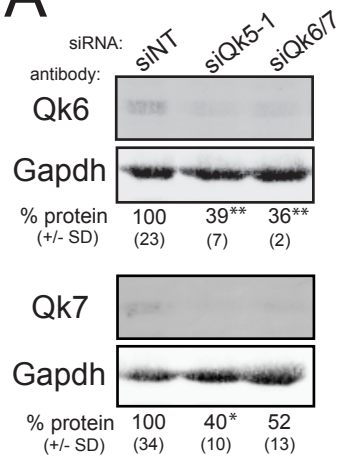
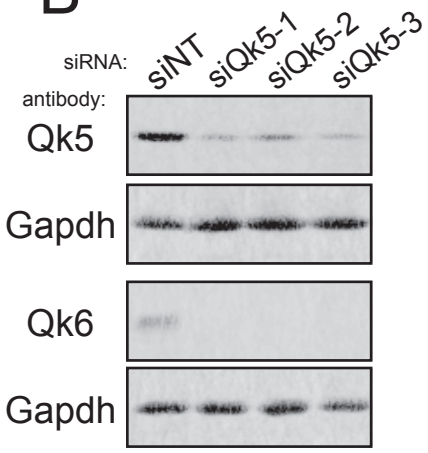
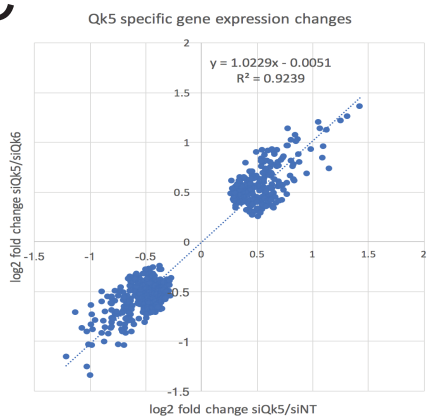
A



B

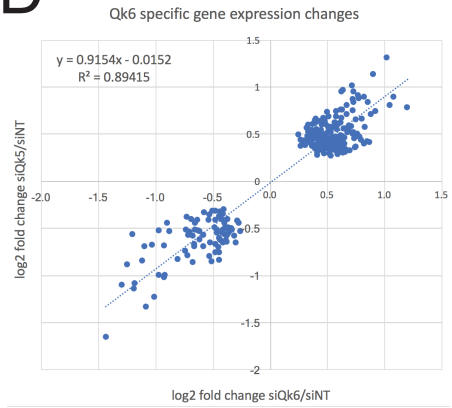


C



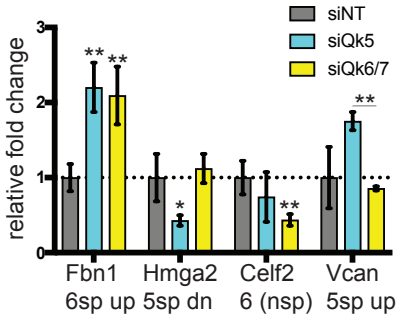
Among genes not significantly changing in siQk6/siNT:
319 down regulated, 225 up regulated upon loss of Qk5

D

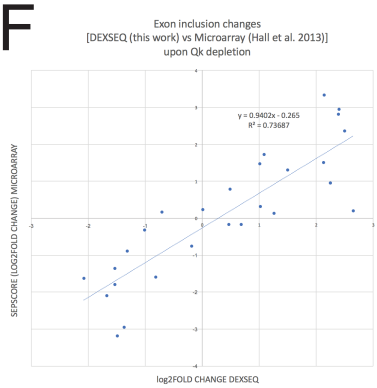


Among genes not significantly changing in siQk5/siQk6:C
86 down regulated, 186 up regulated upon loss of Qk6

E



F

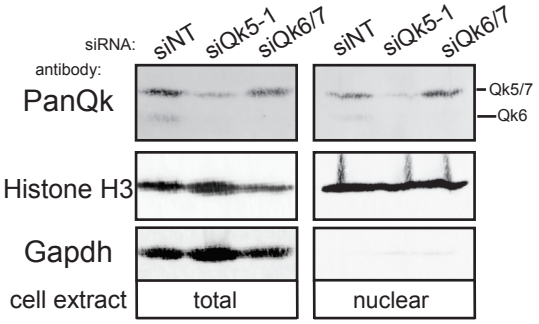


G

Representation of CLIP peaks
relative to expressed genes that do not change upon Qk depletion

Loss of:	gene response:	Qk clip peaks are:	pval
Qk5	up	Enriched	4.4e –6
Qk5	down	Depleted	0.02
Qk6	up	Enriched	3.6e –10
Qk6	down	Not different	0.94

H



I

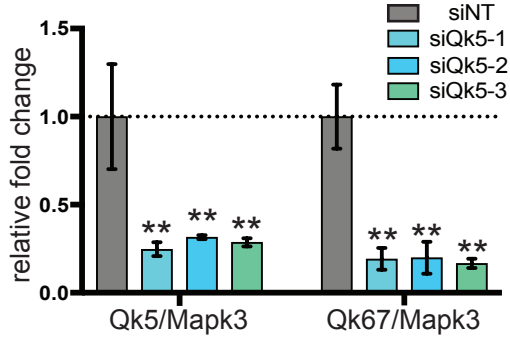


Figure S3 (supplemental to Figure 3): A. Western blots simultaneously probed with Qk6 and Gapdh (top) or Qk7 and Gapdh (bottom) antibodies from whole cell protein lysate from C2C12 myoblasts transfected with siNT, siQk5-1, and siQk6/7; mean percentage of protein abundance relative to siNT is shown below from three independent biological replicates, +/- standard deviation from the mean (** $p < 0.01$; * $p < 0.05$). B. Representative western blot simultaneously probed with Qk5 and Gapdh (top) or Qk6 and Gapdh (bottom) antibodies from whole cell protein extracted from C2C12 myoblasts transfected with siNT, siQk5-1, siQk5-2, and siQk5-3. C. Scatter plot and summary of Qk5-specific RNA abundance changes determined by DESEQ2 analysis of RNA-seq data; y-axis is $\log_2$ fold change of transcripts whose abundance significantly changes under siQk5 treatment relative to siQk6/7 treatment and x-axis is $\log_2$ fold change of transcripts whose abundance significantly changes under siQk5 treatment relative to control siNT treatment, with summary below. D. Scatter plot as in C. but depicting Qk6/7-specific RNA abundance changes; y-axis is $\log_2$ fold change of transcripts whose abundance significantly changes under siQk5 treatment relative to control siNT treatment and x-axis is $\log_2$ fold change of transcripts whose abundance significantly changes under siQk6/7 treatment relative to siNT treatment, with summary below. E. RT-qPCR validation of RNA abundance changes identified by RNA-seq for Fbn1 (Qk6 specific), Hmga2 (Qk5 specific), Celf2 (Qk6 specific), and Vcan (Qk5 specific). F. Scatter plot comparing splicing changes identified here by DEXSEQ analysis of RNA-seq of siQk5 relative to control siNT to splicing changes identified by splicing sensitive microarray of siRNA targeting all Qk isoforms relative to control siNT. G. Correlation of iCLIP peaks with isoform-specific RNA abundance changes identified by RNA-seq described in Fig S3C and S3D. H. Representative western blot of protein lysates from whole cell extract (WCE, left) or nuclear fraction (nuclear, right) C2C12 myoblasts transfected with siNT, siQk5-1, and siQk6/7 probed with antibodies against PanQk,

histone H3, and Gapdh. I. RT-qPCR analysis of RNA extracted from C2C12 myoblast cultures transfected with siNT, siQk5-1,siQk5-2, or siQk5-3 for Qk5 (left) or Qk6/7 (right) RNA normalized to Mapk3 RNA and displayed as fold change relative to siNT; error bars show standard deviation from the mean using three independent biological replicates (** $p < 0.01$).