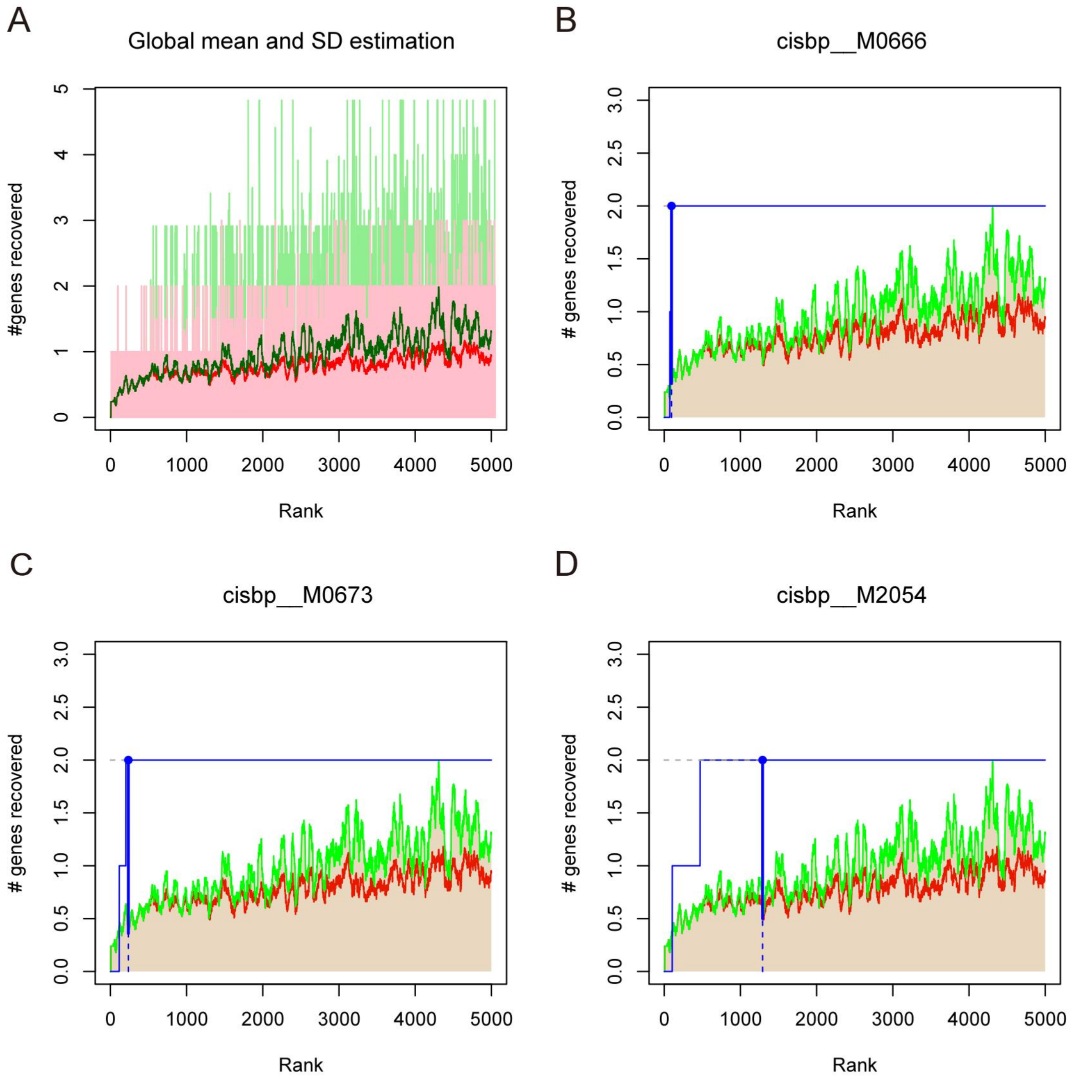
Supplementary Material

Supplementary Table S1. Primer sequences used in this study (5′–3′).

Target	**Forward primer (5′–3′)**	**Reverse primer (5′–3′)**
GAPDH (mouse)	AGGTCGGTGTGAACGGATTTG	TGTAGACCATGTAGTTGAGGTCA
MAPK14 (mouse)	GGCTCGGCACACTGATGAT	TGGGGTTCCAACGAGTCTTAAA
ADM (mouse)	CACCCTGATGTTATTGGGTTCA	TTAGCGCCCACTTATTCCACT
MAPK8 (mouse)	AGCAGAAGCAAACGTGACAAC	GCTGCACACACTATTCCTTGAG

Supplementary Figure S1. Motif enrichment analysis of transcription factor binding motifs for the key-gene set using RcisTarget. Motif enrichment was performed using RcisTarget with rankings from rcistarget.hg19.motifdb.cisbpont.500bp; enrichment was quantified by the area under the recovery curve (AUC), and normalized enrichment scores (NES) was calculated by normalizing motif AUC values to the background distribution across all motifs. The complete list of enriched motifs (NES > 3.0), inferred motif–TF annotations, and enrichment statistics is provided in Supplementary Table S2. (A) Global mean ± SD estimation derived from background motifs. (B–D) Enrichment recovery curves for representative enriched motifs, including cisbp__M0666 (NES = 8.25; enriched genes: ADM and MAPK14) (B), cisbp__M0673 (C), and cisbp__M2054 (D).



Supplementary Table S2. Results of transcription factor motif enrichment analysis for the key-gene set. Significantly enriched motifs (NES > 3.0) are listed with their motif identifiers, high-confidence TF annotations (TF_highConf), normalized enrichment scores (NES), area under the recovery curve (AUC), and enriched genes contributing to each motif.

Motif	**Gene set**	**TF (high confidence)**	**NES**	**AUC**	**nEnrGenes**	**Enriched genes**
cisbp__M0666	key_gene		8.25	0.616	2	ADM; MAPK14
cisbp__M0673	key_gene		7.62	0.571	2	ADM; MAPK14
cisbp__M2054	key_gene		6.54	0.494	2	ADM; MAPK8
cisbp__M0678	key_gene		6.52	0.492	2	ADM; MAPK14
cisbp__M1781	key_gene		6.18	0.468	2	ADM; MAPK14
cisbp__M4536	key_gene	E2F1 (directAnnotation)	5.98	0.454	2	ADM; MAPK14
cisbp__M1789	key_gene		5.76	0.438	2	ADM; MAPK14
cisbp__M0677	key_gene		5.52	0.421	2	ADM; MAPK14
cisbp__M0675	key_gene		5.38	0.411	2	ADM; MAPK14
cisbp__M0613	key_gene	MBD1 (inferredBy_Orthology)	5.17	0.396	2	ADM; MAPK14