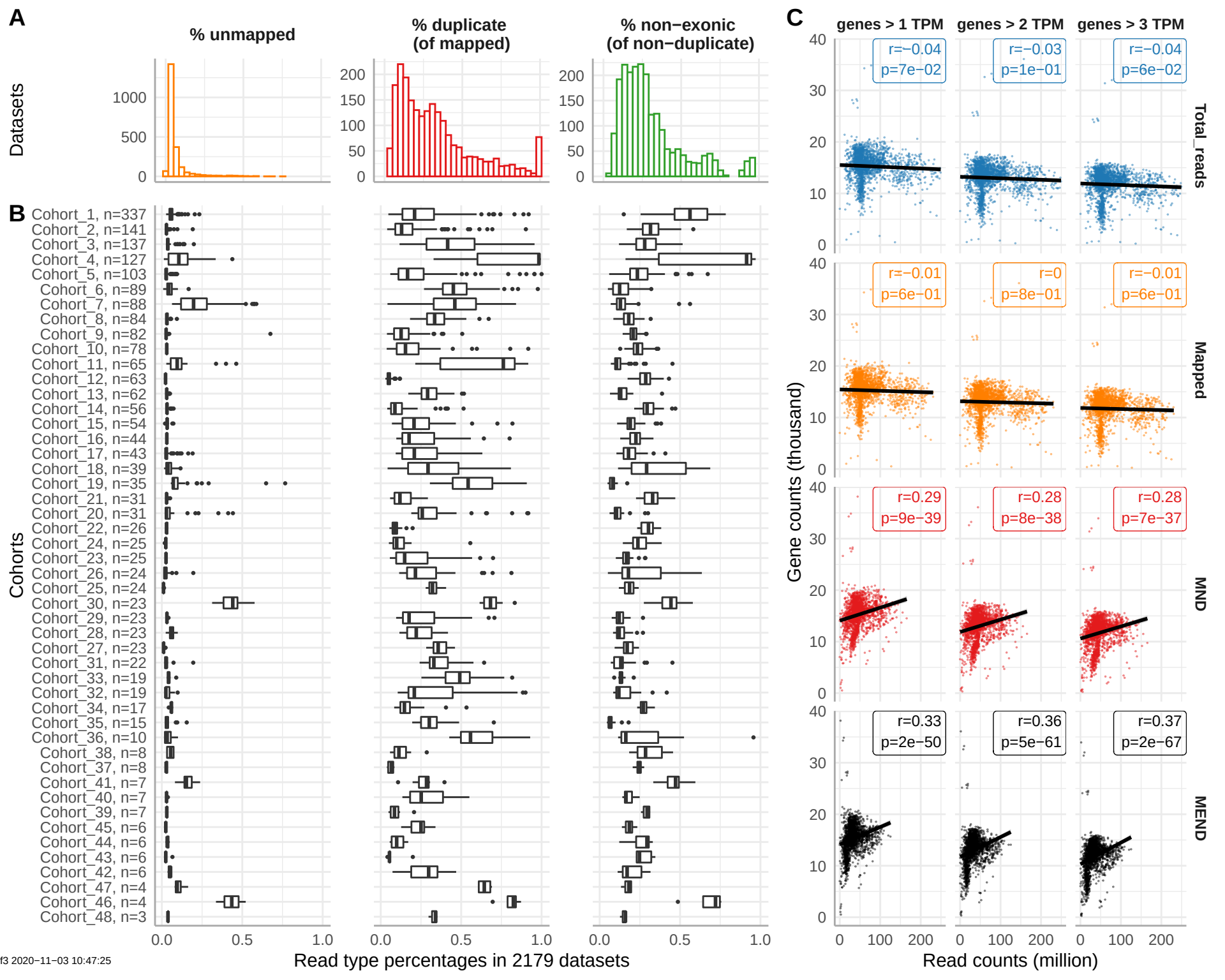
A
% unmapped
% duplicate
(of mapped)
% non−exonic
(of non−duplicate)
Datasets
1000
500
0
200
150
100
50
0
B
Cohorts
Cohort_1, n=337
Cohort_2, n=141
Cohort_3, n=137
Cohort_4, n=127
Cohort_5, n=103
Cohort_6, n=89
Cohort_7, n=88
Cohort_8, n=84
Cohort_9, n=82
Cohort_10, n=78
Cohort_11, n=65
Cohort_12, n=63
Cohort_13, n=62
Cohort_14, n=56
Cohort_15, n=54
Cohort_16, n=44
Cohort_17, n=43
Cohort_18, n=39
Cohort_19, n=35
Cohort_21, n=31
Cohort_20, n=31
Cohort_22, n=26
Cohort_24, n=25
Cohort_23, n=25
Cohort_26, n=24
Cohort_25, n=24
Cohort_30, n=23
Cohort_29, n=23
Cohort_28, n=23
Cohort_27, n=23
Cohort_31, n=22
Cohort_33, n=19
Cohort_32, n=19
Cohort_34, n=17
Cohort_35, n=15
Cohort_36, n=10
Cohort_38, n=8
Cohort_37, n=8
Cohort_41, n=7
Cohort_40, n=7
Cohort_39, n=7
Cohort_45, n=6
Cohort_44, n=6
Cohort_43, n=6
Cohort_42, n=6
Cohort_47, n=4
Cohort_46, n=4
Cohort_48, n=3
0.0
0.5
1.0
Read type percentages in 2179 datasets
C
genes > 1 TPM
genes > 2 TPM
genes > 3 TPM
r=−0.04
p=7e−02
r=−0.03
p=1e−01
r=−0.04
p=6e−02
Total_reads
r=−0.01
p=6e−01
r=0
p=8e−01
r=−0.01
p=6e−01
Mapped
r=0.29
p=9e−39
r=0.28
p=8e−38
r=0.28
p=7e−37
MND
r=0.33
p=2e−50
r=0.36
p=5e−61
r=0.37
p=2e−67
MEND
Gene counts (thousand)
40
30
20
10
0
0
100
200
Read counts (million)
f3 2020−11−03 10:47:25