

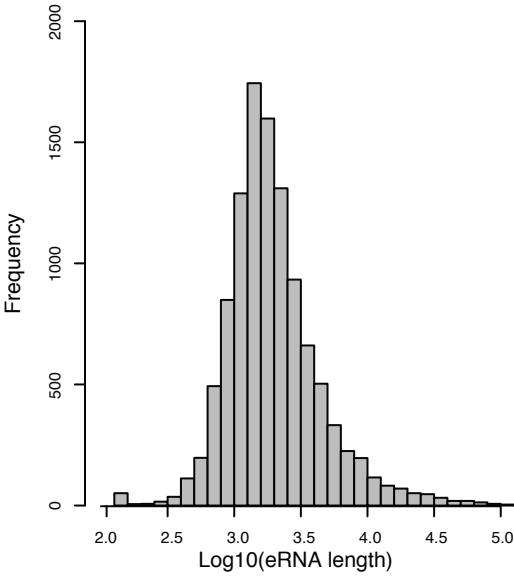
Supplemental Figures

Supplemental Figure 1. Differentially expressed genes and enhancer by SeV virus infection

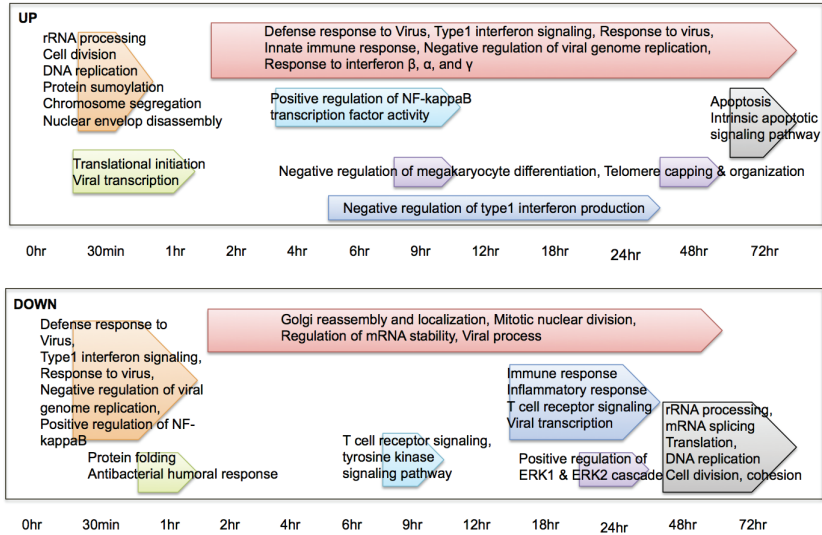
(a) Histogram of eRNA lengths is shown. X-axis represents the $\log_{10}$ of eRNA lengths and Y-axis represents the frequency. **(b)** Gene Ontology terms enriched by up-regulated genes (UP) and down-regulated gene (DOWN) are shown with spans of arrows showing duration of gene activation. **(c)** and **(d)** Representative genome browser track views of activated immune-related genes, MX1, ISG15 and CCL5, and activated enhancers. Epigenetic (DNase HS, H3K4me1 or H3K4me3 and H3K27ac) signals were normalized to the maximum levels in the regions. The y-axis of GRO-seq data represents normalized read density in reads per 10 million. **(e)** and **(f)** The results from t-distributed stochastic neighbor embedding (t-SNE) dimension-reduction analysis for mRNA and eRNA are shown. The plots are color-coded with blue and orange representing early and late time points, respectively. **(g)** K27ac enrichment level at the inducible enhancer with time course after virus infection is shown.

Supplemental Figure S1

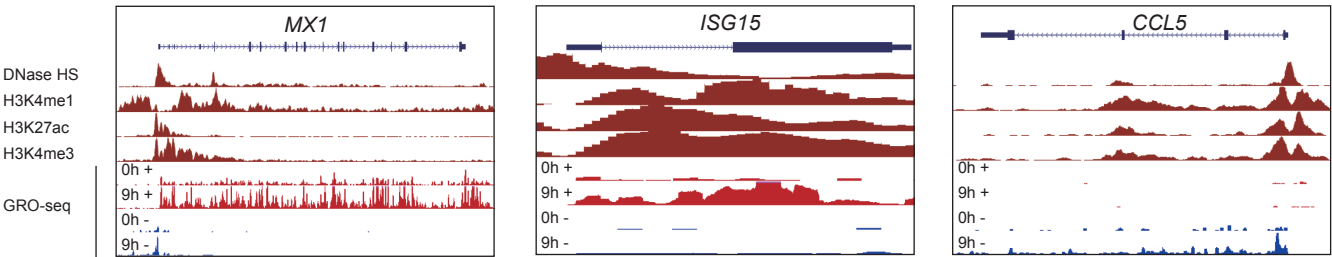
A. distribution of eRNA length



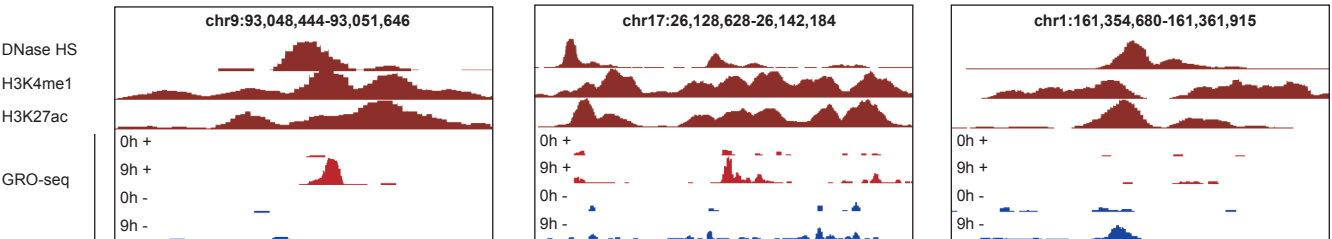
B. functional analysis of DE genes across time course



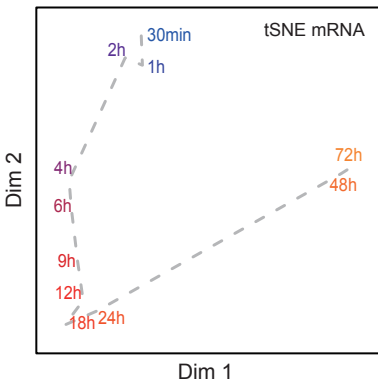
C. examples of SeV-induced genes



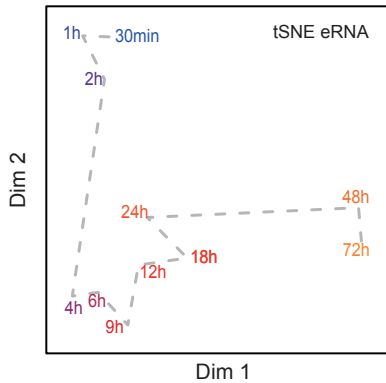
D. examples of SeV-induced eRNA



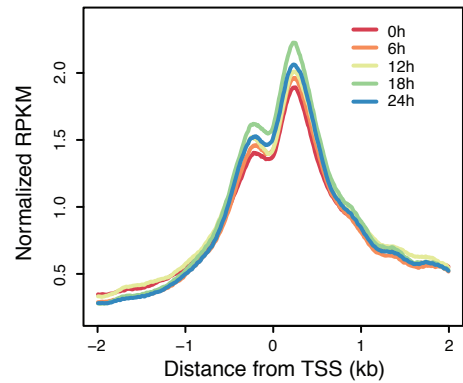
E. tSNE mRNA



F. tSNE eRNA



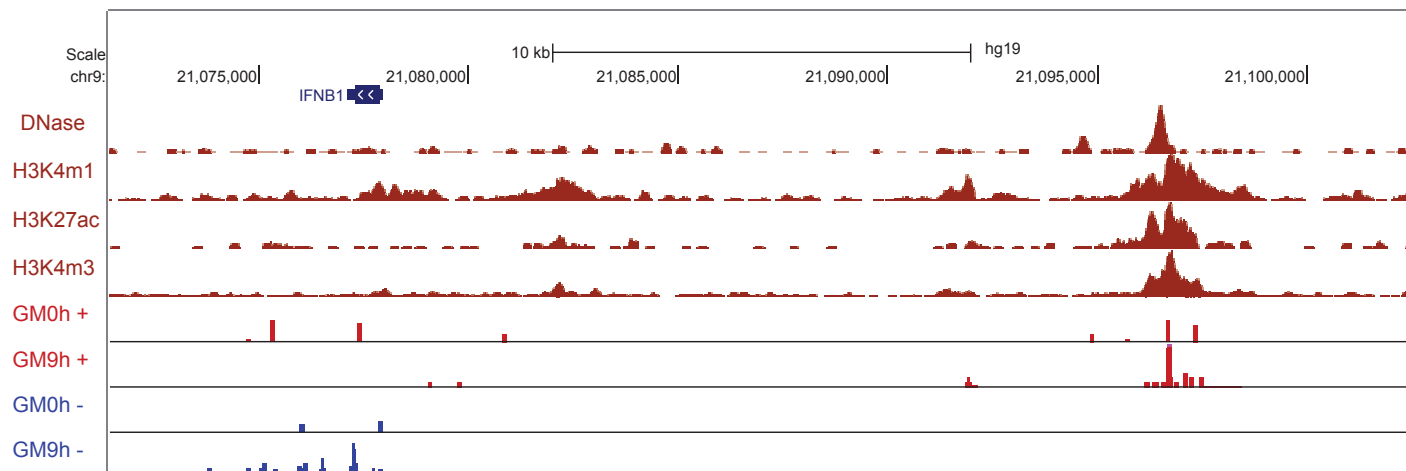
G. K27Ac enrichment at induced enhancer



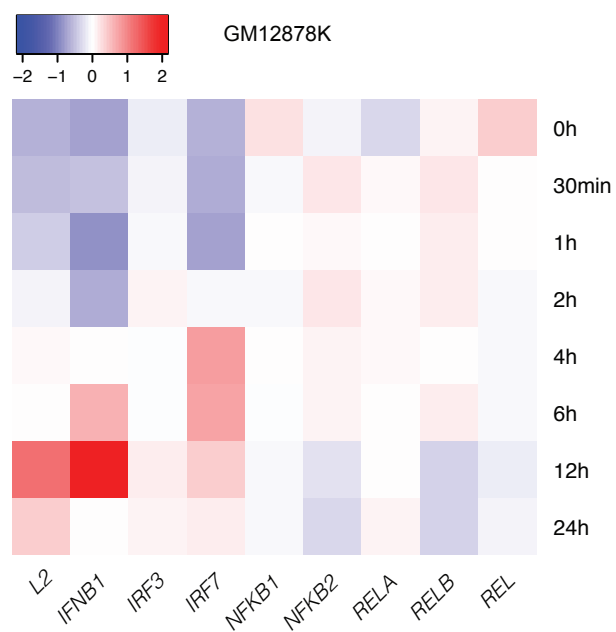
Supplemental Figure 2. *L2*, *IFNB1* enhancer and *IFNB1* transcriptional changes before (0h) and after virus infection (9h). **(a)** Genome browser track of *L2* and *IFNB1* is shown. Epigenetic (Sg1, H3K4me1/3 and H3K27ac) signals were normalized by the maximum levels in the regions. The Y-axis represents GRO-seq signal in reads per 10 million. **(b)** Heat map summarizes GRO-seq RPKM level of *L2* and *IFNB1* as well as its signal related genes, IRFs, NFκBs, and RELs through the incubation times from 0 hour to 24 hours after infection.

Supplemental Figure S2

A.



B.

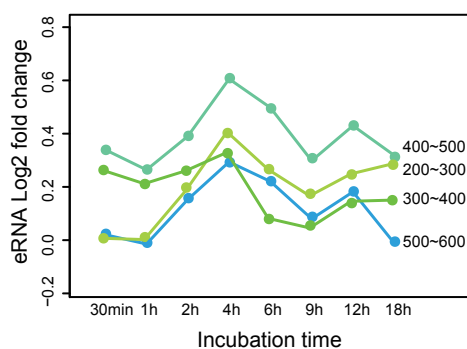
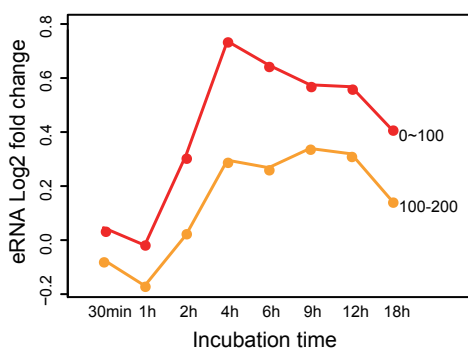


Supplemental Figure 3. Prediction of virus inducible enhancer-promoter (EP) pairs. (a)

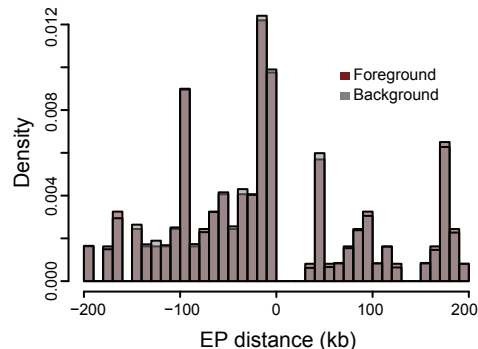
Average logarithm fold-changes of expressed enhancers near inducible genes, divided into two groups according to EP distance are shown: 0-100kb, 100-200kb, 200-300kb, 300-400kb, 400-500kb, and 500-600kb. **(b)** Distribution of EP distance between inducible (red) and background (grey) pairs is shown. **(c)** Average phastCon conservation scores of each mammal and vertebrate across inducible enhancer regions, relative to randomly selected background are shown. **(d)** Percentage of inducible human EP pairs (EP distance < 500kb) that co-exist in other species is shown. **(e)** Violin plots showing the logarithmic fold change values of enhancers at each time point after infection. Enhancers were divided into groups based on distances from inducible genes.

Supplemental Figure S3

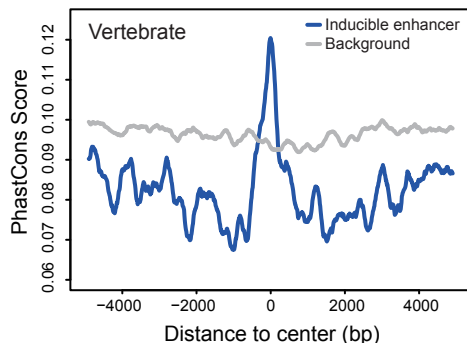
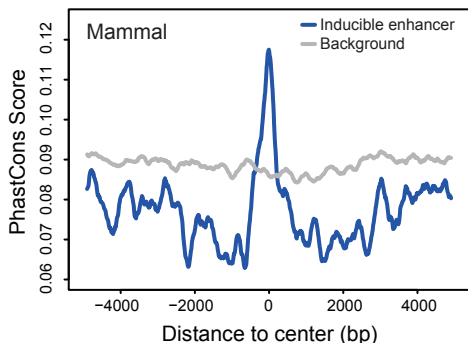
A



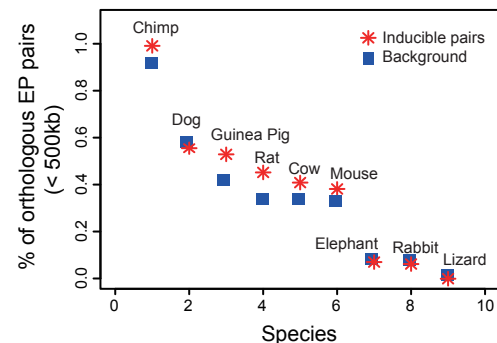
B



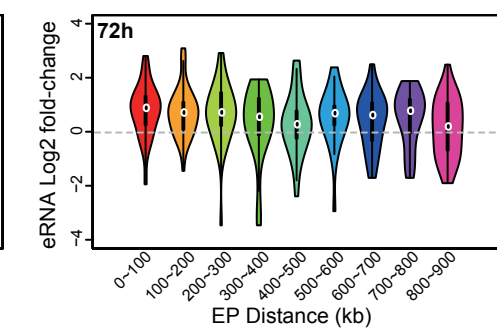
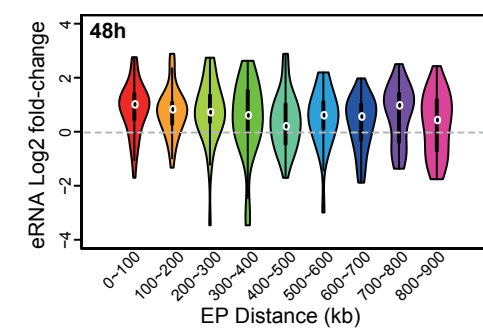
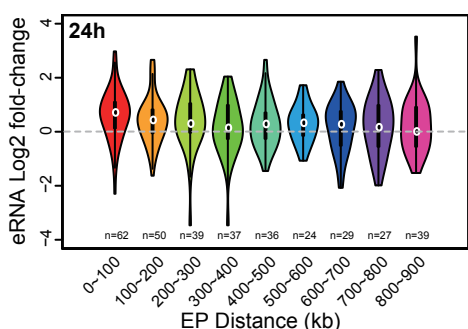
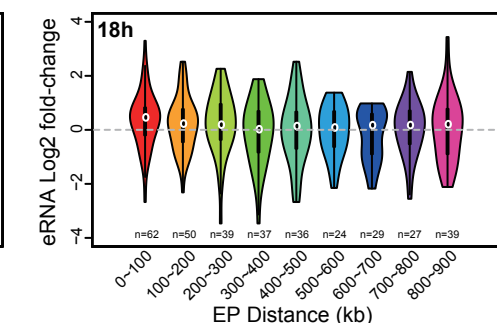
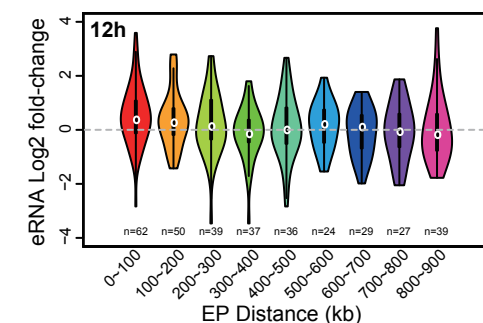
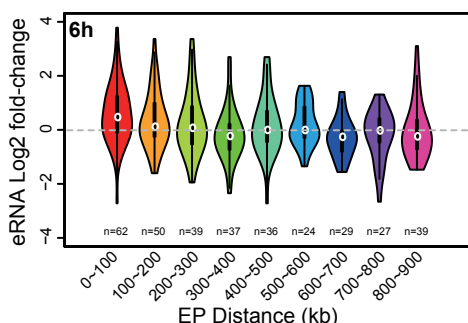
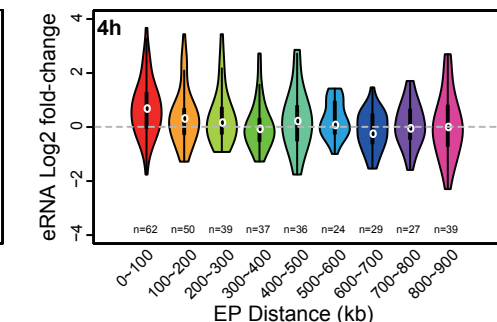
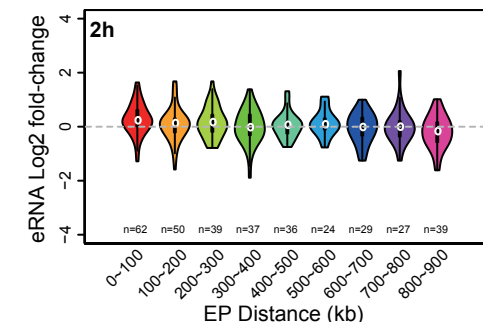
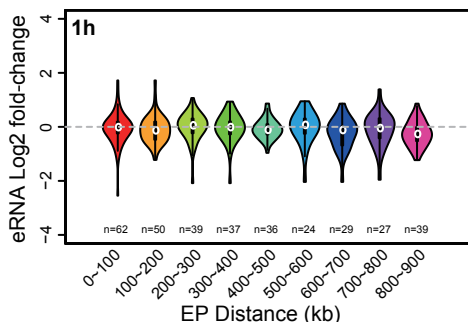
C



D



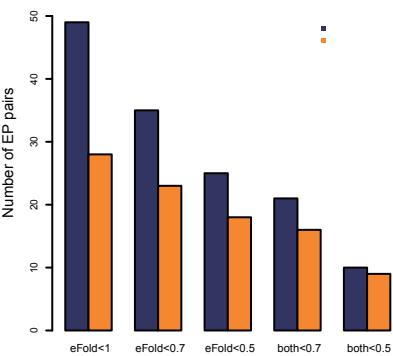
E



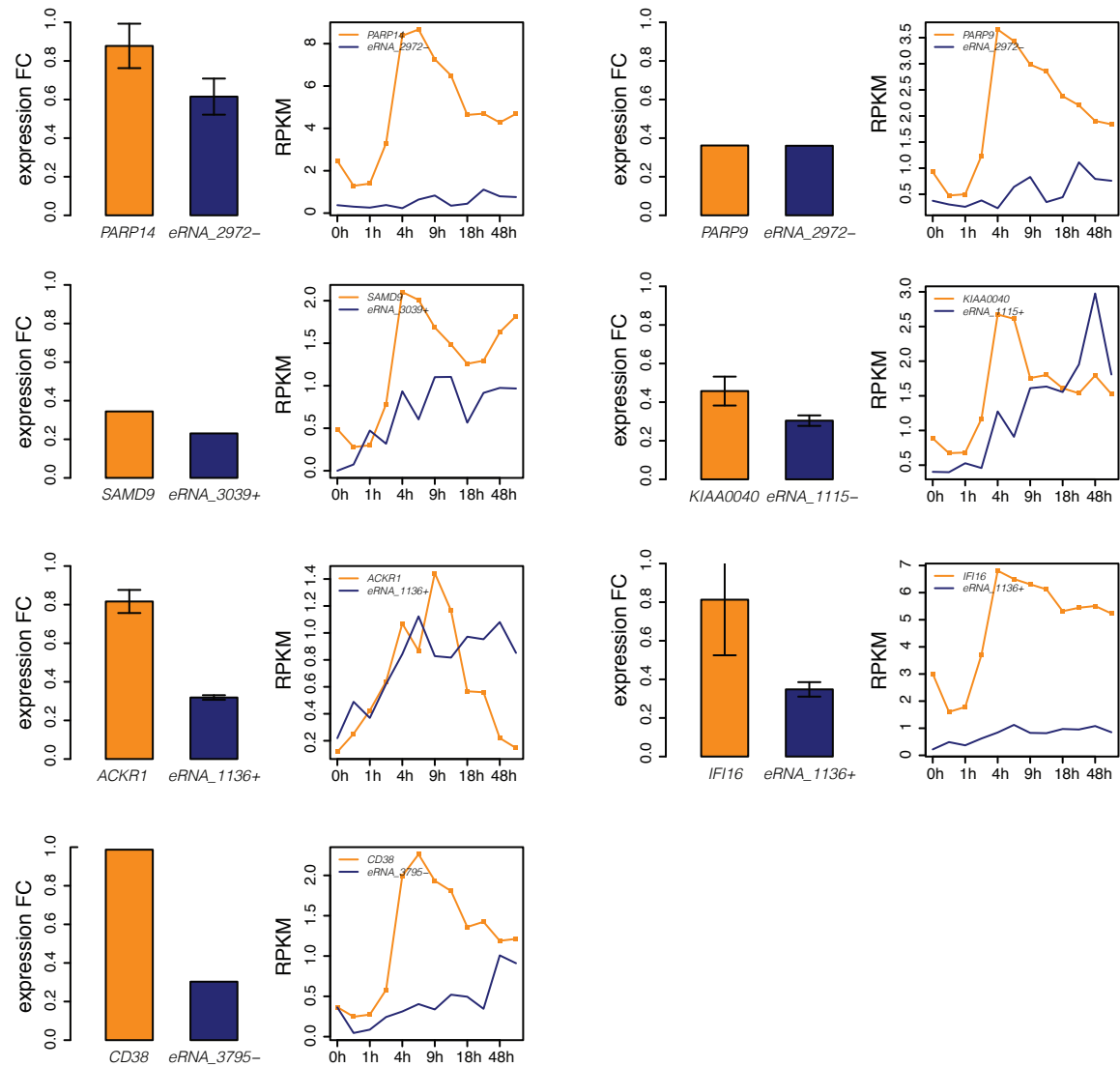
Supplemental Figure 4. Effects of eRNA KD on target gene transcription. Individual KD experiments of inducible EP pairs are shown. Barplots (left) show the ratio of eRNA (blue) / mRNA (orange) expression level before and after siRNA treatment. Expression profiles (right) show GRO-seq signal (RPKM) of eRNA (blue) / mRNA (orange) during virus incubation time.

Supplemental Figure S4

A eRNA knockdown experiments

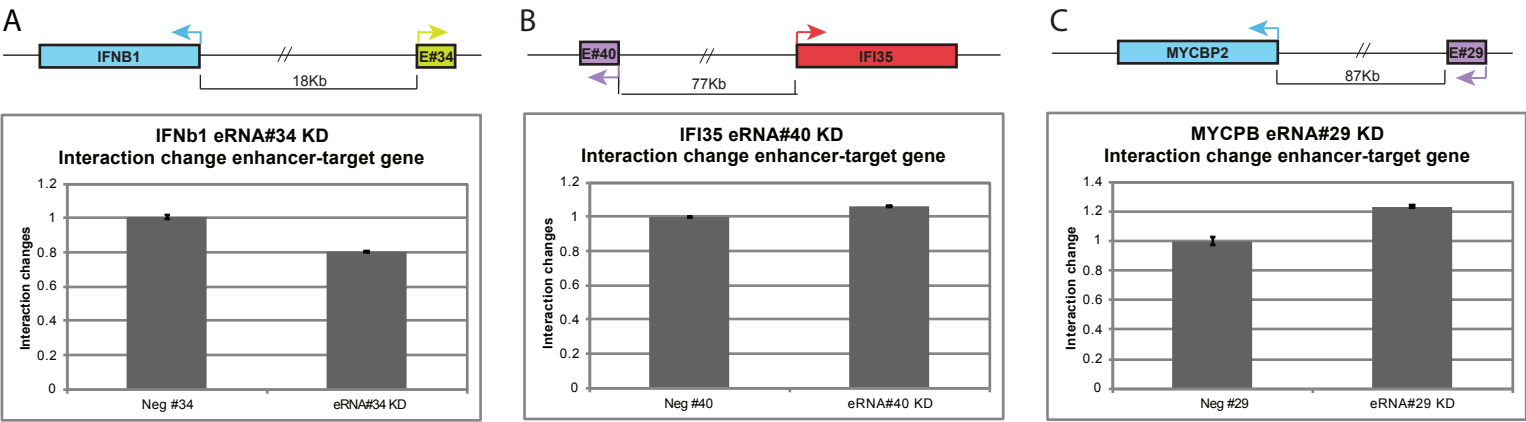


B



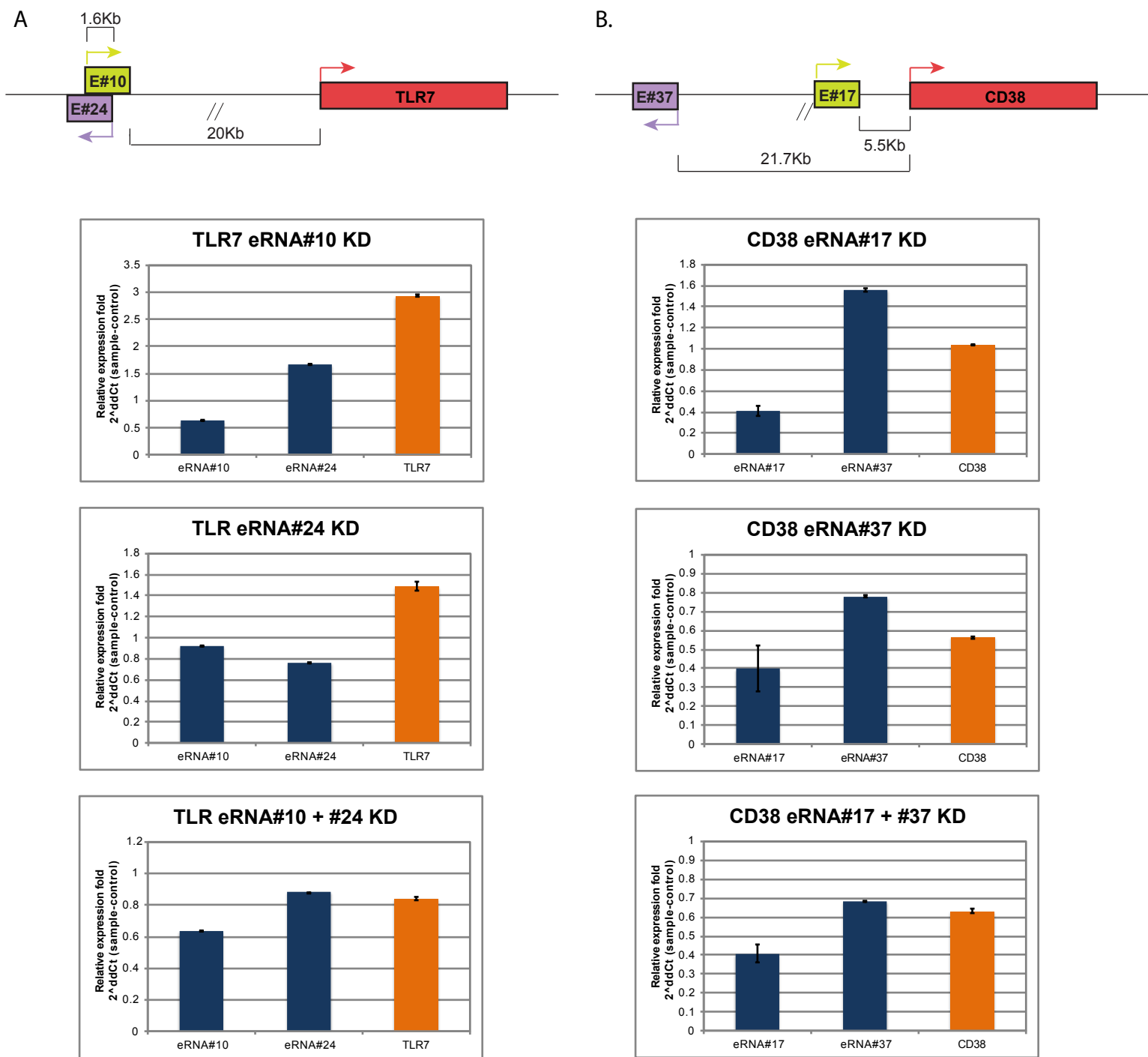
Supplemental Figure 5. eRNA KD effect on physical EP interaction. (a), (b), and(c) (Top)
Schematic diagrams of *IFNB1/IFI35/MYCBP2* and corresponding enhancer are shown. (Lower left)
Fold-change of 3C interaction between EPs after eRNA KD is shown, compared with negative controls.

Supplementary Figure 5



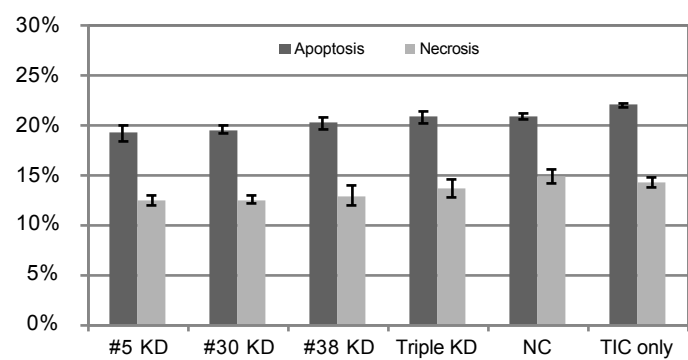
Supplemental Figure 6. Cases of genes with multiple enhancers. (a) and (b) Schematic diagram of *TLR7* and *CD38* and their nearby inducible enhancers is shown (top). Fold changes of eRNA (blue) / mRNA (orange) after individual and combined eRNA KD is plotted.

Supplementary Figure 6



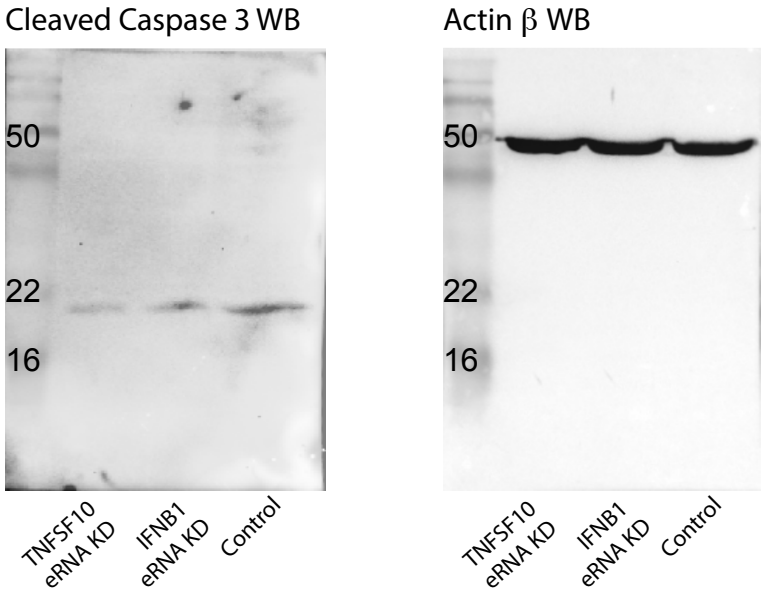
Supplemental Figure 7. eRNA KD and TIC10 treatment. Y-axis shows the fraction of apoptotic and necrotic cells after 48h TIC10 incubation, with single, triple or control eRNA KD.

Supplemental Figure S7



Supplemental Figure 8. Uncropped original view of the western blots in Fig 3C.

Supplemental Figure S8



Supplemental Tables

Table S1. All predicted induced eRNAs and their target genes. Target_genes (Refseq) column notes accession number of target genes paired to inducible enhancer. Enhancer_id column contains unique IDs for inducible enhancers identified. Target-gene (symbol) column notes the gene name assigned to the Refseq accession number. Enhancer_coord_hg19 column refers to the genomic coordinate of the inducible enhancers based on the hg19 build of the human genome.

Table_S1

All induced EP pairs passing our criteria

Target_gene (Refseq)	Enhancer_id	Target_gene (symbol)	Enhancer_coord_hg19
NM_002036	MetaEnhancer_1136_+	ACKR1	chr1 158975648 158977353
NM_001122951	MetaEnhancer_1136_+	ACKR1	chr1 158975648 158977353
NM_004833	MetaEnhancer_1136_+	AIM2	chr1 158975648 158977353
NM_001136540	MetaEnhancer_1799_-	APOL1	chr22 36805195 36806192
NM_001136540	MetaEnhancer_862_-	APOL1	chr22 36846877 36848115
NM_030882	MetaEnhancer_1799_-	APOL2	chr22 36805195 36806192
NM_145637	MetaEnhancer_1799_-	APOL2	chr22 36805195 36806192
NM_030641	MetaEnhancer_3137_-	APOL6	chr22 36030413 36031205
NM_174919	MetaEnhancer_2379_-	ARHGAP27	chr17 43433743 43435137
NM_001128616	MetaEnhancer_2422_+	ARHGEF3	chr3 56726327 56729181
NM_019555	MetaEnhancer_2422_+	ARHGEF3	chr3 56726327 56729181
NM_001731	MetaEnhancer_3101_+	BTG1	chr12 92586863 92587704
NM_001295	MetaEnhancer_258_-	CCR1	chr3 46149958 46152633
NM_001295	MetaEnhancer_1961_+	CCR1	chr3 46150916 46156022
NM_001775	MetaEnhancer_3795_-	CD38	chr4 15757373 15758209
NM_001775	MetaEnhancer_847_-	CD38	chr4 15767579 15773083
NM_001775	MetaEnhancer_1694_+	CD38	chr4 15773236 15774381
NM_001243794	MetaEnhancer_2191_+	CHST12	chr7 2439830 2441170
NM_172210	MetaEnhancer_3084_+	CSF1	chr1 110435830 110436993
NM_172212	MetaEnhancer_3084_+	CSF1	chr1 110435830 110436993
NM_000757	MetaEnhancer_3084_+	CSF1	chr1 110435830 110436993
NM_138287	MetaEnhancer_2972_-	DTX3L	chr3 122380136 122380883
NM_001034194	MetaEnhancer_2326_-	EXOSC9	chr4 122708957 122710268
NM_001034194	MetaEnhancer_1507_-	EXOSC9	chr4 122714858 122717023
NM_001034194	MetaEnhancer_1473_+	EXOSC9	chr4 122716718 122718546
NM_153230	MetaEnhancer_2571_-	FBXO39	chr17 6842901 6843791
NM_014824	MetaEnhancer_94_+	FCHSD2	chr11 72864171 7288511
NM_002053	MetaEnhancer_1625_+	GBP1	chr1 89546827 89547678
NM_052941	MetaEnhancer_1625_+	GBP4	chr1 89546827 89547678
NM_052941	MetaEnhancer_2172_+	GBP4	chr1 89739974 89742358
NM_001206567	MetaEnhancer_1136_+	IFI16	chr1 158975648 158977353
NM_002038	MetaEnhancer_1613_-	IFI6	chr1 28014868 28016573
NM_001270927	MetaEnhancer_2029_-	IFIT1	chr10 91052142 91055958
NM_001270927	MetaEnhancer_3024_+	IFIT1	chr10 91055858 91057638
NM_001547	MetaEnhancer_4002_-	IFIT2	chr10 90922933 90923624
NM_001547	MetaEnhancer_1253_+	IFIT2	chr10 90923524 90925010
NM_001547	MetaEnhancer_2029_-	IFIT2	chr10 91052142 91055958
NM_001547	MetaEnhancer_3024_+	IFIT2	chr10 91055858 91057638
NM_001289758	MetaEnhancer_4002_-	IFIT3	chr10 90922933 90923624
NM_001031683	MetaEnhancer_4002_-	IFIT3	chr10 90922933 90923624

Table_S1

NM_001289758	MetaEnhancer_1253_+	IFIT3	chr10 90923524 90925010
NM_001031683	MetaEnhancer_1253_+	IFIT3	chr10 90923524 90925010
NM_001289758	MetaEnhancer_2029_-	IFIT3	chr10 91052142 91055958
NM_001031683	MetaEnhancer_2029_-	IFIT3	chr10 91052142 91055958
NM_001289758	MetaEnhancer_3024_+	IFIT3	chr10 91055858 91057638
NM_001031683	MetaEnhancer_3024_+	IFIT3	chr10 91055858 91057638
NM_012420	MetaEnhancer_2029_-	IFIT5	chr10 91052142 91055958
NM_012420	MetaEnhancer_3024_+	IFIT5	chr10 91055858 91057638
NM_003641	MetaEnhancer_1268_+	IFITM1	chr11 188083 189410
NM_003641	MetaEnhancer_1341_-	IFITM1	chr11 347562 351028
NM_003641	MetaEnhancer_230_-	IFITM1	chr11 353806 356185
NM_006435	MetaEnhancer_1268_+	IFITM2	chr11 188083 189410
NM_006435	MetaEnhancer_1341_-	IFITM2	chr11 347562 351028
NM_006435	MetaEnhancer_230_-	IFITM2	chr11 353806 356185
NM_002176	MetaEnhancer_1571_+	IFNB1	chr9 21096515 21098279
NM_002198	MetaEnhancer_250_-	IRF1	chr5 131828856 131832505
NM_002198	MetaEnhancer_372_+	IRF1	chr5 131831379 131847154
NM_002163	MetaEnhancer_2143_+	IRF8	chr16 85922550 85923645
NM_002163	MetaEnhancer_259_+	IRF8	chr16 86028925 86034443
NM_005547	MetaEnhancer_3423_+	IVL	chr1 152844459 152845369
NM_005547	MetaEnhancer_2511_+	IVL	chr1 152940836 152941593
NM_001162895	MetaEnhancer_633_-	KIAA0040	chr1 175173105 175173615
NM_001162893	MetaEnhancer_633_-	KIAA0040	chr1 175173105 175173615
NM_001162895	MetaEnhancer_1625_-	KIAA0040	chr1 175201951 175206691
NM_001162893	MetaEnhancer_1625_-	KIAA0040	chr1 175201951 175206691
NM_001162895	MetaEnhancer_3581_-	KIAA0040	chr1 175255261 175256747
NM_001162893	MetaEnhancer_3581_-	KIAA0040	chr1 175255261 175256747
NM_001162895	MetaEnhancer_1115_+	KIAA0040	chr1 175256708 175258040
NM_001162893	MetaEnhancer_1115_+	KIAA0040	chr1 175256708 175258040
NM_002308	MetaEnhancer_606_-	LGALS9	chr17 26131567 26137792
NM_002308	MetaEnhancer_211_+	LGALS9	chr17 26135260 26137784
NM_002308	MetaEnhancer_421_+	LGALS9	chr17 26137777 26140602
NM_002432	MetaEnhancer_1136_+	MNDA	chr1 158975648 158977353
NM_013262	MetaEnhancer_3166_+	MYLIP	chr6 15989743 15990881
NM_022750	MetaEnhancer_1844_+	PARP12	chr7 139910100 139913318
NM_017554	MetaEnhancer_2972_-	PARP14	chr3 122380136 122380883
NM_001146102	MetaEnhancer_2972_-	PARP9	chr3 122380136 122380883
NM_001146104	MetaEnhancer_2972_-	PARP9	chr3 122380136 122380883
NM_001146103	MetaEnhancer_2972_-	PARP9	chr3 122380136 122380883
NM_001146106	MetaEnhancer_2972_-	PARP9	chr3 122380136 122380883
NM_021105	MetaEnhancer_4023_-	PLSCR1	chr3 146268426 146269080
NM_002787	MetaEnhancer_1544_-	PSMA2	chr7 43110543 43112396
NM_006871	MetaEnhancer_844_-	RIPK3	chr14 24741839 24743689

Table_S1

NM_001193307	<i>MetaEnhancer_3039_+</i>	<i>SAMD9</i>	chr7 92666321 92666833
NM_001303496	<i>MetaEnhancer_3039_+</i>	<i>SAMD9L</i>	chr7 92666321 92666833
NM_015474	<i>MetaEnhancer_1375_-</i>	<i>SAMHD1</i>	chr20 35493353 35495639
NM_015295	<i>MetaEnhancer_510_-</i>	<i>SMCHD1</i>	chr18 2634970 2637532
NM_015295	<i>MetaEnhancer_730_-</i>	<i>SMCHD1</i>	chr18 2637665 2641759
NM_013306	<i>MetaEnhancer_2509_+</i>	<i>SNX15</i>	chr11 64918212 64918934
NM_001308205	<i>MetaEnhancer_2826_+</i>	<i>SSR3</i>	chr3 156323933 156325284
NM_001308204	<i>MetaEnhancer_2826_+</i>	<i>SSR3</i>	chr3 156323933 156325284
NM_001308197	<i>MetaEnhancer_2826_+</i>	<i>SSR3</i>	chr3 156323933 156325284
NM_001308205	<i>MetaEnhancer_2114_+</i>	<i>SSR3</i>	chr3 156361733 156363160
NM_001308204	<i>MetaEnhancer_2114_+</i>	<i>SSR3</i>	chr3 156361733 156363160
NM_001308197	<i>MetaEnhancer_2114_+</i>	<i>SSR3</i>	chr3 156361733 156363160
NM_001308205	<i>MetaEnhancer_3846_+</i>	<i>SSR3</i>	chr3 156374076 156375609
NM_001308204	<i>MetaEnhancer_3846_+</i>	<i>SSR3</i>	chr3 156374076 156375609
NM_001308197	<i>MetaEnhancer_3846_+</i>	<i>SSR3</i>	chr3 156374076 156375609
NM_016562	<i>MetaEnhancer_341_-</i>	<i>TLR7</i>	chrX 12859229 12863555
NM_016562	<i>MetaEnhancer_502_+</i>	<i>TLR7</i>	chrX 12862239 12865018
NM_001190942	<i>MetaEnhancer_2005_+</i>	<i>TNFSF10</i>	chr3 172194931 172195631
NM_001190943	<i>MetaEnhancer_2005_+</i>	<i>TNFSF10</i>	chr3 172194931 172195631
NM_001190942	<i>MetaEnhancer_3924_-</i>	<i>TNFSF10</i>	chr3 172263822 172264784
NM_001190943	<i>MetaEnhancer_3924_-</i>	<i>TNFSF10</i>	chr3 172263822 172264784
NM_001190942	<i>MetaEnhancer_3404_-</i>	<i>TNFSF10</i>	chr3 172295508 172299753
NM_001190943	<i>MetaEnhancer_3404_-</i>	<i>TNFSF10</i>	chr3 172295508 172299753
NM_001190942	<i>MetaEnhancer_734_-</i>	<i>TNFSF10</i>	chr3 172308346 172310066
NM_001190943	<i>MetaEnhancer_734_-</i>	<i>TNFSF10</i>	chr3 172308346 172310066
NM_001190942	<i>MetaEnhancer_116_+</i>	<i>TNFSF10</i>	chr3 172310235 172315325
NM_001190943	<i>MetaEnhancer_116_+</i>	<i>TNFSF10</i>	chr3 172310235 172315325
NM_001190942	<i>MetaEnhancer_811_-</i>	<i>TNFSF10</i>	chr3 172310301 172313961
NM_001190943	<i>MetaEnhancer_811_-</i>	<i>TNFSF10</i>	chr3 172310301 172313961
NM_025195	<i>MetaEnhancer_733_-</i>	<i>TRIB1</i>	chr8 126614669 126617093
NM_001282985	<i>MetaEnhancer_733_-</i>	<i>TRIB1</i>	chr8 126614669 126617093
NM_025195	<i>MetaEnhancer_1012_+</i>	<i>TRIB1</i>	chr8 126617345 126619945
NM_001282985	<i>MetaEnhancer_1012_+</i>	<i>TRIB1</i>	chr8 126617345 126619945
NM_030961	<i>MetaEnhancer_931_+</i>	<i>TRIM56</i>	chr7 100893754 100895706
NM_001301144	<i>MetaEnhancer_501_-</i>	<i>TRIM69</i>	chr15 45073139 45076695
NM_001301144	<i>MetaEnhancer_1609_+</i>	<i>TRIM69</i>	chr15 45076646 45078317
NM_020830	<i>MetaEnhancer_512_-</i>	<i>WDFY1</i>	chr2 224812655 224817461
NM_017523	<i>MetaEnhancer_2571_-</i>	<i>XAF1</i>	chr17 6842901 6843791
NM_001160417	<i>MetaEnhancer_1451_+</i>	<i>ZBP1</i>	chr20 56008141 56009316
NM_001160419	<i>MetaEnhancer_1451_+</i>	<i>ZBP1</i>	chr20 56008141 56009316

Table S2. Genomic information for eRNAs and target genes of induced EP pairs analyzed by 3C and siRNA knockdown experiments. Enhancer_ID column contains unique IDs (from Table S1) for annotated eRNAs and corresponding strand information. Whole region column contains genomic coordinates for the full eRNA transcript that was detected across the entire time course. High enrichment region column contains genomic coordinates of a region within eRNAs with high GRO-seq signal that was used for designing the siRNAs. eRNA length column denotes the length of the annotated eRNA encompassing the whole region of the annotated eRNAs. Target Genes column contains the gene name and DNA strand information for the assigned target genes. Whole region column contains genomic coordinate information of the target genes. First exon region columns contains coordinate of first exon region. Gene length column notes target gene length. All genomic coordinates and names are based on the hg19 build of the human genome.

Table_S2

eRNA and target genes of induced EP pairs

eRNA			Whole region			High enrichment region			eRNA length	Target Genes			Whole region			First exon region			Gene length
Enhancer_ID	strand		chr	start	end	chr	start	end		Gene name	strand		chr	start	end	chr	start	end	
<i>MetaEnhancer_1136_+</i>	+		chr1	157242272	157243977	chr1	157242460	157242561	1705	<i>ACKR1</i>	+		chr1	157440426	157442914	chr1	157440426	157441394	2488
<i>MetaEnhancer_258_-</i>	-		chr3	46124962	46127637	chr3	46127469	46127636	2675	<i>CCR1</i>	-		chr3	46218203	46224836	chr3	46224776	46224836	6633
<i>MetaEnhancer_1694_+</i>	+		chr4	15382334	15383479	chr4	15382463	15382581	1145	<i>CD38-1</i>	+		chr4	15389028	15459804	chr4	15389028	15389368	70776
<i>MetaEnhancer_3795_-</i>	-		chr4	15366471	15367307	chr4	15366966	15367155	836	<i>CD38-2</i>	+		chr4	15389028	15459804	chr4	15389028	15389368	70776
<i>MetaEnhancer_1136_+</i>	+		chr1	157242272	157243977	chr1	157242460	157242561	1705	<i>IFI16</i>	+		chr1	157246305	157291569	chr1	157246305	157246575	45264
<i>MetaEnhancer_1571_+</i>	+		chr9	21086515	21088279	chr9	21086643	21086794	1764	<i>IFNB1</i>	-		chr9	21067103	21067943	chr9	21067103	21067943	840
<i>MetaEnhancer_259_+</i>	+		chr16	84586426	84591944	chr16	84586456	84586609	5518	<i>IRF8</i>	+		chr16	84490274	84513712	chr16	84490274	84490330	23438
<i>MetaEnhancer_1115_+</i>	+		chr1	173523331	173524663	chr1	173523395	173523541	1332	<i>KIAA0040</i>	-		chr1	173392745	173428852	chr1	173428618	173428852	36107
<i>MetaEnhancer_1136_+</i>	+		chr1	157242272	157243977	chr1	157242460	157242561	1705	<i>MNDA</i>	+		chr1	157067791	157085894	chr1	157067791	157067971	18103
<i>MetaEnhancer_2972_-</i>	-		chr3	123862826	123863573	chr3	123863236	123863394	747	<i>PARP14</i>	+		chr3	123882361	123932377	chr3	123882361	123882607	50016
<i>MetaEnhancer_2972_-</i>	-		chr3	123862826	123863573	chr3	123863233	123863404	747	<i>PARP9</i>	-		chr3	123729449	123766213	chr3	123765975	123766213	36764
<i>MetaEnhancer_3039_+</i>	+		chr7	92504257	92504769	chr7	92504452	92504536	512	<i>SAMD9</i>	-		chr7	92566761	92585272	chr7	92585111	92585272	18511
<i>MetaEnhancer_502_+</i>	+		chrX	12772160	12774939	chrX	12772218	12772389	2779	<i>TLR7-1</i>	+		chrX	12795122	12818401	chrX	12795122	12795163	23279
<i>MetaEnhancer_341_-</i>	-		chrX	12769150	12773476	chrX	12771691	12771969	4326	<i>TLR7-2</i>	+		chrX	12795122	12818401	chrX	12795122	12795163	23279
<i>MetaEnhancer_116_+</i>	+		chr3	173792929	173798019	chr3	173796865	173797019	5090	<i>TNFSF10-1</i>	-		chr3	173705991	173723991	chr3	173723736	173723991	18000
<i>MetaEnhancer_734_-</i>	-		chr3	173791040	173792760	chr3	173792248	173792364	1720	<i>TNFSF10-2</i>	-		chr3	173705991	173723991	chr3	173723736	173723991	18000
<i>MetaEnhancer_2005_+</i>	+		chr3	173677625	173678325	chr3	173677765	173677876	700	<i>TNFSF10-3</i>	-		chr3	173705991	173723991	chr3	173723736	173723991	18000
<i>MetaEnhancer_512_-</i>	-		chr2	224520899	224525705	chr2	224525490	224525639	4806	<i>WDFY1</i>	-		chr2	224448308	224518296	chr2	224518108	224518296	69988

Table S3. Genomic information for eRNAs and target genes of control EP pairs analyzed by 3C and siRNA knockdown experiments. Enhancer_ID column contains unique IDs (from Table S1) for annotated eRNAs and corresponding strand information. Whole region column contains genomic coordinates for the full eRNA transcript that was detected across the entire time course. High enrichment region column contains genomic coordinates of a region within eRNAs with high GRO-seq signal that was used for designing the siRNAs. eRNA length column denotes the length of the annotated eRNA encompassing the whole region of the annotated eRNAs. Target Genes column contains the gene name and DNA strand information for the assigned target genes. Whole region column contains genomic coordinate information of the target genes. First exon region columns contains coordinate of first exon region. Gene length column notes target gene length. All genomic coordinates and names are based on the hg19 build of the human genome.

Table_S3

eRNA and target gene of Control EP pairs

eRNA			Whole region			High enrichment region			eRNA length	Target Genes			Whole region			First exon region			Gene length
Enhancer ID	strand	chr	start	end	chr	start	end			Gene name	strand		chr	start	end	chr	start	end	
MetaEnhancer_600_+	+	chr22	37680218	37682221	chr22	37680446	37680578	2003		APOBEC3B	+		chr22	37708349	37718730	chr22	37708349	37708421	10381
MetaEnhancer_600_+	+	chr22	37680218	37682221	chr22	37680446	37680578	2003		APOBEC3D-1	+		chr22	37747063	37759202	chr22	37747063	37747487	12139
MetaEnhancer_94_-	-	chr22	37677998	37680141	chr22	37679910	37680116	2143		APOBEC3D-2	+		chr22	37747063	37759202	chr22	37747063	37747487	12139
MetaEnhancer_1529_+	+	chr6	47490687	47491589	chr6	47490697	47490886	902		CD2AP	+		chr6	47553483	47702955	chr6	47553483	47553943	149472
MetaEnhancer_699_+	+	chr5	118395014	118397954	chr5	118395699	118396002	2940		DMXL1-1	+		chr5	118434982	118612721	chr5	1.18E+08	1.18E+08	177739
MetaEnhancer_454_-	-	chr5	118393146	118396611	chr5	118396304	118396575	3465		DMXL1-2	+		chr5	118434982	118612721	chr5	1.18E+08	1.18E+08	177739
MetaEnhancer_475_+	+	chr6	33103702	33107329	chr6	33105577	33105889	3627		HLA-DMA	-		chr6	33024368	33028877	chr6	33028703	33028877	4509
MetaEnhancer_157_-	-	chr6	32546422	32549330	chr6	32548510	32548783	2908		HLA-DRA	+		chr6	32515596	32520802	chr6	32515596	32515787	5206
MetaEnhancer_157_-	-	chr6	32546422	32549330	chr6	32548510	32548783	2908		HLA-DRB5	-		chr6	32593131	32605984	chr6	32605879	32605984	12853
MetaEnhancer_820_-	-	chr17	38333528	38334970	chr17	38334705	38334946	1442		IFI35	+		chr17	38412267	38420002	chr17	38412267	38412511	7735
MetaEnhancer_311_+	+	chr17	34064382	34065788	chr17	34064375	34064679	1406		MLLT6	+		chr17	34115398	34139582	chr17	34115398	34115520	24184
MetaEnhancer_544_-	-	chr13	76886469	76887807	chr13	76887554	76887756	1338		MYCBP2	-		chr13	76516792	76799178	chr13	76798609	76799178	282386
MetaEnhancer_327_+	+	chr2	64303953	64307226	chr2	64303970	64304149	3273		PELI1	-		chr2	64173289	64225109	chr2	64224718	64225109	51820
MetaEnhancer_1477_-	-	chr16	11297248	11299746	chr16	11297809	11297902	2498		SOCs1-1	-		chr16	11255774	11257540	chr16	11257436	11257540	1766
MetaEnhancer_810_-	-	chr16	11308132	11312802	chr16	11312513	11312648	4670		SOCs1-2	-		chr16	11255774	11257540	chr16	11257436	11257540	1766
MetaEnhancer_1228_+	+	chr20	55489469	55491648	chr20	55489512	55489777	2179		ZBP1	-		chr20	55612307	55629038	chr20	55628723	55629038	16731
MetaEnhancer_804_+	+	chr18	58324203	58326493	chr18	58324896	58325080	2290		ZCCHC2	+		chr18	58341637	58396798	chr18	58341637	58342576	55161
MetaEnhancer_246_+	+	chr15	78096744	78104705	chr15	78100853	78101069	7961		ZFAND6	+		chr15	78138964	78217790	chr15	78138964	78139206	78826

Table S4. 3C assay primers and BAC clone for induced EP interaction (a) and control EP interaction (b). eRNA column contains Enhancer ID (from Table S2) and primer sequence from eRNA region for 3C assay (eRNA – primer). Target genes column contain gene name of the corresponding target genes and primer sequences for promoter region (Target promoter – primer 1 and Target promoter – primer 2). Control column contains primer sequence from control region used for 3C assay. BAC clone column contains clone identifier for BAC clones used for 3C assay controls.

3C assay primers and BAC clone

A. Induced EP interaction

eRNA		Target genes			Control	BAC clone
Enhancer ID	eRNA - primer	Target gene name	Target promoter - primer1	Target promoter - primer2	Control primer	
<i>MetaEnhancer_1136_+</i>	TCACGAACACCCAGAGATGT	<i>ACKR1</i>	AACTCTGATGGCCTCCTCTG	TTGGTCACCCTTTCTCCAGG	TCCGTAGTGAAAGTTTTGGGA	RP11-621D16 +RP11-1065J8
<i>MetaEnhancer_258_-</i>	ACCACCAGACATTAGCCAG	<i>CCR1</i>	GGAGGGCAGTGTTGTTCAAA	CTTCCTCACGGCATTGCTAC	CTGCTCTTGTCTCCACTGC	RP11-793E15
<i>MetaEnhancer_1694_+</i>	TGCTGCCACAAGAACATTTG	<i>CD38-1</i>	TCCTGTTGTGTACCTGGCTT	GGAGTCCAAGGCAGTCTCT	TGATCCTTTCTTGGCCTCA	RP11-640L4
<i>MetaEnhancer_3795_-</i>	GTGTGTGTGTGTGTGTGT	<i>CD38-2</i>	GGAGACCCAGGGAAGAGTTG	TCCTGTTGTGTACCTGGCTT	ATTACAGCACTTTGGGAGGC	RP11-640L4
<i>MetaEnhancer_1136_+</i>	TCACGAACACCCAGAGATGT	<i>IFI16</i>	GCAGTGATCAAAATTATGTCCCA	TCCAAGGCCATCTACAGAGC	GTGCTGTCTCCCTTCTGTCT	RP11-265E4
<i>MetaEnhancer_1571_+</i>	TCCCCAGTCATTAGCACAGT	<i>IFNβ1</i>	GCAAAGGAAAGCAACGACC	TCCCCAGTGCCTTGTTTATA	TCAGGTAATGTGATGCCTCCA	RP11-372B20
<i>MetaEnhancer_259_+</i>	ATAGCCTGCCCAATCACT	<i>IRF8</i>	GAAGTGCTCTGCTTCCGAG	TGGGCATTGTTGGGAATTG	TGTTAATTACCTGAAGCGCGT	RP11-478M13+RP11-152O13
<i>MetaEnhancer_1115_+</i>	TCTTGGGACCGTGAAAGTGT	<i>KIAA0040</i>	ATCCAAGTGTTCACACCGC	CTTTCTCCGAACGCTCAAGG	AAAGAAAATGCCAGGCCAG	RP11-661N21
<i>MetaEnhancer_1136_+</i>	TCACGAACACCCAGAGATGT	<i>MNDA</i>	CAAAATCAACGGGAGCAAGCT	ATCATGAGAACAGCACGGGA	TGAGTTGGCTGTAATGTGTGT	RP11-110D10 + RP11-1065J8
<i>MetaEnhancer_2972_-</i>	TGGTTGGACAGTAGGGGAAG	<i>PARP14</i>	TCATATCTCTCTGGCTGCTCC	TCTTGGTCCAATGCAGTCTT	GGGTCAAAGAGATGGCAGGA	RP11-90P23
<i>MetaEnhancer_2972_-</i>	TGGTTGGACAGTAGGGGAAG	<i>PARP9</i>	ATCTCTTGGCCTGAGGCTT	TGAGGACCTACTGTTGCTG	TTACAGGCACGTACCACTAT	RP11-90P23
<i>MetaEnhancer_3039_+</i>	AGCATTTAGGAGTGCACGTT	<i>SAMD9</i>	GATGTTAGGGGCTCTGCAGA	TGAGCACTTTGGAAGGCAAG	TTTGCTGTAAGTCCCCTCT	RP11-962H11
<i>MetaEnhancer_502_+</i>	CTGTCCCACACACCCCATAT	<i>TLR7-1</i>	CAGGAAGAGGGAGAGCAGAG	GAGGGTTTCATTTGCTGGGG	GTAACCACTGCAAGACTGGC	RP11-166H19
<i>MetaEnhancer_341_-</i>	CTGTCCCACACACCCCATAT	<i>TLR7-2</i>	CAGGAAGAGGGAGAGCAGAG	GAGGGTTTCATTTGCTGGGG	CATGCCAAGATCTGTAGACATCT	RP11-166H19
<i>MetaEnhancer_116_+</i>	TCTCCATGGGTACAGTTGTT	<i>TNFSF10-1</i>	TACAGGTTCTTTGGTGCCCA	GAGCTGAGATCATGCACTGC	GCCATGCGCGGATATAATC	RP11-240B20
<i>MetaEnhancer_734_-</i>	CTCCATGTTTCTCCCGTGTG	<i>TNFSF10-2</i>	TACAGGTTCTTTGGTGCCCA	GAGCTGAGATCATGCACTGC	GAGGACTACAGTAACGACCTT	RP11-183A2
<i>MetaEnhancer_2005_+</i>	GCAATAAACGTGGGAATGCC	<i>TNFSF10-3</i>	GAGCAGGACACGTAGACTCA	TGCCCATTTCAGCATACAAA	ACATTGTGCCCAGATGTTCC	RP11-259F22
<i>MetaEnhancer_512_-</i>	CACAGAAAGCATTGCCCTT	<i>WDFY1</i>	AGGCTGGTCTTGAACCTCAA	TGTAGGAGGAGCAGGTTTGG	CTGGCAGACACCTCCACTTA	RP11-79C2

B. Control EP interaction

eRNA		Target genes			Control	BAC clone
Enhancer ID	eRNA - primer	Target gene name	Target promoter - primer1	Target promoter - primer2	Control primer	
<i>MetaEnhancer_600_+</i>	CTGGTCTTCTCTTCCCCACT	<i>APOBEC3B</i>	GCCTCAGCCTCTAGAGTAGC	CCTAGGGTAGCCTCACGTG	GGGATTACAGGTGCCAGAA	RP11-358G23
<i>MetaEnhancer_600_+</i>	CTGGTCTTCTCTTCCCCACT	<i>APOBEC3D-1</i>	ACTCCCAACCTCATGATCCG	CACCTCTCTGTGCCTCTGAC	GGGATTACAGGTGCCAGAA	RP11-358G23
<i>MetaEnhancer_94_-</i>	CTGCTGGTCTTCTCTTCCCC	<i>APOBEC3D-2</i>	TCGAACCTCCCAACCTCATGA	CACCTCTCTGTGCCTCTGAC	ACAGAGTTCAGGACAGTGGT	RP11-358G23
<i>MetaEnhancer_1529_+</i>	ACAATCAGTCACTAGGAGGAGG	<i>CD2AP</i>	AAGGATTGGGGAGTCTCTCG	GTATGTGTGGGCATTTGTGC	TGGTAGGAGCCCAGATTCTG	RP11-947C14
<i>MetaEnhancer_699_+</i>	CCATGTTTGCTAGGCTGGTC	<i>DMXL1-1</i>	ATCCCTGCGGCCGAAATAT	CTGCATGCCAACTTAAACCTT	CCCTGCTGCTTCCCTTTGAA	RP11-119J15
<i>MetaEnhancer_454_-</i>	CCATGTTTGCTAGGCTGGTC	<i>DMXL1-2</i>	TCCACACACTTCTGTGGAC	AGAAAAGGTGTTGTGGTGCA	ATCCACAGAACCATGCTCCA	RP11-119J15
<i>MetaEnhancer_475_+</i>	CACCTTCTCATTTCTCCAACCACA	<i>HLA-DMA</i>	GGCCGAAGTACCTAGCATGT	CAAGCTACTCAGGAGGCTGA	GACCCAGGAAGAGCTGATGT	RP11-260B12
<i>MetaEnhancer_157_-</i>	TCCAAACATGCAGCAGTCAC	<i>HLA-DRA</i>	TCCAAAGGCACCTGAATGAG	TCTGCTCAGGATCACTAGGT	CTGAAGAGTGACACCTCCTCA	RP11-379F19
<i>MetaEnhancer_157_-</i>	TCACCACCTTCCGACTTTT	<i>HLA-DRB5</i>	ATTCCCCATACAGCACTTCC	TTGCTTCTCTGTTTTCTTTCCC	CTGAAGAGTGACACCTCCTCA	RP11-379F19
<i>MetaEnhancer_820_-</i>	CCAAAAGCACAGACAGCCT	<i>IFI35</i>	GAGAGAGACCACAGCCCTTT	AAACTCTCCACGTTCAACC	CCAGCCCCTTATGCCTCTTA	RP11-948G15
<i>MetaEnhancer_311_+</i>	CTGTGGGTCAAATGGGAGGA	<i>MLLT6</i>	TATTCAGGGCCTAGAACGG	CATCTCCCTCTTGGCTTCCA	CAGCTTGAAGTGCCTTGTGG	RP11-607B2
<i>MetaEnhancer_544_-</i>	AGGGACAAGCAAGCATCTCT	<i>MYCBP2</i>	GAAGGGGTGGAGGTGAGTAC	CTCCTTCAGCCACTTCAGGA	TTTCATGGCTCCAACACCT	RP11-775N1
<i>MetaEnhancer_327_+</i>	AACTTGAGCCCAGACAACCT	<i>PELI1</i>	CGATGCGTTTTCTTTATAGCCA	GCCCGGCCAAATATCAGTAG	CACCTTCTGGTTTCTATTCTCGA	RP11-46K17
<i>MetaEnhancer_1477_-</i>	CGTTGCCTGTTTGGCTTA	<i>SOCS1-1</i>	GCGTCTTATGTGGTGGCTT	AGTCAAGATCCTGGTGGCTT	CTCTGCCAGCCTAGGA	RP11-697G17
<i>MetaEnhancer_810_-</i>	CCTTGGTTTCTGGCCTCTA	<i>SOCS1-2</i>	AGTCAAGATCCTGGTGGCTT	GCGGTCTTATGTGGTATGCC	CAGGAGGCTCTGGGAAGAAT	RP11-697G17
<i>MetaEnhancer_1228_+</i>	TGCATGAGGCAGACTTGTTT	<i>ZBP1</i>	CCCAAGTCTCCCTTCTACCA	GTGTGAAGTCAGGTGCATGG	AACGGGAGCTTCGACTGTAA	RP11-1105M4 +RP11-877E5
<i>MetaEnhancer_804_+</i>	TGTGGTCCATATCCCGTAGA	<i>ZCHC2</i>	CCAGGCTGGCAAATTGAGTT	CCACTCTTACGCTACTCGT	CAAGTCTGCCCTGGTTTAC	RP11-645G19
<i>MetaEnhancer_246_+</i>	CACGCCAGCTAATGTTGT	<i>ZFAND6</i>	GCGGAGACTTTAAGGGCTTG	TAAACATTTTAGCATCCCCAGG	GAACAAAAGCTCCTGAGGCC	RP11-916P11

Table S5. siRNAs targeting eRNA of induced EP pairs. siRNA name column contains assigned name for each siRNA pool. Target gene column contains gene names. Enhancer_ID column contains assigned Enhancer_ID for each eRNA tested. eRNA region column contains sequence of the high enrichment eRNA region from Table S2. siRNA ID contain unique identifier for each siRNAs tested. siRNA target sequence column contains DNA sequence of eRNA targeted by siRNAs. Sense column contains RNA sequence of the sense strand of siRNA duplex (5' to 3'). Antisense contains RNA sequence of the anti-sense strand of siRNA duplex (5' to 3').

siRNAs targeting eRNA of induced EP pairs

siRNA name	Target gene	Enhancer_ID	eRNA region	siRNA ID	siRNA target sequence	Sense	Antisense
siRNA#5A	TNFSF10-1	MetaEnhancer_116_+	TAAACCAAGGATCTTCTCAGCCTCCAAAGTAAAGGAATGTGTATCTCCAAGCTCCCTCTTGTA	116A	GCCACTGTCTCAGAAGAGAAA	GCCACUGUCAGAAGAGAAA	UUUCUCUUCGACAGUGGC
siRNA#5B			TGTATTGTGAACGCCACTGTCAAGAGAAACACCAAGTATTACCTCGGAATGTTCAGT	116B	TCTTCAGCCTCCAAGGTAA	UCUUCAGCCUCCAAGGUAA	UUACCUUGGAGGCGUAGGA
siRNA#5C			ATGAAGACCATGTATTGTAGTGAGAGG	116C	GGAAATGTGTGATCTCCAA	GGAAAUUGUGUAUCUCCAA	UUUGGAGUAUCACAUUCC
siRNA#7A	IRF8	MetaEnhancer_259_+	GGCTCAGGCTGAGAGGATATTCTGCCGTTGTAGTTTGTCTCGGGCCATTCTGTTTAAAGAAGA	259A	GAGAGGATATTCTGCCGTT	GAGAGGAUUAUUCGCCUU	AACGGCAGAAUUAUCCUC
siRNA#7B			CTGGAGAGTCAGTTCCAGTTTGTCTTGGGGACTAAGTCTTATCATGTGGTTTCTACTGTGTG	259B	GGTTTCTACTGTGTGGCTTA	GGUUUCUACUGUGGCUUA	UAAGCCACCAGUAGAAACC
			GCTTATTAGAACACATGCAGGTACAG				
siRNA#8A	MLL76	MetaEnhancer_311_+	CCCAGCCCTCAGTGGCCCCACAGCAGCTGGCTGTTCTTGTTGTTTCTCTGCTTCTGCA	311A	CTCTGCTTCTGCATGATAT	CUCUGCUUCUGCAUGAUU	AUAUCAUGCAGAGCAGAG
siRNA#8B			TGATATCTTTGAACAAAAGTCCCAAGGTACAAAAAGTCCGAAAGCGTTTCGCAAAACCACT	311B	GAGGGCATCCCTTTACATA	GAGGGCAUCCUUUACAUA	UAUGUAAAGGGAUGCCCU
			GACCTAGATGGAGGAATGTGAGGAGCAGAGGACCCCTTATAAATAGCTGTACTTCG				
siRNA#10	TLR7-1	MetaEnhancer_502_+	GTGCAGGGTTTGGTGGTGCGCCGTTGGAGGCCCTTAAAGCTTCTCACTCCTGTGCACTG	502A	GGCTCAAGGTATCTGCAAA	GGCUCAAGGUUAUCUGCAA	UUUGCAGAUACCUUGAGCC
			GTGGATGGTGGGTGCCGCGCAGGAGGCATCCCTTACATAGGGGCTCATTG				
siRNA#17A	CD38	MetaEnhancer_1694_+	GGGGAATGAGAAACAAAGACAAGGTTAATTATGACACCGGGCTTACAATGCTAAAAATA	1694A	AGCATTCTGTGCTCATTTA	AGCAUUCUGUGCUCAUUUA	UAAUAGAGCAGAGAUUGCU
siRNA#17B			TCCTATATACAAAGGATATGTAGGCTGTGTTCTTTTCCATGTCTATACAAAGAACAGGCTCA	1694B	GAGTGTATGTACTTGGACA	GAGUGUAUGUACUUGGACA	UGUCCAAGUACAUACACUC
siRNA#23A			AGGTATCTGCAAAATTTCTAATAAAAAATATTACTTGAAAAATG	258A	GAGTGTCTTCTCACACTCTA	GAGUGUUUCUCACACUCUA	UAGAGUGUGAGAAACACUC
siRNA#23B	CCR1	MetaEnhancer_258_-	GTCCACTTTTAGGAGTGTATGTACTTGGACACCTAAAAATATGCTGCCACAAGAACATTTGTT	258B	GGAGGTATCTTCTCAAGAA	GGAGGUUAUCUUAAGAA	UUUUGAAGAGAUACCUCC
			GTAGCATTCTGTCTCATTTATACAGGTCTAGTTAAGTAACTCTAGCACTACTA				
siRNA#24A	TLR7-2	MetaEnhancer_341_-	GCCTTTGAAAGTCTCGCATCTGCTGTTTTTTCAGGTCTCCAAGTCCATCTTTGTTGGAGCTG	341A	GAGGCACCATTCATTATA	GAGGCACCAUCAUUAUAA	UUUUGAAGAUAGGUGCCUC
siRNA#24B			GTGAGTGTCTTCTCACACTCTATAATCCGCAAGTAGGGAGGTATCTTCAAGAAGACAAGTGT	341B	CTCACCATCTGAGACTCAT	CUCACCAUCUGAGACUCAU	AUGAGUCUCAGAUUGGUGAG
			CATTCAATATTTCTGCATAACAACAGACAAAACTTA				
siRNA#28A	WDFY1	MetaEnhancer_512_-	AGACTATTTATGATGATGCTTGGCTTTGAGCTGTTCCGCTGCTGTCTTGTAAACTCAGAAGCA	512A	GGCTTAGTCCAACTTAA	GGCUUUGAGUCCAACUUA	UUAAGUUGGACUAAAGCC
siRNA#28B			GTTTTCTGAGGTGGGATTATCTGACCATCTAGCTCACCATCTGAGACTATAAGTAGATTGTG	512B	GCCATAATTGTATCAGTCA	GCCAUAAUUGUAUCAGUCA	UGACUGAUACAUAUUGGC
siRNA#28C			GAGTGTGAGGTGTAGTGAAGACCACTGTTTGGGATTCAACATACATGCCAGCCAATGAA	512C	TAGGTCTACTGTGACTGA	UAGGUUACACUGUGUACUGA	UCAGUACACAGUGAACCUA
siRNA#30	TNFSF10-2	MetaEnhancer_734_-	ATGTTAACTCACATCTGCATATGCCCTCATCTGTTATGGAAGTGGAGGCACCATTCATAAT	734A	CACACTGAGCAATTGCTGA	CACACUGAGCAAUUGCUGA	UCAGCAAUUGCUCAGUGUG
			GCTTGAACCCACAGTACAGATCACCATCTGGGCCATCACACTGAGCAATTGCTGACCTGC				
siRNA#34A	IFN1	MetaEnhancer_1571_+	ATCTCTGTGGAGTGGAGCCCCAGGAGACAAGTAAAGACCCCAAGCCACAC	1571A	CTGTCTACATCTGGGATA	CUGUCUACAUCUGGGGAUA	UAUCCAGGAUGUAGACAG
siRNA#34B			TTCTCTGGCTGCTCGGAAGTGCCTCTGTTATTATTAGTAAACATTAGCTCTCGAAAGGT	1571B	TAAAGTGTGCCATTGTAGA	UAAAGUGUGCCAUUGUAGA	UCUACAUAUGGCACACUUUA
siRNA#35A			AGAGAGAACCAAGAGGTAAGGTGTCATTGTAGACAGCTGTGTGTGCGAGGTAGCAG				
siRNA#35B	IFI16	MetaEnhancer_1136_+	TGTTCTGTCTACATCTCGGGATAAT	1136A	CTTATATTGTGTACCCAA	CUUUAUUGUUGUACCCAA	UUUGGUUACAACAUAUAAG
siRNA#36A			GTCTGCTATCTAGATCTTTGACTACCAACAGCCAGGAGTGGTGCCTCTCTTTGGTCTGA	1136B	CTATCTAGATCTTTGACTA	CUAUCUAGAUUUUGACUA	UAGUCAAGAUUCUAGUAG
siRNA#36B			GCTTGCCCTTGTCTTATATTGTTGACCCAAGCGAGT	2972A	CAACTTCTCTGTTCTGTA	CAACUUCUCUUGUUCUGUA	UACAGAACAGAGAAGUUG
siRNA#36C	PARP14	MetaEnhancer_2972_-	CGCGACCGTTCATCTTCTGAGTTTCTTCACTTTGCCAGCTTGGGTGTCTCTCCGAGGCCGTC	2972B	CTCTGTCTGTAGCATTT	CUCUUGUUCUGUAGCAUUU	AAUUGCUACAGAACAGAG
siRNA#37A			GTCTAGTTATGGCTCATCCAGCTGACGCTGCACTCTCTGTTCTGTAGCATTTCTTCTACTT	2972C	CCGTTCCATCTTGTGAGTT	CCGUUCCAUCUUGAGUUU	AAACUCAAGAAUGGAACGG
siRNA#37B			CTCTTCTTCTACAGCTGTGTCAACCGGCT	3795A	GAGGGTCTTTGACAGCTCA	GAGGGUCUUGACAGCUCA	UGAGCUGUCAAAGACCCUC
siRNA#37C	CD38	MetaEnhancer_3795_-	CACATCTACCCCCAGACCTGCCATTGGCATGCACATCTTAAACCAAAACACGATTGAAAAAT	3795B	CTGCCATTGGCATGCACAT	CUGCCAUGGCCAUGCACAU	AUGUGCAUGCCAUUGGCAG
siRNA#38A			GAGAAAGAAAACTCTCTTAGCTGGGCGCTTCATAGGACTAGCCAGGTACGACCATCTCTG	3795C	GCATGCACATCTTAAACA	GCAUGCACAUCUUUAACA	UGGUUAAAGAUUGUAGUC
siRNA#38B			AGGGTCTTTGACAGCTGCACTTTTACTGCATAATCTGTTTCAAGACCCCTTAAAGACCATGAT	2005A	CTGATTATCTCGTCTGCAT	CUGAUUAUCUCUGUCGAU	AUGCAGACGAGAUUAUCAG
siRNA#38C	TNFSF10-3	MetaEnhancer_2005_+	CATAACTACCAGAAGCAATTGGTGGCAAGATCTCAATCAGGACATGTCGATCAATGCTCTGA	2005B	CTGCATCCCTGATTACTTA	CUGCAUCCUGAUUACUUA	UAAGUAUACAGGGAUGCAG
siRNA#41A			TTATCTCGTCTGCATCCCTGATTACTTATGGTCCAGATATAAATCTACT	2005C	TACTTATGTGTCAGATATA	UAUCUUAUGGUCCAGAUUA	UAUAUCUGGACCAUAAGUA
siRNA#41B			GTCTTAAGGCTGATGTGAATCTCTGCCCTTTCCAATGTGTATGTGATTGCTCCAAATAAAA	3039A	GAATCTCTGCTTCTTCCAA	GAUUCUGGCCUUUCCAA	UUUGGAAAGGGCAGAGAUUC
siRNA#42A	KIAA0040	MetaEnhancer_1115_+	CACCTATTATTATTATTTG	3039B	TCCAATGTGTATGTGATT	UCCAAGUGUGUAGUGAUU	AAUCACAUGACACAUUGGA
siRNA#42B			CACCTCACTCTGTTTCTGTCCATTAAATGCTTCTGCCACGTTGGGGAGGAGCTCTCTGA	1115A	CAATTAACTCTAAATCT	CAAUUAAACUCCUAAUUCU	AGAUUUAAGGAGUUUAUUG
siRNA#42C			ACCTCTGCTGCTTCTGAGGAGATTCAAGAATAATTTTGTCTCAATTAACTCTAAATCTAATT	1115B	CTGAGGGATTCAAGAATAT	CUGAGGGAUUCAAGAAUUA	AUAUUCUUGAAUCCUCAG
siRNA#43A	PARP9	etaEnhancer_2972_-	GTCTAAAGCTTTTCTT	1115C	CTGAACCTCTGCTGCTTCT	CUGAACCCUGUGUCUUCU	AGAAGCAGCAGAGGUUCAG
siRNA#43B			ACTTCTGTCCGCGACCGTTCATTCTTGAGTTTCTTCACTTTGCCAGCTTGGGTGCTCTCCC	2972A	CAACTTCTCTGTTCTGTA	CAACUUCUCUUGUUCUGUA	UACAGAACAGAGAAGUUG
siRNA#46A			GAGGCGTGTCTTATGTTATGGCTCATCCAGCTGACGCTGCAACTTCTGTTCTGTAGCATTT	2972B	CCGTTCATTCTTGAGTTT	CCGUUCCAUCUUGAGUUU	AAACUCAAGAAUGGAACGG
siRNA#46A	ZBP1	MetaEnhancer_1228_+	TCTTCTACTTCTTCTTCTACCAAGCTGTGTCAACCGGCTTTG	1228A	CCGACAGAATGCTGAACA	CCGACAGAUGCUGAAACA	UGUUUCAGCAUUCUGUCGG
siRNA#46A			TGATTACTCACTCTCATGCGAGGCTGAATATTACTGTTTCCCTGTTAAACAAGGGTGTATTA	1228B	GGGTGATTACTTCCGAAA	GGGUGUAUUAUCCGAAA	UUUCGGAAGUAUACACCC
siRNA#46A			CTTCCGAAATCTGACAAACCAAGCACAAGGTTTAAAAATATCTCGAGATTGTAAAGCCT	1228C	CTCATGCAAGGCTGAATAT	CUCUAGCAGGGCUGAAUUA	AUAUUCAGCCUGCUGAUG
siRNA#47&48A	MND4 & ACKR1	MetaEnhancer_1136_+	CCGACAGAATGCTGAACAGGATTGCACAGTTGACCAAGGAGCTTCTGAGTTGTGGCGGAC	1136A	CTATATTGTTGTACCCAA	CUUUAUUGUUGUACCCAA	UUUGGUACAACAUAUAG
siRNA#47&48B			CCTCCATGTTTCTGACTGCGGACAGTCAAGCCCTCTTCCCTAATGCACAGGAGTTTCCC	1136B	CTATCTAGATCTTTGACTA	CUAUCUAGAUUUUGACUA	UAGUCAAGAUUCUAGUAG
			TGGGACACCTGCC				
			TTTCTGCTATCTAGATCTTGTACTACCAACAGCAGGAGTGGTCTGCTCTTCTTGTGCTGA				
			GCTTGCCTGTGCTTATATTGTGTACCAAGCGAGT				

Table S6. siRNAs targeting eRNA of control EP pairs. siRNA name column contains assigned name for each siRNA pool. Target gene column contains gene names. Enhancer_ID column contains assigned Enhancer_ID for each eRNA tested. eRNA region column contains sequence of the high enrichment eRNA region for each eRNA. siRNA ID contain unique identifier for each siRNAs tested. siRNA target sequence column contains DNA sequence of eRNA targeted by siRNAs. Sense column contains RNA sequence of the sense strand of siRNA duplex (5' to 3'). Antisense contains RNA sequence of the anti-sense strand of siRNA duplex (5' to 3').

Table_S6

siRNAs targeting of control EP pairs

siRNA name	Target gene	Enhancer_ID	eRNA region	siRNA ID	siRNA target sequence	Sense	Antisense
siRNA#1A	HLA-DMA	MetaEnhancer_475_+	ACAGTCTACAAGAGGCCGTGGAGCTGTCGGGGAAGGAGAATGTTCAAGTAGCACAGGC	475A	CACCTGATGTTAGTCGTCA	CACCUUGAUUUAGUCGUCA	UGACGACUAACAUAGGUG
siRNA#1B			AATCAAACTCTCTATTGCTCAGGTGCAAGCAGGAATGAAACCTGTCCCTCTGTTGA	475B	CTCTCTCTTCACTCCTA	CUCUUCUUCUACUCCUA	UAGGAGUGAAGAAGAAGAG
siRNA#2&3A			ATACTCTCTCTTCACTCCTAAAACACACACTGATGTAGTCTGACGCCCTCTTCTATCACT	157A	CTTTCTAACTCAATGTTT	CUUUCUACUCCAAUGUUU	AAACAUUGGAGUUGAAGAG
siRNA#2&3B			CTACACCTGTCTGTCTGGAGAACTATCCAGGCCTGTGGCTCCCTGCACGCTCTACACTAGTAA	157B	GTATGTAGGTCTCTGACA	GUAUGUAGGUUCUCUGACA	UGUCAGAGAACCUCACUAC
siRNA#2&3C	HLA-DRA & DRB5	MetaEnhancer_157_-	CCTCTGAATCCACGGTCTCCAGCACTCCCTCTGCTCCATCCCCAGGTGGCAGTCAGGT	157C	CCTCAAATGTGAGGATGTA	CCUCAAUUGAGUGAUGUA	UACAUCCUCACAUUUGAGG
siRNA#6A			GAATTCAAAGGGTCTCTCTAGAGGATCTGGGTATGTCTCCACAGGAACCTTGGTGTGG	246A	CTCTGAGTCTCCAGCAATT	CUCUGAGUCCACAGAAU	AAUUGCUGGAGACUCAGAG
siRNA#6B			CCCTCTCTCAAATGTGAGGATGTACCAATGGCCTCCCATATCTCTCTTTCTTTCTTCTA	246B	GTGAGAACCTGTTAGAACT	GUGAGAACCUUGUAGAACU	AGUUCUAAACAGGUUCUCAC
siRNA#9A			ATGCTTGTCTTCTCCCTCTCCCTGTAGAACACAAAGGGATTTTCTCTGATAATCATTGTGA	327A	CTGTAACCTGTGTTGCTA	CUGUAAUCUUGUUCGCUA	UAGCGAACACAGAUUACAG
siRNA#9B	PELI1	MetaEnhancer_327_+	GAACCTGTTAGAATCTCTGGAGGTAAAACCTAAAGATATGGCGGCCCTGAAATGAGTCTT	327B	GAGAGAAATCTAGAAGAT	GAGAGAAAUUCUAGAAGAU	AUCUUCUAGAAUUCUCUC
siRNA#11&12A			CCTGGAATTAAGTCAAACTGCCACTCTGAGTCTCCAGCAATCTTGAAATTAATTCAGAT	600A	TTGTGAGAGCCAGAAATCA	UUGUCAGAGCCAGAAUCA	UGAUUCUGGGUCUCAGAA
siRNA#11&12B			TTTCTATCTGCTGACAGGTTCTCTGT	600B	GCTCCAGGGCAATGTTGA	GCUCCACGGGCAUUGUUA	UCACAUUGCCCGUGGAGC
siRNA#13A			TACCAATGTCTCTGGGCTTGTCTACTAGTACAACAGAGGAGAGAGAAATCTAGAAGATTT	699A	CTAACTCCCTCAATTCTTT	CUAACUCCUCAAUUCUUU	AAAGAAUUGAGGGAGUUG
siRNA#13B	DMXL1-1	MetaEnhancer_699_+	TCAACTCCCTCTGCTGTGAATCTGTTCTGCTATGTGCTAAATGCACCTGAAATAAACAC	699B	CTGTCACTGCTAGTCTCT	CUCGUCACCUGCUAGUCCU	AGGACUAGCAGUGACGAG
siRNA#14A			TTCTTTGTGTGTGTGTGCGGGGTGAATCCTCACTTTACAGAAAGAGGA	804A	GTGTTCTGGCTTGATTTA	GUGUUCUGGGCUUGAUUUA	UAAAUCAAGCCACGAACAC
siRNA#14B			ACCAATGACTCACCTCTTCTCTGCTACCTGCTAGTCTCCCACTTCACTCCCTTCAGTCATATT	804B	TTGAGAACTCTTGAGCTA	UUCAGAAUUCUUGAGCUA	UAGCUCAGGAAGUUCUGAA
siRNA#14C			GGCCTTGCTTCTTTCAGACGGGCGAGCACACTCAGGGCCTTTCGACTGACTTCTCTCTG	804C	CTGACACCTCTGATGAGCT	CUGACACCCUGAUUAGCCU	AGGCUAAUCAGGGUGUCAG
siRNA#16A	CD2AP	MetaEnhancer_1529_+	CCTGGAATTTCTCTCCAAGATATCCATGCTCACTTACAGAAAGGGA	1529A	CAGCTTTCTCCAAGAGAT	CAGCUUCCUCCAAGAGAU	AUCUCUUGGAGGAAAGCUG
siRNA#16B			ACAAGGCGTTTCCAAATAAGTCTCTCTGCTACCTCTTTAAATTTTAACCCACCTCTT	1529B	GCCACAGTTTCACTTTGTT	GCCACAGUUCACUUGUUU	AACAAGUGAAACUGUGGC
siRNA#16C			ACATTTATATACTCCCTCTCTGCTTTTTCAGCTCTTGTCT	1529C	CTCTGCCAACCTCTGAAA	CUCUGCCAACCCUCUGAAA	UUUCAGAGGGUUGGAGAG
siRNA#18A			CAATCGCTGCTGAGTACCTATGTCTGCTGGCTGATTACCTTCTGTAATCTCTGGATGT	94A	CACTGTCTGTGTGCTTAA	CACUGUCUGUGUGUCUUA	UAGCACACACAGACAGUG
siRNA#18B	APOBEC3D-2	MetaEnhancer_94_-	TAAAGGACACCAAAATCTCTGACACCTGATTAGCTCACTTGAAGAACCAAGCCAGG	94B	CTGTGTTTGGCCACAGA	CUGUGUUCUUGCCACAGA	UCUGGUGGCAAGACACAG
siRNA#23A			ATTTCTGCCCTTGCTAGAAAAAGACTGATTCAAGAACTCTCGAGCTACCTAGATATT	258A	GAGTGTCTTCTACACTCTA	GAGUGUUCUACACACUUA	UAGAGUGUGAGAAACACUC
siRNA#23B			CACAATGAGAGTGTCCCTGATTTCACTGGAATGAAATAAAGCCCTGATCATTCTCACTGC	258B	GGAGGTATCTTCAAGAA	GGAGGUUUCUUCUACAGAA	UUCUUGAAGAGAUACCUCC
siRNA#26A			TCGACAGCCACAGTTTCACTTGTCTTCATGGCTCTGCCAACCTCTGAAACTCTCACTGACG	454A	CTCTCTCTTCTAGGTTCA	CUCUCUUCUUCUAGGUGUA	UGACCCAUAGAAAGAGAGAG
siRNA#26B	DMXL1-2	MetaEnhancer_454_-	GGGACTGTGCTCTCAGCTTCTCCAAGAATTTCTCACTGCAATTGCTCTGTTTTT	454B	CTGTGTTTCTGTTCAATTG	CUGUGUUCUUGUUCAUUGU	ACAUAAGACAGAAACACAG
siRNA#26C			ATCCTCTGACTTGGGACAGAGCTGAGGTAGACATCTGGGTGTGTCTGGGAAACCCGGGGA	454C	CCCACAGTAGGGTAGGGAA	CCCACAGUAGGUAGGGAA	UUCCUACCCUACUGUGGG
siRNA#29A			AGGTTCCTTCTGTCTGTCACTGTGTGTGTGCTTATGTGTCTGTGTGTGTGTCTTTTGC	544A	GATGGTACCTCTTACATGA	GAUGGUACCUUUAUAGUA	UCAUGUAAGAGGUACCAUC
siRNA#29B			CACCAGAAAGGATTTGGGCTGTGTGCTCATGAGCAGCTGTGAGGAGGCCACTGTGTACC	544B	TGCTCTGTGTGATCCACA	UGUCUCUGUGCAUCCACA	UGUGGAGUACACAGAGGCA
siRNA#29C	MYCBP2	MetaEnhancer_544_-	ACATATGCGGCTCTGAGG	544C	GGGAGATACTGAGAAAGCA	GGGAGAUACUGAGAAAGCA	UGCUUUCUCAGUAUUCUCC
siRNA#33			GCCTTTGAAAGTCTGCACTGTGCTTTTTTCAAGTCTCCAAGTCCATTCTTGTGTTGGACTG	1477A	GTGTCAAGCTCTCTGCTGT	GUGUCAGGCUCUCUGCUGU	ACAGCAGAGAGCCUGACAC
siRNA#39A			GTGAGTGTCTTCTCACTCTATAATCGAAAGTAGGGAGGTATCTTCTCAAGAGACAAGTGT	810A	GGGTCAATTTCTTTGTTTA	GGGUCAAUUUCUUGUUUA	UAAACAAGAAAUUGACCC
siRNA#39B			CATTCAAATATTTCTGCATAAACAACAGACAAAACCTTA	810B	GTCTTTCTGATATAGAA	GUCCUUCUGAUUAGAA	UUCUUAUACAGGAAGGAC
siRNA#40A	IFI35	MetaEnhancer_810_-	CTATCTCTCTTTTATGGGTGAGTTCTATTTCCCTCTGTGTTTCTGTTCAATGTTCTCTGGTG	810C	CAATTTCTTTGTTATAGA	CAAUUUCUUGUUUAUCCA	UGGAUAAACAAGAAAUUG
siRNA#40B			GCTAACTCTGCTTATAGTTTCTGCTCCTTTTAACTCTGTGTGCACATGACTTGGACTTGTA	820A	CAGTGTGTATCTTGATAAA	CAGUGUGAUUCUAGUAAA	UUUAUCAAGAUACACACUG
siRNA#46A			TGGTACTATGCTCTGTGCTGGAACGTAGCGGTGAGTAAGGCAAGCCTGACTTCTCAGCTCT	820B	GAGTCAGTGTATCTTGA	GAGUCAGUGUGAUUCUUGA	UCAAGAUACACUCAGACUC
siRNA#46B			GCATAGGACCCACAGTAGGGTAGGGAATAAACACACACACACACACACACACACACACA	1228A	CCGACAGAATGCTGAAACA	CCGACAGAAUGCUGAAACA	UGUUUCAGCAUUCUGUGCG
siRNA#46C	ZBP1	MetaEnhancer_1228_+	AGGAACTAGCTAACATAGGTTTTGTTATCTGCTTCGAGTGTGCTCTGTGTGCATCCACACCA	1228B	GGGTGTATTACTCCGAAA	GGGUGUAUUAUCCGAAA	UUUCGGAAGUAUACACCC
siRNA#46D			AGTCCAGGCCCAAGAGTCTGTGTGGAGCTGTGTGATGGGCTGATGTAACCTCTTACATGA	1228C	CTCATGCAGGGCTGAATAT	CUCAUGCAGGGCUGAAUUA	AUAUUCAGCCUGCUGAUG
siRNA#46E			GGCCTTTTGGGAGATAGTGAAGAACCTGACTAGGAGTTGAGGCTCCACCCACAGATAGTCT				
siRNA#46F			ATCATCTGTGTGT				
siRNA#46G			TGTAATTTATTTTACTGTAGGCTCCCTTTGATGAGGAGGCCCTGGGAGTGTCAAGCTC				
siRNA#46H			TCTGCTGTCCCCCAGCACGACGACAAGGC				
siRNA#46I			TTAGTTTCAGTCTTTGATACTTTTGTAGAGGGCTGAAGGTCTTCTCTGATATAGAACTCACG				
siRNA#46J			TAAACAAATAAAGCTTCAAGTTTTTAAGACAGAAGGGTCAATTTCTTGTATTCAAAAAAC				
siRNA#46K			TATCTA				
siRNA#46L			CCTACACTGAAAGCCCTAGGGGTTGAAGCAGGATTTGGTTCAAGCTAGAACTCTGAGAGTCT				
siRNA#46M			AGTGTGTATCTGTAAACAGCAACAGAGCTTAGTCTAGTGTCCCTGTAAGTGGTCTGCTCAG				
siRNA#46N			AGAGTTTGTCTCCCACTCTGGGGAGAACTTACTGGGAAGAGGGCAATGTTCTATCTAA				
siRNA#46O			GCCTGTCCGCTCTGTAGTTTCAACCTCTTCAATTTCACTGTGGAGTGGCTC				
siRNA#46P			TGATTACCTCACTCTCATGACGGGCTGAATATTACTGTTTCCCTGTTAAACAGGGTGTATTAT				
siRNA#46Q			CTTCGAAATCTGACAAACCCCAAGCACCAAAAGGTTTAAATAATCTCGAGATTGTAAAGCTC				
siRNA#46R			CCGACAGAATGTGAAACAGGATTGCACAGTTGACAGGAGCTCTGAGGTTGTGGCGGAC				
siRNA#46S			CCTCATGTTTCTGACTGCCGGACAGTCAACGCCCTCTTCTCTAATGTCACAGATGTCTTC				
siRNA#46T			CTGGGACACTGCCC				

Table S7. eRNA and target gene expression fold changes after eRNA KD with siRNA. siRNA name column contains assigned name for each siRNA used. Distance column contains approximate distance between enhancer and target gene promoter. fold changes of eRNA expression fold column contains normalized fold change in eRNA expression upon eRNA KD. mRNA expression fold column contains normalized fold change in mRNA expression of the target gene upon eRNA KD.

.

eRNA expression and mRNA expression fold change after eRNA KD with siRNA

siRNA name	Target gene	Enhancer_ID	Distance	eRNA expression fold	mRNA expression fold
#1A siRNA	HLA-DMA	MetaEnhancer_475_+	75000	0	1.423721208
#1B siRNA			75000	0.540862333	0.878430468
#2A siRNA			26000	2.163449332	1.016281451
#2B siRNA	HLA-DRA	MetaEnhancer_157_-	26000	0.615600653	0.668948321
#2C siRNA			26000	1.689660424	0.366012967
#3A siRNA			44000	2.163449332	0.79922115
#3B siRNA	HLA-DRB5	MetaEnhancer_157_-	44000	0.615600653	0.628506687
#3C siRNA			44000	1.689660424	0.268563162
#5A siRNA			69000	0.60149862	0.695730272
#5B siRNA	TNFSF10-1	MetaEnhancer_116_+	69000	0.684600064	0.874542257
#5C siRNA			69000	0.77916458	1.228246391
#6A siRNA			34000	2.518677954	0.963707118
#6B siRNA	ZFAND6	MetaEnhancer_246_+	34000	0.827405623	0.33140486
#7A siRNA			73000	0.707106781	0.649169294
#7B siRNA			73000	1.194687532	0.52123288
#8A siRNA	MLLT6	MetaEnhancer_311_+	50000	2.795810671	0.831237896
#8B siRNA			50000	7.193364285	2.434007027
#9A siRNA			82000	1.713096791	2.750969224
#9B siRNA	PELI1	MetaEnhancer_327_+	82000	0.983915733	1.018613446
#10 siRNA			20000	0.631417726	2.934944726
#11A siRNA			65000	1.580082624	1.701334322
#11B siRNA	APOBEC3D-1	MetaEnhancer_600_+	65000	0.763129604	1.990779358
#12A siRNA			26000	1.580082624	1.2397077
#12B siRNA			26000	0.381564802	0.552227
#13A siRNA	DMXL1-1	MetaEnhancer_699_+	37000	0.625320044	1.815038311
#13B siRNA			37000	1.006722921	1.624504793
#14A siRNA			15000	1.447336117	5.277909696
#14B siRNA	ZCCHC2	MetaEnhancer_804_+	15000	6.573826285	6.276527763
#14C siRNA			15000	0	4.469045294
#16A siRNA			62000	2.417082417	1.781797436
#16B siRNA	CD2AP	MetaEnhancer_1529_+	62000	0.990777721	1.74916534
#16C siRNA			62000	0.692538733	1.280463977
#17A siRNA			5500	0.409896999	1.040059934
#17B siRNA	CD38-1	MetaEnhancer_1694_+	5500	3.863745316	0.369249191
#18A siRNA			65000	0.287114879	1.594790224
#18B siRNA			65000	2.356588726	3.256600313
#23A siRNA	APOBEC3D-2	MetaEnhancer_94_-	91000	2.328929014	0.604270604
#23B siRNA			91000	3.49833068	0.759576231
#24A siRNA			22000	6.320330495	8.186991136
#24B siRNA	TLR7-2	MetaEnhancer_341_-	22000	0.761368436	1.487957514
#26A siRNA			38000	0.835087919	1.353473524
#26B siRNA			38000	3.792283097	1.543993487
#26C siRNA	DMXL1-2	MetaEnhancer_454_-	38000	0	4.9588308
#28A siRNA			2600	0.174742204	0.104627452
#28B siRNA			2600	1.522736872	2.075319318
#28C siRNA	WDFY1	MetaEnhancer_512_-	2600	0.540862333	0.169184191
#29A siRNA			87000	3.023039857	0.664327558
#29B siRNA			87000	4.845458993	1.11984573
#29C siRNA	MYCBP2	MetaEnhancer_544_-	87000	0.422395587	0.084785811
#30 siRNA			67000	0.835087919	0.733736182
#34A siRNA			18000	0	0.502315837
#34B siRNA	IFN β 1	MetaEnhancer_1571_+	18000	0.410845157	0.57567774
#35A siRNA			2300	0.23648036	0.439316726
#35B siRNA			2300	0.34268249	1.25411241
#36A siRNA	IFI16	MetaEnhancer_1136_+	18000	0.434280777	0.993115441
#36B siRNA			18000	0.720315074	1.887792242
#36C siRNA			18000	0.699001117	0.667435348
#37A siRNA	PARP14	MetaEnhancer_2972_-	22000	1.032923445	1.135504429
#37B siRNA			22000	0.779182582	0.562529242
#37C siRNA			22000	0.240376317	0.92444966
#38A siRNA	CD38-2	MetaEnhancer_3795_-	27000	0.801069878	0.279954964
#38B siRNA			27000	0.92873141	1.219762273
#38C siRNA			27000	0.930879716	0.391368623
#39A siRNA	TNFSF10-3	MetaEnhancer_2005_+	48400	1.587364376	2.244872228
#39B siRNA			48400	1.498272459	3.160092233
#39C siRNA			48400	1.674000548	1.286364948
#40A siRNA	IFI35	MetaEnhancer_820_-	77000	0.550952558	0.237061508
#40B siRNA			77000	0.217637641	0.390483457
#41A siRNA			62000	0.848664754	0.304243849
#41B siRNA	SAMD9	MetaEnhancer_3039_+	62000	0.168007786	0.281908718
#42A siRNA			94000	0.187712939	0.554425941
#42B siRNA			94000	0.295917448	0.255678012
#42C siRNA	KIAA0040	MetaEnhancer_1115_+	94000	0.251146313	0.425058505
#43A siRNA			96000	0.297982601	0.299369676
#43B siRNA			96000	0.751059963	0.402390086
#46A siRNA	PARP9	etaEnhancer_2972_-	120000	0.227930622	0.903335201
#46B siRNA			120000	5.051341805	2.06575143
#46C siRNA			120000	0.082469244	0.342300032
#47A siRNA	ZBP1	MetaEnhancer_1228_+	156000	0.23981603	0.430275719
#47B siRNA			156000	0.273573425	0.733736182
#48A siRNA			196000	0.23981603	0.673616788
#48B siRNA	MND4	MetaEnhancer_1136_+	196000	0.273573425	0.842841545
#48C siRNA			196000	0.273573425	0.842841545
#48D siRNA			196000	0.273573425	0.842841545
#48E siRNA	ACKR1	MetaEnhancer_1136_+	196000	0.273573425	0.842841545
#48F siRNA			196000	0.273573425	0.842841545
#48G siRNA			196000	0.273573425	0.842841545

Table S8. eRNA primers. Target gene column contains gene names. Enhancer_ID column contains assigned Enhancer_ID for each eRNA tested. eRNA-F column contains name of forward primers used for realtime PCR detection of eRNA expression. Forward primer sequence column contains forward primer sequences. eRNA-R column contains name of reverse primers used for realtime PCR detection of eRNA expression. Reverse primer sequence column contains reverse primer sequences.

Table_S8

eRNA primers

Target gene	Enhancer_ID	eRNA-F	Forward primer sequence	eRNA-R	Reverse primer sequence
HLA-DMA	MetaEnhancer_475_+	eRNA#1A-F	CTTCTTCACTCCTAAACTACACACC	eRNA#1A-R	AGAGTGATAAAGAGAGGGCTGA
HLA-DRA & DRB5	MetaEnhancer_157_-	eRNA#1B-F	AATGAAAACCTGTCCCCTCTG	eRNA#1B-R	AGGTGTGTAGTTTTAGGAGTGAAGAA
		eRNA#2-3A-F	CTCCCCATTATCTCCTTTCTTTT	eRNA#2-3A-R	AGGGATATAGGCTTTATAAACATTGG
		eRNA#2-3B-F	GTGTATGTAGGTTCTCTGACAGAAGT	eRNA#2-3B-R	TTTTTCCCATAAGAAAGACAGA
TNFSF10-1	MetaEnhancer_116_+	eRNA#2-3C-F	TCCTCCACAGGAACCTTGGT	eRNA#2-3C-R	GGCCATTGGTACATCCTCAC
		eRNA#5A-F	TTGTATGTATTGTGAACGCCACT	eRNA#5A-R	CATTTCCAGGTGAATAACTTTGG
		eRNA#5BC-F	AGGATCTTCTTCAGCCTCCA	eRNA#5BC-R	AATACATACAAGAGGGAGCTTGG
ZFAND6	MetaEnhancer_246_+	eRNA#6A-F	TCTTCCTGGAATTAAGTGTCAAA	eRNA#6A-R	TGTAATTCAAGAATTGCTGGAGAC
		eRNA#6B-F	GGGATTTTTCTCTGATAATCATTGTG	eRNA#6B-R	TTGAGTTTTACCTCCAGGAGTTCT
		eRNA#7A-F	TGAGAGGATATTCTGCCGTTG	eRNA#7A-R	GAAGTGAAGTCTCCAGTCTTCTTAAA
IRF8	MetaEnhancer_259_+	eRNA#7B-F	TGGGGGACTAAGTTCTTATCATGT	eRNA#7B-R	CCTGCATGTGTTCTCAATAAGC
		eRNA#8A-F	TGGCTGTTCTTGGTTTTGTTT	eRNA#8A-R	CGGGACTTTTTGTACACTTGG
		eRNA#8B-F	ACTCCTGTCACTGGTGGATG	eRNA#8B-R	GCCCTATGTAAGGGATGC
PELI1	MetaEnhancer_327_+	eRNA#9A-F	TTTTCAACTCCCCTCCTGCT	eRNA#9A-R	TTTCAAGGTGCATTTAGCAC
		eRNA#9B-F	TCTCTGGGCTTGTCTACT	eRNA#9B-R	GCAGGAGGGGAGTTGAAAT
		eRNA#10-F	AGGCTGTGTTCTTTTCCATGT	eRNA#10-R	AGAAATTTGCAGATACCTTGAGC
APOBEC3D-1 & APOBEC3B	MetaEnhancer_600_+	eRNA#11-12A-F	CCTTGCCTCTAGGCTGAGGA	eRNA#11-12A-R	TCCTCTGGCTTTGATTCTGG
		eRNA#11-12B-F	AGGTGGACGCTGAGACTGT	eRNA#11-12B-R	CCAGATGCCCACTTCAACAT
		eRNA#13A-F	CTGGAATGTTCTCCTCCAA	eRNA#13A-R	AAGCGCCTTGTTGGTTAAAGA
DMXL1-1	MetaEnhancer_699_+	eRNA#13B-F	ACCCTCTTTCTCTGTCACCT	eRNA#13B-R	GCAAGGCCAATATGACTGAA
		eRNA#14A-F	CCTATGTGTTCTGGGCTTGA	eRNA#14A-R	TTTGGTGTCTTTTAACTCCA
		eRNA#14B-F	AAGAACCACAGCCGAGAT	eRNA#14B-R	GCTCAGGAAGTTCTGAATCAGTC
ZCCHC2	MetaEnhancer_804_+	eRNA#14C-F	AAGACACCAAAATCTCTGACA	eRNA#14C-R	ATCCTGGGCTTGGGTTCTT
		eRNA#17A-F	GTAGCATTCTGTCTCATTATAC	eRNA#17A-R	TAAATGAGCACAGAATGC
		eRNA#17B-F	CCACTTTTAGGAGTGTATGTACTTGG	eRNA#17B-R	CAAATGTTCTTGTGGCAGCA
APOBEC3D-2	MetaEnhancer_94_-	eRNA#18A-F	ATCTGGGTGTCTCTGGGAAA	eRNA#18A-R	GCACACACAGACAGTGACAGG
		eRNA#18B-F	ATGACAGCTGTGCGAGGAG	eRNA#18B-R	ACACAGACAGTGCCCTCAGGA
		eRNA#23A-F	TCCATTCTTTGTGTTGGACTG	eRNA#23A-R	TGCGATTATAGAGTGTGAGAAACA
CCR1	MetaEnhancer_258_-	eRNA#23B-F	CGCAAGTAGGGAGGTATCTCTT	eRNA#23B-R	TGCAGAAATATTTGAATGACACTTG
		eRNA#24A-F	TATGGAACTGGAGGCACCAT	eRNA#24A-R	TGCAGGTGTTTTATTTTAAAGCA
		eRNA#24B-F	TGACCATCTAGCTCACCATCTG	eRNA#24B-R	TCCCAAACAAGTGGTCTTCA
TLR7-2	MetaEnhancer_341_-	eRNA#26AB-F	TCTCTTTTTCATGGGTGAGTTTC	eRNA#26AB-R	GCAGAAAGTTAGCCACAGGA
		eRNA#26C-F	CAGCCCTGACTTCTCAGCTC	eRNA#26C-R	CAACTGTGTGTGTGTGTGTG
		eRNA#28A-F	GGCCAAAATTAATATGTACAACG	eRNA#28A-R	ACTGTTAAATTAAGTTTGGACTAAAGC
WDFY1	MetaEnhancer_512_-	eRNA#28B-F	CAACGGAGGCTTTAGTCCAA	eRNA#28B-R	GACTGATACAATTTAGCAATACTGA
		eRNA#28C-F	GGTTACATATCAAGTTAGGTTCACTG	eRNA#28C-R	TTTTGGCCTAAAGGTTTTTCA
		eRNA#29A-F	CTGTGTGGAGCTGTGTGATG	eRNA#29A-R	CTCCCAAAGGCCCTCATGTA
MYCBP2	MetaEnhancer_544_-	eRNA#29B-F	CTGCTTCCGATGTGCTCTGT	eRNA#29B-R	TCACACAGCTCCACACAGACT
		eRNA#29C-F	GGCCTTTGGGAGATACTGA	eRNA#29C-R	GGTTGGAGCCTCAACTCCTA
		eRNA#30-F	CCATCTTGGGCCTATCACAC	eRNA#30-R	CTCCACAGAGATGCAGGTCA
TNFSF10-2	MetaEnhancer_734_-	eRNA#34A-F	TTTAGCTCCTCGAAAGGTAGAGA	eRNA#34A-R	TTTAGCTCCTCGAAAGGTAGAGA
		eRNA#34B-F	GCCTGGAAGATGCCTCTGTT	eRNA#34B-R	CTACCTGGCACACACACCAG
		eRNA#35-F	CTGCTATCTAGATCTTTG	eRNA#35-R	CTCGCTTGGGTACAACAT
IFN1	MetaEnhancer_1136_+	eRNA#36AB-F	CGACCGTCCATTCTTTGAGT	eRNA#36AB-R	AGAGAAGTTGCAGCGTCAGC
		eRNA#36C-F	CGACCGTCCATTCTTTGAGT	eRNA#36C-R	AGAGAAGTTGCAGCGTCAGC
		eRNA#37A-F	TGGGCGCTTCATAGGACT	eRNA#37A-R	TCTGGTCTTTTAAAGGGTCTTGA
PARP14	MetaEnhancer_2972_-	eRNA#37BC-F	ACATCTCACCCCGACACCT	eRNA#37BC-R	CTATGAAGCGCCAGCTAGA
		eRNA#38AB-F	TGGTGGCAAGATCTCAATCA	eRNA#38AB-R	TCAGGGATGCAGACGAGATA
		eRNA#38C-F	CGGTACAATGCTCTGATTATCTCG	eRNA#38C-R	GGACCATAAGTAATCAGGGATGC
SOCS1	MetaEnhancer_810_-	eRNA#39AC-F	TCACGTAAACAATAAAAGCTTCA	eRNA#39AC-R	CAAAAGAAATTGACCTTCTTGTG
		eRNA#39B-F	TTTTTGAGAGGCTGAAGGT	eRNA#39B-R	TGAAGCTTTTATTTGTTACGTGAG
		eRNA#40-F	ATGGGTTTGAAGCAGGATTT	eRNA#40-R	CAGCCAGTTACAGGGAAGTCA
SAMD9	MetaEnhancer_3039_+	eRNA#41-F	AAGGCTGATGTGAATCTCTGC	eRNA#41-R	TGGAGCAATCACATGACACA
		eRNA#42A-F	TCTGCTGCTTCTGAGGGATT	eRNA#42A-R	GATTTAGGAGTTTAATTGAGCAAAAA
		eRNA#42BC-F	CCAGCTTGTGGGGAGGAG	eRNA#42BC-R	GAATCCCTCAGAAGCAGCAG
KIAA0040	MetaEnhancer_1115_+	eRNA#43A-F	GGCCGTCTGTTCTAGTTATGG	eRNA#43A-R	CCGGTTGACACAGCTGGTAG
		eRNA#43B-F	CGACCGTTCCATTCTTGAGT	eRNA#43B-R	TCAGCTGGATGAGCCATAACT
		eRNA#46A-F	ACCAAAAGGTTTAAAAATATCTCG	eRNA#46A-R	ACCTCAGAAGCTCCTGGTCA
PARP9	MetaEnhancer_2972_-	eRNA#46BC-F	CACCTCTCATGCAGGGCTGA	eRNA#46BC-R	GTGCTTGGGGTTGTGAGATT
		eRNA#47-48A-F	CAGGAGTGGTCTGCCTCTTC	eRNA#47-48A-R	ACTCGCTTGGGTACAAACAT
		eRNA#47-48B-F	TGCTATCTAGATCTTTGACTACCAACC	eRNA#47-48B-R	GAAGAGGCAGACCCTCTCTG

Table S9. mRNA primers. Gene name column lists target gene analyzed. Forward primer column contains sequence of the forward primer and Reverse primer column contains sequence of the reverse primer used for detecting mRNA expression.

Table_S9

mRNA primers

Gene name	Forward primer	Reverse primer
<i>HLA-DMA</i>	GATCTAAGGCCACCCTCTCG	GCAGCTCCTTG GTTCTGTTC
<i>HLA-DRA</i>	TCCCGAGCTCTACTGACTCC	TGATAGCCCATGATTCCTGA
<i>HLA-DRB5</i>	CCAGCATGGTGTGTCTGAAG	AGCCAGTGGGGAGCTCAG
<i>TNFSF10</i>	AAGGAAGGGCTTCAGTGACC	GACTGCAGGAGCACTGTGAA
<i>ZFAND6</i>	CCAATCCAGTGGCTCTCCT	CCTCCGTCCGCTGTTTATTA
<i>IRF8</i>	TCGACACCAGCCAGTTCTTC	CTCTTCCCAGCCTCTTCTGC
<i>MLLT6</i>	AGCTCATGGGAGTATGAAGGA	AGTAGACCAGCGGGTTCTCG
<i>PELI1</i>	CCCTCCTTGCGAGTGTATGT	CCGCTGCTGCTAGTGGAG
<i>TLR7</i>	TCCCATCAGAGGCTCATGGA	ATGATTGTCTGTGGCCAGGG
<i>APOBEC3D</i>	AACTTGGCTCACTGCAACCT	GAGTTCGAGACCAGCCTGAC
<i>APOBEC3B</i>	TGCTGGGACACCTTTGTGTA	CCATCCTTCAGTTTCCCTGA
<i>DMXL1</i>	GTGTCCGTTGCAGGACTAGG	CCACGGAGAAGCAGTGGT
<i>ZCCHC2</i>	CCTGAGGGAACACTTGGAGA	AACTTGCACGGCTCTACCTC
<i>CD2AP</i>	GCGCTGAAGAGACTGGTAGG	GCTCCTCCTCCTCCTCCTC
<i>CD38</i>	GGGAGGTGCAGTTTTCAGAAC	CGAGGATCAGGACCAGGATA
<i>CCR1</i>	CATCTCCAACCAAGGACCCC	CACACAGTGGGCACATTTTGT
<i>SEMA4D</i>	AACACTCACCGTGAAGGTCTG	CGTCTGGAGTCTGTCCCTTC
<i>WDFY1</i>	GGCCGAAATCCACTCCAG	CTCCTTGGGGATGAGCAG
<i>MYCBP2</i>	GAAGGAGGTCGCTGTCTTTG	ACACACAGCCCTTTTCCAAC
<i>SOCS1</i>	CTGGAGCACTACGTGGCG	AGGGGAAGGAGCTCAGGTAG
<i>IFNB1</i>	TCTCCTAGCCTGTGCCTCTG	GCCATCAGTCACTTAAACAGCA
<i>IFI16</i>	GAATAGGAGCAAGCCAGCAC	AAGTTCCCAGAAACGGAACC
<i>PARP14</i>	TACTTCCAGAGCCCGAAGAG	CGGGTAGAAGAACACCAGGA
<i>CD38</i>	GGGAGGTGCAGTTTTCAGAAC	CGAGGATCAGGACCAGGATA
<i>IFI35</i>	AGGGATTTACGGAAATGAA	AAGGGCTGTGGTCTCTCTCA
<i>SAMD9</i>	CCGTTAAAACCAGAATGAGGA	TGTGGGGAAAACCATCTCTT
<i>KIAA0040</i>	TTCAGGAAGTTGTGCCTGTG	TGTGTTCCCTGCCTTCCTAC
<i>PARP9</i>	CTGCCCTTTCACTGAACTCC	CGAAGGAAGCTGGAGAGCTA
<i>ZBP1</i>	GCATCTATTTCCGGGCTGTA	CTGCAAGGAGTCGGAGAGAC
<i>MNDA</i>	TGGCTCTAACAAGTGCCATT	CACTGTCCGTAAAGCTTTGGA
<i>ACKR1</i>	CTGTCCCATTGTCCCCTAGA	CTGTGAGGCTGCATAATGA