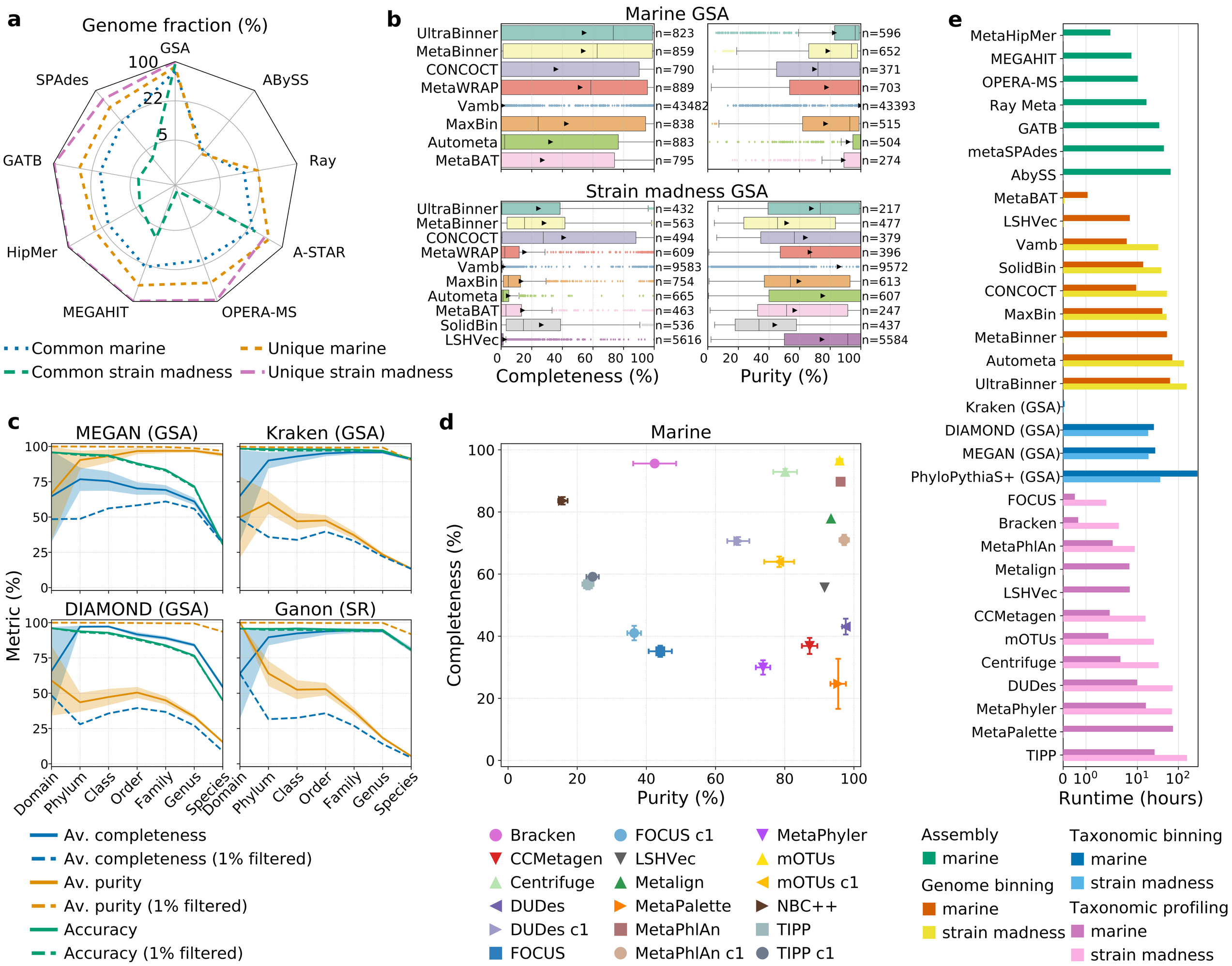
a
Genome fraction (%)
GSA
ABySS
Ray
A-STAR
OPERA-MS
MEGAHIT
HipMer
GATB
SPAdes
100
22
5
Common marine
Unique marine
Common strain madness
Unique strain madness
b
Marine GSA
UltraBinner n=823 n=596
MetaBinner n=859 n=652
CONCOCT n=790 n=371
MetaWRAP n=889 n=703
Vamb n=43482 n=43393
MaxBin n=838 n=515
Autometa n=883 n=504
MetaBAT n=795 n=274
Strain madness GSA
UltraBinner n=432 n=217
MetaBinner n=563 n=477
CONCOCT n=494 n=379
MetaWRAP n=609 n=396
Vamb n=9583 n=9572
MaxBin n=754 n=613
Autometa n=665 n=607
MetaBAT n=463 n=247
SolidBin n=536 n=437
LSHVec n=5616 n=5584
0 20 40 60 80 100
Completeness (%)
Purity (%)
c
MEGAN (GSA)
Kraken (GSA)
DIAMOND (GSA)
Ganon (SR)
Metric (%)
Domain Phylum Class Order Family Genus Species
Av. completeness
Av. completeness (1% filtered)
Av. purity
Av. purity (1% filtered)
Accuracy
Accuracy (1% filtered)
d
Marine
Completeness (%)
Purity (%)
Bracken
CCMetagen
Centrifuge
DUDes
DUDes c1
FOCUS
FOCUS c1
LSHVec
Metalign
MetaPalette
MetaPhlAn
MetaPhlAn c1
MetaPhyler
mOTUs
mOTUs c1
NBC++
TIPP
TIPP c1
e
MetaHipMer
MEGAHIT
OPERA-MS
Ray Meta
GATB
metaSPAdes
AbySS
MetaBAT
LSHVec
Vamb
SolidBin
CONCOCT
MaxBin
MetaBinner
Autometa
UltraBinner
Kraken (GSA)
DIAMOND (GSA)
MEGAN (GSA)
PhyloPythiaS+ (GSA)
FOCUS
Bracken
MetaPhlAn
Metalign
LSHVec
CCMetagen
mOTUs
Centrifuge
DUDes
MetaPhyler
MetaPalette
TIPP
0 10^0 10^1 10^2
Runtime (hours)
Assembly
marine
Genome binning
marine
strain madness
Taxonomic binning
marine
strain madness
Taxonomic profiling
marine
strain madness