

Supplemental Figure 6:

Number of Strains missing in each platform

Number of Uptags missing
Bar-seq Array

	Bar-seq	Union	Array
# BC missing	169	968	954
% BC correct (82%)	64.5	50.72	68.76
% BC error (17.6%)	27.81	25	30.24
% U1 error (19.8%)	48.52	44.83	13
% U2 error (17%)	14.79	25.52	14.25
% U1 or U2 error (30%)	59.17	68.18	25.16

Number of Downtags missing
Bar-seq Array

	Bar-seq	Union	Array	
# BC missing	599	831	350	# BC missing
% BC correct (81.7%)	62.6	47.41	52.57	% BC correct (81.7%)
% BC error (18.3%)	35.06	35.02	45.14	% BC error (18.3%)
% D1 error (19.04%)	38.06	48.5	11.14	% D1 error (19.04%)
% D2 error (15.9%)	36.73	19.86	5.71	% D2 error (15.9%)
% D1 or D2 error (29%)	68.11	66.91	16.57	% D1 or D2 error (29%)

Number of strains missing both tags (Up and Down tag)

