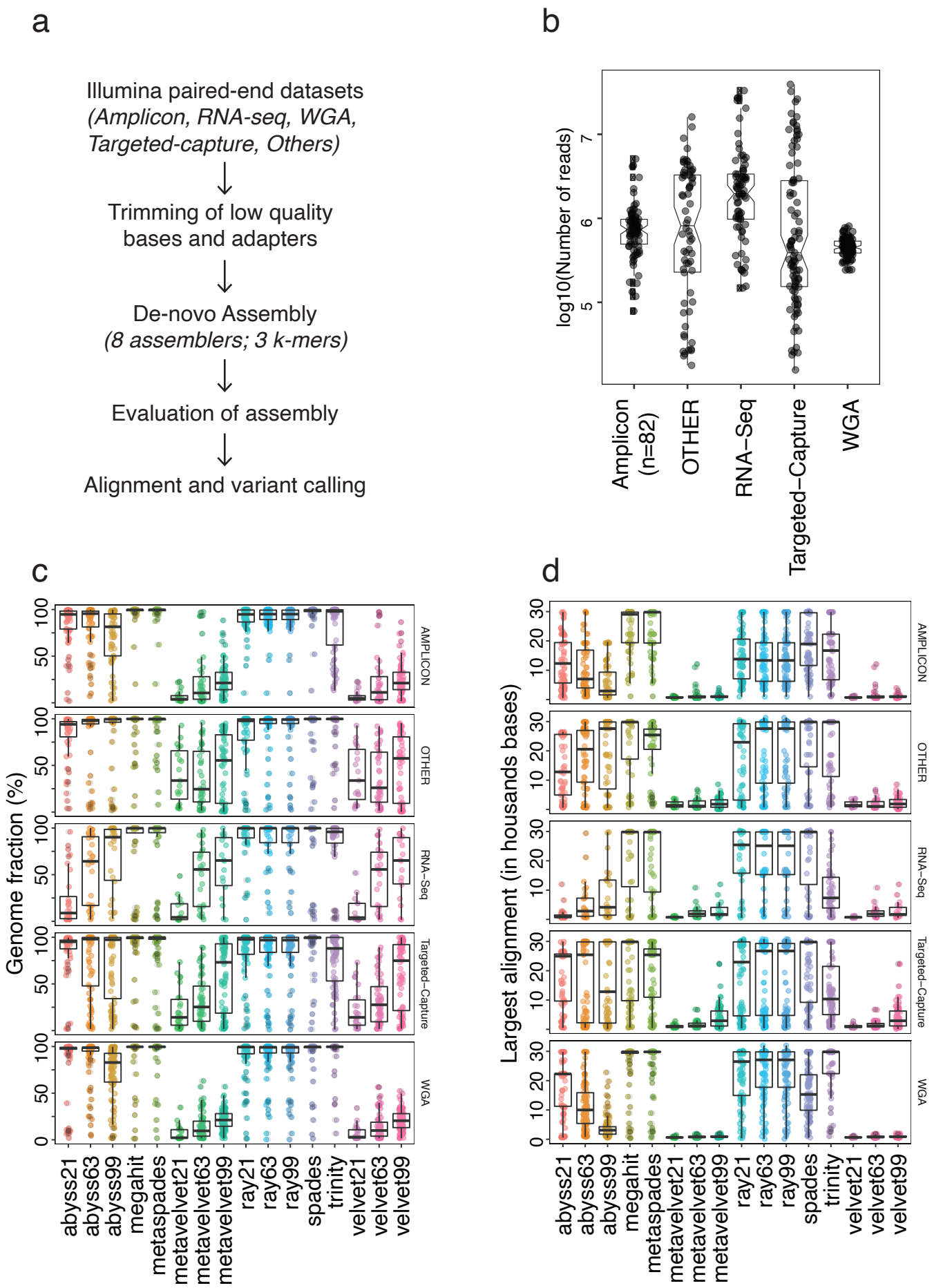
a
Illumina paired-end datasets
(Amplicon, RNA-seq, WGA,
Targeted-capture, Others)
Trimming of low quality
bases and adapters
De-novo Assembly
(8 assemblers; 3 k-mers)
Evaluation of assembly
Alignment and variant calling
b
log10(Number of reads)
Amplicon
(n=82)
OTHER
RNA−Seq
Targeted−Capture
WGA
c
Genome fraction (%)
AMPLICON
OTHER
RNA−Seq
Targeted−Capture
WGA
abyss21
abyss63
abyss99
megahit
metaspades
metavelvet21
metavelvet63
metavelvet99
ray21
ray63
ray99
spades
trinity
velvet21
velvet63
velvet99
d
Largest alignment (in housands bases)