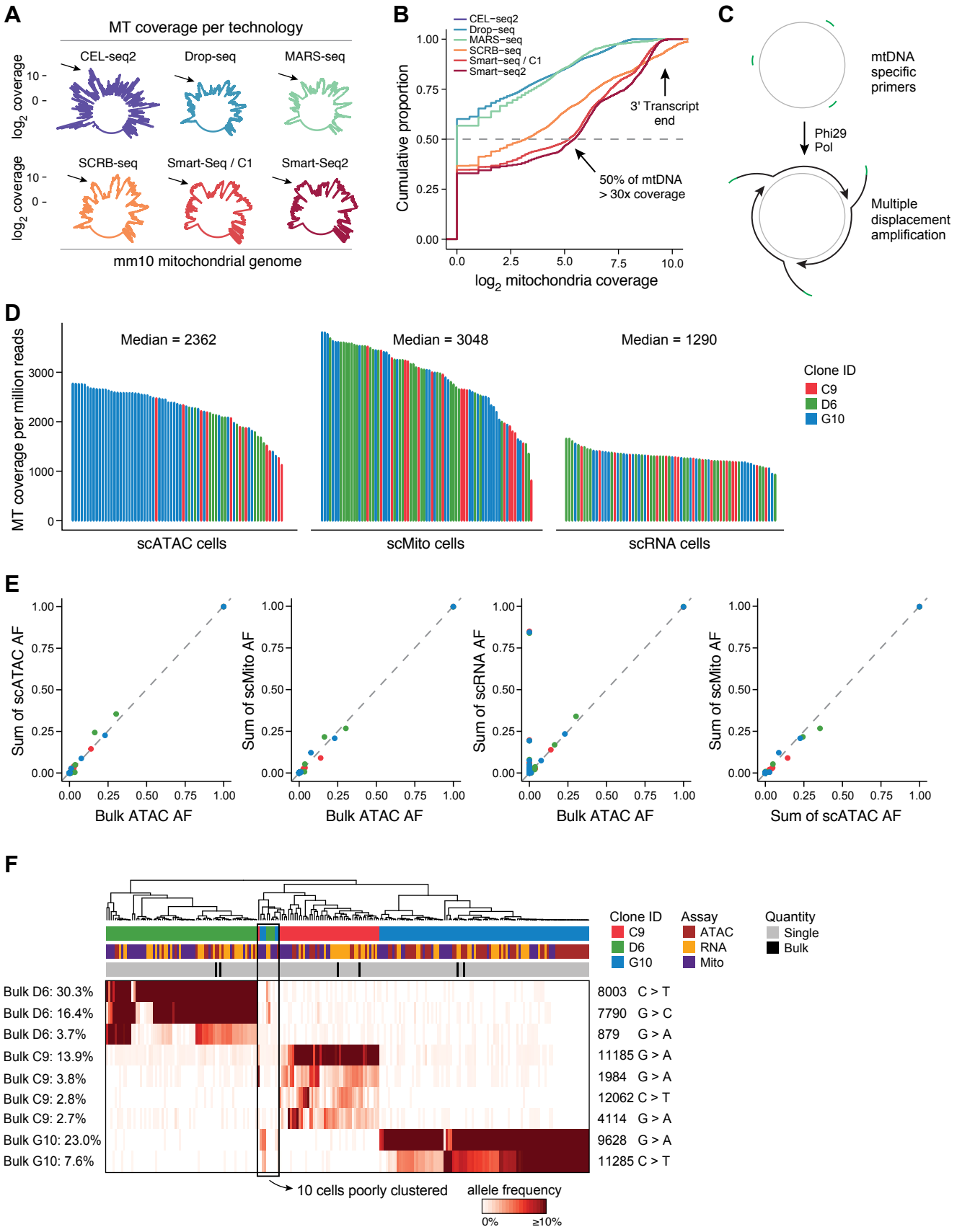
Figure S2


A
MT coverage per technology
CEL-seq2
Drop-seq
MARS-seq
SCRB-seq
Smart-Seq / C1
Smart-Seq2
log2 coverage
10
0
mm10 mitochondrial genome
B
CEL−seq2
Drop−seq
MARS−seq
SCRB−seq
Smart−seq / C1
Smart−seq2
Cumulative proportion
1.00
0.75
0.50
0.25
0.00
3' Transcript end
50% of mtDNA > 30x coverage
0.0
2.5
5.0
7.5
10.0
log2 mitochondria coverage
C
mtDNA specific primers
Phi29 Pol
Multiple displacement amplification
D
MT coverage per million reads
Median = 2362
Median = 3048
Median = 1290
3000
2000
1000
0
scATAC cells
scMito cells
scRNA cells
Clone ID
C9
D6
G10
E
Sum of scATAC AF
Sum of scMito AF
Sum of scRNA AF
Bulk ATAC AF
Sum of scATAC AF
0.00
0.25
0.50
0.75
1.00
F
Clone ID
C9
D6
G10
Assay
ATAC
RNA
Mito
Quantity
Single
Bulk
Bulk D6: 30.3%
Bulk D6: 16.4%
Bulk D6: 3.7%
Bulk C9: 13.9%
Bulk C9: 3.8%
Bulk C9: 2.8%
Bulk C9: 2.7%
Bulk G10: 23.0%
Bulk G10: 7.6%
8003 C > T
7790 G > C
879 G > A
11185 G > A
1984 G > A
12062 C > T
4114 G > A
9628 G > A
11285 C > T
10 cells poorly clustered
allele frequency
0%
≥10%