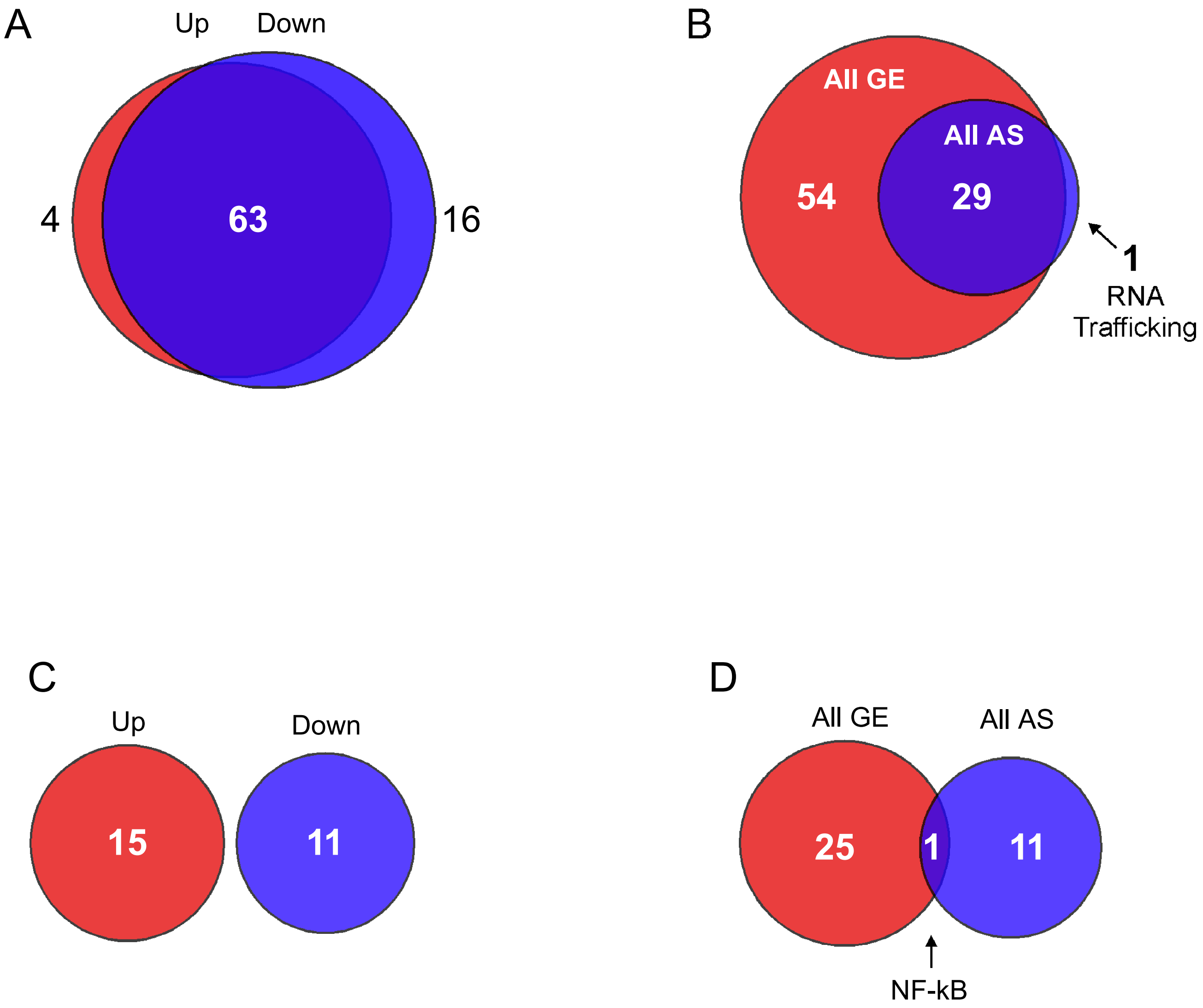
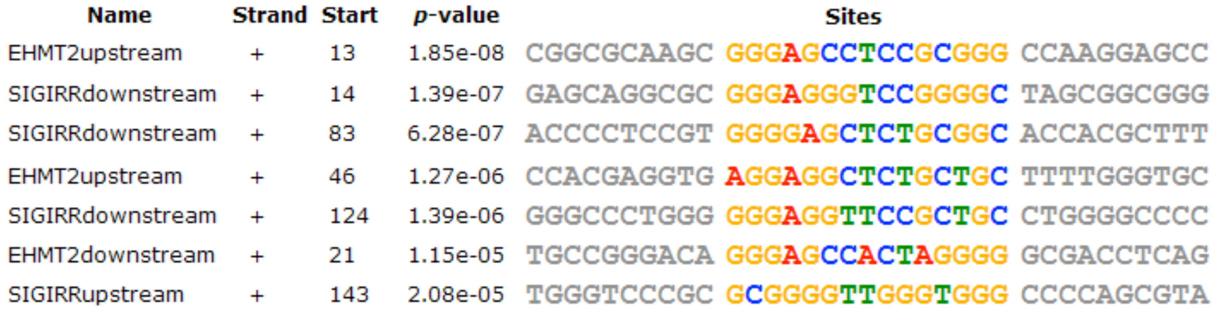


Supplemental Figure 1: Comparison of IPA analysis of gene expression (GE) changes upon stimulation of JSL1 cells. (A) Functional categories enriched in genes up-regulated (red) vs. down-regulated (blue) upon stimulation. (B) Functional categories enriched in all genes that change expression (GE, red) vs. splicing (AS, blue). (C) Signaling pathways enriched in genes up-regulated (red) vs. down-regulated (blue) upon stimulation. (D) Signaling pathways enriched in all genes that change expression (GE, red) vs. splicing (AS, blue). See supplemental table 5 for further detail.

Supplemental Figure 2

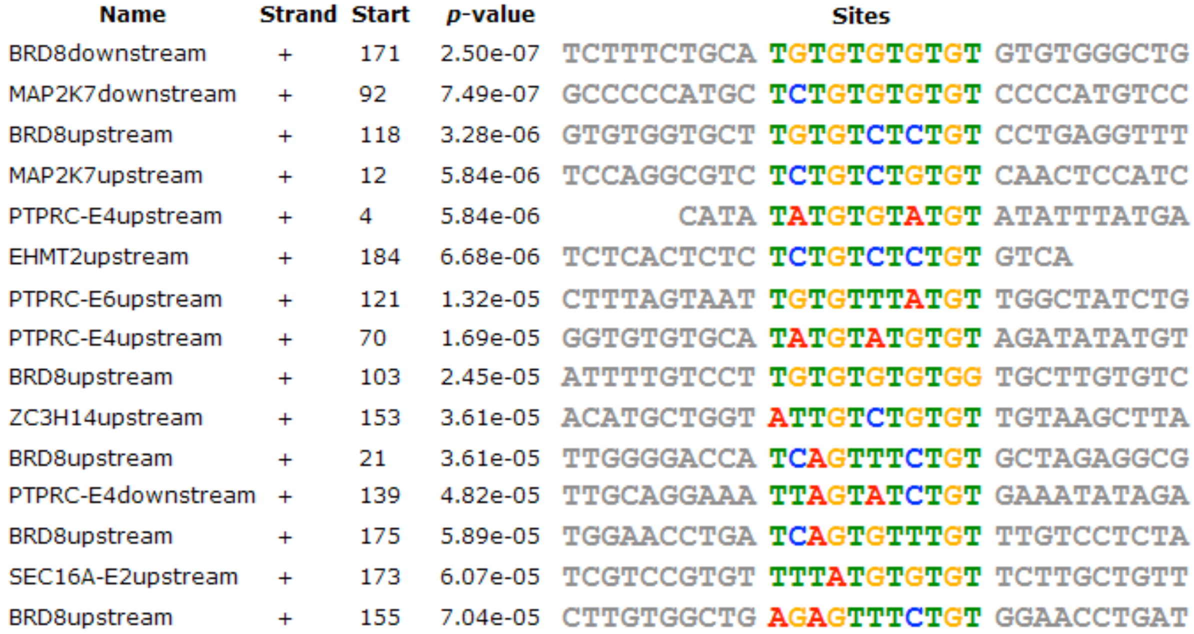
Category I

Motif 1



Name	Strand	Start	*p*-value	Sites
EHMT2upstream	+	13	1.85e-08	CGGCGCAAGC GGGAGCCTCCGCGGG CCAAGGAGCC
SIGIRRdownstream	+	14	1.39e-07	GAGCAGGCGC GGGAGGGTCCGGGGC TAGCGGCGGG
SIGIRRdownstream	+	83	6.28e-07	ACCCCTCCGT GGGGAGCTCTGCGGC ACCACGCTTT
EHMT2upstream	+	46	1.27e-06	CCACGAGGTG AGGAGGCTCTGCTGC TTTTGGGTGC
SIGIRRdownstream	+	124	1.39e-06	GGGCCCTGGG GGGAGGTTCCGCTGC CTGGGGCCCC
EHMT2downstream	+	21	1.15e-05	TGCCGGGACA GGGAGCCACTAGGGG GCGACCTCAG
SIGIRRupstream	+	143	2.08e-05	TGGGTCCCGC GCGGGGTTGGGTGGG CCCCAGCGTA

Motif 2

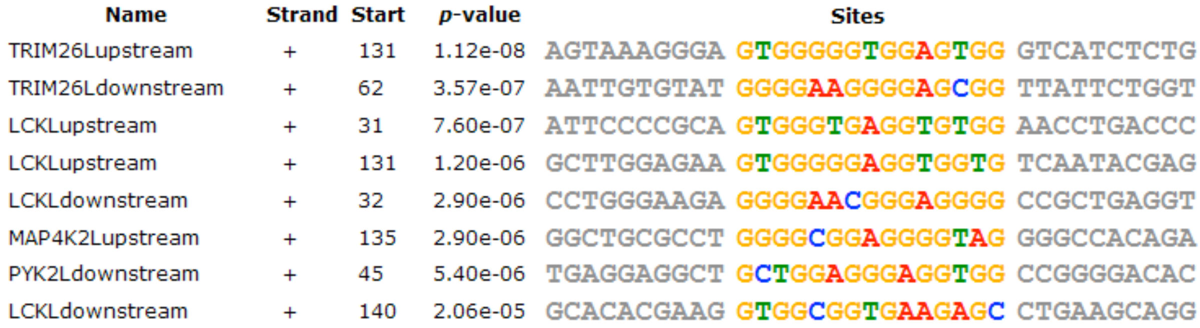


Name	Strand	Start	*p*-value	Sites
BRD8downstream	+	171	2.50e-07	TCTTTCTGCA TGTGTGTGTGT GTGTGGGCTG
MAP2K7downstream	+	92	7.49e-07	GCCCCCATGC TCTGTGTGTGT CCCCATGTCC
BRD8upstream	+	118	3.28e-06	GTGTGGTGCT TGTGTCTCTGT CCTGAGGTTT
MAP2K7upstream	+	12	5.84e-06	TCCAGGCGTC TCTGTCTGTGT CAACTCCATC
PTPRC-E4upstream	+	4	5.84e-06	CATA TATGTGTATGT ATATTTATGA
EHMT2upstream	+	184	6.68e-06	TCTCACTCTC TCTGTCTCTGT GTCA
PTPRC-E6upstream	+	121	1.32e-05	CTTTAGTAAT TGTGTTTATGT TGGCTATCTG
PTPRC-E4upstream	+	70	1.69e-05	GGTGTGTGCA TATGTATGTGT AGATATATGT
BRD8upstream	+	103	2.45e-05	ATTTTGTCCT TGTGTGTGTGG TGCTTGTGTC
ZC3H14upstream	+	153	3.61e-05	ACATGCTGGT ATTGTCTGTGT TGTAAGCTTA
BRD8upstream	+	21	3.61e-05	TTGGGGACCA TCAGTTTCTGT GCTAGAGGCG
PTPRC-E4downstream	+	139	4.82e-05	TTGCAGGAAA TTAGTATCTGT GAAATATAGA
BRD8upstream	+	175	5.89e-05	TGGAACCTGA TCAGTGTTTGT TTGTCCTCTA
SEC16A-E2upstream	+	173	6.07e-05	TCGTCCGTGT TTTATGTGTGT TCTTGCTGTT
BRD8upstream	+	155	7.04e-05	CTTGTGGCTG AGAGTTTCTGT GGAACCTGAT

Supplemental Figure 2

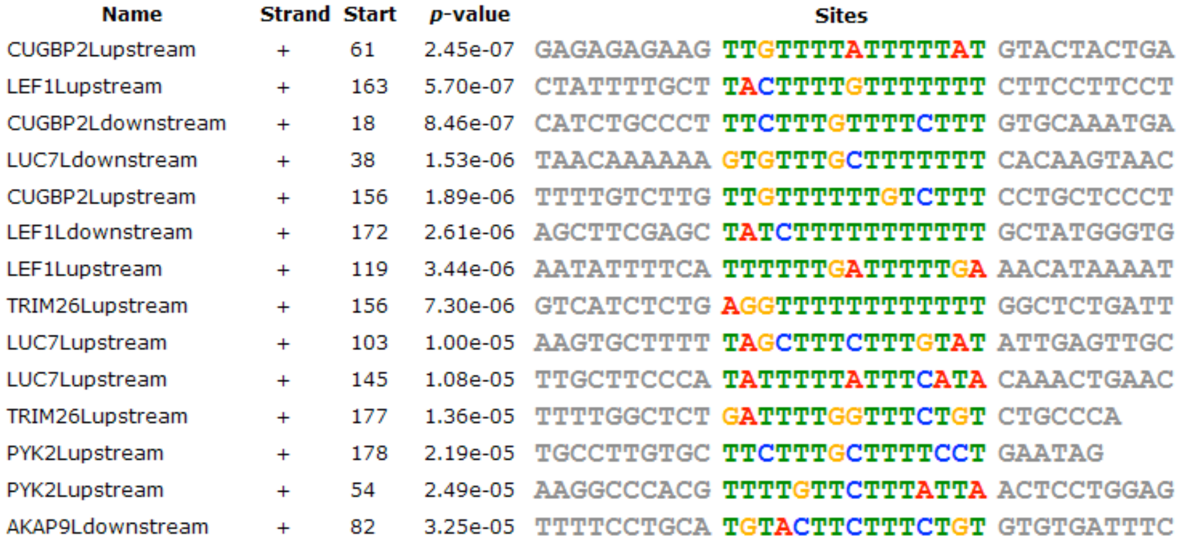
Category II

Motif 1



Name	Strand	Start	*p*-value	Sites		
TRIM26Lupstream	+	131	1.12e-08	AGTAAAGGGA	GTGGGGGTGGAGTGG	GTCATCTCTG
TRIM26Ldownstream	+	62	3.57e-07	AATTGTGTAT	GGGGAAGGGGAGCGG	TTATTCTGGT
LCKLupstream	+	31	7.60e-07	ATTCCCCGCA	GTGGGTGAGGTGTGG	AACCTGACCC
LCKLupstream	+	131	1.20e-06	GCTTGGAGAA	GTGGGGGAGGTGGTG	TCAATACGAG
LCKLdownstream	+	32	2.90e-06	CCTGGGAAGA	GGGGAACGGGAGGGG	CCGCTGAGGT
MAP4K2Lupstream	+	135	2.90e-06	GGCTGCGCCT	GGGGCGGAGGGGTAG	GGGCCACAGA
PYK2Ldownstream	+	45	5.40e-06	TGAGGAGGCT	GCTGGAGGGAGGTGG	CCGGGGACAC
LCKLdownstream	+	140	2.06e-05	GCACACGAAG	GTGGCGGTGAAGAGC	CTGAAGCAGG

Motif 2



Name	Strand	Start	*p*-value	Sites		
CUGBP2Lupstream	+	61	2.45e-07	GAGAGAGAAG	TTGTTTTATTTTTAT	GTACTACTGA
LEF1Lupstream	+	163	5.70e-07	CTATTTTGCT	TACTTTTGTTTTTTT	CTTCCTTCCT
CUGBP2Ldownstream	+	18	8.46e-07	CATCTGCCCT	TTCTTTGTTTTCTTT	GTGCAAATGA
LUC7Ldownstream	+	38	1.53e-06	TAACAAAAAA	GTGTTTGCTTTTTTT	CACAAGTAAC
CUGBP2Lupstream	+	156	1.89e-06	TTTTGTCTTG	TTGTTTTTTGTCTTT	CCTGCTCCCT
LEF1Ldownstream	+	172	2.61e-06	AGCTTCGAGC	TATCTTTTTTTTTTT	GCTATGGGTG
LEF1Lupstream	+	119	3.44e-06	AATATTTTCA	TTTTTTGATTTTTGA	AACATAAAAT
TRIM26Lupstream	+	156	7.30e-06	GTCATCTCTG	AGGTTTTTTTTTTTT	GGCTCTGATT
LUC7Lupstream	+	103	1.00e-05	AAGTGCTTTT	TAGCTTTCTTTGTAT	ATTGAGTTGC
LUC7Lupstream	+	145	1.08e-05	TTGCTTCCCA	TATTTTTATTTCATA	CAAACTGAAC
TRIM26Lupstream	+	177	1.36e-05	TTTTGGCTCT	GATTTTGGTTTCTGT	CTGCCCA
PYK2Lupstream	+	178	2.19e-05	TGCCTTGTGC	TTCTTTGCTTTTCCT	GAATAG
PYK2Lupstream	+	54	2.49e-05	AAGGCCCACG	TTTTGTTCTTTATTA	ACTCCTGGAG
AKAP9Ldownstream	+	82	3.25e-05	TTTTCCTGCA	TGTACTTCTTTCTGT	GTGTGATTTC

Category III

Name	Strand	Start	*p*-value	Sites		
PIGQupstream	+	63	4.36e-16	GCGACGGAGG	GGGCGGGGAGAGCTTCGTGGGTGGCCACGGCCAGCAGCAC	CCGGGTGCCC
PIGQupstream	+	9	1.11e-12	GCCTGGCTG	CAGGAGGCTTTGATGCCGGCCTGGCAGCCAGCTCCAGGAG	TTGGGCGACG
PIGQdownstream	+	60	9.20e-12	ACGGTGGGGT	CAGCTGGGTGTAGTGTCTGGGTGGCACCACGCCAGCCTGC	GATGAGGTAC
H2AFYdownstream	+	10	2.40e-10	TAATGCCTAG	CCGGGTGCTGCCGAGTGTGTGTGTGCATGGTCAGTCGGCC	GCTGCAGACA