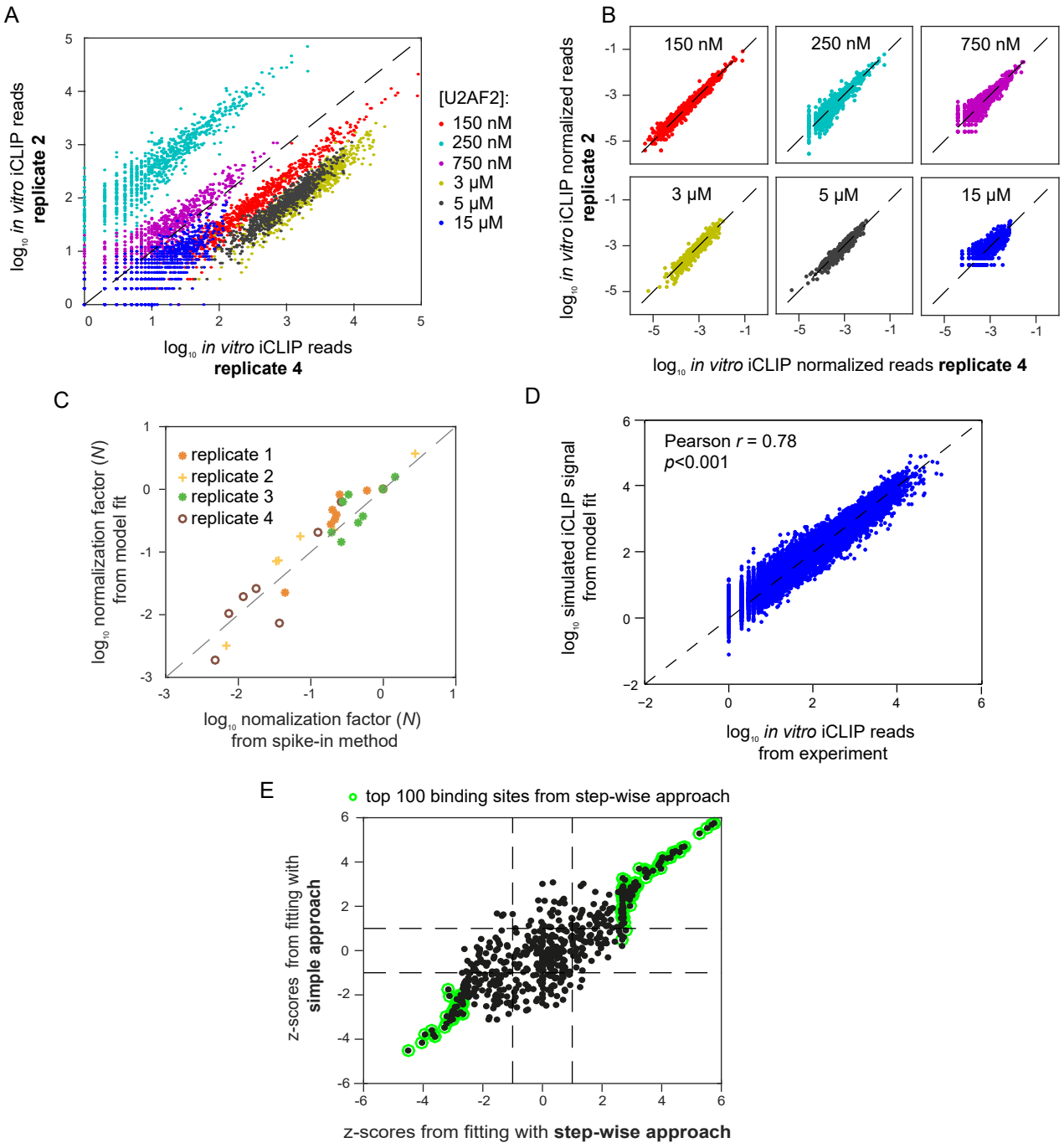

Supplemental figure S6, related to Supplementary Methods. The mathematical model quantitatively describes U2AF2 binding. (A) *In vitro* iCLIP signal is well correlated between replicates. Scatter plot showing correlation of $\log_{10}$-transformed non-normalized *in vitro* iCLIP read counts from replicates 2 and 4 of the K_d titration experiment. Different concentrations of added U2AF2^{RRM12} are indicated by colors. **(B)** Comparison of the same replicate samples as in (A) after normalization to the total number of reads within each library (**Supplemental Table S7**). **(C)** Normalization factors (*N*) estimated from the model fit and a *NUP133* spike-in control are well correlated in quadruplicate experiments. All normalization factors are given on $\log_{10}$-transformed scale relative to the normalization factor for the lowest U2AF2^{RRM12} concentration in each replicate. **(D)** Best-fit model accurately describes the experimental data. Scatter plot showing correlation between $\log_{10}$-transformed measured and simulated *in vitro* iCLIP signals (arbitrary units) for all U2AF2^{RRM12} concentrations and replicate experiments. Pearson correlation coefficients (*r*) are given at the top. **(E)** Scatter plot showing correlation of z-scores for *in vivo* regulated U2AF2 binding sites defined by the simple and step-wise fitting approaches. Green circles indicate top 100 binding sites according to ranked z-scores from the step-wise fitting approach.