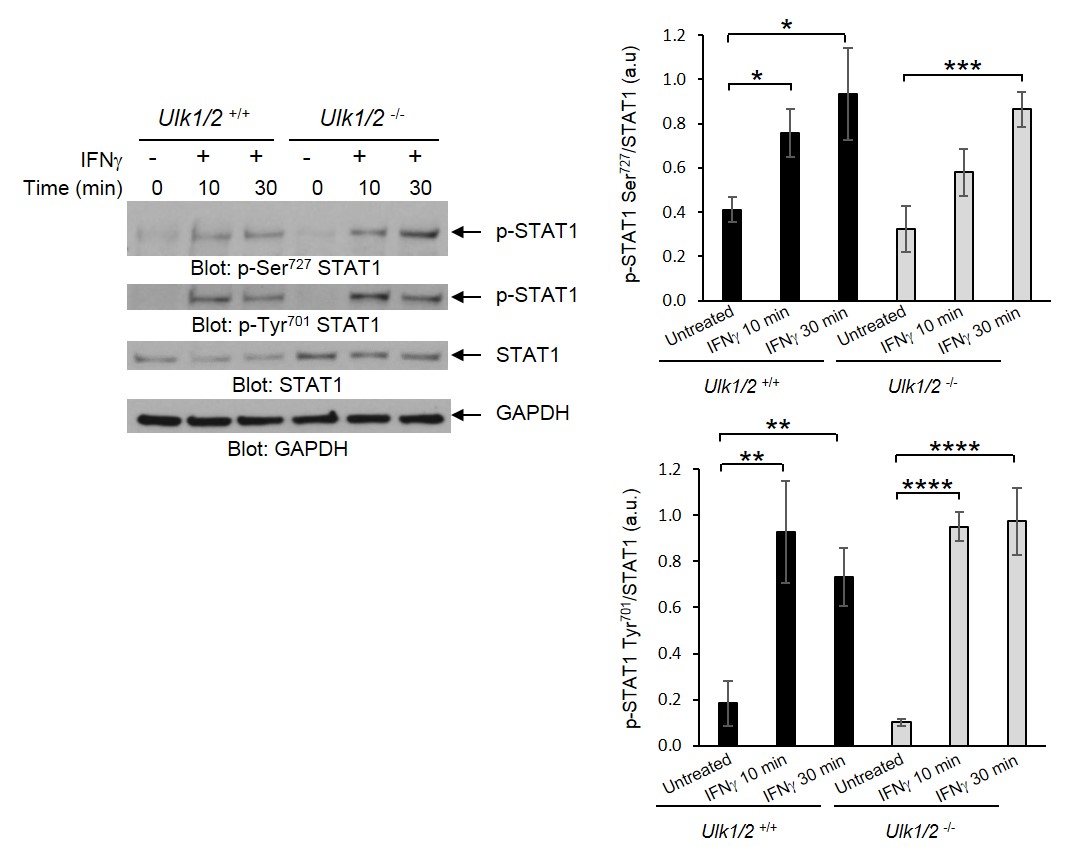
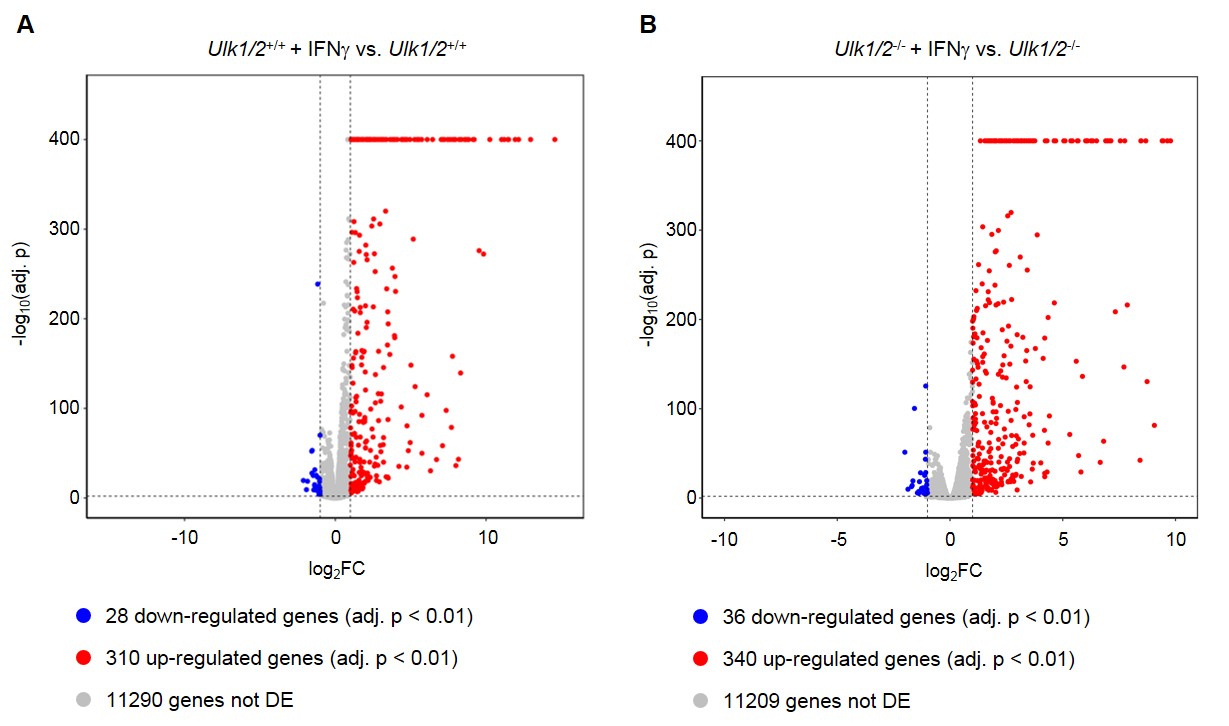
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**Fig. S1. ULK1/2 activity is not required for IFNγ-induced phosphorylation of STAT1.** Western blot analysis of pSTAT1 in lysates from *Ulk1/2*+/+ and *Ulk1/2*-/- MEFs treated with IFNγ for the indicated times. Blots (left) are representative of 4 independent experiments. Quantified band intensity values are means ± SEM from all experiments. \*P< 0.05, \*\*P< 0.01, \*\*\*P< 0.001, and \*\*\*\*P< 0.0001 by two-way ANOVA and post-hoc t-tests.



**Fig. S2.** **Effects of targeted disruption of *Ulk1/2* gene expression on IFNγ-dependent gene transcription.** **(A** to **B)** RNAseq analysis of transcript expression in *Ulk1/2*+/+ and *Ulk1/2*-/- MEFs treated with IFNγ, as indicated.Volcano plots of differentially expressed genes after IFNγ treatment from (A) *Ulk1/2*+/+ and (B) *Ulk1/2*-/- MEFs are from 4 biological replicates per condition.

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**Fig. S3.** **Genes differentially expressed in both *Ulk1/2*+/+ and *Ulk1/2*-/- MEFs after IFNγ treatment.** RNAseq analysis of transcript expression in *Ulk1/2*+/+ and *Ulk1/2*-/- MEFs treated with IFNγ, as indicated. Data are from 4 biological replicates per condition. Genes are listed in Table S3.



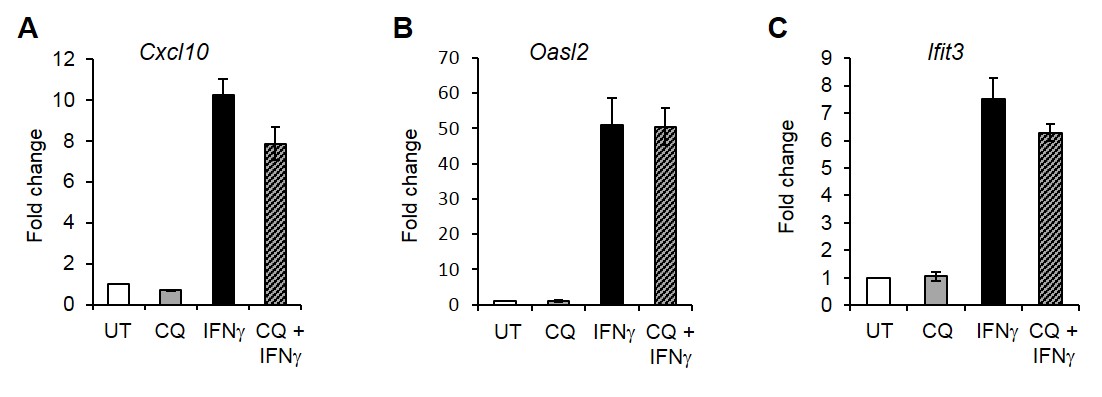
**Fig. S4.** **Genes differentially expressed only in *Ulk1/2*+/+ MEFs after IFNγ treatment.** RNAseq analysis of transcript expression in *Ulk1/2*+/+ and *Ulk1/2*-/- MEFs treated with IFNγ, as indicated. Data are from 4 biological replicates per condition. Genes are listed in Table S4.

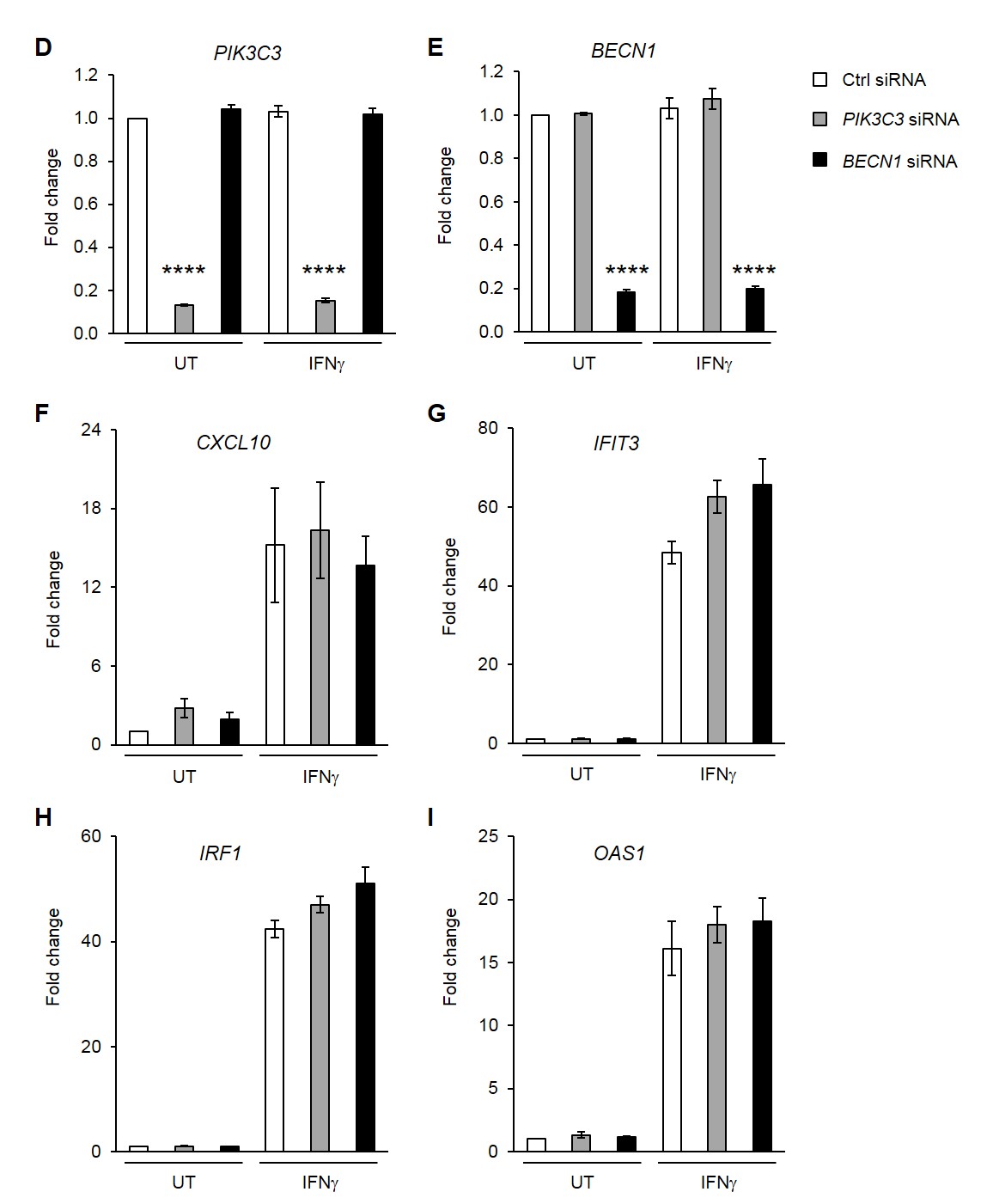


**Fig. S5. Genes differentially expressed only in *Ulk1/2*-/- MEFs after IFNγ treatment.** RNAseq analysis of transcript expression in *Ulk1/2*+/+ and *Ulk1/2*-/- MEFs treated with IFNγ, as indicated. Data are from 4 biological replicates per condition. Genes are listed in Table S5.

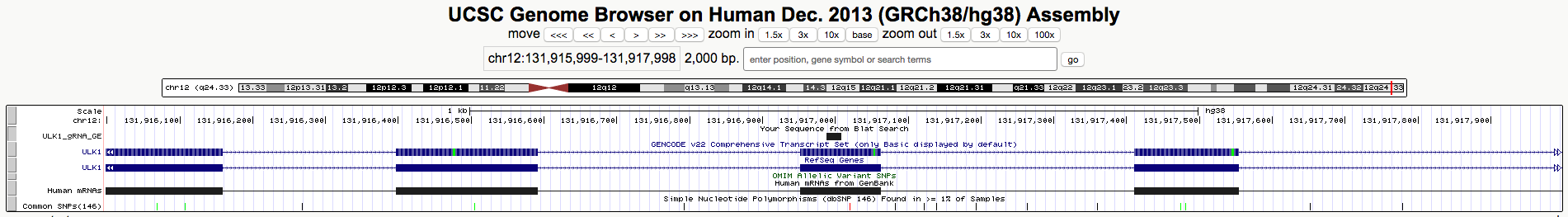
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**Fig. S6.** **Gene ontology analysis of IFNγ-dependent differentially expressed genes.** (**A**) Gene ontology analysis of the 268 differentially expressed genes identified in both *Ulk1/2*+/+ and *Ulk1/2*-/- MEFs after IFNγ treatment.(**B**) Gene ontology analysis of the 70 differentially expressed genes identified only in *Ulk1/2*+/+ MEFs. (**C**) Gene ontology analysis of the 108 differentially expressed genes identified only in *Ulk1/2*-/- MEFs. Data are from 4 biological replicates per condition.

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**Fig. S7. Inhibition of autophagy does not affect transcription of antiviral ISGs.** (**A** to **C**) qRT-PCR analysis of expression of the indicated genes in MEFs left untreated (UT) or treated with chloroquine (CQ) and/or IFNγ. Data are means ± SEM from 3 independent experiments. (**D** to **I**) qRT-PCR analysis of expression of the indicated genes in KT-1 cells transfected with control (Ctrl) siRNA, *PIK3C3*, or *BECN1*-specific siRNA and left untreated (UT) or treated with IFNγ. Data are means ± SEM from 3 independent experiments. \*\*\*\*P< 0.0001 by one-way ANOVA analysis followed by Tukey’s multiple comparisons test.



**Fig. S8. Genomic location for the ULK1 single-guide RNA in the human *ULK1* open reading frame** (red rectangle)**.**

**Supplementary Tables**

**Table S1. Putative ULK1 interactors in untreated versus IFNγ-treated KT-1 cells identified by mass spectrometry analysis.** Gene ontology groups of proteins found to interact with ULK1 under untreated, IFNγ-treated, and both conditions are shown.

**Table S2. Putative ULK1 interactors identified after IFNγ stimulation by mass spectrometry analysis.** Gene ontology groups of proteins found to interact with ULK1 only after IFNγ treatment are shown.

**Table S3. Genes differentially expressed in both *Ulk1/2*+/+ and *Ulk1/2*-/- MEFs after IFNγ treatment.** Log2 Fold change and FDR adjusted p values between IFNγ-treated and untreated samples for each genotypic group are presented. Data are from 4 biological replicates per condition.

**Table S4. Genes differentially expressed only in *Ulk1/2*+/+ MEFs after IFNγ treatment.** Log2 Fold change and FDR adjusted p values between IFNγ-treated and untreated *Ulk1/2*+/+ samples are presented. Data are from 4 biological replicates per condition.

**Table S5. Genes differentially expressed only in *Ulk1/2*-/- MEFs after IFNγ treatment.** Log2 Fold change and FDR adjusted p values between IFNγ-treated and untreated *Ulk1/2*-/- samples are presented. Data are from 4 biological replicates per condition.

**Table S6. Gene ontology analysis of differentially expressed genes identified in both *Ulk1/2*+/+ and *Ulk1/2*-/- MEFs after IFNγ treatment.** Genes, –log10 p values, enrichment, and z-scores are shown for the top 25 gene ontology groups.

**Table S7. Gene ontology analysis of differentially expressed genes identified only in *Ulk1/2*+/+ MEFs after IFNγ treatment.** Genes, –log10 p values, enrichment, and z-scores are shown for the top 25 gene ontology groups.

**Table S8. Gene ontology analysis of differentially expressed genes identified only in *Ulk1/2*-/- MEFs after IFNγ treatment.** Genes, –log10 p values, enrichment, and z-scores are shown for the top 25 gene ontology groups.