Table SI. Sequences of the primers used for reverse transcription-quantitative PCR.

Gene	Primer sequence (5'- 3')
JUNB	Fwd: ATACACAGCTACGGGATACGG
	Rev: GCTCGGTTTCAGGAGTTTGT
JUN	Fwd: CCAAAGGATAGTGCGATGTTT
	Rev: CTGTCCCTCTCCACTGCAAC
FOS	Fwd: CTACCACTCACCCGCAGACT
	Rev: AGGTCCGTGCAGAAGTCCT
JUND	Fwd: CAGCGAGGAGCAGGAGTT
	Rev: GAGCTGGTTCTGCTTGTGTAAAT
ATF3	Fwd: TCTCATCTTCTGGAGTCCTC
	Rev: TTGAGGAGCTCAAGAACG
ATF7	Fwd: AAGATCCAGATGAGCGAC
	Rev: TTCTTCTCTAGGGAGGACAC
JDP2	Fwd: TCAATCTGGGTCTTCAGC
	Rev: AGAACAAAGTCGCAGCAG
CREB1	Fwd: TTGGACTTGTGGAGACTG
	Rev: TCATGCAACATCATCTGC
CREB3L4	Fwd: ACAACCTCATAGAGCATAGGAG
	Rev: TCAAGAGAGTGAGCCTGAAG
PVRL4	Fwd: CTCCAGGACCAAAGGATCAC
	Rev: TCAAGGCCCCTCACAGAG
HPRT1	Fwd: TGACCTTGATTTATTTTGCATACC
	Rev: CGAGCAAGACGTTCAGTCCT

Fwd, forward primer; Rev, reverse primer; ATF, activating transcription factor; CREB, cAMP responsive element binding protein; HPRT1, hypoxanthine phosphoribosyltransferase 1; JDP2, Jun dimerization protein 2.

Table SII. Target sequence of the siRNAs used in the present study.

Gene	Target sequence (5'- 3')
Control	UGGUUUACAUGUCGACUAA UGGUUUACAUGUUGUGUGA UGGUUUACAUGUUUUCUGA UGGUUUACAUGUUUUCCUA
JUN	AUAUGGAAUUGCUUACCAAAGGATA
JUNB	GAAACACGCACUUAGUCUCUAAAGA
JUND	CGAGUCCACAUUCCUGUUUGUAATC
FOS#1	GGGGCAAGGUGGAACAGUUAUCUCC
FOS#2	CAGUGGAACCUGUCAAGAGCAUCAG
FOS#3	CUGAUUAGAAAUGACCAAUAUUATA
ATF3	GCAUUUGAUAUACAUGCUCAACCTT
ATF7	GCUAGCUCCUUUGAACAUGAAUUCA
JDP2	CGUGAAAAGUGAGCUAGAUGAGGAA
CREB1	GAGAGAGGUCCGUCUAAUG
CREB3L4	GCUAAUUGCUCAAACUUCCAACAAA
PVRL4#1	CCAAACUCUUCUUAGUCUGAAAUCT
PVRL4#2	CAAGGGAUUCUCAGGUCACUGUGGA

ATF, activating transcription factor; CREB1, CAMP responsive element binding protein 1; CREM, cAMP responsive element modulator; FOSL2, FOS-like 2; HPRT1, hypoxanthine phosphoribosyltransferase 1; JDP2, Jun dimerization protein 2.

Table SIII. Sequences of the primers used for the cloning of reporter plasmids.

Region cloned into pGL4.23, bp	Primer sequence (5' - 3')[a]	Restriction enzyme
5'-flanking region #1, -3402/-2093	Fwd: ccgctcgagcggTCTTCTCTGACCTGGGACTTC	*Xho*I
	Rev: gaagatcttcAGGAGAAACTGAGGCACAG	*Bgl*II
5'-flanking region #2, -4687/-3352	Fwd: cggggtacccgTTCGGTAGGACCCATACTTG	*Kpn*I
	Rev: cccaagcttgggTGGTGAGTAATATCCTGTCTGC	*Hin*dIII
5'-flanking region #3, -6717/-5455	Fwd: ccgctcgagcggTCTGCAGTGGTCTATAATGACC	*Xho*I
	Rev: cccaagcttgggTCAGTCAAAGGAGCTCTCAAG	*Hin*dIII
5'-flanking region #4, -7420/-6689	Fwd: ccgctcgagcggTCCCAACTATAGCTTTCCCTG	*Xho*I
	Rev: cccaagcttgggTGACAAGGTCATTATAGACCACTG	*Hin*dIII
5'-flanking region #5, -8058/-7270	Fwd: ccgctcgagcggACTCCTACCCTTCCCTGATATC	*Xho*I
	Rev: gaagatcttcTAGCCAGTGAGAAAGAAGCC	*Bgl*II
intron #6, +671/+910	Fwd: ccgctcgagcggTGGTGACCCAGTGTAGATG	*Xho*I
	Rev: cccaagcttgggTCCTGGTGCTCTAGAACATC	*Hin*dIII
intron #7, +4277/+4498	Fwd: ccgctcgagcggAATCTGGTGTGTCCTGAGAG	*Xho*I
	Rev: cccaagcttgggAGCTCCCAGCACAGATAAG	*Hin*dIII
intron #8, +5164/+5421	Fwd: ccgctcgagcggTAGTGGTGAGAAGGTTGGC	*Xho*I
	Rev: cccaagcttgggTCTGTGGTATGTGGCTGTG	*Hin*dIII
intron #9, +5433/+6630	Fwd: ccgctcgagcggATAGCCTCACATGCGTTTG	*Xho*I
	Rev: gaagatcttcTATACTAGCCAACCACCTGC	*Bgl*II
Intron #10, +14831/+15174	Fwd: ccgctcgagcggTCCAATTACCTCTACACCCAG	*Xho*I
	Rev: cccaagcttgggAAGACAGGGAAGCTGAAGG	*Hin*dIII
intron #11, +15750/+15891	Fwd: ccgctcgagcggCAAGTATGCACACGCACA	*Xho*I
	Rev: cccaagcttgggAAGGTGAGCCTATCCTGG	*Hin*dIII
intron #12, +16185/+16582	Fwd: ccgctcgagcggTGTCTTTCCCAGTGAGGAG	*Xho*I
	Rev: cccaagcttgggAACAGGTCCATTCTCTCCTG	*Hin*dIII
3'-flanking region #13, +55848/+56085	Fwd: ccgctcgagcggTTAGCCAGGTGTGGTGAC	*Xho*I
	Rev: cccaagcttgggAGTGCATAATCATGGCTCAC	*Hin*dIII
3'-flanking region #14, +98811/+99037	Fwd: ccgctcgagcggTTACAGGCACGTGCTACTAC	*Xho*I
	Rev: cccaagcttgggTTCAACCTGCTCTACTGTCC	*Hin*dIII

[a]Text in uppercase denotes the sequence in the genome; underlined text denotes the restriction enzyme site. Fwd, forward primer; Rev, reverse primer.

Table SIV. Primer sequences for the #10 region for the cloning of reporter plasmids.

Region	Primer sequence (5' - 3')[a]	Restriction enzyme
10-I	Fwd: ccgctcgagcggTCCAATTACCTCTACACCCAG	*Xho*I
	Rev: cccaagcttgggAACGTGTCCAGACAGCTC	*Hin*dIII
#10-II	Fwd: ccgctcgagcggTCCAATTACCTCTACACCCAG	*Xho*I
	Rev: cccaagcttgggAGAGGTCCTTTCTCCCTGC	*Hin*dIII
#10-III	Fwd: ccgctcgagcggGAGCAGGGAGAAAGGACCTC	*Xho*I
	Rev: cccaagcttgggAACGTGTCCAGACAGCTC	*Hin*dIII

[a]Text in uppercase denotes the sequence in the genome; underlined text denotes the restriction enzyme site. Fwd, forward primer; Rev, reverse primer.

Table SV. Sequences of the primers used for the cloning of mutant plasmids.

Mutant	Primer sequence (5' - 3')
#10-III FOS binding site Mut-1	Fwd: GCCTGCGGCTCTGGGCAACGTCATGGGGGTGG
	Rev: CCACCCCCATGACGTTGCCCAGAGCCGCAGGC
#10-III FOS binding site Mut-2	Fwd: CGGCTCTGGGTGACGCAATGGGGGTGGAGGGT
	Rev: ACCCTCCACCCCCATTGCGTCACCCAGAGCCG
#10-III FOS binding site Mut-1 + 2	Fwd: GCCTGCGGCTCTGGGCAACGCAATGGGGGTGG
	Rev: CCACCCCCATTGCGTTGCCCAGAGCCGCAGGC

Fwd, forward primer; Rev, reverse primer.

Table SVI. Primer sequences for the pCMV-FOS plasmid.

Gene	Primer sequence (5' - 3')[a]	Restriction enzyme
FOS	Fwd: ccggaattcggATGATGTTCTCGGGCTTCAA	*Eco*RI
	Rev: ccgctcgagTCACAGGGCCAGCAGCGTGG	*Xho*I

[a]Text in uppercase denotes the sequence in the genome; underlined text denotes the restriction enzyme site. Fwd, forward primer; Rev, reverse primer.

Table SVII. Primer sequences for the Assay for Transposase-Accessible Chromatin Sequencing.

Region	Primer sequence (5' - 3')
#10	Fwd: TCCAATTACCTCTACACCCAG
	Rev: AAGACAGGGAAGCTGAAGG
#11	Fwd: CAAGTATGCACACGCACA
	Rev: AAGGTGAGCCTATCCTGG
#13	Fwd: TTAGCCAGGTGTGGTGAC
	Rev: AGTGCATAATCATGGCTCAC
#14	Fwd: TTACAGGCACGTGCTACTAC
	Rev: TTCAACCTGCTCTACTGTCC

Fwd, forward primer; Rev, reverse primer.

Table SVIII. Primer sequences for the chromatin conformation capture assay.

PCR	Region	Primer sequence (5' - 3')
1st PCR	Promoter	
	5'	AGAACTCTGCAGCTTCCTG
	3'	ATCCTCCTTGCTCTCAACC
	Enhancer	
	5'	AGAGAGTAGGAGTTGAGGTGAG
	3'	AAGTCCACACAACAGGACAC
Nested PCR	Promoter	
	5'	TCCTTATTCAAGTCTGCAGC
	3'	AATCCAGGACCACAGTATGG
	Enhancer	
	5'	TCTGGATGTTTCTCTGGGTTG
	3'	TGATGTTGCATGGCAGGATAC

Table SIX. *PVRL4* enhancer region and NC primer sequences for the chromatin immunoprecipitation sequencing.

Region	Primer sequence (5' - 3')
PVRL4 enhancer	Fwd: GAGCAGGGAGAAAGGACCTC
	Rev: AACGTGTCCAGACAGCTC
NC (exon 1 of *GAPDH*)	Fwd: AGCTCAGGCCTCAAGACCTT
	Rev: AAGAAGATGCGGCTGACTGT

GAPDH, glyceraldehyde-3-phosphate dehydrogenase; NC, negative control; Fwd, forward primer; Rev, reverse primer.

Table SX. Changes in expression of genes related to "Cytokine Signaling in Immune System" upregulated following treatment with siPVRL4#1 and #2.

Gene	siPVRL4#1			siPVRL4#2		
	Relative expression, Log_2FC	P-value	q-value	Relative expression, Log_2FC	P-value	q-value
IFIT1	11.45	$9.5x10^{-13}$	$1.2x10^{-9}$	4.62	0.004	0.107
IFI44	10.90	$7.4x10^{-9}$	$2.6x10^{-6}$	4.23	0.029	0.301
IFI44L	9.88	$3.6x10^{-7}$	$7.5x10^{-5}$	3.51	0.084	0.490
MX1	9.82	$5.5x10^{-14}$	$1.0x10^{-10}$	3.30	0.012	0.190
XAF1	9.67	$2.6x10^{-6}$	$4.5x10^{-4}$	4.05	0.052	0.391
OAS2	9.22	$1.5x10^{-13}$	$2.6x10^{-10}$	2.95	0.020	0.254

IFIT1, interferon induced protein with tetratricopeptide repeats 1; IFI44, interferon induced protein 44; IFI44L, interferon induced protein 44-like; MX1, MX dynamin-like GTPase 1; XAF1, XIAP associated factor 1; OAS2, 2'-5'-Oligoadenylate Synthetase 2; si, small interfering; FC, fold change.