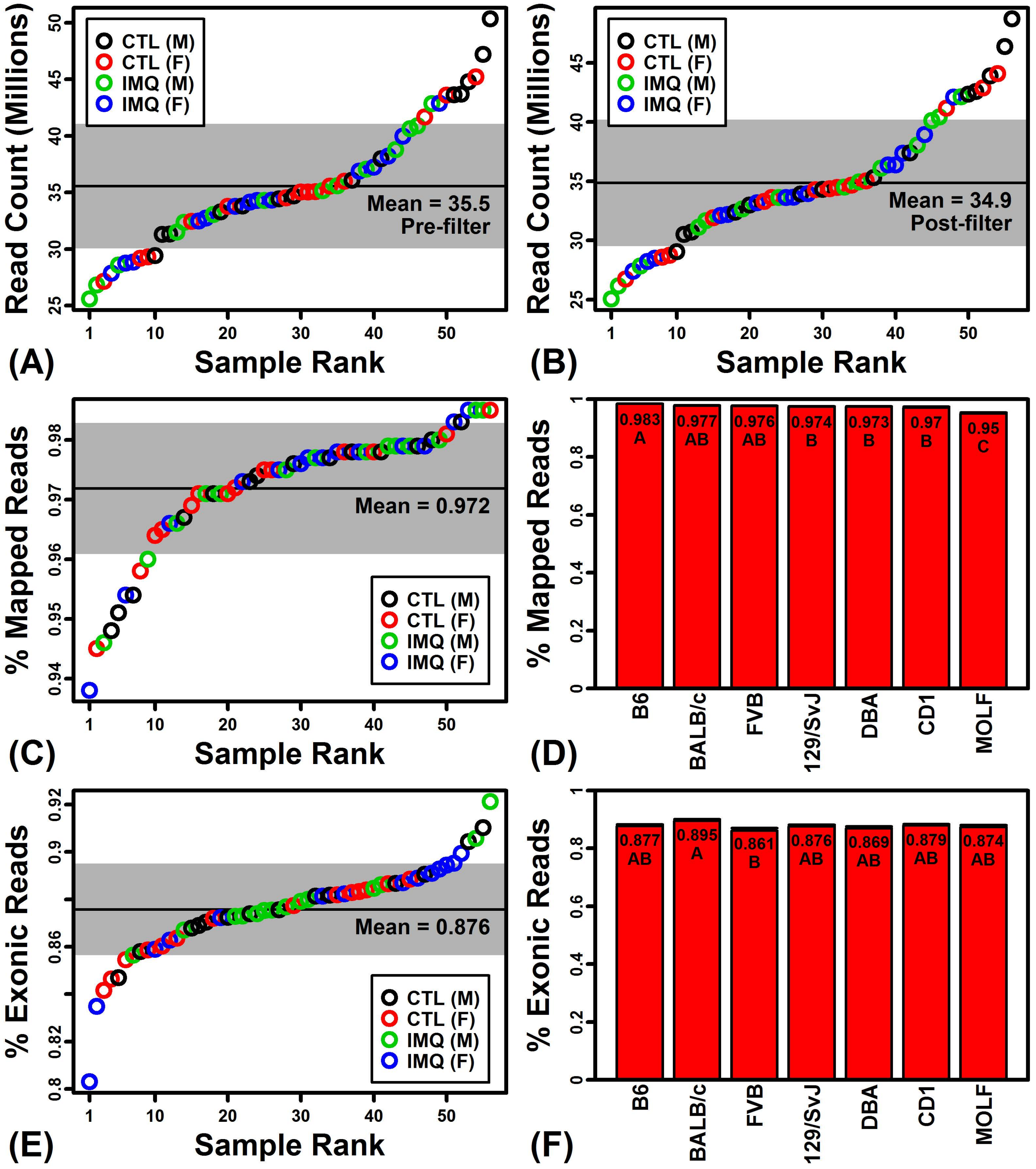
Additional File 2. Mapping of reads to mouse genome (*n* = 56 samples). (A) Reads per sample. (B) Quality-filtered reads per sample. (C) Percentage of quality-filtered reads mapped to the mouse genome (GRCm38/mm10). (D) Average percentage of mapped quality-filtered reads per strain. (E) Percentage of reads mapped to exonic regions. (F) Average percentage of exonic reads per strain. In (D) and (F), groups without the same letter differ significantly ($P < 0.05$, Tukey honest significant difference).


(A)
Read Count (Millions)
Sample Rank
CTL (M)
CTL (F)
IMQ (M)
IMQ (F)
Mean = 35.5
Pre-filter
25
30
35
40
45
50
1
10
20
30
40
50
(B)
Read Count (Millions)
Sample Rank
CTL (M)
CTL (F)
IMQ (M)
IMQ (F)
Mean = 34.9
Post-filter
25
30
35
40
45
1
10
20
30
40
50
(C)
% Mapped Reads
Sample Rank
Mean = 0.972
CTL (M)
CTL (F)
IMQ (M)
IMQ (F)
0.94
0.95
0.96
0.97
0.98
1
10
20
30
40
50
(D)
% Mapped Reads
0
0.2
0.4
0.6
0.8
1
0.983 A
0.977 AB
0.976 AB
0.974 B
0.973 B
0.97 B
0.95 C
B6
BALB/c
FVB
129/SvJ
DBA
CD1
MOLF
(E)
% Exonic Reads
Sample Rank
Mean = 0.876
CTL (M)
CTL (F)
IMQ (M)
IMQ (F)
0.8
0.82
0.86
0.9
0.92
1
10
20
30
40
50
(F)
% Exonic Reads
0
0.2
0.4
0.6
0.8
1
0.877 AB
0.895 A
0.861 B
0.876 AB
0.869 AB
0.879 AB
0.874 AB
B6
BALB/c
FVB
129/SvJ
DBA
CD1
MOLF