Supplementary Figure 6. Higher density of uTSSs near genes facilitates high level expression, which increases upon loss of NELF. A, 4sU RNA-seq signal (normalized counts) is shown for the genes associated with enhancers (black, N=4,459) or super-enhancers (green, N=231) in mES cells. P-values are from Mann-Whitney test. **B**, Expression levels increase concomitantly with the number of associated uTSSs. The 4sU RNA-seq signal is shown for the genes with 0-4 (black, N=3,694), 5-49 (blue, N=10,788) and 50 or more (green, N=583) associated uTSSs in mES cells. **C**, Comparison of Pausing Indices across genes with 0-4 (black, N=3,694), 5-49 (blue, N=10,788) and 50 or more (green, N=583) associated uTSSs in mES cells. **D**, Fold change in 4sU RNA-seq upon deletion of NELF-B at genes associated with different numbers of uTSSs (black, N=3,694; blue, N=10,788; and green, N=583). **E**, Fold change in Start-RNA levels at uTSSs clusters upon deletion of NELF-B. 5'-end Start-RNA reads (±50bp) were counted from control versus NELF-B KO ESCs within clusters of 0-4 (black, N=3,694), 5-49 (blue, N=10,788) and ≥50 uTSSs (green, N=583). Box plots show 25th-75th percentiles and error bars depict 10-90th percentiles. (B-E) P-values are from Kruskal-Wallis test. Related to Fig. 6.