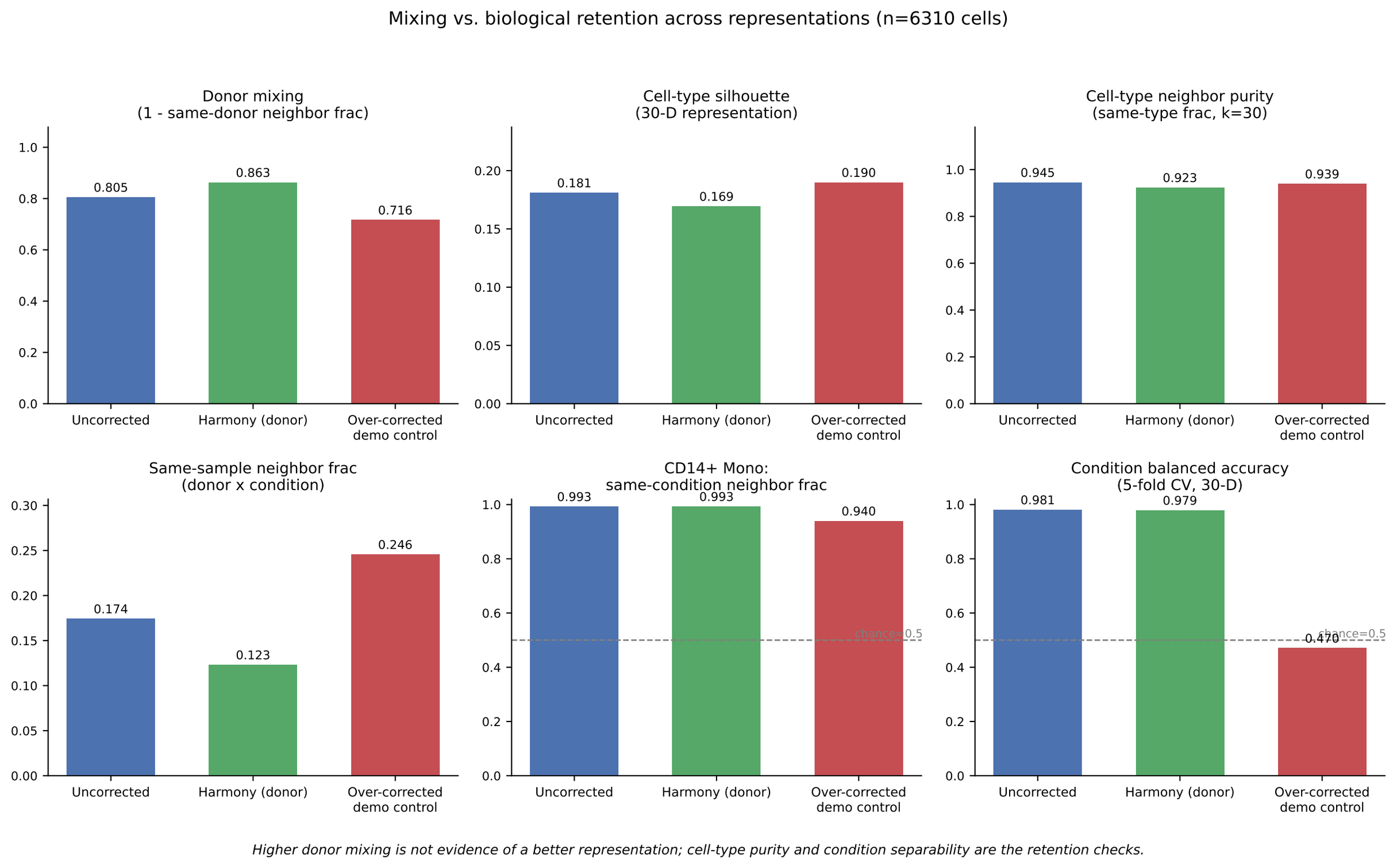

Mixing vs. biological retention across representations (n=6310 cells)
Donor mixing
(1 - same-donor neighbor frac)
0.805
0.863
0.716
Cell-type silhouette
(30-D representation)
0.181
0.169
0.190
Cell-type neighbor purity
(same-type frac, k=30)
0.945
0.923
0.939
Same-sample neighbor frac
(donor x condition)
0.174
0.123
0.246
CD14+ Mono:
same-condition neighbor frac
0.993
0.993
0.940
chance=0.5
Condition balanced accuracy
(5-fold CV, 30-D)
0.981
0.979
0.470
chance=0.5
Uncorrected
Harmony (donor)
Over-corrected
demo control
Higher donor mixing is not evidence of a better representation; cell-type purity and condition separability are the retention checks.