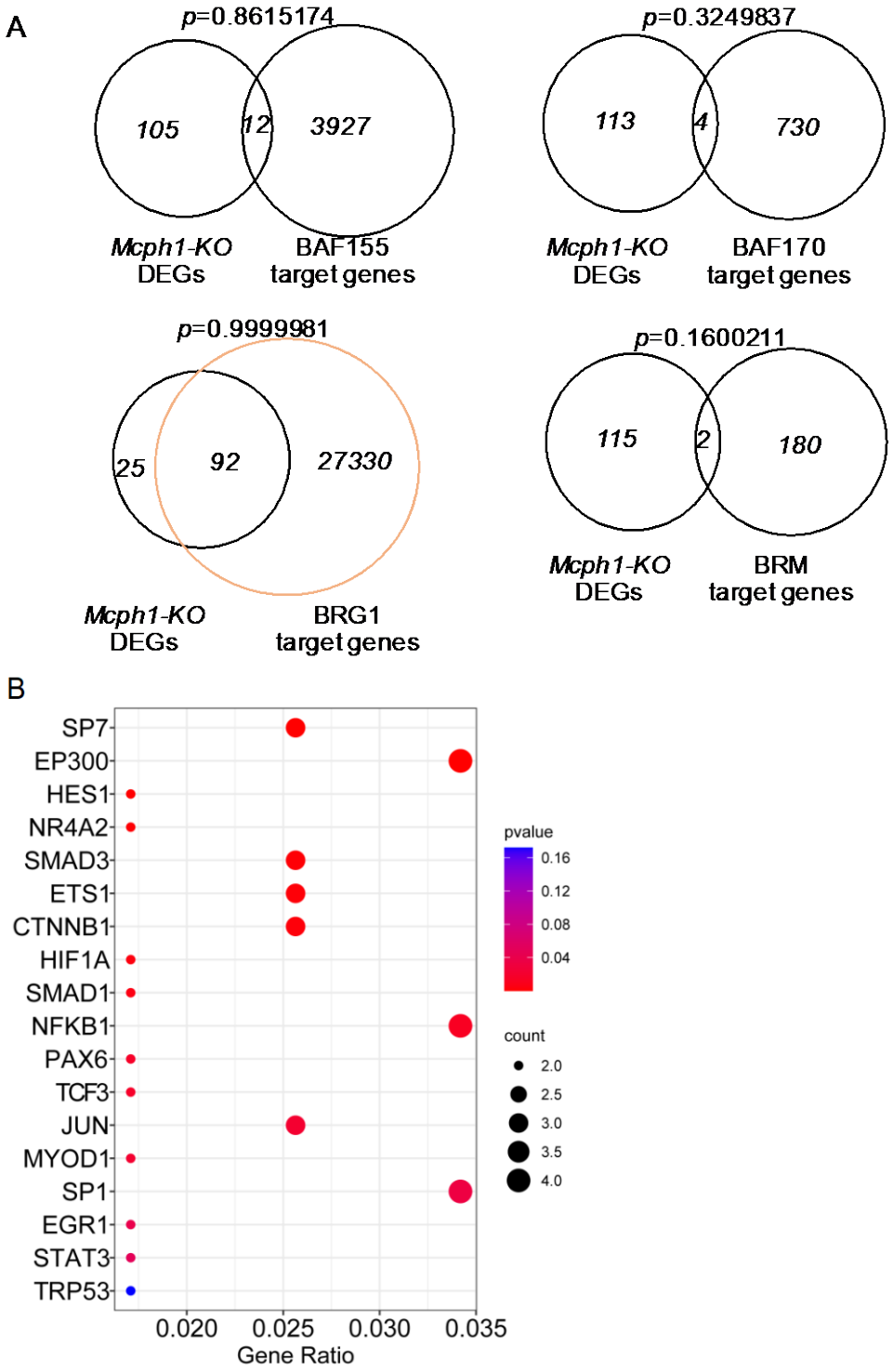

Figure S1. *Mcph1* DEGS were not associated with transcriptional regulation of the SWI/SNF complex and E2F1. (A) The Venn diagrams represent the number of intersecting genes between *Mcph1-KO* DEGs and the target genes of the core proteins of the SWI/SNF complex. The core proteins in this complex are BAF155, BAF170, BRG1, and BRM. $p > 0.05$ indicates no statistical significance. Statistical analysis was performed using Fisher's exact test. (B) *Mcph1-KO* DEGs transcription factor prediction analysis.

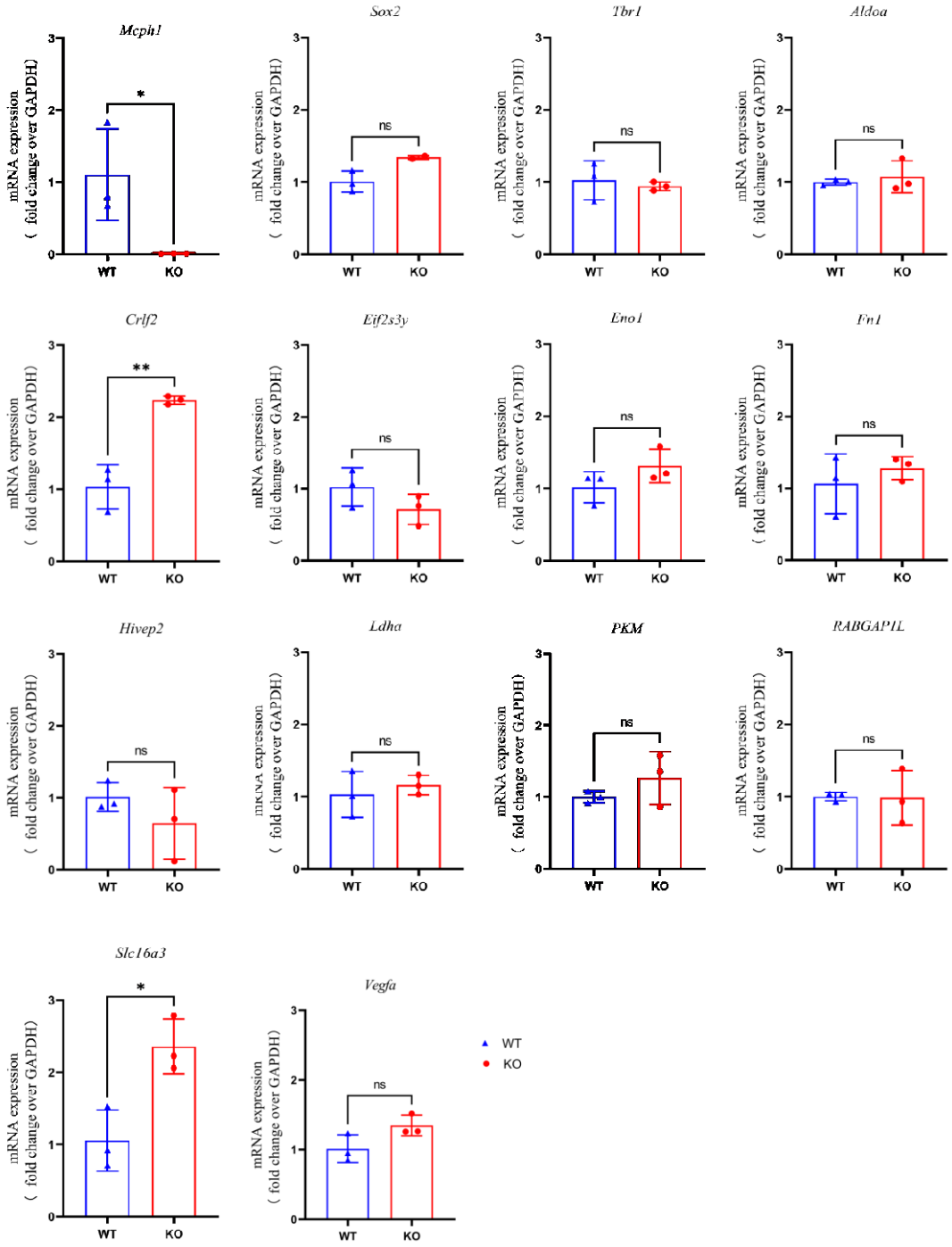

Figure S2. Expression verification of intersecting genes related to neurodevelopment. WT is the control group, and KO is the knockout of the *Mcph1* group. The expression of DEGs in the control and *Mcph1-KO* groups was detected by RT-qPCR.

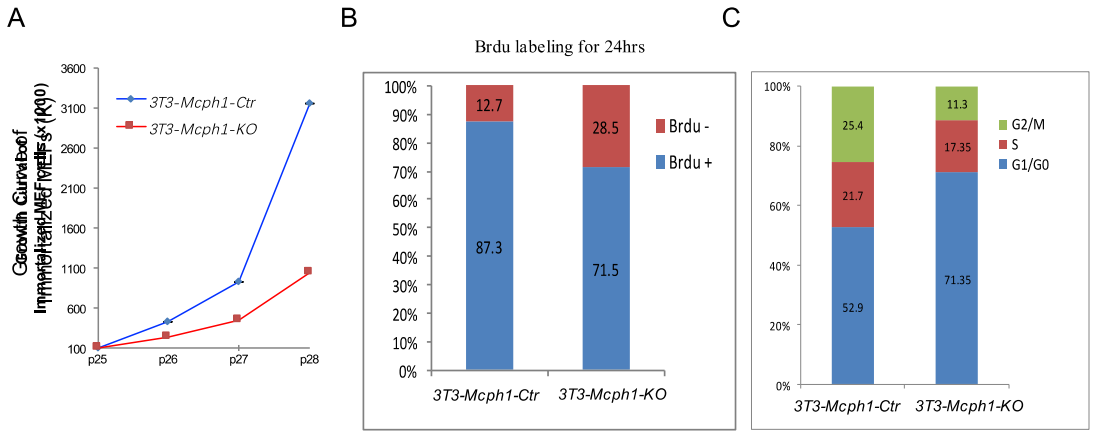

Figure S3. *Mcph1* affects cell proliferation in immortalized MEFs. (A) Growth curves of *Mcph1-Ctr* and *Mcph1-KO* immortalized MEFs. The immortalized cells have a good proliferation capability. Cells were harvested by trypsinization and counted once per passage. P25, cells at passage 25; P26, cells at passage 26; P27, cells at passage 27, and P28, cells at passage 28. (B) Immobilized MEFs, stained with BrdU antibody, and quantitative flow cytometric analysis showed that BrdU-labeled *Mcph1-KO* cells decreased at 24 h. (C) The distribution of the cell cycle was detected by flow cytometry with PI staining. The percentages of the G1, S, and G2/M phases were calculated.

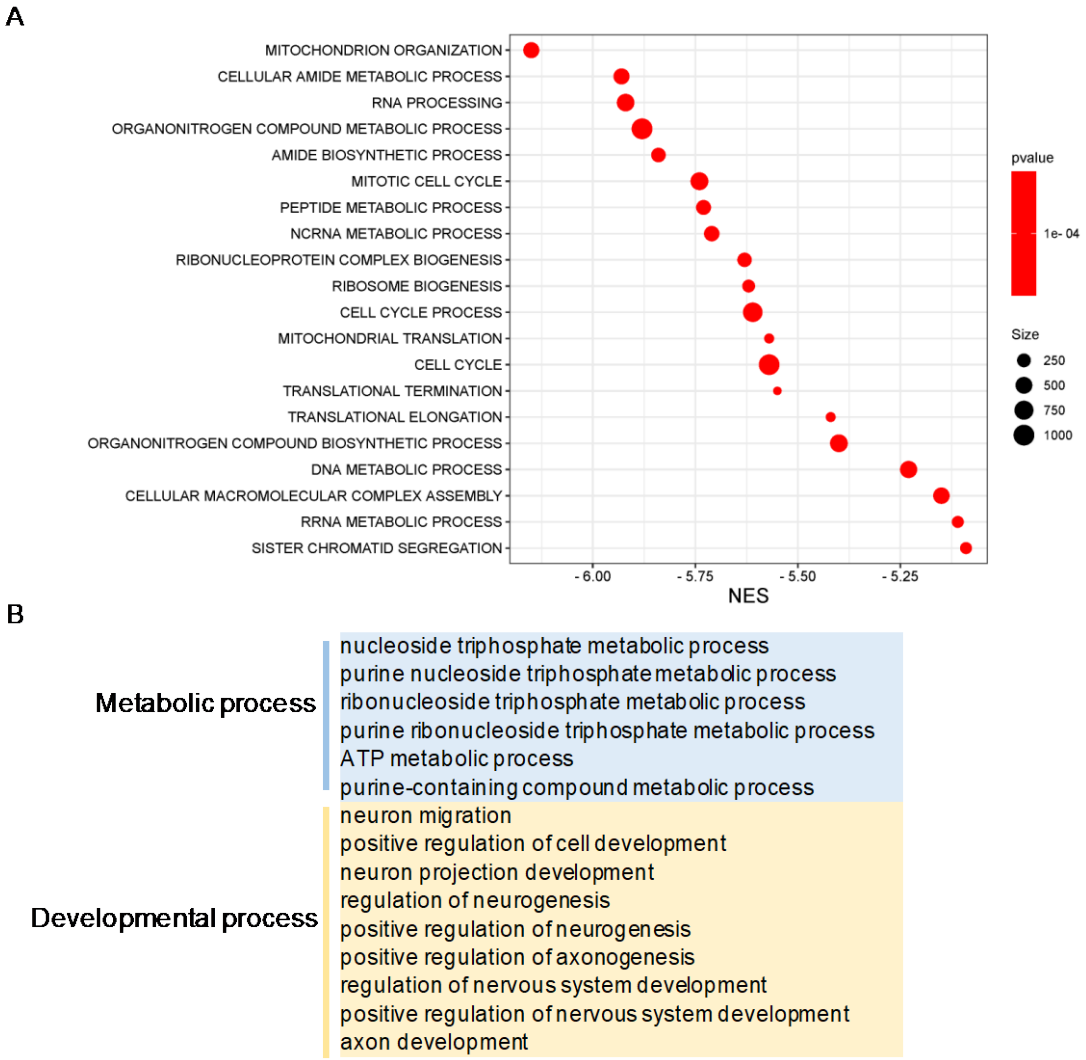

Figure S4. *Mcph1* may cause cell cycle-dependent metabolic changes (A) The biological process of the DEGs in the results of Nathalie Journiac et al[1]. The figure shows the top 20 biological processes, including metabolism-related and cell cycle related (B) We used metascape to perform the same analysis on our DEGs and their DEGs[1]. The intersection of the two different genes focuses on metabolism and development.

Table S1. Summary of intersecting genes information

NO.	Intersecting Gene	log2FoldChange	*P* adj	Site Count*	Remark
1	*Ldha*	0.53258291	1.40E-06	4	*Ldha* can affect neuronal excitability[2].
2	*Tcf7l1*	0.534401708	0.047987897	4	-
3	*Vegfa*	0.584031025	0.00033305	3	*Vegfa* affects embryonic angiogenesis[3].
4	*Hey1*	0.460385188	0.029574475	3	-
5	*Aldoa*	0.310349563	0.047987897	3	*Aldoa* is related to cytoskeletal development and function[4].
6	*Slc16a3*	1.274481753	9.16E-06	2	Deletion of *Slc16a3* is likely to result in decreased lactate in the embryo's blood and a decrease in the embryo's growth[5, 6].
7	*Tpi1*	0.444301423	8.25E-05	2	-
8	*Eno1*	0.436598496	0.000176167	2	*Eno1* inactivation causes delayed brain development[7, 8].
9	*Crlf2*	0.884397108	0.000936195	2	Crlf2 is involved in neuronal signaling, and patients have symptoms of microcephaly[9].
10	*Fn1*	0.378091826	0.001353569	2	Mouse embryos lacking *Fn1* have defects in mesoderm and neural tube development[10].
11	*Lcp1*	0.521461793	0.002515204	2	-
12	*Pkm*	0.338713642	0.003225653	2	*Pkm* is related to synaptic plasticity[2, 11].
13	*Rabgap1l*	-0.342916124	0.00422707	2	*Rabgap1l* is differentially methylated in Zika-induced microcephaly[12].
14	*Spp1*	1.198484624	0.011059793	2	-
15	*Hivep2*	-0.348226286	0.016053953	2	Mutations in the *Hivep2* gene cause developmental delay/intellectual disability[13].
16	*Nxn*	0.40763114	0.01743748	2	-
17	*Eif2s3y*	-0.42710408	0.019913806	2	*Eif2s3y* can inhibit the pluripotency state of embryonic stem cells in mice[8].
18	*Gm37844*	-0.88957664	0.021387194	2	-
19	*Inhba*	-0.8904405	0.046788412	2	-
20	*Ddit4*	0.469127086	0.047987897	2	-
21	*Satb2*	-0.72840142	2.19E-06	1	Mutations in the *Satb2* gene cause developmental delay/intellectual disability[6].
22	*Sla*	-0.603553268	0.000122916	1	-
23	*9130024F11Rik*	-0.710580795	0.00033305	1	-

Table S1.（*Continued*）

NO.	Intersecting Gene	log2FoldChange	*P* adj	Site Count*	Remark
24	*Mef2c*	-0.414368576	0.001570872	1	-
25	*Fam49a*	-0.342475004	0.002471334	1	-
26	*Alas2*	-1.196964327	0.002515204	1	-
27	*Crb2*	0.509924247	0.002920479	1	-
28	*Pfkl*	0.373654061	0.003110287	1	-
29	*Dlk1*	0.556029226	0.003225653	1	-
30	*2610318N02Rik*	0.754241912	0.003260079	1	-
31	*Dok6*	-0.398228958	0.004321018	1	-
32	*Pgk1*	0.352225734	0.006154432	1	-
33	*Gnai1*	-0.359240218	0.007113982	1	-
34	*Dll3*	0.612639822	0.009379012	1	-
35	*Cdkn1c*	0.335603094	0.011059793	1	Mutations in the *Cdkn1c* gene cause developmental delay/intellectual disability[14].
36	*Fut10*	-0.926136173	0.011932979	1	-
37	*Neurog2*	0.401683379	0.011932979	1	-
38	*Ccnd3*	0.44717396	0.019519963	1	-
39	*1700048O20Rik*	0.804420254	0.019519963	1	-
40	*Slc2a1*	0.399721042	0.030723065	1	-
41	*Nr4a3*	-0.425268553	0.030892622	1	-
42	*Kcnn1*	0.55633904	0.031913054	1	-
43	*Gria2*	-0.279563023	0.032771223	1	-
44	*Tmem132b*	-0.320917809	0.032952499	1	-
45	*Mctp1*	-0.698451514	0.03545619	1	-
46	*Neurog1*	0.770946401	0.040967524	1	-
47	*Rhbdl3*	0.390346143	0.043599623	1	-
48	*Necab1*	-0.486480137	0.046488149	1	-
49	*Mpped1*	-0.309551635	0.047922476	1	-
50	*Ntrk3*	-0.277612814	0.047987897	1	-
51	*Zic3*	0.368405971	0.049918514	1	-

* Count of E2F1 binding sequence

Table S2. Primers used in this study

Gene name	Primer	Sequence (5'to 3')
Satb2	Forward Primer	GAGATGAGTTGAAGAGGGCTAGTG
	Reverse Primer	CCCTGTGTGCGGTTGAAT
Ldha	Forward Primer	AGCGTACCCGTGATGCTAAC
	Reverse Primer	CAGGGTTGGCAGATCGACAT
Aldoa	Forward Primer	AACGGTCACACACTTCGTCG
	Reverse Primer	TACTTTCCTTGACAAGCGAGGC
Vegfa	Forward Primer	GCAGGCTGCTGTAACGATGAA
	Reverse Primer	TGCTTTCTCCGCTCTGAACAA
Eif2s3y	Forward Primer	ATCTTGTCCTCAACCTCAGACT
	Reverse Primer	TTCTTTAGCCTGGCTTTCTTTCA
Hivep2	Forward Primer	CTCCTTTCTCCTCCCGAGCG
	Reverse Primer	GATCCCGAGGCTACTGGCTG
Rabgap1l	Forward Primer	ACTGGGAATCTTCATGAGAAGCTGA
	Reverse Primer	TCACATTACTGTGCTTGATACACCA
Pkm	Forward Primer	GGAGGAGGAATGCAGGACTGG
	Reverse Primer	GGAGTGCACAAGAAGTGGGGA
Fn1	Forward Primer	AACAAGAGACCACTGGCACC
	Reverse Primer	AGAGGATTGCTTTCCCTGCC
Eno1	Forward Primer	CGACTGTATGGAATCCAAGGCA
	Reverse Primer	CCAGCTTTGCAGACAGCCA
Crlf2	Forward Primer	GCAGGTGATGTCACAGTCGT
	Reverse Primer	GCGCTGCCTAGCCTTAAACA
Slc16a3	Forward Primer	GGCTGTTTTATCATCACGGGTT
	Reverse Primer	GTGTCGCTGTAGCCAATCCC
Cdkn1c	Forward Primer	AGCTGAAGGACCAGCCTCTCTC
	Reverse Primer	ACGTCGTTCGACGCCTTGTTCT
mGapdh	Forward Primer	GCACAGTCAAGGCCGAGAAT
	Reverse Primer	GCCTTCTCCATGGTGGTGAA
1000-Cdkn1c-pGL3	Forward Primer	TTACGCGTGCTAGCCCGGGCTCGAGGTTG GAGGGCTAGATGGGGAACTT
	Reverse Primer	ACCTTAGTTGGCTGGAAGTAGTTATGCTA GAAAAG
2000-Cdkn1c-pGL3	Forward Primer	TTACGCGTGCTAGCCCGGGCTCGAGGGGG GTCGAATATGGCCTGA
	Reverse Primer	atgcagatcgcagatctcgagCTGCACCAACTGATT AGGGCTT

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