0 | Site FDR | 0.01 |
| Min. peptide Length | 7 | Site tables | Oxidation (M)Sites.txt<br>Phospho (STY)Sites.txt |
| Min. peptide length for unsp.. | 8 | Stabilize large LFQ ratios | True |
| Min. peptides | 1 | Temporary folder | E:\MQ_Temp |
| Min. razor peptides | 1 | Top MS/MS peaks per Da inter.. | 12 |
| Min. score for modified pept.. | 40 | Top MS/MS peaks per Da inter.. | 8 |
| Min. score for unmodified pe.. | 0 | Top MS/MS peaks per Da inter.. | 10 |
| Min. unique peptides | 0 | Top MS/MS peaks per Da inter.. | 8 |
| Modifications included in pr.. | Oxidation (M)<br>Acetyl (Protein N−term)<br>Carbamidomethyl (C) | Use delta score | False |
| MS/MS ammonia loss (FTMS) | True | Use Normalized Ratios For Oc.. | True |
| MS/MS ammonia loss (ITMS) | True | Use only unmodified peptides.. | True |
| MS/MS ammonia loss (TOF) | True | User name | ProteHomics |
| MS/MS ammonia loss (Unknown) | True | Variation mode | None |
| MS/MS deisotoping (FTMS) | True | Version | 1.6.5.0 |
| MS/MS deisotoping (ITMS) | False | Write accumulatedPasefMsmsSc.. | True |
| MS/MS deisotoping (TOF) | True | Write allPeptides table | True |
| MS/MS deisotoping (Unknown) | False | Write ms3Scans table | True |
| MS/MS deisotoping tolerance .. | 7 | Write msmsScans table | True |
| MS/MS deisotoping tolerance .. | ppm | Write msScans table | True |
| MS/MS deisotoping tolerance .. | 0.15 | Write mzRange table | True |
| MS/MS deisotoping tolerance .. | Da | Write pasefMsmsScans table | True |

ortho_orf1.fasta


PG: PCA of 'raw intensity'
(excludes contaminants)
..44t_igg_10c
..44t_igg_10b
..44t_orf1_9c
.44t_orf1_9b
44t_igg_10a
44t_orf1_9a
..44t_orf1_1a
..44t_orf1_1c
..59n_orf1_5c
..59n_orf1_5a
..59n_orf1_5b
50
25
0
−25
−50
0
25
50
75
PC #1 (26% var)
PC #2 (17% var)
ord
30
20
10

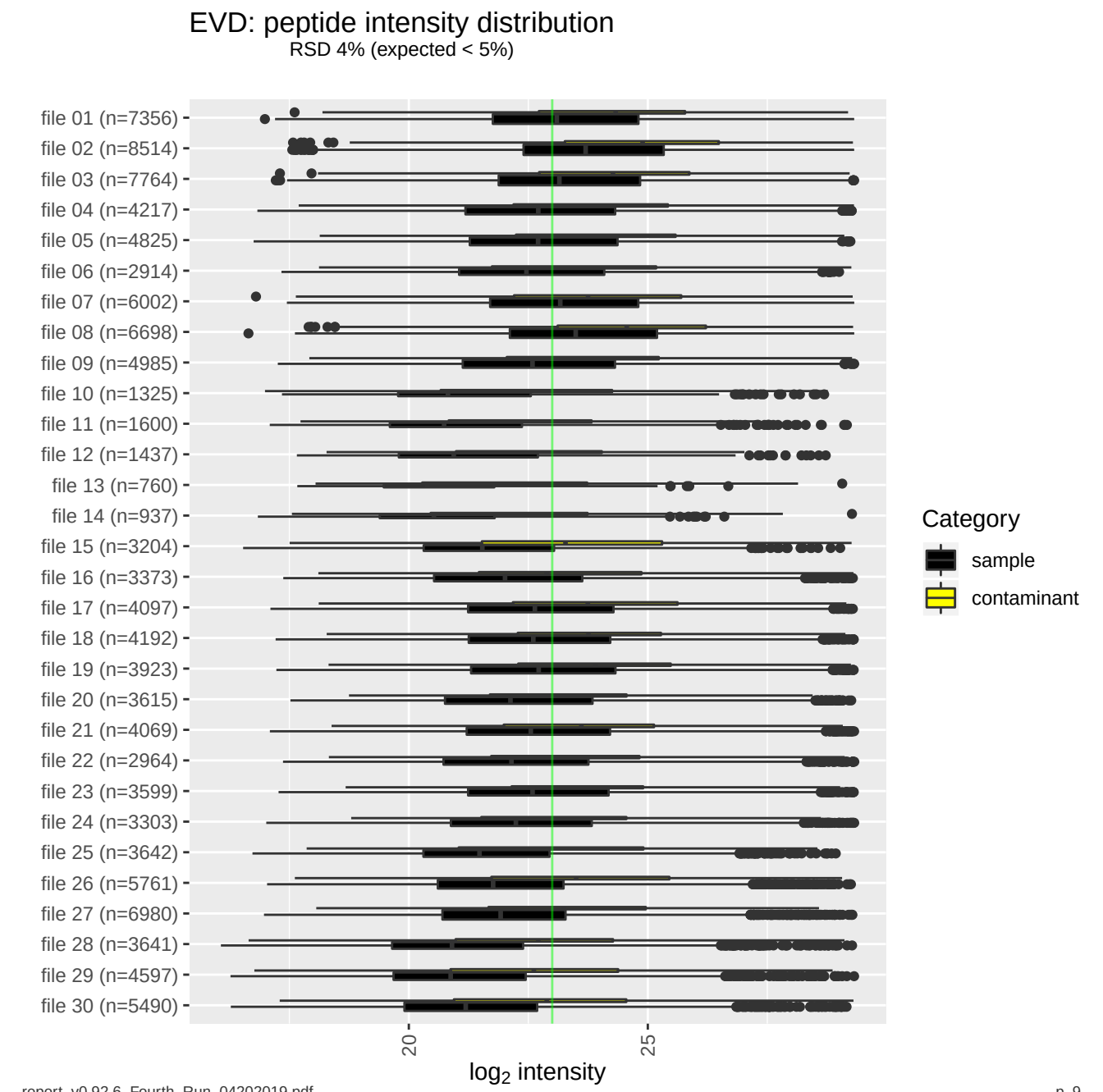

PG: PCA of 'lfq intensity'
(excludes contaminants)
..59n_orf1_5b
..59n_orf1_5a
..59n_orf1_5c
..63t_orf1_6c
..44t_igg_2c
..44t_igg_2a
..44t_igg_2b
..44t_igg_10a
..44t_orf1_9a
..44t_orf1_9b
..44t_orf1_9c
..44t_igg_10b
..44t_orf1_1a
..44t_orf1_1c
4t_orf1_1b
..44t_igg_1
ord
30
20
10
PC #2 (14% var)
PC #1 (15% var)
20
0
−20
−40
−40
−20
0
20

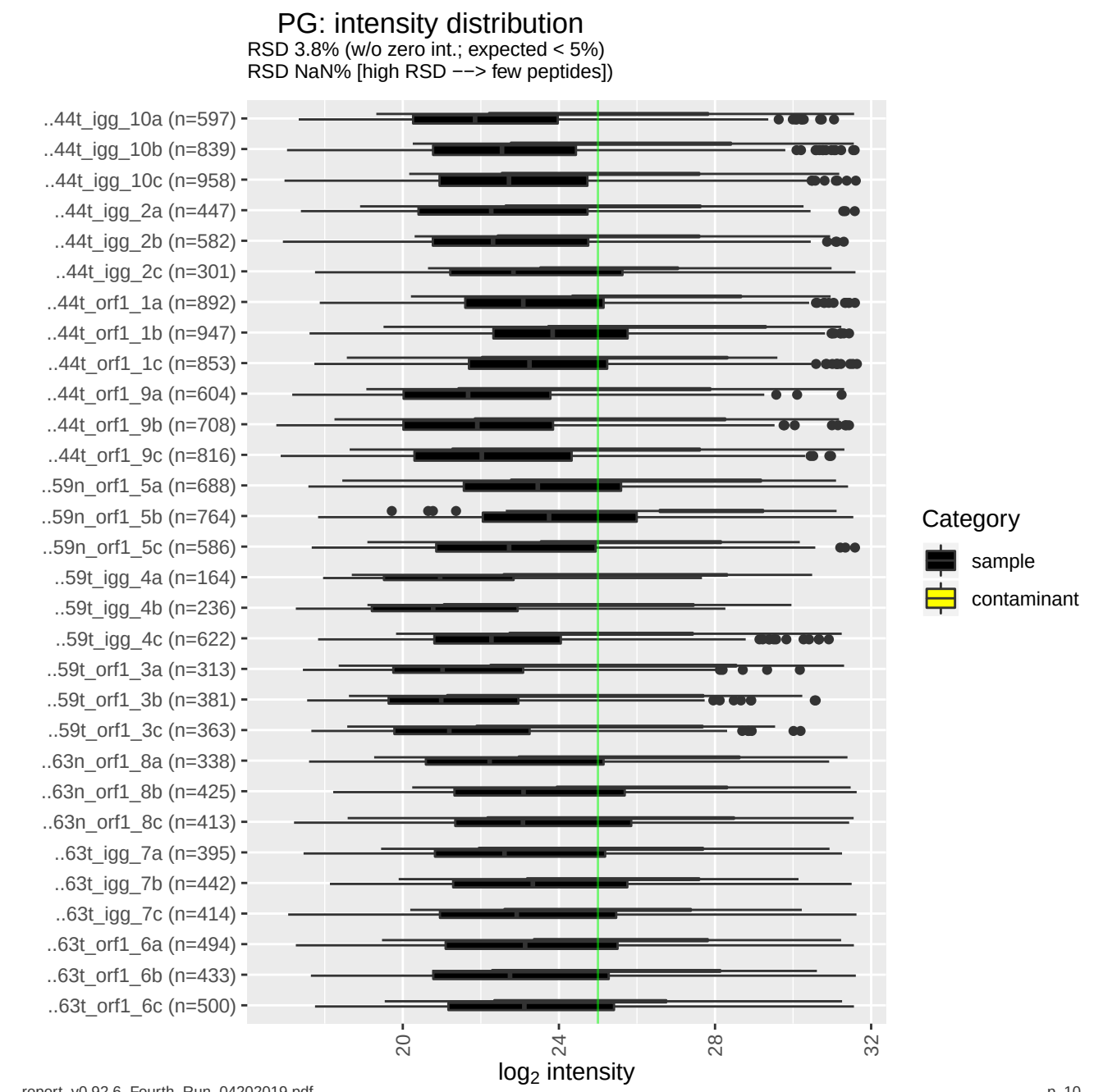

EVD: Top5 Contaminants per Raw file
file 01
file 02
file 03
file 04
file 05
file 06
file 07
file 08
file 09
file 10
file 11
file 12
file 13
file 14
file 15
file 16
file 17
file 18
file 19
file 20
file 21
file 22
file 23
file 24
file 25
file 26
file 27
file 28
file 29
file 30
0
20
40
60
80
contaminant (% intensity)
Protein
other
CON__P00761
Desmin;Keratin, type..;..
Keratin, type..
Keratin, type..;Vimentin;..
Abundance class
low
mid
high

# EVD: Contaminants

Contaminant 'MYCOPLASMA' was not found in any sample.

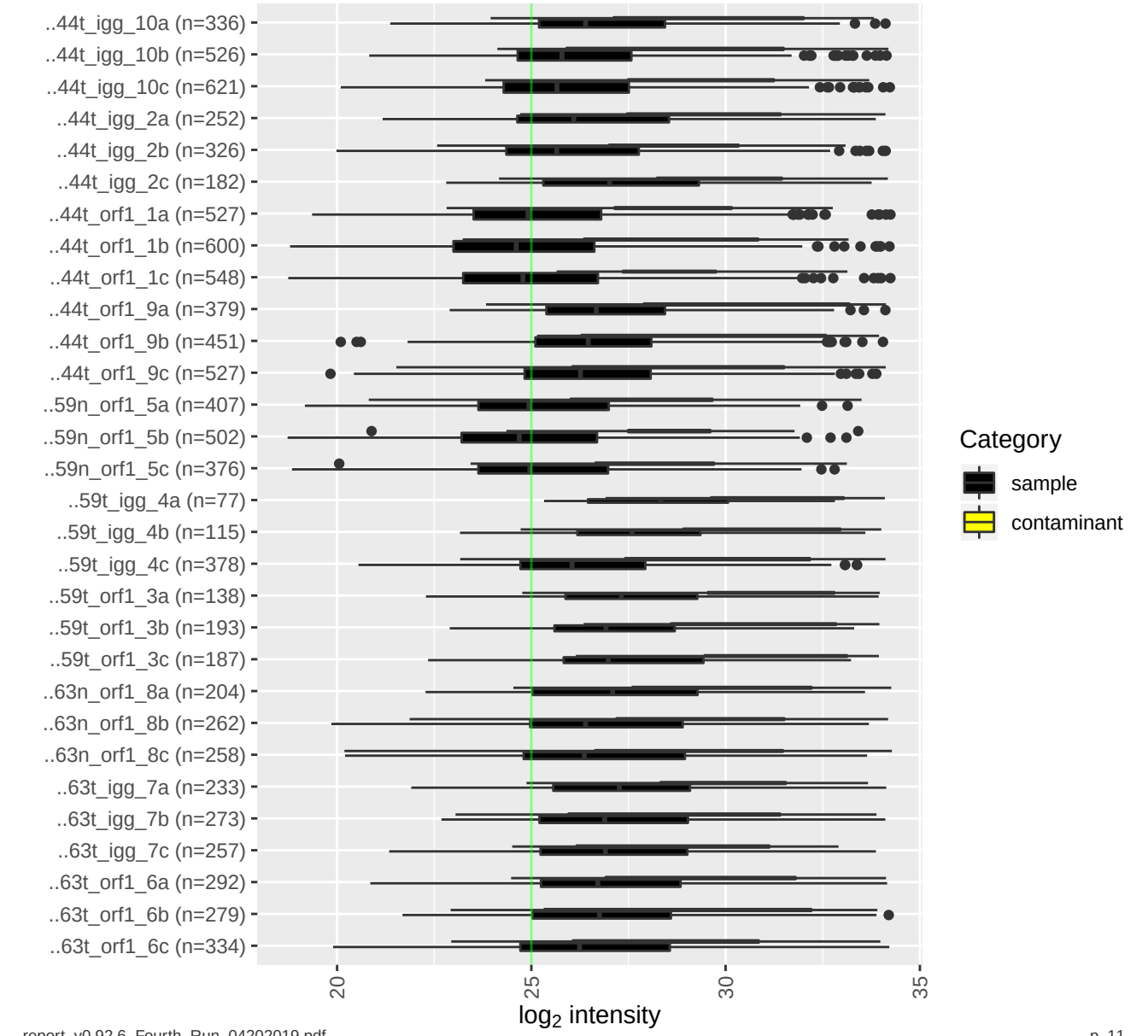
Did you use the correct database?

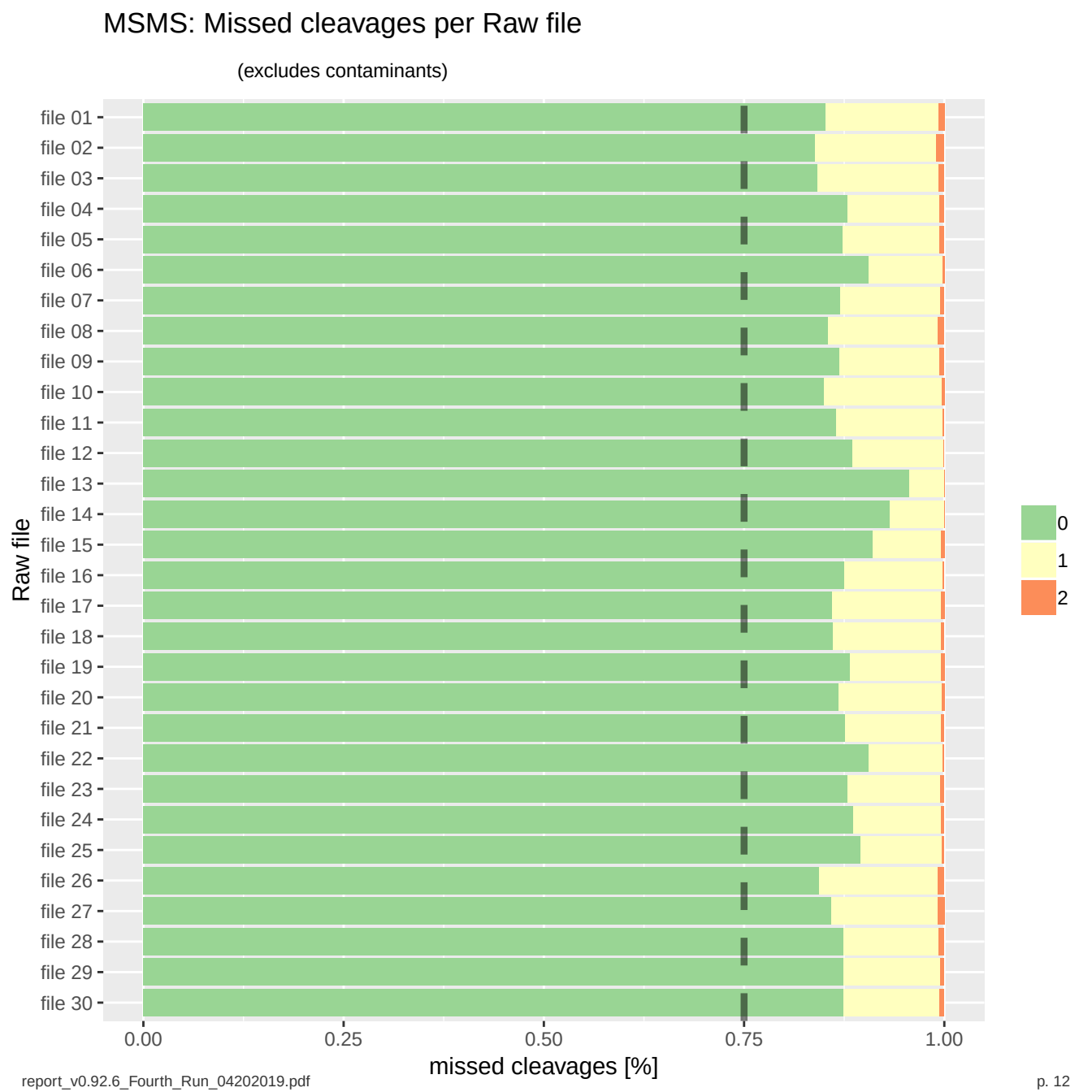

EVD: peptide intensity distribution
RSD 4% (expected < 5%)
file 01 (n=7356)
file 02 (n=8514)
file 03 (n=7764)
file 04 (n=4217)
file 05 (n=4825)
file 06 (n=2914)
file 07 (n=6002)
file 08 (n=6698)
file 09 (n=4985)
file 10 (n=1325)
file 11 (n=1600)
file 12 (n=1437)
file 13 (n=760)
file 14 (n=937)
file 15 (n=3204)
file 16 (n=3373)
file 17 (n=4097)
file 18 (n=4192)
file 19 (n=3923)
file 20 (n=3615)
file 21 (n=4069)
file 22 (n=2964)
file 23 (n=3599)
file 24 (n=3303)
file 25 (n=3642)
file 26 (n=5761)
file 27 (n=6980)
file 28 (n=3641)
file 29 (n=4597)
file 30 (n=5490)
20
25
log2 intensity
Category
sample
contaminant

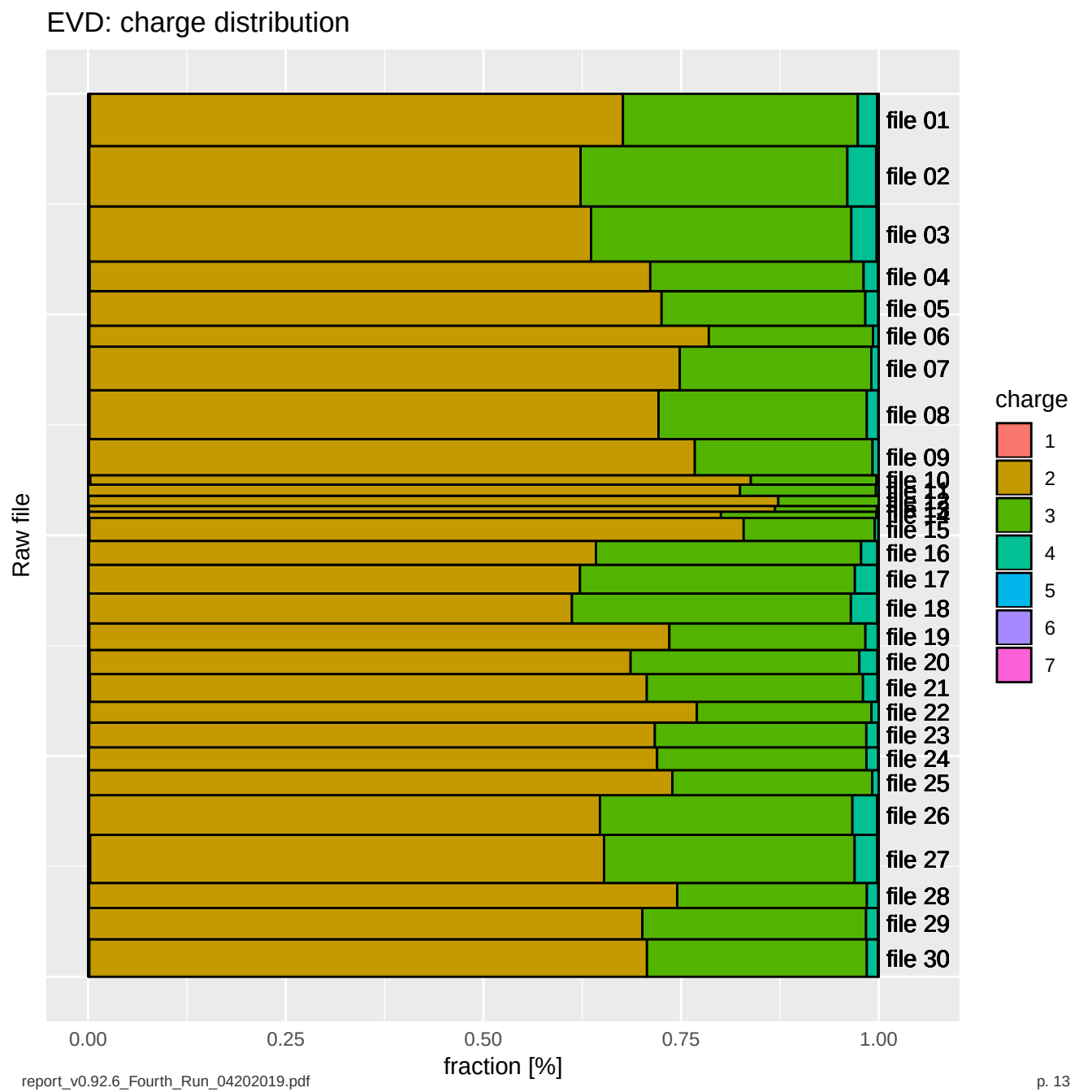

PG: intensity distribution
RSD 3.8% (w/o zero int.; expected < 5%)
RSD NaN% [high RSD −−> few peptides])
..44t_igg_10a (n=597)
..44t_igg_10b (n=839)
..44t_igg_10c (n=958)
..44t_igg_2a (n=447)
..44t_igg_2b (n=582)
..44t_igg_2c (n=301)
..44t_orf1_1a (n=892)
..44t_orf1_1b (n=947)
..44t_orf1_1c (n=853)
..44t_orf1_9a (n=604)
..44t_orf1_9b (n=708)
..44t_orf1_9c (n=816)
..59n_orf1_5a (n=688)
..59n_orf1_5b (n=764)
..59n_orf1_5c (n=586)
..59t_igg_4a (n=164)
..59t_igg_4b (n=236)
..59t_igg_4c (n=622)
..59t_orf1_3a (n=313)
..59t_orf1_3b (n=381)
..59t_orf1_3c (n=363)
..63n_orf1_8a (n=338)
..63n_orf1_8b (n=425)
..63n_orf1_8c (n=413)
..63t_igg_7a (n=395)
..63t_igg_7b (n=442)
..63t_igg_7c (n=414)
..63t_orf1_6a (n=494)
..63t_orf1_6b (n=433)
..63t_orf1_6c (n=500)
20
24
28
32
log2 intensity
Category
sample
contaminant

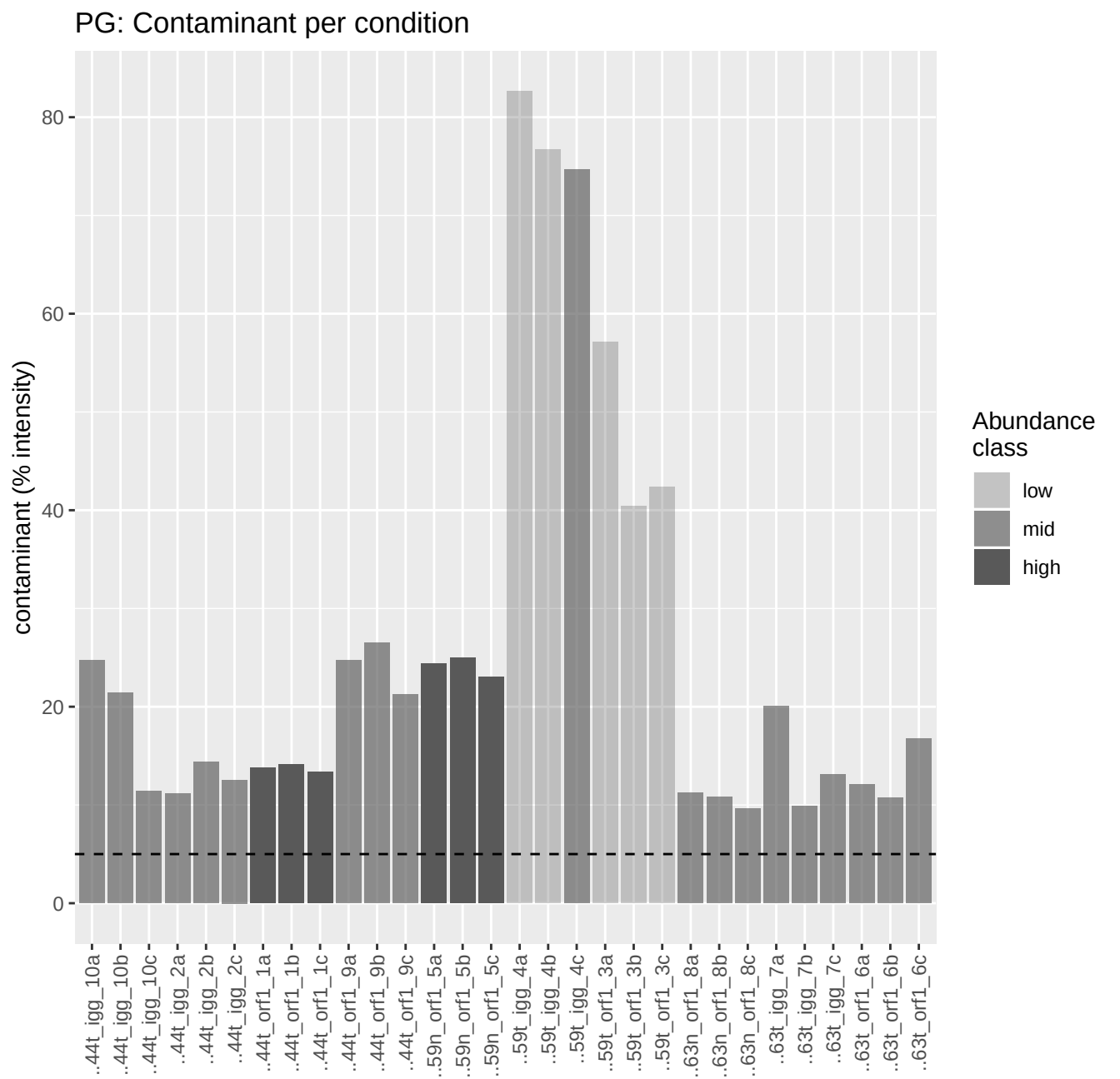
# PG: LFQ intensity distribution

RSD 3.9% (w/o zero int.; expected < 5%)
RSD NaN% [high RSD −−> few peptides])

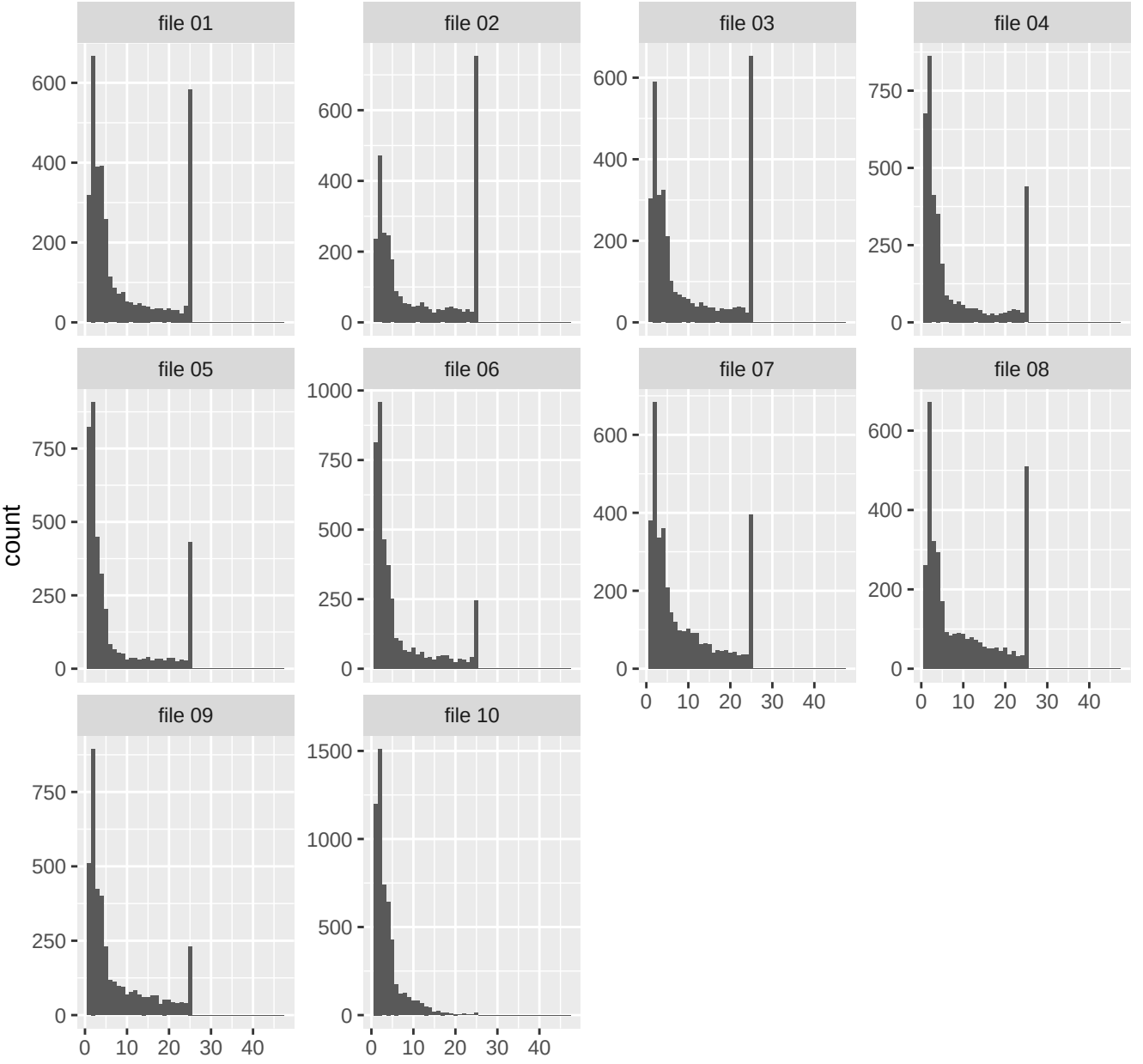



MSMS: Missed cleavages per Raw file
(excludes contaminants)
Raw file
file 01
file 02
file 03
file 04
file 05
file 06
file 07
file 08
file 09
file 10
file 11
file 12
file 13
file 14
file 15
file 16
file 17
file 18
file 19
file 20
file 21
file 22
file 23
file 24
file 25
file 26
file 27
file 28
file 29
file 30
0.00
0.25
0.50
0.75
1.00
missed cleavages [%]
0
1
2

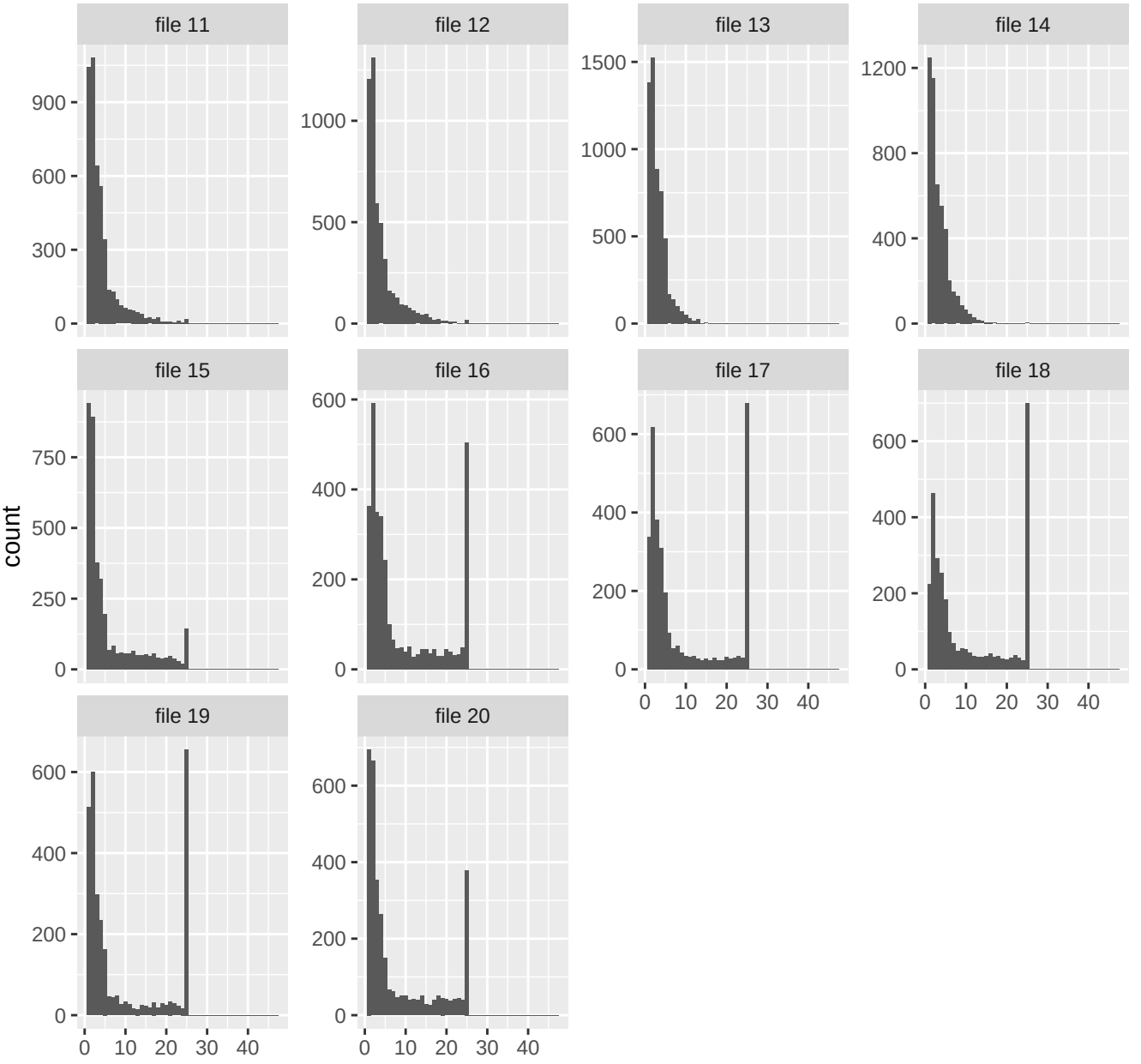

EVD: charge distribution
Raw file
file 01
file 02
file 03
file 04
file 05
file 06
file 07
file 08
file 09
file 10
file 15
file 16
file 17
file 18
file 19
file 20
file 21
file 22
file 23
file 24
file 25
file 26
file 27
file 28
file 29
file 30
charge
1
2
3
4
5
6
7
0.00
0.25
0.50
0.75
1.00
fraction [%]


PG: Contaminant per condition
contaminant (% intensity)
0
20
40
60
80
..44t_igg_10a
..44t_igg_10b
..44t_igg_10c
..44t_igg_2a
..44t_igg_2b
..44t_igg_2c
..44t_orf1_1a
..44t_orf1_1b
..44t_orf1_1c
..44t_orf1_9a
..44t_orf1_9b
..44t_orf1_9c
..59n_orf1_5a
..59n_orf1_5b
..59n_orf1_5c
..59t_igg_4a
..59t_igg_4b
..59t_igg_4c
..59t_orf1_3a
..59t_orf1_3b
..59t_orf1_3c
..63n_orf1_8a
..63n_orf1_8b
..63n_orf1_8c
..63t_igg_7a
..63t_igg_7b
..63t_igg_7c
..63t_orf1_6a
..63t_orf1_6b
..63t_orf1_6c
Abundance class
low
mid
high

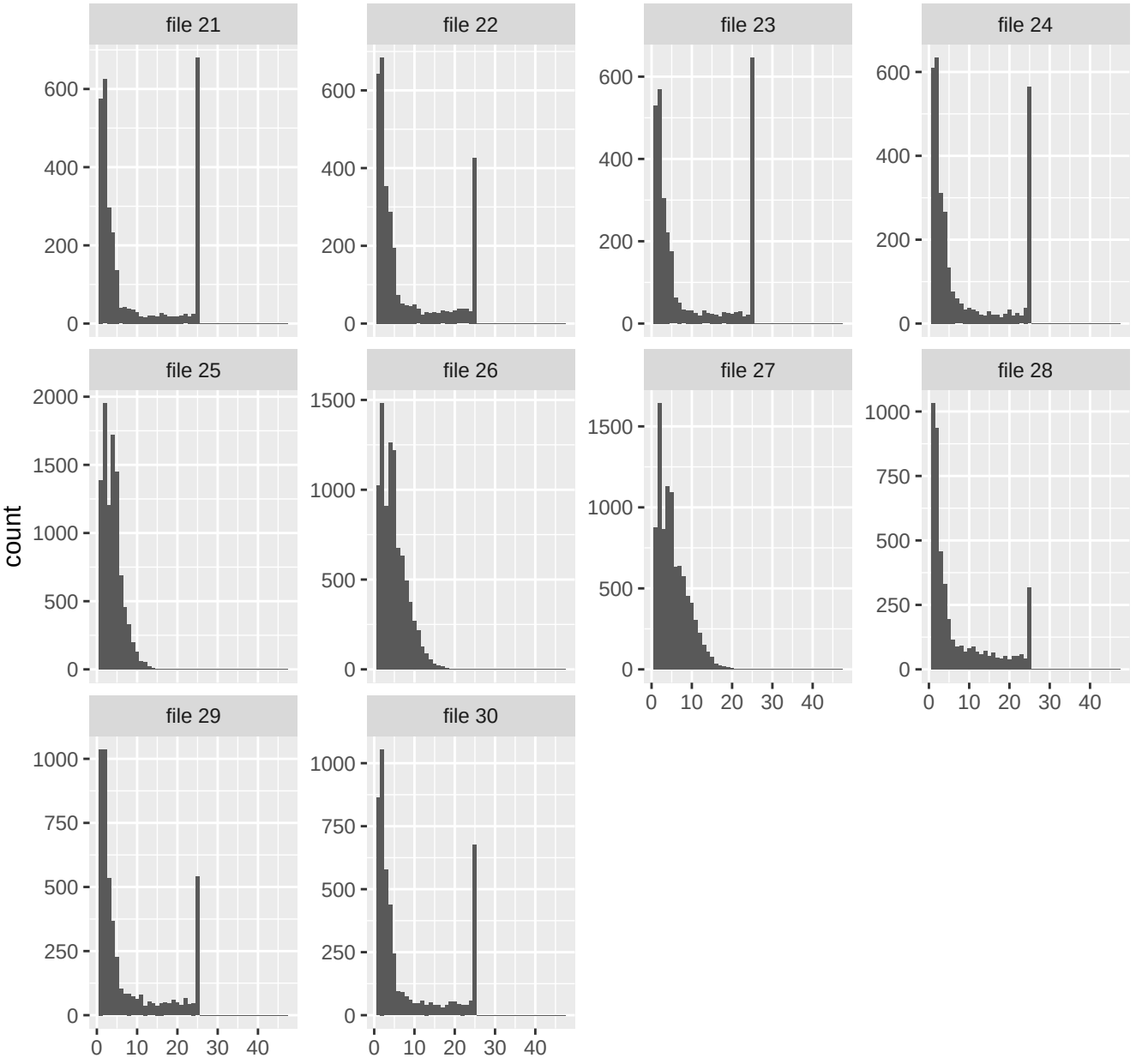
# MSMSscans: TopN

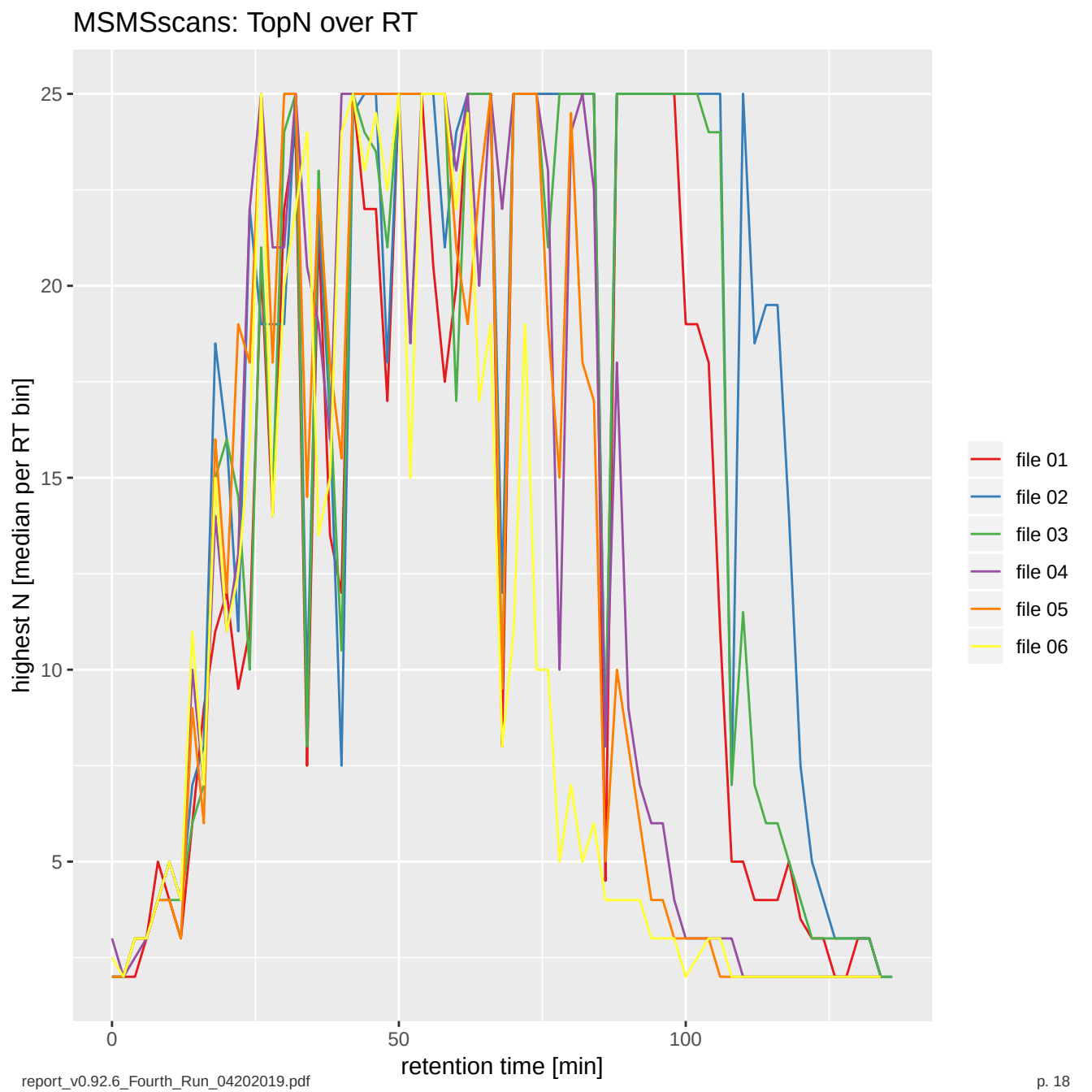


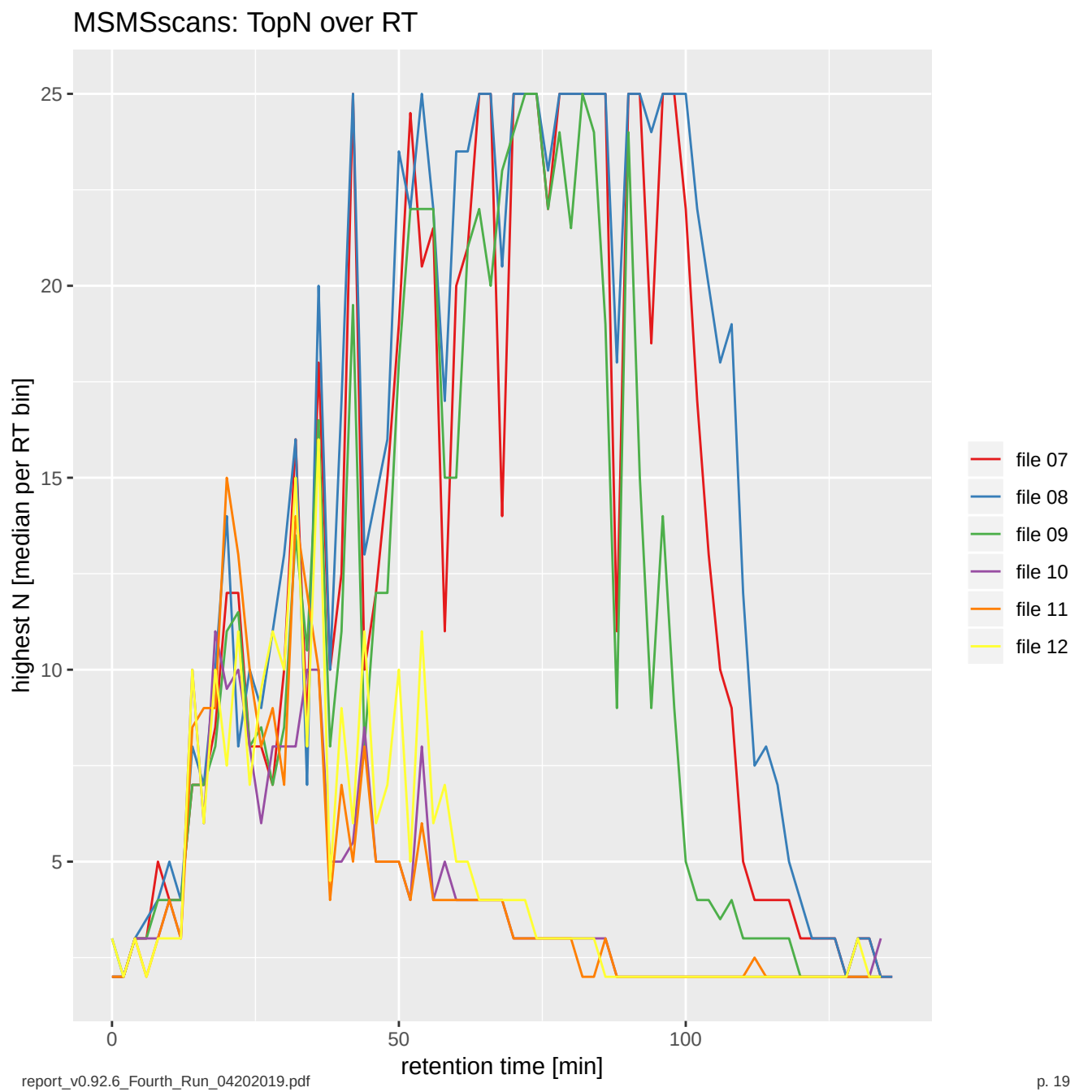
# MSMSscans: TopN

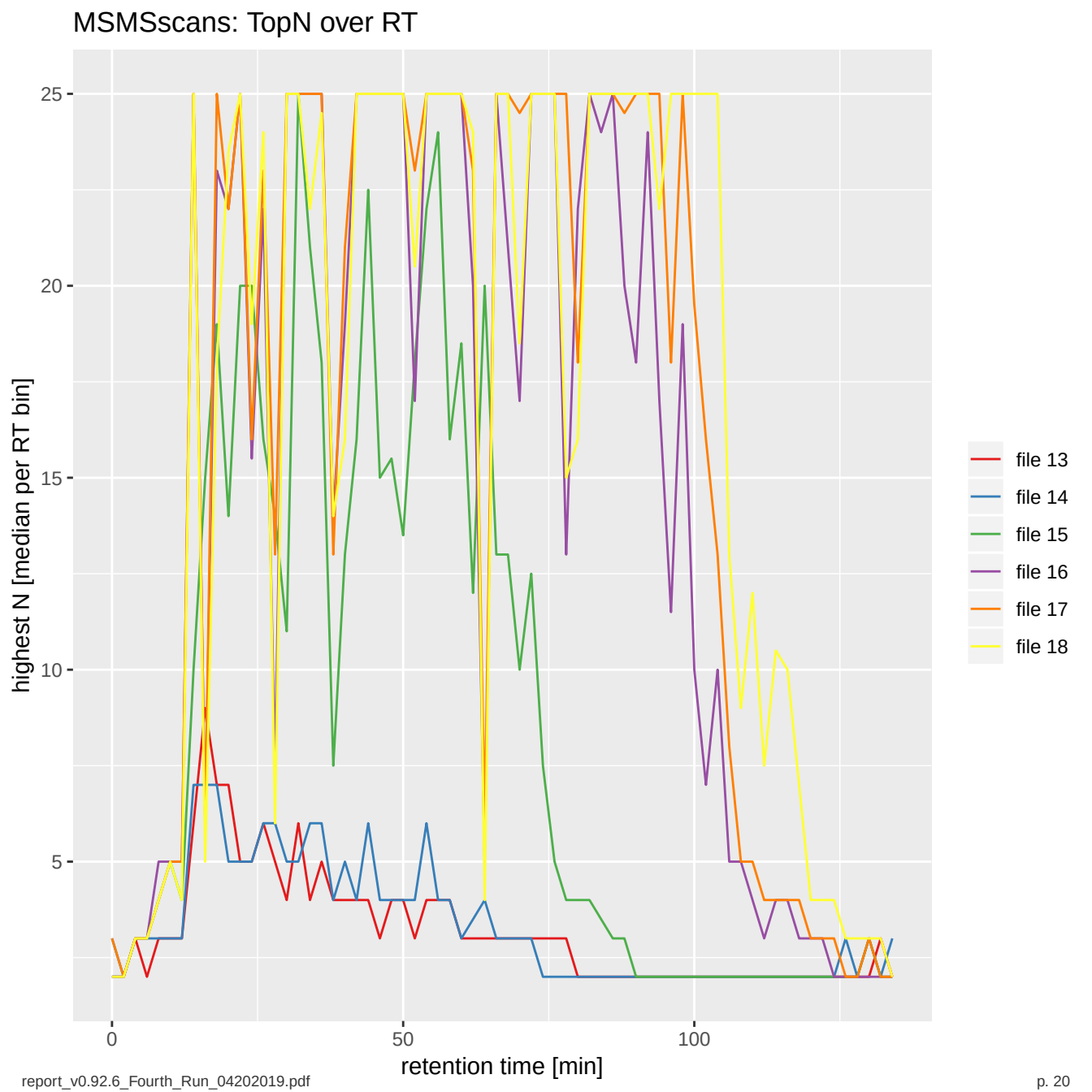


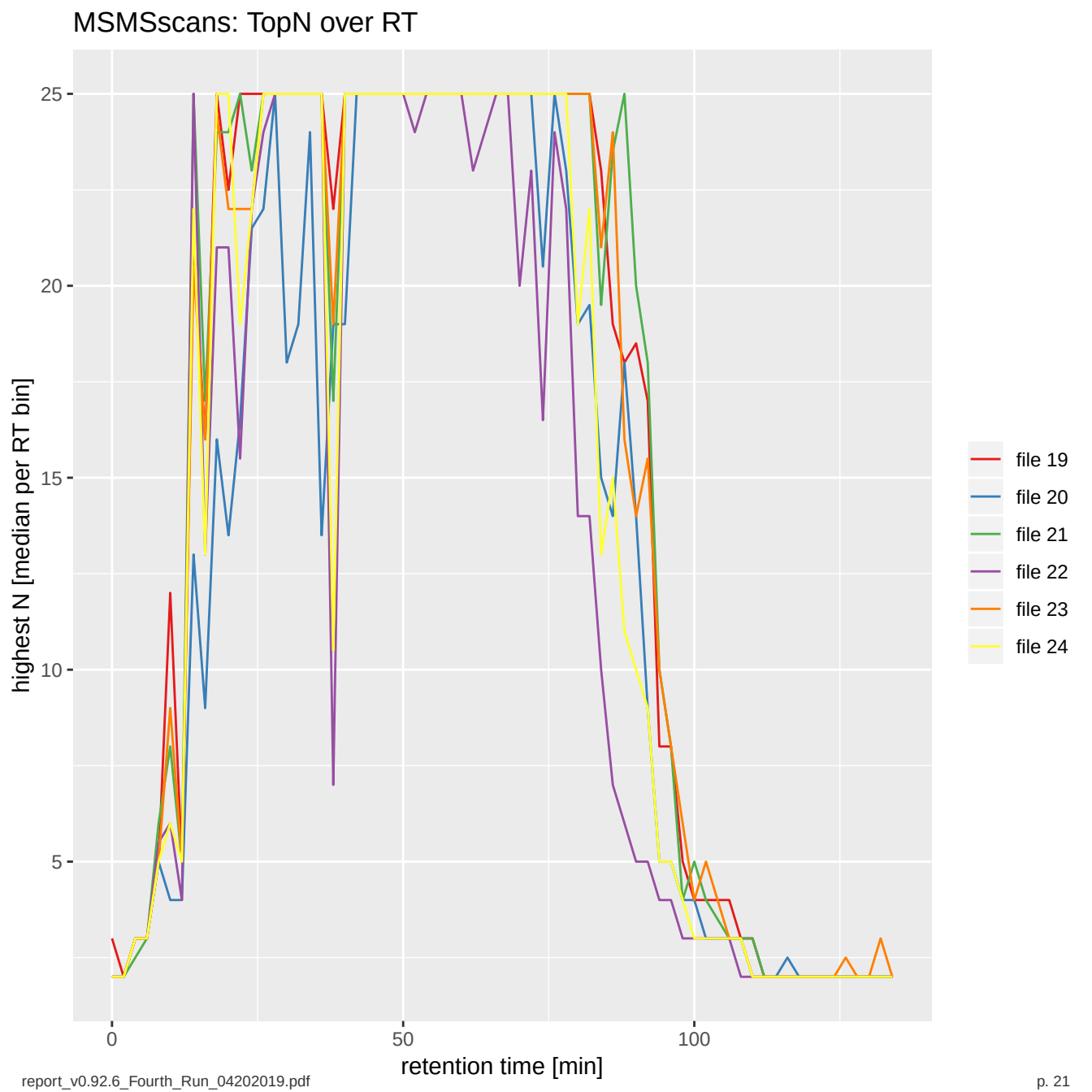
# MSMSscans: TopN

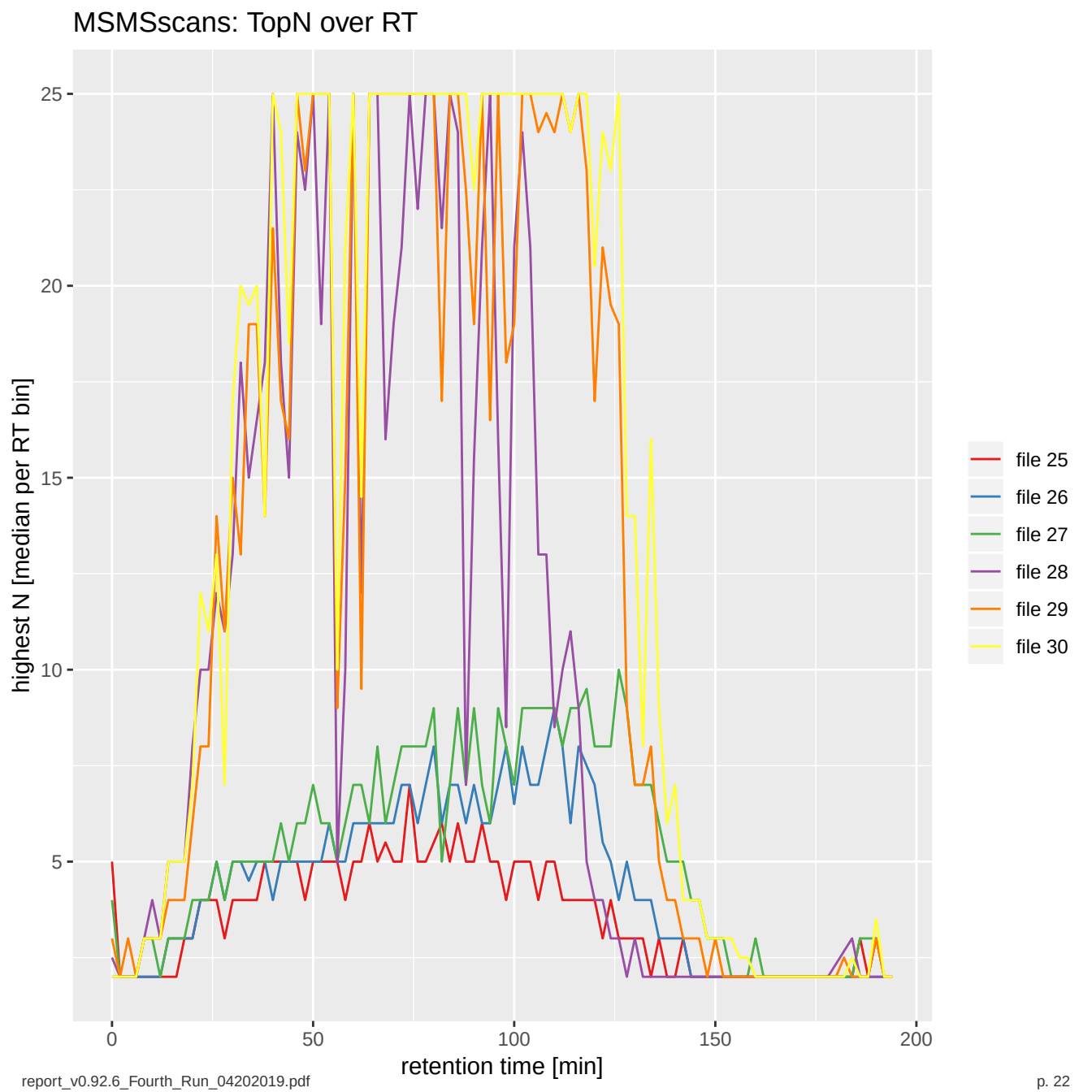


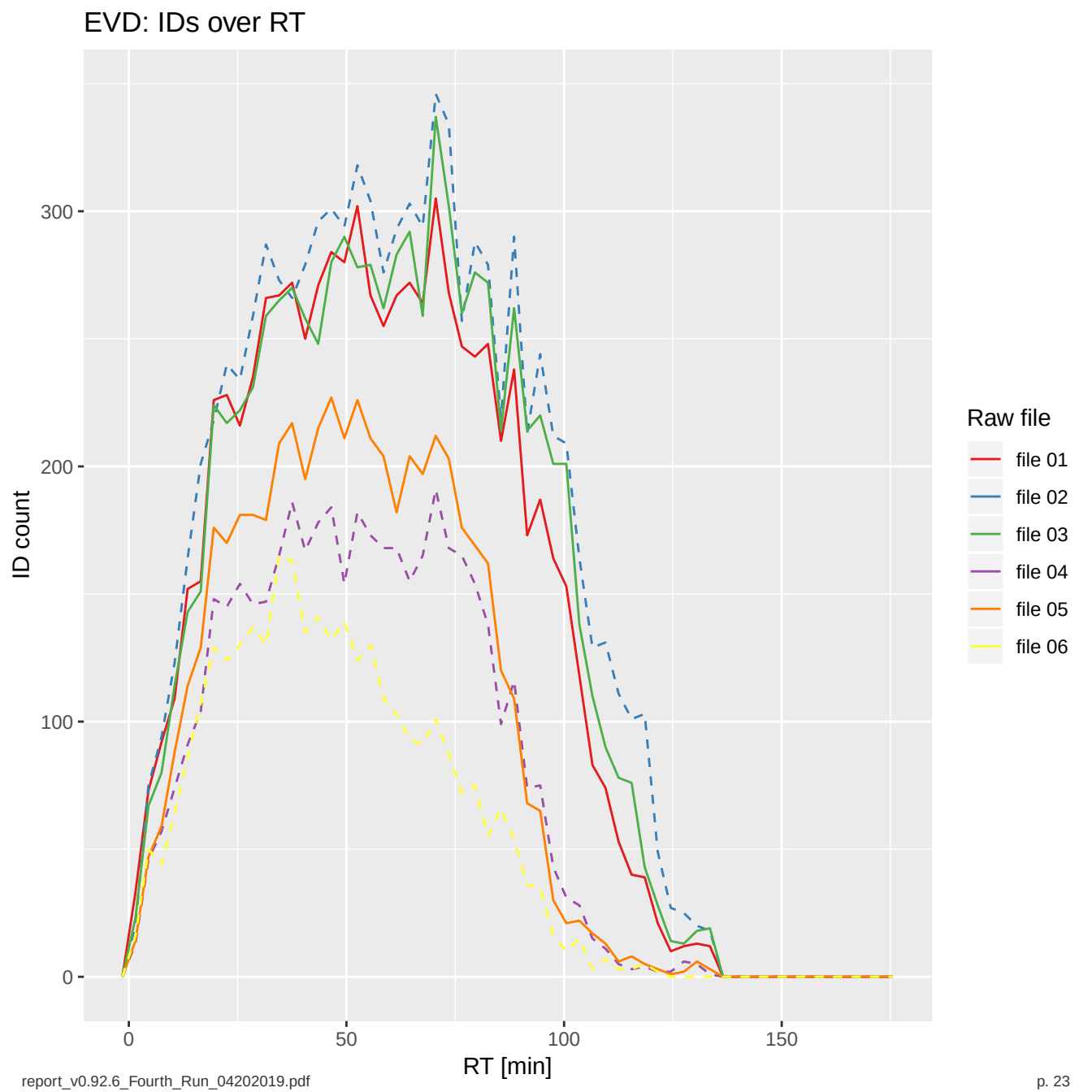

MSMSscans: TopN over RT
highest N [median per RT bin]
25
20
15
10
5
0
50
100
retention time [min]
file 01
file 02
file 03
file 04
file 05
file 06

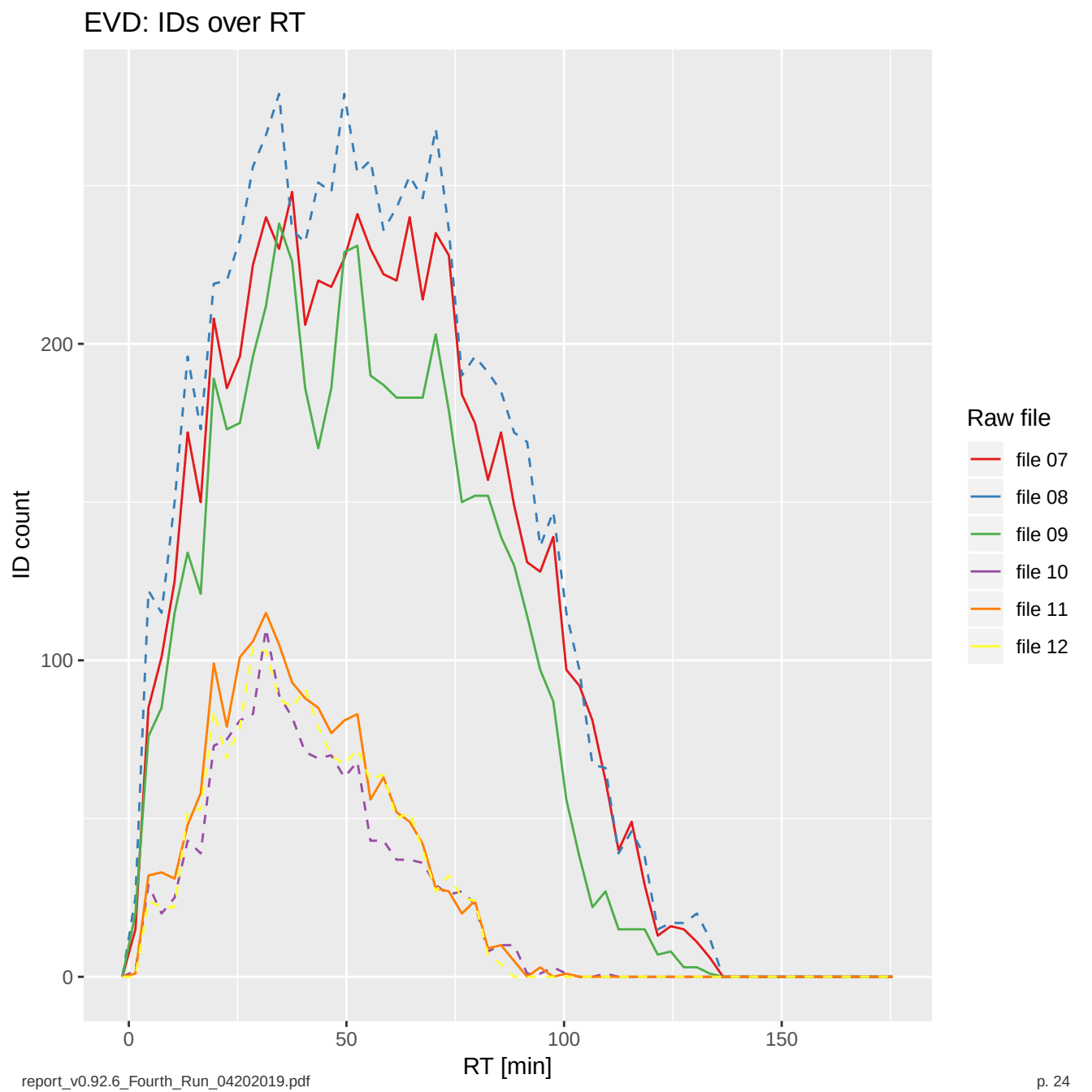

MSMSscans: TopN over RT
highest N [median per RT bin]
25
20
15
10
5
0
50
100
retention time [min]
file 07
file 08
file 09
file 10
file 11
file 12

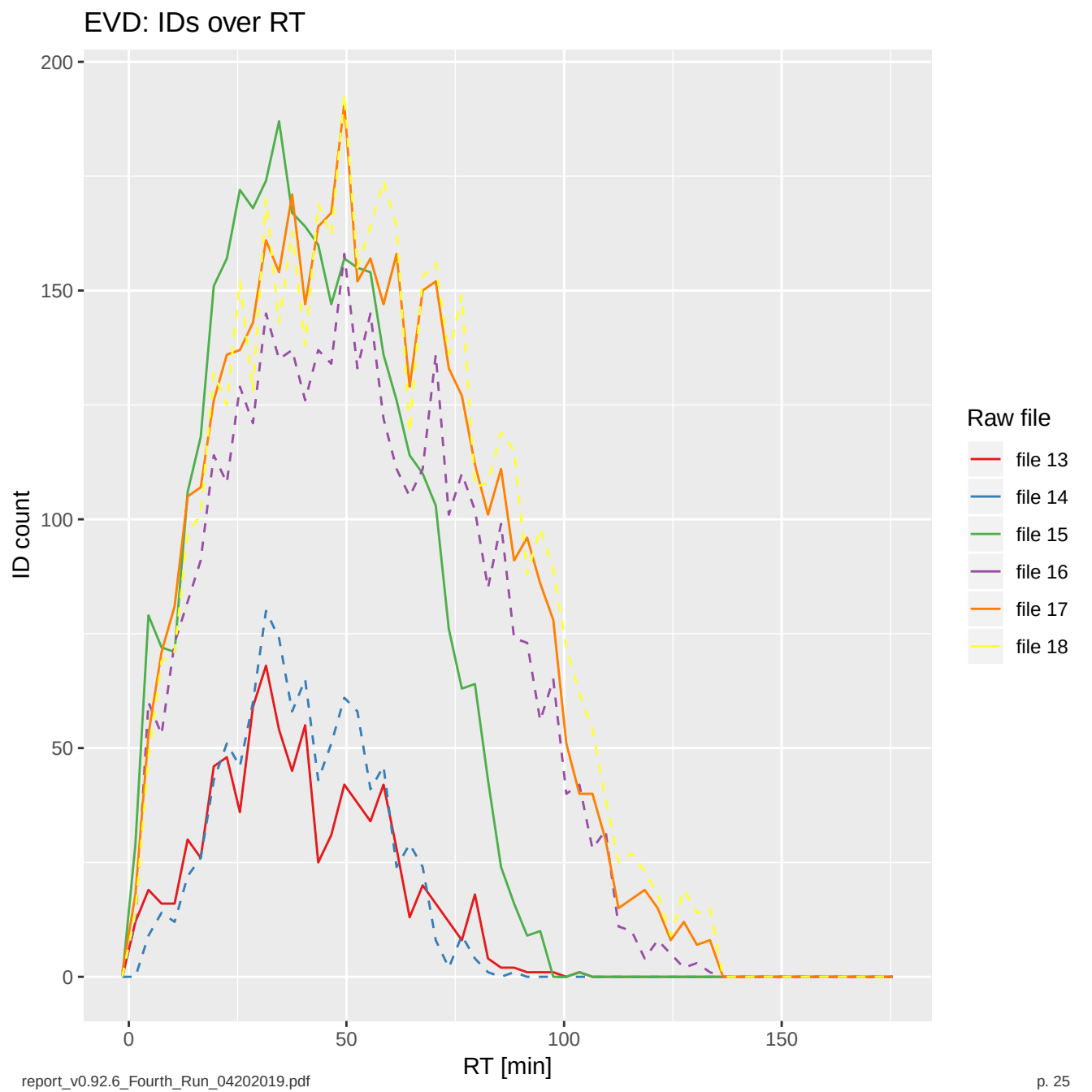

MSMSscans: TopN over RT
highest N [median per RT bin]
25
20
15
10
5
0
50
100
retention time [min]
file 13
file 14
file 15
file 16
file 17
file 18

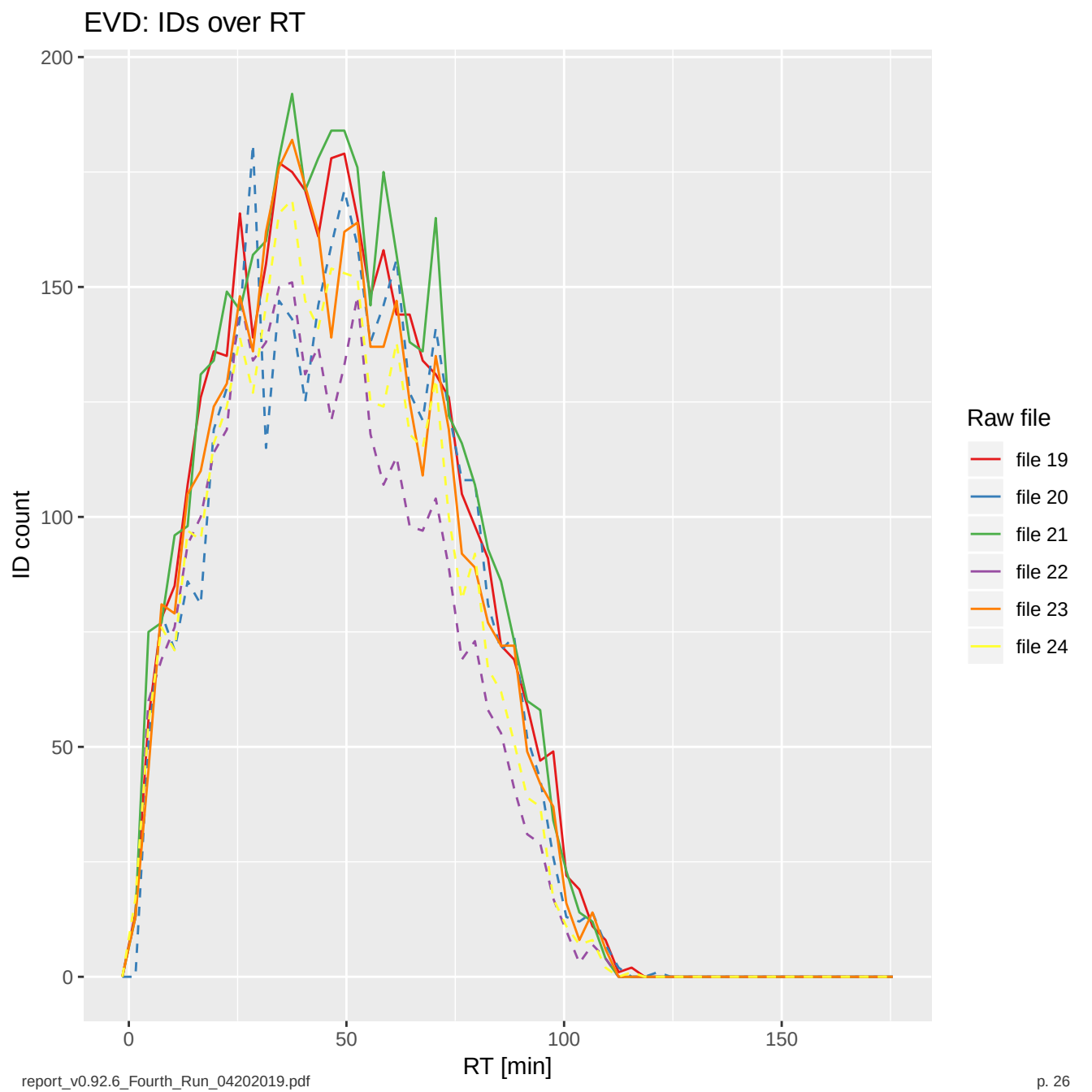

MSMSscans: TopN over RT
highest N [median per RT bin]
25
20
15
10
5
0
50
100
retention time [min]
file 19
file 20
file 21
file 22
file 23
file 24

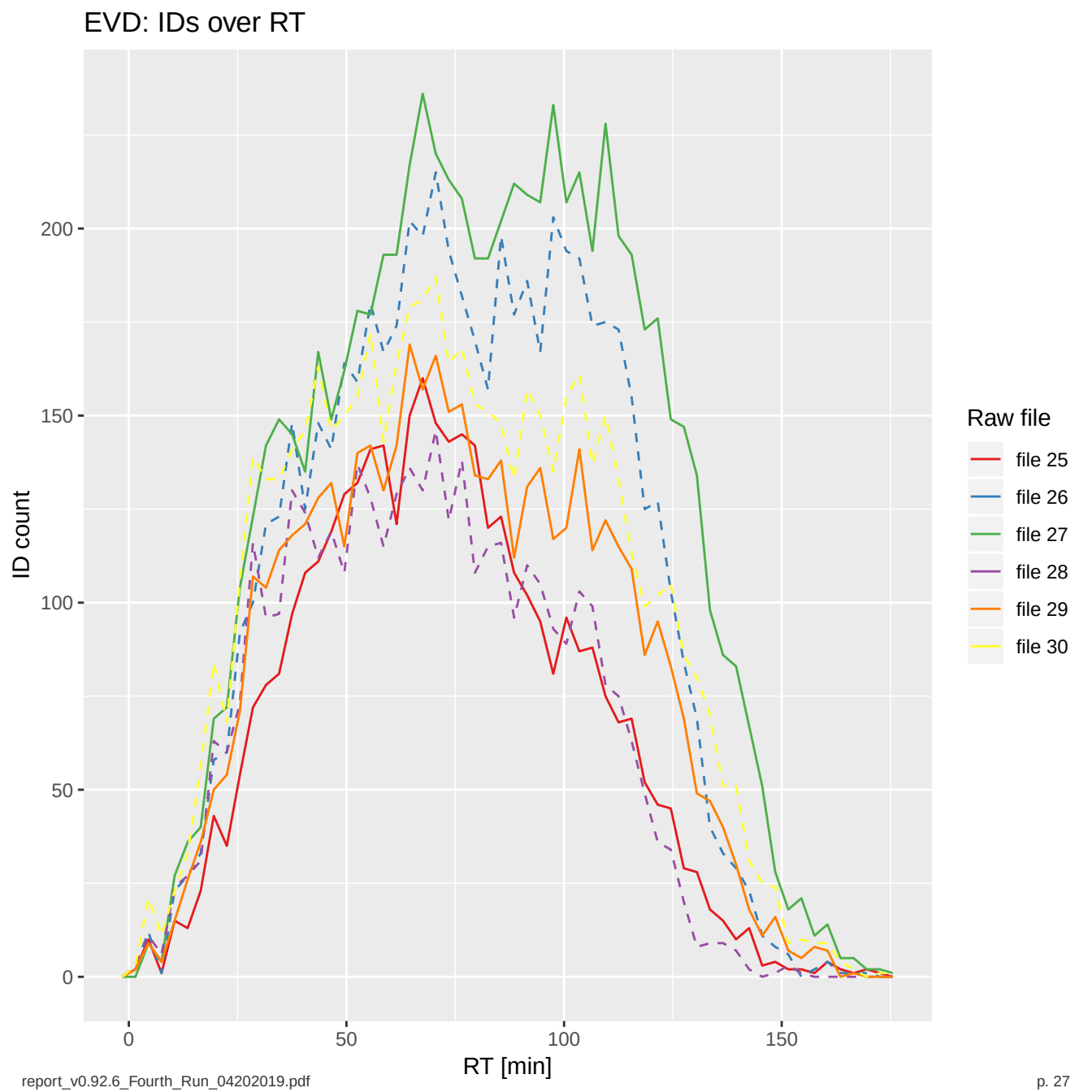

MSMSscans: TopN over RT
highest N [median per RT bin]
25
20
15
10
5
0
50
100
150
200
retention time [min]
file 25
file 26
file 27
file 28
file 29
file 30

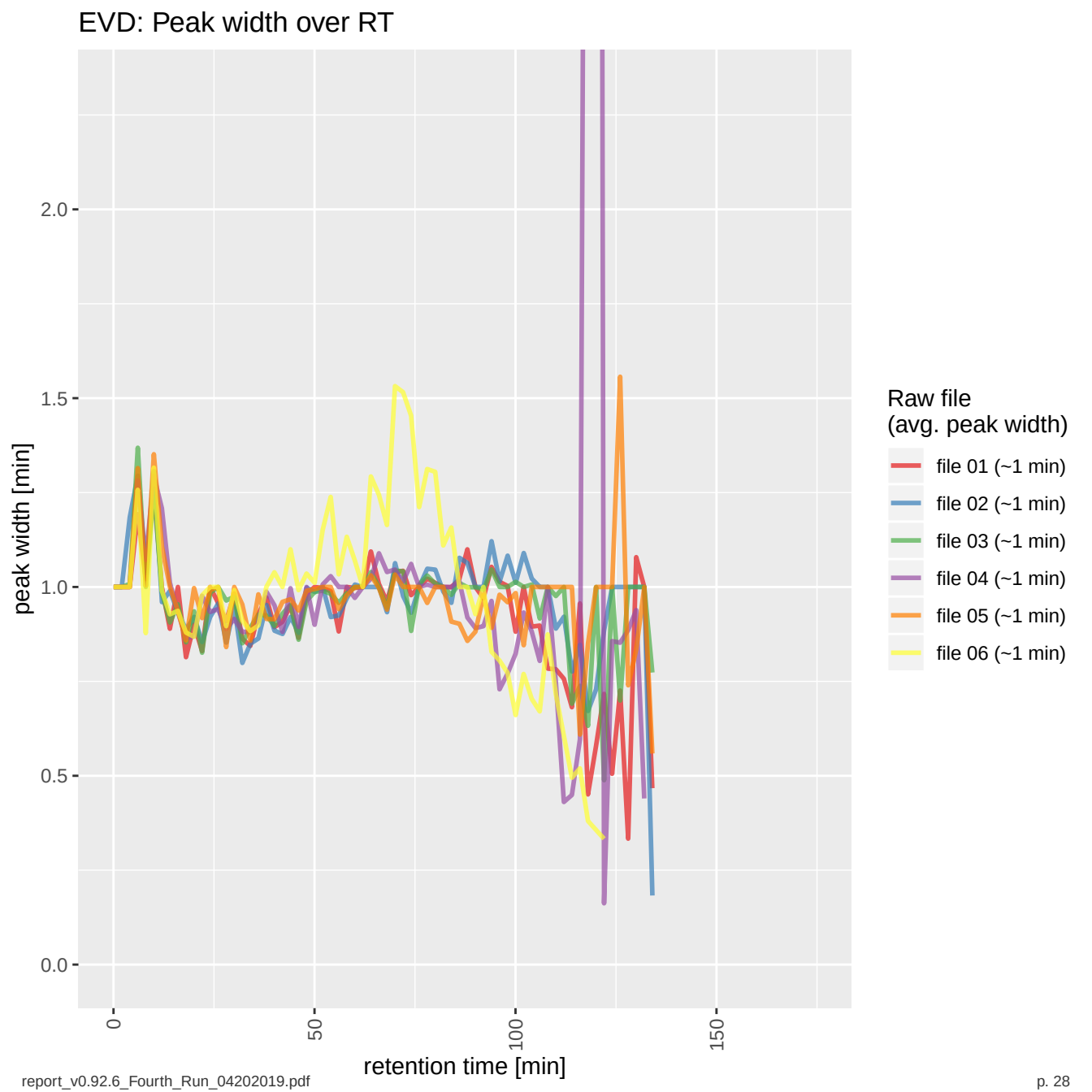

EVD: IDs over RT
ID count
300
200
100
0
0
50
100
150
RT [min]
Raw file
file 01
file 02
file 03
file 04
file 05
file 06

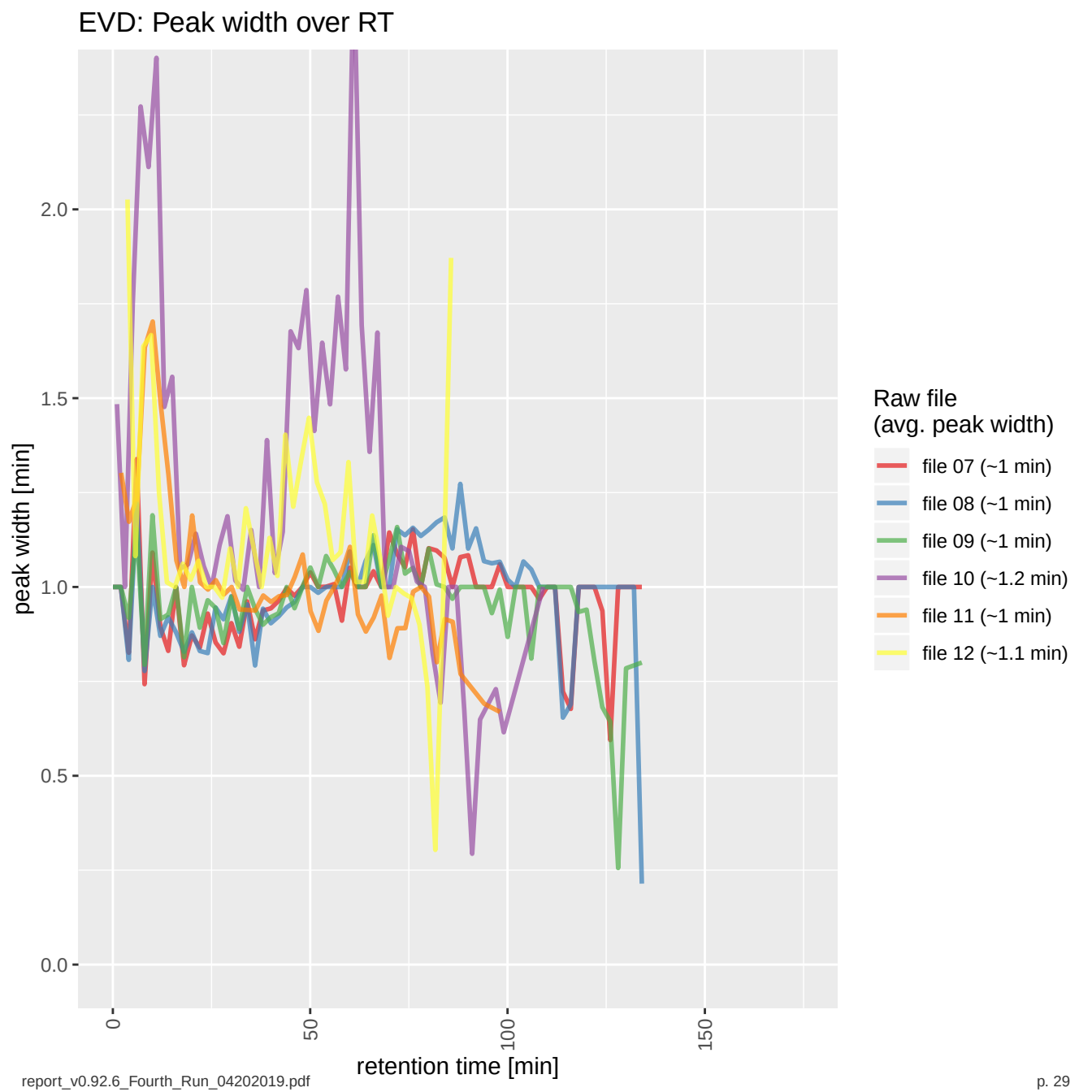

EVD: IDs over RT
ID count
200
100
0
0
50
100
150
RT [min]
Raw file
file 07
file 08
file 09
file 10
file 11
file 12

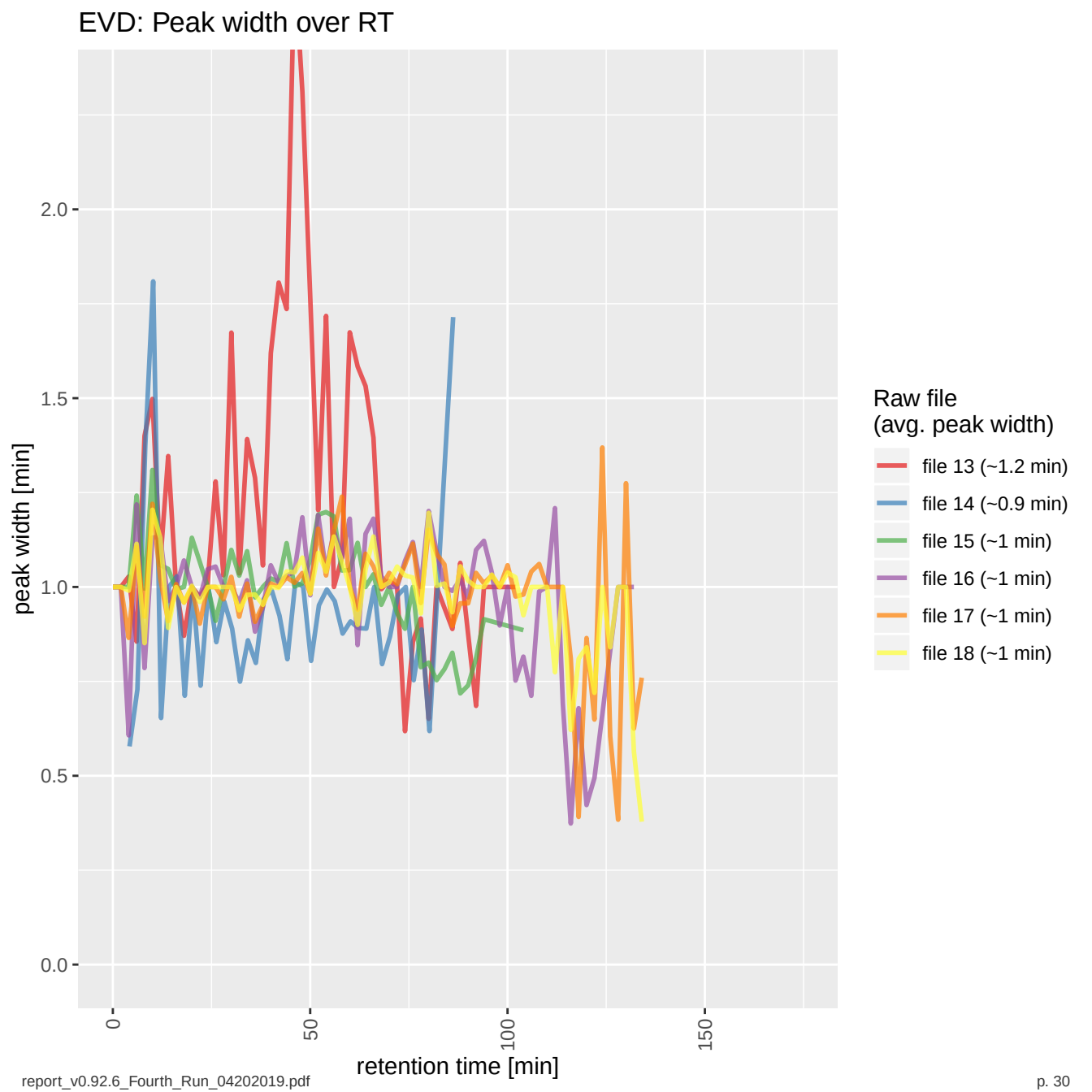

EVD: IDs over RT
ID count
RT [min]
0
50
100
150
200
Raw file
file 13
file 14
file 15
file 16
file 17
file 18

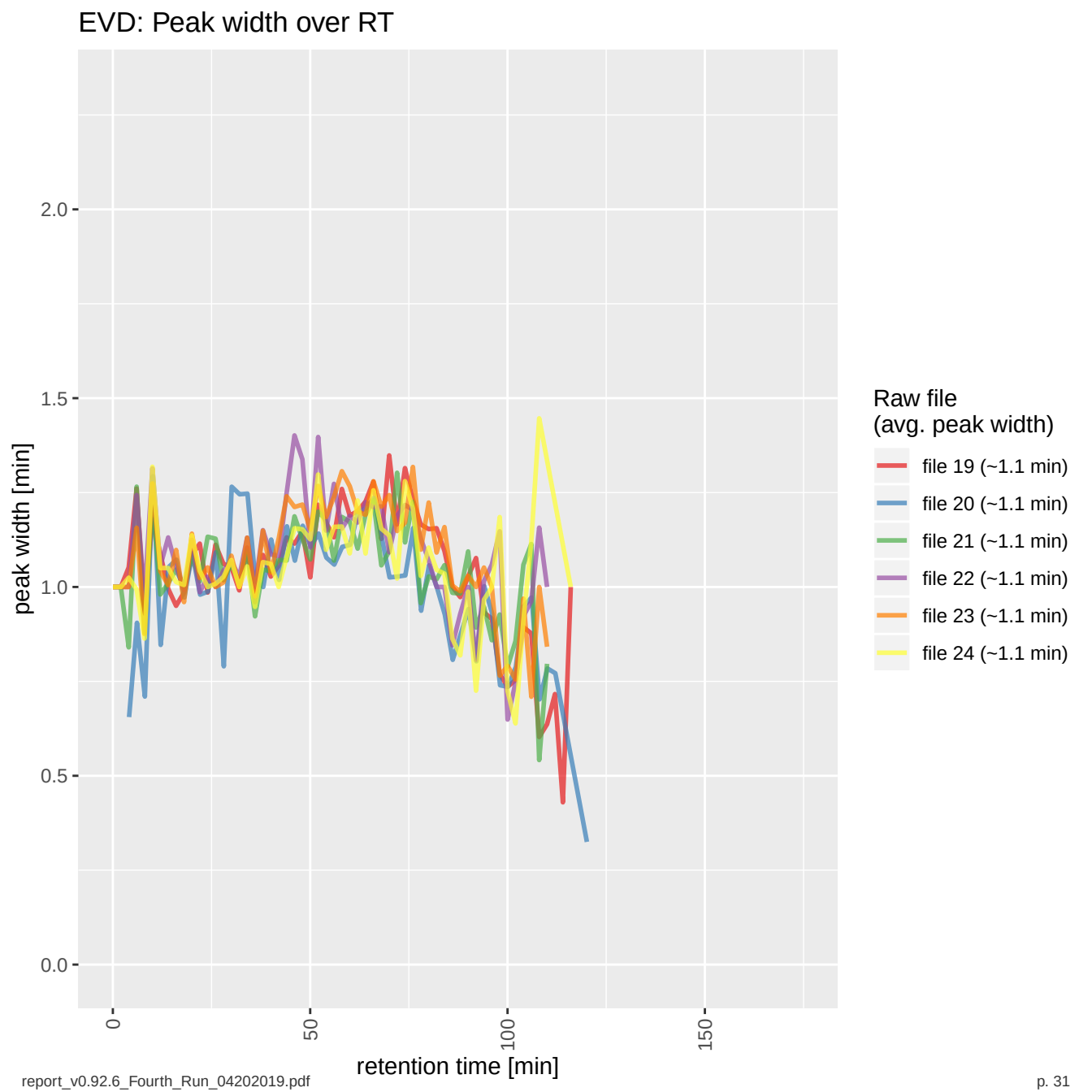

EVD: IDs over RT
200
150
100
50
0
ID count
0
50
100
150
RT [min]
Raw file
file 19
file 20
file 21
file 22
file 23
file 24

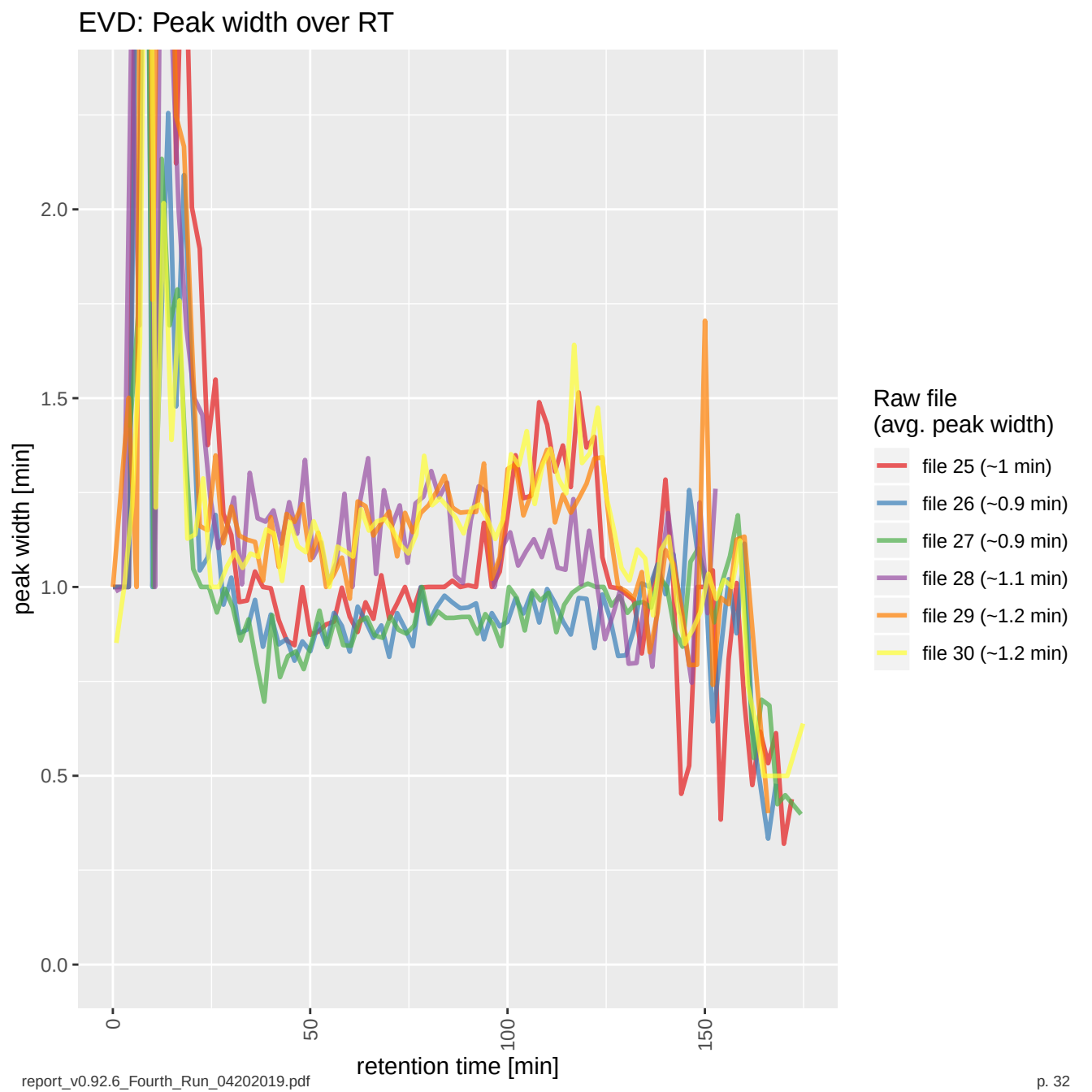

EVD: IDs over RT
ID count
RT [min]
0
50
100
150
200
Raw file
file 25
file 26
file 27
file 28
file 29
file 30

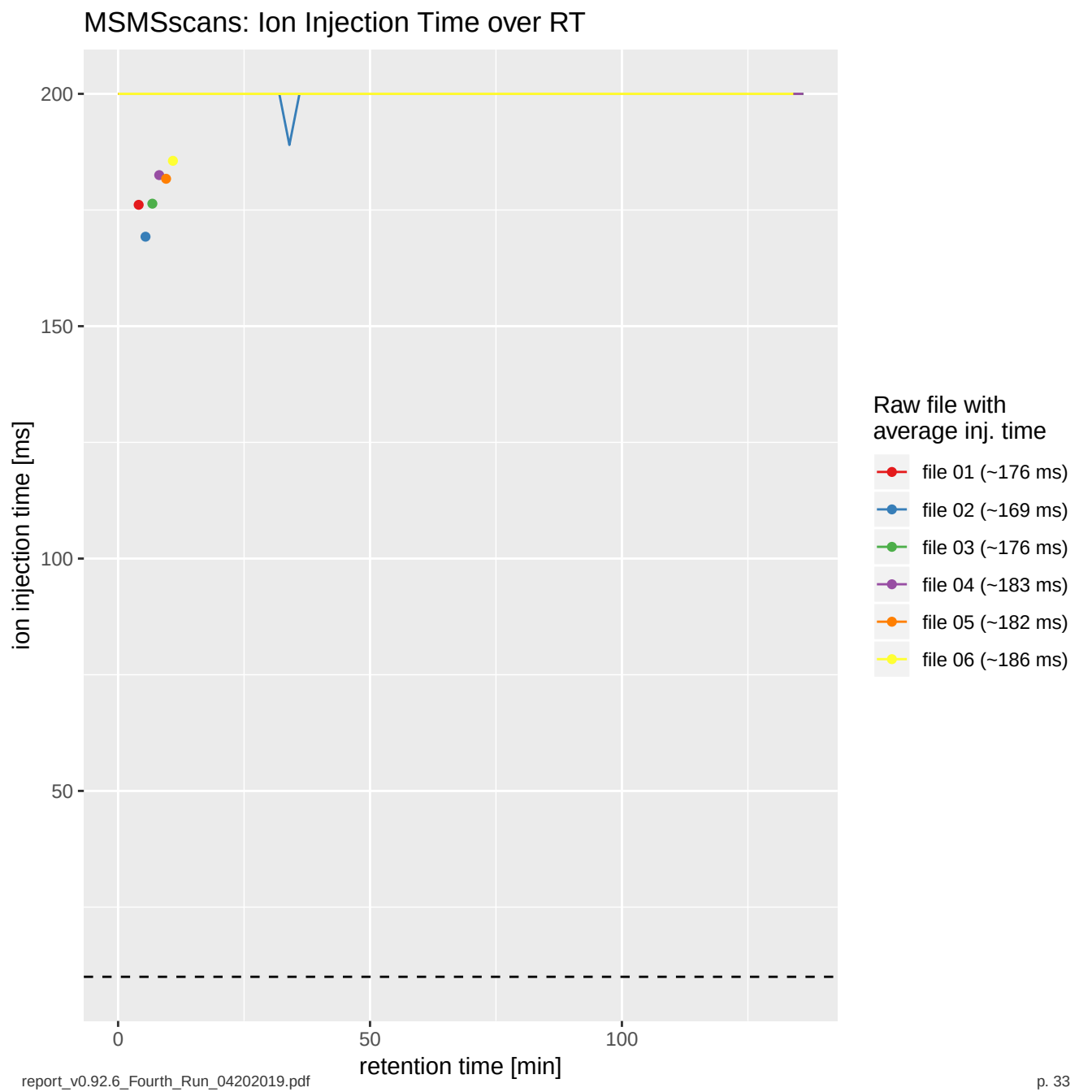

EVD: Peak width over RT
peak width [min]
2.0
1.5
1.0
0.5
0.0
0
50
100
150
retention time [min]
Raw file
(avg. peak width)
file 01 (~1 min)
file 02 (~1 min)
file 03 (~1 min)
file 04 (~1 min)
file 05 (~1 min)
file 06 (~1 min)

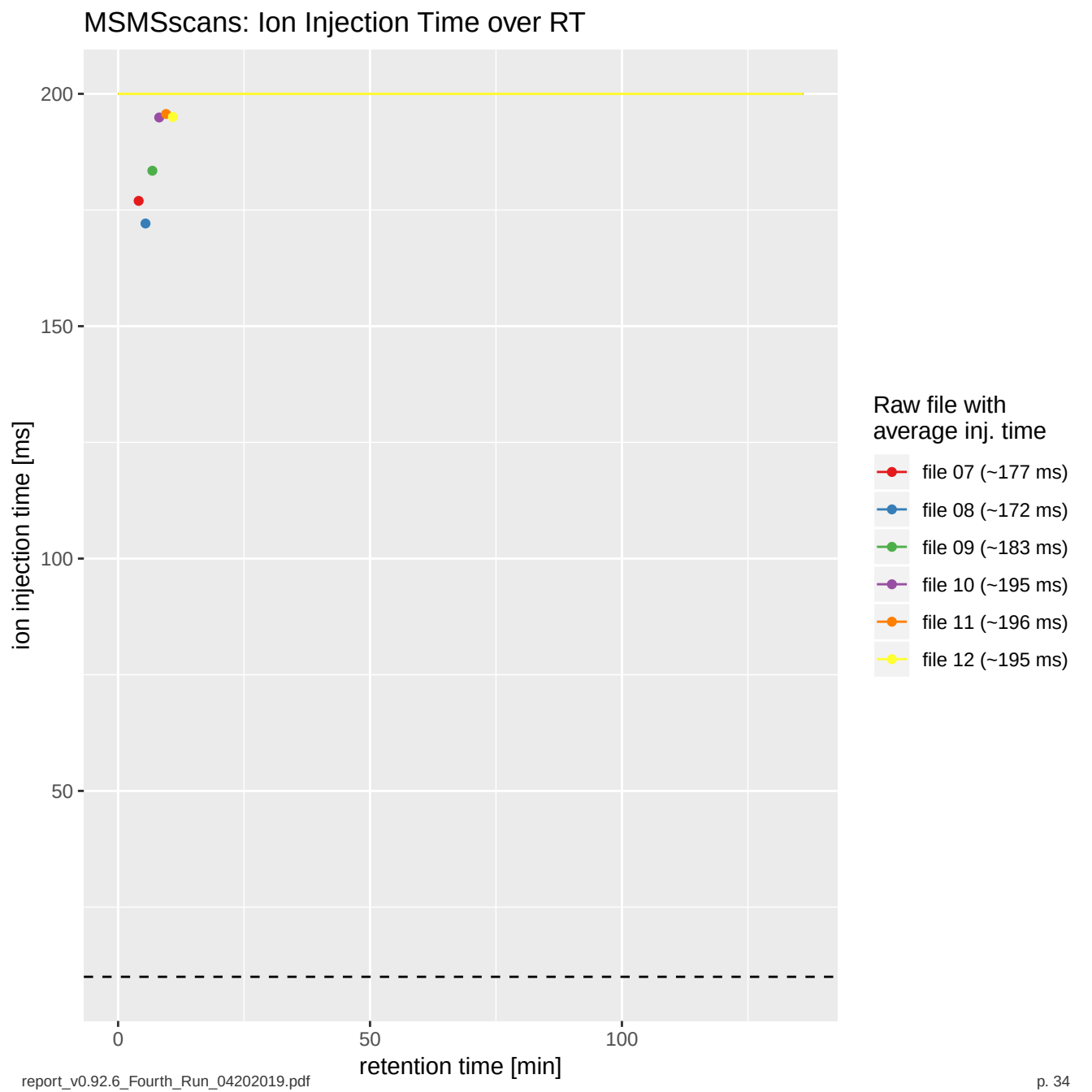

EVD: Peak width over RT
peak width [min]
2.0
1.5
1.0
0.5
0.0
0
50
100
150
retention time [min]
Raw file
(avg. peak width)
file 07 (~1 min)
file 08 (~1 min)
file 09 (~1 min)
file 10 (~1.2 min)
file 11 (~1 min)
file 12 (~1.1 min)

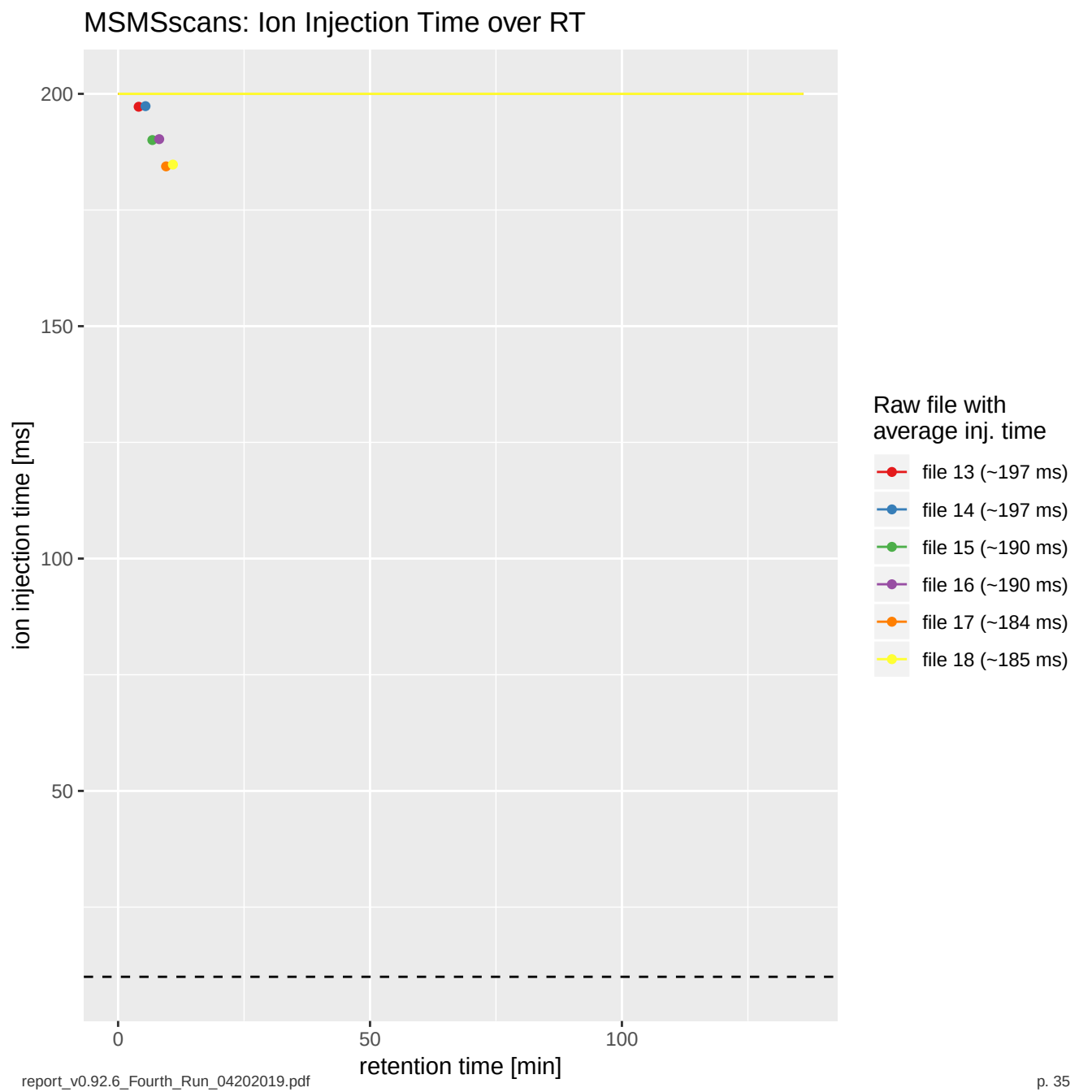

EVD: Peak width over RT
peak width [min]
2.0
1.5
1.0
0.5
0.0
0
50
100
150
retention time [min]
Raw file
(avg. peak width)
file 13 (~1.2 min)
file 14 (~0.9 min)
file 15 (~1 min)
file 16 (~1 min)
file 17 (~1 min)
file 18 (~1 min)

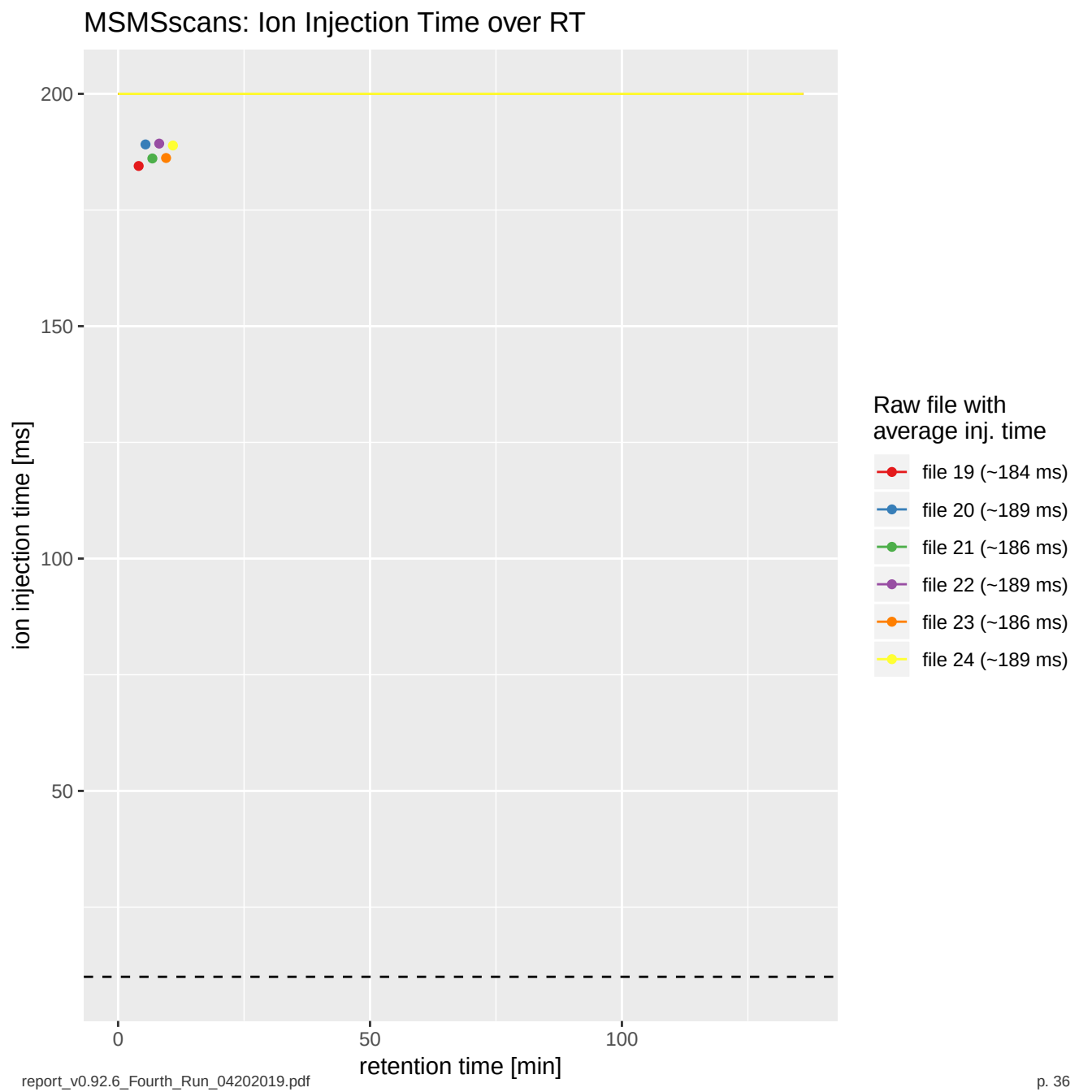

EVD: Peak width over RT
peak width [min]
2.0
1.5
1.0
0.5
0.0
0
50
100
150
retention time [min]
Raw file
(avg. peak width)
file 19 (~1.1 min)
file 20 (~1.1 min)
file 21 (~1.1 min)
file 22 (~1.1 min)
file 23 (~1.1 min)
file 24 (~1.1 min)

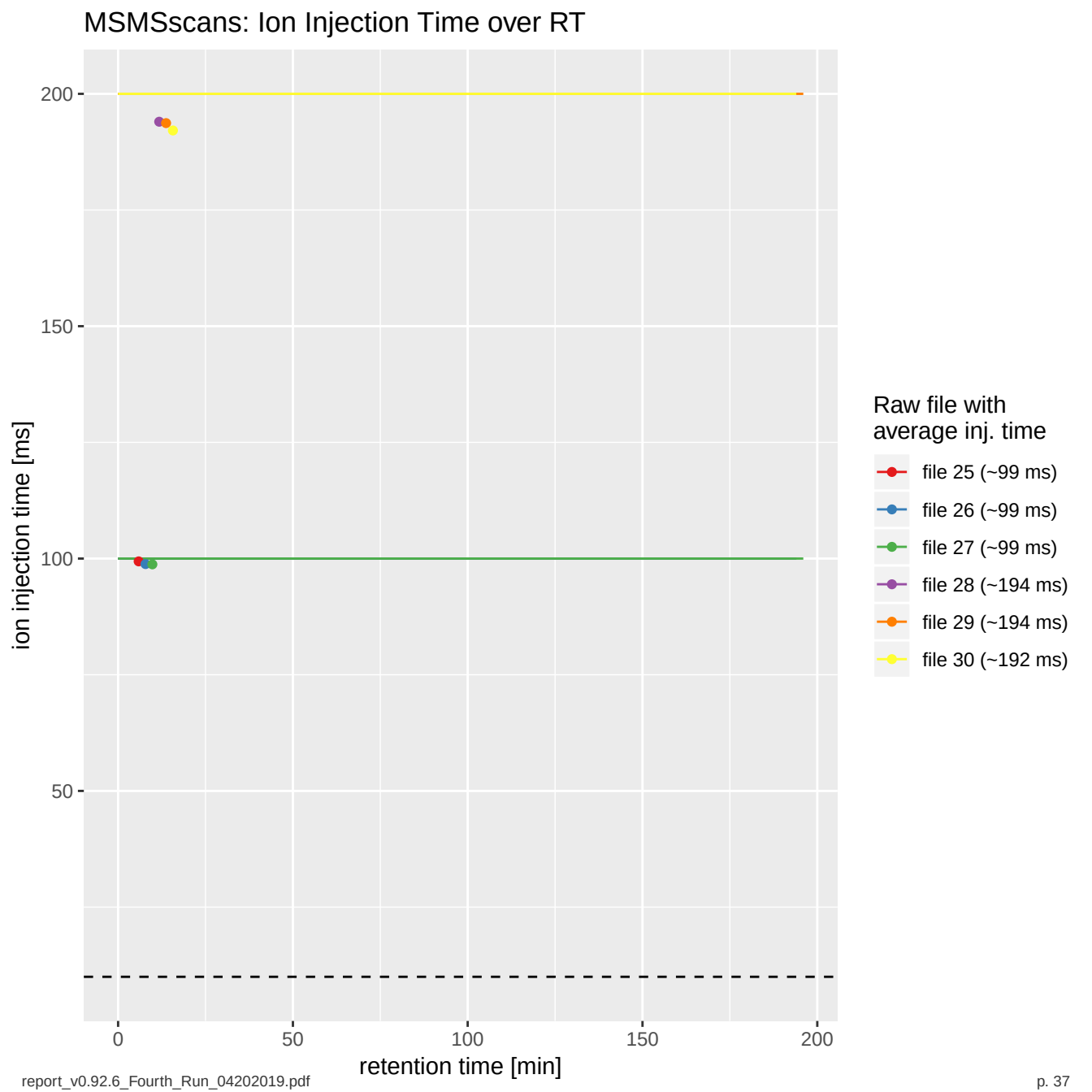

EVD: Peak width over RT
peak width [min]
2.0
1.5
1.0
0.5
0.0
0
50
100
150
retention time [min]
Raw file
(avg. peak width)
file 25 (~1 min)
file 26 (~0.9 min)
file 27 (~0.9 min)
file 28 (~1.1 min)
file 29 (~1.2 min)
file 30 (~1.2 min)

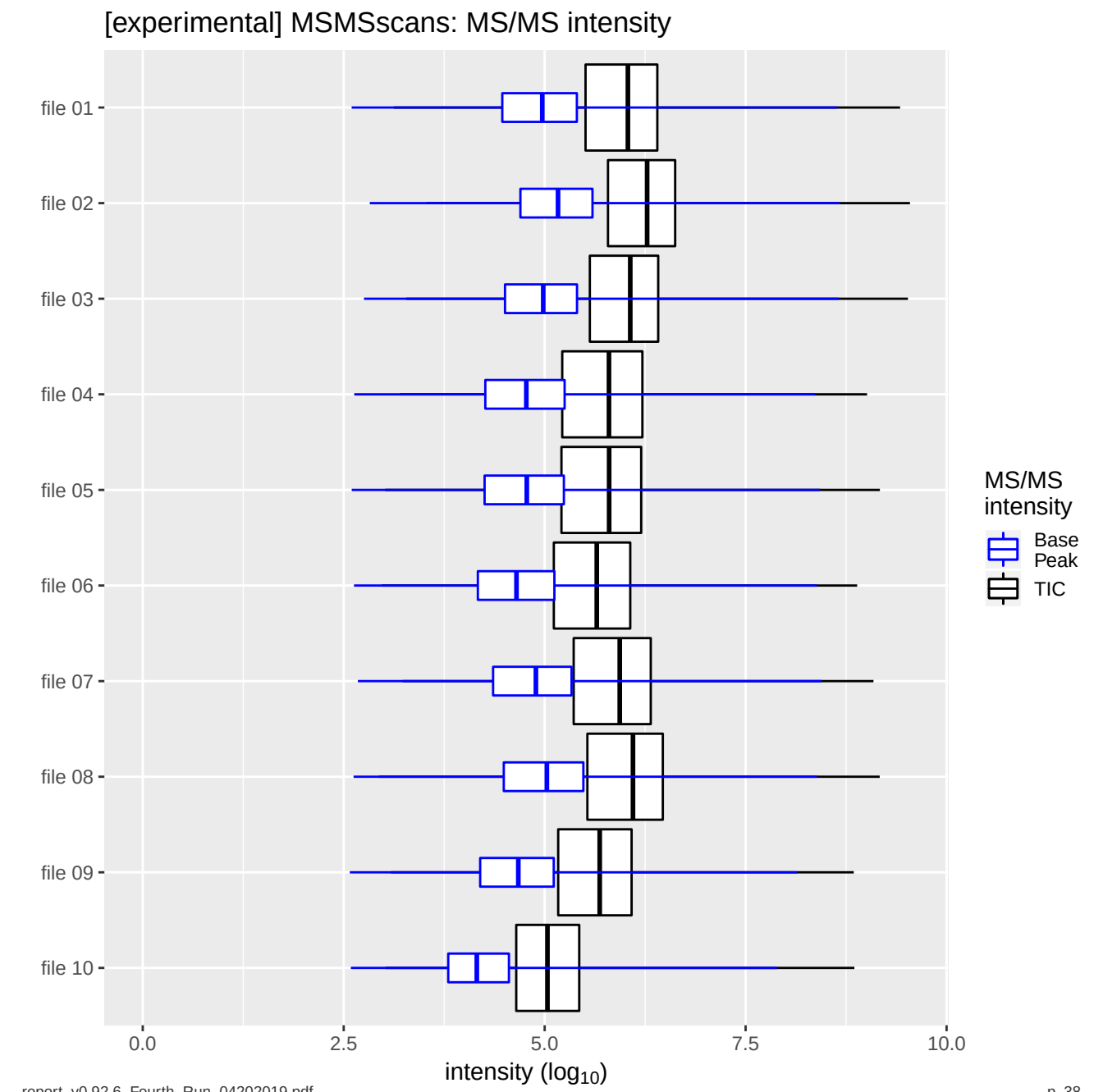

MSMSscans: Ion Injection Time over RT
ion injection time [ms]
200
150
100
50
0
50
100
retention time [min]
Raw file with average inj. time
file 01 (~176 ms)
file 02 (~169 ms)
file 03 (~176 ms)
file 04 (~183 ms)
file 05 (~182 ms)
file 06 (~186 ms)

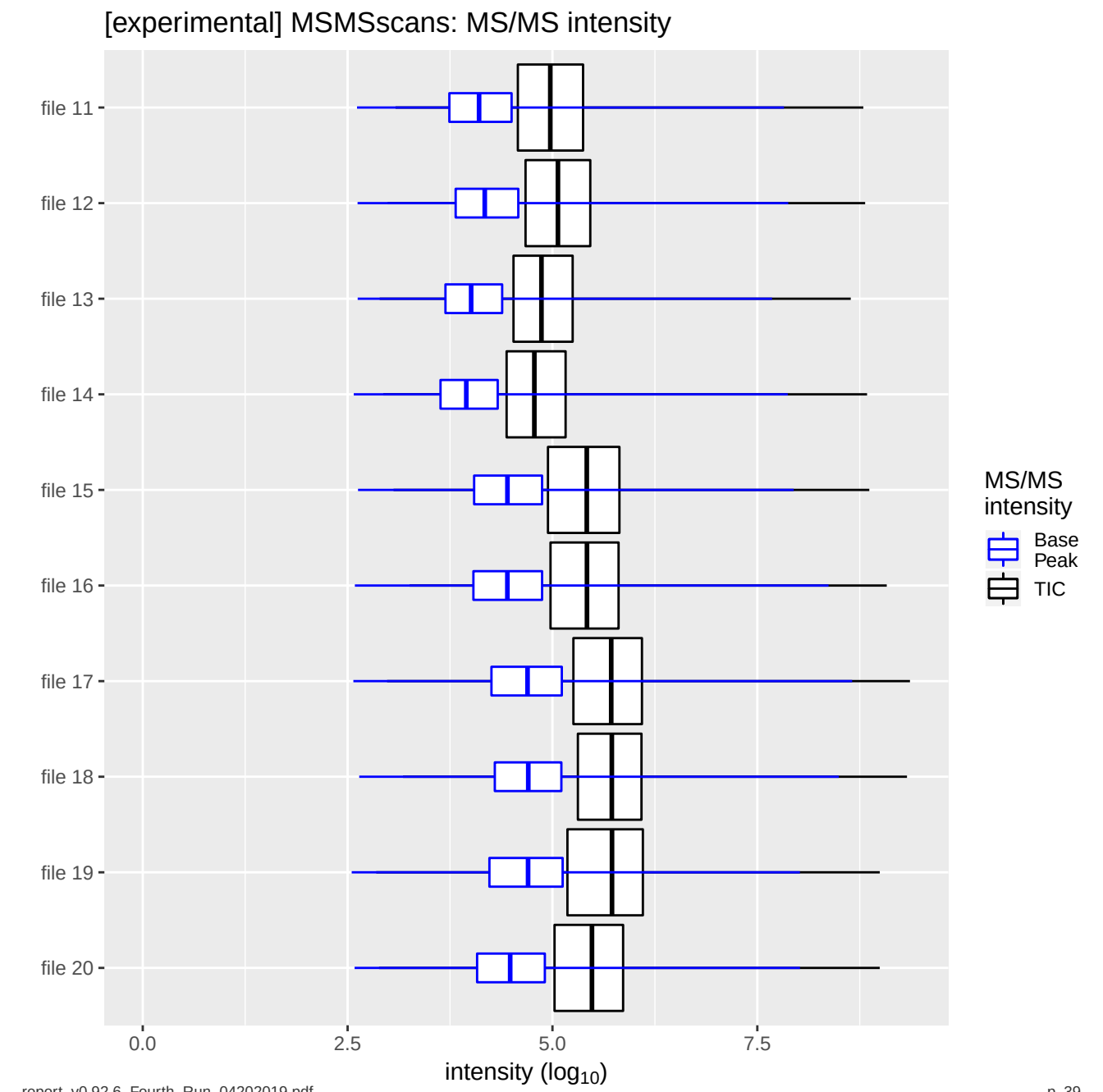

MSMSscans: Ion Injection Time over RT
ion injection time [ms]
200
150
100
50
0
50
100
retention time [min]
Raw file with average inj. time
file 07 (~177 ms)
file 08 (~172 ms)
file 09 (~183 ms)
file 10 (~195 ms)
file 11 (~196 ms)
file 12 (~195 ms)

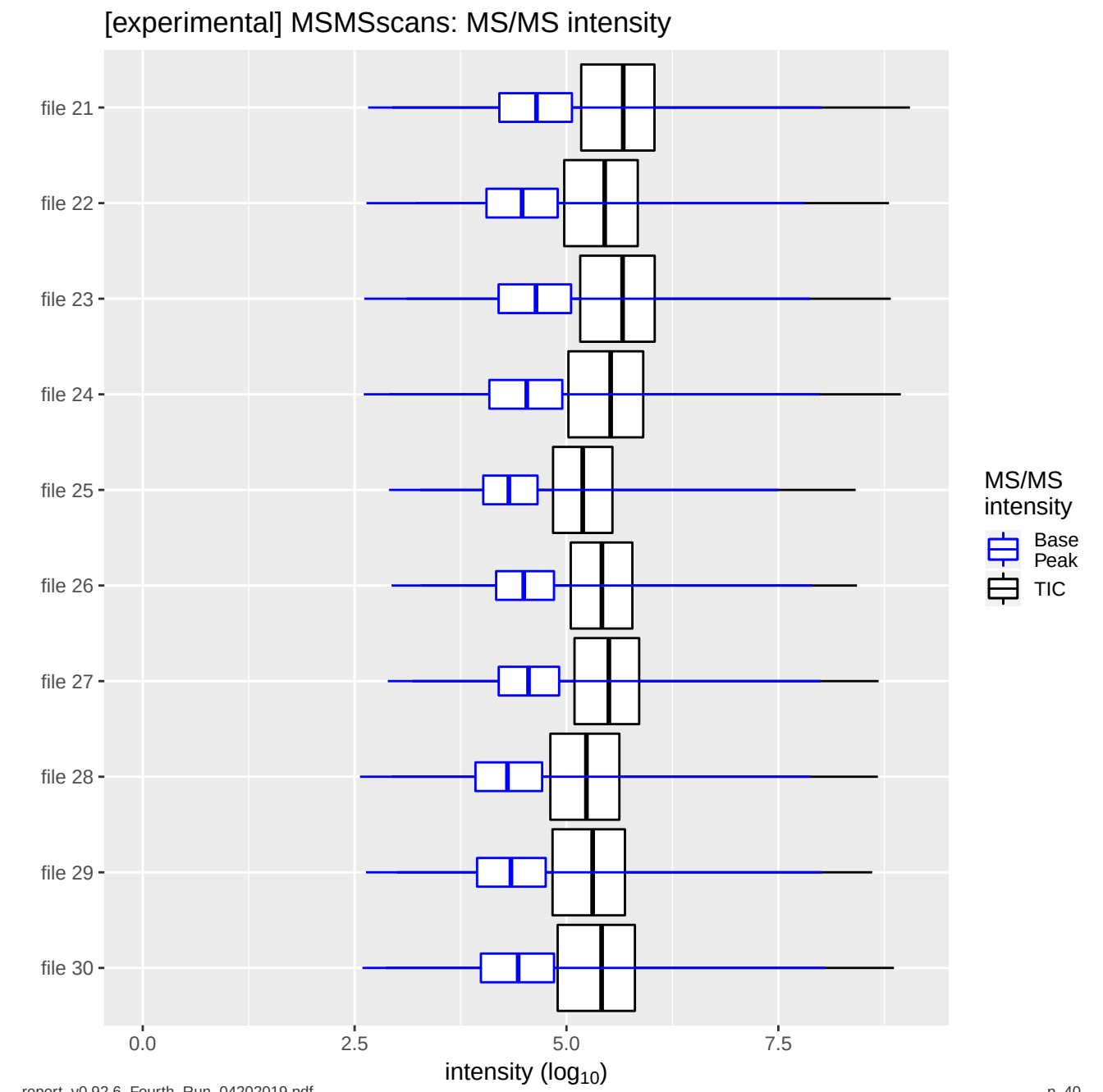

MSMSscans: Ion Injection Time over RT
ion injection time [ms]
200
150
100
50
0
50
100
retention time [min]
Raw file with average inj. time
file 13 (~197 ms)
file 14 (~197 ms)
file 15 (~190 ms)
file 16 (~190 ms)
file 17 (~184 ms)
file 18 (~185 ms)

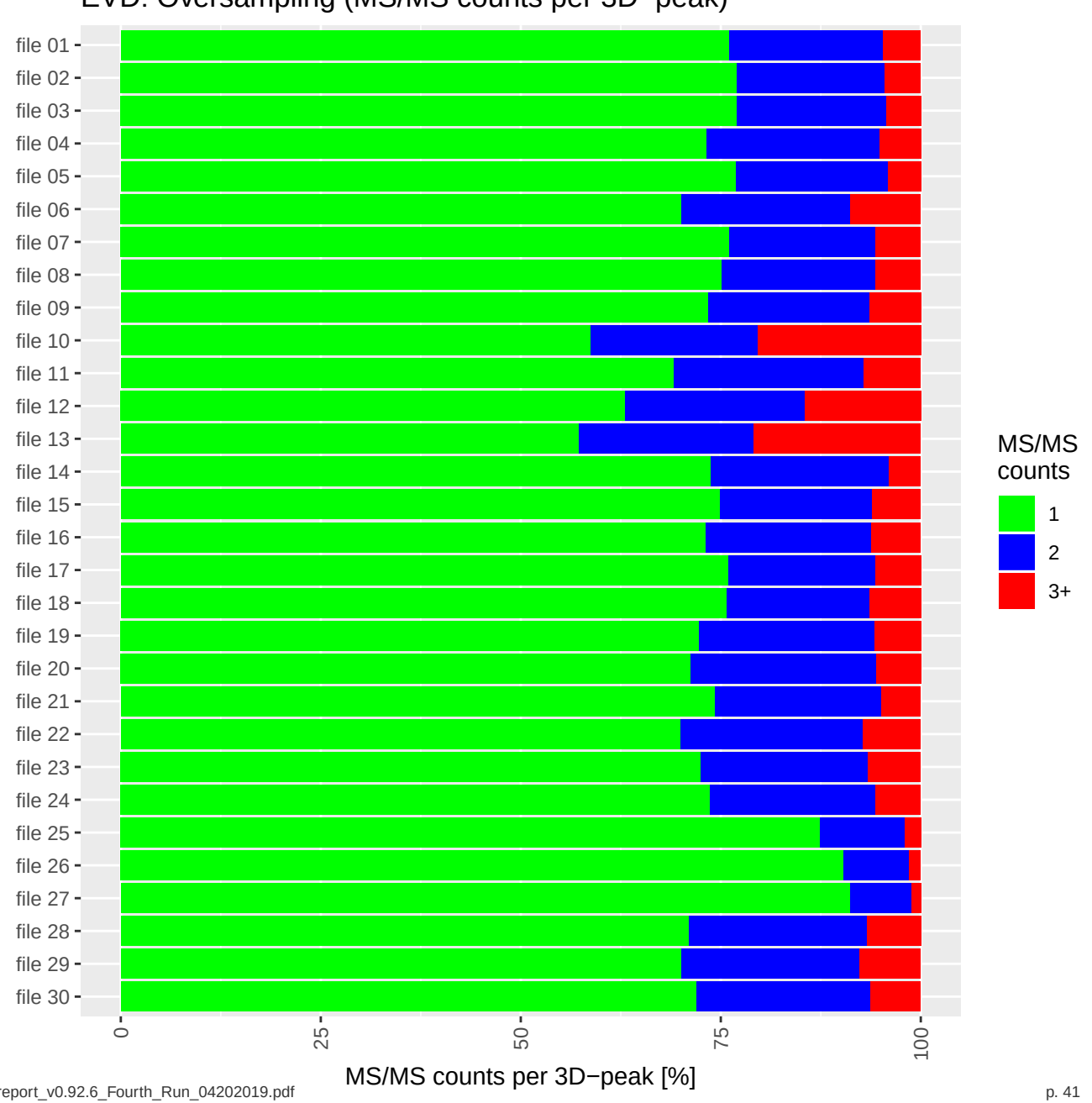

MSMSscans: Ion Injection Time over RT
ion injection time [ms]
200
150
100
50
0
50
100
retention time [min]
Raw file with average inj. time
file 19 (~184 ms)
file 20 (~189 ms)
file 21 (~186 ms)
file 22 (~189 ms)
file 23 (~186 ms)
file 24 (~189 ms)

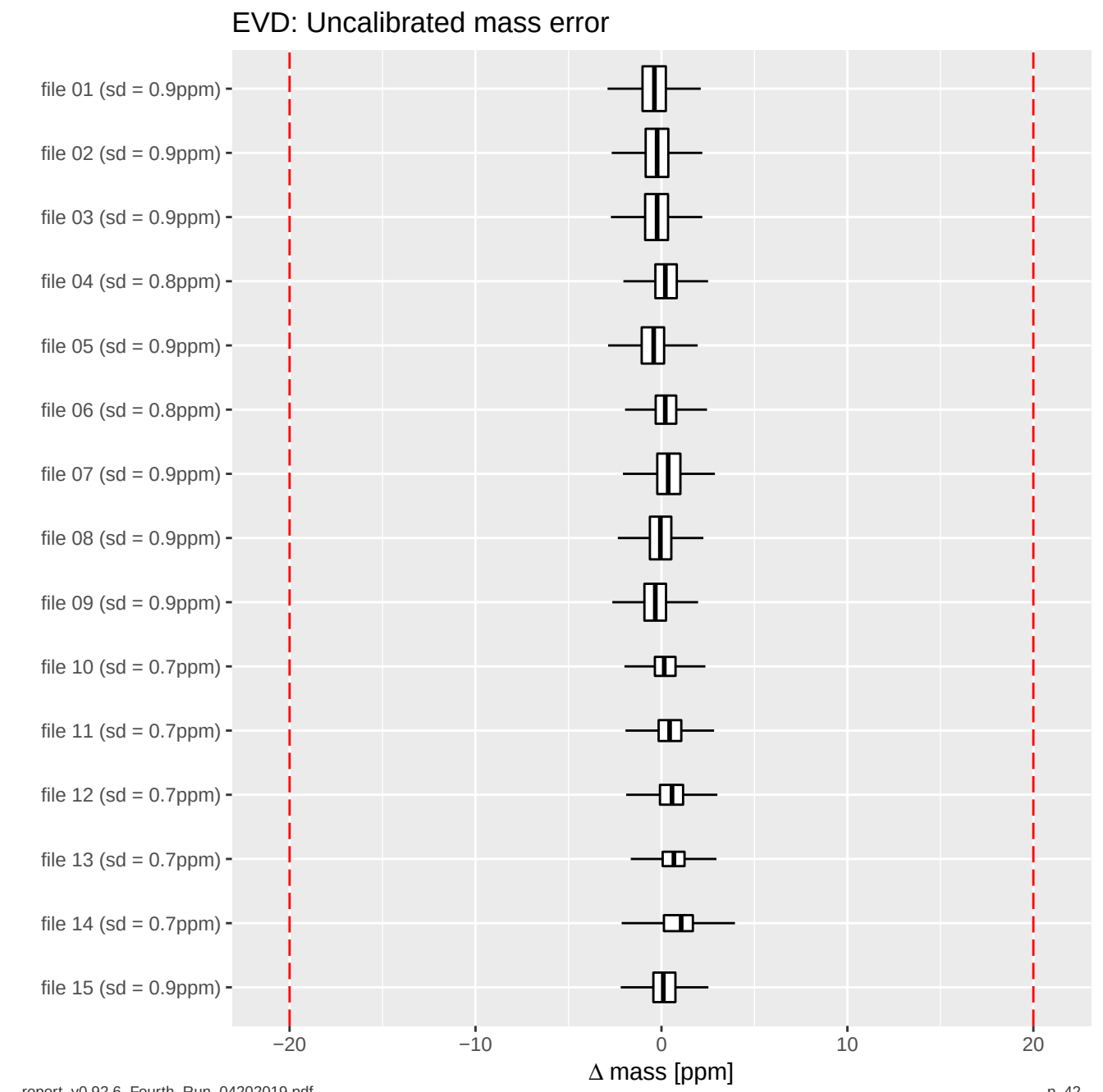

MSMSscans: Ion Injection Time over RT
ion injection time [ms]
200
150
100
50
0
50
100
150
200
retention time [min]
Raw file with average inj. time
file 25 (~99 ms)
file 26 (~99 ms)
file 27 (~99 ms)
file 28 (~194 ms)
file 29 (~194 ms)
file 30 (~192 ms)

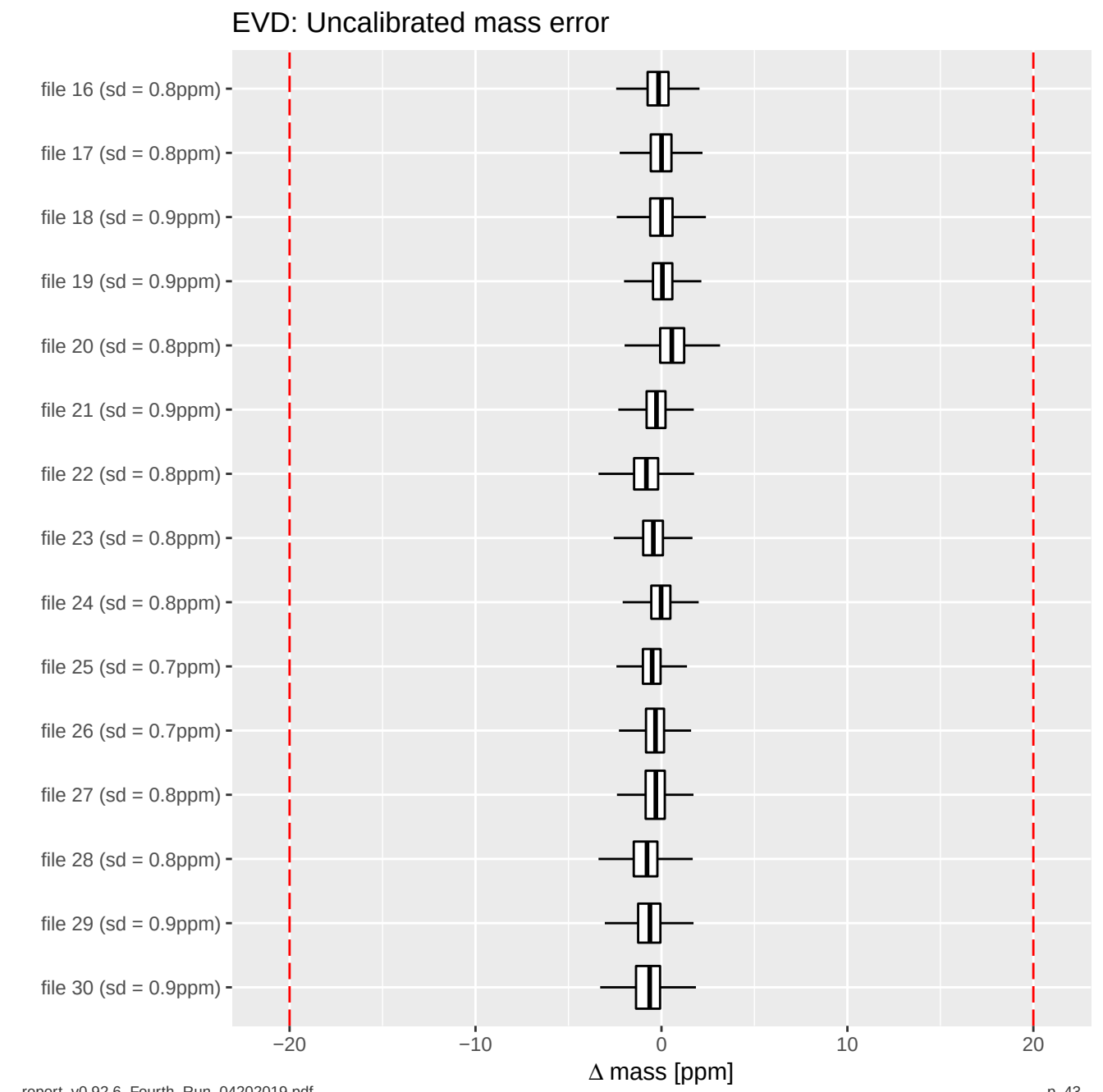

[experimental] MSMSscans: MS/MS intensity
file 01
file 02
file 03
file 04
file 05
file 06
file 07
file 08
file 09
file 10
0.0
2.5
5.0
7.5
10.0
intensity (log10)
MS/MS intensity
Base Peak
TIC

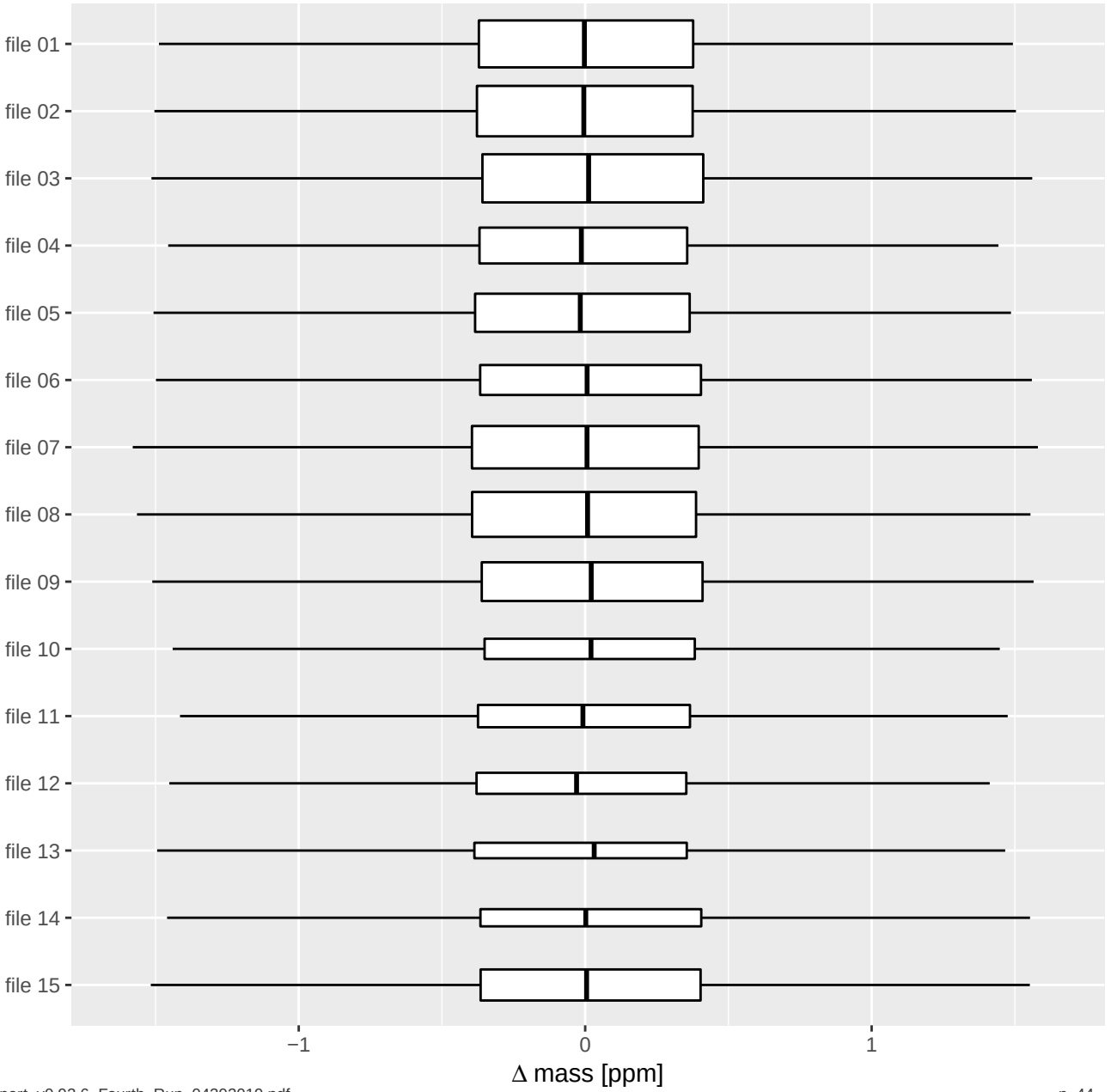

[experimental] MSMSscans: MS/MS intensity
file 11
file 12
file 13
file 14
file 15
file 16
file 17
file 18
file 19
file 20
0.0
2.5
5.0
7.5
intensity (log10)
MS/MS intensity
Base Peak
TIC

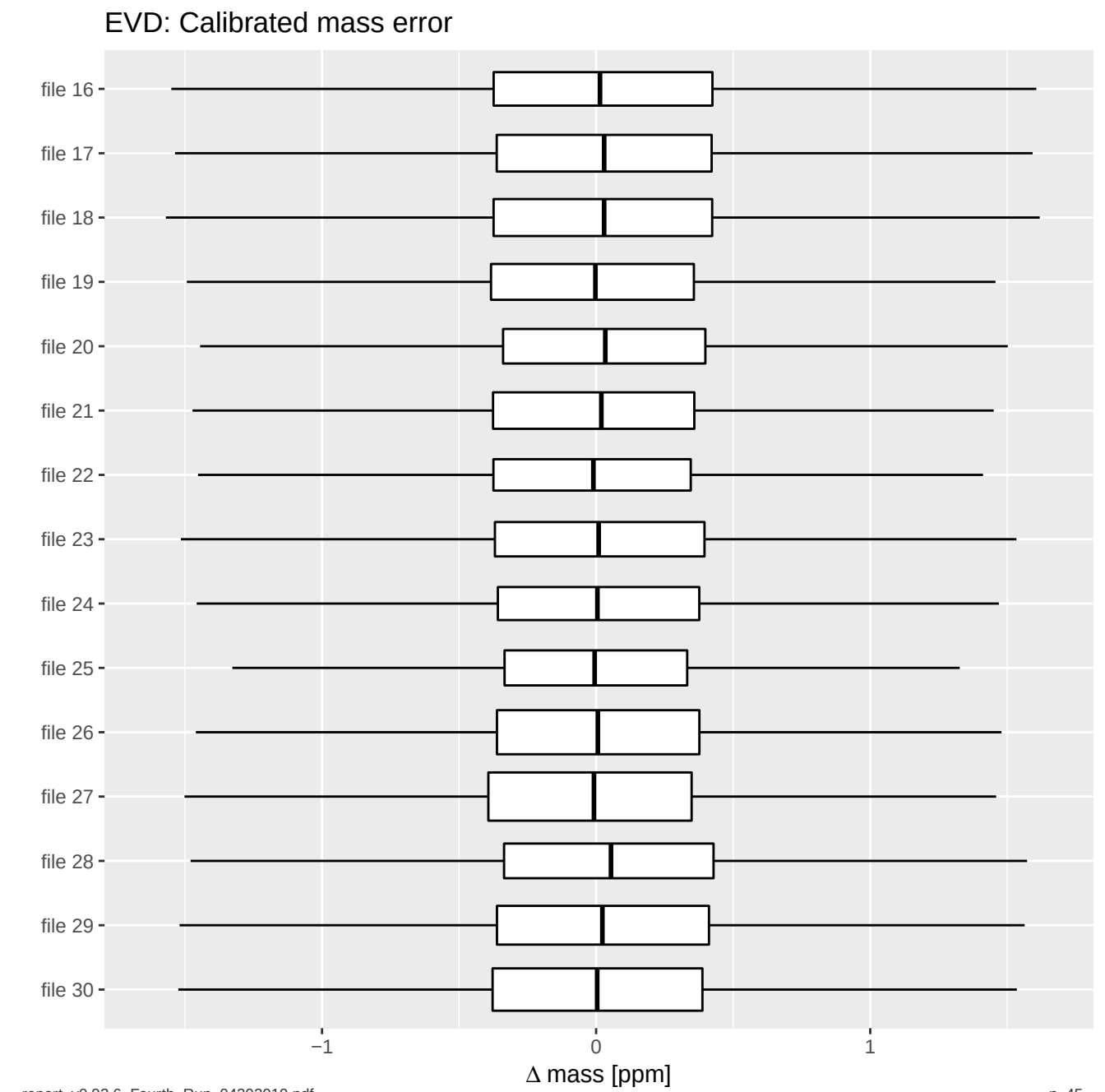

[experimental] MSMSscans: MS/MS intensity
file 21
file 22
file 23
file 24
file 25
file 26
file 27
file 28
file 29
file 30
0.0
2.5
5.0
7.5
intensity (log10)
MS/MS intensity
Base Peak
TIC

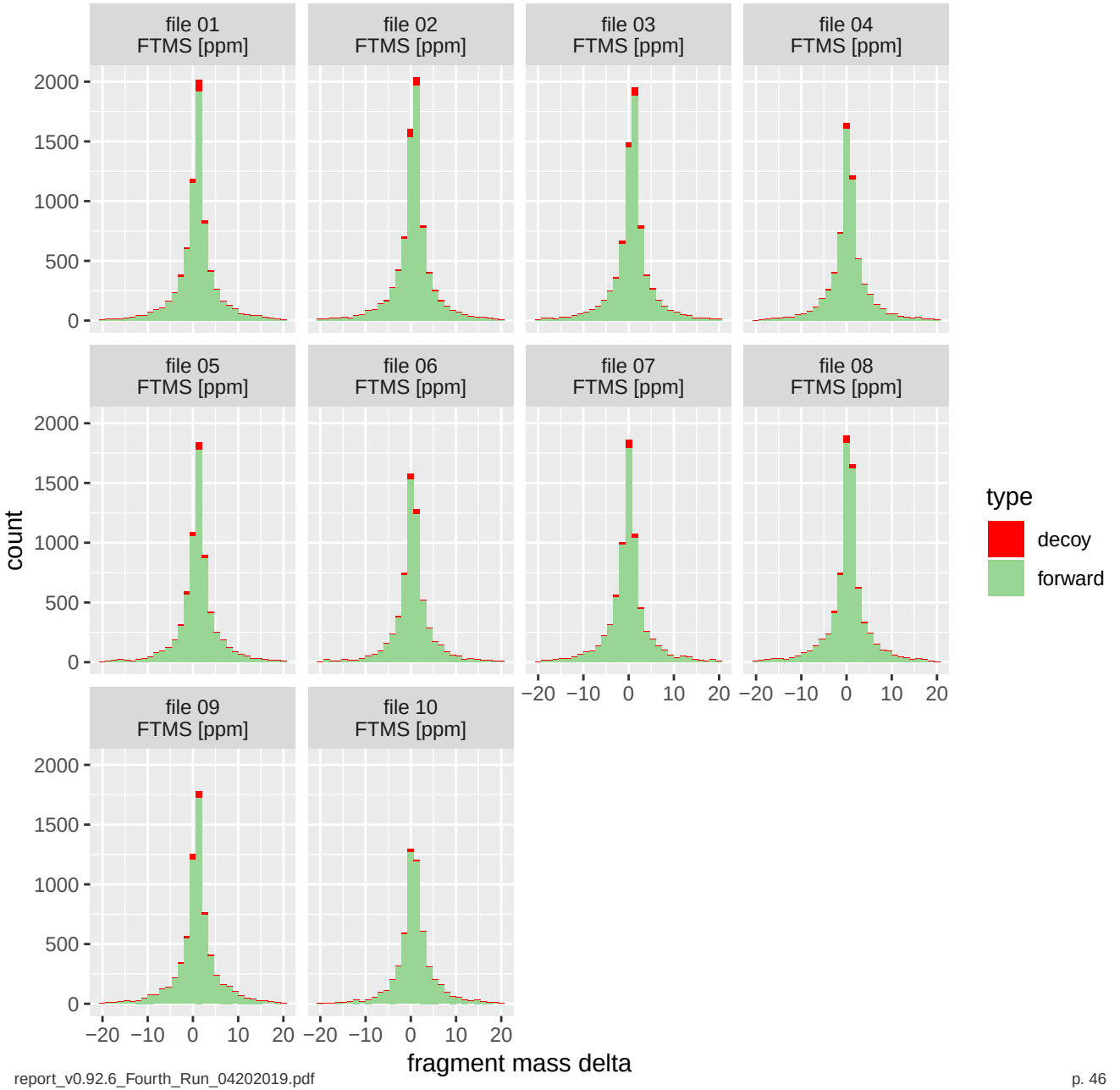

EVD: Oversampling (MS/MS counts per 3D−peak)
file 01
file 02
file 03
file 04
file 05
file 06
file 07
file 08
file 09
file 10
file 11
file 12
file 13
file 14
file 15
file 16
file 17
file 18
file 19
file 20
file 21
file 22
file 23
file 24
file 25
file 26
file 27
file 28
file 29
file 30
0
25
50
75
100
MS/MS counts per 3D−peak [%]
MS/MS counts
1
2
3+

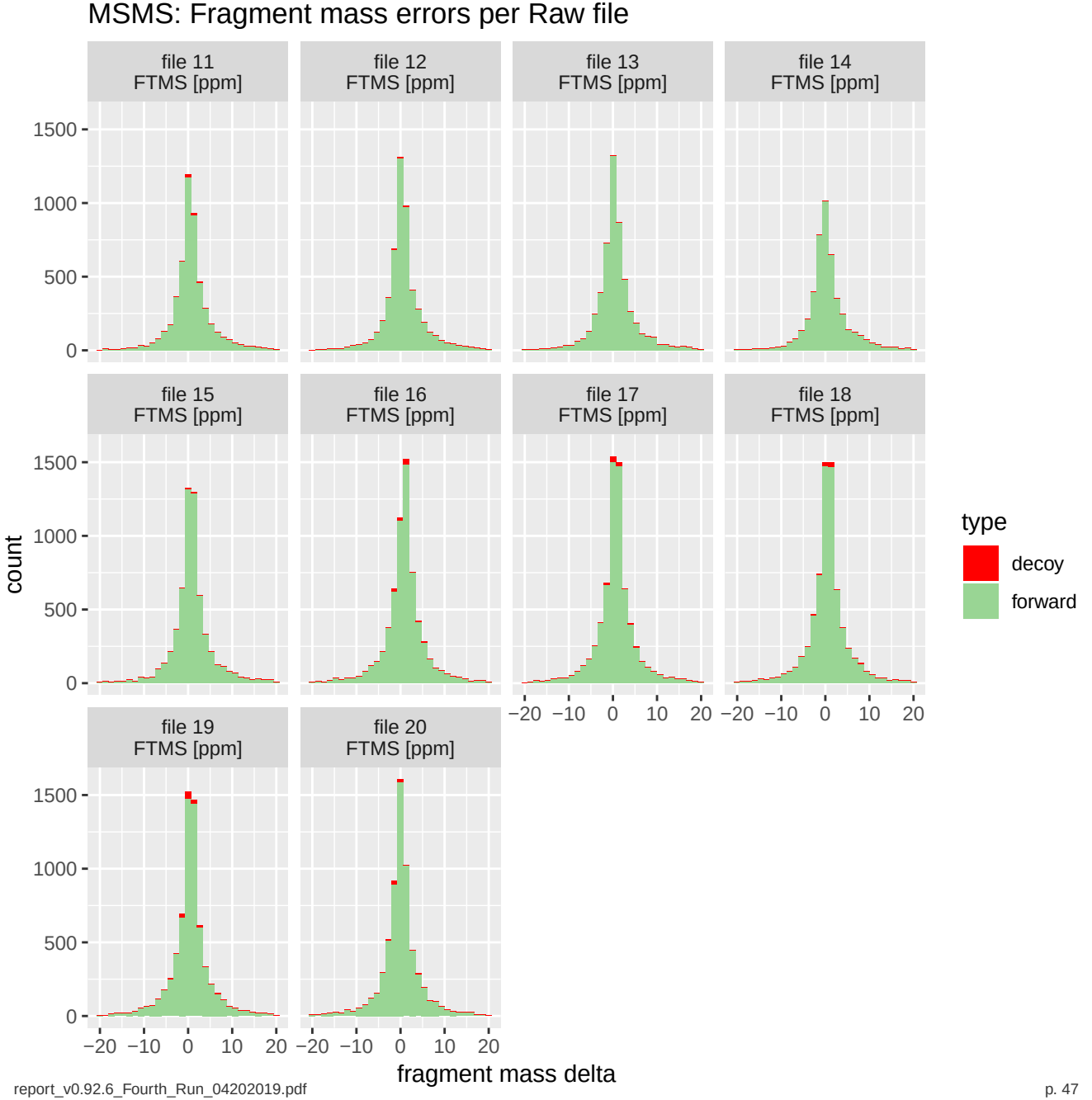

EVD: Uncalibrated mass error
file 01 (sd = 0.9ppm)
file 02 (sd = 0.9ppm)
file 03 (sd = 0.9ppm)
file 04 (sd = 0.8ppm)
file 05 (sd = 0.9ppm)
file 06 (sd = 0.8ppm)
file 07 (sd = 0.9ppm)
file 08 (sd = 0.9ppm)
file 09 (sd = 0.9ppm)
file 10 (sd = 0.7ppm)
file 11 (sd = 0.7ppm)
file 12 (sd = 0.7ppm)
file 13 (sd = 0.7ppm)
file 14 (sd = 0.7ppm)
file 15 (sd = 0.9ppm)
−20
−10
0
10
20
Δ mass [ppm]


EVD: Uncalibrated mass error
file 16 (sd = 0.8ppm)
file 17 (sd = 0.8ppm)
file 18 (sd = 0.9ppm)
file 19 (sd = 0.9ppm)
file 20 (sd = 0.8ppm)
file 21 (sd = 0.9ppm)
file 22 (sd = 0.8ppm)
file 23 (sd = 0.8ppm)
file 24 (sd = 0.8ppm)
file 25 (sd = 0.7ppm)
file 26 (sd = 0.7ppm)
file 27 (sd = 0.8ppm)
file 28 (sd = 0.8ppm)
file 29 (sd = 0.9ppm)
file 30 (sd = 0.9ppm)
−20
−10
0
10
20
Δ mass [ppm]

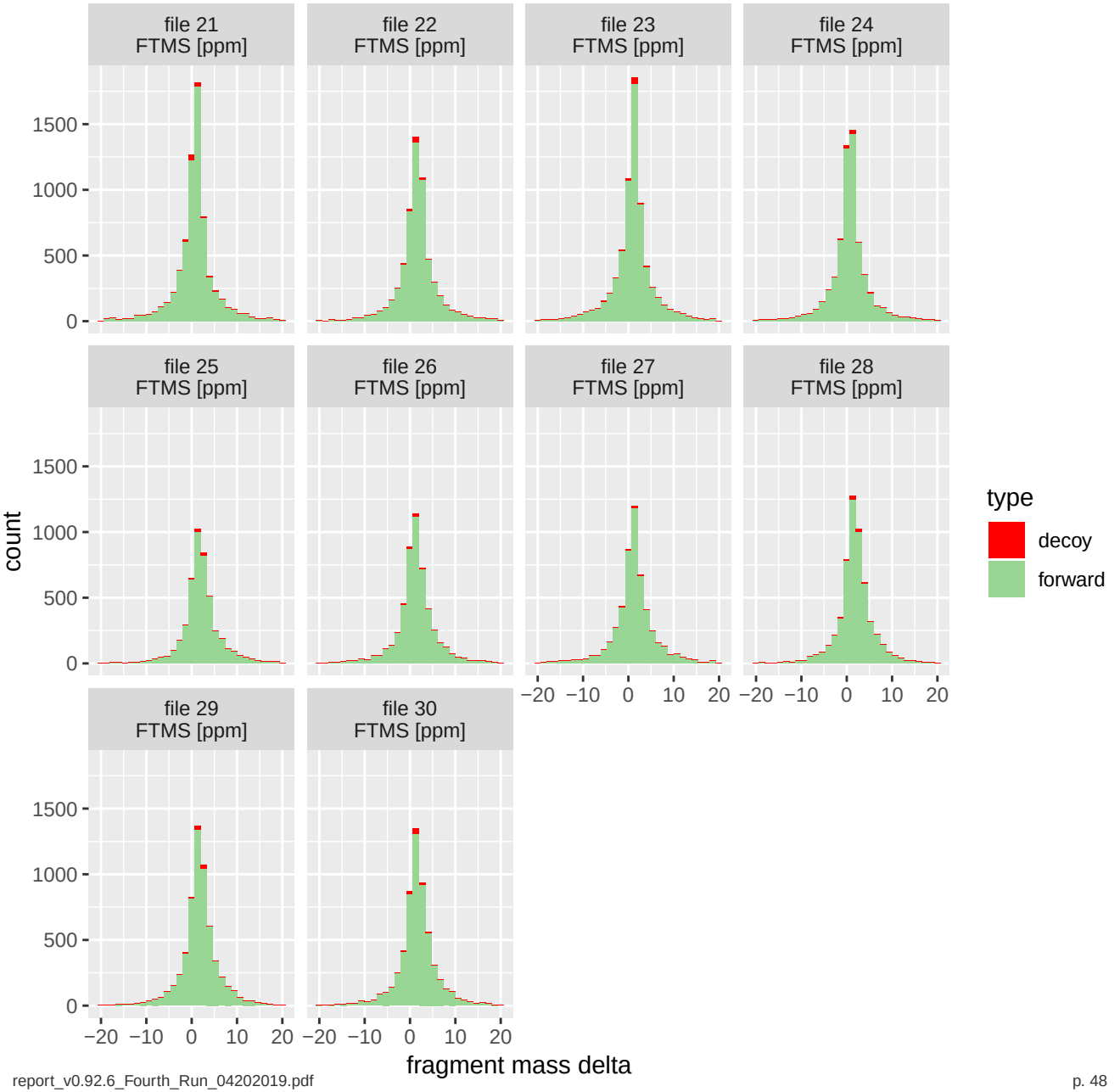

EVD: Calibrated mass error
file 01
file 02
file 03
file 04
file 05
file 06
file 07
file 08
file 09
file 10
file 11
file 12
file 13
file 14
file 15
−1
0
1
Δ mass [ppm]

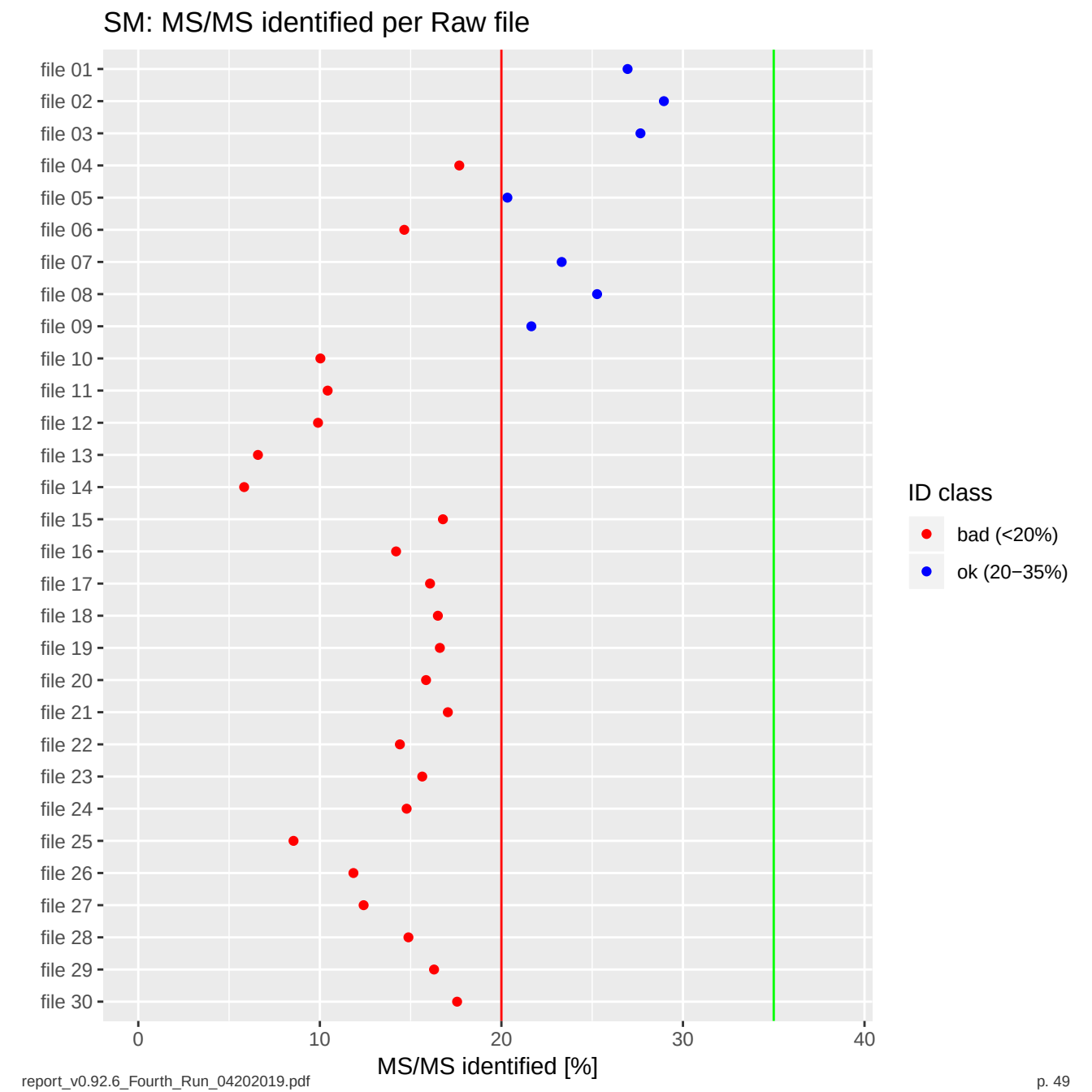

EVD: Calibrated mass error
file 16
file 17
file 18
file 19
file 20
file 21
file 22
file 23
file 24
file 25
file 26
file 27
file 28
file 29
file 30
−1
0
1
Δ mass [ppm]


MSMS: Fragment mass errors per Raw file
file 01
FTMS [ppm]
file 02
FTMS [ppm]
file 03
FTMS [ppm]
file 04
FTMS [ppm]
file 05
FTMS [ppm]
file 06
FTMS [ppm]
file 07
FTMS [ppm]
file 08
FTMS [ppm]
file 09
FTMS [ppm]
file 10
FTMS [ppm]
count
0
500
1000
1500
2000
−20
−10
0
10
20
fragment mass delta
type
decoy
forward


MSMS: Fragment mass errors per Raw file
file 11
FTMS [ppm]
file 12
FTMS [ppm]
file 13
FTMS [ppm]
file 14
FTMS [ppm]
file 15
FTMS [ppm]
file 16
FTMS [ppm]
file 17
FTMS [ppm]
file 18
FTMS [ppm]
file 19
FTMS [ppm]
file 20
FTMS [ppm]
count
0
500
1000
1500
−20
−10
0
10
20
fragment mass delta
type
decoy
forward

# MSMS: Fragment mass errors per Raw file

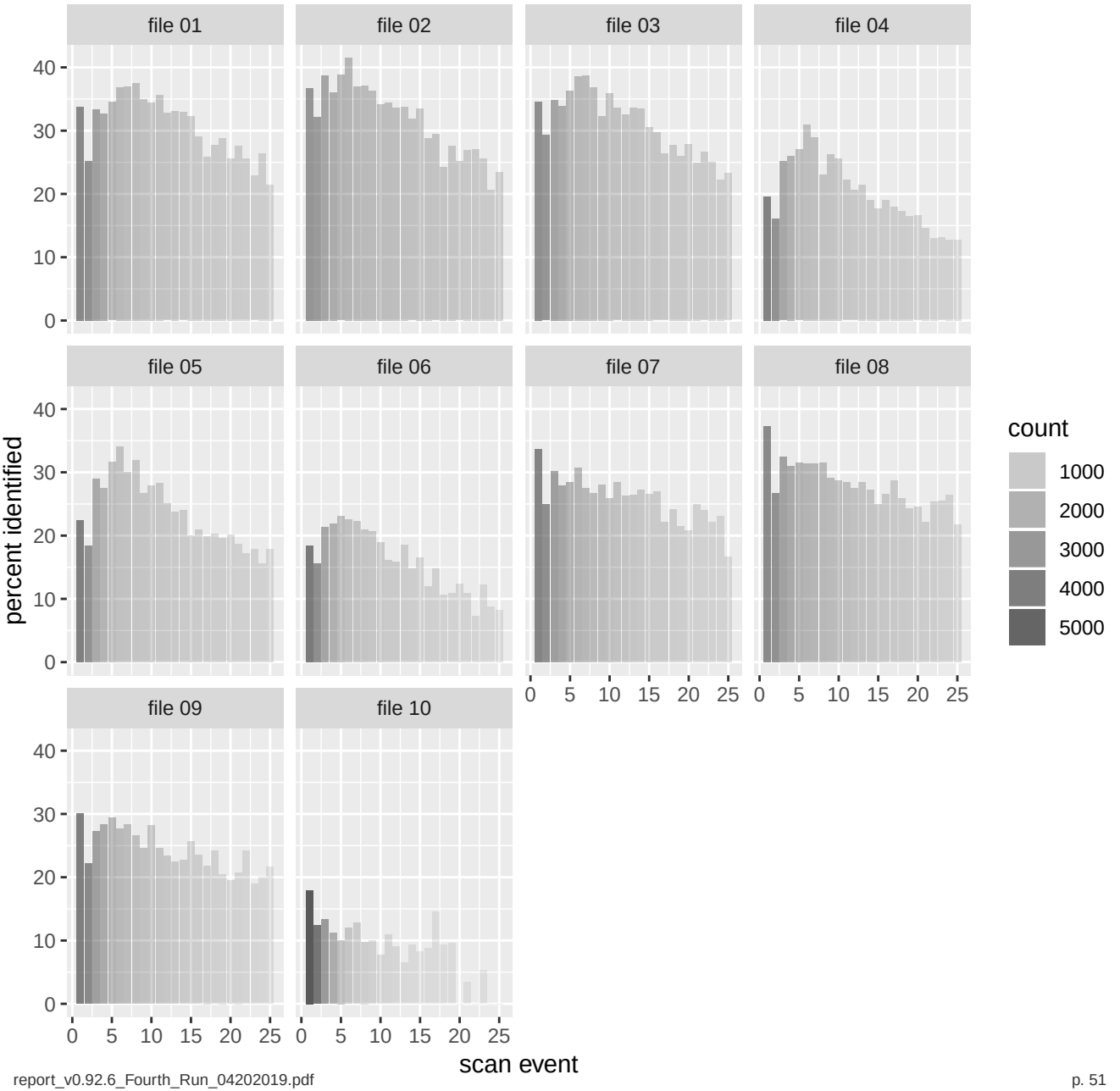


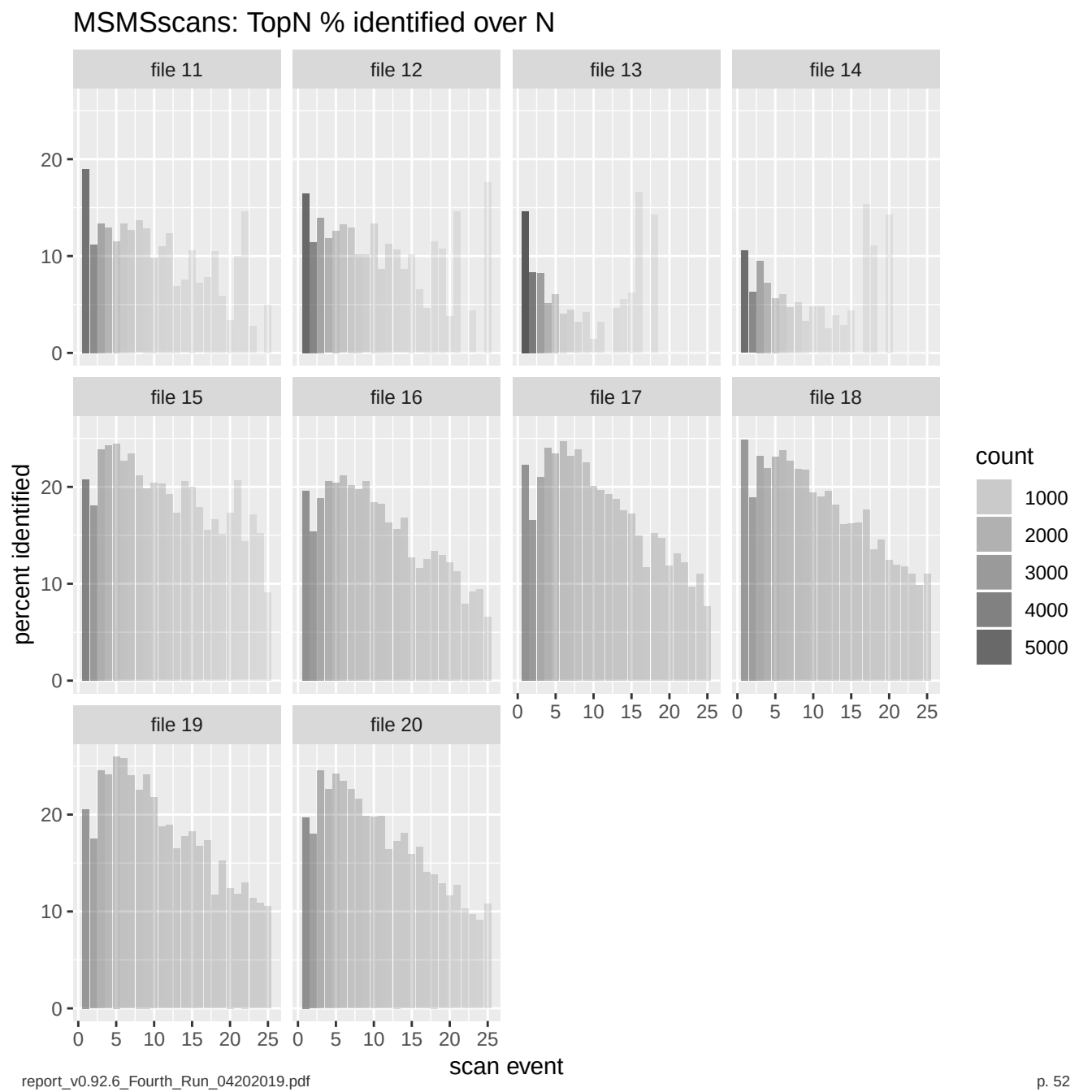

SM: MS/MS identified per Raw file
file 01
file 02
file 03
file 04
file 05
file 06
file 07
file 08
file 09
file 10
file 11
file 12
file 13
file 14
file 15
file 16
file 17
file 18
file 19
file 20
file 21
file 22
file 23
file 24
file 25
file 26
file 27
file 28
file 29
file 30
0
10
20
30
40
MS/MS identified [%]
ID class
bad (<20%)
ok (20−35%)

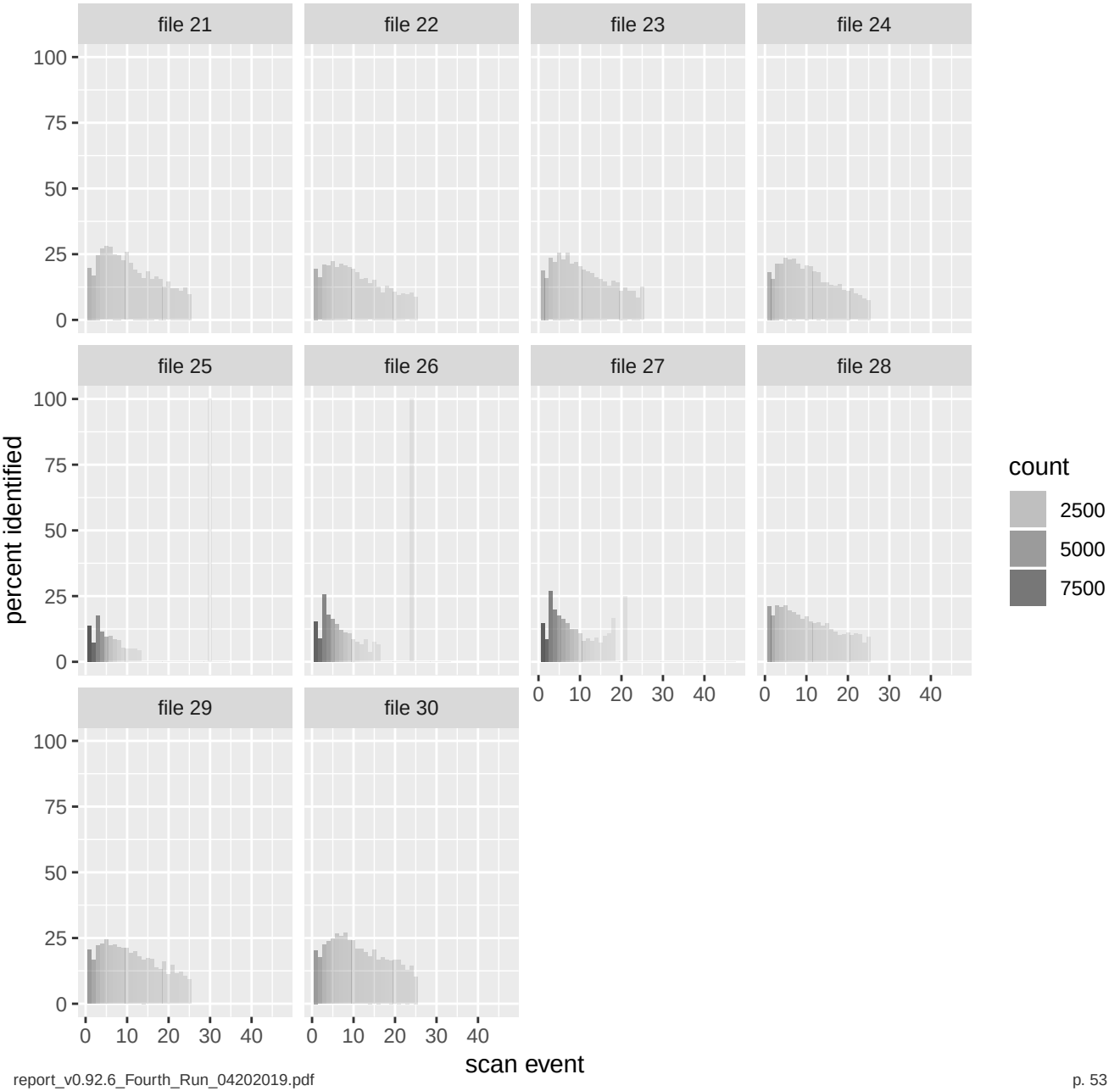
# SM: Files with 'red' ID rate

| Raw file | % identified |
|---|---|
| 20170427_144T_2a | 17.68 |
| 20170427_144T_2c | 14.65 |
| 20170427_159T_3a | 10.03 |
| 20170427_159T_3b | 10.43 |
| 20170427_159T_3c | 9.90 |
| 20170427_159T_4a | 6.59 |
| 20170427_159T_4b | 5.83 |
| 20170427_159T_4c | 16.78 |
| 20170427_163N_8a | 14.20 |
| 20170427_163N_8b | 16.07 |
| 20170427_163N_8c | 16.50 |
| 20170427_163T_6a | 16.61 |
| 20170427_163T_6b | 15.85 |
| 20170427_163T_6c | 17.05 |
| 20170427_163T_7a | 14.41 |
| 20170427_163T_7b | 15.64 |
| 20170427_163T_7c | 14.78 |
| 144T_mIgG1 | 8.55 |
| 144T_mIgG2 | 11.85 |
| 144T_mIgG3 | 12.41 |
| 144T_Orf1_1 | 14.88 |
| 144T_Orf1_2 | 16.29 |
| 144T_Orf1_3 | 17.56 |

77% of samples)

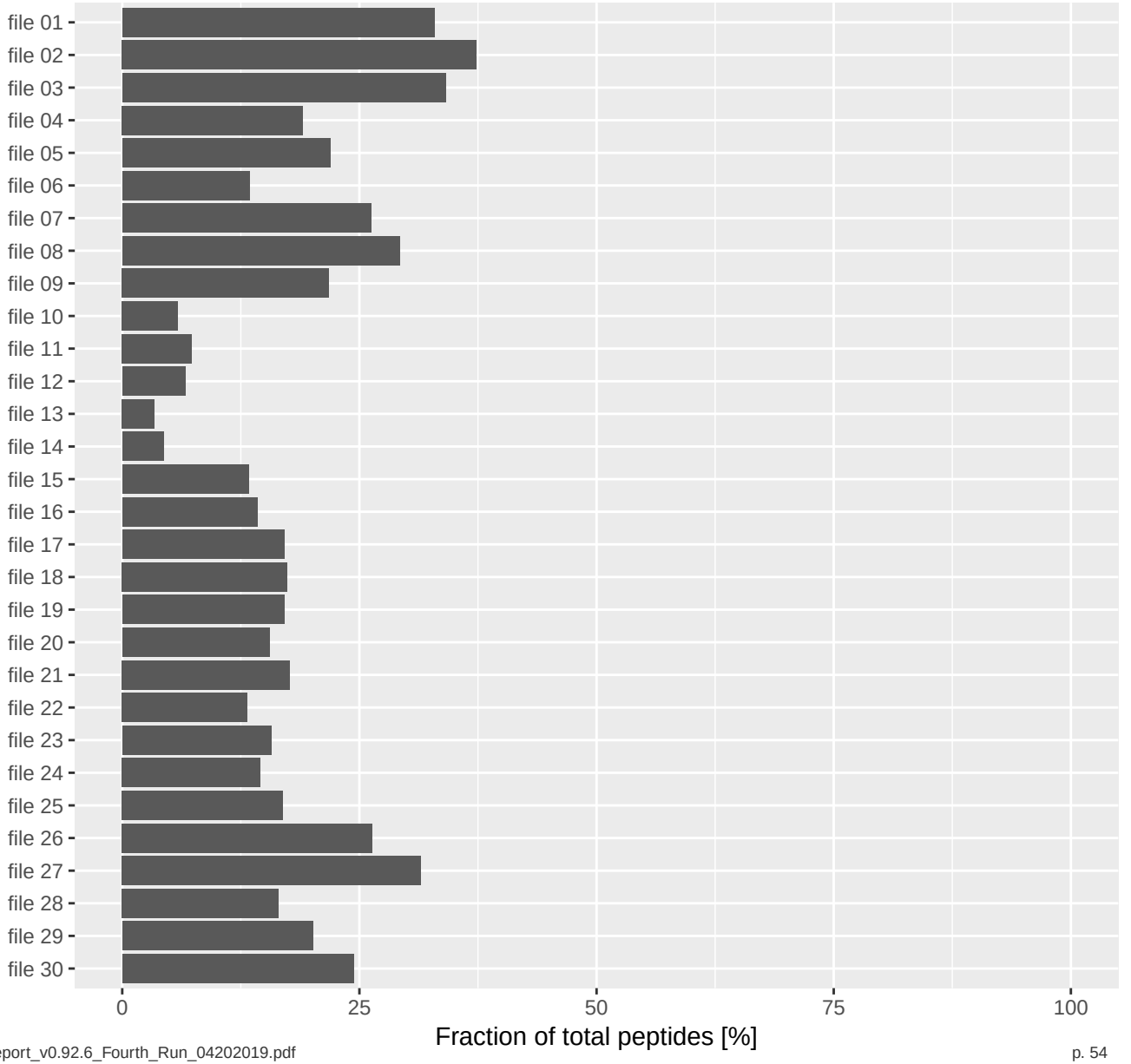

MSMSscans: TopN % identified over N
file 01
file 02
file 03
file 04
file 05
file 06
file 07
file 08
file 09
file 10
percent identified
scan event
count
1000
2000
3000
4000
5000

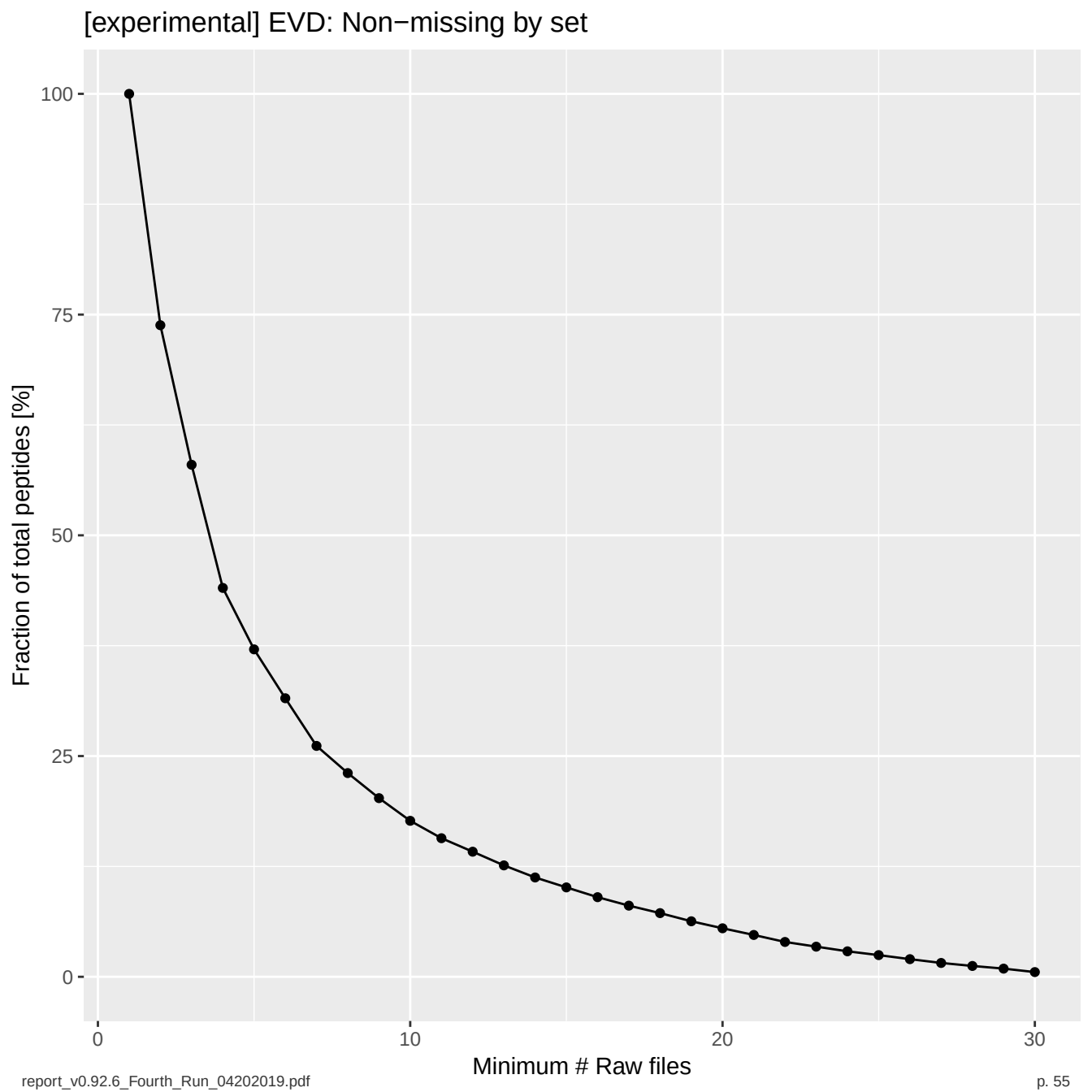

MSMSscans: TopN % identified over N
file 11
file 12
file 13
file 14
file 15
file 16
file 17
file 18
file 19
file 20
percent identified
scan event
count
1000
2000
3000
4000
5000


MSMSscans: TopN % identified over N
file 21
file 22
file 23
file 24
file 25
file 26
file 27
file 28
file 29
file 30
percent identified
scan event
count
2500
5000
7500

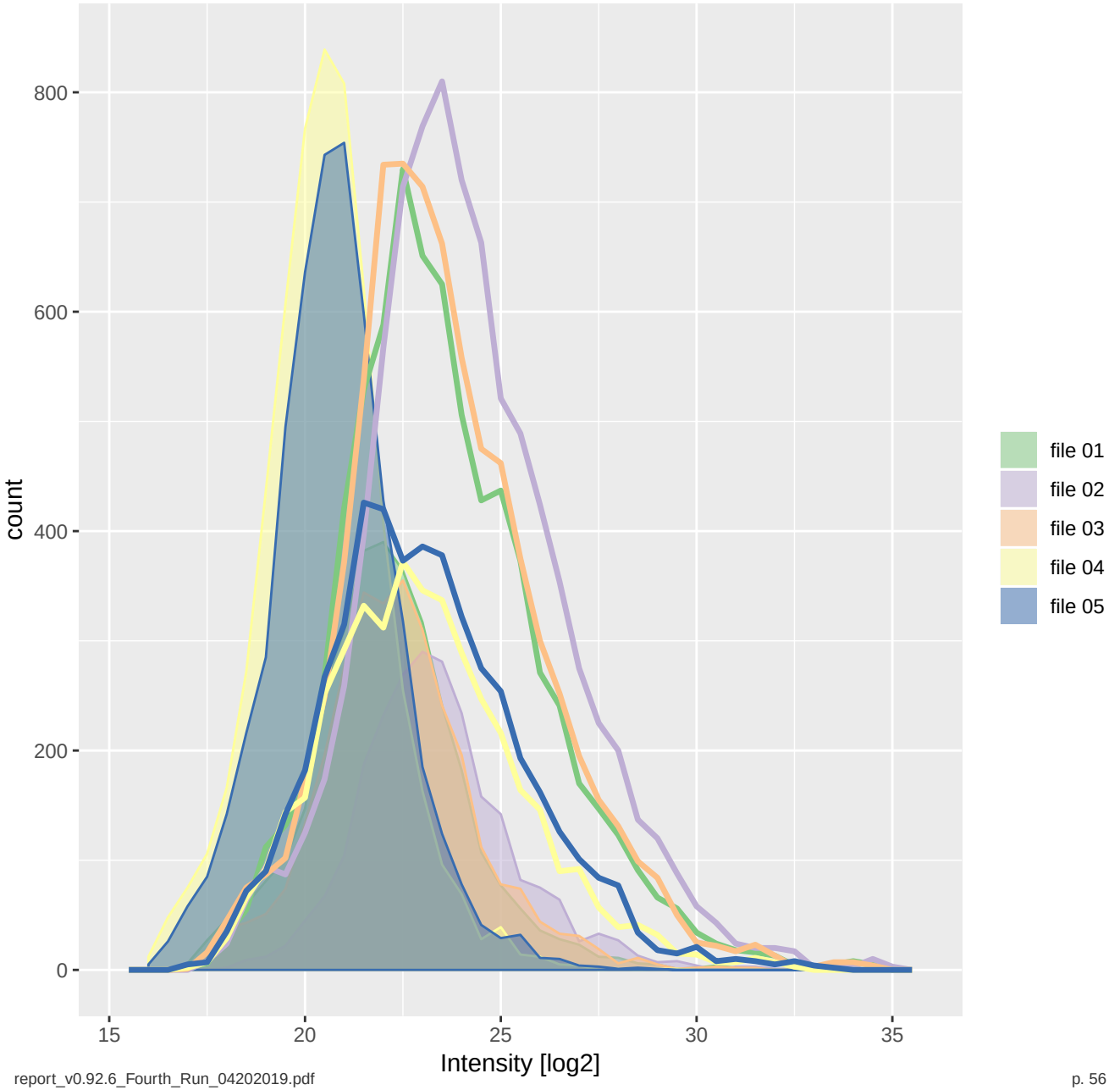
# [experimental] EVD: Non−Missing Peptides

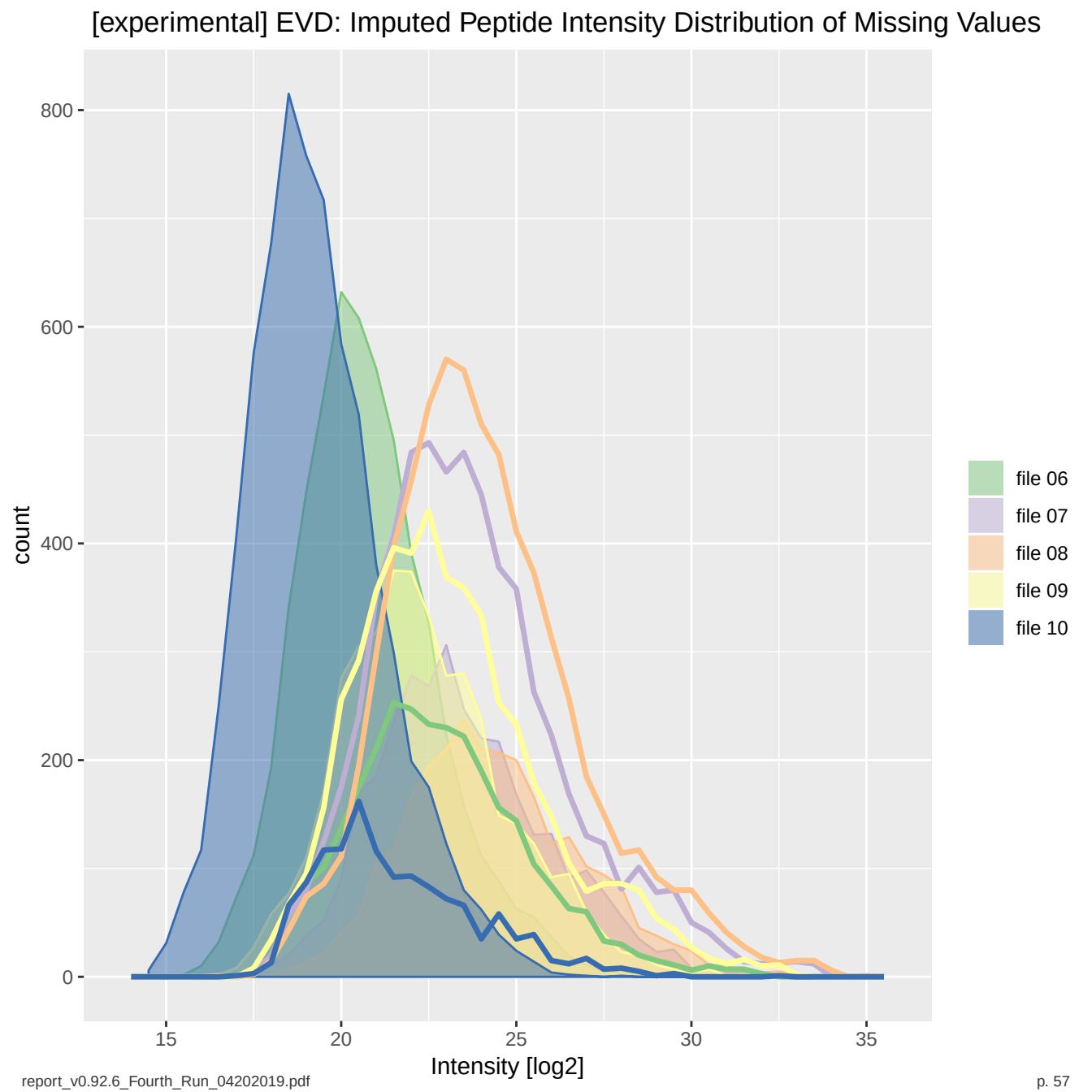
compared to all peptides seen in experiment

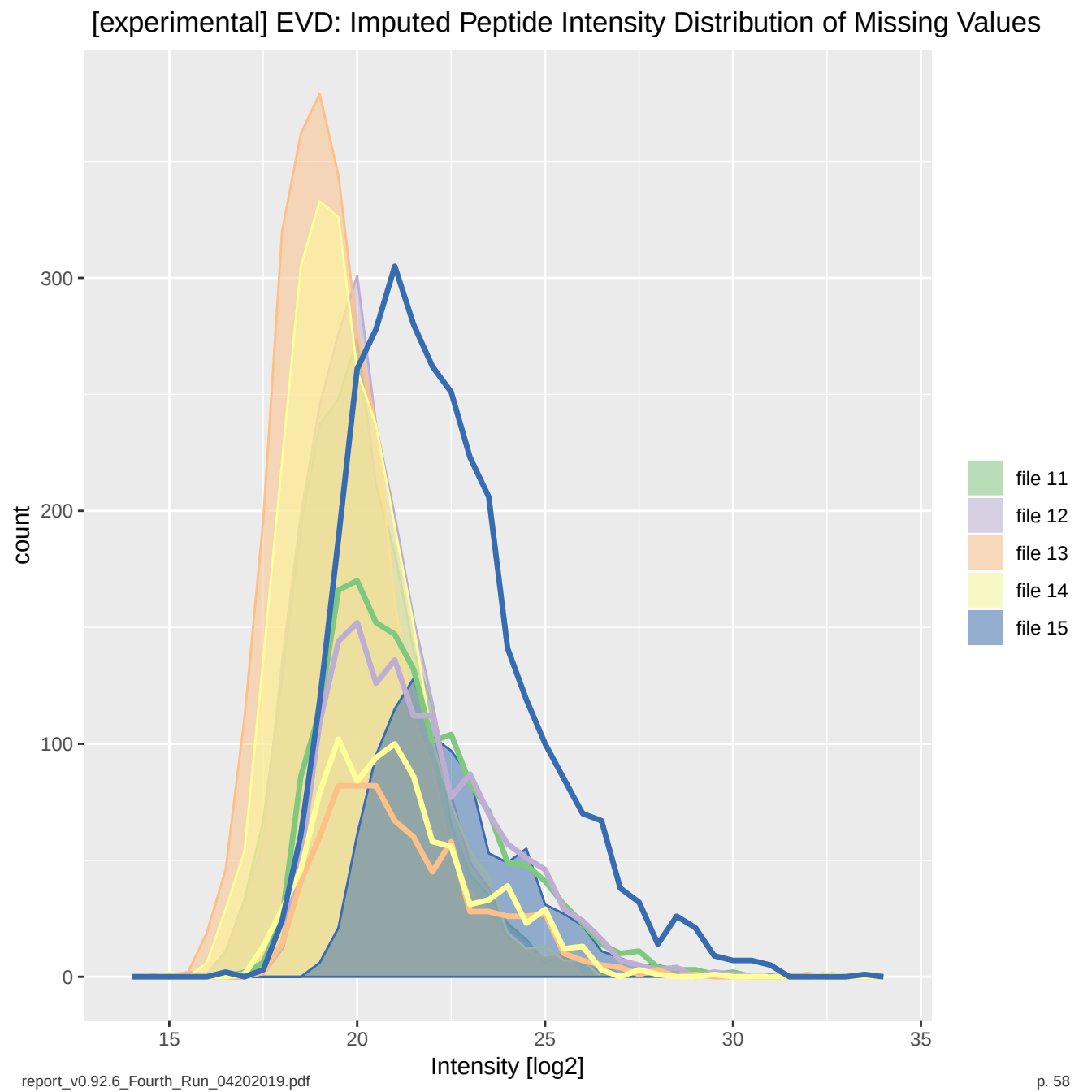


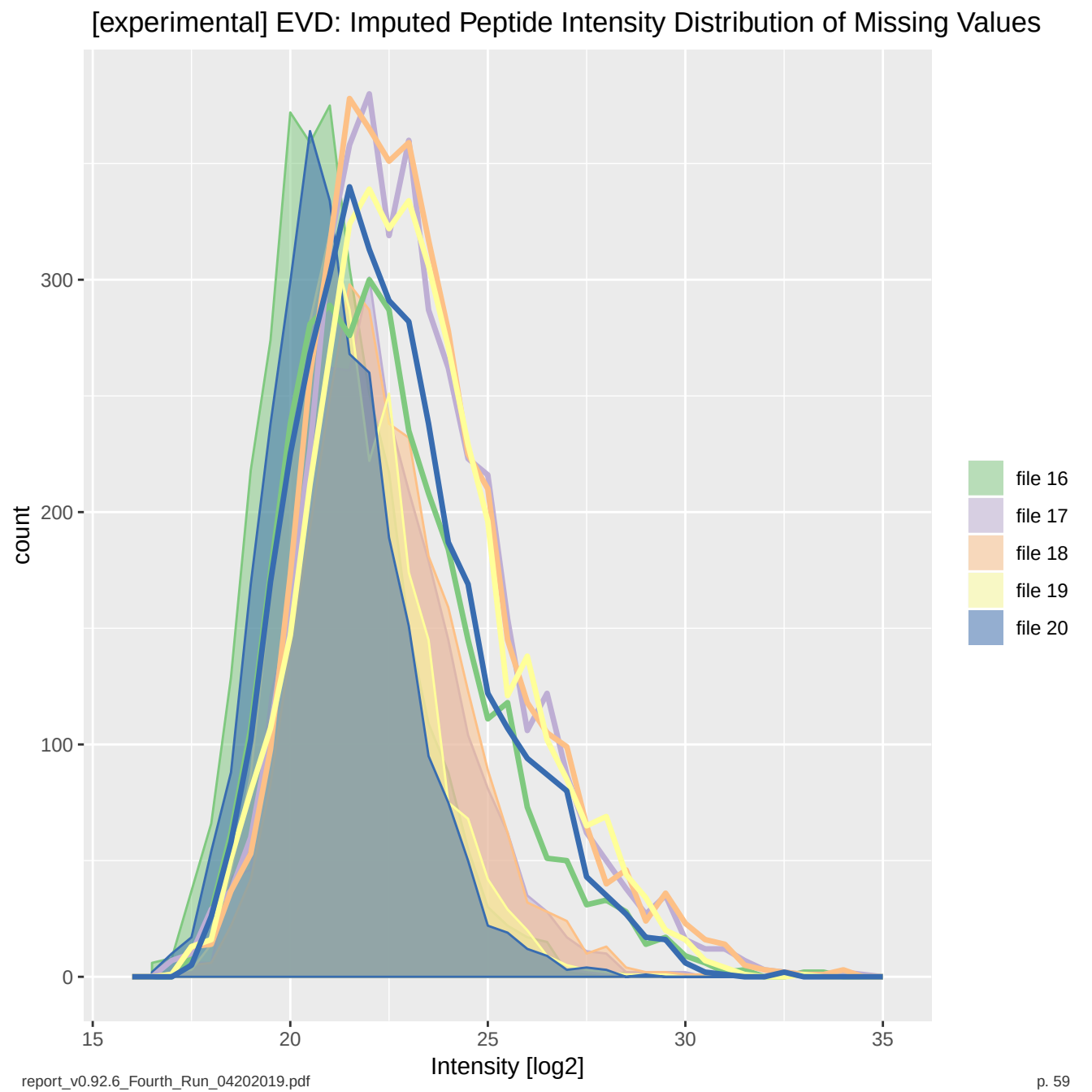

[experimental] EVD: Non−missing by set
Fraction of total peptides [%]
100
75
50
25
0
0
10
20
30
Minimum # Raw files

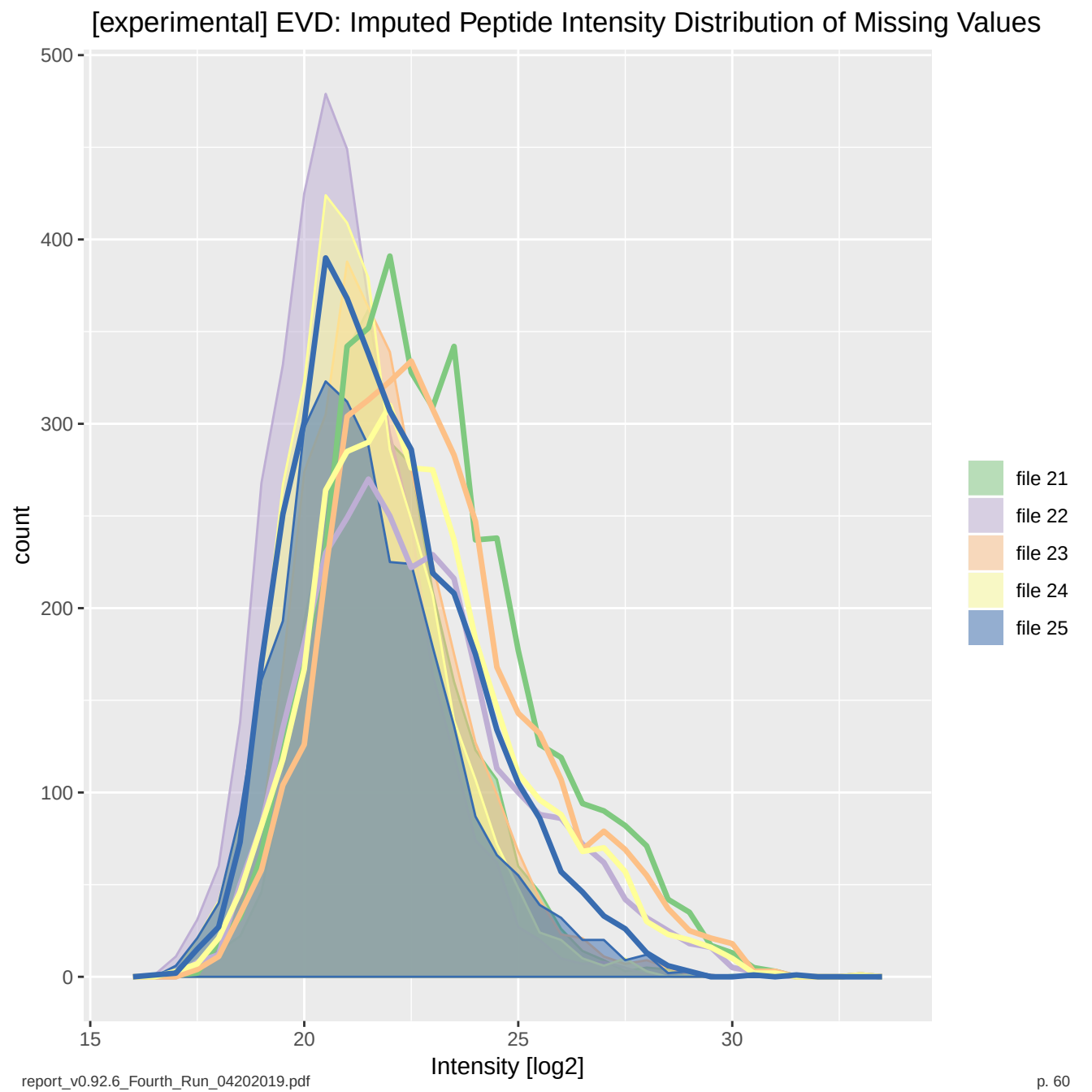
# [experimental] EVD: Imputed Peptide Intensity Distribution of Missing Values

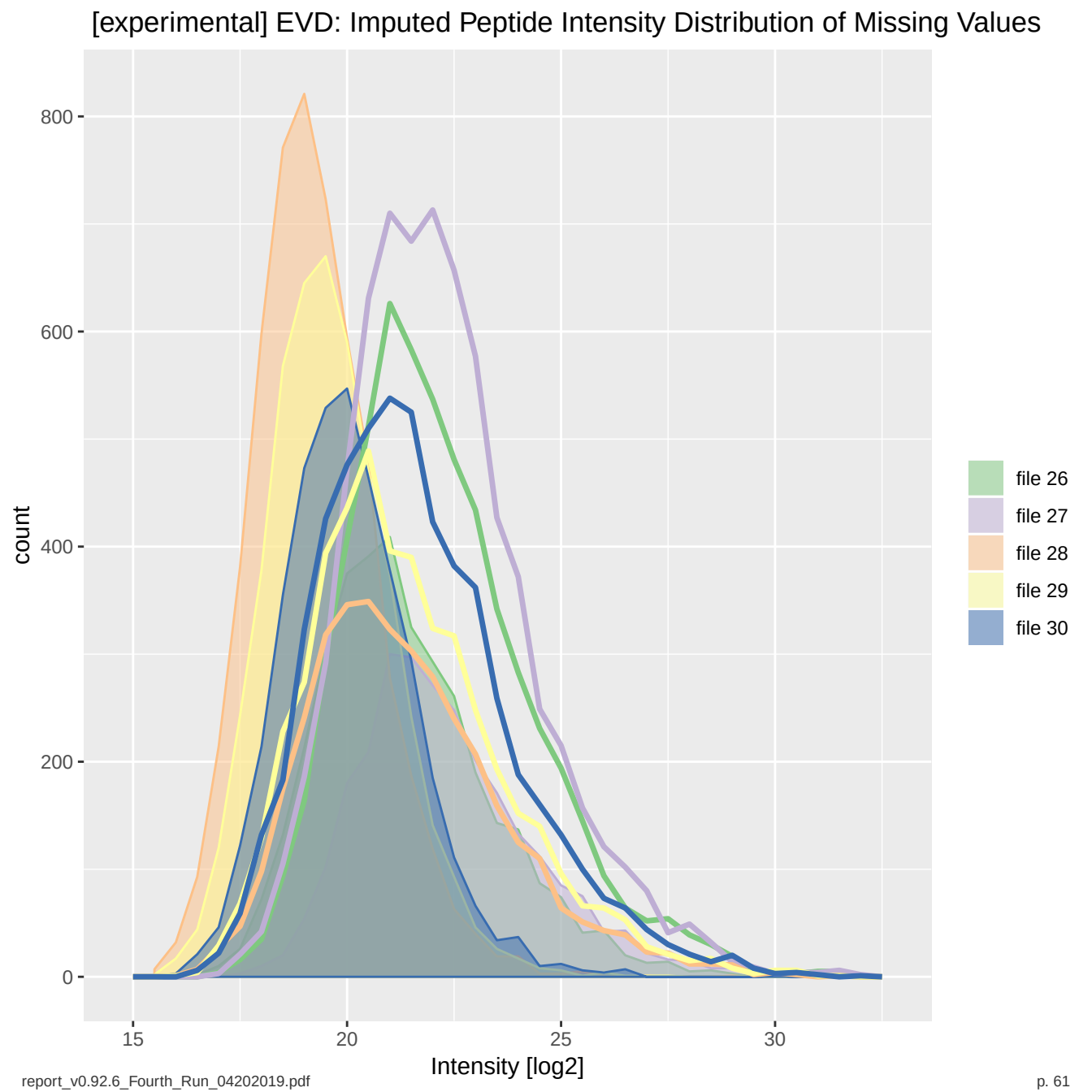


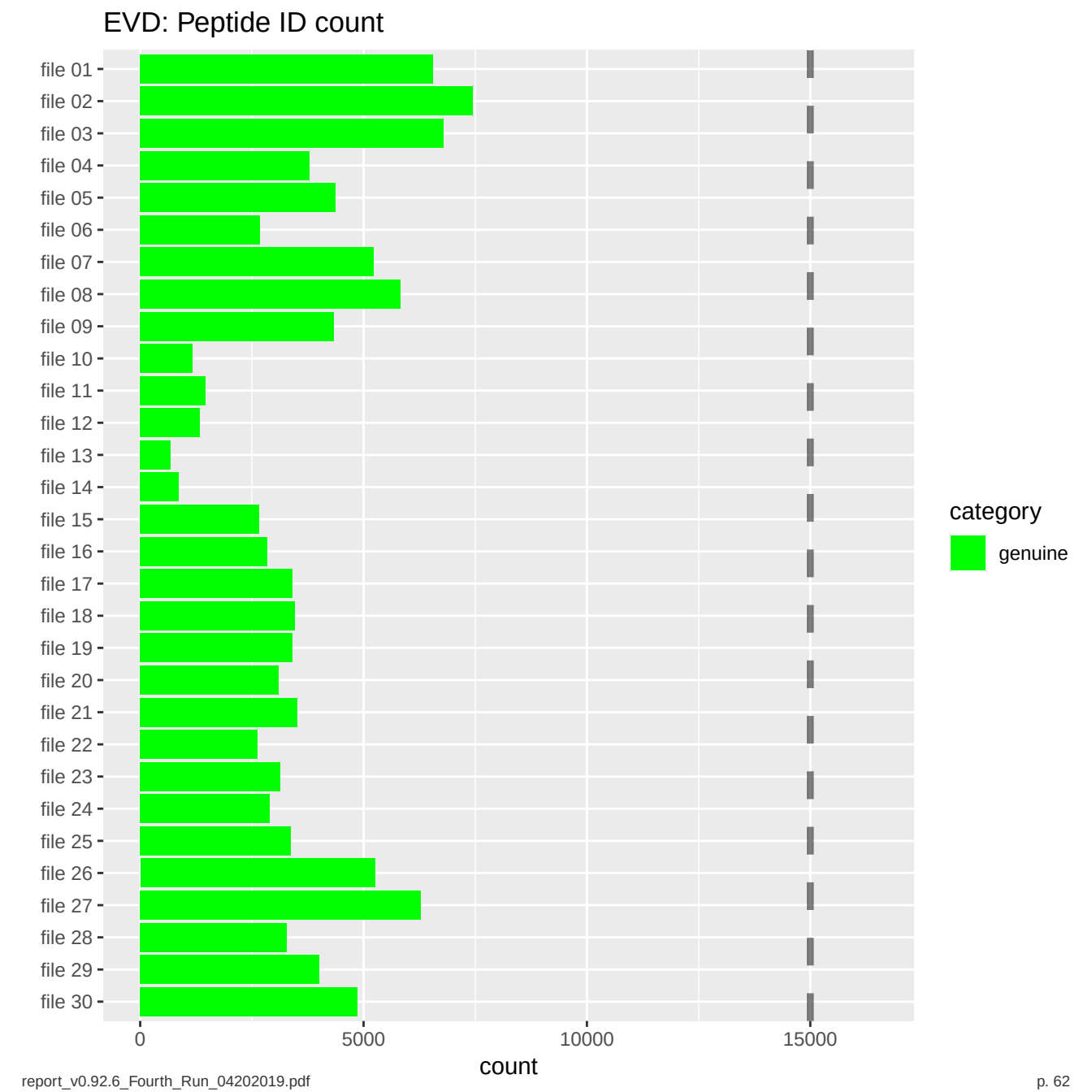

[experimental] EVD: Imputed Peptide Intensity Distribution of Missing Values
count
800
600
400
200
0
15
20
25
30
35
Intensity [log2]
file 06
file 07
file 08
file 09
file 10

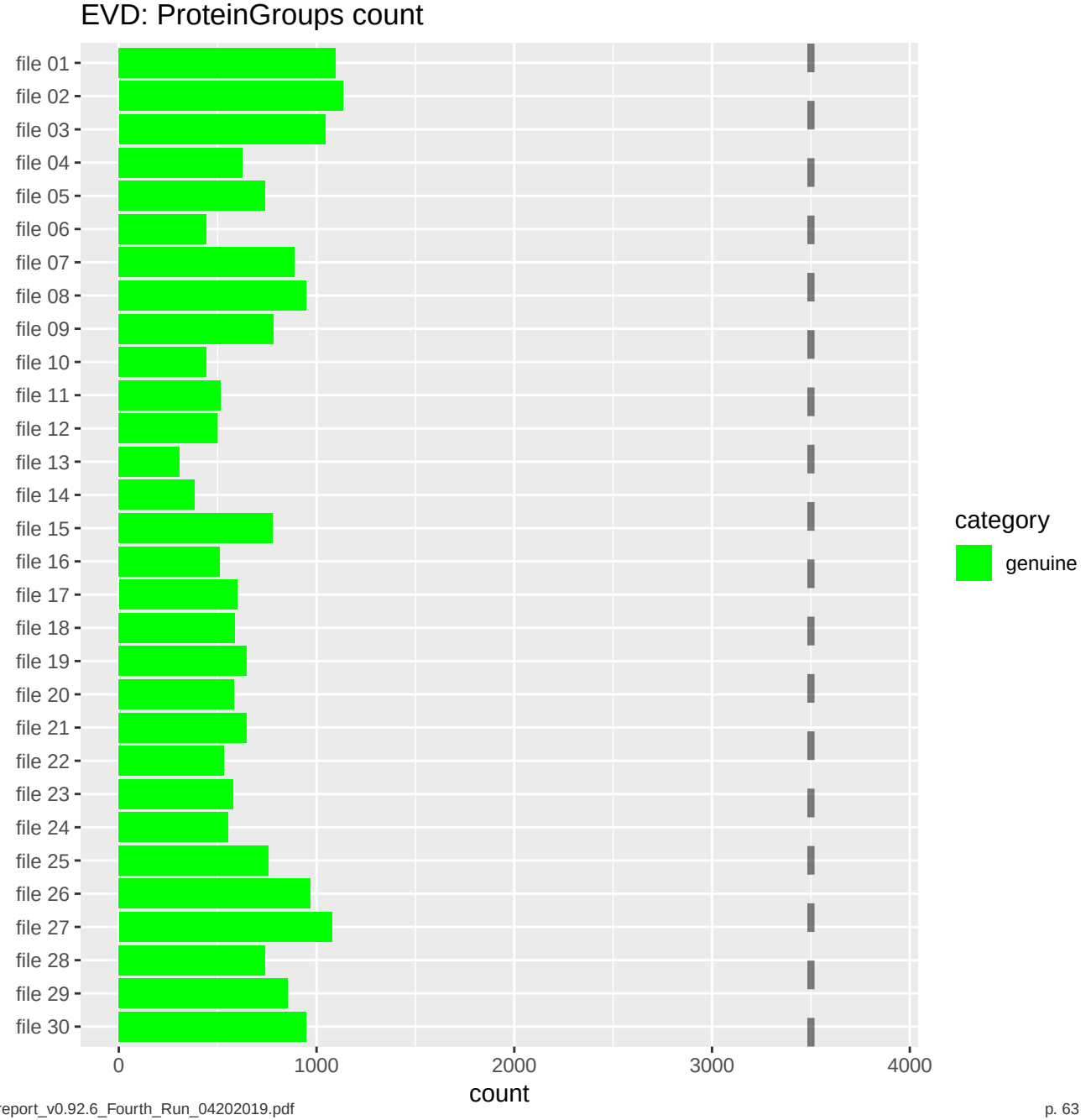

[experimental] EVD: Imputed Peptide Intensity Distribution of Missing Values
count
300
200
100
0
15
20
25
30
35
Intensity [log2]
file 11
file 12
file 13
file 14
file 15


[experimental] EVD: Imputed Peptide Intensity Distribution of Missing Values
count
300
200
100
0
15
20
25
30
35
Intensity [log2]
file 16
file 17
file 18
file 19
file 20


[experimental] EVD: Imputed Peptide Intensity Distribution of Missing Values
count
500
400
300
200
100
0
15
20
25
30
Intensity [log2]
file 21
file 22
file 23
file 24
file 25


[experimental] EVD: Imputed Peptide Intensity Distribution of Missing Values
count
800
600
400
200
0
15
20
25
30
Intensity [log2]
file 26
file 27
file 28
file 29
file 30


EVD: Peptide ID count
file 01
file 02
file 03
file 04
file 05
file 06
file 07
file 08
file 09
file 10
file 11
file 12
file 13
file 14
file 15
file 16
file 17
file 18
file 19
file 20
file 21
file 22
file 23
file 24
file 25
file 26
file 27
file 28
file 29
file 30
0
5000
10000
15000
count
category
genuine


EVD: ProteinGroups count
file 01
file 02
file 03
file 04
file 05
file 06
file 07
file 08
file 09
file 10
file 11
file 12
file 13
file 14
file 15
file 16
file 17
file 18
file 19
file 20
file 21
file 22
file 23
file 24
file 25
file 26
file 27
file 28
file 29
file 30
0
1000
2000
3000
4000
count
category
genuine