
Figures and figure supplements

A mammalian pseudogene lncRNA at the interface of inflammation and anti-inflammatory therapeutics

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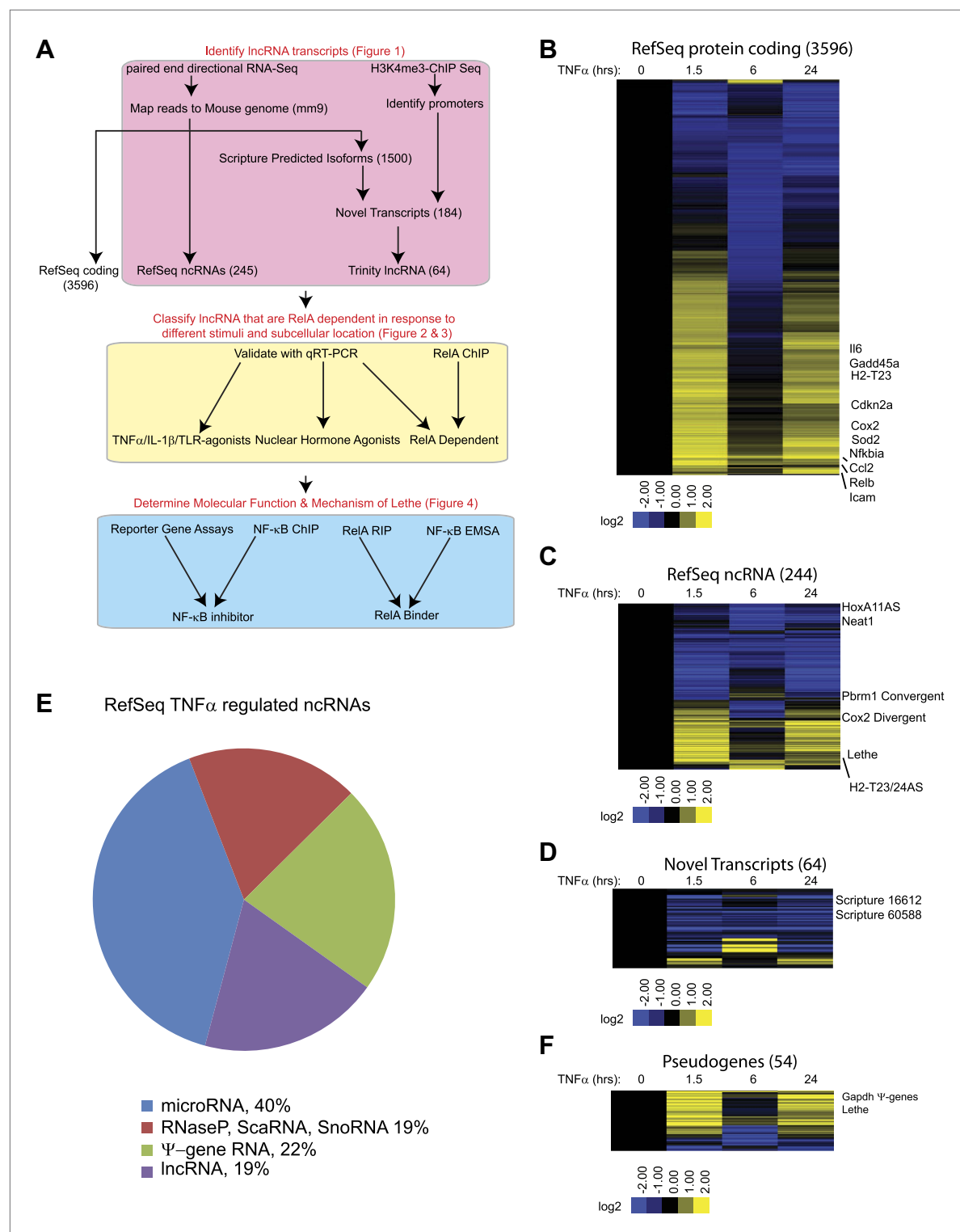


Figure 1. TNF α regulates the transcription of many coding and noncoding genes. **(A)** Workflow for strategy for discovery of NF- κ B regulated lncRNAs. **(B)** 3596 RefSeq protein coding genes are regulated by TNF α . Values are normalized to the 0 hr time point. **(C)** 244 RefSeq ncRNAs are regulated by TNF α . **(D)** 64 de novo lncRNAs are regulated by TNF α . **(E)** The fraction of all RefSeq ncRNAs for each class of transcript. **(F)** 54 pseudogene lncRNAs are regulated by TNF α .

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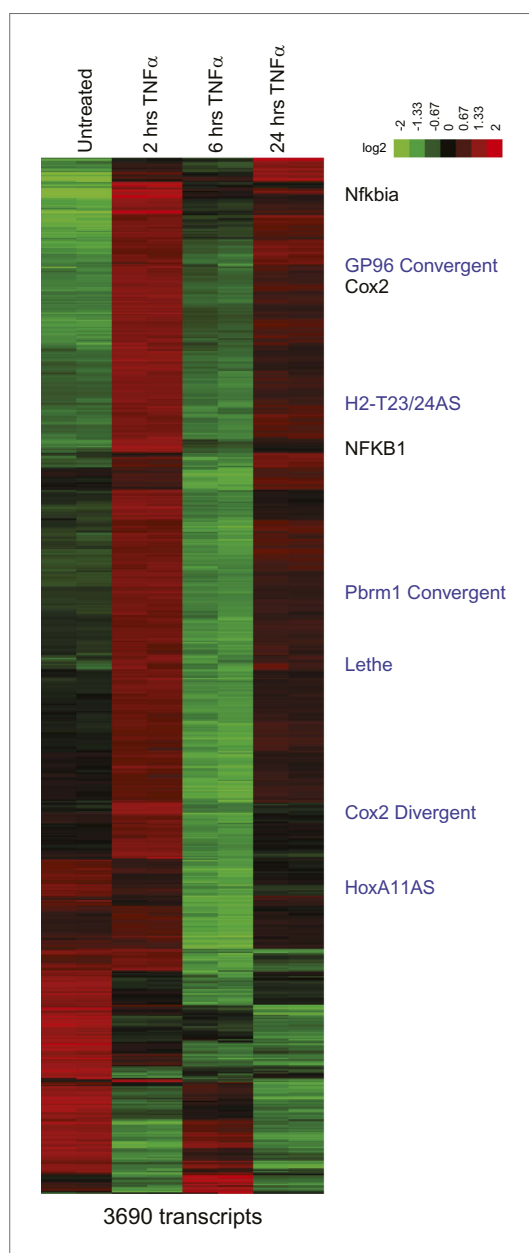


Figure 1—figure supplement 1. Heatmap of RefSeq genes. Mean centered heatmap of RefSeq protein coding genes and RefSeq lncRNAs.
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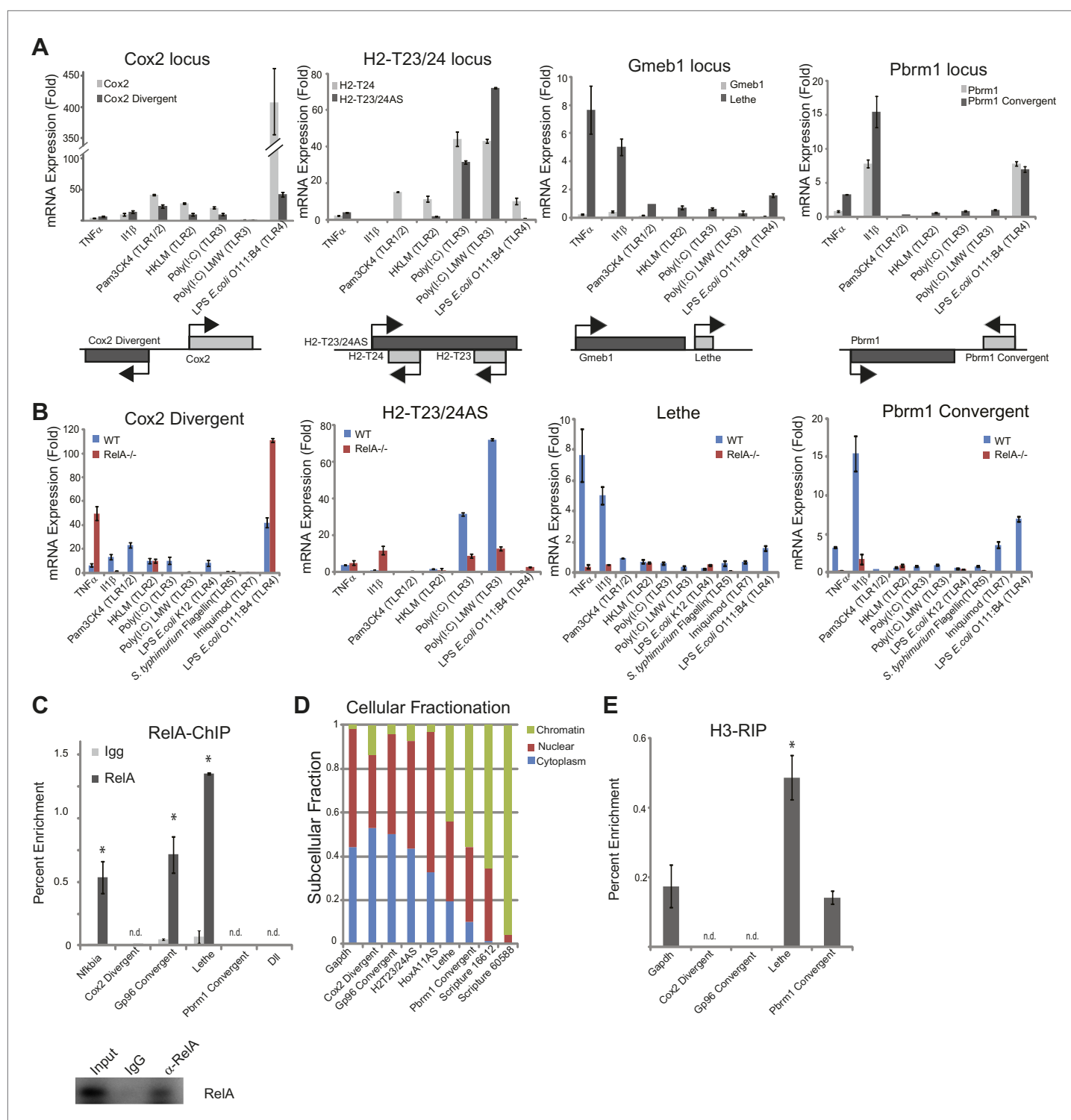


Figure 2. LncRNAs distinguish between different stimuli and are regulated by NF- κ B. **(A)** Validation of lncRNAs expression alongside the closest protein coding gene under a variety of different stimuli by qRT-PCR. Genomic organization is shown below. MEFs were treated with 20 ng/ml TNF α for 0 and 6 hr. Quantitative Taqman real time RT-PCR of the indicated RNAs is normalized to Actin levels (mean \pm SD). **(B)** LncRNAs are regulated by RelA. qRT-PCR in WT and RelA $^{-/-}$ littermate cells under a variety of different stimuli. MEFs were treated with 20 ng/ml TNF α for 0 and 6 hr. Quantitative Taqman real time RT-PCR of the indicated RNAs is normalized to Actin levels (mean \pm SD). **(C)** Endogenous RelA is recruited to the promoters of lncRNAs. MEFs were treated with 20 ng/ml TNF α for 0 and 15 min. ChIP with α -RelA antibodies was performed and RelA percent enrichment relative to input is shown (mean \pm SD, *Nkfbia*, $p < 0.0518$; *Gp96* Convergent, $p < 0.007$; *Lethe*, $p < 0.002$). **(D)** LncRNAs are found throughout the cell. Cellular fractionation was performed Figure 2. Continued on next page

Figure 2. Continued

and fraction found in the chromatin, nucleus and cytoplasm is shown. MEFs were treated with 20 ng/ml TNF α for 6 hr. Quantitative Taqman real time RT-PCR of the indicated RNAs is shown (mean \pm SD is shown). **(E)** LncRNAs are found on the chromatin. MEFs were treated with 20 ng/ml TNF α for 6 hr. RNA-IP with α -H3 antibodies was performed. RNA was isolated and Quantitative Taqman real time RT-PCR of the indicated RNAs is shown (mean \pm SD, Lethe $p < 0.004$).

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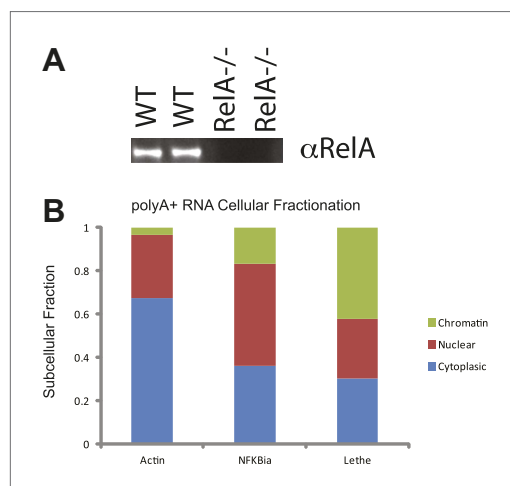


Figure 2—figure supplement 1. **(A)** Western analysis of RelA protein levels. **(B)** PolyA+ Lethe is found on the chromatin. Immunoblot of wildtype and RelA^{-/-} MEFs. Cellular fractionation was performed, total RNA was purified and polyA+ selection was performed. The fraction polyA+ RNA found in the chromatin, nucleus and cytoplasm is shown. MEFs were treated with 20 ng/ml TNF α for 6 hr. Quantitative Taqman real time RT-PCR of the indicated RNAs is shown (mean \pm SD is shown).

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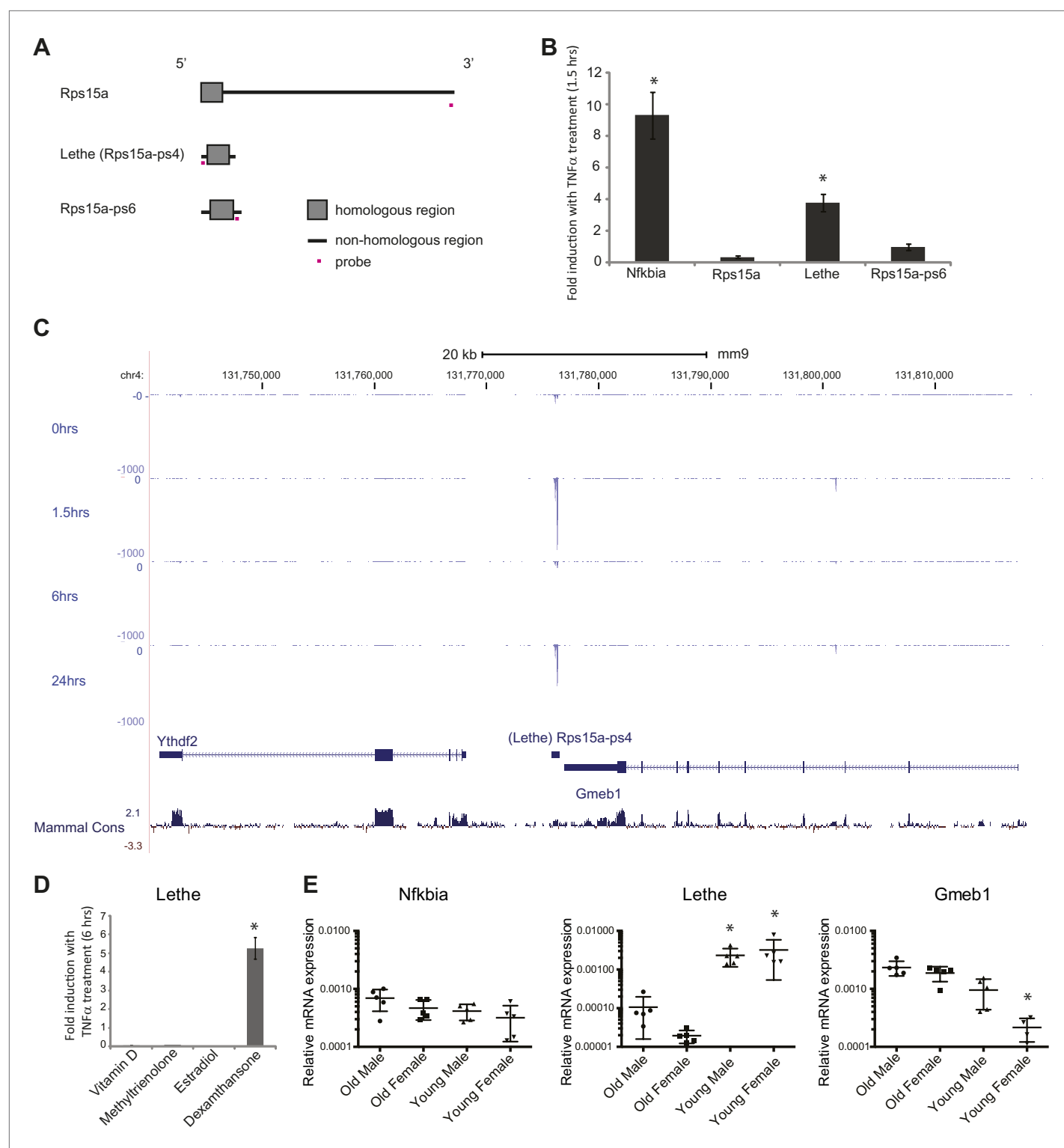


Figure 3. Lethe is a pseudogene lncRNAs that is regulated by NF- κ B, Glucocorticoid Receptor and in aging. **(A)** Gene structure, homology and Taqman probe design of *Rps15a* and pseudogene family members. **(B)** Lethe is induced by TNF α , but other family members are not. MEFs were treated with 20 ng/ml TNF α for 0 and 1.5 hr. Quantitative Taqman real time RT-PCR of the indicated RNAs is shown normalized to Actin levels (mean \pm SD, $p < 0.012$). **(C)** Genomic organization of Lethe with RNA-Seq data at time 0, 1.5, 6 and 24 hr post TNF α treatment. Lethe is located on mouse chromosome 4 between *Gmeb1* and *Ythdf2*. *Gmeb1* and *Ythdf2* are not induced by TNF α stimulation. **(D)** Lethe is induced by dexamethasone treatment, but not other nuclear hormone receptor agonists. MEFs were treated with either 10 nM vitamin D, 100 nM methyltrienolone, 100 nM estradiol, or 1 μ M dexamethasone. **(E)** Lethe and *Gmeb1* expression in aging. MEFs were treated with either 10 nM vitamin D, 100 nM methyltrienolone, 100 nM estradiol, or 1 μ M dexamethasone. Figure 3. Continued on next page

Figure 3. Continued

dexamethasone for 0 and 6 hr. Quantitative Taqman real time RT-PCR of the indicated RNAs is shown normalized to Actin levels (mean \pm SD, $p < 0.003$). (E) Lethe is down-regulated in aged mice. Lethe is expressed in young spleen from male and female mice. Five mice were used for each sex and time point. Quantitative Taqman real time RT-PCR of the indicated RNAs is shown normalized to Actin levels (mean \pm SD, Lethe $p < 0.001$, Gmeb1 $p < 0.003$). ANOVA analysis was performed to determine significance.

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CLUSTAL 2.1 multiple sequence alignment

Lethe	-----AGG--TAAACA---CCCAGAGCCCAGTTTGTCCAAGGGACCCCA	39
Rps15a-6	TCTGCTGGTGAAACAGAGGCGTAGATAGGTTTAAAGCCTAGGTAGTTAA--AACTCCA	58
	*** ** *	
Lethe	G---GGGA-----CTCTTCCTC-----TTCAA-	59
Rps15a-6	GATATGGGATGAGTGATGGTTAAGAGCACTGGCTGTTTCTCCACAAGACCCAGGTCAAT	118
	* **** *	
Lethe	----AGC-----CTGTTC-----TCTGTCCC-----TCTGTTC	84
Rps15a-6	TCCCAGCACATACATGGCTGCTCACACCTGTCTGTTCCAGGAGATCTAATGCTCTCTTT	178
	*** ** *	
Lethe	GGA CTGAGGAGG-----ACAT-----CAGAAA-----	106
Rps15a-6	GGCCTCTGGGGGCATCAAGCATGCACATGGGTACAGAAATATATGGTGGCAAAACATTC	238
	** * ** *	
Lethe	-----GAACTCAGAATCCGCAC---TCTTTCTGCCATCTTCCCTCGCCGCCACCATG	155
Rps15a-6	ATGCATATAAAATTAACCAACCAACACCTTCTGCCATCTTCTCGCCGCCACCATG	298
	** * * * *	
Lethe	GTGCGAATGAATGTTCTGGCGGATGCTCTCAGGAGCATCAACAACGCTGAGAAGAGAGGC	215
Rps15a-6	GTGTGAATGAATGTTCTGGCGGATGCTCTCAAGAGCATCAACAACGCTGAGAAGAGAGGC	358
	*** ****	
Lethe	AAACGCCAGGTCTCATCAGGCCATGTTCTAAAGTCATCGTTCGGTCTCTTAACCGTGATG	275
Rps15a-6	AAACGCCAGGTCTCATCAGGCCATGTTCTAAAGTCATCGTTCGGTCTCTTAACGTGTGATG	418

Lethe	GTGAAGCACGGGTACATTGGTGAATTCGAGATCATTGATGATCACAGAGCTGGGAAGATT	335
Rps15a-6	ATGAAGCACGGATACATTGGTGAATTCGAGATCATTGATGATCACAGAGCTGGGAAGATT	478

Lethe	GTTGTGAACCTCACAGGAAGGTGAACAAGTGTGGCGTTATAAGCCCTAGATTTGATGTT	395
Rps15a-6	GTTGTGAACCTCACAGGAAGGTGAACAAGTGTGGCGTTATAAGCCCTAGATTTGATGTT	538

Lethe	CAACTCAAAGACCTAGAGAAATGGCAGAACACCTGCTCCCTTCACGGCAGTTTGGCTTC	455
Rps15a-6	CAACTCAAAGACCTAGAGAAATGGCAGAACACCTGCTCCCTTCACGTACGTTTGGCCTC	598

Lethe	ATTGTGCTGACAACTAGGCTGGCATCATGAACCATGAAGAGGCAAGACGAAAACATACA	515
Rps15a-6	ATTGTGCTGACAACTCGGCTGGCATTATGGACCATGAAGAGGCAAGACGAAAACATACA	658

Lethe	GGAGGGAAAATCCTGGGATTCTTTTAAATGTAAAGCATAAATAAAAAGCCTTCGTGG	575
Rps15a-6	GGAGGGAAAATCCTGGGATTCTTTTAAATGTAAAGCATAAATAAAAAGCCTTTGTGG	718

Lethe	ACTGTGAAAAAAAAAAAAAAAAAGAACTCAGAACTCCTTGATCTACACTCCTCTCTGCATC	635
Rps15a-6	ACTGTGAAAAAAAAAAAAAAAA-----CCAAAACAACCAACAAAACCTCC-----CCAAACA	770

Lethe	ATCTTTTCAGCTCCTAAAAAGCCATAGTTTGATTCTCATGCTCTGCCACA-TTAGTAACT	694
Rps15a-6	AACCCCCCGAAACCAAGAACCGCAACCCAG-----ATACCCAGATGTAGTCTATAAT-	824
	* * * * *	
Lethe	TCC	697
Rps15a-6	---	

Figure 3—figure supplement 1. Alignment of Lethe with Rps15a-ps6. ClustalW2 alignment was performed on Lethe (Rps15a-ps4) and Rps15a-ps6.

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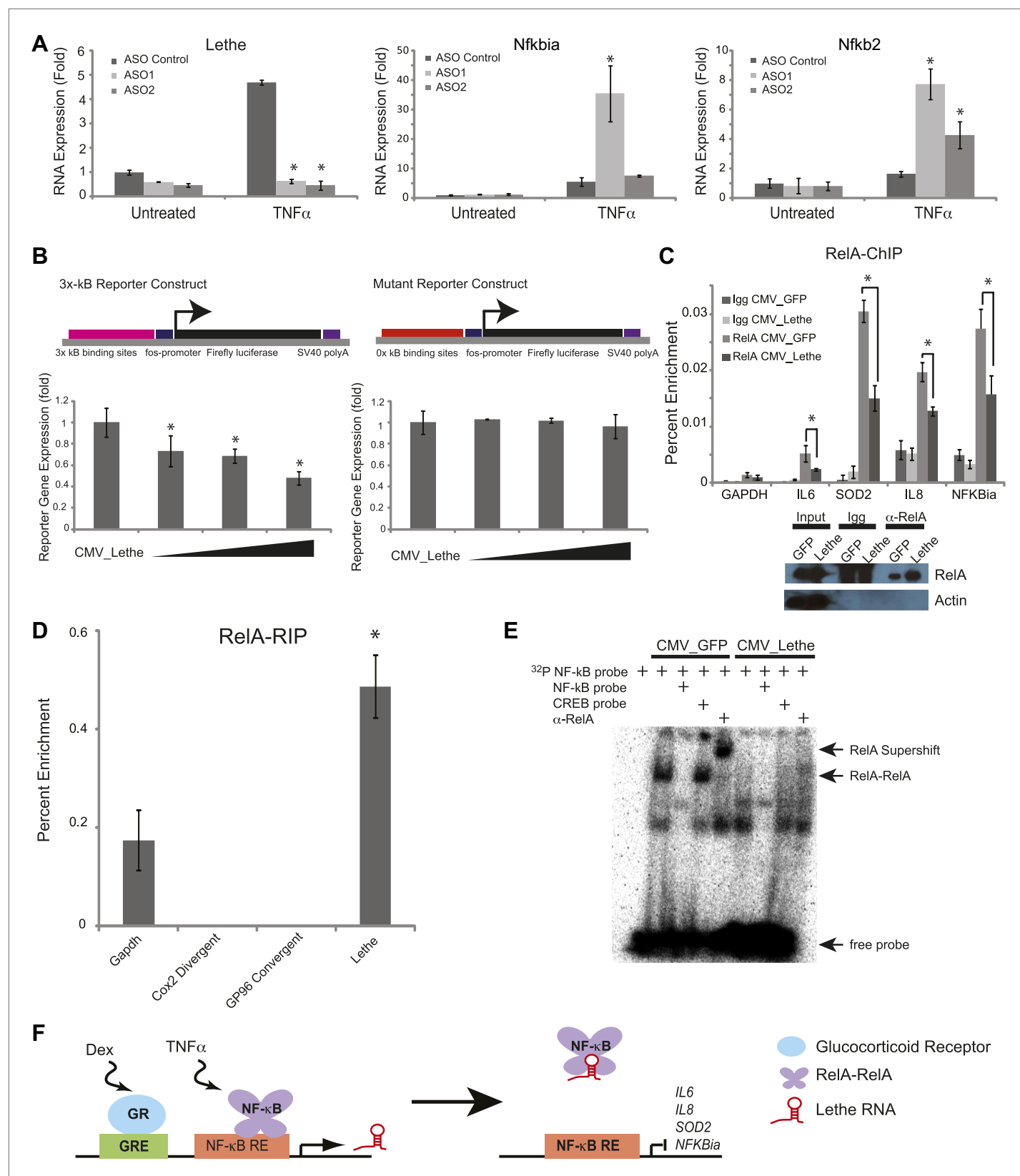


Figure 4. Lethe Binds to RelA and inhibits RelA occupancy of DNA. **(A)** Increased expression of NF- κ B regulated genes in Lethe knockdown cells. Quantitative Taqman real time RT-PCR of the indicated RNAs is shown normalized to Actin levels (mean \pm SD, $p < 0.05$ is shown) **(B)** Lethe inhibits TNF α Figure 4. Continued on next page

Figure 4. Continued

induced reporter gene expression. RLU of 3x- κ B reporter activity and mutant reporter activity (mean \pm SD, $p < 0.05$ is shown) in CMV_Lethe transfected 293T cells. Reporter constructs are diagrammed above. **(C)** Endogenous RelA recruitment to the promoters of target genes is reduced in the presence of Lethe. 293T expressing CMV_GFP or CMV_Lethe were treated with 20 ng/ml TNF α for 15 min. ChIP with α -RelA antibodies was performed and RelA percent enrichment relative to input is shown (mean \pm SD; *Il6*, $p < 0.033$; *Sod2*, $p < 0.001$; *Il8*, $p < 0.003$; *Nfkb1a*, $p < 0.015$). **(D)** Lethe binds to RelA. MEFs were treated with 20 ng/ml TNF α for 6 hr. RNA-IP with α -RelA antibodies was performed. RNA was isolated and Quantitative Taqman real time RT-PCR of the indicated RNAs is shown (mean \pm SD, $p < 0.020$). **(E)** Lethe expression blocks DNA binding of the RelA homodimer to its target. NF- κ B EMSA of GFP or Lethe transfected 293T nuclear extracts treated with 20 ng/ml TNF α for 15 min. Extracts were pretreated with unlabeled NF- κ B (specific) or CREB (nonspecific competitor), or α -RelA antibodies for 15 min prior to incubation with probe. **(F)** Model for Lethe regulation of gene expression. Upon addition of TNF α or dexamthasone, Lethe is transcribed. Lethe can then bind to RelA–RelA homodimers and block binding to other NF- κ B response elements, inhibiting NF- κ B.

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