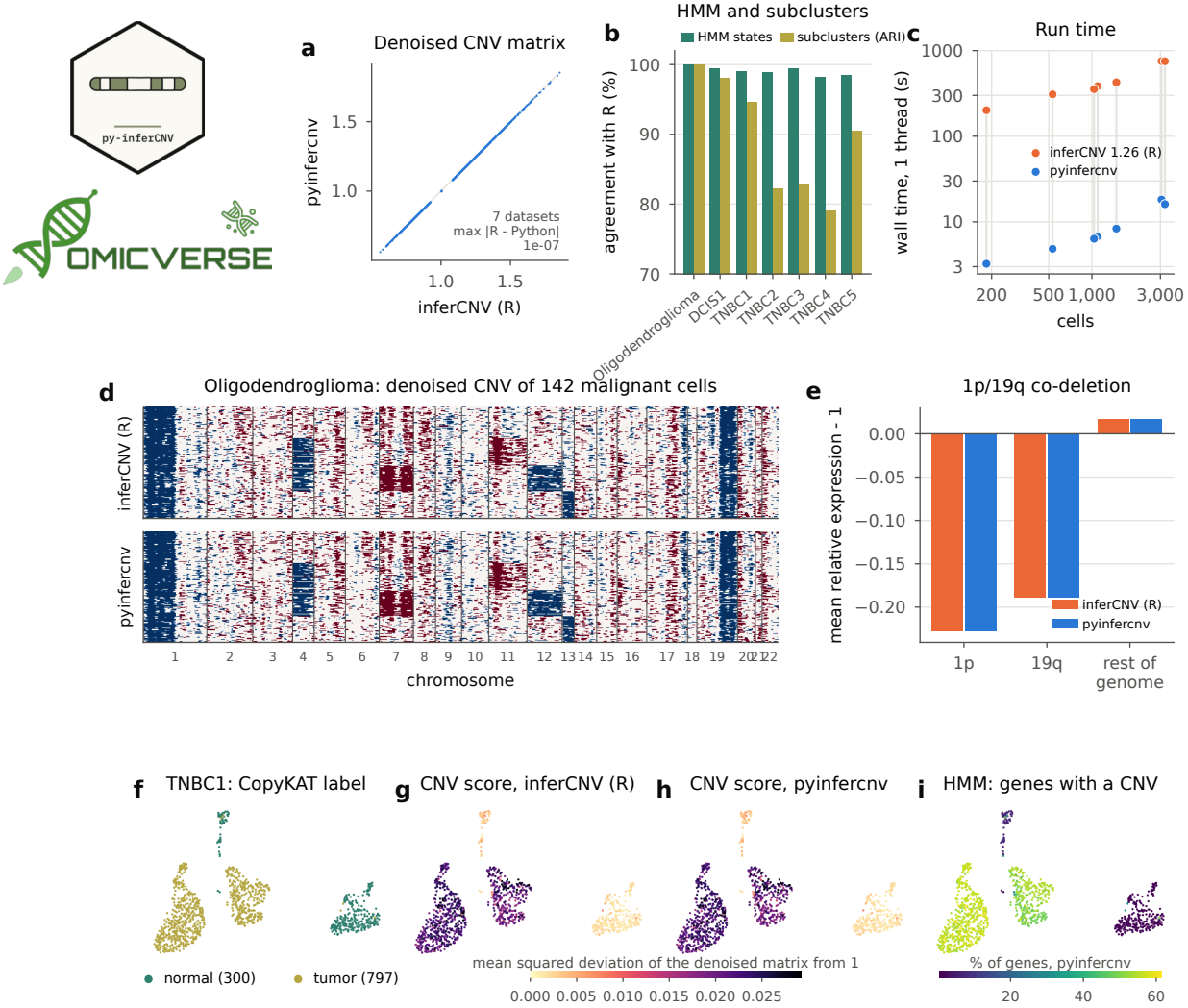

py-inferCNV
OMICVERSE
a
Denoised CNV matrix
pyinfercnv
inferCNV (R)
7 datasets
max |R - Python|
1e-07
b
HMM and subclusters
HMM states
subclusters (ARI)
agreement with R (%)
Oligodendroglioma
DCIS1
TNBC1
TNBC2
TNBC3
TNBC4
TNBC5
c
Run time
wall time, 1 thread (s)
inferCNV 1.26 (R)
pyinfercnv
cells
d
Oligodendroglioma: denoised CNV of 142 malignant cells
inferCNV (R)
pyinfercnv
chromosome
e
1p/19q co-deletion
mean relative expression - 1
inferCNV (R)
pyinfercnv
1p
19q
rest of genome
f
TNBC1: CopyKAT label
normal (300)
tumor (797)
g
CNV score, inferCNV (R)
h
CNV score, pyinfercnv
mean squared deviation of the denoised matrix from 1
i
HMM: genes with a CNV
% of genes, pyinfercnv