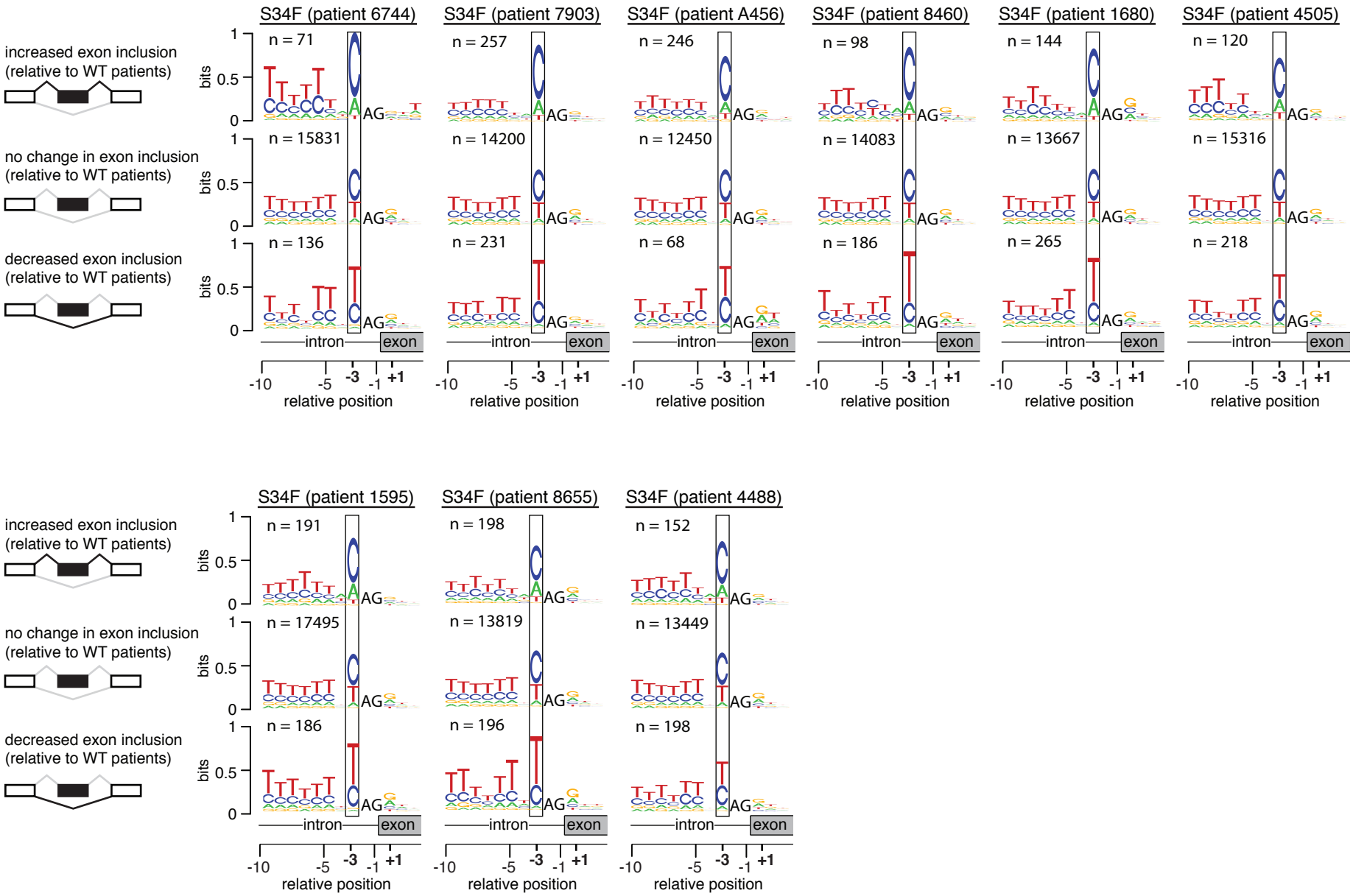
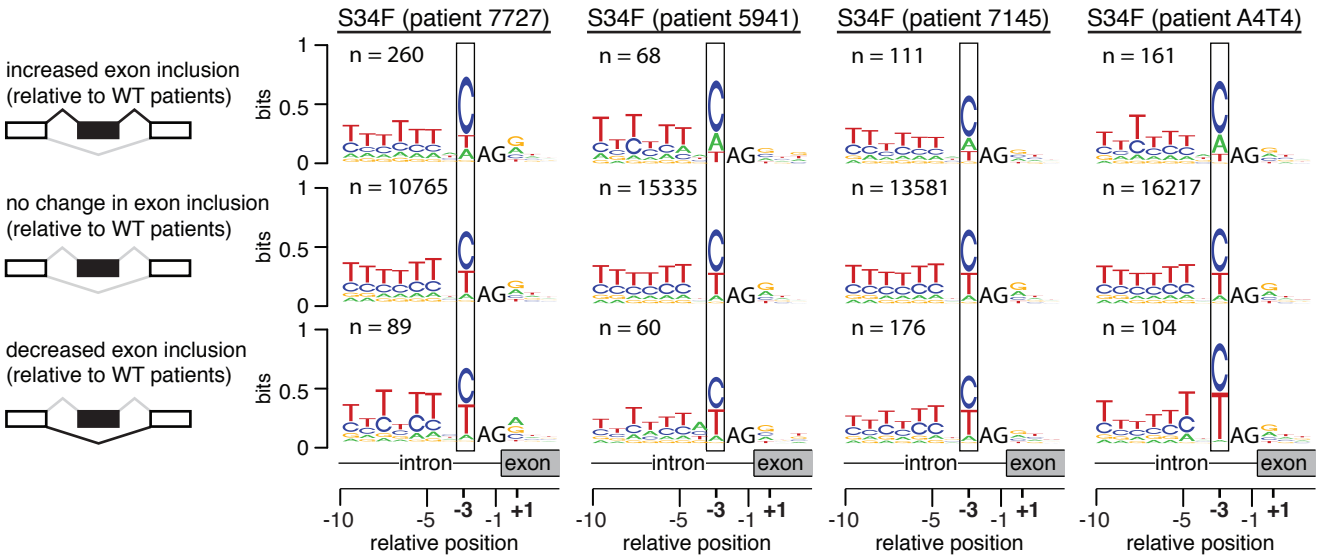
A. “Typical S34F” consensus 3' splice sites from mutant LUAD Transcriptomes



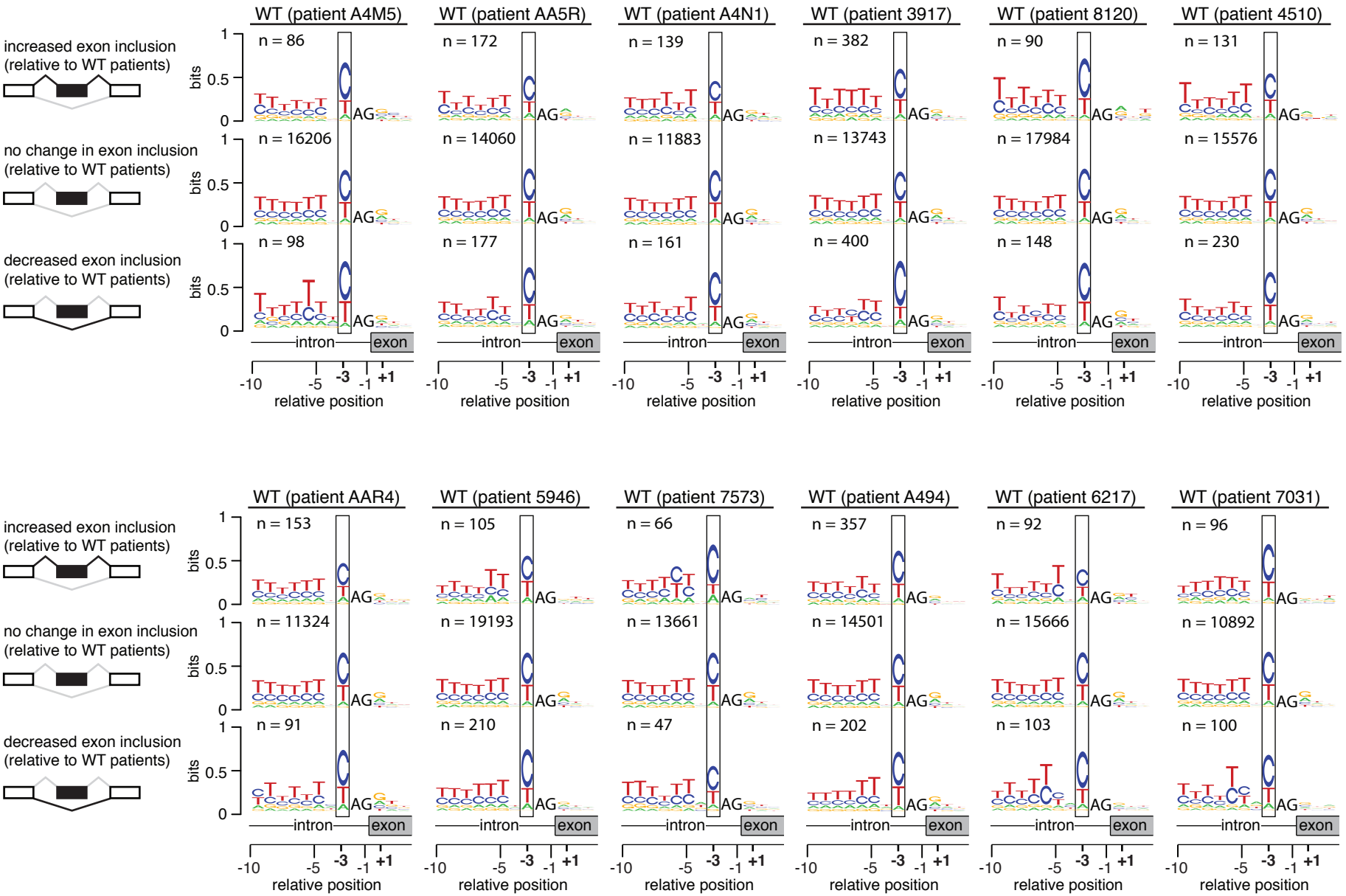
Supplemental Fig. S1 (to be continued on the next page)

B. “Quasi-WT” consensus 3' splice sites from mutant LUAD Transcriptomes



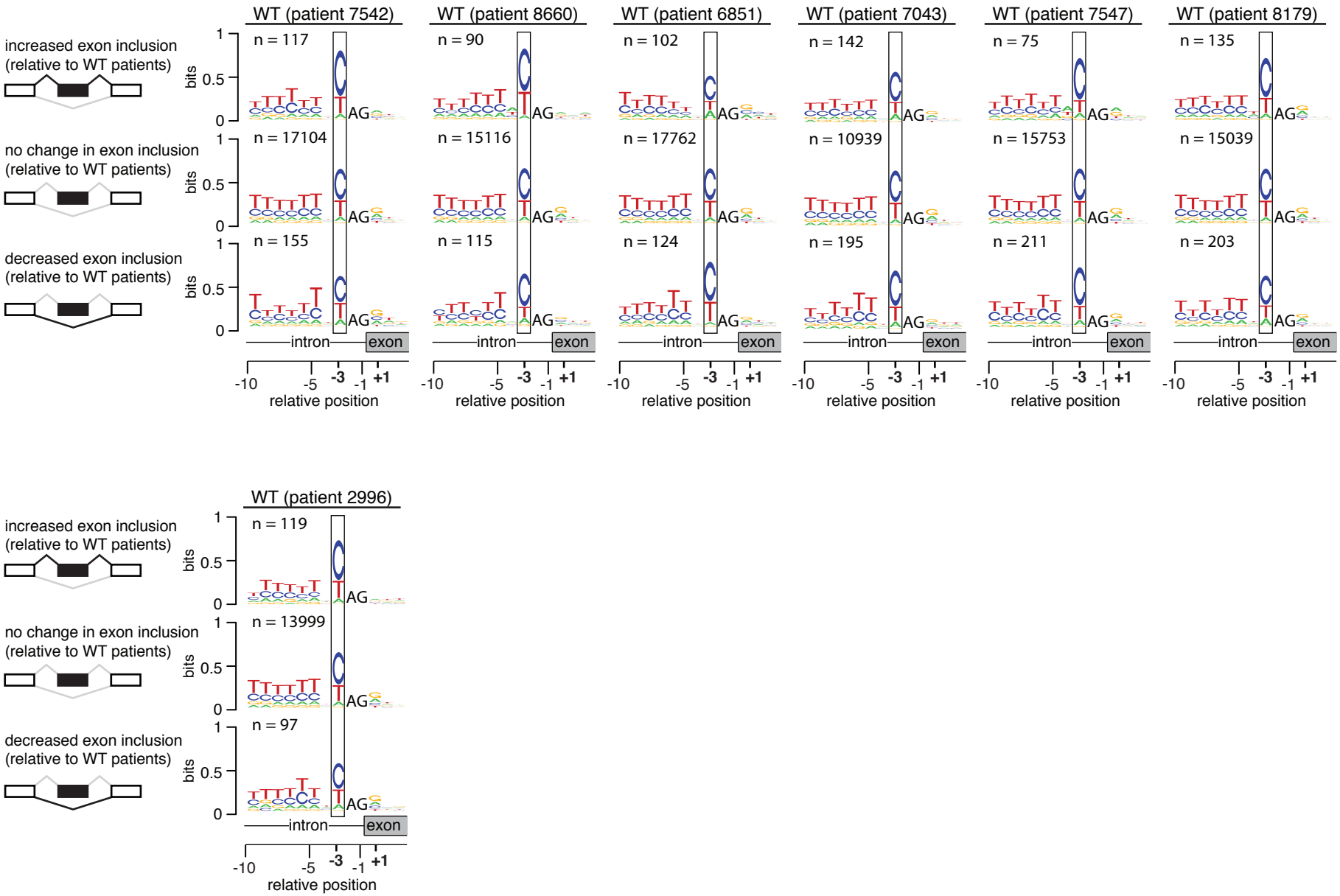
Supplemental Fig. S1 (to be continued on the next page)

C. Wild-type consensus 3' splice sites from wild-type LUAD Transcriptomes

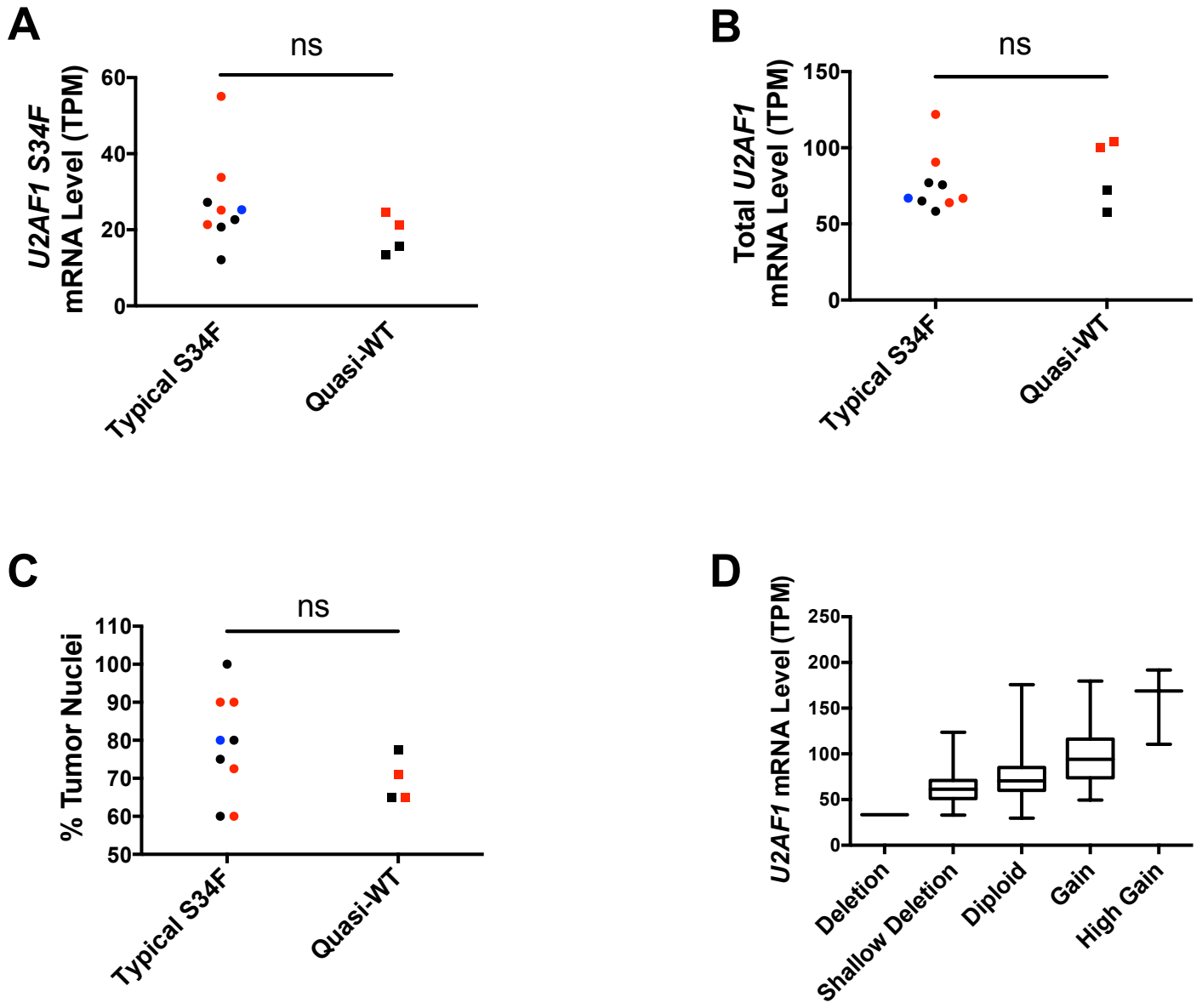


Supplemental Fig. S1 (to be continued on the next page)

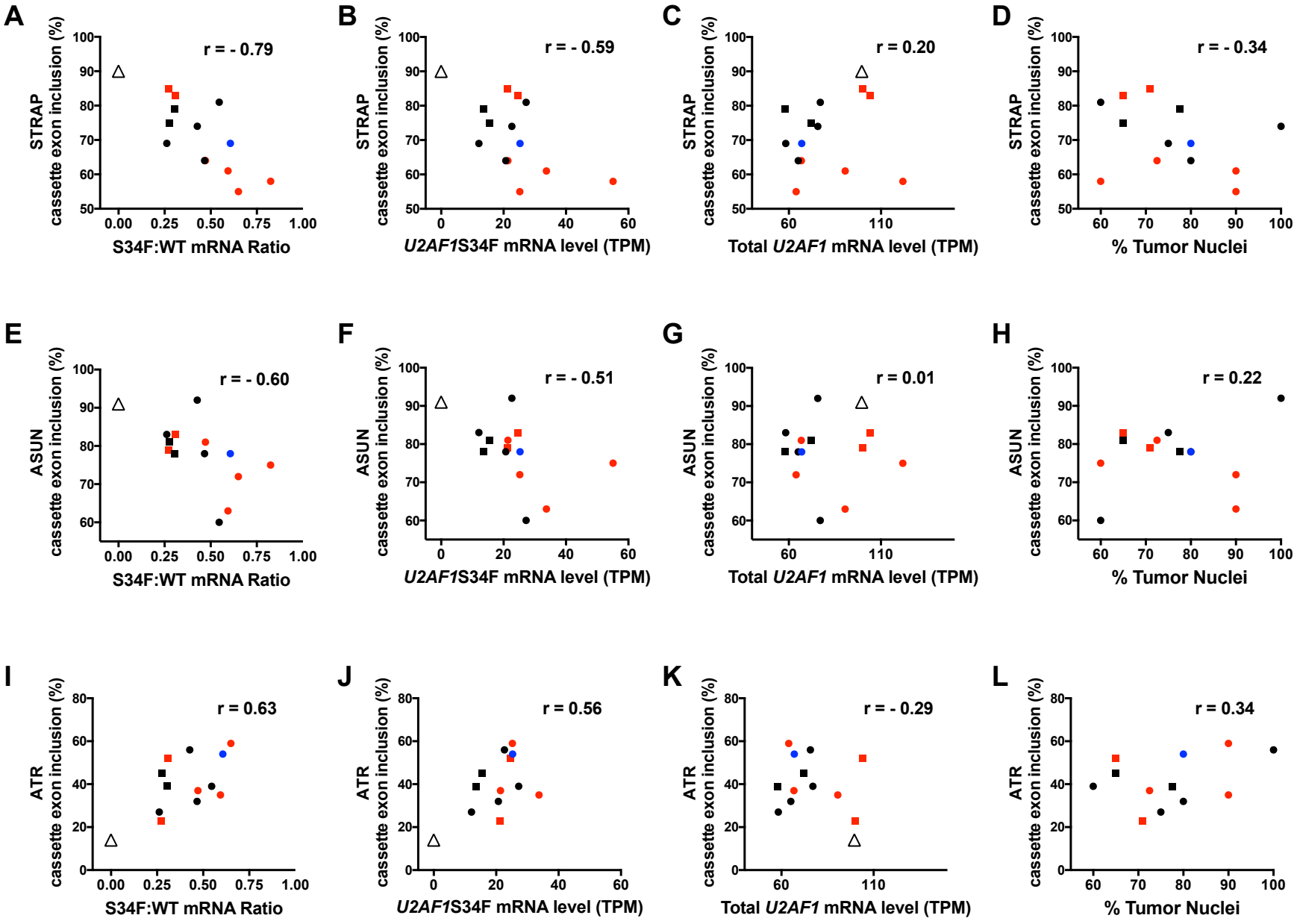
C. Wild-type consensus 3' splice sites from wild-type LUAD Transcriptomes



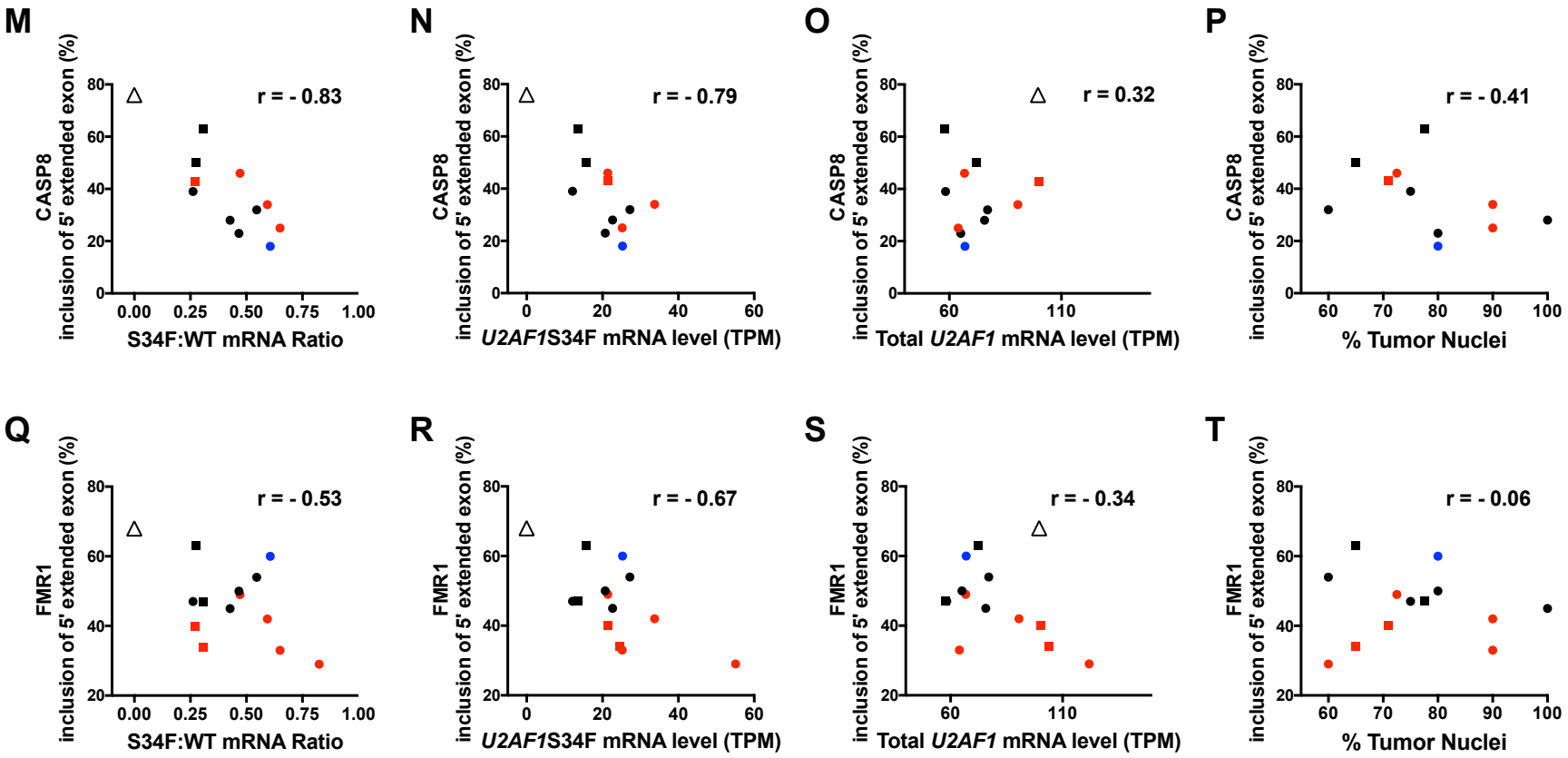
Supplemental Fig. S1



Supplemental Fig. S2



Supplemental Fig. S3 (to be continued on the next page)



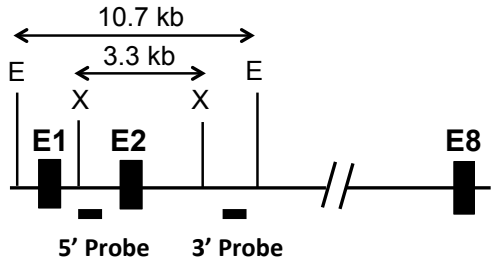
Supplemental Fig. S3

A

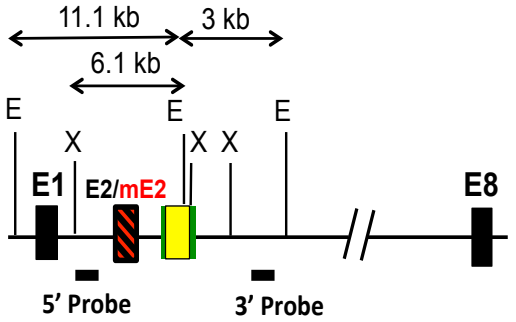
Southern Blot Strategy

	5' Probe (Xho I cut)	3' Probe (EcoR I cut)
Wild type allele	3.3 kb	10.7 kb
Intermediate allele	6.1 kb	3.0 kb

Wild-type *U2AF1* Allele

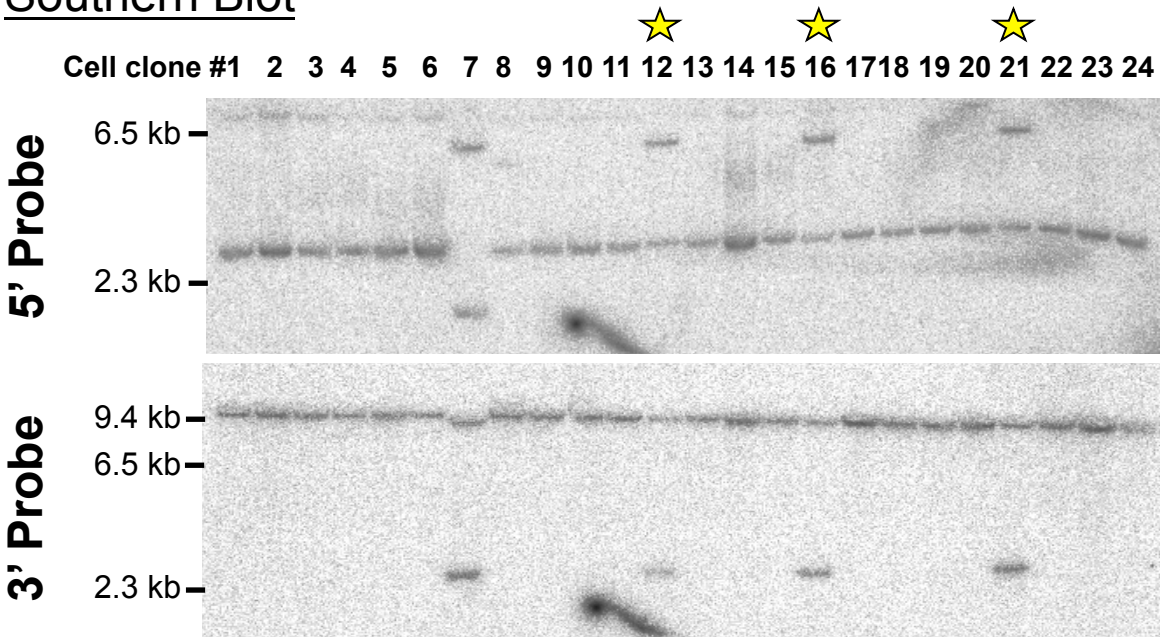


Mutant or Wild-type Intermediate Allele

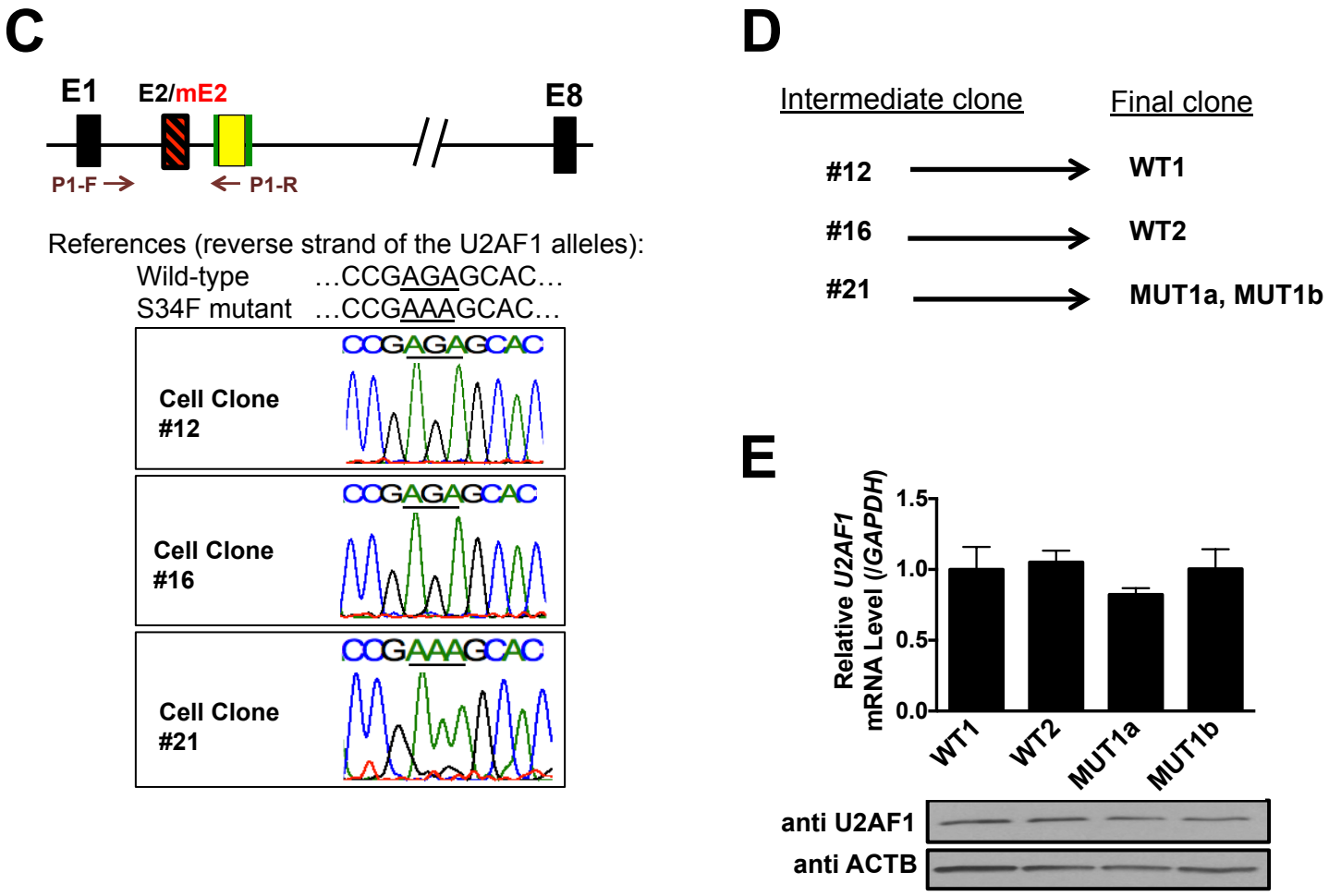


B

Southern Blot



Supplemental Fig. S4 (to be continued on the next page)

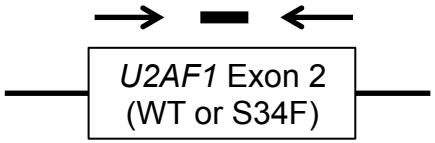


Supplemental Fig. S4

A

Taqman S34F/WT SNP Assay

Forward primer: AATTGGAGCATGTCGTCATGGA
Reverse primer: CTGGCTAAACGTCGGTTTATTGT
WT Probe: [VIC]-CAACCGAGAGCACC-[MGB]
S34F Probe: [FAM]-CAACCGAAAGCACC-[MGB]



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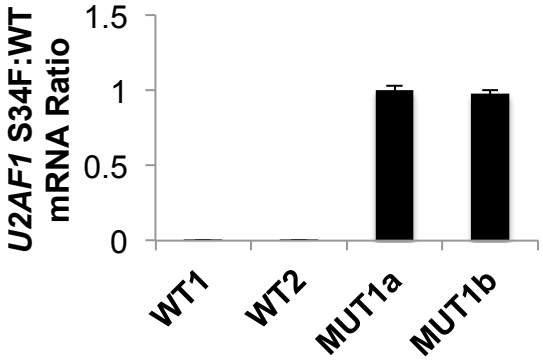
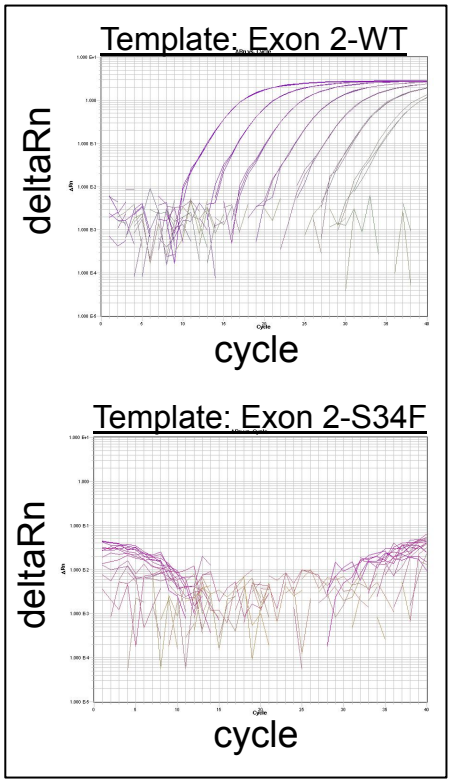
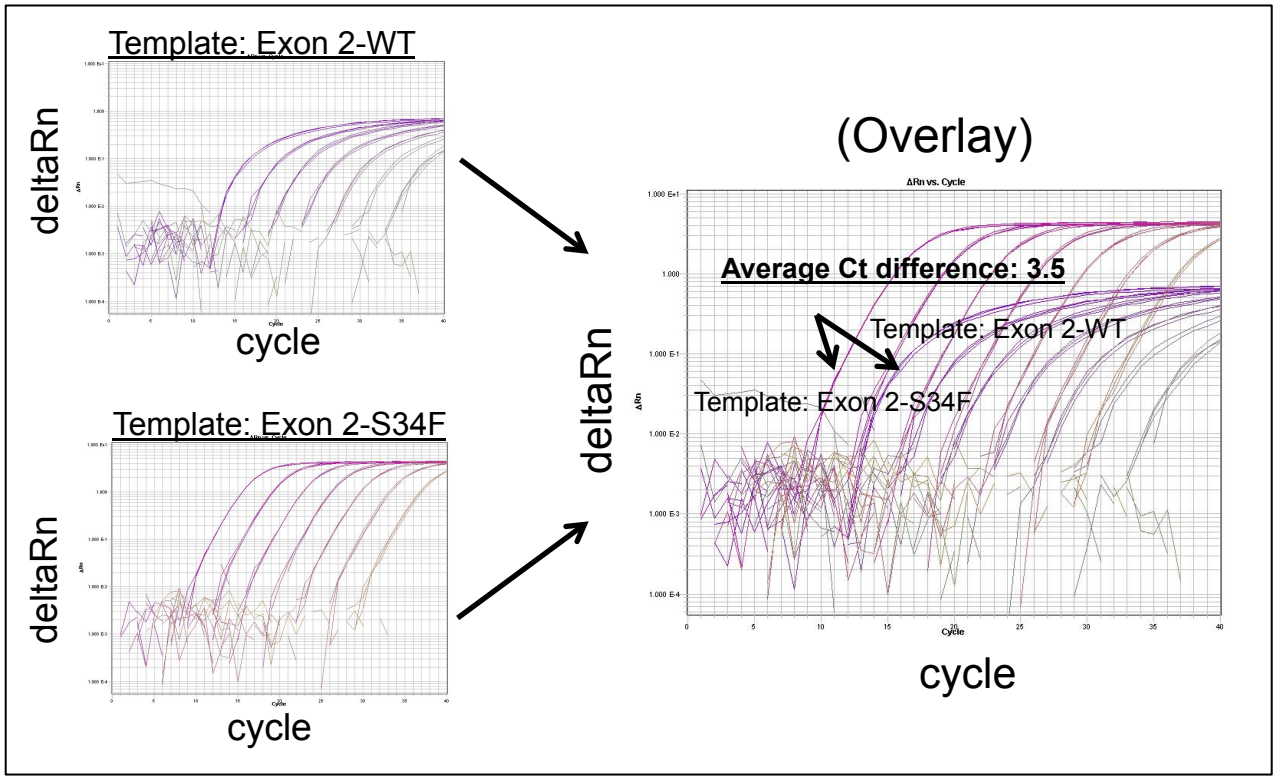


B **qPCR amplification curves**

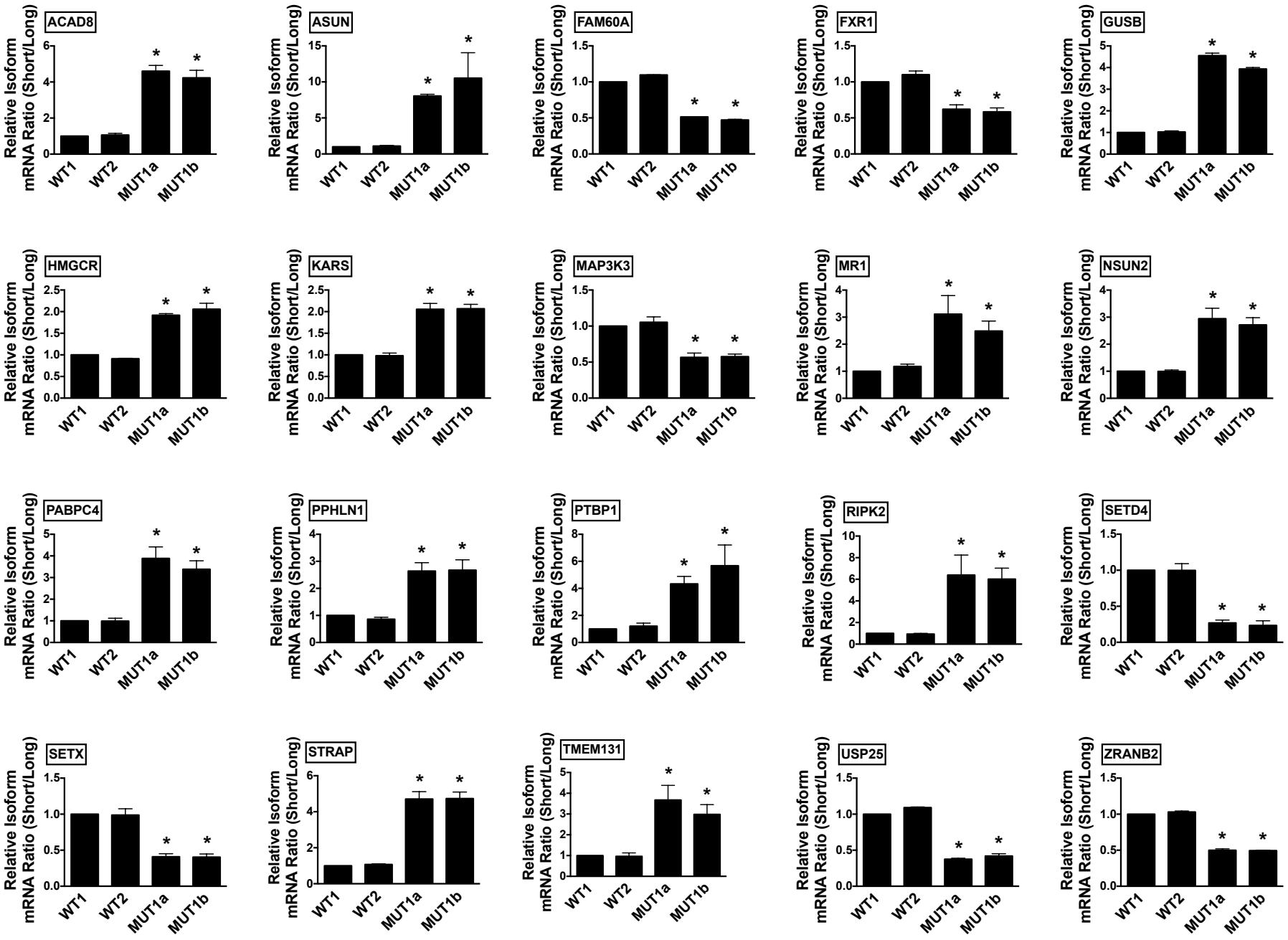
By the WT probe



By the S34F probe



Supplemental Fig. S5



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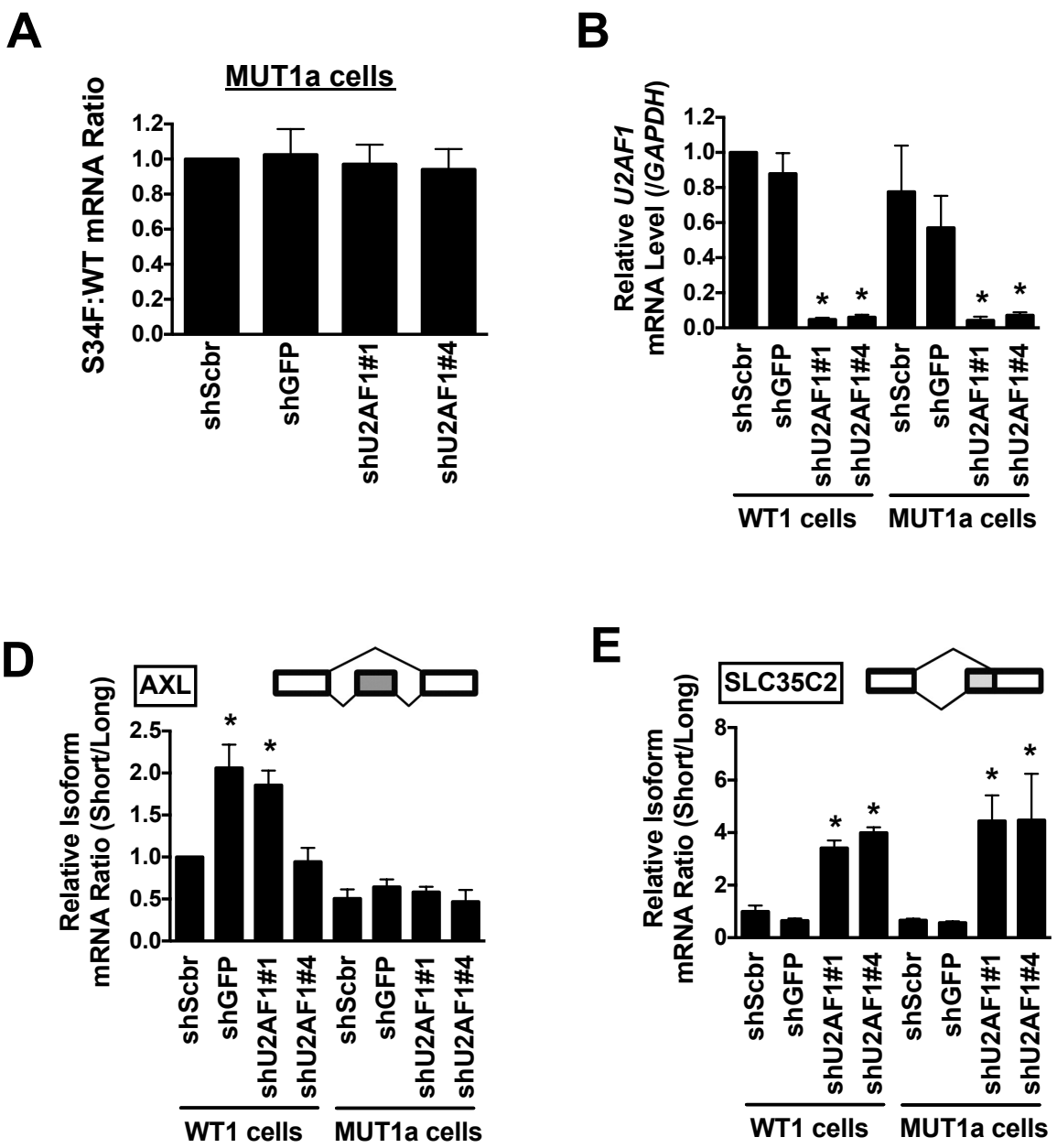
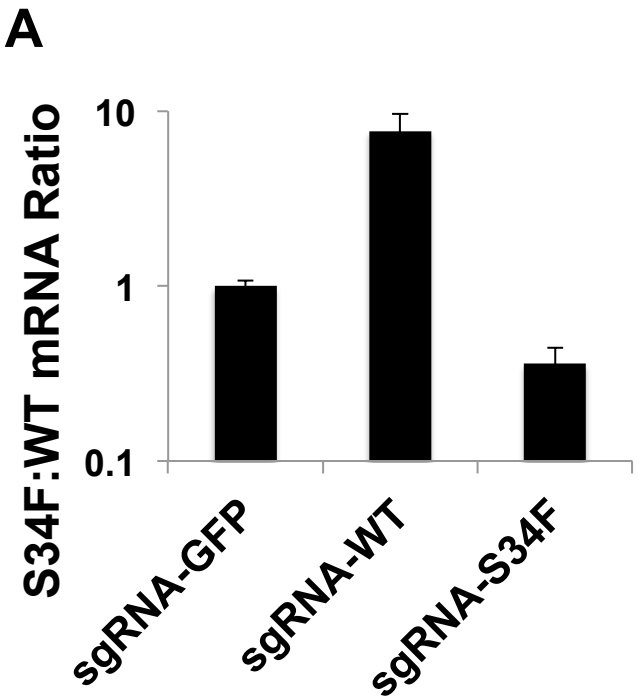
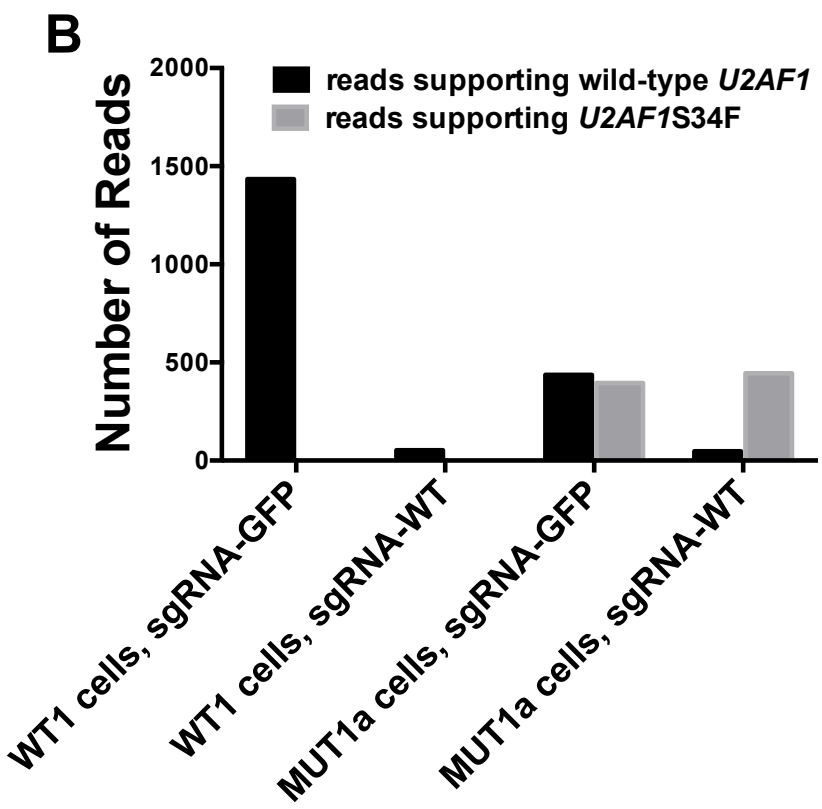


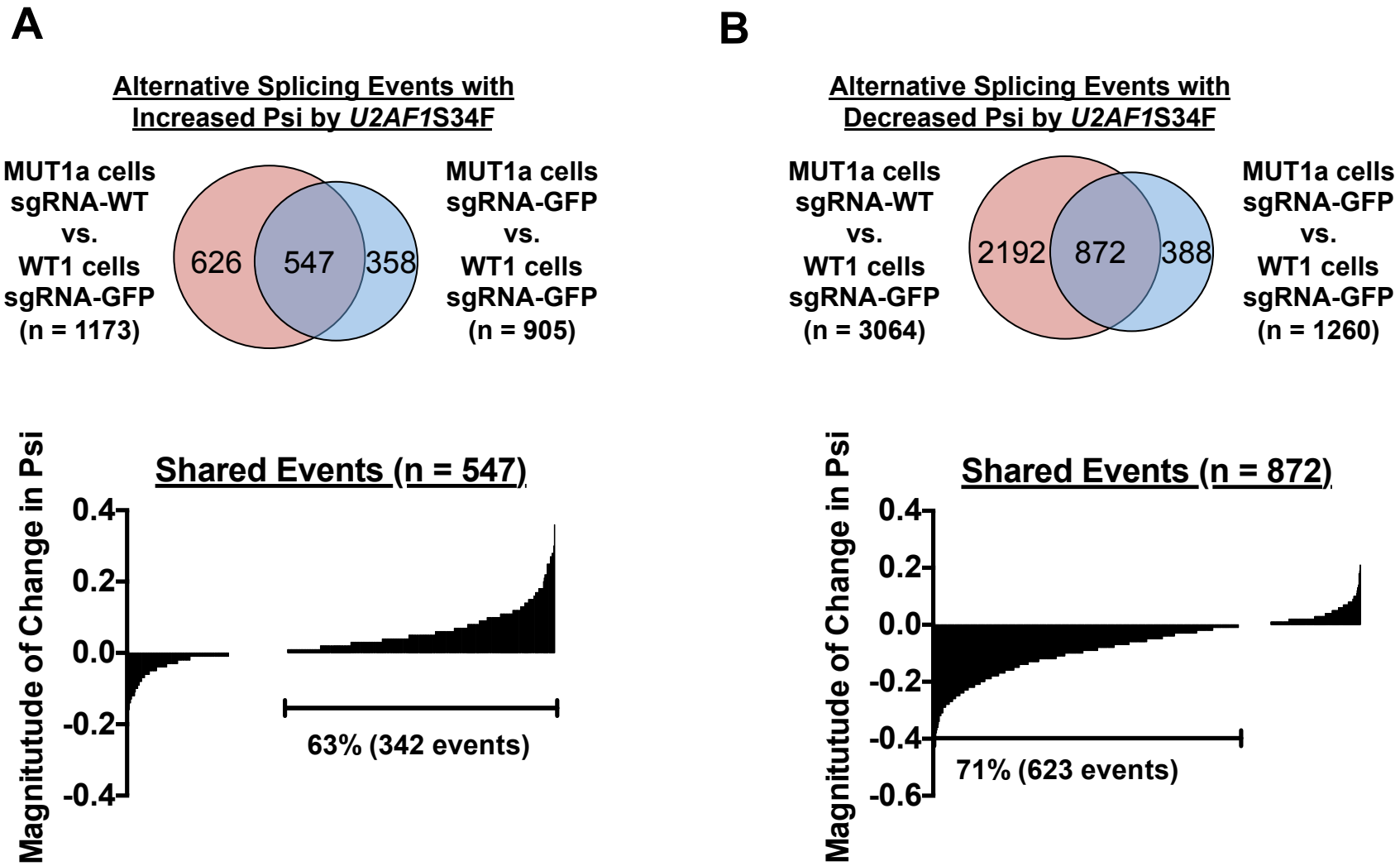
Supplemental Fig. S7

Supplemental Fig. S8

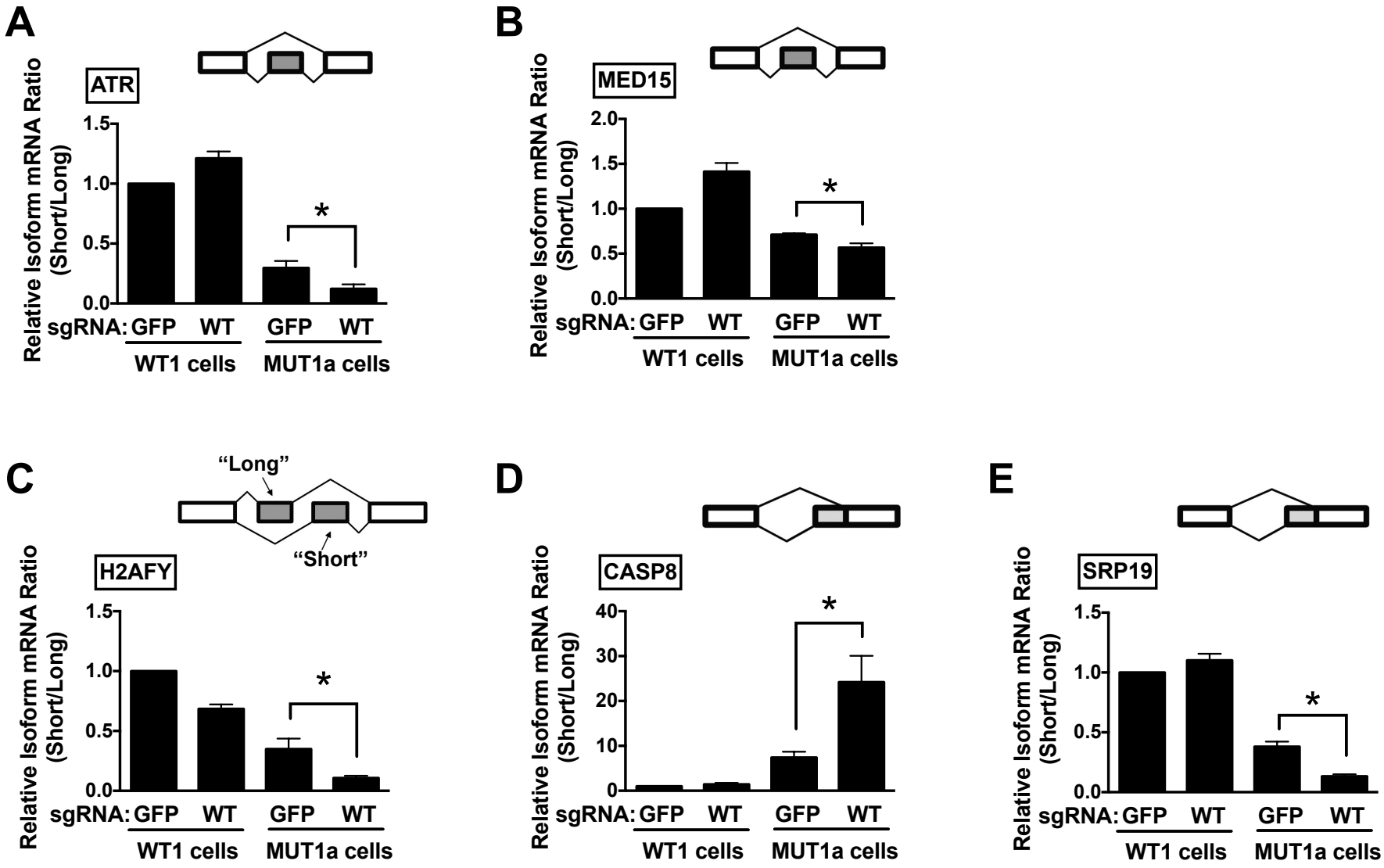




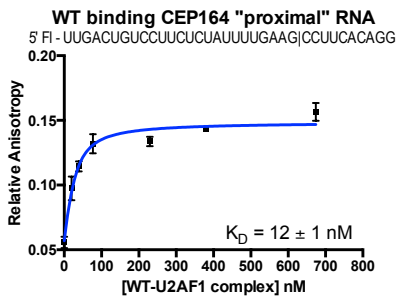
Supplemental Fig. S9

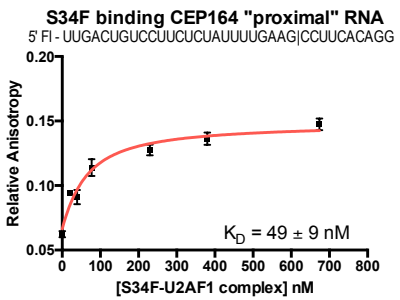


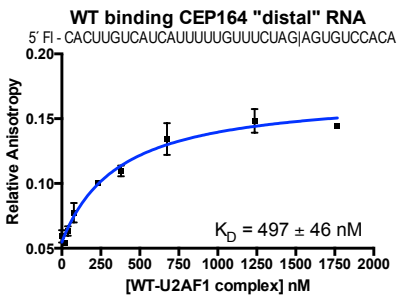
Supplemental Fig. S10

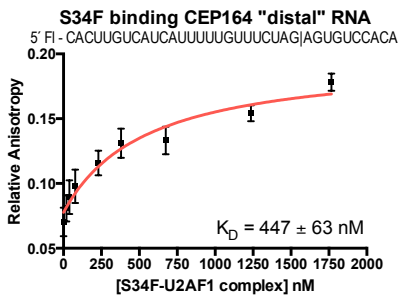


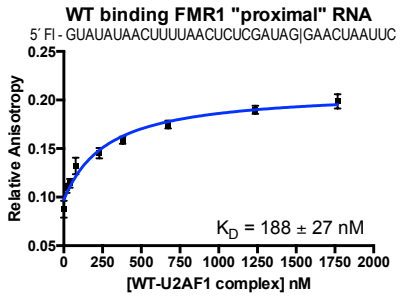
Supplemental Fig. S11

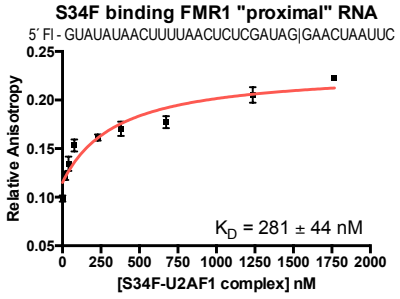


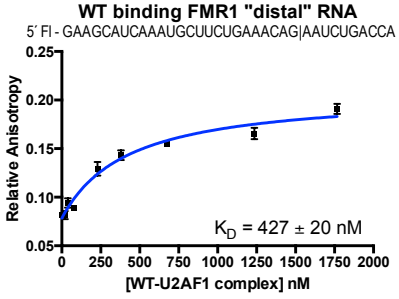


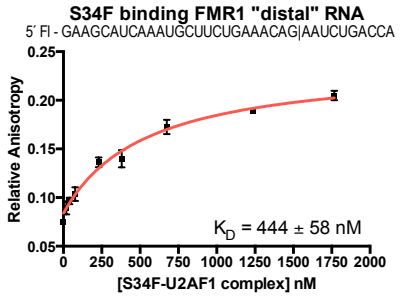


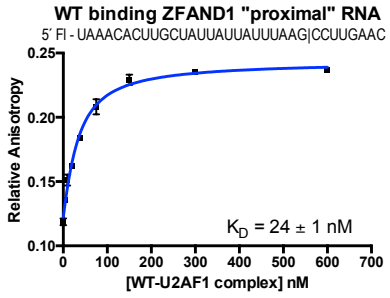


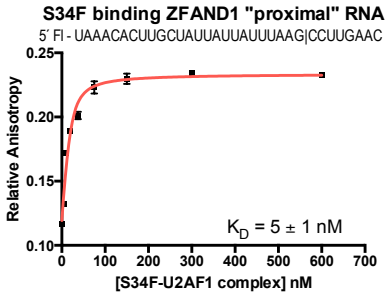


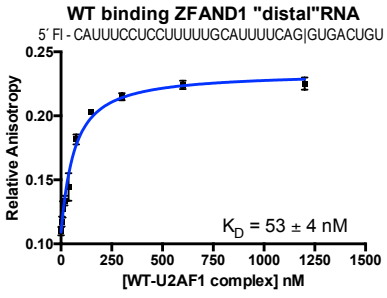


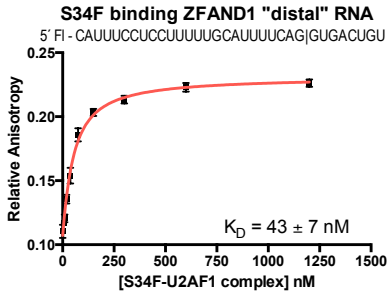




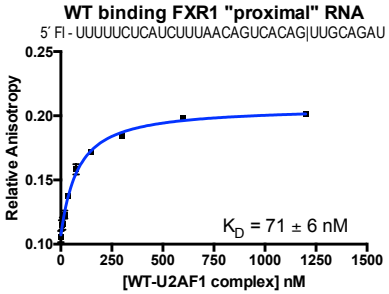


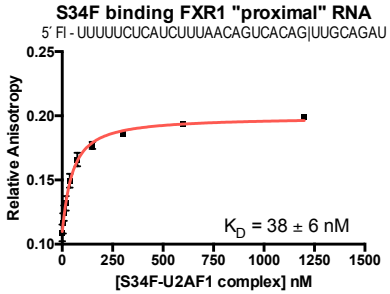


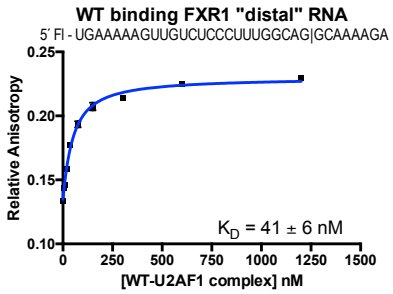


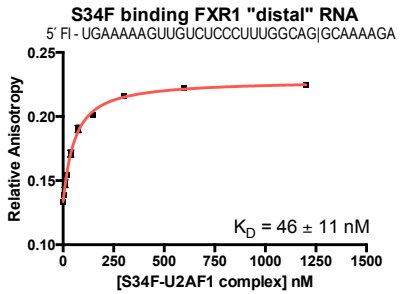


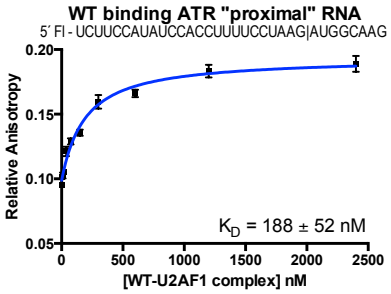
Supplemental Fig. S12 (to be continued on the next page)

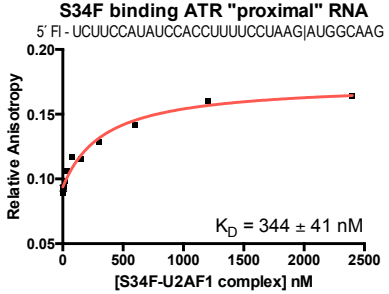


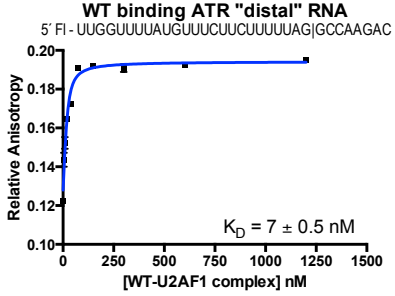


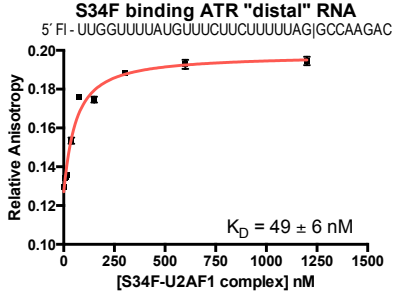


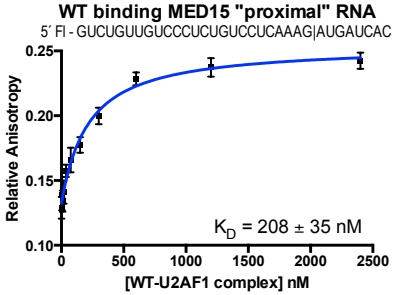


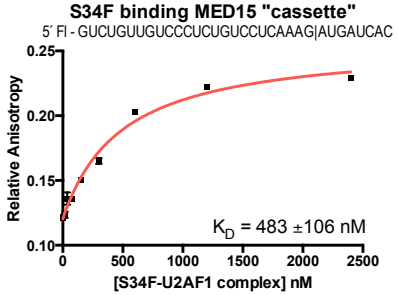


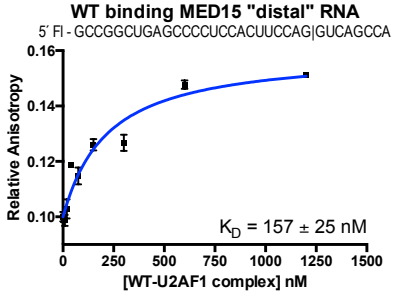


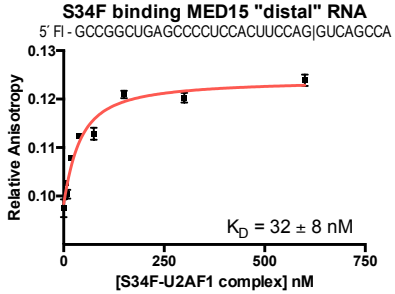




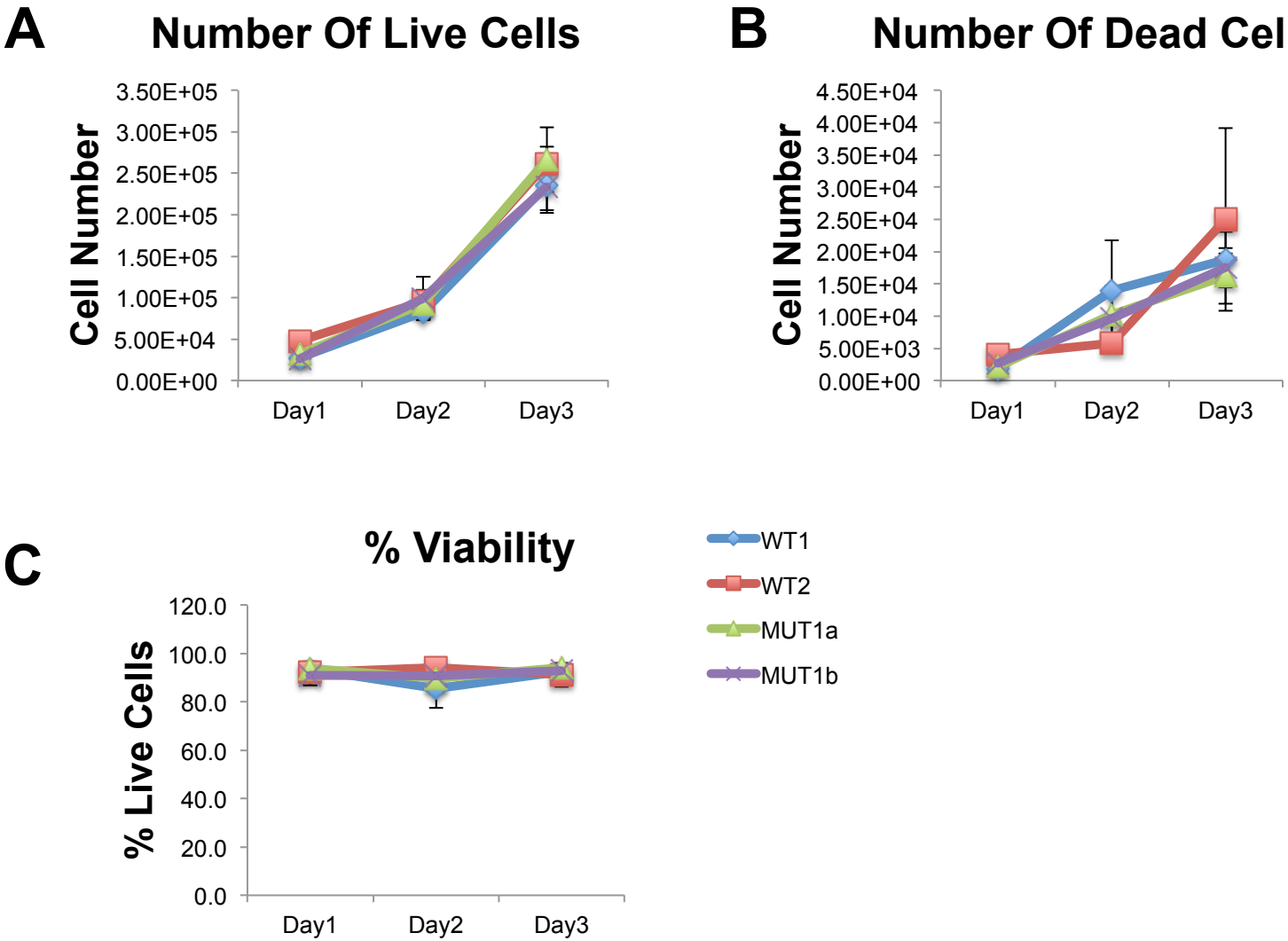








Supplemental Fig. S12



Supplemental Fig. S13

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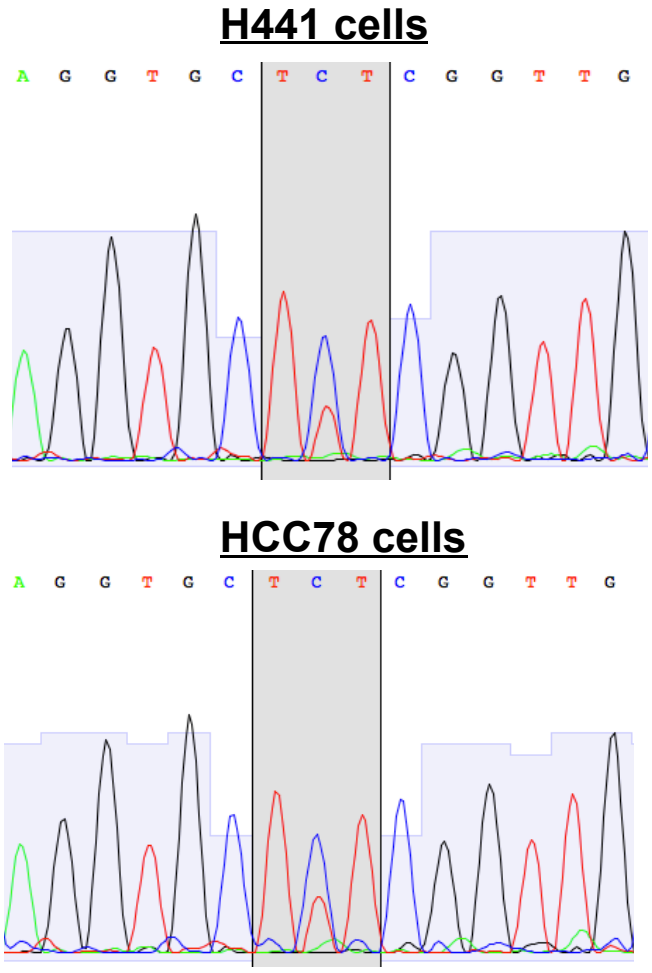

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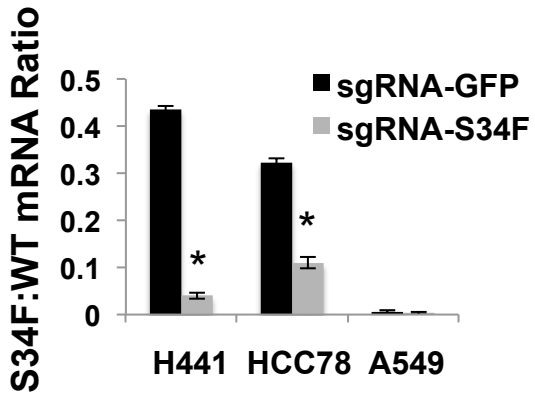

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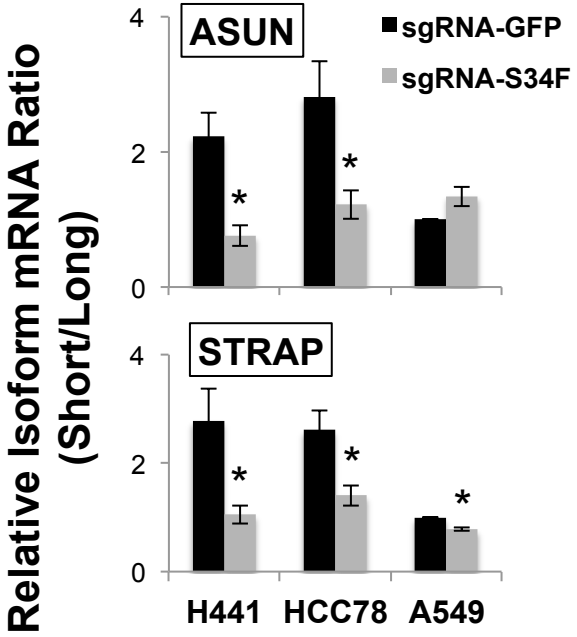
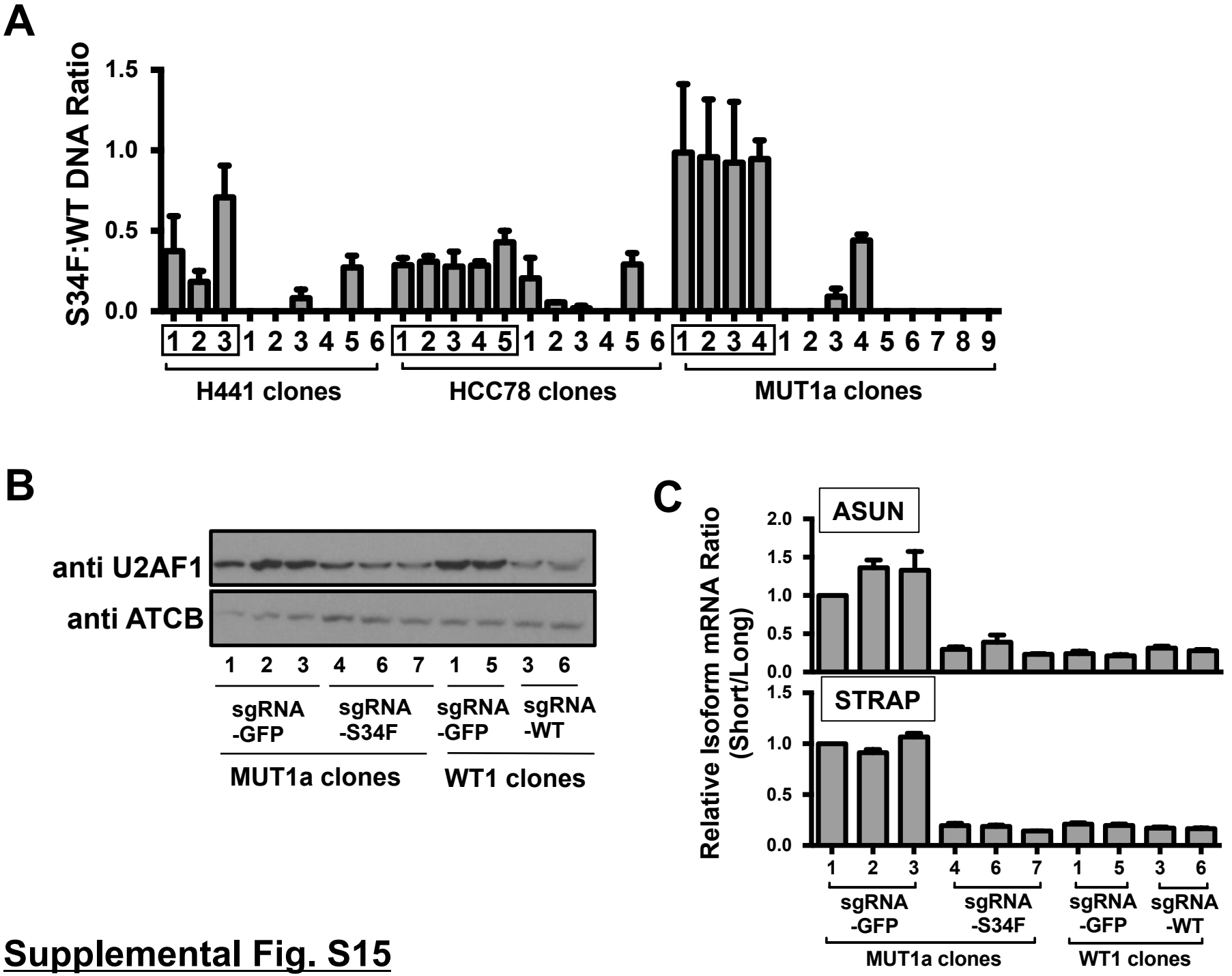


Supplemental Fig. S14



Supplemental Fig. S15

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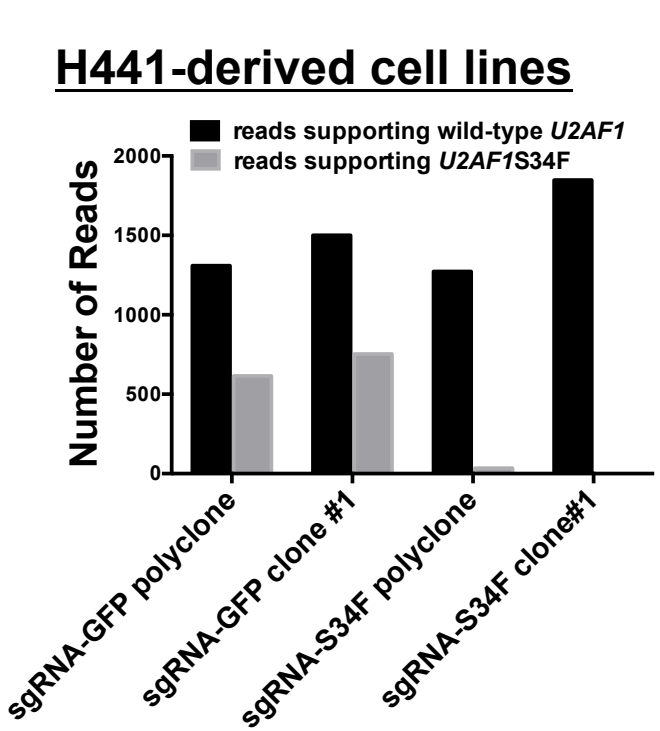

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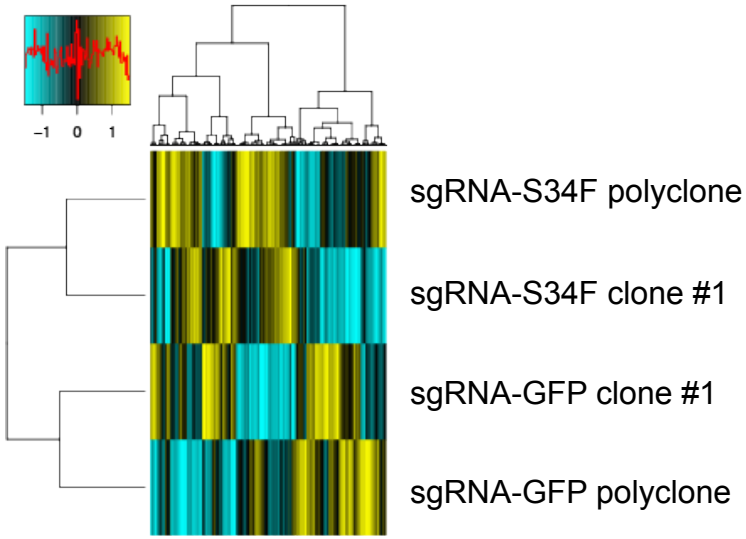

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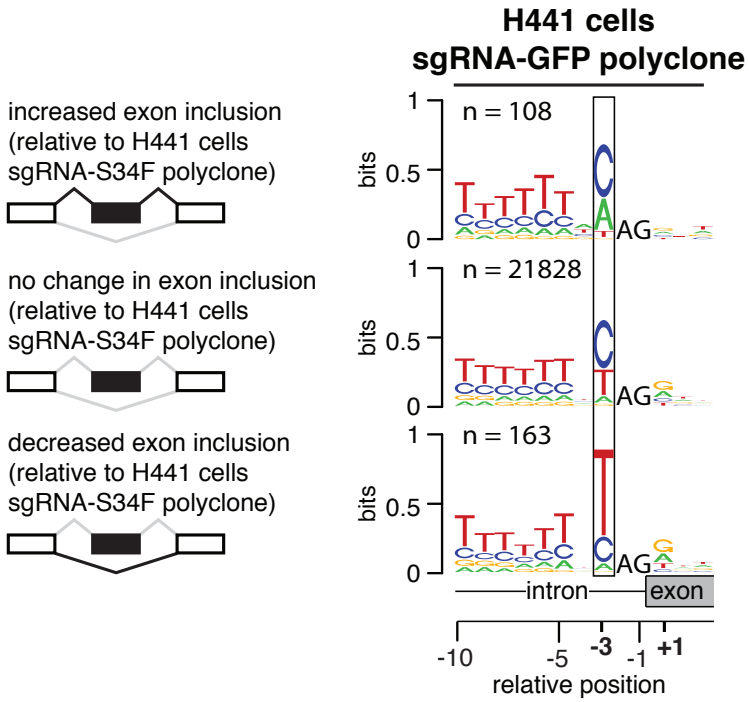

Supplemental Fig. S16

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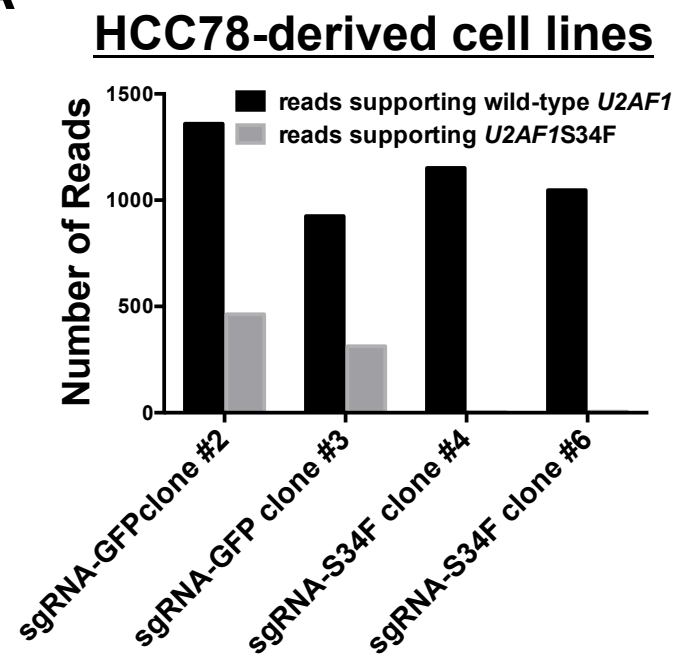

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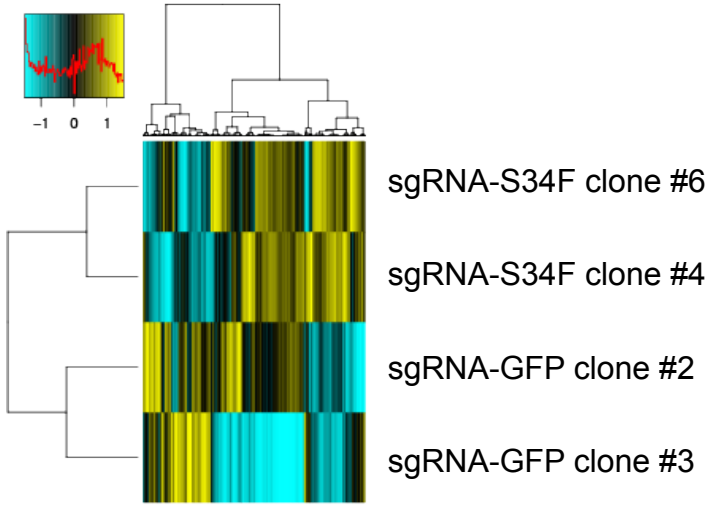
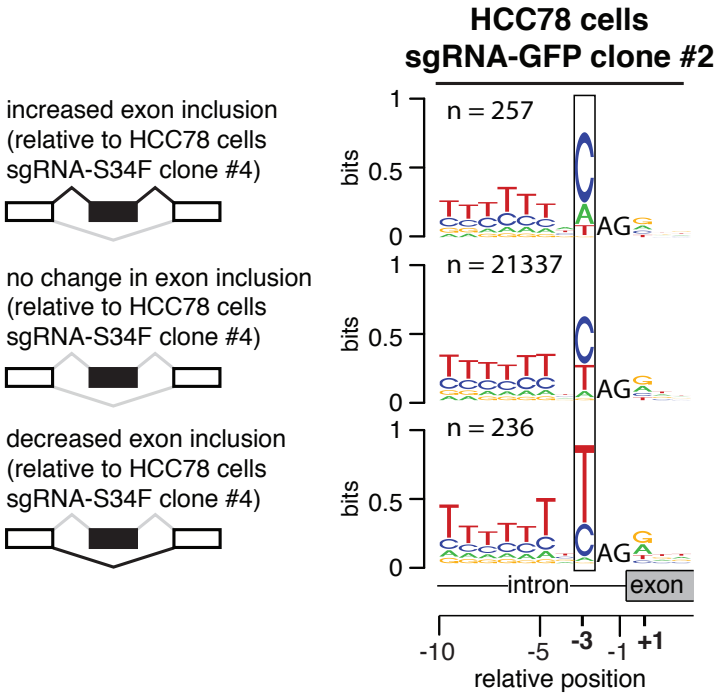
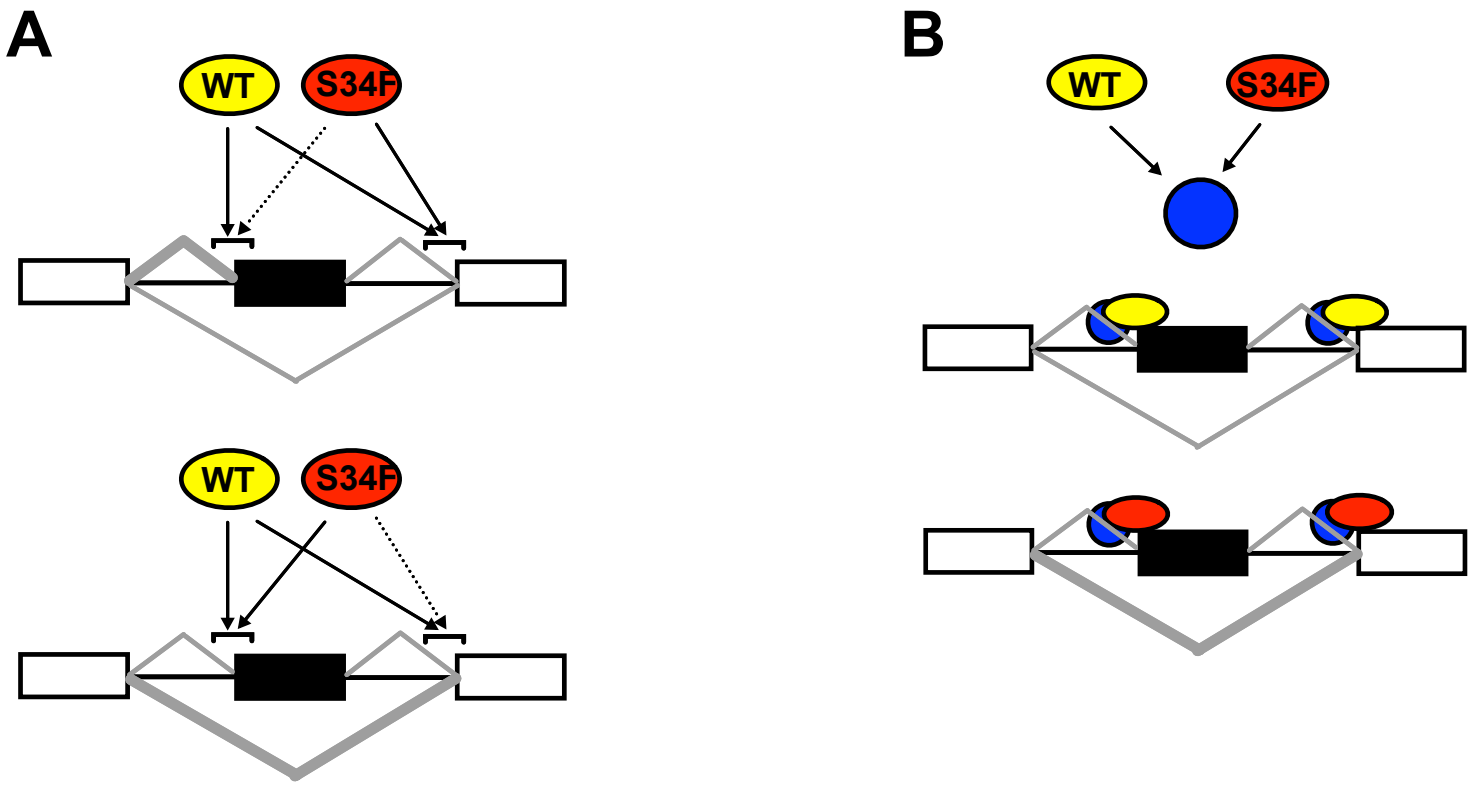


C



Supplemental Fig. S17



Supplemental Fig. S18