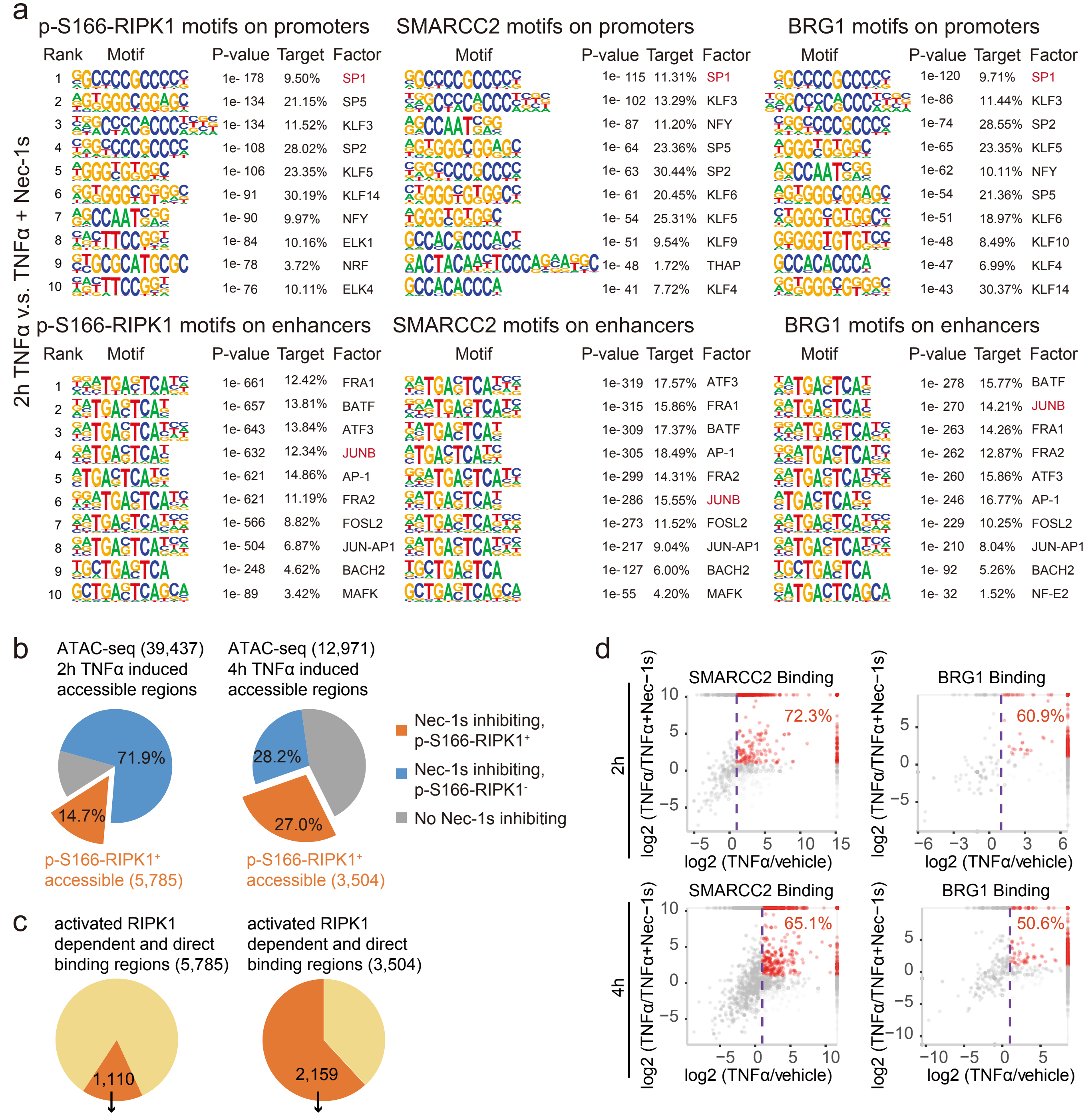
Figure S3



a

2h TNFα v.s. TNFα + Nec-1s

p-S166-RIPK1 motifs on promoters

Rank	Motif	P-value	Target	Factor
1		1e- 178	9.50%	SP1
2		1e- 134	21.15%	SP5
3		1e- 134	11.52%	KLF3
4		1e- 108	28.02%	SP2
5		1e- 106	23.35%	KLF5
6		1e- 91	30.19%	KLF14
7		1e- 90	9.97%	NFY
8		1e- 84	10.16%	ELK1
9		1e- 78	3.72%	NRF
10		1e- 76	10.11%	ELK4

SMARCC2 motifs on promoters

Motif	P-value	Target	Factor
	1e- 115	11.31%	SP1
	1e- 102	13.29%	KLF3
	1e- 87	11.20%	NFY
	1e- 64	23.36%	SP5
	1e- 63	30.44%	SP2
	1e- 61	20.45%	KLF6
	1e- 54	25.31%	KLF5
	1e- 51	9.54%	KLF9
	1e- 48	1.72%	THAP
	1e- 41	7.72%	KLF4

BRG1 motifs on promoters

Motif	P-value	Target	Factor
	1e-120	9.71%	SP1
	1e-86	11.44%	KLF3
	1e-74	28.55%	SP2
	1e-65	23.35%	KLF5
	1e-62	10.11%	NFY
	1e-54	21.36%	SP5
	1e-51	18.97%	KLF6
	1e-48	8.49%	KLF10
	1e-47	6.99%	KLF4
	1e-43	30.37%	KLF14

p-S166-RIPK1 motifs on enhancers

Rank	Motif	P-value	Target	Factor
1		1e- 661	12.42%	FRA1
2		1e- 657	13.81%	BATF
3		1e- 643	13.84%	ATF3
4		1e- 632	12.34%	JUNB
5		1e- 621	14.86%	AP-1
6		1e- 621	11.19%	FRA2
7		1e- 566	8.82%	FOSL2
8		1e- 504	6.87%	JUN-AP1
9		1e- 248	4.62%	BACH2
10		1e- 89	3.42%	MAFK

SMARCC2 motifs on enhancers

Motif	P-value	Target	Factor
	1e-319	17.57%	ATF3
	1e-315	15.86%	FRA1
	1e-309	17.37%	BATF
	1e-305	18.49%	AP-1
	1e-299	14.31%	FRA2
	1e-286	15.55%	JUNB
	1e-273	11.52%	FOSL2
	1e-217	9.04%	JUN-AP1
	1e-127	6.00%	BACH2
	1e-55	4.20%	MAFK

BRG1 motifs on enhancers

Motif	P-value	Target	Factor
	1e- 278	15.77%	BATF
	1e- 270	14.21%	JUNB
	1e- 263	14.26%	FRA1
	1e- 262	12.87%	FRA2
	1e- 260	15.86%	ATF3
	1e- 246	16.77%	AP-1
	1e- 229	10.25%	FOSL2
	1e- 210	8.04%	JUN-AP1
	1e- 92	5.26%	BACH2
	1e- 32	1.52%	NF-E2

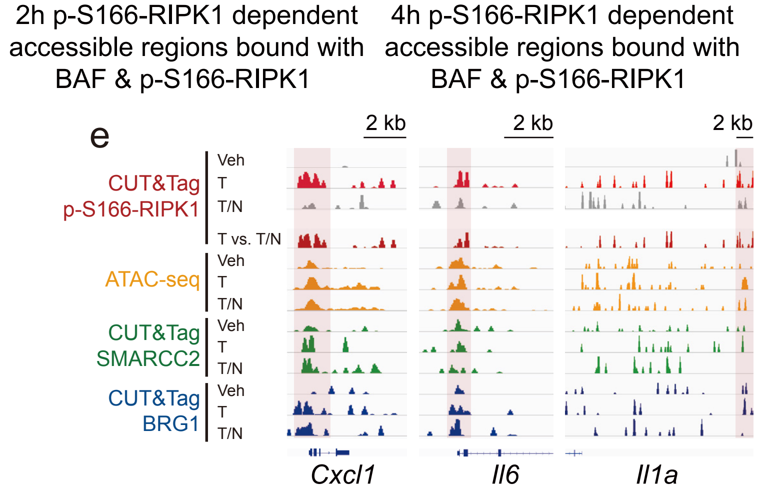


Fig. S3 Genome-wide analysis of the transcriptional targets of RIPK1 and BAF complex in *Ripk1$^{D325A/D325A}$;Ripk3$^{-/-}$* MEFs. a Top 10 results found by HOMER motif analysis of p-S166-RIPK1, SMARCC2 or BRG1 binding peaks on promoters or enhancers under the treatment of TNFα versus TNFα plus Nec-1s were shown. **b** Pie chart showed the distribution of p-S166-RIPK1 dependent regions (orange and blue) derived from TNFα induced accessible regions. p-S166-RIPK1 dependent regions (orange and blue) include regions directly bound by p-S166-RIPK1 (orange) and regions without p-S166-RIPK1 binding (blue). **c** Pie chart showed the distribution of SMARCC2, BRG1 and p-S166-RIPK1 co-binding peaks (orange) derived from p-S166-RIPK1+ accessible regions. These regions were used for Figure 3, c, d and e.**d** The log2 ratio of binding scores of SMARCC2 or BRG1 upon the treatment of TNFα versus vehicle, and TNFα versus TNFα plus Nec-1s were plotted. **e** The ATAC-seq profiles (orange) and CUT&Tag profiles of p-S166-RIPK1 (red), SMARCC2 (green) and BRG1 (blue) genomic binding upon the treatment of vehicle, TNFα and TNFα plus Nec-1s on the indicated gene loci.